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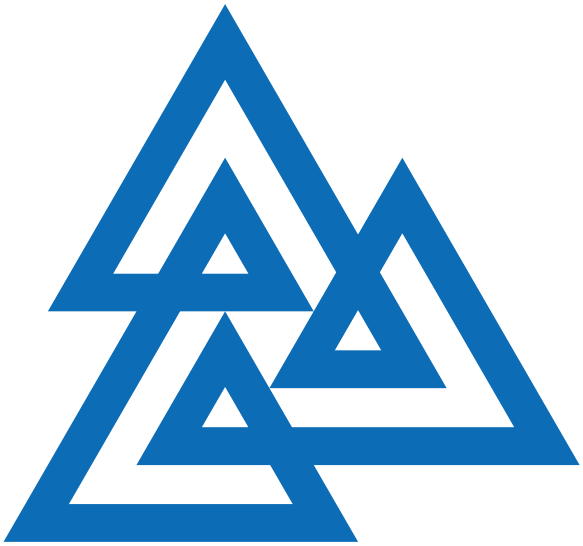

BIRS

Contents

Five-day Workshop Reports

Chapter 1

Fractons and Beyond (20w5064)

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Overview of the Field

The field of condensed matter physics studies the complex and often surprising collective behavior of systems containing many particles. One of the most striking examples of new physics which arises in such many-body systems is the concept of an emergent quasiparticle. Strong interactions between the microscopic particles can often drive the formation of emergent quasiparticle excitations with vastly different properties from any known fundamental particle. The concept of a quasiparticle dates back to Landau's theory of Fermi liquids, in which interactions between electrons lead to the formation of quasiparticle excitations with the same charge as an electron, but with a different mass. A more dramatic example of an emergent quasiparticle was later found in the context of fractional quantum Hall systems, where Laughlin quasiparticles carry only a fraction of the elementary electric charge. Since then, a wide array of quasiparticles has been discovered, often possessing fractionalized quantum numbers or anyonic quantum statistics.

Recently, however, a new type of emergent quasiparticle has been encountered which differs from all previously known particles in an unusual way. Fractons are quasiparticles which lack an ability previously assumed to be inherent to all particles: namely the ability to move. A fracton is a quasiparticle which, in isolation, is unable to move in response to an applied force [6, 10, 33, 34, 20]. However, depending on the details of the model, fractons

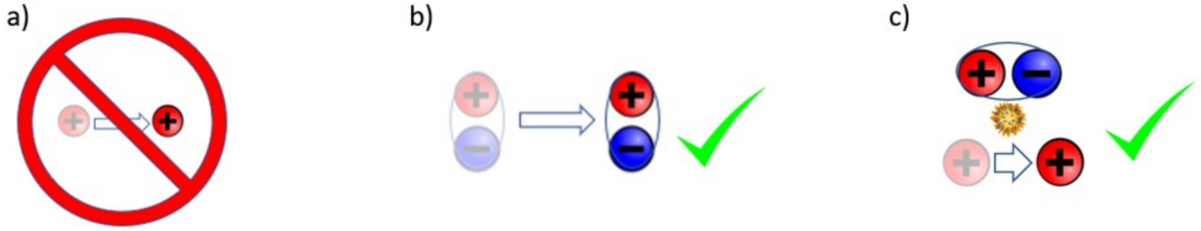

Figure 1.1: a) A single fracton cannot move freely in any direction. b) Fractons can sometimes move by forming certain bound states, such as dipoles. c) It is also possible for a fracton to move at the expense of creating new particles out of the vacuum.

can sometimes move by combining to form certain bound states, as depicted in Figure 1.1. Fracton models are often classified as "type-I" if they possess stable mobile bound states, and as "type-II" if all mobile bound states can decay directly into the vacuum [34]. It is also possible for an individual fracton to move at the cost of creating new fractons out of the vacuum at each step of its motion. However, in the absence of a constant energy input to sustain this particle creation, an individual fracton will remain immobile. These unusual new particles were first encountered in certain exactly-solvable three-dimensional spin and Majorana models [6, 5, 10, 33, 34, 2, 38], but have since been shown to arise in contexts ranging from topological crystalline defects [21] to plaquette-ordered paramagnets [39] (see also precursor work in Ref. [15]). Furthermore, the restricted mobility of fractons causes them to exhibit a variety of unusual properties, such as nonergodic behavior [16, 14] and even gravitational physics [18, 37]. At a practical level, there is hope that the immobility of fractons may even be harnessed for the purposes of quantum information storage [10, 1, 31, 3].

It is generally agreed upon that the first manifestation of fracton behavior was encountered in a spin model exhibiting glassy dynamics constructed by Chamon [6], though there is also important conceptual overlap between fractons and earlier work on kinetically constrained models [23, 13, 7]. Later, Haah designed the paradigmatic type-II fracton model, featuring a characteristic fractal structure, with the goal of creating a self-correcting quantum memory [10]. However, the significance of these two models, often known as the Chamon model and Haah's code respectively, was not immediately appreciated. It was not until the seminal work of Vijay, Haah, and Fu that it became clear that these models were only two examples of a much larger class of fracton systems, representing a fundamentally new type of phase of matter [33, 34]. Vijay, Haah, and Fu constructed several now-prototypical fracton models in three dimensions, such as the X-cube model. Additionally, they recognized the existence of several close cousins of fractons: particles which can only move along a one- or two-dimensional subspace of a three-dimensional system. These particles have since come to be known as lineons and planons respectively, or sometimes more generally as subdimensional particles.

The next major advance in the understanding of fractons came with the realization by Pretko that the restricted mobility of fractons can be naturally understood in terms of a set of higher moment conservation laws, which often arise as a consequence of an emergent symmetric tensor gauge theory [20, 19]. For example, the simplest such gauge theories feature conservation of both charge and dipole moment, which immobilizes individual charges but allows for motion of stable dipolar bound states. Building on earlier work on symmetric tensor gauge theories [35, 22, 9, 8, 36], Pretko showed that these gauge theories provide an effective description of a broad class of fracton phases featuring emergent gapless gauge modes. It was later shown by Ma, Hermele, and Chen [11], and independently by Bulmash and Barkeshli [4], that certain symmetric tensor gauge theories give rise to the previously studied gapped fracton models via the Higgs mechanism. From this viewpoint, various spin-1/2 fracton models can be understood as types of Z_2 symmetric tensor gauge theories. In addition to shedding internal light on the field of fractons, the symmetric tensor gauge theory formalism has also drawn unexpected connections between fractons and other areas of physics, such as elasticity theory [21] and gravity [18].

Recently, there has been further significant progress on the understanding of fracton phases in gapped spin models. Useful tools have now been developed for relating such fracton phases to more familiar topological phases of matter. For example, it has been shown how certain three-dimensional fracton phases can arise via strongly coupling together layers of two-dimensional topological phases [12, 32]. Various schemes have also been proposed for generalizing the string-net condensate picture for ordinary topological phases to fracton phases [17, 30]. Moreover, an idea based on the notion of "foliation" was used to define "fracton phases" by Shirley, Slagle, and Chen [29, 28, 26, 25, 24, 27]. Based on this definition, various universal quantities were identified which lead to the classification of many of the known spin models into different fracton phases.

While much of the work on fractons takes place in the context of abstract spin models and gauge theories, it is important to note that fracton physics has a very concrete realization as the topological lattice defects of ordinary crystals. Specifically, the disclinations and dislocations of two-dimensional crystals exhibit the restricted mobility of fractons and lineons, respectively. This connection is made precise via a duality transformation, often referred to as "fracton-elasticity duality," which maps the elasticity theory of crystals onto a symmetric tensor gauge theory [21].

Open Problems

Beyond established results, there are also numerous open questions in the field of fractons, which range from the practical to the highly abstract.

First of all, the types of models that are known to exhibit fracton order are still very limited. New toy models and new approaches to construct toy models are being proposed constantly. This would not only expand our knowledge about what kind of fracton phenomena is possible, but also bring new perspective to study them. For example, there has also been only limited exploration of fractons in fermion systems, and the known models all have natural analogues in boson systems. Are there examples of intrinsically fermionic fracton models? Can fermion systems give rise to tensor gauge theories with half-integer higher-spin gauge modes? On the other hand, one important line of research is a push towards a complete classification of fracton systems, with a full characterization of all statistical processes. This line of effort is trying to extract universal properties of the fracton models and organize what we know about individual models into a more systematic framework.

One major issue in the field of fracton is its connection to field theory. Field theory has been very successful in describing almost all other phenomena in condensed matter systems – symmetry breaking, topological order, etc. Fracton models, on the other hand, exhibit features that seem hard to fit into a continuous framework. For example, the growth of ground state degeneracy with system size, fractal pattern of coordinated fracton motion, etc. Whether we can still capture fracton physics using continuous field theory or whether we need to extend the field theory framework in some fundamental way to accommodate them is an issue that is being actively investigated.

On the more practical side, one important line of research is the search for more experimentally-relevant spin models which may be realized in actual materials exhibiting frustrated magnetism. It will also be important to develop more experimental signatures of fractons in spin systems, particularly for gapped models. However, recent developments have made it clear that fracton physics is a much broader paradigm than its humble beginnings in exactly solvable spin models. Fractons are already known to be realized in a diverse set of systems, such as elasticity theory, plaquette paramagnets, hole-doped antiferromagnets, and more. As such, it is natural to ask what other platforms may host fractons, and how fracton physics is concretely manifested in experimental signatures.

Given that fractons are on the cusp of physical realization, it is also important to ask what we will do with fractons once we have them. How can we practically manipulate fractons in some useful way? It has been widely suggested that the properties of fractons will be useful for the purpose of quantum information storage [10, 1, 31, 3], but we lack any concrete roadmap for the precise implementation of this proposal. Much more work will be required to figure out how to usefully store and manipulate quantum information using a fracton system. It is also unclear whether or not the mobility restrictions of fractons can be harnessed for constructing any other sort of useful quantum devices. These questions are fundamentally related to the dynamics of the fracton models, which are now being explored in various settings.

Another interesting question is what we can learn about real gravitational systems from the connection between fractons and gravity. Can fracton physics provide new insights into more traditional gravitational theories? Can fracton models be used to simulate more complicated gravitational phenomena, such as black holes?

Presentation Highlights

At this workshop, a variety of fracton related topics were addressed, including the construction of toy models, classification of fracton phases, field theory description, physical realization schemes, dynamics in fracton models, etc. Due to the closeness of the topic of fracton to several other actively-developing topics in condensed matter nowadays, such as topological order, non-ergodic dynamics, etc., there were also talks which focused on ‘beyond fracton’ topics but with ideas highly pertinent to the study of fracton. Here are the highlights of the talks given on each topic.

Model construction

Sheng-Jie Huang introduced a class of gapped non-Abelian fracton models, dubbed “cage-net fracton models,” which host immobile fracton excitations in addition to non-Abelian particles with restricted mobility. Starting from layers of two-dimensional string-net models, whose spectrum includes non-Abelian anyons, the extended one-dimensional “flux strings” built out of pointlike excitations are condensed. This flux-string condensation generalizes the concept of anyon condensation familiar from conventional topological order and allows us to establish properties of the fracton phase, such as its ground-state wave function and spectrum of excitations. To illustrate the main idea, Huang focused on a simple example: doubled-Ising cage-net model. He showed that there are non-Abelian excitations with restricted-mobility in this model and these are a fundamentally three-dimensional phenomenon, as they cannot be understood as bound states among two-dimensional non-Abelian anyons and Abelian particles.

Hao Song talked about his study of novel three-dimensional gapped quantum phases of matter which support quasiparticles with restricted mobility, including immobile ”fracton” excitations. So far, most existing fracton models may be instructively viewed as generalized Abelian lattice gauge theories. Here, by analogy with Dijkgraaf-Witten topological gauge theories, Song and collaborators discovered a natural generalization of fracton models, obtained by twisting the gauge symmetries. Introducing generalized gauge transformation operators carrying an extra phase factor depending on local configurations, they constructed a plethora of exactly solvable three-dimensional models, which they dub ”twisted fracton models.” A key result of their approach is to demonstrate the existence of rich non-Abelian fracton phases of distinct varieties in a three-dimensional system with finite-range interactions. For an accurate characterization of these novel phases, the notion of being inextricably non-Abelian is introduced for fractons and quasiparticles with one-dimensional mobility, referring to their new behavior of displaying braiding statistics that is, and remains, non-Abelian regardless of which quasiparticles with higher mobility are added to or removed from them. Song also analyzed these models by embedding them on a three-torus and computing their ground state degeneracies, which exhibit a surprising and novel dependence on the system size in the non-Abelian fracton phases.

Jeongwan Haah presented an exactly solvable model for a 4+1D beyond-cohomology symmetry protected topological phase. It has been proposed that there are four symmetry protected topological phases in 4+1D under internal Z_2 symmetry. One generator of these phases is a well understood Dijkgraaf-Witten cohomology theory, but the other is speculatively identified with the so-called generalized double semion theory. Haah discussed a new construction of an exactly solved model that was believed to represent the beyond cohomology phase. It is a decorated domain wall construction by the Walker-Wang state based on three-fermion anyon theory. An important property of this state is that the induced action of the symmetry on a 3+1D boundary is a nontrivial quantum cellular automaton — a locality preserving unitary that does not admit any constant depth quantum circuit decomposition.

Universal properties and Classification

Wilbur Shirley talked about entanglement renormalization of gapped fracton models. Gapped fractonic gauge theories are fracton models that arise from gauging the discrete subsystem symmetries of a quantum paramagnet. The entanglement renormalization group transformation for such theories is known to exhibit novel bifurcation phenomena. In this talk, Shirley discussed how these bifurcation phenomena reflect the structure of the subsystem symmetry of the ungauged model. He illustrated this principle in the case of both foliated and fractal fractonic orders.

Sagar Vijay presented a set of constraints on the ground-state wavefunctions of fracton phases, which provide a possible generalization of the string-net equations used to characterize topological orders in two spatial dimensions. He demonstrated that the solutions to these equations yield both Type I and Type II gapped fracton phases – which are distinct as as translationally-invariant quantum phases — along with their dual subsystem symmetry-protected topological phases (SSPT). These constraint conditions present a constructive starting point for finding new fracton orders and provide a complementary perspective to understanding fracton phases through “foliated” equivalence relations. He noted that their constraint conditions are derived after taking a translation symmetry group and a subsystem symmetry group as input; he commented on (i) possible generalizations of this prescription with more general objects, beyond subsystem symmetry groups, and (ii) how these constraint equations may be parametrized to extract “universal” data that may characterize fracton orders.

Daniel Bulmash’s talk focused on Type-II fracton models, in which all nontrivial point-like excitations are immobile. These models have eluded most systematic descriptions of fractons. Bulmash and collaborators showed that Haah’s B code, which is a type-II model, can be described by using networks of defects in topological quantum field theories. They explicitly showed how type-II excitations can be created in these models using fractal-like networks of TQFT operators. Taken together with their results (described in prior talks) that show that defect networks can also describe examples of both Abelian and non-Abelian type-I fracton models, they conjecture that all fracton models can be described by a suitable defect network.

Dominic Williamson presented an overview of the origin of fracton topological order, recent progress that has been made towards classifying and characterizing fracton phases, and preliminary results of ongoing work to find a unified framework for the construction and classification of all gapped fracton phases of matter.

Field theory description

Kevin Slagle talked about how fracton phases can be described by a topological quantum field theory (TQFT) with a network of defects. Slagle focused on the X-cube model as the primary example. This helped to understand the new and novel fracton physics by making use of the much more mature TQFT formalism.

Michael Hermele's talk on "Symmetry in fracton phases" began with a discussion of one motivation to study fracton phases, namely the relationship between quantum phases of matter and continuum quantum field theory (QFT). By challenging our usual assumptions, fraction phases make it clear that this relationship needs to be understood better. Symmetry plays an important role as a tool for understanding both phases and QFT that is independent of particular models or constructions. The talk then proceeded to discuss two pieces of work exploring the role of symmetry in fracton phase. In the first part, Hermele used symmetry and duality arguments to explain how to think about one of the simplest fracton models – the so-called rank-2 $U(1)$ scalar charge theory in 2+1 dimensions – as a conventional theory but with unusual symmetries. In the second part, Hermele discussed using higher form symmetries as a means to understand p-string condensation mechanisms, where one starts in a conventional phase and enters a fracton phase by condensing certain extended objects.

Han Ma discussed the quantum critical points described by an emergent tensor gauge theory featuring sub-dimensional excitations, in close relation to fracton theories. She also showed that the critical theory of the Lifshitz transition between two valence bond solid (VBS) phases can be mapped to a symmetric tensor gauge theory featuring one-dimensional particles. Also, the same tensor gauge theory describes a quantum critical point between a two-dimensional superfluid and a finite-momentum Bose condensate. Furthermore, she presented a new finite-temperature phase of bosons at this critical point, in which boson-hole pairs are condensed but individual bosons are not. Finally, the whole finite temperature phase diagram of this system was discussed.

Realization

Michael Pretko gave an overview of progress towards connecting the field of fractons with experiments. Pretko provided a brief introduction to fractons, describing some of the models and phenomenology encountered in the field. He then described some advances in proposed spin models realizing fracton behavior, such as a putative fracton spin ice. He also described some experimental diagnostics which are useful for detecting fractons. Finally, he discussed some new platforms for realizing fracton physics, such as hole-doped antiferromagnets and electric circuits.

Leo Radzihovski first gave a review of quantum crystal elasticity to fracton gauge theory duality, then discussed anisotropic quantum melting of the crystal into a smectic. Dualizing the latter, Radzihovski will discuss the resulting gauge theory whose charges capture the restricted mobility of disclinations in the quantum smectic. As a consistency check this smectic description can also be obtained by Higgs'ing the dual gauge theory of the quantum smectic.

Dynamics

Juan P. Garrahan discussed constrained dynamics, both in classical and quantum systems. Garrahan reviewed the the rich dynamics that emerges in simple models endowed with kinetic constraints. He considered the classification of stochastic kinetically constrained models (KCMs), and the range of behaviour that they can display. He emphasised the connection between KCMs and classical "fractons" and how these ideas were in partly the origin of the current interest in quantum fractons. He discussed how these classical ideas can be adapted to the problem of slow thermalisation and (apparent) non-ergodicity in quantum systems in the absence of quenched disorder. In particular he focussed on the quantum East model as a paradigmatic quantum KCM displaying a range of interesting dynamical behaviour. He explained how as a consequence of constraints one can construct analytically a very large class of non-thermal excited states with low entanglement. Towards the end he provided a trailer on similar concepts in the context of discrete "Floquet" circuit settings.

Frank Pollmann talked about ergodicity-breaking arising from Hilbert space fragmentation in dipole-conserving Hamiltonians. Pollmann and collaborators showed that the combination of charge and dipole conservation—characteristic of fracton systems—leads to an extensive fragmentation of the Hilbert space, which in turn can lead to a breakdown of thermalization. As a concrete example, they investigated the out-of-equilibrium dynamics of one-dimensional spin-1 models that conserve charge (total Sz) and its associated dipole moment. First, they considered a minimal model including only three-site terms and find that the infinite temperature auto-correlation saturates to a finite value. The absence of thermalization is identified as a consequence of the strong fragmentation of the Hilbert space into exponentially many invariant subspaces in the local Sz basis, arising from the interplay of dipole conservation and local interactions. Second, they extended the model by including four-site terms and found that this perturbation leads to a weak fragmentation: the system still has exponentially many invariant subspaces, but they are no longer sufficient to avoid thermalization for typical initial states. More generally, for any finite range of interactions, the system still exhibits non-thermal eigenstates appearing throughout the entire spectrum.

Igor Lesanovsky's talk focused on Rydberg quantum simulators, i.e. highly excited atoms held in optical tweezer arrays. The Rydberg quantum simulators belong to the currently most advanced platforms for the implementation and study of strongly interacting spin systems. An interesting dynamical regime is reached when one atom that is brought to a Rydberg states facilitates the excitation of another nearby one. The resulting dynamics can be similar to that of epidemic spreading and also may form an ingredient for observing non-equilibrium phase transitions. In this talk, Lesanovsky discussed recent results concerning the analysis of constrained spin dynamics on Rydberg quantum simulators.

Scientific Progress Made

Extensive discussion was carried about among the workshop participants on all kinds of questions. Here are some of the scientific progress made at the conference as reported by the participants.

Dominic Williamson had many useful discussions about topics of current interest, including the role of 1-form symmetries in fracton topological order, the topological defect network construction of fracton phases, and linear subsystem SSPTs that are dual to topologically ordered models.

Michael Hermele had numerous useful discussions while in Banff. Particular notable was a discussion with Nat Tantivasadakarn, Hao Song, Sheng-Jie Huang and Juven Wang. Tantivasadakarn had recently constructed a new model where it appeared that the fractons were behaving like fractons. Together they came up with new statistical processes by which two fractons can in some sense be exchanged with one another, and showed that these processes give rise to a robust statistical phase of -1 in the model. Many open questions remain, and Tantivasadakarn and Hermele and others are planning to explore this further. Hermele also discussed this progress with Wilbur Shirley, who had been working on similar ideas, and Wilbur immediately had a number of very interesting further observations and questions. Also notable were productive discussions with Wilbur Shirley, Kevin Slagle and Xie Chen, where it seems like some progress was made on a project they have been working on.

Juan P. Garrahan had discussions mostly on the connections between classical and quantum concepts relating to slow dynamics and non-ergodicity, the emergence of constraints, and how idealized models can be realized in atomic settings.

Michael Pretko had the opportunity to discuss with numerous experts from around the globe, both in the fracton field and from the broader condensed matter community. These discussions provided various ideas for future investigations into fractons, as well as other topics at the forefront of condensed matter research. For example, Fakher Assad and Pretko discussed several potential interesting features of fracton behavior in hole-doped antiferromagnets with unusual lattice structures. They suspected that the Bethe lattice may provide a platform for exact fracton behavior, which would provide an exciting new result. Pretko had a variety of other discussions about fractons, such as an exploration with Han Ma about extensions of the fracton gauge principle, as well as with

Yongbaek Kim about new fracton spin models. Pretko also had discussions on other topics, such as an engaging conversation with Sagar Vijay about quantum chaos.

Leo Radzihovski discussed physics with a number of people: with Andrey Gromov he discussed his multipole gauge theory of fractons, as well as a way to couple vortex lattice in a superfluid to gauge fields; with Maissam Barkeshli he discussed critical phases and also the breakdown of homotopy classification of orientational defects in systems that break rotational and translational symmetry (e.g., smectics and crystals); with Sagar Vijay he discussed critical phases, quantum smectics and relation to the KPZ nonequilibrium dynamics; with Sheng-Jie Huang he discussed elasticity duality to gauging spatial symmetries; with Michael Pretko and Andrey Gromov he discussed my quantum GL theory and its relation to Michael's highly nonlinear theory of fractons.

Han Ma was mainly inspired by the studies about global symmetry of the fracton phase. It is a very unusual symmetry and may be important for the formation of the phases. There will be a lot to explore along this direction. She plans to study this type of global symmetry and also study its interplay with other ordinary global symmetries, and even generalized global symmetries.

Kevin Slagle and his collaborators explained the results of their forthcoming works and receive many useful comments. Michael Hermele, Xie Chen, Wilbur Shirley, and Slagle made progress on their ongoing project regarding how to coarse grain the gapless $U(1)$ fracton models.

Nat Tantivasadakarn had many helpful discussions about his upcoming work on Jordan-Wigner transformations for translation-invariant Hamiltonians in higher dimensions. By bosonizing a fermion model with subsystem fermion parity symmetry, he can obtain a ”twisted” X-cube model where fractons behave like fermions. In particular, he had an insightful discussion with Mike Hermele, Sheng-Jie Huang, Hao Song, and Juven Wang about a certain braiding process that can give a minus sign in this model, but not in the usual X-cube model. This opens the question of whether there are in general meaningful ways one can braid immobile objects such as fractons without pairing them up into mobile particles, an aspect they hope to explore in the future.

Hao Song learned about the latest progress in the study of fracton orders, especially about the idea of realizing fractons as defect networks of topological orders. It is very insightful and he would like to explore problems like whether other interesting gapped non-liquid states can also be constructed in this way. During the workshop, he also had good discussions with many people, especially Mike Hermele, Sheng-Jie Huang, Nathanan Tantivasadakarn, and Juven Wang. These discussions improved his understanding on some field theoretical descriptions of fracton phases. They also got stimulated and made some new progress on characterizing fractons by exchange and braiding, which they will explore further.

Arpit Dua talked to various scientists including Xie Chen, Jeongwan Haah and Zhenghan Wang about his recent work on the structure of three-dimensional stabilizer models. Also, the visit led to a new project on the entanglement renormalization and ungauging of Chamon's model with Xie Chen's group. Dua also discussed with Dominic Williamson and others about an ongoing project of entanglement renormalization of subsystem symmetry protected topological phases and potential future ideas like structure theorems for models described by X-S stabilizer formalism.

Daniel Bulmash made progress on writing his defect network paper, and had discussions on issues such as uses of defect networks to classify fracton phases, the relation between local operator structure and excitation mobility, and dualities in generalized gauge theories.

Sagar Vijay find the workshop very helpful in furthering his understanding of fracton orders, in making progress in new directions and in understanding open questions within this field. In particular, he had several useful discussions with colleagues (Andrey Gromov, Maissam Barkeshli, Jeongwan Haah, Zhenghan Wang, Michael Pretko) on understanding $U(1)$ fracton orders that may lie beyond what we currently understand using tensor gauge theories. As an example, he discussed generalizations of an algebraic framework for understanding gapped fracton orders (originally proposed by Haah) and how this may be useful for understanding when two $U(1)$ fracton orders — specified by a generalized “Gauss' law” — are distinct and/or are stable quantum phases. he is now pursuing these ideas and other open questions related to $U(1)$ fracton orders as a consequence of this workshop.

Wilbur Shirley find this conference to be a great opportunity to discuss new ideas with colleagues. He had stimulating discussions about a variety of topics related to fractons, including: fracton exchange statistics, fracton models with emergent fermionic gauge theory, TQFT defect network constructions of fracton models, fermionic ‘strong' SSPTs, ‘panoptic' fracton orders and new types of SPT and SET phases, and potential structure theorems for fractonic stabilizer codes. Several of these discussions have evolved into ongoing fruitful collaborations with various participants, including Mike Hermele, Nathanan Tantivasadakarn, Hao Song, Juven Wang, Arpit Dua, and Dominic Williamson.

Participants

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Bibliography

[1] Sergey Bravyi and Jeongwan Haah. Quantum self-correction in the 3d cubic code model. *Phys. Rev. Lett.*, 111:200501, Nov 2013.

[2] Sergey Bravyi, Bernhard Leemhuis, and Barbara M. Terhal. Topological order in an exactly solvable 3d spin model. *Annals of Physics*, 326(4):839 – 866, 2011.

[3] Benjamin J. Brown and Dominic J. Williamson. Parallelized quantum error correction with fracton topological codes. 2019.

[4] Daniel Bulmash and Maissam Barkeshli. Higgs mechanism in higher-rank symmetric u(1) gauge theories. *Phys. Rev. B*, 97:235112, Jun 2018.

[5] Claudio Castelnovo and Claudio Chamon. Topological quantum glassiness. *Philosophical Magazine*, 92(1-3):304–323, Jan 2012.

[6] Claudio Chamon. Quantum glassiness in strongly correlated clean systems: An example of topological overprotection. *Phys. Rev. Lett.*, 94:040402, Jan 2005.

[7] Juan P. Garrahan and M. E. J. Newman. Glassiness and constrained dynamics of a short-range nondisordered spin model. *Phys. Rev. E*, 62:7670–7678, Dec 2000.

[8] Zheng-Cheng Gu and Xiao-Gang Wen. A lattice bosonic model as a quantum theory of gravity. 2006.

[9] Zheng-Cheng Gu and Xiao-Gang Wen. Emergence of helicity ± 2 modes (gravitons) from qubit models. *Nuclear Physics B*, 863(1):90 – 129, 2012.

[10] Jeongwan Haah. Local stabilizer codes in three dimensions without string logical operators. *Phys. Rev. A*, 83:042330, Apr 2011.

[11] Han Ma, Michael Hermele, and Xie Chen. Fracton topological order from the higgs and partial-confinement mechanisms of rank-two gauge theory. *Phys. Rev. B*, 98:035111, Jul 2018.

[12] Han Ma, Ethan Lake, Xie Chen, and Michael Hermele. Fracton topological order via coupled layers. *Phys. Rev. B*, 95:245126, Jun 2017.

[13] M. E. J. Newman and Cristopher Moore. Glassy dynamics and aging in an exactly solvable spin model. *Phys. Rev. E*, 60:5068–5072, Nov 1999.

[14] Shriya Pai, Michael Pretko, and Rahul M. Nandkishore. Localization in fractonic random circuits. *Physical Review X*, 9(2), Apr 2019.

[15] S. Pankov, R. Moessner, and S. L. Sondhi. Resonating singlet valence plaquettes. *Phys. Rev. B*, 76:104436, Sep 2007.

[16] Abhinav Prem, Jeongwan Haah, and Rahul Nandkishore. Glassy quantum dynamics in translation invariant fracton models. *Physical Review B*, 95(15), Apr 2017.

[17] Abhinav Prem, Sheng-Jie Huang, Hao Song, and Michael Hermele. Cage-net fracton models. *Phys. Rev. X*, 9:021010, Apr 2019.

[18] Michael Pretko. Emergent gravity of fractons: Mach's principle revisited. *Physical Review D*, 96(2), Jul 2017.

[19] Michael Pretko. Generalized electromagnetism of subdimensional particles: A spin liquid story. *Phys. Rev. B*, 96:035119, Jul 2017.

[20] Michael Pretko. Subdimensional particle structure of higher rank $u(1)$ spin liquids. *Phys. Rev. B*, 95:115139, Mar 2017.

[21] Michael Pretko and Leo Radzihovsky. Fracton-elasticity duality. *Phys. Rev. Lett.*, 120:195301, May 2018.

[22] Alex Rasmussen, Yi-Zhuang You, and Cenke Xu. Stable gapless bose liquid phases without any symmetry. 2016.

[23] F. Ritort and P. Sollich. Glassy dynamics of kinetically constrained models. *Advances in Physics*, 52(4):219–342, 2003.

[24] Wilbur Shirley, Kevin Slagle, and Xie Chen. Foliated fracton order from gauging subsystem symmetries. *SciPost Physics*, 6(4), Apr 2019.

[25] Wilbur Shirley, Kevin Slagle, and Xie Chen. Foliated fracton order in the checkerboard model. *Physical Review B*, 99(11), Mar 2019.

[26] Wilbur Shirley, Kevin Slagle, and Xie Chen. Fractional excitations in foliated fracton phases. *Annals of Physics*, 410:167922, Nov 2019.

[27] Wilbur Shirley, Kevin Slagle, and Xie Chen. Twisted foliated fracton phases. 2019.

[28] Wilbur Shirley, Kevin Slagle, and Xie Chen. Universal entanglement signatures of foliated fracton phases. *SciPost Physics*, 6(1), Jan 2019.

[29] Wilbur Shirley, Kevin Slagle, Zhenghan Wang, and Xie Chen. Fracton models on general three-dimensional manifolds. *Phys. Rev. X*, 8:031051, Aug 2018.

[30] Kevin Slagle, David Aasen, and Dominic Williamson. Foliated field theory and string-membrane-net condensation picture of fracton order. *SciPost Physics*, 6(4), Apr 2019.

[31] Barbara M. Terhal. Quantum error correction for quantum memories. *Rev. Mod. Phys.*, 87:307–346, Apr 2015.

[32] Sagar Vijay. Isotropic layer construction and phase diagram for fracton topological phases. 2017.

[33] Sagar Vijay, Jeongwan Haah, and Liang Fu. A new kind of topological quantum order: A dimensional hierarchy of quasiparticles built from stationary excitations. *Phys. Rev. B*, 92:235136, Dec 2015.

[34] Sagar Vijay, Jeongwan Haah, and Liang Fu. Fracton topological order, generalized lattice gauge theory, and duality. *Phys. Rev. B*, 94:235157, Dec 2016.

[35] Cenke Xu. Gapless bosonic excitation without symmetry breaking: An algebraic spin liquid with soft gravitons. *Phys. Rev. B*, 74:224433, Dec 2006.

[36] Cenke Xu and Petr Hořava. Emergent gravity at a lifshitz point from a bose liquid on the lattice. *Phys. Rev. D*, 81:104033, May 2010.

[37] Han Yan. Hyperbolic fracton model, subsystem symmetry, and holography. *Physical Review B*, 99(15), Apr 2019.

[38] Beni Yoshida. Exotic topological order in fractal spin liquids. *Phys. Rev. B*, 88:125122, Sep 2013.

[39] Yizhi You, Zhen Bi, and Michael Pretko. Emergent fractons and algebraic quantum liquid from plaquette melting transitions. 2019.

Chapter 2

Dynamics in Geometric Dispersive Equations and the Effects of Trapping, Scattering and Weak Turbulence II (20w5013)

February 3 - 7, 2020

Organizer(s): Stephen Gustafson (University of British Columbia), Jeremy Marzuola (University of North Carolina), Daniel Tataru (University of California, Berkeley)

Overview of the Field

Of late, the primary advances in the field of dispersive PDE seem to be occurring in the study of models in Mathematical Physics that result in quasilinear equations, or at low regularity where semilinear equations take on more of a quasilinear structure. Many dispersive (and non-dispersive but related) PDE of this type arise naturally in applications, in such diverse areas as general relativity, plasma models, magnetics, optics, and water waves. These advances have opened doors to new models and new techniques, as well as strengthened the developing connections of the area to fluid dynamics. They have also provided pathways to connect to non-local operators through careful study of for instance the Dirichlet-to-Neumann map in fluids models, and opened up a host of questions regarding stability and dynamics in domains with an array of boundary conditions.

Moreover, some of the key physical examples of super-critical equations, such as the Einstein equations, and the gauge theories of particle physics, are inherently geometric. As a result, the field seems to be moving towards an inflection point, where we will see maximal advances on existence and stability theory for solutions to supercritical equations, quasilinear equation and/or equations very rough initial data with researchers moving strongly to find models and explore some of these challenging new directions.

This workshop brought together a group of people working in dispersive Partial Differential Equations five years beyond our first meeting. While many attendees were the same, we also had a host of new people come speak about progress in the field. A main take-away currently is that much progress is starting to be made in areas that have previously been somewhat unexplored due to the difficulties with understanding the equations. These include quasilinear models that include either complicated metrics or very low-regularity initial data for well-studied problems, detailed analysis of integrable systems, and blow-up dynamics in supercritical problems. As a result, complicated models in quantum field theories, fluids, geometric waves and more are becoming more tractable analytically.

Recent Developments and Open Problems

The workshop saw topics that could easily fit into a few developing areas: (i) development of quasilinear or degenerate dispersive models, (ii) stability in critical/super-critical models, (iii) Dispersive theory in fluids, (iv) applications of ideas from integrable systems to low-regularity studies of dispersive equations and/or stochastic PDE, (v) linear/nonlinear theory in domains and with variable coefficients. We will discuss the major topics in each category and summarize the results presented.

Quasilinear and Degenerate Schrödinger/Wave models

The workshop featured talks by Mihaela Ifrim, Jason Metcalfe, Sung-Jin Oh, and Benoit Pausader about solutions to nonlinear PDE in various settings where wave interactions take on a very different character on long time scales due to the lack of dispersion.

- Mihaela Ifrim - Low dimensional quasilinear systems of wave equations

  In joint work with A. Stingo [26], the authors study the system

  $$\begin{aligned}(\partial_t^2 - \Delta)u &= N_1(v, \partial v) + N_2(u, \partial v),\\ (\partial_t^2 - \Delta + 1)u &= N_1(v, \partial u) + N_2(u, \partial u)\end{aligned}$$

  where N_1 and N_2 are built to have classical quadratic null forms. For small data solutions of sufficient regularity, the authors are able to prove almost global well-posedness using a combination of vector field methods and local energy decay to establish pointwise decay estimates. These equations arise in the study of general relativity and are related to equations for the wave equation on wave-guides. In $3d$ and higher, these types of problems have been solved for some time using more classical techniques, but for low dimensions the weak dispersive decay makes the problem quite challenging. The use of local energy decay to get pointwise bounds for wave decay originated in the work of Tataru on Price's Law [48] and the dyadic version that appears here is due to Metcalfe-Tataru-Tohaneanu [40]. The spherical hyperbolic coordinates introduced by Tataru in [47] also play a major role. The authors are hoping to enhance the result to global by introducing the idea of testing by wave packets (see [24, 27, 25]), though this is work in progress. The takeaway is that long time dynamics are possible for low-dimensional quasilinear wave/Klein-Gordon systems, but that to do so one needs very good energy estimates for the linearized system to get good pointwise bounds and even then the decay properties of the waves are much more subtle. However, the authors have now laid a foundation for these pursuits to be explored.

- Jason Metcalfe - Quasilinear Schrödinger equations

  In joint with with J.L. Marzuola and D. Tataru [38], the authors study local well-posedness for large data Quasilinear Schrödinger equations of the form

  $$i\partial_t u + g^{jk}(u, \nabla u, \bar{u}, \bar{\nabla} u)\partial_j \partial_k u = F(u, \nabla u, \bar{u}, \bar{\nabla} u).$$

  Quasilinear Schrödinger models arise in various forms, but specifically in Density Functional Theory models for many body systems in electronic structure, plasma models, superfluid thin film models, in the study of rotating fluids and in the study of Hall/electron magnetohydrodynamics. The result establishes a robust short-time existence theorem the requires some care due to the metric dependence upon the solution in the dispsersion. In particular to pair with the author's small data results that relied upon a combination of energy estimates and local smoothing properties that were perturbative in the small data case, [37, 39], one must establish robust incoming estimates and non-trapping estimates that are stable under rough perturbations. This moves past prior work by Kenig-Ponce-Vega, Kenig-Ponce-Rolvung-Vega [31, 30] by defining translation invariant spaces and dramatically reducing regularity requirements. A paradifferential framework is introduced that simplifies some of the arguments from the authors previous works and provides a unifying framework for applications of the ideas contained within the result.

- Sung-Jin Oh - Degenerate Schrödinger equations from the Magnetic Hall Dynamics

  In joint work with I.J. Jeong (see [29] and forthcoming extensions), the authors study the equations

  $$\begin{aligned}&\partial_t u + u \cdot \nabla + \nabla p = \nu \Delta u + J \times B,\\ &\partial_t B + \nabla \times E = 0,\\ &\nabla \cdot u = 0,\ \nabla B = 0\end{aligned}$$

  with the assumptions that

  $$\begin{aligned}&J = \nabla \times B \text{ (Ampere's Law)},\\ &E + u \times B = \eta J + cJ \times B \text{ (Ohm's Law \& Hall Current)}.\end{aligned}$$

  If $\eta = 0$, there is no resistivity and the model becomes a degenerate dispersion equation. Other degenerate dispersive models relating to hydrodynamic equations were studied recently in [17, 18]. The authors use the degeneracy to construct a strong ill-posedness result near trivial magnetic field backgrounds, but in forthcoming work will prove existence in a neighborhood of a non-trivial magnetic field.

- Benoit Pausader - Derivation of the Ion equation

  In joint work with Grenier, Guo and Suzuki [21], the authors derive a ”Low Electron Mass Number” equation for ions built around the Euler-Poisson plasma model of interacting electrons and ions. The model is hydrodynamic again is is of the form

  $$\begin{aligned}&\partial_t \rho_i + \operatorname{div}(\rho_i u_i) = 0,\\ &\rho_i(\partial_t u_i + u_i \cdot \nabla u_i) + \nabla p_i + \rho_i \nabla \phi = 0,\\ &-\Delta \phi + e^{\phi} = \rho_i.\end{aligned}$$

  The original plasma model is a compressible two-fluid electrostatic model, but the ion equation looks somewhat incompressible. However, the ion equation is a singular limit of the two-fluid model, hence the convergence must be managed carefully. This is similar to the Euler equation as the limit of a ’low Mach number’ compressible fluid. Energy estimates must be done very carefully to get uniform convergence in ε, and the resulting system is somewhat Klein-Gordon-like but with variable coefficients depending upon the ion equation solution. To get the correct energy estimates, one must use normal form analysis, as well as forms of local energy decay and equipartition of energy must be developed here that generalize the notion of the fluid momentum coordinates.

Related Open Problems

Large data blow-up for couple wave/Klein-Gordon quasilinear systems, non-flat geometries for coupled wave/Klein-Gordon systems, Global existence in low dimensions of wave/Klein-Gordon quasilinear systems, inclusion of Coulomb-like singular potentials in quasilinear Schrödinger models, improvements in well-posedness for quasilinear equations with Hamiltonian structure, ill-posedness and well-posedness for other degenerate Schrödinger models in physics, external magnetic fields or geometry in the ion equation, results and dynamics for problems without coercive energy quantities.

Stability in Critical/Super-critical equations

The workshop featured talks by Enno Lenzmann, Wilhelm Schlag and Birgit Schörkhuber about solutions to nonlinear PDE in various settings where wave interactions take on a very different character on long time scales due to the lack of dispersion.

- Enno Lenzmann - A new L^2 critical NLS equation In joint forthcoming work with Patrick Gerard, the authors introduce the equation

  $$iu_t = -u_{xx} = 2(D_+(|u|^2))u,$$

  where $D_+ = \Pi_+ D$, $D = -i\partial_x$. The operator Π_+ is thus a projection onto positive frequencies and is related to the Szegő equation (see the recent survey of results in [16]). It is L^2 critical and has a stationary solution of the form

  $$Q(x) = \frac{\sqrt{2}}{x+i},$$

  which can be seen to be unique in a sense up to symmetries. In ways, the equation has both defocusing and focusing tendencies, as it can be converted via a transformation to an equation of such a type. A Lax Pair can be constructed and the integrability of the model understood to some extent. However, many questions remain about the nature of the dynamics and behavior of solutions to this model.

- Wilhelm Schlag - Non-equivariant in/stability of critical wave maps

  In joint work with J. Krieger and C. Miao, the authors explore the stability of blow-up solutions near the equivariant 1 wave map in the non-equivariant class. The work is based upon extending the contstruction of blow-up solutions in [35] to the setting where the perturbations are not equivariant, and as a result extending the blow-up rigidity result of [34]. Weighted dispersive estimates are required of the form [15, 45, 46]. The functional equivalent of 'one-pass' theorems are required to ensure that the dynamics are not effected by energy that has radiated away to a certain extent.

- Birgit Schörkhuber - Self-similar blow-up solutions for super-critical wave equations

  In joint work with Glogić and Maliborski (see [20, 19]), the authors explore the stability of blow-up solutions constructed for supercritical wave equations in high dimensions. A key example is

  $$\left(\partial_t^2 - \partial_r^2 - \frac{d-1}{r}\partial_r\right) u = u^3$$

  for $d \geq 5$. The solutions themselves are constructed explicitly, then studied in self-similar coordinates. A main issue is understanding the linear stability properties of the proposed states. Related models in include the symmetric version of Yang-Mills.

Related Open Problems

Other integrable models from Szegő type nonlinearities, Stability or blow-up solutions for wave maps with different targets and different domains, spectral properties of special solutions from the work of Schörkhuber et al, verification of the numerically observed dynamics and blow-up for supercritical waves.

Fluids

The workshop featured talks by about various aspects of fluids models by Albert Ai, Thomas Alazard, Roberto Camassa, Marcelo Disconzi, Jon Wilkening.

- Albert Ai and Thomas Alazard - Water Waves and Hele-Shaw equations

  The gravity wave equations have recently seen a great deal of progress as quasilinear techniques have become more readily available and the equations better understood. Through a combination of different methods, various groups have made progress on the problem recently, especially for gravity-waves in $2d$ on global time scales. Reports on this progress were made by Thomas Alazard and Albert Ai. The gravity-capillary wave equations can be represented as

$$\begin{cases} \partial_t h = |D|\,\psi + \{G(h)\psi - |D|\,\psi\} \\ \partial_t \psi = (\tau\Delta - g)\,h + \left\{ \tau \left(\operatorname{div}\left(\dfrac{\nabla h}{\sqrt{1+|\nabla h|^2}} \right) - \Delta h \right) \right. \\ \qquad\qquad \left. -\dfrac{1}{2}\,|\nabla\psi|^2 + \dfrac{(G(h)\psi + \nabla h\cdot\nabla\psi)^2}{2\left(1+|\nabla h|^2\right)} \right\}. \end{cases}$$

for h the height of the fluid at the interface and ψ a trace of a related velocity field.

Ai reported on recent work with Ifrim and Tataru in [1] where improvements to small data well-posedness for the gravity wave system ($\tau = 0$) are established. The key observation is the new energy estimate for the equations in holomorphic coordinates given by

$$\partial_t E^s \leq A^2_{\frac{1}{4}} E^s,$$

where $A_{\frac{1}{4}} \sim \| |D|^{\frac{1}{4}} \cdot \|_{BMO}$. This improved diagonalized energy estimate allows for a dramatic improvement of the local Cauchy theory and opens up the possibility of further improvement using refined Strichartz estimates as well. Very sharp energy estimates on the linearized paradifferential form of the equation are essential since one cannot apply normal form methods to the problem.

Alazard reported in improvements for the Dirichlet-to-Neumann map achieved with Lazar and at a similar time by Nguyen-Pausader [42, 3], as well as on identities and monotonic quantities for the Hele-Shaw flow. While not technically a dispersive equation, its evolution relies on the Dirichlet-to-Neumann map and can be related to key quantities in the so-called good unknown determination of the water wave problem, namely vertical, horizontal and time derivatives of the velocity potential restricted to the surface.

- Marcelo Disconzi - Strichartz estimates for relativistic fluids

  In joint work with C. Luo, G. Mazzone and J. Speck in [14], the authors introduce finite-time Strichartz estimates for compressible Euler equations with vorticity in order to construct local solutions. This can be written as a system of quasilinear wave equations, though to get low-regularity results one needs careful dispersive theory and control on the characteristic geometry. Generically, the transport terms make the terms non-perturbative. Vorticity is required for the argument by giving elliptic estimates for the transport variables. Hölder regularity is required on part of the data to make sense of the mapping properties.

- Roberto Camassa and Jon Wilkening - Water wave numerical and asymptotic models.

  These topics by applied mathematicians were about phenomenological fluids results relating to singularity formation in the hydrodynamic models for Euler equations in long-wave shallow water [12] and quasiperiodic waves in the gravity-capillary system [49]. In the first, self-similar solutions to asymptotic models are constructed for singularity formation in two-fluid systems with singular shock-like formation resulting from dry singularities. In the second, a zoo of special solutions to the gravity-capillary waves are computed numerically with remarkable structure, $u(\vec{k}x + \vec{\omega}t + \vec{z})$. Both results were supported by strong modeling and numerical calculations, and provide a rich landscape of theory questions to consider.

Related Open Problems

Analytic solutions from works of Camassa et al for generic construction of dry solutions and comparison to full Euler, existence and stability for the quasiperiodic waves of Wilkening et al, generalizations of existence times for small data from conformal coordinates to more general fluid domains and other formulations of Euler, long time dynamics in compressible Euler.

Integrable Systems, low-regularity and SPDEs

The workshop featured talks by about various aspects of wave equation models by Valeria Banica, Ben Harrop-Griffiths, Herbert Koch, Adrian Nachman and Hiro Oh.

- Valeria Banica - The binormal flow and singular initial data for cubic NLS

  In joint work with Luis Vega (see [6, 7, 8, 9, 10], motivated by regularly recurring polygons in the study of vortex rings, the consider finite dirac mass initial data for the cubic NLS in $1d$, which can be connected to the binormal flow via a transformation. Such low regularity creates complications with even defining the flow and must be done with great care.

- Ben Harrop-Griffiths - Low regularity NLS/mKdV

  In joint forthcoming work with Rowan Killip and Monica Visan based upon the work [33, 32], the authors construct a modified NLS flow built around the conserved quantities from the theory of complete integrability and use such a flow to construct solutions in H^s for $s > -\frac{1}{2}$. The key ideas relate to local smoothing estimates and tightness bounds to make the limits of the model flows converge to a solution of the actual flow.

- Herbert Koch - Multiple solitons in NLS

  In joint work with Tataru building off of [33], the authors construct multiple soliton solutions through the use of inverse scattering theory, and in the process observe stability and construct the soliton manifold for a large class of multi-soliton solutions that are close in the $H^{-\frac{1}{2}}$ norm to an N-soliton solution at time 0.

- Adrian Nachman- The Calderon Problem and the Davey-Stewartson system

  In joint work with Regev and Tataru in [41], the authors explore the invertibility of an inverse scattering transformation that both describes the evolution of the elliptic Davey-Stewartson system and also plays a major role in the reconstruction problem for the Calderon problem. The map

  $$Sq(k) = \frac{1}{2\pi i} \int_{\mathbb{R}^2} e_k(z)\overline{q(z)}(m_+(z,k) + m_-(z,k)dz$$

  where $m_\pm$ are solutions to

  $$\frac{\partial}{\partial \overline{z}} m_\pm = \pm e_{-k} q \overline{m_\pm}$$

  and

  $$e_k(z) = e^{i(zk + \overline{zk})}.$$

  serves as a nonlinear Fourier transform of sorts, and the authors prove it is an L^2 norm preserving map. The fundamental result is a beautiful exercise in harmonic analysis using maximal function estimates with far reaching implications in inverse problems.

- Tadahiro Oh - On the Stochastic Dispersive PDE

  In joint work with many authors, the speaker has explored well-posedness in a variety of stochastically forced dispersive models. Elements of renormalization theory must be used to make sense of the low-regularity of noise in the equation. See [43, 23, 22, 44] for some related results.

Related Open Problems

The fractional or non-linear Calderon problem and possible reconstruction algorithms, δ function regularity in NLS and the binormal flow (the Dirac comb solution), soliton gas in NLS, existence theory and Gibbs measures for stochastic models with other types of nonlinearities and noise.

Linear and Nonlinear Effects of Domains

The workshop featured talks by about various geometric aspects of dispersive equations by Zaher Hani, Nicolas Burq, Jonas Lührmann. Hani discussed kinetic equations for modeling frequency cascades NLS on the torus, Burq discussed boundary control theory in annuli and Luhrmann discussed 1d variable coefficient wave models.

- Zaher Hani - Kinetic equations in NLS

  In joint work with Yu Deng in [13], the authors derive a nonlocal equation known as wave kinetic equation from the dynamics of cubic NLS on large tori in certain scaling limits. These equations can then describe the statistics of how random waves behave the possibilities of cascades leading to weakly turbulent behaviors.

- Nicolas Burq - Boundary observability for the linear Schrödinger equation in annuli

  Based upon a paper by Anantharaman-Léautaud-Macia in [4] on the disc, Burq presented work on boundary observability for the Schrödinger equation on the annulus that builds off his previous works such as [11]. While he cannot get to the full disc, the results on the annulus follow from relatively well-understood tools involving semi-classical defect measures and positive commutators with commuting vectors. These control and observability results can generally be extended to nonlinear, small-data problems and relates as well to damped waves and other interesting geometric models, see [2, 5].

- Jonas Lührmann - Variable coefficient nonlinear $1d$ Klein-Gordon equations

  In joint work with Lindblad and Soffer in [36], the authors explore the equation

  $$(\partial_t^2 - \partial_x^2 + 1)u = (\alpha_0 + \alpha(x))u^2 + (\beta_0 + \beta(x))u^3,$$

  where serves as a model for the equation linearized around a kink solution in a nonlinear wave equation of the form

  $$(\partial_t^2 - \partial_x^2)\phi = -V'(\phi)$$

  with $V(x) \geq 0$ something like a double-well potential that is not decaying a 0. This type of problem can lead to the existence of kink solutions, and the goal is to develop a dispersive machinery for kind stability. So far, the authors can create a vector-field type approach to these problems using hyperbolic coordinates to prove pointwise decay in the cubic nonlinear case where $\alpha_0 + \alpha(x) = 0$. For the quadratic case, they have results for $\alpha_0 = 0$ depending upon the Fourier modes of $\hat{\alpha}$. Combining both results and getting to the actual kink problem requires future work, but the methods are robust. In any case, the decay is rather weak $t^{-\frac{1}{2}}$ since it is a $1d$ problem. See also recent work of [28] about kink-anti-kink pair rigidity and dynamics.

Related Open Problems

Classification, statistics and dynamics of weakly turbulent cascades in NLS, Nonlinear control and observability for NLS, Generalizations of control/observability with other metrics, Applications of control/observability to kink dynamics and stability in 1d Klein-Gordon.

Scientific Progress Made

Numerous collaborations and discussions took place between people in various sub-fields of PDE and numerical analysis. Many young people attended the conference and were thus able to learn a great deal about pioneering areas in the field. Several ongoing collaborations were strengthened at the same time. In the end the meeting was quite useful for bringing together many areas of dispersive PDE strongly impacted by geometry and nonlinearity and solidifying new highly nonlinear directions and applications in the field.

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Bibliography

[1] Albert Ai, Mihaela Ifrim, and Daniel Tataru. Two dimensional gravity waves at low regularity i: Energy estimates. *arXiv preprint arXiv:1910.05323*, 2019.

[2] Thomas Alazard and Pietro Baldi. Gravity capillary standing water waves. *Archive for Rational Me- chanics and Analysis*, 217(3):741–830, 2015.

[3] Thomas Alazard and Omar Lazar. Paralinearization of the muskat equation and application to the cauchy problem. *arXiv preprint arXiv:1907.02138*, 2019.

[4] Nalini Anantharaman, Matthieu Léautaud, and Fabricio Macià. Wigner measures and observability for the schrödinger equation on the disk. *Inventiones mathematicae*, 206(2):485–599, 2016.

[5] Pietro Baldi, Giuseppe Floridia, and Emanuele Haus. Exact controllability for quasilinear perturbations of kdv. *Analysis & PDE*, 10(2):281–322, 2017.

[6] Valeria Banica and Luis Vega. On the dirac delta as initial condition for nonlinear schrödinger equations. In *Annales de l'IHP Analyse non linéaire*, volume 25, pages 697–711, 2008.

[7] Valeria Banica and Luis Vega. On the stability of a singular vortex dynamics. *Communications in mathematical physics*, 286(2):593, 2009.

[8] Valeria Banica and Luis Vega. The initial value problem for the binormal flow with rough data. *Ann. Sci. Éc. Norm. Supér*, 48(4):1423–1455, 2015.

[9] Valeria Banica and Luis Vega. Evolution of polygonal lines by the binormal flow. *arXiv preprint arXiv:1807.06948*, 2018.

[10] Valeria Banica and Luis Vega. On the energy of critical solutions of the binormal flow. *arXiv preprint arXiv:1907.08789*, 2019.

[11] Nicolas Burq and Maciej Zworski. Geometric control in the presence of a black box. *Journal of the American Mathematical Society*, 17(2):443–471, 2004.

[12] Roberto Camassa, G Falqui, G Ortenzi, M Pedroni, and C Thomson. Hydrodynamic models and con- finement effects by horizontal boundaries. *Journal of Nonlinear Science*, 29(4):1445–1498, 2019.

[13] Yu Deng and Zaher Hani. On the derivation of the wave kinetic equation for nls. *arXiv preprint arXiv:1912.09518*, 2019.

[14] Marcelo M Disconzi, Chenyun Luo, Giusy Mazzone, and Jared Speck. Rough sound waves in 3d compressible euler flow with vorticity. *arXiv preprint arXiv:1909.02550*, 2019.

[15] Roland Donninger, Wilhelm Schlag, and Avy Soffer. On pointwise decay of linear waves on a schwarzschild black hole background. *Communications in Mathematical Physics*, 309(1):51–86, 2012.

[16] Patrick Gérard and Sandrine Grellier. A survey of the Szegő equation. *Sci. China Math.*, 62(6):1087– 1100, 2019.

[17] Pierre Germain, Benjamin Harrop-Griffiths, and Jeremy L Marzuola. Compactons and their variational properties for degenerate kdv and nls in dimension 1. *arXiv preprint arXiv:1709.05031*, 2017.

[18] Pierre Germain, Benjamin Harrop-Griffiths, and Jeremy L Marzuola. Existence and uniqueness of solutions for a quasilinear kdv equation with degenerate dispersion. *Communications on Pure and Applied Mathematics*, 72(11):2449–2484, 2019.

[19] Irfan Glogić, Maciej Maliborski, and Birgit Schörkhuber. Threshold for blowup for the supercritical cubic wave equation. *arXiv preprint arXiv:1905.13739*, 2019.

[20] Irfan Glogić and Birgit Schörkhuber. Co-dimension one stable blowup for the supercritical cubic wave equation. *arXiv preprint arXiv:1810.07681*, 2018.

[21] E Grenier, Y Guo, B Pausader, and M Suzuki. Derivation of the ion equation. *Quarterly of Applied Mathematics*, 2019.

[22] Massimiliano Gubinelli, Herbert Koch, and Tadahiro Oh. Paracontrolled approach to the three- dimensional stochastic nonlinear wave equation with quadratic nonlinearity. *arXiv preprint arXiv:1811.07808*, 2018.

[23] Massimiliano Gubinelli, Herbert Koch, and Tadahiro Oh. Renormalization of the two-dimensional stochastic nonlinear wave equations. *Transactions of the American Mathematical Society*, 370(10):7335–7359, 2018.

[24] Benjamin Harrop-Griffiths, Mihaela Ifrim, and Daniel Tataru. The lifespan of small data solutions to the kp-i. *arXiv preprint arXiv:1409.4487*, 2014.

[25] Benjamin Harrop-Griffiths, Mihaela Ifrim, and Daniel Tataru. Finite depth gravity water waves in holomorphic coordinates. *Annals of PDE*, 3(1):4, 2017.

[26] Mihaela Ifrim and Annalaura Stingo. Almost global well-posedness for quasilinear strongly coupled wave-klein-gordon systems in two space dimensions. *arXiv preprint arXiv:1910.12673*, 2019.

[27] Mihaela Ifrim and Daniel Tataru. Global bounds for the cubic nonlinear schrödinger equation (nls) in one space dimension. *Nonlinearity*, 28(8):2661, 2015.

[28] Jacek Jendrej, Michał Kowalczyk, and Andrew Lawrie. Dynamics of strongly interacting kink-antikink pairs for scalar fields on a line. *arXiv preprint arXiv:1911.02064*, 2019.

[29] In-Jee Jeong and Sung-Jin Oh. On the cauchy problem for the hall and electron magnetohydrody- namic equations without resistivity i: illposedness near degenerate stationary solutions. *arXiv preprint arXiv:1902.02025*, 2019.

[30] Carlos E Kenig, Gustavo Ponce, Christian Rolvung, and Luis Vega. The general quasilinear ultrahyper- bolic schrödinger equation. *Advances in Mathematics*, 206(2):402–433, 2006.

[31] Carlos E. Kenig, Gustavo Ponce, and Luis Vega. The Cauchy problem for quasi-linear Schrödinger equations. *Invent. Math.*, 158(2):343–388, 2004.

[32] Rowan Killip and Monica Vişan. Kdv is well-posed in h–1. *Annals of Mathematics*, 190(1):249–305, 2019.

[33] Herbert Koch, Daniel Tataru, et al. Conserved energies for the cubic nonlinear schrödinger equation in one dimension. *Duke Mathematical Journal*, 167(17):3207–3313, 2018.

[34] Joachim Krieger, Shuang Miao, et al. On the stability of blowup solutions for the critical corotational wave-map problem. *Duke Mathematical Journal*, 2020.

[35] Joachim Krieger, Wilhelm Schlag, and Daniel Tataru. Renormalization and blow up for charge one equivariant critical wave maps. *Inventiones mathematicae*, 171(3):543–615, 2008.

[36] Hans Lindblad, Jonas Luhrmann, and Avy Soffer. Decay and asymptotics for the 1d klein-gordon equation with variable coefficient cubic nonlinearities. *arXiv preprint arXiv:1907.09922*, 2019.

[37] Jeremy L Marzuola, Jason Metcalfe, and Daniel Tataru. Quasilinear schrödinger equations i: Small data and quadratic interactions. *Advances in Mathematics*, 231(2):1151–1172, 2012.

[38] Jeremy L Marzuola, Jason Metcalfe, and Daniel Tataru. Quasilinear schrödinger equations iii: Large data and short time. *arXiv preprint arXiv:2001.01014*, 2020.

[39] Jeremy L Marzuola, Jason Metcalfe, Daniel Tataru, et al. Quasilinear schrödinger equations, ii: Small data and cubic nonlinearities. *Kyoto Journal of Mathematics*, 54(3):529–546, 2014.

[40] Jason Metcalfe, Daniel Tataru, and Mihai Tohaneanu. Price's law on nonstationary space–times. *Ad- vances in Mathematics*, 230(3):995–1028, 2012.

[41] Adrian Nachman, Idan Regev, and Daniel Tataru. A nonlinear plancherel theorem with applications to global well-posedness for the defocusing davey–stewartson equation and to the inverse boundary value problem of calderón. *Inventiones mathematicae*, pages 1–57, 2017.

[42] Huy Q Nguyen and Benoît Pausader. A paradifferential approach for well-posedness of the muskat problem. *Archive for Rational Mechanics and Analysis*, pages 1–66, 2020.

[43] Tadahiro Oh, Mamoru Okamoto, and Oana Pocovnicu. On the probabilistic well-posedness of the non- linear schrödinger equations with non-algebraic nonlinearities. *arXiv preprint arXiv:1708.01568*, 2017.

[44] Tadahiro Oh, Tristan Robert, and Nikolay Tzvetkov. Stochastic nonlinear wave dynamics on compact surfaces. *arXiv preprint arXiv:1904.05277*, 2019.

[45] Wilhelm Schlag, Avy Soffer, and Wolfgang Staubach. Decay for the wave and schrödinger evolutions on manifolds with conical ends, part i. *Transactions of the American Mathematical Society*, 362(1):19–52, 2010.

[46] Wilhelm Schlag, Avy Soffer,and Wolfgang Staubach. Decay for the wave and schrödinger evolutions on manifolds with conical ends, part ii. *Transactions of the American Mathematical Society*, 362(1):289– 318, 2010.

[47] Daniel Tataru. Strichartz estimates in the hyperbolic space and global existence for the semilinear wave equation. *Transactions of the American Mathematical society*, 353(2):795–807, 2001.

[48] Daniel Tataru. Local decay of waves on asymptotically flat stationary space-times. *American Journal of Mathematics*, 135(2):361–401, 2013.

[49] Jon Wilkening and Xinyu Zhao. Quasi-periodic traveling gravity-capillary waves. *arXiv preprint arXiv:2002.09487*, 2020.

Chapter 3

Geometric Tomography (20w5037)

February 9 - 14, 2020

Organizer(s): Alexander Koldobsky (University of Missouri), Dmitry Ryabogin (Kent State University), Vladyslav Yaskin (University of Alberta), Artem Zvavitch (Kent State University)

Overview of the Field

Geometric Tomography is the area of Mathematics where one investigates properties of solids based on the information about their sections and projections. It shares ideas and methods from many fields of Mathematics, such as Differential Geometry, Functional Analysis, Harmonic Analysis, Combinatorics and Probability. But the most significant overlap is with Convex Geometry and in particular with the classical Brunn-Minkowski theory. The workshop brought together a number of top researchers as well as students and postdocs with the aim of discussing most recent developments in the area.

The topics of the workshop included harmonic analysis on the sphere, spherical operators and special classes of bodies, geometric inequalities, discrete geometry, probability and random matrices.

Presentation Highlights

We start the description with the results of Mark Agranovsky. Let f be a continuous function on the unit sphere S^{n-1}, and let $F_a f$ be the *shifted* spherical Funk transform with respect to the center $a \in \mathbb{R}^n$, i.e.,

$$(F_a f)(E) = \int\limits_{S^{n-1}\cap E} f(x) dA_E.$$

Here E is a k-dimensional subspace passing through a and dA_E is the surface area measure on the $(k-1)$-dimensional sphere $S^{n-1} \cap E$. It is known that every operator F_a with $|a| \neq 1$ has a non-trivial kernel. On the other hand, the kernel is trivial, provided $|a| = 1$. Given $A = \{a_1, \dots, a_s\} \subset \mathbb{R}^n$, define

$$F_A f = \{F_{a_1} f, \dots, F_{a_s} f\}.$$

The problem is to describe all sets such that $\mathrm{ker} F_A = \{0\}$. Agranovsky's approach relies on the action of the group $Aut(B^n)$ of automorphisms of the unit ball and exploits group-invariance arguments. Denote by $G(A)$ the group generated by the symmetries $\tau_{a_j} : S^{n-1} \to S^{n-1}$,

$$\tau_{a_j}(x) = x + 2\frac{1 - \langle x, a_j \rangle}{|a - x|^2}(a - x), \quad j = 1, \dots, s.$$

In the case of two points, $s = 2$, it is shown that the paired transform $f \to (F_{a_1}f, F_{a_2}f)$ fails to be injective iff the group $G(A)$ generated by τ_{a_1}, τ_{a_2}, is finite. In the general case it is also shown that if $\operatorname{Ker} F_A \neq \{0\}$, then $G(A)$ is a Coxeter group (every subgroup with two generators is finite). It would be very interesting to see if the converse is true.

Jan Boman presented uniqueness results related to supports of distributions. Let $f \neq 0$ be a compactly supported distribution in $\mathbb{R}^n$, $n \geq 2$, and let Rf be its Radon transform. It is shown that if the Radon transform is supported on the set of tangent planes to the boundary ∂D of a bounded convex domain D, then ∂D must be an ellipsoid. As a corollary one gets a new proof of a recent theorem of Koldobsky, Merkurjev, and Yaskin, who settled a special case of a conjecture of Arnold that was motivated by a famous lemma of Newton. The following questions are left open and deserve an attention. Let D be a domain in $\mathbb{R}^n$ and let $\overline{D_0}$ be its sub-domain. Does there exist a non-trivial function f supported by $\overline{D}$ such that Rf vanishes for every line that meets D_0? What about polygons? Which subsets of the manifold of lines in the plane can be the support of Rf for some compactly supported function or distribution f in $\mathbb{R}^2$?

Mark Rudelson spoke about their joint results with Herman König. They considered the problem of maximal and minimal (in volume) non-central sections of the cube $Q_n = [-\frac{1}{2}, \frac{1}{2}]^n$ by subspaces $E \subset \mathbb{R}^n$, $\dim(E) = n-d$, $d = 1, \dots, n-1$. It was proved by Vaaler that the minimal central section of the cube is the one orthogonal to the coordinate direction, and after K. Ball we know that

$$\mathrm{vol}_{n-d}(Q_n \cap E) \leq (\sqrt{2})^d.$$

Several results for non-central sections that have distance $t > \frac{\sqrt{n-1}}{2}$ from the origin were also obtained by Moody, Stone, Zach and Zvavitch. Rudelson and König proved that

$$\mathrm{vol}_{n-d}(Q_n \cap (x+E)) > c(d)$$

for $|x| \leq \frac{1}{2}$, $x \in E^{\perp}$. They got a control on $C(d)$ in the case $d = 1$ by showing that

$$\mathrm{vol}_{n-1}(Q_n \cap (x+E)) > \frac{1}{17}$$

and also obtained a similar result for the complex cube with $\frac{1}{27}$ instead of $\frac{1}{17}$.One of the open problems is to consider the case of general polytopes instead of Q_n.

Herman König gave a talk about non-central sections of the simplex, cube and cross-polytope. Let $a \in S^{n-1}$ and $t \in \mathbb{R}$. Given a convex body $K \subset \mathbb{R}^n$ consider the parallel section and the perimeter functions,

$$A_K(a,t) = \mathrm{vol}_{n-1}(\{x \in K : \langle x, a\rangle = t\}),$$

$$P_{\partial K}(a,t) = \mathrm{vol}_{n-2}(\{x \in \partial K : \langle x, a\rangle = t\}).$$

König was motivated by the aforementioned results of Moody, Stone, Zach and Zvavitch, who proved that

$$A_{Q_n}(a,t) \leq A(a^{(n)}, t)$$

for $a^{(n)} = \frac{(1,\dots,1)}{\sqrt{n}}$, provided $\frac{\sqrt{n-2}}{2} < t \leq \frac{\sqrt{n}}{2}$, and by the recent results of Liu and Tkocz, who proved that

$$A_{B_1^n}(a,t) \leq A_{B_1^n}(e_1,t),$$

for $\frac{1}{\sqrt{2}} < t \leq 1$.

Let $\Delta^n = \{x \in \mathbb{R}_+^{n+1} : \sum_{j=1}^{n+1} x_j = 1\}$ be a simplex and let $a \in S^n \subset \mathbb{R}^{n+1}$ be such that $\sum_{j=1}^{n+1} a_j = 0$. It was shown by Webb that

$$A_{\Delta^n}(a,0) \leq A_{\Delta^n}(\tilde{a},0) = \frac{\sqrt{n+1}}{\sqrt{2}(n-1)!}$$

for $\tilde{a} = \frac{(1,-1,0,\ldots,0)}{\sqrt{2}}$. König's results include the estimate

$$A_{\Delta^n}(\tilde{a}, t) \leq A(a^{[n]}, t) = \frac{\sqrt{n+1}}{(n-1)!}\Big(\frac{n}{n+1}\Big)^{\frac{n}{2}}\Big(\sqrt{\frac{n}{n+1}} - t\Big)^{n-1},$$

where

$$a^{[n]} = \left(\sqrt{\frac{n}{n+1}}, -\frac{1}{\sqrt{n(n+1)}}, \ldots, -\frac{1}{\sqrt{n(n+1)}}\right) \in S^n, \qquad n \geq 3.$$

A similar result is obtained for $P_{\partial\Delta^n}(a,t)$ as well as several new results for $A_{B_1^n}(a,t)$, $P_{\partial B_1^n}(a,t)$ and for $A_{Q_n}(a,t)$, $P_{\partial Q_n}(a,t)$. Several questions about local minima and maxima of the parallel section and the perimeter functions are left open.

Tomasz Tkocz together with Han Huang, Boaz Slomka and Beatrice-Helen Vritsiou attacked the famous illumination problem, posed independently by Levi (1955), Hadwiger (1957) and Gohberg-Marcus (1960). Let $K \subset \mathbb{R}^n$ be a convex body. How many translates $N(K)$ of the interior of K are needed to cover K, or, equivalently, how many external sources $l(K)$ of light are needed to illuminate ∂K? The conjecture is that

$$N(K) = l(K) \leq 2^n$$

with equality iff K is a cube (up to an affine map). Many partial results are known, in particular,

$$N(K) \leq 4^n \frac{1 + o(1)}{\sqrt{\pi}} \sqrt{n} \log n.$$

Following the ideas of independent approaches of Artstein-Avidan-Slomka and Naszodi, it was proved by Huang, Slomka, Tkocz and Vritsiou that

$$N(K) \leq C4^n e^{-c\sqrt{n}}.$$

They do it by showing that

$$\frac{|K|}{|K \cap -K|} \leq 2^n e^{-c\sqrt{n}},$$

provided the barycenter of K is at the origin.

Galyna Livshyts brought a discussion of the Log-Brunn-Minkowski conjecture and related questions. Let $0 \leq \lambda \leq 1$ and let

$$\lambda K +_0 (1-\lambda)L = \bigcap_{u \in S^{n-1}} \{x \in S^{n-1} : |\langle u, x\rangle| \leq h_K(u)^\lambda h_L(u)^{1-\lambda}\}$$

be the logarithmic sum of two convex bodies K and L, where $h_K(u) = \sup\limits_{x \in K} \langle x, u\rangle$ is the support function of K.

Böröczky, Lutwak, Yang and Zhang asked if

$$|\lambda K +_0 (1-\lambda)L| \geq |K|^\lambda |L|^{1-\lambda}.$$

Galyna presented several related results, in particular, she asked if

$$8|K|\text{span}(e_1, e_2)^\perp| + \int\limits_{S^{n-1}} \frac{(|u_1| + |u_2|)^2}{h_K(u)} dS_K(u) \leq 4\frac{|K|e_1^\perp| + |K|e_2^\perp|}{|K|}.$$

Here $K|e_1^\perp$ stands for the orthogonal projection on the subspace $e_1^\perp$.

Eli Putterman continued the discussion about log-Brunn-Minkowski inequality. He showed how one can obtain the global log-BM from the local log-BM.

Apostolos Giannopoulos gave several results related to the conjecture posed by V. Milman. Let K be a symmetric convex body. For an n-tuple $C = (C_1, \dots, C_s)$ of convex symmetric bodies C_j, $j = 1, \dots, s$, consider the norm of the vector $T = (t_1, \dots, t_s) \in \mathbb{R}^n$ defined by

$$\|T\|_{C,K} = \frac{1}{\prod_{j=1}^{s} |C_j|} \int\limits_{C_1} \cdots \int\limits_{C_s} \| \sum_{j=1}^{s} t_j x_j \|_K dx_1 \dots dx_s.$$

Is it true that if $C_1 = \dots = C_s = C$, $|C_j| = 1$, then $\|T\|_{C,K}$ is equivalent to the Euclidean norm up to a logarithm in dimension? Giannopoulos, Chasapis and Skarmogiannis gave an alternative proof of the lower estimate of Gluskin and Milman,

$$\|T\|_{C,K} \geq \frac{n}{e(n+1)} \|T\|_2.$$

The upper bound is reduced to obtaining a constant of the order $L_C \sqrt{n} M(K_{\text{iso}})$, $M(K) = \int\limits_{S^{n-1}} \|\xi\|_K d\sigma(\xi)$, provided K is in isotropic position, and L_K is the isotropic constant. They hope that

$$L_C \sqrt{n} M(K_{\text{iso}}) \leq c (\log n)^b$$

for some absolute constant $b > 0$, however the best currently know estimate of Giannopoulos and E. Milman is

$$M(K_{\text{iso}}) \leq c \frac{(\log n)^{\frac{2}{5}}}{\sqrt[10]{n} L_K}.$$

The presented upper bound is

$$\|T\|_{C,K} \leq c \max\{\sqrt[4]{n}, \sqrt{\log(1+s)}\} L_C \sqrt{n} M(K) \|T\|_2,$$

provided $C_1 = \dots = C_s = C$ and C is in isotropic position. Other non-trivial upper bounds are obtained in the unconditional, ψ_2 and co-type-2 cases.

Carsten Shütt presented their joint results with Matthias Reitzner and Elisabeth Werner about convex hull of random points on the boundary of a simple polytope. Given a convex body $K \subset \mathbb{R}^n$ and N random points $x_1, \dots, x_N$ in K, let $K_N = [x_1, \dots, x_N]$ be the convex hull of these points. What is the expected number of vertices $\mathbb{E} f_0(K_N)$, facets $\mathbb{E} f_{n-1}(K_N)$ and the volume difference $\text{vol}_n(K) - \mathbb{E}\text{vol}_n(K_N)$? They show that choosing N points on the boundary of a simple convex polytope $P \subset \mathbb{R}^n$,

$$\mathbb{E}(f_{n-1}(P_N)) = c_{n,n-1} f_0(P) (\ln N)^{n-2} (1 + O(\ln N)^{-1}), \quad c_{n,n-1} > 0,$$

and

$$\text{vol}_n(P) - \mathbb{E}\text{vol}_n(P_N) = \frac{c_{n,P}}{N^{\frac{n}{n-1}}} (1 + O(N^{-\frac{1}{(n-1)(n-2)}}).$$

They expect that for arbitrary polytopes, one has

$$\text{vol}_n(P) - \mathbb{E}\text{vol}_n(P_N) = c_n \frac{\text{flag}(P) \text{vol}_n(P)}{N^{\frac{n}{n-1}}} (1 + O(N^{-\frac{1}{(n-1)(n-2)}})).$$

Here the flag is an n-tuple $(f_0(P), f_1(P), \dots, f_{n-1}(P))$ of k-dimensional faces of P, and $\text{flag}(P)$ is the number of flags of P. It would be interesting to evaluate the constant c_n.

Grigoris Paouris talked about his joint results with Boris Hanin on non-asymptotic behavior of the spectrum of products of many random matrices (square or rectangular). Let A be a $n \times n$ random matrix with mean zero Gaussian entries $a_{ij} \sim \frac{1}{\sqrt{n}} N(0,1)$, and let $s_1(A) \geq \dots \geq s_n(A)$ be its singular values. The Lyapunov exponents are defined as

$$\lambda_k = \frac{1}{n} \log s_k(X_N),$$

where X_N is the product of N independent random matrices, $X_N = A_N \cdot \dots \cdot A_1$. They proved that for small n and large N if

$$H_{n,N}(t) = \frac{1}{n} \{j \leq n : \lambda_j \leq \log t\},$$

and $N \geq T^n \log n$, $\delta \sim \frac{1}{T}$, then

$$\|H_{n,N} - H\|_{L^\infty[\delta,1-\delta]} \leq \frac{1}{T}$$

with probability $\geq 1 - e^{-cn^4 \frac{N}{T^4}}$. Here

$$H(t) = \int\limits_{-\infty}^{t} h(x)dx, \qquad h(x) = 2x1_{[0,1]}(x).$$

They conjecture that this statement should be true for not Gaussian variables only. It is also shown that for fixed n and N, one has

$$d(\Lambda_k, N(1,\varepsilon)) \leq C\frac{k^{\frac{3}{4}}\log N\sqrt{n}}{\sqrt{N}},$$

where $\Lambda_k = (\lambda_1, \dots, \lambda_k)$ is a Gaussian Random vector with some mean and variance.

Rafal Latala described his joint results with Petr Nayar and Marta Strzelecka. The general problem is to compare the strong and weak moments of random n-dimensional vectors X in $(\mathbb{R}^n, \|\cdot\|)$, say,

$$(\mathbb{E}\sup_{\|t\|_*\leq 1} |\langle t, X\rangle|^p)^{\frac{1}{p}} \leq C_{n,p} \sup_{\|t\|_*\leq 1} (\mathbb{E}|\langle t, X\rangle|^p)^{\frac{1}{p}},$$

where $\|\cdot\|_*$ is the dual norm. They show, in particular, that for any non-empty set $T \subset \mathbb{R}^n$ and $p \geq 2$, one has

$$(\mathbb{E}\sup_{t\in T} |\langle t, X\rangle|^p)^{\frac{1}{p}} \leq 2\sqrt{e}\sqrt{\frac{n+p}{p}}\sup_{t\in T}(\mathbb{E}|\langle t, X\rangle|^p)^{\frac{1}{p}}.$$

Paouris proved that for a log-concave vector X,

$$(\mathbb{E}|X|^p)^{\frac{1}{p}} \leq c_1\mathbb{E}|X| + c_2\sup_{t\in T}(\mathbb{E}|\langle t, x\rangle|^p)^{\frac{1}{p}}.$$

Is it possible to take $c_1 = 1$? What other norms can you take? Let X be log-concave, $r < \infty$ and let $(\mathbb{R}^n, \|\cdot\|)$ embeds isometrically in l_r. Is it true that

$$(\mathbb{E}\|X\|^p)^{\frac{1}{p}} \leq Cr(\mathbb{E}\|X\| + \sup_{\|t\|_*\leq 1}(\mathbb{E}|\langle t, x\rangle|^p)^{\frac{1}{p}})$$

holds with C instead of Cr?

Alexander Litvak reported about his results with Konstantin Tikhomirov. The general problem is as follows. Let B be a random matrix $n \times n$ with i.i.d. ± 1 entries. What is $P_n := \mathbb{P}(B\,\text{is singular})$? Equivalently, let $X_1, \dots, X_n$ be independent random vectors uniformly distributed on the vertices of the n-dimensional cube $[-1, 1]^n$. What is the probability that the vectors are linearly independent? It is known that

$$P_n \geq (1 - o(1))2n^2 2^{-n},$$

and the conjectures are that

$$P_n \leq (\frac{1}{2} + o(1))^n = 2^{-(1+o(1))n}$$

(solved recently by Tikhomirov) and

$$P_n \leq (1 + o(1))2n^2 2^{-n}.$$

They also ask the same question about Bernoulli $0/1$ random matrices and the conjecture is that

$$P_n = (1 + o(1))\mathbb{P}\{\exists\text{a zero row or a zero column}\} = (1 + o(1))2n(1-p)^n.$$

Basak and Rudelson proved that

$$P_n \leq e^{-cnp},$$

provided $p \geq \frac{C \ln n}{n}$ and that

$$P_n \leq (1+o(1))2n(1-p)^n,$$

provided $p \leq \frac{\ln n}{n} + o(\ln \ln n)$. Tikhomirov proved that

$$P_n \leq (1-p+o(1))^n$$

for $p \in (0, \frac{1}{2}]$. Recently, Litvak and Tikhomirov showed that for $C\frac{\ln n}{n} \leq p \leq c$,

$$P_n \leq (1+o(1))2n(1-p)^n.$$

Arnaud Marsiglietti gave a talk that was devoted to his joint results with James Melbourne about localization technique for discrete log-concave random variables. The main idea is to translate the “continuous” results from convex geometry to the “discrete” ones. In this lecture the results related to the 1993 Theorem of Lovasz and Simonovits were presented. A function $f : \mathbb{N} \to (0, \infty)$ is called discrete log-concave if

$$f(n)^2 \geq f(n-1)f(n+1)$$

$\forall n \in \mathbb{N}$ and f has a contiguous support, i.e., $\forall a \leq b$, $a, b \in \{f > 0\}$ iff $\forall k \in \{a, \ldots, b\}$, k must belong to $\{f > 0\}$. A random variable is discrete log-concave if its probability mass function is discrete log-concave. Let $N \in \mathbb{N}$ and let $[N] = \{0, \ldots, n\}$. For a measure γ with contiguous support and a function h define the set

$$P_h^\gamma([N]) = \{P_X \in P([N]) : X \quad \text{log-concave}/\gamma \quad \text{and} \quad \mathbb{E}(h(X)) \geq 0\},$$

where $P([N])$ stands for the set of all probability measures with the support on $[N]$, and $X \sim p$ is log-concave with respect to an integer-valued measure γ with mass function q means that $\frac{p}{q}$ is log-concave. It is proved that if $\varphi : P_h^\gamma([N]) \to \mathbb{R}$ is convex, then

$$\sup_{P_X \in P_h^\gamma([N])} \varphi(P_X) \leq \sup_{P_{X^\sharp} \in A_h^\gamma([N])} \varphi(P_{X^\sharp}),$$

where

$$A_h^\gamma([N]) = P_h^\gamma([N]) \cap \{X \, \text{log-affine}/\gamma\}$$

(i.e., inequalities become equalities). As one of the applications in the case $\varphi(P_X) = P_X(A)$, $A \subset \mathbb{R}$, one can prove bounds or every log-concave discrete X,

$$\mathbb{P}(X > t) \leq c_1 e^{-\frac{c_2 t}{\mathbb{E}(X)}}, \quad (\mathbb{E}[X^s])^{\frac{1}{s}} \leq C(r,s)(\mathbb{E}[X^r])^{\frac{1}{r}},$$

with some explicit constants. It would be interesting to verify if they are sharp.

Peter Pivovarov described his joint results with Jesus Rebollo Bueno about stochastic Prékopa-Leindler inequality for log-concave functions. For $x, y \in \mathbb{R}^n$, and $\lambda \in [0,1]$, let

$$(f \star_\lambda g)(v) = \sup\{f(x)^\lambda g(y)^{1-\lambda} : \, v = \lambda x + (1-\lambda)y\}.$$

Given a log-concave integrable function $f : \mathbb{R}^n \to [0, \infty)$, define

$$G_f = \{(x,z) \in \mathbb{R}^n \times [0,\infty) : z \leq f(x)\},$$

and let the vectors $\{(X_i, Z_i)\}_{i=1}^N \subset \mathbb{R}^n \times [0,\infty)$ be i. i. d. uniform in G_f. For two integrable log-concave functions $f, g : \mathbb{R}^n \to [0, \infty)$, $\lambda \in (0,1)$ and $N, M > n+1$, it is proved that for all $\alpha > 0$,

$$\mathbb{P}\Big(\int\limits_{\mathbb{R}^n} ([f]_N \star_\lambda [g]_M)(v)dv > \alpha\Big) \geq \mathbb{P}\Big(\int\limits_{\mathbb{R}^n} ([f^*]_N \star_\lambda [g^*]_M)(v)dv > \alpha\Big),$$

where

$$[f]_N(x) = e^{\sup\{z : \, (x,z) \in H_f\}}, \quad H_f = \text{conv}\{(X_1, \log Z_1), \ldots, (X_N, \log Z_N)\},$$

and $*$ stands for a non-decreasing rearrangement. In particular, for one function they get a stochastic functional Groemer-type inequality.

Petros Valettas gave a talk about lower deviation estimates in normed spaces. Let $\|\cdot\|$ be an arbitrary norm on $\mathbb{R}^n$ and let G be a Gaussian vector. The main goal is to provide upper bounds for $\mathbb{P}(\|G\| \leq \delta\mathbb{E}(\|G\|))$. Jointly with Grigoris Paouris they obtain the estimate

$$\mathbb{P}(f(G) \leq \mathbb{E}f(G) - t\sqrt{\mathrm{Var}[f(G)]}) \leq e^{-ct^2}, \quad t > 0.$$

Giorgos Chasapis presented several results about random polytopes related to Lutwak's conjecture. Let K be a convex body and let $1 \leq l \leq n-1$. Define

$$\Phi_{[l]}(K) = |K|^{-\frac{1}{n}} \Big(\int\limits_{G_{n,l}} |P_F K|^{-n} dv_{n,l}(F) \Big)^{-\frac{1}{ln}},$$

the l-th normalized affine quermassintegral. Prove that

$$\Phi_{[l]}(K) \geq \Phi_{[l]}(B_2^n).$$

Another conjecture of Dafnis and Paouris is that there exist two constants c_1 and c_2 such that for all l,

$$c_1\sqrt{\frac{n}{e}} \leq \Phi_{[l]}(K) \leq c_2\sqrt{\frac{n}{e}}.$$

Piotr Nayar's talk was devoted to Khinchin's inequality which is stated as follows. Let $\{\varepsilon_j\}_{j=1}^N$ be i.i.d random variables with $\mathbb{P}(\varepsilon_j = \pm 1) = \frac{1}{2}$ for $j = 1, \ldots, N$, i.e., a sequence with Rademacher distribution. Let $0 < p < \infty$ and let $x_1, \ldots, x_N \in \mathbb{C}$. Then

$$A_p\Big(\sum_{j=1}^n |x_j|^2\Big)^{\frac{1}{2}} \leq \Big(\mathbb{E}\Big|\sum_{j=1}^n \varepsilon_j x_j\Big|^p\Big)^{\frac{1}{p}} \leq B_p\Big(\sum_{j=1}^n |x_j|^2\Big)^{\frac{1}{2}},$$

where A_p and B_p are some absolute constants. Together with Tomasz Tkocz Petr Nayar gave a beautiful elementary proof of this inequality for even p. It would be very interesting to obtain an elementary proof for odd p.

Elisabeth Werner gave a talk about her joint work with O. Giladi, H. Huang and C. Schütt on constraint convex bodies with maximal affine surface area. Given a convex body $K \subset \mathbb{R}^n$, the L_p-affine surface area is defined as

$$\mathrm{as}_p(K) = \int\limits_{\partial K} \frac{k(x)^{\frac{p}{n+p}}}{\langle x, N(x)\rangle^{\frac{n(p-1)}{n+p}}} d\mu_K(x), \quad p \neq -n,$$

where the integration is with respect to the usual surface area measure μ_K over the boundary ∂K, N is the normal vector, and k is the Gauss curvature. The quantity is affine (linear) invariant, but not continuous in K, so the question is if one can get continuous affine invariants. They study the inner and outer maximal and minimal surface areas

$$\mathrm{IS}_p(K) = \sup_{C\subset K}(\mathrm{as}_p(C)), \qquad \mathrm{OS}_p(K) = \sup_{C\supset K}(\mathrm{as}_p(C)),$$
$$\mathrm{is}_p(K) = \inf_{C\subset K}(\mathrm{as}_p(C)), \qquad \mathrm{os}_p(K) = \inf_{C\supset K}(\mathrm{as}_p(C)),$$

for relevant ranges of p. In particular, they showed that for $p \in [0, n]$, $p \in [n, \infty]$, $[-n, 0]$, the maps $K \to \mathrm{IS}_p(K)$, $K \to \mathrm{OS}_p(K)$ and $K \to \mathrm{os}_p(K)$ are continuous in the Hausdorff metric correspondingly. They also study the bodies at which the corresponding $\sup$ or $\inf$ is reached. Following the results of Barany in the case $n = 2$, $p = 1$, they attack the questions about estimating the "size" of $\mathrm{IS}_p(K)$, $\mathrm{OS}_p(K)$ and $\mathrm{os}_p(K)$ in all dimensions for all relevant p.

Maria de los Angeles Alfonseca-Cubero spoke about her joint results with F. Nazarov, D. Ryabogin and V. Yaskin on a local solution to the eighth Busemann-Petty problem. In 1956, Busemann and Petty posed ten problems about symmetric convex bodies, of which only the first one has been solved. Their fifth and the eighth problems are as follows. If for an origin-symmetric convex body $K \subset \mathbb{R}^n$, $n \geq 3$, one has

$$\forall \theta \in S^{n-1} \quad h_K(\theta) vol_{n-1}(K \cap \theta^{\perp}) = C,$$

where the constant C is independent of θ, must K be an ellipsoid? If for an origin-symmetric convex body $K \subset \mathbb{R}^n$, $n \geq 3$, one has

$$f_K(\theta) = C(vol_{n-1}(K \cap \theta^{\perp}))^{n+1} \qquad \forall \theta \in S^{n-1},$$

where the constant C is independent of θ, must K be an ellipsoid? Here f_K is the curvature function, which is the reciprocal of the Gaussian curvature viewed as a function of the unit normal vector. They prove that if an origin-symmetric convex body $K \subset \mathbb{R}^n$, $n \geq 3$, satisfies one of the above conditions and is sufficiently close to the Euclidean ball in the Banach-Mazur metric, then K must be an ellipsoid.

Sudan Xing talked about dual curvature measures and the Orlicz-Minkowski problem which is about finding necessary and sufficient conditions on a finite Borel measure μ and a function $\varphi : (0, \infty) \to (0, \infty)$ so that there exists a convex body $K \subset \mathbb{R}^n$ containing the origin in its interior and $\mu = \tau \varphi(h_K) S(K, \cdot)$ for some constant $\tau > 0$. Here h_K is the support function of the body K and $S(K, \cdot)$ is the surface area measure of K.

Shiri Artstein's talk was devoted to polarity, transportation and potentials. She started describing the "parallels" between the relations of the Legendre transform

$$\mathcal{A}\varphi(x) = \sup \frac{(\langle x, y \rangle - 1)_-}{\varphi(y)}$$

(both $\mathcal{L}$ and $\mathcal{A}$ are order reversing involutions) and the Prekopa-Leindler inequality and the polarity transform $\mathcal{A}\varphi$ and the inequality recently discovered with D. Florentin and A. Segal. Next, she talked about the source of other order reversing involutions, coming from a cost function $c(x, y) : \mathbb{R}^n \times \mathbb{R}^n \to (-\infty, \infty]$. Given a function $\varphi : \mathbb{R}^n \to [-\infty, \infty]$ she defined the c-transform of φ as

$$\varphi^c(y) = \inf_x (c(x, y) - \varphi(x))$$

and explained that different choices of the cost function lead to different transforms. In particular, the choice $c(x, y) = -\langle x, y \rangle$ yields $-\varphi^c = \mathcal{L}(-\varphi)$ and the choice $c(x, y) = -\ln(\langle x, y \rangle - 1)$ yields $e^{-\varphi^c} = \mathcal{A}(e^{-\varphi})$. Finally, she presented a result on the $\mathcal{A}$-transport of measures that is analogous to the famous Brenier, McCann and Cafarelli theorem (which measures can be mapped to one another using the "dual" gradient , i.e., the $\mathcal{A}$-gradient?)

Luis Carlos Garcia Lirola talked about volume product and metric spaces. Given a finite metric space (M, d), $M = \{a_0, \ldots, a_n\}$ one can associate a polytope $P = P(M) \subset \mathbb{R}^n$ as

$$B_{\mathcal{F}(M)} = \operatorname{conv} \left\{ \frac{e_i - e_j}{d(a_j, a_j)} \right\}, \qquad i \neq j.$$

The volume product of a metric space is

$$\mathcal{P}(M) = |B_{\mathcal{F}(M)}| \cdot |B_{\mathrm{Lip}_0(M)}|,$$

where

$$B_{\mathrm{Lip}_0(M)} = \left\{ f : \frac{f(a_i) - f(a_j)}{d(a_j, a_j)} \leq 1 \ \forall i \neq j \right\},$$

and a function f is identified with a vector $(f(a_1), \ldots, f(a_n)) \in \mathbb{R}^n$, $B^*_{\mathrm{Lip}_0(M)} = B_{\mathcal{F}(M)}$. Together with M. Alexander, M. Fradelizi and A. Zvavitch they showed, in particular, if M is a finite metric space with minimal volume product such that $B_{\mathcal{F}(M)}$ is a simplicial polytope, then M is a tree (and so $\mathcal{P}(M) = \frac{4^n}{n!}$). In addition, they obtained several results related to a metric-graph characterization of $B_{\mathcal{F}(M)}$ being a Hanner polytope.

Michael Roysdon presented a slicing inequality of the Rogers-Shephard type. Michael generalized the original result of Mark Rudelson who proved that, for any m-dimensional subspace H of $\mathbb{R}^n$ and any convex body $K \subset \mathbb{R}^n$, one has

$$\operatorname{vol}((K + (-K) \cap H) \leq \left[c \cdot \min\{n/m, \sqrt{m}\} \right]^m \sup_{y \in \mathbb{R}^n} \operatorname{vol}(K \cap (y + H)),$$

where the volume here is interpreted as the restriction of the Lebesgue measure of the m-dimensional subspace H and $c > 0$ is some absolute constant.

Michael worked on the case, when $\min\{n/m, \sqrt{m}\} = n/m$ for general measures μ on $\mathbb{R}^n$ having radially decreasing densities. The main result presented in the talk asserts that for any convex body $K \subset \mathbb{R}^n$, any measure μ on $\mathbb{R}^n$ having a radially decreasing density, and any m-dimensional subspace H of $\mathbb{R}^n$, and any measures η defined on $\mathbb{R}^n$ whose density satisfies certain concavity conditions and such that $\eta(K) > 0$ one has

$$\mu((K + (-K)) \cap H) \leq \frac{\binom{n+m}{m}}{\eta(K)} \int_K \mu((-y + K) \cap H) d\eta(y).$$

The inequality was further extended to the setting of $(1/s)$-concave functions, with $s \in (0, \infty)$. In particular, it was shown that, for any such function and any measure μ, one has

$$\int_H \sup_{x=x_1-x_2} (f(x_1)^{1/s} + f(x_2)^{1/s})^s d\mu(x) \leq C(n, m, s) \cdot \sup_{y\in\mathbb{R}^n} \left\{ \int_{(\mathrm{supp}(f)-y)\cap H} f(x) d\mu(x) \right\},$$

where $C(n, m, s) > 0$ is a constant depending only on n, m and s.

Martin Henk delivered a lecture about slicing properties of the lattice point enumerator based on ongoing joint work with Ansgar Freyer. He presented the results about the discrete Meyer inequality for $n \geq 3$. Let K be an origin-symmetric convex body, and let

$$c(n) = \inf \left\{ \frac{G(K)^{\frac{n-1}{n}}}{\prod_{j=1}^{n} G(K \cap e_j^{\perp})^{\frac{1}{n}}} \right\},$$

where $G(K) = \sharp(K \cap \mathbb{Z}^n)$ stands for the lattice point enumerator. Gardner, Gronchi and Zong proved that

$$c(2) = 3^{-\frac{1}{2}} \quad \text{and} \quad c(n) \leq \frac{(n!)^{\frac{1}{n}}}{n}.$$

In general, $c(n) \leq 3^{\frac{1-n}{n}}$. Henk and Freyer showed that $c(n) \geq 4^{-(n+o(n))}$ and for the class of unconditional bodies $c(n) \geq 3^{-n}$.

Krzysztof Oleszkiewicz gave a lecture about some recent developments of harmonic analysis on the discrete cube $\{-1, 1\}^n$. He discussed an improvement of a result of Friedgut, Kalai and Naor who have shown that if the variance of the absolute value of a sum of weighted Rademacher variables is much smaller than the variance of the sum, then one of the summands dominates the sum. He also gave new proofs of some results of K. Tanguy. Let

$$\mathrm{Inf}_{ij}(f) = \sum_{i,j\in S} (\widehat{f}(S))^2,$$

where $\widehat{f}(S) = \mathbb{E}(f \cdot w_S)$ and w_S is the Walsh function associated with a subset S of $[n]$. If $\forall i, j$,

$$Inf_{ij}(f) \leq \frac{1}{1000}(\frac{lnn}{n})^2,$$

then f is close to ± 1 or $\pm r_k$ (Rademacher functions of order k). He asked if given two finite 1-separated sets A, B in a Banach space $(F, \|\cdot\|)$, the Minkowski sum set $A+B$ contains a 1-separated subset of cardinality $|A|+|B|-1$. Right after the conference Fedor Nazarov gave a negative answer to this question for A , B consisting of 3 points.

Yair Shenfeld talked about polytope extremals of the Alexandrov-Fenchel inequality. He presented results about 1985 Conjecture of R. Schneider. Let

$$V(K, L, C_1, \ldots, C_{n-2}) = \int_{S^{n-1}} h_K dS_{L,C_1,\ldots,C_{n-2}}.$$

If C_j are full-dimensional and we have an equality in

$$V(K, L, C_1, \dots, C_{n-2})^2 \geq V(K, K, C_1, \dots, C_{n-2})V(L, L, C_1, \dots, C_{n-2}),$$

then $h_K = h_{cL+t}$. Together with Ramon Van Handel they prove that the conjecture is true if all C_j are equal to each other, or if C_j are polytopes.

Oscar Adrian Ortega Moreno discussed the results related to the classical Tarski plank problem, asking if an n-dimensional convex body is covered by a collection of planks, then the sum of the widths of the planks should be at least the minimal width of the convex body they cover. Following Jiang, Polyanski he reproves the conjecture of Toth about zones on the unit sphere S^{n-1}. He asks if, given vectors $v_1, \dots, v_n \in S^{n-1}$, there exists $v \in S^{n-1}$ such that

$$\prod_{j=1}^{n} |\langle v_j, v \rangle| \geq n^{-\frac{n}{2}}.$$

Gideon Schehtman's talk was devoted to the dimension reduction in the trace class norm. Let (M, d) be a metric space, and let $(X, \| \cdot \|)$ be a normed space. One says that M embeds into X with distortion C if there is a function $f : M \to X$ such that

$$d(x, y) \leq \|x - y\| \leq Cd(x, y) \qquad \forall x, y \in M.$$

The best C is denoted by $C_X(M)$. The interest is in $k_n^C(X)$-the smallest k such that for all $S \subset X$ with $|S| = n$ there is a subspace $Y \subset X$ of dimension k such that $C_Y(S) \leq C$ (one thinks that, say, $C = 2$). Together with A. Naor and G. Pisier they proved the strengthening of a Brinkman-Charikar result that

$$k_n^C(S_1) \geq n^{\frac{\alpha}{C^2}}$$

for a universal $\alpha > 0$. Here S_1 is the trace class (Schatten-Von-Neumann 1, Nuclear norm). The meaning of this result is that for all n there are n points in S_1 such that if Y is a subspace of S_1 of dimension k into which these n points embed with distortion C, then $k \geq n^{\frac{\alpha}{C^2}}$. Given k what is the order of the smallest m such that $\forall k$-dimensional subspace of S_1 2-embeds into S_1^m? He conjectured that there is no polynomial bound on m in terms of k.

Semyon Alesker spoke about a complex analogue of the algebra of even valuations on convex sets. Valuations on convex sets are a classical object in convexity with traditionally strong relations to integral geometry. A valuation is a finitely additive measure on the class of all convex compact sets in $\mathbb{R}^n$. Translation invariant valuations continuous in the Hausdorff metric are studied particularly well. During the last 25 year there was a considerable progress in their study and in their integral geometric applications. It was realized that continuous valuations are particularly rich in structure. Some years ago the speaker has introduced a canonical product on them. Several non-trivial properties of it has been found, as well as applications to integral geometry. The first part of the talk contained a review of some of the relevant background on valuations and the product on them. The focus was on versions of the Poincaré duality and hard Lefschetz theorem. They served as a motivation for the new results. The main new result was the introduction of a complex non-Archimedean analogues of the algebra of even translation invariant valuations. While at the moment these algebras lack a geometric interpretation, they have non-trivial algebraic properties. In particular they satisfy versions of the Poincaré duality and hard Lefschetz theorem. Behind these properties stay results on the Radon and cosine transform on Grassmannians over local fields.

Outcome of the Meeting

The meeting was very successful. We brought together mathematicians from many countries and many research areas, such as convex geometry, discrete geometry, probability, functional and harmonic analysis. Besides the leading scientists, we also had 1 undergraduate student, 4 graduate students and 4 postdocs or recent PhDs participating in the workshop. Female participation was about 22%. The friendly atmosphere created during the workshop helped many participants not only to identify the promising ways to attack old problems but also to get acquainted with many open new ones.

Participants

Agranovsky, Mark (Bar-Ilan University)
Alesker, Semyon (Tel Aviv University)
Alfonseca-Cubero, Maria de los Angeles (North Dakota State University)
Artstein, Shiri (Tel-Aviv University)
Boman, Jan (Stockholm University)
Chasapis, Giorgos (University of Crete)
Dann, Susanna (Universidad de los Andes)
García-Lirola, Luis C. (Universidad de Zaragoza)
Giannopoulos, Apostolos (National and Kapodistrian University of Athens)
Gordon, Yehoram (Technion)
Henk, Martin (Technische Universität Berlin)
Hosle, Johannes (UCLA)
Koenig, Hermann (Universitaet Kiel)
Koldobsky, Alexander (University of Missouri)
Latala, Rafal (University of Warsaw)
Litvak, Alexander (University of Alberta)
Livshyts, Galyna (Georgia Institute of Technology)
Ludwig, Monika (Technische Universität Wien)
Marsiglietti, Arnaud (University of Florida)
Myroshnychenko, Sergii (University of Alberta)
Nayar, Piotr (University of Warsaw)
Oleszkiewicz, Krzysztof (University of Warsaw)
Ortega Moreno, Oscar Adrian (Technische Universität Wien)
Paouris, Grigoris (Texas A & M University)
Pivovarov, Peter (University of Missouri)
Putterman, Eli (Tel Aviv University)
Rotem, Liran (Technion)
Roysdon, Michael (Brown University)
Rudelson, Mark (University of Michigan, Ann Arbor)
Ryabogin, Dmitry (Kent State University)
Schechtman, Gideon (Weizmann Institute)
Schütt, Carsten (Christian-Albrechts-Universitaet)
Shenfeld, Yair (Princeton University)
Tatarko, Kateryna (University of Alberta)
Tkocz, Tomasz (Carnegie Mellon University)
Tomczak-Jaegermann, Nicole (University of Alberta)
Valettas, Petros (University of Missouri)
Werner, Elisabeth (Case Western Reserve University)
Xing, Sudan (University of Arkansas at Little Rock.)
Yaskin, Vladyslav (University of Alberta)
Zvavitch, Artem (Kent State Univeristy)

Chapter 4

New Perspectives in Colouring and Structure 20w5143 (20w5143)

March 15 - 20, 2020

Organizer(s): Bojan Mohar (Simon Fraser University), Alex Scott (University of Oxford), Paul Seymour (Princeton University)

Organization of the meeting

The workshop was planned for 42 participants. However, with the date of the workshop approaching, many cancellations were received due to the emerging Covid-19 pandemic that made international travel impossible. In the week preceeding the workshop, less than half of the original participants were expected (the remaining participants were either from Canada, or international visitors that were already in Canada). Just two days before the meeting, the province of Alberta announced ban on international gatherings, and the workshop was cancelled.

However, in a couple of days the organizers together with the technical help from BIRS, were able to organize the online event featuring most of the intended lectures. The event was a great success as the audience was about 60 participants for most of the talks.

Presentations

In the end, almost all the originally scheduled presentations took place. The final schedule was as follows:

Monday

9:00-10:00 Sergey Norin 10:30-11:30 Luke Postle
2:30-3:00 Andrew Thomason 3.30-4:00 Vaidy Sivaraman (remote) 4:00 problem session

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Tuesday

9:00-10:30 Maria Chudnovsky (survey+talk)
11:00-11:30 Nicolas Trotignon
2:00-2:30 Carla Groenland 2:30-3:30 David Conlon
3:30-4:00 Bhargav Narayanan

Wednesday

9:00-10:00 David Wood (survey) 10:30-11:00 Vida Dujmovic 11:00-11:30 Chun-Hung Liu

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Thursday

9:00-9:30 Bartosz Walczak 9:30-10:00 Penny Haxell 10:30-11:00 Robert Samal
2:00-2:30 Jon Noel 2:30-3:00 Tom Trotter

Overview of the subject area of the workshop

The study of graph colouring is a central theme in combinatorics. Calculating the chromatic number of a graph is well-known to be NP-hard (indeed it is NP-hard even to approximate the chromatic number), and so it is perhaps not surprising that graph colouring has a rich theory, with many important open problems. The colouring of graphs, and more generally of directed graphs and hypergraphs, also has connections and applications in many other areas, including algorithm design, scheduling and resource allocation, statistical physics, and social choice theory.

A common theme in colouring problems is the relationship between chromatic number and graph structure. For instance, one of the oldest problems in graph theory was the celebrated Four Colour Conjecture on colouring planar graphs, which was raised in 1852 and inspired a huge body of work (it was only proved in 1976). It was shown by Wagner in 1937 that planar graphs can be characterized in structural terms: a graph is planar if and only if it does not have two specific subgraphs as minors. Thus the Four Colour Theorem provides a connection between structure and chromatic number.

A vastly more general conjecture was made by Hadwiger in 1943: the conjecture asserts that if a graph cannot be properly coloured with $k-1$ colours then it must contain the complete graph on k vertices as a minor. The conjecture has been proved when k is at most 6 (Wagner showed already that the result for $k = 5$ is equivalent to the Four Colour Theorem; the proof of the $k = 6$ case by Robertson, Seymour and Thomas won the 1994 Fulkerson Prize). For $k \geq 7$, the problem is still open, although there are some promising partial results. In the last few years, there has been a lot of interesting work work looking at defective forms of Hadwiger's Conjecture, where colour classes do not need to be stable sets. This has led to a broader and rapidly advancing theory of defective colouring.

Another important structural question is to understand what induced subgraphs must be contained in graphs of large chromatic number. For instance, it has long been known from work of Tutte and then Erdos that graphs of large chromatic number need not contain large complete subgraphs (or even short cycles). A celebrated result in this area is the Strong Perfect Graph Theorem, conjectured by Berge in 1961 and proved by Chudnovsky, Robertson, Seymour and Thomas in 2006 (and subsequently awarded the 2009 Fulkerson Prize): every graph with chromatic number larger than clique number contains either an odd hole or an odd antihole. The Strong Perfect Graph Theorem gives a precise structural characterization, but it is natural to ask what more can be said when the chromatic number is *much* larger than the clique number. Gyarfas made a sequence of beautiful conjectures concerning such graphs, and there has been major progress on these in the last three years, and a new structural theory is beginning to emerge. More generally, there has been a large burst of research on chi-bounded classes of graphs, and on the algorithmic problem of colouring graphs with specific forbidden induced subgraphs.

Another important collection of problems concerns flows (which arise as a dual problem to colouring). Tutte's 3-Flow and 5-Flow Conjectures have been open for decades, and there are many interesting related problems. Recent progress by Thomassen and his coauthors has introduced some new techniques, and it seems there is potential for further progress.

This is only a small sample of the many open questions and theoretical advances on colouring. Many questions have been open now for decades with seemingly little progress. However, some powerful new techniques have been developed in the last few years. These have led to significant breakthroughs, and their full potential is yet to be ascertained. We believe that the new methods are robust and powerful enough to be used to resolve other important coloring questions and can be extended beyond their original application to attack new areas. By bringing the originators of these new tools, other respected researchers in graph coloring and bright young minds together, we hope that collaboration at this conference will spur the development of these new techniques to attack some of the remaining important open questions in graph coloring.

Workshop press release

The study of graph colouring is a central theme in combinatorics. Calculating the chromatic number of a graph is well-known to be NP-hard (indeed it is NP-hard even to approximate the chromatic number), and so it is perhaps not surprising that graph colouring has a rich theory, with many important open problems. The colouring of graphs, and more generally of directed graphs and hypergraphs, also has connections and applications in many other areas, including algorithm design, scheduling and resource allocation, statistical physics, and social choice theory.

A common theme in colouring problems is the relationship between chromatic number and graph structure. For instance, one of the oldest problems in graph theory was the celebrated Four Colour Conjecture on colouring planar graphs, which was raised in 1852 and only proved in 1976. A vastly more general conjecture made by Hadwiger in 1943 is still open: if a graph cannot be properly coloured with $k-1$ colours then it must contain the complete graph on k vertices as a minor. In the last few years, there have been some important steps forward on Hadwiger's Conjecture, and major progress on some of the many other important questions on graph and digraph colouring. This workshop brings together the originators of these new developments, as well as other respected researchers and bright young minds in graph colouring, to explore these new breakthroughs and the new territory they have opened up.

Participants

Bradshaw, Peter (Simon Fraser University)
Chudnovsky, Maria (Princeton)
Conlon, David (California Institute of Technology)
DeVos, Matt (Simon Fraser University)
Dibek, Cemil (Princeton University)
Dujmović, Vida (University of Ottawa)
Fox, Jacob (Stanford University)
Groenland, Carla (TU Delft)
Haxell, Penny (University of Waterloo)
Johnston, Tom (University of Oxford)
Liu, Chun-Hung (Texas A & M University)
Masařík, Tomáš (University of Warsaw)
Mohar, Bojan (Simon Fraser University)
Morrison, Natasha (University of Victoria)
Narayanan, Bhargav (Rutgers University)
Noel, Jonathan (University of Victoria)
Norin, Sergey (McGill University)
Oum, Sang-il (Institute for Basic Science)
Postle, Luke (University of Waterloo)
Roberts, Alexander (Oxford University)
Samal, Robert (Charles University)
Scott, Alex (University of Oxford)
Seymour, Paul (Princeton University)
Sivaraman, Vaidy (Mississippi State University)
Stein, Maya (University of Chile)
Tan, Jane (University of Oxford)
Thomason, Andrew (University of Cambridge)
Trotignon, Nicolas (CNRS, France)
Trotter, William (Georgia Tech)
Walczak, Bartosz (Jagiellonian University)
Wood, David (Monash University)

Chapter 5

Connections in Infinite Dimensional Dynamics (20w5145)

May 17 - 22, 2020

Organizer(s): Konstantin Mischaikow (Rutgers University), Jan Bouwe van den Berg (VU Amsterdam), Jean-Philippe Lessard (McGill University), Jason Mireles James (Florida Atlantic University)

Overview of the Field

Understanding dramatic changes in the dynamics of physical systems is a critical part of describing real world phenomena like the formation of hurricanes, booms and busts in the stock market, and even the progression of global pandemics. Such dynamical transitions are described by connecting orbits in nonlinear dynamical systems, mainly in the form of ordinary differential equations, partial differential equations and delay differential equations. This workshop focused on combining computational techniques with abstract mathematics to improve our fundamental understanding of transitions in dynamical systems.

Open Problems

The meeting was moved to an online, zoom-enabled workshop in response to travel restrictions. Since participants were dispersed through multiple time zones we decided to have a very small number of short talks, leaving as much time for open discussion as possible and making the best use of the roughly 5 hours per day work window.

The idea was to start the meeting with short 15 minutes talks on major open problems in the area, each followed by 15 minutes of conversation. The slogan for the talks was “don’t tell us what you know how to do, tell us what you don’t know how to do”. Six volunteers were found to give such presentations:

1. Connecting orbits for strongly indefinite problems/ill posed PDEs (Jonathan Jaquette)
2. DSGRN and Hill Function Continuation (Konstantin Mischaikow)
3. Stability of nonlinear waves for delayed PDEs (Blake Barker)
4. Forcing and topology from partial information in infinite dimensions (Jan Bouwe van den Berg)
5. Hopf bifurcations in the FitzHugh-Nagumo PDE (Elena Queirolo)
6. Traveling waves for a fourth order problem with exponential nonlinearity (Michael Plum)

Scientific Progress Made

While progress was made on all six open problems during the week, for brevity we have opted to report here on three of these.

Concerning *Open Problem 1*, an approach was proposed for computing the connecting orbits between critical points which comprise the boundary operator in Hamiltonian Floer homology. While a semiflow in this problem cannot be defined, there is a well defined notion of stable and unstable eigenvectors about a critical point. By using a variation of constants formula, a solution to the connecting orbit problem may be defined as the fixed point of an integral equation which integrates forward along the stable eigendirections, and backwards along the unstable eigendirections. This approach could be applied to extend recent work on stable manifolds in parabolic PDEs (a topic of discussion at the BIRS 14w5098 workshop) to the strongly indefinite case. Again, by integrating forward along stable directions and backwards along unstable directions, the infinite length connecting orbit problem may be formulated as a finite length boundary value problem, imposing Dirichlet boundary conditions to connect the infinite dimensional (un)stable manifolds at either ends. During the conference, the feasibility of this approach was discussed. It turns out that recently developed techniques for rigorously integrating parabolic PDEs, developed as a result of discussions at another previous BIRS workshop, namely 17w5141, are expected to provide some of the tools we need to rigorously carry out those forward and backward integrations between the manifolds.

Concerning *Open Problem 3*, in recent years rigorous numerics have been used to prove existence and uniqueness of solutions to boundary value problems in DDEs, and also to prove stability of traveling waves in non-delay PDEs with a single spatial dimension. To prove stability of traveling waves with one spatial dimension, the Evans function is a very useful tool because zeros of the Evans function correspond to eigenvalues of the linearized PDE problem. Samaey and Sandstede have recently proposed a strategy for determining stability of pulses for partial differential equations with time delays using the Evans function. During the BIRS workshop, it was proposed to combine this Evans function approach with rigorous numerics to prove stability of traveling wave solutions to PDEs with delay. Through discussions at this workshop, a group of five participants began working and made significant progress on this problem for a particular traveling wave system. By the end of the workshop, they already had the outline of a paper written up and several steps of the numerical proof completed or in progress.

Concerning *Open Problem 5*, the main challenge is to prove that the relevant derivative operator has a simple eigenvalue crossing the imaginary axes, satisfies a shifted Fredholm operator index condition, and a non-resonance condition is met. Promising ideas were put forwards by the participants for each of the three issues mentioned. First, concerning eigenvalue counting, one could attempt to obtain precise information on the eigenvalues of an approximation of the derivative operator, interpret them as approximations of the eigenvalues of the derivative operator and derive analytic bounds on the error. Second, regarding the Fredholm index condition, it was proposed to deduce the operator's Fredholm index from the adjoint operator's properties, possibly combined with using compact perturbations and the continuation property of the Fredholm index. Third, concerning the non-resonance condition, one approach is to construct rough analytic bounds on the position of the eigenvalues and rigorously verify using computer-assistance the non-resonance condition only within the finite region provided by these bounds.

Outcome of the Meeting

It was fantastic and extremely valuable to have this opportunity to focus on open problems and meet with collaborators during the Covid-19 pandemic when travel was not feasible. We made substantial progress on a number of problems that would not have otherwise been possible, as discussed above. The BIRS staff were incredibly helpful and the meeting would not have worked at all without their diligent support. What we missed in this online format, as opposed to an in person meeting, were all the side conversations and new contacts that develop naturally in a typical Banff meeting.

Participants

Akitoshi, Takayasu (University of Tsukuba)
Barker, Blake (Brigham Young University)
Beck, Margaret (Boston University)
Breden, Maxime (Ecole Polytechnique)
Church, Kevin (McGill University)
Duchesne, Gabriel William (McGill University)
Gameiro, Marcio (Rutgers University)
Hénot, Olivier (École Polytechnique)
Hetebrij, Wouter (Vrije Universiteit Amsterdam)
Jaquette, Jonathan (Boston University)
Kepley, Shane (Rutgers University)
Lessard, Jean-Philippe (McGill University)
Mireles James, Jason (Florida Atlantic University)
Mischaikow, Konstantin (Rutgers University)
Murray, Maxime (Florida Atlantic University)
Plum, Michael (Karlsruhe Institute of Technology)
Queirolo, Elena (Rutgers University)
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Chapter 6

Model Theory of Differential Equations, Algebraic Geometry, and their Applications to Modeling (20w5204)

May 31 - June 5, 2020

Organizer(s): Marisa Eisenberg (University of Michigan), Rahim Moosa (University of Waterloo), Alexey Ovchinnikov (City University of New York), Gleb Pogudin (École Polytechnique), Thomas Scanlon (University of California, Berkeley)

Context and goals of the workshop

Growing complexity of models used in the sciences makes it harder to use conventional numeric and simulation-based techniques (e.g., due to the computational complexity and curse of dimensionality) and get reliable results. One way to tackle this challenge is to empower these techniques by combining them with a *structural analysis* of the models. It is natural to expect that suitable tools for structural analysis come from the areas of Algebra and Logic. For example, *algebraic geometry* and *differential algebra* have been recently successfully applied to problems of parameter identifiability of dynamical models, multistationarity of biochemical reaction networks, and reconstruction of phylogenetic trees. Moreover, these applications gave rise to intriguing questions in differential algebra and algebraic geometry of practical importance and theoretical interest together with valuable intuition behind the approaches to these questions.

On the other hand, in the past decades, algebraic geometry and differential algebra themselves interacted a lot with *model theory*, and this interaction resulted in new impressive directions and results on both sides. In particular, model theory of differential and difference fields has been developed and used to provide insights about the Galois theory of differential and difference equations and deep structural results for differential-algebraic varieties (that is, solution sets of systems of differential equations).

Thus, there are two actively studied connections

differential algebra & algebraic geometry $\longleftrightarrow$ modeling (see [2, 5])

differential algebra & algebraic geometry $\longleftrightarrow$ model theory (see [6, 12, 3]).

Moreover, resent results on multi-experiment parameter identifiability [8, 9] combined all three areas. It turned out that the similarity between definability, a fundamental notion in model theory, and identifiability, a structural property of dynamical models, goes beyond phonetics: in an appropriate context, identifiability is a special case of definability.

The goal of the workshop was to bring together researchers working in between these areas and discuss existing and potential interactions of these areas altogether. In short: what could be a model theory of modeling?

Format of the workshop: going online

Since the scope of the workshop was broad and the mathematical background of the participants was ranging from pure logic to applied mathematics, the program included three tutorials:

1. *Model theory, quantifier elimination, and differential algebra* by D. Marker;
2. *Challenges in the study of algebraic models of biochemical reaction networks* by E. Feliu;
3. *Structural parameter identifiability with a view towards model theory* by G. Pogudin.

The official program of the workshop consisted of five three-hour slots (one slot for each day from Monday to Friday). Each slot consisted of either two tutorials or three research talks followed by "coffeebreaks". Each coffeebreak was a discussion dedicated to one of the talks or the tutorials, and it was always moderated by one of the organizers or a senior participant. The coffeebreaks in the first days usually started with the participants introducing themselves. A Slack workspace of the workshop turned out to be a great platform for following up on the talks, discussions, and exchanging the materials.

Outcomes of the meeting

Based on the discussions during the talks, coffeebreaks and in the Slack workspace, we would like to outline the following potential topics for three-way interactions between model theory, algebraic geometry/differential algebra, and modeling:

- *O-minimal structures and nonpolynomial functions.* One of the limitations of many popular algebraic methods used in modeling is the fact that they typically manipulate with polynomial functions. On the other hand, numerous nonpolynomial functions (e.g., exponential, logarithmic) appear in practice. For example, in chemical reactor design, one is often interested in considering convex hulls of trajectories of solutions of ODE systems [7]. Such convex hull while being inconvenient from the algebraic standpoint can be naturally viewed from the point of view of the theory of bounded analytic functions, its o-minimality and quantifier elimination [4].
- *Valued fields and initial conditions.* The majority of dynamical models used in sciences consist of equations of some type together with the initial conditions describing the initial state of the system. Many important properties of the model (boundedness, identifiability, controllability) may substantially depend on the values of the initial conditions. A natural way to treat the initial conditions from the algebraic point of view is using valued differential fields. Model theoretic approach has already been proved to be fruitful for these objects [1], so it is natural to conjecture that these tools can now be applied to study dynamical models with initial conditions.
- *Real algebraic geometry, ordered fields, and models over the real numbers.* Many existing algorithms for studying structural properties of dynamical models using techniques from algebraic geometry work over the field of complex numbers. This is not always realistic in the context of applications in the sciences in which most of the unknowns are real (or even nonnegative) functions. A natural approach would be to refine and extend the existing algorithms using tools from real algebraic geometry and model theory of ordered differential fields [1, 11].
- *Symmetries of models and differential Galois theory.* Some structural questions about dynamical models (such as identifiability and order reduction) can be viewed as questions about the symmetries of models. One common framework to study symmetries of differential equations is differential Galois theory, in which model theoretic techniques have been already successfully used [10]. Turning these theory into algorithms can help gain deep insights into the structure of dynamical models.

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Bibliography

[1] M. Aschenbrenner, L. van den Dries, J. van der Hoeven, *Asymptotic differential algebra and model theory of transseries*, Princeton University Press, 2017.

[2] F. Boulier and F. Lemaire, Differential Algebra and System Modeling in Cellular Biology, *International Conference on Algebraic Biology* (2008), 22-39.

[3] E. Bouscaren (editor), *Model theory and algebraic geometry*, Lecture Notes in Mathematics, Springer, Berlin, Heidelberg, 1998.

[4] J. Denef and L. van den Dries, P-adic and real subanalytic sets, *Annals of Mathematics*, **128** (1988), 79–138.

[5] A. Dickenstein, Biochemical reaction networks: an invitation for algebraic geometers, In *Mathematical Congress of the Americas*, Contemp. Math., **656**, 65-–83. American Mathematical Society, 2016.

[6] D. Marker, Model theory of differential fields, In D. Marker, M. Messmer, and A. Pillay, *Model Theory of Fields*, Lecture Notes in Logic, Cambridge University Press (2017), 38-113.

[7] D. Ming, D. Glasser, D. Hildebrandt, B. Glasser, and M. Metzger, *Attainable region theory: an introduction to choosing an optimal reactor*, Wiley, 2016.

[8] A. Ovchinnikov, A. Pillay, G. Pogudin, T. Scanlon, Computing all identifiable functions for ODE models, arXiv:2004.07774, 2020.

[9] A. Ovchinnikov, A. Pillay, G. Pogudin, T. Scanlon, Multi-experiment parameter identifiability of ODEs and model theory, arXiv:2011.10868, 2020.

[10] A. Pillay, Differential Galois theory I, *Illinois Journal of Mathematics*, **42:4** (1998), 678–699.

[11] M. Singer, The model theory of ordered differential fields, *The Journal of Symbolic Logic*, **43:1** (1978), 82–91.

[12] T. Scanlon, Model theory and differential algebra, *Differential Algebra and Related Topics*, World Scientific (2002), 125-150.

Chapter 7

Interactions of gauge theory with contact and symplectic topology in dimensions 3 and 4 (20w5088)

June 7 - 12, 2020

Organizer(s): John Baldwin (Boston College), Hans U. Boden (McMaster University), John Etnyre (Georgia Institute of Technology), Liam Watson (University of British Columbia)

Introduction

This workshop is the sixth in a series of BIRS "Interactions" workshops, with earlier meetings having taken place in 2007, 2009, 2011, 2013, and 2016. The talks covered recent results in gauge theory, contact and symplectic geometry, and low-dimensional topology. Each of these subjects is an active area of current research and interactions between them have led to breakthroughs on many long standing problems. The schedule included time for group work with break-out rooms after the talks. This encouraged lively discussion and allowed for a rich exchange of ideas.

As result of the pandemic, the meeting was conducted in an online format. While some were disappointed they were not able to travel and visit the Banff area, the new format had the benefit of allowing for the inclusion of many more mathematicians. Indeed, the sheer number of confirmed participants (155 people!) is evidence of the popularity of this meeting.

Apart from not meeting in person, one other notable difference was that we hosted fewer talks. This was a deliberate, and it was done in recognition of the challenges of parenting in the face of stay-at-home orders, as well as the difficulty of finding suitable times for such a large number of participants distributed over so many different time zones. As a result, the workshop featured an average of only two talks per day. In recognition of the #ShutDownAcademia #ShutDownSTEM #Strike4BlackLives movement, we did not schedule any talks on June 10.

In our survey of participants, we asked them "What are the main takeaways from the virtual delivery format? What worked, what didn't?"

According to the replies, the main advantage was that many more people could attend, and BIRS may choose to continue making the meetings open via Zoom even after BIRS resumes in person meetings. The main disadvantage was that it is more difficult to engage in a dialogue with the speaker or with other participants in the virtual format. As one of the respondents wrote, "The main disadvantage is that a virtual meeting lacks the 'electricity' (or 'energy' or 'vitality') of an in-person gathering

Brief overview of subject area

Over the last several decades it has become clear that the topology of manifolds in dimensions 3 and 4 is subtly and beautifully intertwined with various flavors of geometry (hyperbolic, symplectic and contact), as well as with ideas from physics, such as gauge theories and topological quantum field theories. Collaborations among people working in these diverse areas have exploded over the last ten years, resulting in the remarkable solutions to long-standing conjectures in topology as well as the birth of entire new sub-fields and perspectives. Some of the more spectacular recent results include the solution to the triangulation conjecture for higher dimensional manifolds, the proof that Khovanov homology detects the unknot, characterizations of fibered knots in terms of Floer homologies, etc.

Critical to these developments has been the information provided by a vast array of new invariants whose definitions were motivated by gauge theory and topological quantum field theory. These invariants – Donaldson-Floer, Seiberg-Witten, Ozsváth-Szabó, Khovanov homology, Embedded Contact Homology to name a few – have intriguing relations among them, and a better understanding has led to significant progress on key problems in geometric topology, contact and symplectic geometry, and mathematical physics. An even more promising direction is the interplay between these invariants and more constructive approaches to low-dimensional manifolds – open book decompositions of contact 3-manifolds, symplectic fillings, Lefschetz fibrations, surgery constructions among many others. This interaction between powerful invariants and constructive methods is now more than ever a major driving force in the subject.

Highlights from the Workshop

The workshop featured ten talks on recent results in gauge theory, contact and symplectic topology, including:

- the Atiyah-Floer conjecture,
- unification of various Floer-theoretic invariants,
- spectral sequences relating Floer and Khovanov homologies,
- bordered and sutured versions of Floer-type invariants, and
- adjunction inequalities and applications.

In particular, the talks on the Atiyah-Floer conjecture (Daemi) and on the rectangular peg problem (Greene) were striking for the fresh ideas that were brought to bear and the many related open questions. Lambert-Cole's talk was also an impressive for his proof of the adjunction inequalities using topological/symplectic techniques instead of gauge theory.

Featured Talks

Below is a detailed list of speakers, titles, and brief descriptions of their talks.

1. **Matt Hedden** (Michigan State) *Relative adjunction inequalities and their applications*
   This talk discussed joint work [HR1, HR2] with Katherine Raoux on proving relative adjunction inequalities and applying them to define concordance invariants of links in a general setting, and to prove new results about contact structures, to motivate a 4-dimensional interpretation of tightness, and to show that knots with simple Floer homology in lens spaces (or L-spaces) minimize rational slice genus.

2. **Robert Lipshitz** (Oregon) *Khovanov homology detects split links*
   This talk discussed joint work [LS] with Sucharit Sarkar giving a proof, in terms of the Ozsváth-Szabó and Kronheimer-Mrowka spectral sequences, that the module structure on Khovanov homology detects split links.

3. **Vera Vertesi** (Vienna) *Bordered contact invariants*
   This talk discussed using foliated open books to extend the definition of the contact invariant for bordered Floer homology and applications to questions in low-dimensional topology.

4. **Peter Lambert-Cole** (Georgia Tech) *Symplectic trisections and the adjunction inequality*
   This talk discussed trisections for symplectic 4-manifolds with applications including a new proof of the adjunction inequality as well as new results on the minimal genus problem [LC1, LC2]

5. **Kristen Hendricks** (Rutgers) *Rank inequalities for the Heegaard Floer homology of branched covers*
   This talk discussed joint work [HLL] with T. Lidman and R. Lipshitz giving a proof that, for any nullhomologous knot K in a 3-manifold Y, there is a spectral sequence relating the Heegaard Floer homologies of Y with its 2-fold cover branched along K, along with a rank inequality for $\widehat{HF}$.

6. **Joshua Greene** (Boston College) *The rectangular peg problem*
   This talk discussed joint work [GL1, GL2] with Andrew Lobb giving a solution of the rectangular peg problem. This asserts that for every smooth Jordan curve and rectangle in the Euclidean plane, one can place four points on the curve at the vertices of a rectangle similar to the one given. The proof utilizes techniques of symplectic geometry in a surprising way.

7. **Aliakbar Daemi** (Washington University in St. Louis) *Lagrangians, $SO(3)$-instantons and the Atiyah-Floer Conjecture*
   This talk discussed joint work with Kenji Fukaya and Maksim Lipyanskyi on a variant of the Atiyah-Floer conjecture relating the framed Floer homology (as defined by Kronheimer and Mrowka) to symplectic framed Floer homology (as defined by Wehrheim and Woodward).

8. **Jonathan Hanselman** (Princeton) *Knot Floer homology as immersed curves*
   This talk discussed a new approach to understanding knot Floer homology via decorated immersed curves in the torus, along with applications to problems in Dehn surgery such as the cosmetic surgery conjecture.

9. **Juanita Pinzon-Caicedo** (Notre Dame) *Instanton and Heegaard Floer homologies of surgeries on torus knots*
   This talk discussed joint work with Tye Lidman and Christopher Scaduto relating the instanton and Heegaard Floer homologies of 3-manifolds obtained by Dehn surgery on torus knots.

10. **Artem Kotelskiy** (Indiana) *The earring correspondence on the pillowcase*
    This talk discussed joint work [CHKK] with G. Cazassus, C. Herald and P. Kirk on Lagrangian correspondences in pillowcase homology induced by the earring tangle.

Scientific Progress Made

The workshop created a virtual community with a nice mix of graduate students, early career researchers, and more senior members. The talks included many exciting new developments in the field. One purpose of the interactions workshops is to help develop new collaborative relationships as well as to support longer-term collaborative projects. Another goal was to encourage early career mathematicians.

One of the questions in our survey was "How well did it (the meeting) encourage early-career mathematicians?" One younger mathematician wrote in response that he "found the conference encouraging and the mathematics exciting." Another wrote "I benefitted from talking to other participants in the discussion sessions after the talks, where interesting questions and ideas were communicated." A mid-career participant replied that "the main value for me was getting to meet some of the young people in the field who I might otherwise have seen at a conference, and getting more feedback on my work from young and senior people." Another replied that "A good number of the talks were by early-career mathematicians, which was good."

These are tall orders for an online workshop. This is one of the distinct advantages of holding in-person workshop in Banff. We tried to find an alternative way to encourage collaborative research, and we decided to propose a conference proceedings for the first time in the series of "Interactions" workshops. These efforts are currently underway, but many participants have expressed an interest in contributing their work, and we have secured a commitment from Geometry and Topology Monographs to publish the volume. We are currently soliciting research and expository articles, which will be reviewed for inclusion and eventual publication in the forthcoming "Interactions" volume.

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Bibliography

[AFHLPV] Akram Alishahi, Viktória Földvári, Kristen Hendricks, Joan Licata, Ina Petkova, and Vera Vértesi, *Bordered Floer homology and contact structures*, **arXiv:2011.08672**.

[CHKK] Guillem Cazassus, Christopher M. Herald, Paul Kirk, and Artem Kotelskiy, *The correspondence induced on the pillowcase by the earring tangle*, **arXiv:2010.04320**.

[DK] Aliakbar Daemi and Kenji Fukaya, *Atiyah-Floer conjecture: a formulation, a strategy to prove and generalizations*, **arXiv:1707.03924.**

[GL1] Joshua Greene and Andrew Lobb, *The rectangular peg problem*, **arXiv:2005.09193**.

[GL2] Joshua Greene and Andrew Lobb, *Cyclic quadrilaterals and smooth Jordan curves*, **arXiv:2011.05216**.

[H] Jonathan Hanselman, *Heegaard Floer homology and cosmetic surgeries in S^3*, **arXiv:1906.06773**.

[HRW] Jonathan Hanselman, Jake Rasmussen, and Liam Watson, *Heegaard Floer homology for manifolds with torus boundary: properties and examples*, **arXiv:1810.10355**.

[HW] Jonathan Hanselman and Liam Watson, *Cabling in terms of immersed curves*, **arXiv:1906.06773**.

[HR1] Matthew Hedden and Katherine Raoux, *Knot Floer homology and relative adjunction inequalities*, **arXiv:2009.05462**.

[HR2] Matthew Hedden and Katherine Raoux, *4-dimensional aspects of tight contact 3-manifolds*, **arXiv:2010.13162**.

[HLL] Kristen Hendricks, Tye Lidman, and Robert Lipshitz *Rank inequalities for the Heegaard Floer homology of branched covers*, **arXiv:2007.03023.**

[LC1] Peter Lambert-Cole, *Lecture notes on trisections and cohomology*, **arXiv:2009.11263.**

[LC2] Peter Lambert-Cole, *Symplectic trisections and the adjunction inequality*, **arXiv:2009.06028.**

[LV] Joan E. Licata and Vera Vertesi, *Foliated Open Books*, **arXiv:2002.01752.**

[LPS] Tye Lidman, Juanita Pinzon-Caicedo, and Christopher Scaduto, *Framed instanton homology of surgeries on L-space knots*, **arXiv:2003.03329**.

[LPZ] Tye Lidman, Juanita Pinzon-Caicedo, and Raphael Zentner, *Toroidal homology spheres and SU(2)-representations*, **arXiv:2101.02621**.

[LS] Robert Lipshitz and Sucharit Sarkar, *Khovanov homology also detects split links*, **arXiv:1910.04246.**

Chapter 8

Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types (20w5197)

June 14 - 19, 2020.

Organizer(s): Aedin Culhane (Harvard TH Chan School of Public Health), Elana Fertig (Johns Hopkins University), Kim-Anh LeCao (University of Melbourne)

Community-wide hackathons establish foundations for emerging single cell data integration

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Abstract

Multi-omics hackathon studies illustrate standards and computational challenges in cell biology

Single-cell multimodal omics has claimed the title of method of the year only six years after single-cell sequencing [1], demonstrating the rapid pace of technological development in biology. Multi-omics technologies provide a unique opportunity to characterize cellular systems at both the spatial and molecular level. While each high-throughput measurement technology can resolve specific biological scales, complementary data integration techniques can reveal multi-scale interactions between modalities. While advances in multi-omics have coincided with the formation of tremendous new data resources and atlas-based initiatives to characterize biological systems, computational techniques and benchmarking strategies to integrate these datasets remains an active area of research.

To determine the optimal methods and new developments required to analyze multi-modal data effectively, we selected hackathon studies focused on data integration for the Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Workshop. The first challenge included spatial molecular profiling. While this technology is rapidly emerging, it often provides lower molecular resolution than its non-spatial counterparts. Integration strategies that merge spatial and omics datasets have the promise to enhance the molecular resolution of spatially resolved profiling. Thus, we designed a hackathon using spatially resolved transcriptional data from seqFISH with corresponding non-spatial single-cell profiling data from the mouse visual cortex [2]. The second challenge dealt with the limited availability of tissue to obtain multiple measurements in samples from identical conditions, raising the question as to whether information can be transferred from datasets between distinct sample cohorts. Therefore, we designed the second hackathon to contain two triple-negative breast cancer cohorts profiled with single-cell proteomics profiling from mass cytometry (CyTOF) [4] and spatial in-situ proteomics from Multiplexed Ion Beam Imaging (MIBI) [5]. In contrast to the previous challenges, the third challenge presented data at different molecular scales but from the same cells to investigate how genetic and epigenetic alterations to DNA drive the transcriptional regulation underlying cellular state transitions. Our third hackathon was designed with scNMT-seq data to obtain concurrent DNA methylation, chromatin accessibility, and RNA expression from the same cells to delineate the regulatory networks that underlie mouse gastrulation [6].

Altogether, the analysis approaches employed to address these hackathons provide a unique opportunity to identify technology-specific challenges and unifying themes across disparate biological contexts, which are essential to effectively leverage multi-omics datasets for new biological knowledge. This article presents the study-specific and common challenges faced during this workshop. We provide guidelines and articulate the needs of technologies, data, tools, and computational methods to model the multi-scale regulatory processes of biological systems.

scRNA-seq + seqFISH as a case study for spatial transcriptomics

Overview and biological question

The first hackathon aimed to leverage the complementary strengths of sequencing and imaging-based single-cell transcriptomic profiling by using computational techniques to integrate scRNA-seq and seqFISH data in the mouse visual cortex. While single cells are considered the smallest units and building blocks of each tissue, they still require proper spatial and structural three-dimensional organization in order to assemble into a functional tissue that can exert its physiological function. In the last decade, single-cell RNA-seq (scRNA-seq) has played a key role in capturing single-cell gene expression profiles, allowing us to map different cell types and states in whole organisms. Despite this remarkable achievement, this technology is based on cellular dissociation and hence does not maintain spatial relationships between single cells. Emerging technologies can now profile the transcriptome of single cells within their original environment, offering the possibility to examine how gene expression is influenced by cell-to-cell interactions and how it is spatially organized. One such approach is sequential single-molecule fluorescence in situ hybridization (seqFISH [7]), which can identify single molecules at (sub)cellular resolution with high sensitivity.

In contrast with scRNA-seq, seqFISH and many other spatial transcriptomic technologies often pose significant technological challenges, resulting in a small number of profiled genes per cell (10-100s). The newer generation of seqFISH technology (called seqFISH+ [9]) has dramatically enhanced its capacity to profile up to 10,000 genes, but this technology is more complex and costly than seqFISH.

New computational approaches are needed to integrate scRNA-seq and seqFISH data effectively. This first hackathon provided seqFISH and scRNA-seq data corresponding to the mouse visual cortex ([3], [2]) and our participants were challenged to accurately identify cell types. The scRNA-seq data included transcriptional profiles at a high molecular resolution whereas the seqFISH data provided spatial characterization at a lower molecular resolution. Two key computational challenges were identified to enable high-resolution spatial molecular resolution. First, we explored several strategies to identify the most likely cell types in the seqFISH dataset based on information obtained from the scRNA-seq dataset. Second, we sought to transfer spatial information obtained from the seqFISH dataset to that of the scRNA-seq dataset. Cell type labels were derived from scRNA-seq analysis [2] and previous seqFISH/scRNA-seq integration [3] were also provided as reference. Data were preprocessed by the organizers and consisted in 113 matching genes between the scRNA-seq dataset and the seqFISH dataset, with 1723 cells for the scRNA-seq data and 1597 cells for the seqFISH data.

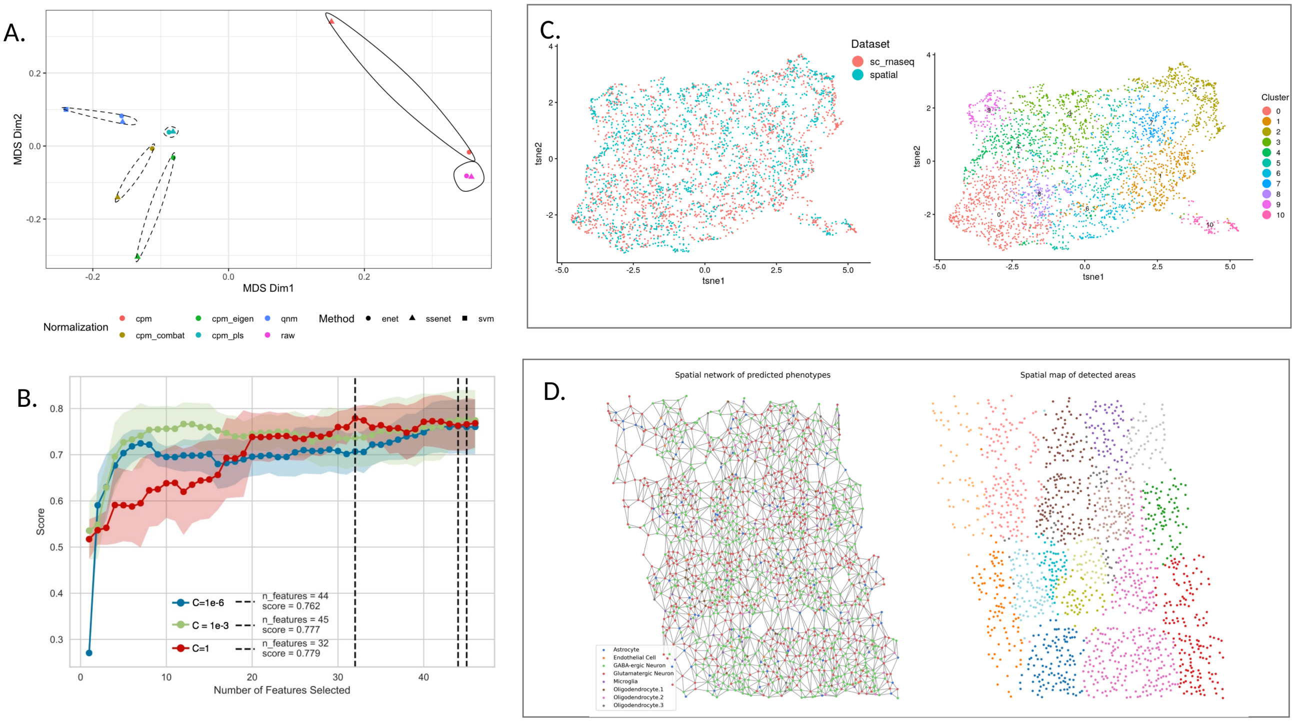


Figure 1:

Caption Figure: **Overview of seqFISH and scRNA-seq integration analysis**. **A.** Assessment of cell type prediction using different data normalizations and classifiers. Normalization strategies included none (raw), counts per million (cpm), ComBat batch correction applied to cpm (cpm_combat), scRNA-seq and seqFISH scaled using the first eigenvalue (cpm_eigen), latent variables retained for both datasets after applying Partial Least Squares regression to cpm_eigen normalized data (cpm_pls). Classifiers approaches included a supervised multinomial classifier with elastic net penalty (enet), a semi-supervised multinomial classifier with elastic net penalty (ssenet) and Support Vector Machine (SVM, supervised). Each classifier was trained using the scRNA-seq data and the known (provided) cell type labels, then predicted the cell type labels in the seqFISH data; for the SVM predictions from the original study were used (Challenge 1). Gower distance between each method-normalization pair is depicted on a multidimensional scaling plot. The first dimension (x-axis) separates methods that normalize the scRNA-seq and seqFISH data together (dashed) and separately (solid), showing that normalization had a stronger impact on cell type predictions than the classification method used. **B.** SVM classification models with different C parameters were trained with different number of genes in scRNA-seq data using Recursive Feature Elimination (RFE) to evaluate the minimal number of genes required for data integration. The results show that a smaller gene list than what the original study proposed was sufficeint to identify cell types in both data types (Challenge 1). **C.** LIGER was applied to combine spatial and single cell transcriptomic datasets. From the separate and integrative analyses, plots of identified and known clusters were generated and metrics of integration performance were compared, showing some loss of information as a result of the integration (Challenge 1). **D.** Construction of a spatial network from cells' positions using Voronoi tessellation, where cell types were inferred from SVM trained on scRNA-seq data. Left: A neighbors aggregation method computes aggregation statistics on the seqFISH gene expression data for each node and its first order neighbors (Challenge 2). Right: Identification of spatially coherent areas that can contain one or several cell types and can be used to detect genes whose expression is modulated by spatial factors rather than cell type.

Computational challenges

Challenge 1: overlay of scRNA-seq onto seqFISH for resolution enhancement

The mouse visual cortex consists of multiple complex cell types. However, the seqFISH dataset was limited to 125 profiled genes, which were not prioritized based on their ability to discriminate between cell types. Assigning the correct cell identity presents an important challenge. In contrast, the scRNA-seq dataset is transcriptome-wide and includes the 125 genes profiled by seqFISH. This challenge proposed to use all genes to identify the cell type labels for each cell in the scRNA-seq data with high certainty. Next, we leveraged the cell type information to build a classifier based on a subset of the 125 genes shared between both datasets. The classifier was then applied to the seqFISH dataset to assign cell types.

During the hackathon, participants aimed to test various machine learning and data integration models (see Vignettes). Preliminary analyses highlighted that normalization strategies had a significant impact on the final results (Figure 1A). In addition, although unique molecular identifier (UMI) based scRNA-seq and seqFISH can both be considered as count data, we observed dataset specific biases that could be attributed to either platform (imaging vs. sequencing batch effects) or sample specific sources of variation. We opted to apply a quantile normalization approach that forces a similar expression distribution for each shared gene.

Two classification approaches were considered: supervised and semi-supervised generalized linear model regularized with elastic net penalty (enet and ssenet) and supervised support vector machines (SVM). The ssenet approach builds a model iteratively: it combines both datasets and initially only retains the highest confidence labels, then gradually adds more cell type labels until all cells are classified (Figure 1A). This type of self-training approach might be promising to generalize information to other datasets. To improve the SVM model, several combinations of kernels and optimal hyperparameters were assessed using a combination of randomized and zoomed search. In addition, different flavors of gene selection using recursive feature elimination were considered to identify the optimal or minimal number of genes needed to correctly classify the majority of the cells (Figure 1A). Finally, different classification accuracy metrics were considered to alleviate the major class imbalance in the dataset. More than 90% of cells were excitatory or inhibitory neurons, using balanced classification error rates. We applied LIGER, an approach based on integrative non-negative matrix factorization (NMF) to integrate both datasets in a subspace based on shared factors. This enabled the transfer of cell type labels using a nearest neighbor approach (Figure 1D).

Challenge 2: Identifying spatial expression patterns at the tissue level through the integration of gene expression and spatial cellular coordinates

While most tools originally developed for scRNA-seq data can be adapted for spatial transcriptomic datasets (see common challenges section), methods to extract sources of variation from spatial factors are still lacking. Novel methods that can integrate the information obtained from gene expression with that of the spatial coordinates from each cell or transcript (for sub-cellular resolution) within a tissue of interest are needed.

To identify spatial expression patterns in the seqFISH dataset, the participants first formed a spatial network based on Voronoi tessellation ([10]). The gene expression of each cell was spatially smoothed by calculating the average gene expression of all neighboring cells. UMAP was applied to the smoothed and aggregated data matrix to identify cell clusters with a density-based clustering approach (Figure 1D). Interestingly, these results showed that the obtained clusters themselves are spatially separated and do not necessarily overlap with specific cell types, suggesting that the spatial dimension cannot be captured from the expression data only.

An unanswered question is whether the identified combinatorial spatial patterns can be extracted directly from scRNA-seq data, as previous studies have shown cellular mapping between gene expression profiles and known spatial locations [11,12]. However, this still constitutes both a technological and analytical challenge that will require careful benchmarking in the near future (see benchmarking section).

Spatial proteomics as a case for cross-study and cross-platform analysis

Overview and biological question

Whereas the first hackathon with seqFISH and scRNA-seq data included samples from the same biological conditions, our second hackathon challenged participants to analyze two datasets obtained from different single cell targeted proteomics (antibody-based) technologies, applied to breast cancer tissue of different patient cohorts, from different laboratories. Both studies examined the tumor-immune microenvironment in primary breast cancer: Wagner, et al. used Mass Cytometry (CyTOF) to assay 73 proteins across two panels (tumor and immune) in 194 tissue samples from 143 subjects, of which 6 patients had triple-negative negative breast cancer [4], while Keren, et al. applied Multiplexed Ion Beam Imaging (MIBI) to quantify spatial in-situ expression of 36 proteins in 41 triple-negative breast cancer patients [5] (Figure 2A).

This hackathon focused on integrative data analysis across studies and platforms, given limited overlap in features (Section @ref{sec:common}). Three main challenges emerged. The first challenge was whether analytical methods could integrate partially-overlapping proteomic data collected on different patients with similar phenotypes, and whether measurements from one technology (MIBI spatial location and expression of proteins) could be transferred and used to predict information in the second technology (e.g., spatial expression patterns of proteins measured on CyTOF). The second challenge pertained to the added value of spatial technologies and whether integrated analyses of spatial single cell data could uncover additional information about immune cell populations in breast cancer beyond cell composition. The third challenge was whether data from patients with heterogeneous phenotypes could still be integrated, given few common features and no overlap in biological samples.

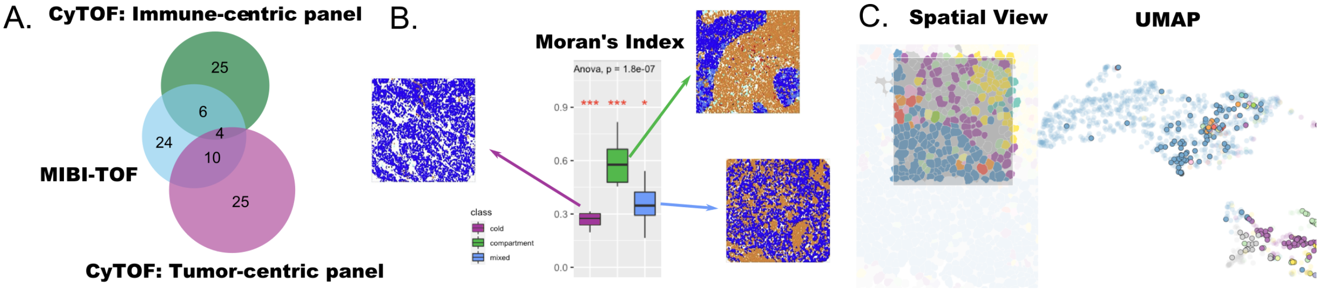


Figure 2:

Caption figure: **A** The datasets selected for this hackathon had limited overlap in features (MIBI-TOF, CyTOF immune-centric panel, and CyTOF tumor-centric panel; illustrating **Challenge 1**) **B** Spatial analysis with Moran's index computed on Gabriel graph shown in boxplot according to tumor/immune status showing a significant difference between groups (Red asterisks indicate significance of an ANOVA of each group with all others with p-value from an overall ANOVA across the three groups reported; exploring **Challenge 2**). **C** Cells can be studied through either spatial or gene expression relationships, and correspondences between both representations can be highlighted through linked brushing, an interactive visualization technique (exploring **Challenge 2**).

Computational challenges

Challenge 1: Limited overlap between protein features across studies

There were only 20 proteins that were assayed in both the CyTOF [4] and MIBI-TOF [5] studies (Figure 2A), which precluded integration of features at the level of gene set or pathways and required the use of surrogate measures for cross-study association. The majority of proteins were cell-type markers or biomarkers targets of breast cancer therapeutic intervention, providing the opportunity to perform cross-study integration of cell type proportions in tumor tissue samples.

Several semi-supervised and supervised algorithms were applied to transfer cell labels and cell compositions from one dataset to the second (see Vignettes). Random forest was considered to capture the hierarchical structure of cell lineage and perform feature transfer learning of cell type labels, using an adaptation of the prediction strength approach [13] to assess model robustness: first, a model was trained on the labeled dataset, then used to predict labels in the unlabeled dataset; next, a second model was trained based on the second dataset with the newly predicted labels; finally, the ability of the second model to recover the correct original labels when making predictions on the labeled dataset was assessed. Mapping cells from CyTOF to imaging with spatial information was handled by solving an entropic regularization optimal transport problem [14] [15], using the cosine distance of the common proteins between the two datasets as transport cost. The constructed optimal transport plan can be considered as likelihood of cells from one modality mapped to cells from the other modality, which allows the prediction of protein expression measured only in CyTOF on imaging data. After cluster analysis of the resulting imputed expression matrix, sub tumour cell type could be identified that was not revealed in the original matrix.

Another issue encountered with this challenge was that the different scales of protein expression across technologies meant that cell compositions could not be integrated using correlation of the expression of protein markers, as some cell markers were expected on a range of cell types (e.g. CD45), while others were more specialized and appeared in only a subset of those cells (e.g. CD4). Other challenges associated with cell composition analysis of proteomics data included uncertainty about antibody specificity and consistency between studies; specific sensitivity and specificity of protein markers for cell types and tissues; and disease heterogeneity. Cell type assignment was also a significant challenge, as it relied on manually curated protein annotation, and was therefore dependent on domain-specific knowledge (e.g. CD4 is expressed by T-cells). To date, methods for cell type assignment, classification or extraction of differentially expressed proteins cannot easily be applied to targeted proteomics. There is thus an urgent need for a unifying map between cells present in different datasets, and for annotation resources to provide quality metric or priors of protein cell type markers. The construction of protein expression atlases would support cell type classification, even if antibodies used and their performances might vary between labs.

Challenge 2: spatial analysis of protein expression

CyTOF mass spectrometry data provided protein expression and counts/composition of cells in breast tumor-immune environment, while the MIBI-TOF data provided spatial information that quantified cell attributes (shape, size, spatial coordinates) in addition to expression levels. These two data sets thus provide the opportunity to examine protein expression, cell microenvironment, and predict cell-cell interactions and the cellular community ecosystem.

Spatial information can be encoded as a set of XY coordinates (cell centroid), a line (e.g. tumor-immune boundary), or a polygon, which is a closed plane defined by a number of lines and can define complex shapes such as a cell or a community of cells. Spatial protein expression can be summarized using spatial descriptive statistics, such as the autocorrelation of the expression of a protein within a neighborhood of polygons, using techniques developed in geographical information science or ecology to assess whether a spatially measured variable has a random, dispersed or clustered pattern [16].

We investigated whether expression data could be used to predict spatial properties of tissue samples using a variety of approaches (see Vignettes). A K-nearest neighbor graph was used to build spatial response variables and random forest model trained from expression data to predict spatial features. A topic model was trained on protein expression of CyTOF and MIBI-TOF data to predict cell co-locations of CyTOF immune cells where 10% of MIBI-TOF considered test data. Among the five topics identified, the first topic was dominated in most of the immune cells from CyTOF data and the other four dominated in all other cells. Prognostic performance of different higher level spatial metrics was also examined using Moran’s Index with a sphere distance, cell type localisation using nearest neighbour correlation, or cell type interaction composition with Ripley’s L-function. Cox models with fused lasso penalty and random forest survival models were then fitted based on clinical features such as tumor stage, tumor grade, age and tumor size, as well as cell type composition. The spatial metrics were found to be predictive, especially in triple negative breast cancer where clinical features such as grade are often poor prognostics. Further investigation of Moran’s Index using a graph-based neighborhood measure (Gabriel graph, based on Delaunay triangulation; as opposed to sphere distance) found the values of this metric differed significantly between the three prognostic tumor scores described by [5](Figure 2B). This challenge demonstrated the prognostic potential of spatial single cell proteomics data and underscores the need to develop new spatial measures specifically for these data.

Challenge 3: Fourth corner Integration of data at the level of phenotype

Cross-study integration also raises the challenge of non-overlapping biological samples but with similar phenotypes. Here the aim was to identify biomarkers from the different data types to predict phenotype, and, more importantly, to explore concordance among markers selected across multiple studies and datasets. Depending upon how well these markers can be transferred across datasets, as well as the amount of distinctive information encoded by different markers, integrating datasets with only some overlap in markers could potentially provide more biological insight than from individual ‘omics studies. To consider this third challenge, phenotypic data (such as the cell attributes) were the critical factors that should be used to link the two datasets (Figure 4D).

Integrating patient phenotype measures such as grade, stage and overall survival is one first step that we were able to achieve. However, integrating proteins from data sets that used different approaches to cell type annotation and had limited proteins in common was extremely challenging. Borrowing from ecology and the French school of ordination, this problem can be described as a case of the fourth corner problem (or RLQ, Figure 4D). Briefly, given two ’omics data where both features and samples are non overlapping, and phenotypical data are available for each omics data, multiplying the two phenotypical factors should derive a bridging matrix that links the features of two omics data. This requires the two phenotypical matrices to be multiplicable, i.e. describing the same phenotypical factors. The fourth corner RLQ can be solved using matrix decomposition [17; doi:10.1111/ecog.02302]. However, this approach was not attempted in this hackathon.

scNMT-seq as a case-study for epigenetic regulation

Overview and biological question

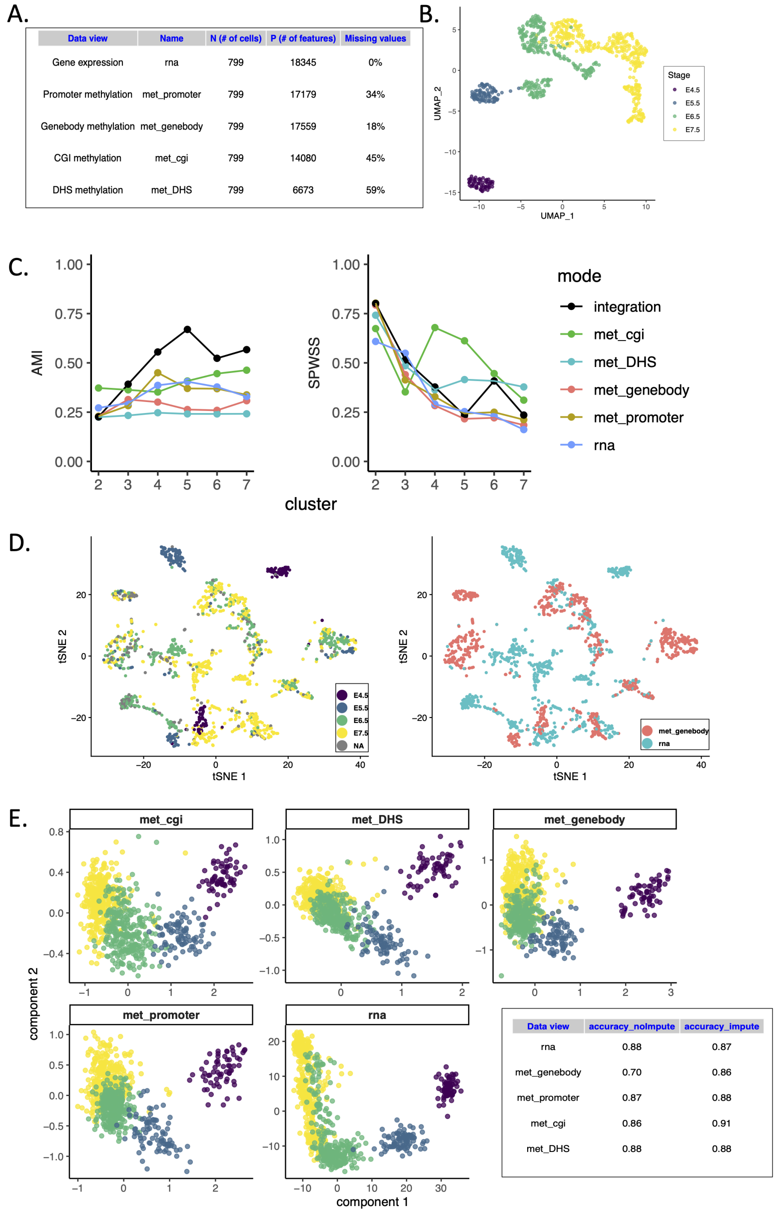
scRNA-seq technologies have enabled the identification of transcriptional profiles associated with lineage diversification and cell fate commitment [18], but the role of epigenetic layers still remains poorly understood [19]. In contrast to the first two hackathons, which leveraged datasets from complementary technologies to enable high molecular and spatial resolution of biological systems, the third hackathon used datasets spanning disparate molecular scales (e.g. DNA and RNA measurements) to improve our understanding of cell fate decisions using scNMT-seq.

scNMT-seq is one of the first experimental protocols that enable simultaneous quantification of RNA expression and epigenetic information from individual cells [20]. Briefly, cells are incubated with a GpC methyltransferase enzyme that labels accessible GpC sites via DNA methylation. Thus, GpC methylation marks can be interpreted as direct read-outs for chromatin accessibility, whereas CpG methylation marks can be interpreted as endogenous DNA methylation. By physically separating the genomic DNA from the mRNA, scNMT-seq can profile RNA expression, DNA methylation and chromatin accessibility read-outs from the same cell. This third hackathon focused on data integration strategies to detect global covariation between RNA expression and DNA methylation variation from scNMT-seq data in a mouse gastrulation study [21].

Gastrulation is a major lineage specification event in mammalian embryos that is accompanied by profound transcriptional rewiring and epigenetic remodeling [6]. In this study, four developmental stages were profiled, spanning exit from pluripotency to germ layer commitment (E4.5 to E7.5). For simplicity in this hackathon, we focused on the integration of RNA expression and DNA methylation, quantified over the following genomic contexts: gene bodies, promoters, CpG islands, and DHS open sites. A total of 799 cells passed quality control (Figure 3A). Preliminary analyses using dimensionality reduction methods confirmed that all four embryonic stages could be separated on the basis of RNA expression (Figure 3B). The main challenge was to leverage the multi-faceted nature of measurements to better resolve the single-cell subpopulations from distinct embyonic stages.

Computational challenges

Our participants considered 3 computational strategies (see Vignettes): MOSAIC (Multi-Omics Supervised Integrative Clustering algorithm inspired by `survClust` [22]) classifies samples by creating weighted distance matrices across data modalities, where the weights are defined as the maximum of the ratio of cluster specifc vs. population log likelihoods (Figure 3C). LIGER is an unsupervised non-negative matrix factorization model for manifold alignment that assumes a common feature space by aggregating DNA methylation over gene-centric elements (promoters or gene bodies) but allows cells to vary between data modalities [12] (Figure 3D). Multi-block sparse Projection to Latent Structures (multiblock sPLS), is a sparse generalization of canonical correlation analysis that maximizes paired covariances between the RNA data set and each of the other genomic context data sets [23] [24] (Figure 3E).



Data view	Name	N (# of cells)	P (# of features)	Missing values
Gene expression	rna	799	18345	0%
Promoter methylation	met_promoter	799	17179	34%
Genebody methylation	met_genebody	799	17559	18%
CGI methylation	met_cgi	799	14080	45%
DHS methylation	met_DHS	799	6673	59%

Data view	accuracy_noImpute	accuracy_impute
rna	0.88	0.87
met_genebody	0.70	0.86
met_promoter	0.87	0.88
met_cgi	0.86	0.91
met_DHS	0.88	0.88

Figure 3:

Caption Figure: **Overview of hackathon analyses for the scNMT-seq challenge. A** Summary of the data modalities analyzed, including different putative regulatory regions. **B** UMAP of RNA measurements using 671 highly variable genes shows separation of the four embryonic stages. **C** Supervised analysis using view-specific and integrative distance measures with MOSAIC: The integration identifies five clusters of cell populations based on Adjusted Mutual Information and Standardized Pooled Within Sum of Squares that outperforms individual (single omics) analyses. **D** LIGER joint alignment using gene body methylation and RNA expression: cells are colored by stage (left) or original data modality (right). **E** Unsupervised integration using multiblock sPLS: cells are projected into the space spanned by each data view components that are maximally correlated. For performance assessment, two types of analyses were considered, either by omitting the missing DNA methylation values or incorporating imputed values. K-means clustering analysis based on the multiblock sPLS components was used to calculate balanced accuracy measures.

Challenge 1: defining genomic features

The first challenge presented in this hackathon concerns the definition of the input data. The output of single-cell bisulfite sequencing are binary DNA methylation measurements for individual CpG sites. Integrative analysis at the CpG level is extremely challenging due to the sparsity levels, the binary nature of the read-outs, and the intricacy in interpretation of individual dinucleotides. To address these problems, DNA methylation measurements are typically aggregated over pre-defined sets of genomic elements (i.e. promoters, enhancers, etc.). This preprocessing step reduces sparsity, permits the calculation of binomial rates that are approximately continuous and can also improve interpretability of the model output.

We observed remarkable differences between genomic contexts on the integration performance. In MOSAIC, stages are better separated when using DNA methylation measurements on promoter regions and at least four clusters (AMI=0.45). Interestingly, this setting performed better than using RNA expression alone (AMI=0.40). Notably, when using an integrated solution across data modalities, stages were better classified (AMI = 0.68) (Figure 3C). LIGER, that was also applied in the first hackathon requires a common feature space to perform alignment of cells when profiled for different data modalities. This hackathon provides unambiguous cell matching between the data modalities and thus represents a gold standard for testing this approach. LIGER was applied to gene expression and gene body methylation: the poor alignment suggested a complex coupling of gene expression and gene body methylation during gastrulation (Figure 3D). Finally, multiblock sPLS identified covarying components between RNA expression and DNA methylation that separated cell stages in all putative regulatory contexts considered (Figure 3E). Taken altogether, these results confirmed that the appropriate selection of the feature space is critical for a successful integration with RNA expression.

Challenge 2: Missing values in DNA methylation

Single-cell bisulfite sequencing protocols are limited by incomplete CpG coverage because of the low amounts of starting material. Nonetheless, in contrast to scRNA-seq, missing data can be distinguished from dropouts. Integrative methods can be divided into approaches that can handle missing values (e.g. MOSAIC, multiblock sPLS which omit the missing values during inference), or approaches that require *a priori* imputation (e.g. LIGER). In this hackathon, missing values were imputed using nearest neighbor averaging (as implemented in the `impute` package [25]) in the methylation data.

We compared the integration performance of multiblock sPLS either with original or with imputed data. The missing values were inferred using nearest neighbor averaging (as implemented in the `impute` package [25]) in the methylation data. The components associated to each data set showed varying degree of separation of the embryonic stages, depending on the genomic contexts (Figure 3E). Accuracy measures based on k-means clustering analysis on the multiblock sPLS components showed that gene body methylation components were better at characterizing embryonic stage after imputation (from 70% with original data to 86% after imputation).

Missing values in regulatory context data represent a topical challenge in data analysis, and further methodological developments are needed to either handle and accurately estimate missing values.

Challenge 3: Linking epigenetic features to gene expression

One of the main advantages of scNMT-seq is the ability to unbiasedly link epigenetic variation with gene expression. Transcriptional activation is associated with specific chromatin states near the gene of interest. This includes deposition of activatory histone marks such as H3K27ac, H3K4me3 and H3K36me3, binding of transcription factors, promoter and/or enhancer demethylation and chromatin remodeling. All these events are closely interconnected and leave a footprint across multiple molecular layers that can only be (partially) recovered by performing an association analysis between a specific chromatin read-out and mRNA expression. However, given the large amount of genes and regulatory regions, this task can become prohibitively large, with the associated multiple testing burden. In addition, some of our analyses have shown that the correlations between epigenetic layers and RNA expression calculated from individual genomic features can be generally weak or spurious.

A practical and straightforward approach from a computational perspective involves considering only putative regulatory elements within each gene's genomic neighborhood. Nonetheless, this might miss important links with regulatory elements located far away from the neighborhood.

In recent years, chromosome conformation capture experiments, have uncovered a complex network of chromatin interactions inside the nucleus connecting regions separated by multiple megabases along the genome and potentially involved in gene regulation. Early genome-wide contact maps generated by HiC uncovered domains spanning on the order of 1 Mb (in humans) within which genes would be coordinately regulated. Thus, a second strategy to associate putative regulatory elements and genes is to build on existing promoter-centered chromatin contact networks to restrict the association analysis to putative regulatory elements that are in 3D contact with genes. Although this is a promising strategy to reduce the complexity of the association analysis, most of our 3D interaction datasets are produced in bulk samples and it is so far unclear how much of these structures are preserved across individual cells. While single-cell conformation capture experiments remain limited by data sparsity and high levels of technical noise, we envision that technological advances in this area will deepen our understanding of the regulatory roles of chromatin states.

Commonalities between analytical multi-omics approaches for hackathons

Each hackathon study highlighted disparate challenges to multi-omics from different measurement technologies. Yet, these studies were unified by the underlying problem of data integration. We summarize the common problems faced across all hackathons and shared approaches adopted by participants. These commonalities highlight the critical computational issues in multi-omics single-cell data analysis.

The choice of methods mostly relied on the biological question to address: data integration was conducted using projection approaches, cell prediction required machine or statistical learning methods (SVM, Enet), and spatial analysis was conducted using Hidden Markov random field or Moran's Index. As computational methodologies span technologies, so do the central challenges highlighted in each hackathon. For example, the accuracy of the analysis critically depended on data pre-processing (e.g. normalization, upstream feature selection), differences in scale across data sets, and overlap (or lack thereof) of features (Figure 4). In many cases, preprocessing can yield data mapping to common molecular features, such as genes, that can be the focus of the integration task. However, the spatial proteomics challenge showed that many multi-omics datasets have limited shared features between studies. In cross-study and cross-platform analyses, methods that investigate hierarchical structure and apply measures of higher order concordance among the omics, cell, and phenotype layers are critical. Even in cases with matching molecular features, such analyses can reveal novel aspects of biology.

The Table summarizes the main methods that were applied across all hackathons. A large number of computational analysis methods that were applied derive from bulk RNA-seq literature, with the exception of projection methods developed for single-cell such as tSNE, UMAP, and LIGER. In this section, we briefly highlight the three common challenges faced across all hackathons, whose reproducible vignettes are in this article.

Common challenge 1: Dependence on pre-processing method and/or variable selection

Pre-processing steps strongly affect downstream analyses. Our participants thoroughly assessed the effect of normalization and data transformation (e.g. spatial transcriptomics, Figure 1A), as well as preliminary feature selection (mostly on based on highly variable genes) or feature summarization (scNMT-seq study). Ease of comparisons between analyses was facilitated by providing processed input data (see software section), which still encountered reproducibility issues between the original published study and the new analyses. For example, in the spatial transcriptomics study, 19 genes were selected in the seqFISH data on one analysis, whereas the original paper selected 43 genes based on the same feature selection process [3]. No consensus was reached across participants' analyses regarding the best way to process such emerging data, as those would require extensive benchmark, ground truth, or established biological results are yet available, which we discuss in benchmarking.

Common challenge 2: Managing differences in scale and size across datasets

Various techniques were used to address the differences in scale or resolution across data sets. For spatial transcriptomics and proteomics, participants focused on a common set of genes (via feature selection in spatial transcriptomics) or proteins. The scNMT-seq study that included overlap between cells raised the issue of differences in data set size with a varying number of features per dataset ranging from 6,673 to 18,345 (Figure 3A). Some projection-based methods, such as MOFA [26], require a similar number of features in each data set, while others such as PLS / sGCCA [23] do not have this limitation and enable more flexible analysis. Differences in data scale may result in one data set contributing to either too much variation or noise during data integration. Techniques such as re-scaling, batch effect removal approaches, such as Combat [27] or weighting specific data sets, were considered and each offered further improvement in the analyses.

Common challenge 3: Addressing partial overlap of information across cells or features

The degree of feature or cell overlap between datasets varied dramatically within each study. Intuitively, to integrate information across modalities, at least one type of overlap (whether on the features or cells, Figure 4) is required. The field has made progress in developing methods to integrate data sets across the same (bulk) samples of single cells, mostly based on dimension reduction techniques. Amongst them, NMF (LIGER) and Projection to Latent Structures (sGCCA [23]) were used for the scNMT-seq study. When there was no cell overlap, such as in the spatial studies, imputation methods were used to predict gene, protein, or spatial expression values based on nearest neighbors, latent variables, or optimal transport. These methods were also used to predict cell types. The most challenging study was the spatial proteomics, which raised the issue of no overlap between cells or features - the so called fourth corner that relies on phenotypes (Challenge 3 in proteomics). We anticipate that this scenario will be avoided once technological progress and increase in data availability is achieved [28].

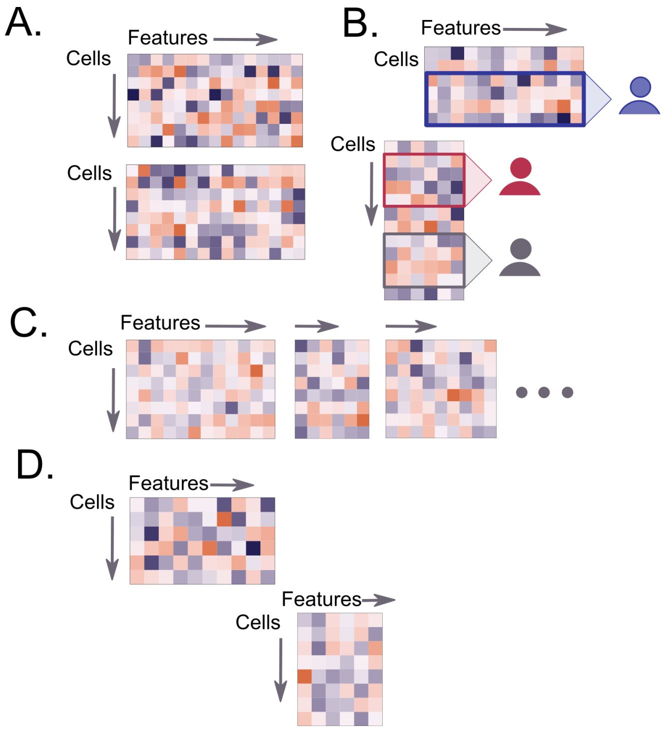


Figure 4:

Caption figure: **Common challenge 3: Addressing partial overlap of information across cells or features A.** Overlap of features (genes) but not cells (e.g. spatial transcriptomics where cell type prediction for seqFISH data was performed based on scRNA-seq where cell types are known. **B.** Partial overlap of features (proteins) but no overlap of cells (e.g. spatial proteomics that required data imputation or cell type prediction). **C.** Overlap of cells across assays, but no overlap of features (e.g. scNMT-seq where data integration was performed). **D.** Lack of overlap between cells and features (the so-called fourth corner problem in spatial proteomics hackathon).

Table: Different methods were used in the hackathon and further available as reproducible vignettes. * indicates that the method was not applied on the hackathon data. For some common challenges, 'bulk' indicates the method was originally developed for bulk omics, 'sc' indicates the method was specifically developed for single-cell data {#tbl:common}

Common challenges	**Tasks**	**sc Spatial**	**sc targeted proteomics**	**sc NMT-seq**
Pre-processing	**Normalization & data transformation**	Data distribution checks (Coullomb, Singh) High Variable Genes selection (Xu)	Variance Stabilization Normalisation [29] (Meng) Arcsinh transformation (Jeganathan). Inverse transformation (Jeganathan) Selection of patients (Jeganathan)	Summaries of DNA measurements (input data provided in hackathon)

Common challenges	**Tasks**	**sc Spatial**	**sc targeted proteomics**	**sc NMT-seq**
Managing differences in scale	**Data integration**	LIGER [30] (Sodicoff) (sc) ComBat (Singh) Projection methods MFA, sGCCA [23] (Singh*) (bulk) UMAP/tSNE (Sodicoff) (sc)	Multi-block PCA [31] Weighting matrices based on their similarities: STATIS, MFA (Chen*)(bulk) Scale MIBI-TOF to the range of CyTOF values (Jenagan)	LIGER [30] (Welch) (sc) Projection method sGCCA [23] (Abadi) (bulk) Multi Omics Supervised Integrative Clustering with weights (Arora) (bulk)
Overlap	**Cell overlap** (features not matching)			**Dimension reduction and projection methods:** LIGER [30] (Welch) (sc) sGCCA [23] (Abadi) (bulk)
	Partial feature overlap (cells not matching)		**Imputation:** Direct inversion with latent variables (Sankaran) Optimal transport to predict protein expression (Lin) K Nearest Neighbor averaging (Jeganathan) **No imputation:** Biological Network Interaction (Foster*)	
	Partial cell overlap (features not matching)		Multi block PCA [31] (Meng*)	
	No cell overlap (complete feature overlap)		Transfer cell type label with Random Forest (Hsu)	LIGER [30] (Welch)
	No cell overlap (partial feature overlap)		Topic modeling to predict cell spatial co-location or spatial expression (Jeganathan, partial feature overlap)	
	No overlap		RLQ [32] (Chen*)	

Common challenges	Tasks	sc Spatial	sc targeted proteomics	sc NMT-seq
Generic approaches	**Classification & feature selection**	Backward selection with SVM (Coullomb) self training ENet (Singh) Balanced error rate (Coullomb, Singh) Recursive Feature Elimination (Xu) (all bulk)		Multi Omics Supervised Integrative Clustering (Arora) (bulk) Lasso penalization in regression-type models (bulk)
	Cell type prediction	Projection with LIGER [30] (Sodicoff) SVM (Coullomb, Xu) ssEnet (Singh) (all bulk)		
	Spatial analysis	Hidden Markov random field Voronoi tesselation (Coullomb) (bulk)	Spatial autocorrelation with Moran’s Index (Hsu, Lin) Selection of spatial discriminative features: Moran’s Index, NN correlation, Cell type, interaction composition, L function (Lin) (all bulk?)	
	Inclusion of additional information		Survival prediction: Cox regression based on spatial features (Lin)	Include annotated hypersensitive sites index to anchor new/unseen data from DNase-seq, (sc)ATAC-seq, scNMT-seq, for *de novo* peak calling (Meuleman*) (bulk)

Challenges for interpretation

The analyses from each hackathon emphasized that regardless of the common difficulties faced by our participants, there is no one method fits all for multi-omics integration. An equally important complement to the diverse computational methods used to solve multi-omics analysis problems rests in the biological interpretation of their solutions, with the notable challenge that the integrated data from these approaches are often of higher dimension than the input datasets. For example, low dimensional representation of the results may require additional contiguous data, such as spatial coordinates to capture higher level cellular structure or prognostics (two of our hackathons). Thus, efforts to interpret multi-omics data require standardized vocabulary, benchmarked methods, and abstracted latent variables that can be compared between studies.

Organizing patterns for interpretation

Interpretation hinges on the analysis method selected for a given dataset. Some methods used in the hackathons and summarized in Table 1 aimed to predict a clearly defined outcome, such as recognizing the environment of tumor cells versus that of healthy cells (see proteomics section). The supervised setting often provides easier interpretations, as one can easily rank the covariates and contiguous data in terms of their predictive potential.

However, when data are collected without the availability of a clear response (e.g. survival time, tumor size, cell growth) using multiple different technologies, data integration requires organizing patterns that enable interpretation. Clustering is often used as one unsupervised method that can use latent variables - for example using a categorical variable such as cell type which was not directly measured on the data but enables simple interpretations [33]. Unfortunately, biological phenomenona are often not as clearcut.

During clustering, overseparating data by forcing the data into types only provides a static description when the variation should often be along a continuum. Indeed, although a latent factor can be a useful first approximation, the development of cells and their fate is a dynamic process. Thus, we recommend referring back to the original data that enabled interpretation of the cell trajectories: in our case, where the underlying latent variable of interest is expressed along a gradient of development (e.g. pseudo-time, disease progression).

Nonetheless, latent variables represent a rich anchor for many multimodal methods and can often be useful in highlighting what the modalities have in “common” and how they differ, as shown in the scNMT-seq hackathon. Disparate sources of evidence, or in this case, data from different technologies, are more compelling than many replicates of the same technology. Thus, if different technologies allow a consensus on underlying latent variables, this information is worth retaining. The commonalities are well understood in the case of classical multivariate factor analyses where the data are decomposed into common and unique components [34]. A schematic summary of the different stages in interpretation is provided in Figure 5).

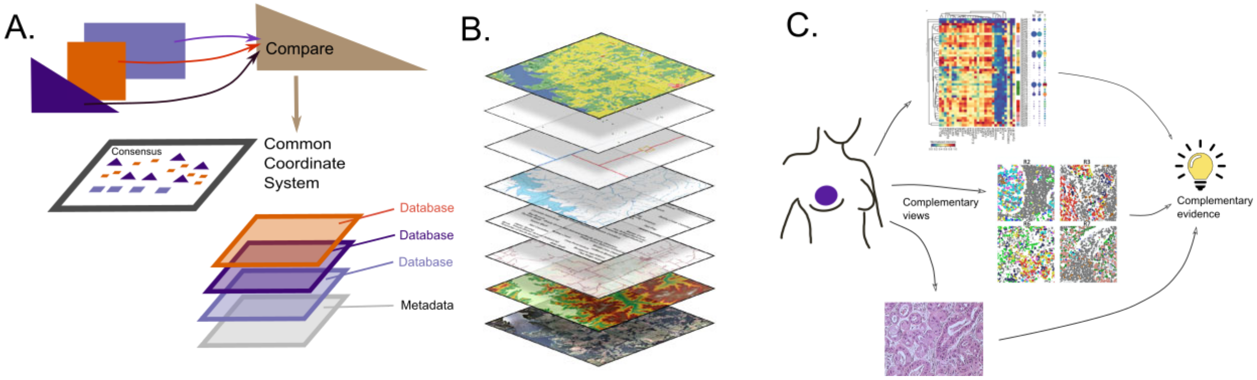


Figure 5:

Caption figure: **A** Schematic diagram of stages of interpretation and integration of data sources. **B** Standards in Geographic Information Systems enable the integration of multiple layers of data. **C** Integrative analysis across multiple modes of data results in complementary evidence, allowing stronger conclusions, an instance of Cardinal Newman’s principle: *‘Supposes a thesis (e.g. the guilt of an accused man) is supported by a great deal of circumstantial evidence of different forms, but in* *agreement with each other; then even if each piece of evidence is in itself insufficient to produce any strong belief, the thesis is decisively strengthened by their joint effect.'*

Reasoning by analogy with geospatial problems

Multiple domains of knowledge can be combined easily if there is a common coordinate system, as in geospatial analyses. This is often a goal in multimodal or conjoint analyses, when the first step is to find a common compromise or consensus on which to project each of the individual modalities. Conjoint analyses also known as STATIS [35] was a very early multimodal method designed as "PCA of PCAs" where the first step in the analyses was to identify the commonalities between different modalities and define a consensus onto which the individual data sets were projected [36]. STATIS can be considered as an extension of the class of matrix decomposition methods to data cubes. Many extensions to matrix decompositions have since been designed for multimodal data, [37] offers an overview of the relations between many of them.

In both spatial transcriptomics and the spatial proteomics hackathons, a spatial dimension was already naturally available, where we could leverage spatial statistics methods to quantify spatial effects. In these studies, contiguity and clustering can be tested and easily understood in the spatial context, and layers of information can be mapped to the natural coordinate system in the same way a GIS system incorporates them (Figure 5B).

The spatial coordinate system analogy can be pursued further by finding a "consensus space" that provides a common coordinate system. Thus, by creating an abstract coordinate space, we can leverage methods developed for true spatial co-occurrences, and evalute these co-occurrences in abstract spatial coordinates as an effective strategy for creating layered maps despite the the absence of a physical coordinate system. There are however pitfalls in using very sophisticated dimension reduction techniques which lead to over-interpretation or misinterpretation of spatial relations. One such example is the size and closeness of clusters in t-SNE which do not represent true densities or similarities in the original data.

Explaining results by linking databases

Figure 5A shows how connections to layers of information from external databases can be incorporated into the final output. Real biological understanding is often limited to the integration of this contiguous information that is available from metadata or from exterior sources such as Gene Ontologies, Biomart [38], Kegg, Human Cell Atlas (HCA) or within software systems (see software section).

As many methods suffer from identifiability issues, redundant biological knowledge can be enlightening. By providing information on the extreme points in a map or brushing a map with known gene expression features, one can delineate orientations and clusters. As an example, it is only through coloring by CD56 across time that we can see the dynamics of immune response [39], similar to the principle behind the interactive brushing illustrated in Figure 5C.

Explaining methods

Simulations can often provide effective and transparent communication tools to shed light into complex analytical methods. By generating data from different probabilistic models, we increase our understanding of the methods' limitations including identifiability problems resulting from overparametrized models. More realistic data can also be simulated by adding constraints on the parameters that reduce or eliminate identifiability issues. By using well defined generative processes during data simulation, we can then benchmark methods to clarify what some complex methods do, as we discuss in the benchmarking section.

Visualization of step-by-step transformations and optimizations of data also help clarify how certain methods fit models or reduce data dimensionality. These visualizations are often very specialized (e.g. correspondence analyses, goodness of fit qqplots or rootograms, mean-variance fitting plots), but serve as intermediary checks to unpack seemingly black boxes analytical processes.

Finally, spanning all of these interpretation challenges is a central communication barriers between data analysts and the community of practitionners who do not have the same vocabulary or background. Many tools are used as black boxes where users do not have a clear understanding on the statistical or mathematical principles underpinning the methods. A clear glossary of terms, and how we are using those terms is crucial to improve communication. For example, many synonyms for multimodal data exist and some have nuances, as we have collated in Table 2. Understanding the relation between methods described by different teams is essential. Data scientist often try to organize the methods first, thus it is useful to create a dichotomy of methods and their underlying properties for our collaborators.

Techniques and challenges for benchmarking methods

Visualizations and biological assessment of marker gene lists resulting from multi-omics analyses provide a critical interpretation of high-throughput data integration, but additional quantitative metrics are necessary to delineate biologically-relevant features from features arising from either computational or technical artifacts. Quantitative benchmarks are also essential to enable unbiased comparisons between analytical methods. For example, the goal of multi-platform single-cell data analysis is often the recovery of known cell types through computational methods. Metrics such as the adjusted Rand Index (ARI) enable a direct assessment of the clustering results with respect to known cell types. When cell types or biological features are not known *a priori*, benchmark methods can also be used to discover known relationships between data modalities. For example, *cis* gene regulatory mechanisms observed between chromatin accessibility and gene expression. Our hackathons highlighted that many of these relationships are not fully understood at the single-cell level, and that benchmarking standards are critically needed for validation (Figure 6A).

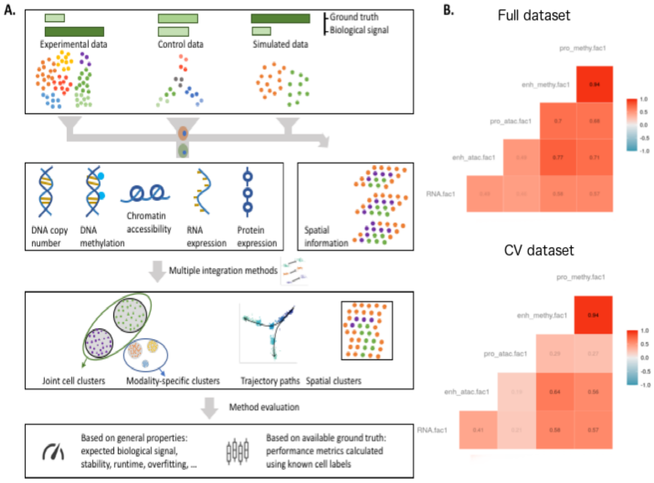


Figure 6:

Caption figure: **A** Systematic benchmarking of single-cell multi-omic analysis methods can involve experimental data (as per our hackathons), custom control datasets, where known structure is imposed through the experimental design or simulated data. The amount of biological signal and ground truth available varies considerably between these types of data. The resulting multi-omics datasets are analysed by competing methods and compared using metrics that have general purpose or take ground truth into account (e.g. cell type labels or number of cell types simulated). **B** scNMT-seq study: correlations with linear projections (MOFA+) evaluated with cross-validation.

Challenges and strategies for benchmarking

Benchmarking multi-modal methods is inherently difficult, as ground truth is rarely known. Ground truth can be introduced through simulating high-throughput data *in silico*, but in the context of data integration, the simulation of a realistic covariance structure across features and across data modalities are challenging [40] and must rely on an underlying generative model that may introduce further biases into the benchmarking analysis. Another strategy is to use cross-validation within a study, or conduct cross-study validation to assess whether solutions found by multi-modal methods generalize to held-out observations or held-out studies. The latter was attempted in the spatial proteomics cross-study hackathon, but where ground truth was unknown.

Challenge 1: creating benchmarking datasets

Benchmark datasets serve two main purposes: to provide ground truth for the intended effect of exposure in a proposed study design, and to provide validation for an analytic task for which a new computational method may be proposed (e.g. data integration in our hackathons), Figure 6A.

For single-cell studies, benchmark datasets have largely focused on measuring sequencing depth and diversity of cell types derived from a single assay of interest (e.g. scRNA-seq). Common experimental designs involve creating artificial samples through the mixing of cells in known proportions [41,42,43] or creating dilution series to simulate variation in cell size [41,44]. Simulating data is also popular and made more convenient through software such as the `splatter` R package [45].

For multi-modal assays, while the intended effects can vary based on the leading biological questions, one may abstract out common data integration tasks such as co-embedding, mapping or correlation, and inferring causal relationships. We distinguish data integration from further downstream analyses that may occur on integrated samples such as differential analysis of both assays with regard to a certain exposure. Both the intended effects and data integration task rely on study design that takes into account the biological and technical variability via replicates, block design, randomization, the power analysis for the intended effect or data integration task, and the dependencies between modalities. For example, gene expression depends on gene regulatory element activity and thus requires that experiment design must also account for spatial and temporal elements in sampling for a given observation.

As such, no universal benchmark data scheme may suit every combination of modalities (e.g. mising cells design does not generalise to the spatial context), and benchmark datasets should be established for commonly used combinations of modalities or technologies towards specific data integration tasks.

Challenge 2: cross-validation within study

Cross-validation within a representative multi-modal study is one possible approach for quantitative assessment for unbiased comparison of methods. We note that the approach of cross-validation – in which observations are split into folds or left out individually for assessing model fit – has been used often for parameter tuning within methods, or for other aspects of model selection [24,40,46,47,48,49,50,51,52,53,54,55].
Similarly, permutation has been used to create null datasets, either as a demonstration that a

particular method is not overfitting, or for parameter tuning, where the optimal parameter setting should result in a model score that is far from the null distribution of model scores [56,57,58]. Cross-validation is particularly useful as a quantitative assessment of a method's self-consistency, even though it cannot determine the *accuracy* of a method in a completely unbiased way if we do not have access to an external test data set for further confirmation.

As part of the third hackathon, a cross-validation analysis of the scNMT-seq dataset using MOFA+ was performed. Strong relationships found among pairs of modalities in training data were often reproduced in held out cells (Figure 6B). This CV analysis also revealed that we could reliably match dimensions of latent space across cross-validation folds. Previous evaluations of multi-modal methods have focused only on the top 'latent factor' [59], however, we showed in our analyses, many latent factors can be reliably discovered in held out cells in studies of complex biological processes such as the differentiation of embryonic cells.

For clustering assessment, several studies have used resampling or data-splitting strategies to determine prediction strength [13,60,61,62]. These techniques could be further extended in a multi-modal setting for clustering of cells into putative cell types or cell states. Community-based benchmarking efforts in the area of multi-modal data analysis could follow the paradigm of the DREAM Challenges, with multi-modal training data provided and test samples held out, in order to evaluate the method submissions from participating groups.

Challenge 3: cross-validation between studies

Our benchmarking hackathons have emphasized the need to access external studies for methods assessment and validation, where either the ground truth is based on biological knowledge of the system being studied, or via high-quality control experiments where the ground truth (e.g. cell type labels) are known (Figure 6A). To take advantage of all data and technologies available, cross-study validation could also extend to cross-platform to assess whether relationships discovered in one dataset are present in other datasets, such as looking across single-cell and bulk omics, as was recently proposed in [63].

Software strategies to enable analyses of multimodal single-cell experiments

Open-source software is essential in bioinformatics and computational biology. Benchmark datasets, analysis pipelines, and the development of multimodal genome-scale experiments are all enabled through community-developed, open-source software, and data sharing platforms. A wide array of genomics frameworks for multi-platform single-cell data have been developed in R and Python. Along with other software, these frameworks use standardized licensing in Creative Commons, Artistic, or GNU so that all components are accessible for full vetting by the community (see List of sofware)). Our hackathons hinged on the central challenges such as widescale adoption, extension, and collaboration to enable inference and visualization of the multimodal single-cell experiments in our analytic frameworks. We designed each case study to leverage and build on these open frameworks to further develop and evaluate robust benchmarking strategies. Easy to use data packages to distribute the multi-omics data and reproducible vignettes were key outputs from our workshop.

Collaboration enabled through continuous integration

Open-source software efforts facilitate a community-level coordinated approach to support collaboration rather than duplication of effort between groups working on similar problems. Real-time improvements to the tool-set should be feasible, respecting the needs for stability, reliability, and continuity of access to evolving components. To that end, exploration and engagement with all these tools is richly enabled through code sharing resources. Our hackathons directly leveraged through GitHub with our reproducible analyses reports to enable continuous integration of changes to source codes (using Github Action), and containerized snapshots of the analyses environments. The hackathons analyses conducted in R were assembled into R packages to facilitate libraries loading, while those conducted in Python enabled automatic installation and deployment

Usability and adoption by the community

Robust software ecosystems are required to build broad user bases [64,65,66]. Bioconductor is one example of such ecosystem, that provides multiplatform and continuous delivery of contributed software while assisting a wide range of users with standardized documentation, tests, community forums, and workshops [67,68,69]. In the case of the hackathons, the R/Bioconductor ecosystem for multi-omics enabled data structures and vignettes to support reproducible, open-source, open development analysis. During this workshop, we identified key software goals needed to advance the methods and interpretation of multi-omics.

Challenge 1: data accessibility

Providing data to the scientific community is a long-standing issue. A particular challenge in our hackathons was that each data modality was characterized by a different collection of features from possibly non-overlapping collections of samples (see common challenges section). Thus, common data structures are needed to store and operate on these data collections, and support data dissemination with robust metadata and implementation of analytical frameworks.

The `MultiAssayExperiment` integrative data class from Bioconductor was our class of choice to enable the collation of standard data formats, easy data access, and processing. It uses the S4 object-oriented structure in R [70,71] and includes several features to support multi-platform genomics data analysis, to store features from multiple data modalities (e.g. gene expression units from scRNA-seq and protein units in sc-proteomics) from either the same or distinct cells, biological specimen of origin, or from multiple dimensions (e.g. spatial coordinates, locations of eQTLs). This class also enables to store sample metadata (e.g. study, center, phenotype, perturbation) and provides a map between the datasets from different assays for downstream analysis.

In our hackathons, pre-processing steps applied to the raw data were fully documented. The input data were stored as `MultiAssayExperiment` objects that were centrally managed and hosted on `ExperimentHub`[72] as a starting point for all analyses. The `SingleCellMultiModal` package was used to query the relevant datasets for each analysis [doi:10.18129/B9.bioc.SingleCellMultiModal] (Figure 7). Text-based machine-readable data were also made available for non-R users, and also to facilitate alternative data preprocessing for participants.

Besides efficient data storage, several hackathon contributors used the `MultiAssayExperiment` class to implement further data processing and extraction of spatial information from raster objects in their analyses. This infrastructure was readily suitable for the spatial and scNMT-seq hackathons but the lack of overlap between samples in the spatial proteomics hackathon revealed an important area of future work to link biologically related datasets without direct feature or sample mappings for multi-omics analysis. Further, our hackathons highlighted the need for scalability of storing and efficiently retrieving single-cell data datasets [73,74]. New algorithms are emerging, that allow for data to be stored in memory or on disk (e.g. [75,76] in R or [77] in Python).

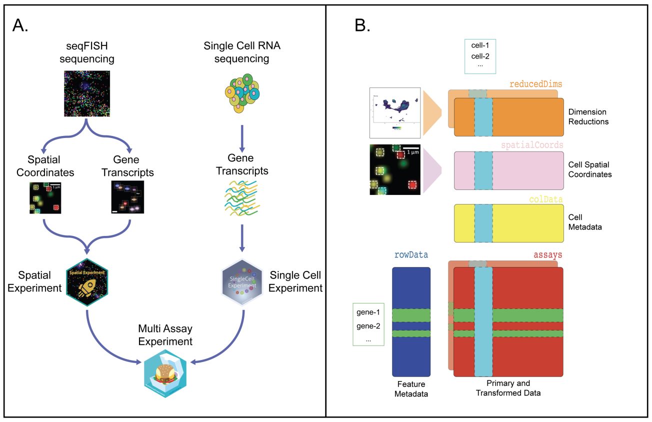


Figure 7:

Caption figure: **A** Software infrastructure using Bioconductor for the first hackathon to combine seqFISH-based `SpatialExperiment` and `SingleCellExperiment` instances into a `MultiAssayExperiment`. **B** To combine these two different experiments, the seqFISH data were stored into a `SpatialExperiment` S4 class object, while the scRNA-seq data were stored into a `SingleCellExperiment` class object [78]. These objects were then stored into a `MultiAssayExperiment` class object and released with the `SingleCellMultiModal` Bioconductor package [79].

Challenge 2: software infrastructure to handle assay-specific features

The hackathons further highlighted emerging challenges to handle different data modalities.

RNA-seq has well-defined units and IDs (e.g., transcript names), but other assays need to be summarized at different genomic scales (e.g., gene promoters, exons, introns, or gene bodies), as was highlighted in the scNMT-seq hackathon. Tools such as the `GenomicRanges` R package [80] have been proposed to compute summaries at different scales and overlaps between signal (e.g., ATAC-seq peaks) and genomic annotation.

Further, the observations of different modalities may not be directly comparable: for instance, gene expression may be measured from individual cells in single-cell RNA-seq, but spatial transcriptomics may have a finer (sub-cellular) or coarser (multi-cellular) resolution. Methods such as SPOTlight [81] can be used to deconvolute multi-cellular spots signal.

Finally, in the absence of universal standards, the metadata available may vary from modalities, or independent studies (e.g. spatial proteomics), thus urging the need from the computational biology community to define the minimum set of metadata variables necessary for each assay, as well as for pairs of assays to be comparable for common analyses.

Challenge 3: accessible vizualization

Our brainstorm discussions on the Data Interpretation Challenge highlighted the importance of novel data visualization strategies to make sens of multi-modal data analyses. Often, these visualization strategies rely on heatmaps or reduced dimension plots, and utilize color to represent the different dimensions. These colors and low dimensional plots facilitate pattern detection and interpretation of increasingly complex and rich data. However, relying on color for interpretation leads to difficulties in perceiving patterns for a substantial proportion of the population with color vision deficiencies and can result in different data interpretations between individuals.

Presenting accessible scientific information requires the inclusion of colorblind friendly visualizations [82,83] standardized as default settings through use of color palettes such as R/viridis [84] and dittoSeq [85] with a limit of 10 colors. Additional visual cues to differentiate regions or cells can also reduce the dependence on colors using hatched areas or point shapes. The inclusion an "accessibility caption" accompanying figures which to guide the reader's perception of the images would also greatly benefit broader data accessibility. Thus, implementing community standards for accessible visualizations is essential for bioinformatics software communities to ensure standardized interpretation of multi-platform single-cell data.

Discussion

The Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Workshop demonstrated the power of hackathons to both inform and develop new analysis methods to capture the complex, multi-scale nature of biological datasets from high-throughput data modalities. Notably, the hackathon studies of the workshop were specifically designed to span state-of-the-art multi-omics challenges to map the epigenetic, molecular, and cellular interaction across time and sample populations. Single-cell measurements spanning molecular modalities can inherently simplify the challenge of linking disparate biological scales, but layering new sets of molecular measurements increases the complexity of the analyses to interpret these data. The computational needs hinge on the underlying biological question being asked as well as the characteristics of the data themselves. In our workshop, different modelling considerations had to be made for multi-modal integration, as higlighted in the seqFISH and scNMT-seq challenges (matching on the same genes, or cells) and the scProteomics challenge (partially unmatched measurements). Regardless, through these hackathons we identified several common analysis themes spanning algorithmic advances, interpretation, benchmarking, and software infrastructure necessary for biological interpretation. All hackathons required methods for dealing with data quality, data loss from summarization, timing variances between and within omics layers, and batch effects. These represent the necessary challenges to overcome in the coming years, along with efficient and insightful data visualization strategies to infer regulatory relationships between different omics.

Technologies to profile biological systems at single-cell resolution and across molecular scales are advancing at an unprecedented pace. Analytically, these advances require the computational community to pursue research that can first enable robust analyses tailored to a specific biology or measurement technology, and second, that can scale and adapt to these rapid advances. Our hackathons highlighted current technologies for spatial molecular profiling. The two technologies used in this study both have limited molecular resolution. Therefore, multi-platform data combining the spatial molecular data from either seqFISH, MIBI, or imaging mass cytometry require complementary data from other single-cell technologies to provide both high spatial and molecular resolution enabled through data integration. We note that additional technologies, such as slide-seq [86] and Visium from 10X Genomics produce spatially resolved molecular measurements approaching measurements of the whole transcriptome, but lack the fine spatial resolution of these alternative imaging technologies. As such, emerging technologies still require further multi-platform data integration for comprehensive analysis. The scNMT-seq challenge did not include spatially resolved data but highlighted the potential of further inference of gene regulation through concurrent profiling of RNA, methylation, and chromatin state. Technological advances for multi-omics spatial data and epigenetics data are rapidly advancing and becoming increasingly available through Nanostring, 10X Genomics, Akoya Biosciences, and others. Our workshop keynote Bernd Bodenmiller presented new research-level technological advances that enable three-dimensional spatial molecular profiling [87]. Other technologies are currently expanding to allow for temporally resolved profiling [88]. Integration strategies aware of these future directions and the mathematical challenges that span technologies will be most adept at advancing biological knowledge: this was the primary aim of this workshop.

The implementation of novel analysis tools requires further robust software ecosystems, including Bioconductor [89], Biopython, and toolkits such as Scanpy [77], Seurat [90], or Giotto [10], in which users can create their analysis approaches and while anticipating stable and adaptive data structures robust for these emerging technologies. The size of these emerging datasets, particularly in the context of their application to atlas projects (e.g. the Human Tumor Atlas Network [91], Human Cell Atlas [92], Allen Brain Initiative, Brain Initiative Cell Census Network, or ENCODE, to cite a few) are key examples that computational efficiency and scalability of these implementations are becoming ever more critical.

In addition to new technologies, we wish to emphasize that arising multi-omics analysis methods can support the generation of new data sources to resolve the multi-scale nature of biological systems. For example, while the workshop posed the scNMT-seq data and spatial molecular datasets as distinct challenges for data integration, integration of matched datasets between these spatial and epigenetic profiling techniques could further resolve the dependence of cell-type and cellular-interactions of regulatory networks. By embedding prior biological knowledge as rules in the analysis approaches, additional sources of data can generate a new representation of a biological system. For example, curated regulatory networks from databases such as KEGG, Biocarta, GO, TRANSFAC, or MSigDB provide commonly used frameworks for this prior knowledge. These gene regulatory networks must be extended to map the impact of cellular context on transcriptional regulation that are being uncovered by emerging single-cell atlases. The regulatory networks and dynamic features captured in single-cell data also provide the potential for future techniques to predict molecular and cellular states. Our hackathons and workshop have shown that merging single-cell data with mathematical models have the potential to predict behaviors in biological systems using rules derived from only prior biological knowledge.

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Online resources (optional as referred above)

- Online resource 1: Three hackathon datasets (github)
- Online resource 2: R packages with open source reproducible vignettes (12 vignettes)

List of software for multi modal single cell analysis.

Type	Brief name (link)	Description
Matlab package	CytoMAP	CytoMAP: A Spatial Analysis Toolbox Reveals Features of Myeloid Cell Organization in Lymphoid Tissues
Matlab package	histoCAT	histoCAT: analysis of cell phenotypes and interactions in multiplex image cytometry data
Python library	PyTorch	General framework for deep learning
Python & R	TensorFlow	General framework for deep learning
Python package	SpaCell	SpaCell: integrating tissue morphology and spatial gene expression to predict disease cells
Python package	Scanpy	Python package for single cell analysis
R data class	MultiAssayExperiment	unify multiple experiments
R data class	SpatialExperiment	SpatialExperiment: a collection of S4 classes for Spatial Data
R package	Giotto	Spatial transcriptomics
R package	cytomapper	cytomapper: Visualization of highly multiplexed imaging cytometry data in R
R package	Spaniel	Spaniel: analysis and interactive sharing of Spatial Transcriptomics data
R package	Seurat	R toolkit for single cell genomics
R package	SpatialLIBD	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex
R package	Cardinal	Cardinal: an R package for statistical analysis of mass spectrometry-based imaging experiments
R package	CoGAPS	scCoGAPS learns biologically meaningful latent spaces from sparse scRNA-Seq data
R package	projectR	ProjectR is a transfer learning framework to rapidly explore latent spaces across independent datasets
R package	SingleCellMultiModal	Serves multiple datasets obtained from GEO and other sources and represents them as MultiAssayExperiment objects
R scripts	SpatialAnalysis	Scripts for SpatialExperiment usage
Self-contained GUI	ST viewer	ST viewer: a tool for analysis and visualization of spatial transcriptomics datasets
Shiny app	Dynverse	A comparison of single-cell trajectory inference methods: towards more accurate and robust tools
R package	mixOmics	R toolkit for multivariate analysis of multi-modal data

Type	Brief name (link)	Description
Python package	totalVI	A variational autoencoder (deep learning model) to integrate RNA and protein data from CITE-seq experiments
Python web application		ImJoy
Python package	napari	Interactive big multi-dimensional 3D image viewer
Software	QuPath	Multiplex whole slide image analysis
Python package	Cytokit	Multiplex whole slide image analysis
Python package	cmIF	Multiplex whole slide image analysis
Software	Facetto	Multiplex whole slide image analysis, not available yet
Software, Python based	CellProfiler	Image analysis

Vignettes summary

Table: Reproducible analyses from the participants.

Hackathon	Participant	Title	Language	Vignette	Additional info
scNMTseq	Al JalalAbadi	PLS	R	○	docker
scNMTseq	Wancen Mu and Michael Love	CV-MOFA	R	○	docker
scNMTseq	Josh Welch	LIGER analysis of scNMT-seq	R	○	docker
scNMTseq	Arshi Arora	MOSAIC analysis of scNMT-seq	R	○	docker
scProteomics	Lauren Hsu	Exploratory analyses	R	○	docker
scProteomics	Chen Meng	Predicting partially overlapping data	R	○	
scProteomics	Pratheepa Jeganathan	Latent Dirichlet Allocation	R	○	
scProteomics	Yingxin Lin	Integrative analysis of breast cancer survival based on spatial features	R	○	docker
scSpatial	Alexis Coullomb	Neighbours Aggregtion	python	○	

Hackathon	Participant	Title	Language	Vignette	Additional info
scSpatial	Joshua Sodicoff	Utilizing LIGER for the integration of spatial transcriptomic data	R		docker
scSpatial	Dario Righelli	SpatialExperiment Analysis	R		docker
scSpatial	Amrit Singh	seqFISH+scRNASeq integration using semi-supervised glmnet	R		docker
scSpatial	Hang Xu	Cortex seq-FISH + scRNA data - gene selection	python		

Glossary

Table 1: Glossary of interchangeable terms in the field of single-cell and bulk multi-omics (multi-source) data analysis.

Consensus Term	Related Terms	Description	Citation
network	graph, adjacency matrix	A set of *nodes*, representing objects of interest, linked by *edges*, representing specific relationships between nodes.	94
node	vertex	Element of interest in a network and linked to other nodes. For example: people, cells, proteins or genes. Nodes can have several properties called *attributes* like cell type or position.	94
edge	link	The relationship between 2 nodes in a network. For example: friendship in social networks, cells in contact in a spatial network, or gene-gene interactions in a gene regulatory network.	94
concordant	common	Agreement between multiple modalities with respect to feature/variable selection and correlation of latent factors.	95, 96
consistent	coherent	Similar performance obtained from applying methods for multimodal data during multiple rounds of data splitting.	59

Consensus Term	Related Terms	Description	Citation
contributions	variable weights, loadings, eigenvector, axis, direction, dimension, coefficients, slopes	Contributions of the original variables in constructing the components.	[24], [97]
latent factors	variates, scores, projections, components, latent/hidden/unobserved variables/factors	Weighted linear combinations of the original variables.	[24], [97]
multimodal	Multiview, multiway arrays, multimodal, multidomain, multiblock, multitable, multi-omics, multi-source data analysis methods, N-integration	Methods pertaining to the analysis of multiple data matrices for the same set of observations.	[24], [37], [98]
conjoint analysis	conjoint analysis, P-integration, meta-analysis, multigroup data analysis	Methods pertaining to the analysis of multiple data matrices for the same set of variables.	[24], [97], [99]
variable	feature, variable	A measurable quantity that describes an observation's attributes. Variables from different modalities include age, sex, gene or protein abundance, single nucleotide variants, operational taxonomic units, pixel intensity *etc.*	[94]
biomarker	marker, biomarker	A variable that is associated with normal or disease processes, or responses to exposures, or interventions. Any change in this variable is also associated with a change in the associated clinical outcome. These variables may be used for diagnostic, monitoring, Pharmacodynamic responses. Examples include LDL cholesterol, CD4 counts, hemoglobin A1C.	[100]
panel	biomarker panel, biomarker signature	A subset of the originally measured variables that are determined to be associated with the outcome or response variable. This may be determined using statistical inference, feature selection methods, or machine/statistical learning.	[101], [102]

Consensus Term	Related Terms	Description	Citation
observation	sample, observation, array	A single entity belonging to a larger grouping. Examples include patients, subjects, participants, cells, biological sample, usually the unit of observation on which the variables are measured *etc.*	94

References

1. **Method of the Year 2019: Single-cell multimodal omics**
   Nature Methods
   (2020-01) https://www.nature.com/articles/s41592-019-0703-5
   DOI: 10.1038/s41592-019-0703-5

2. **Adult mouse cortical cell taxonomy revealed by single cell transcriptomics**
   Bosiljka Tasic, Vilas Menon, Thuc Nghi Nguyen, Tae Kyung Kim, Tim Jarsky, Zizhen Yao, Boaz Levi, Lucas T Gray, Staci A Sorensen, Tim Dolbeare, … Hongkui Zeng
   Nature Neuroscience (2016-01-04) https://doi.org/f778w5
   DOI: 10.1038/nn.4216 · PMID: 26727548 · PMCID: PMC4985242

3. **Identification of spatially associated subpopulations by combining scRNAseq and sequential fluorescence in situ hybridization data**
   Qian Zhu, Sheel Shah, Ruben Dries, Long Cai, Guo-Cheng Yuan
   Nature Biotechnology (2018-10-29) https://doi.org/gfgn8x
   DOI: 10.1038/nbt.4260 · PMID: 30371680 · PMCID: PMC6488461

4. **A Single-Cell Atlas of the Tumor and Immune Ecosystem of Human Breast Cancer**
   Johanna Wagner, Maria Anna Rapsomaniki, Stéphane Chevrier, Tobias Anzeneder, Claus Langwieder, August Dykgers, Martin Rees, Annette Ramaswamy, Simone Muenst, Savas Deniz Soysal, … Bernd Bodenmiller
   Cell (2019-05) https://doi.org/gfzbz7
   DOI: 10.1016/j.cell.2019.03.005 · PMID: 30982598 · PMCID: PMC6526772

5. **A Structured Tumor-Immune Microenvironment in Triple Negative Breast Cancer Revealed by Multiplexed Ion Beam Imaging**
   Leeat Keren, Marc Bosse, Diana Marquez, Roshan Angoshtari, Samir Jain, Sushama Varma, Soo-Ryum Yang, Allison Kurian, David Van Valen, Robert West, … Michael Angelo
   Cell (2018-09) https://doi.org/gd4wms
   DOI: 10.1016/j.cell.2018.08.039 · PMID: 30193111 · PMCID: PMC6132072

6. **Epigenetic regulation in development: is the mouse a good model for the human?**
   Courtney W Hanna, Hannah Demond, Gavin Kelsey
   Human Reproduction Update (2018-09) https://doi.org/gd3d4z
   DOI: 10.1093/humupd/dmy021 · PMID: 29992283 · PMCID: PMC6093373

7. **Single-cell in situ RNA profiling by sequential hybridization**
   Eric Lubeck, Ahmet F Coskun, Timur Zhiyentayev, Mubhij Ahmad, Long Cai
   Nature Methods (2014-03-28) https://doi.org/ggrr5b
   DOI: 10.1038/nmeth.2892 · PMID: 24681720 · PMCID: PMC4085791

8. **In Situ Transcription Profiling of Single Cells Reveals Spatial Organization of Cells in the Mouse Hippocampus**
   Sheel Shah, Eric Lubeck, Wen Zhou, Long Cai
   Neuron (2016-10) https://doi.org/f8875g
   DOI: 10.1016/j.neuron.2016.10.001 · PMID: 27764670 · PMCID: PMC5087994

9. **Transcriptome-scale super-resolved imaging in tissues by RNA seqFISH+**
   Chee-Huat Linus Eng, Michael Lawson, Qian Zhu, Ruben Dries, Noushin Koulena, Yodai Takei, Jina

Yun, Christopher Cronin, Christoph Karp, Guo-Cheng Yuan, Long Cai
Nature (2019-03-25) https://doi.org/gfxgqx
DOI: 10.1038/s41586-019-1049-y · PMID: 30911168 · PMCID: PMC6544023

10. **Giotto, a toolbox for integrative analysis and visualization of spatial expression data**
Ruben Dries, Qian Zhu, Rui Dong, Chee-Huat Linus Eng, Huipeng Li, Kan Liu, Yuntian Fu, Tianxiao Zhao, Arpan Sarkar, Feng Bao, … Guo-Cheng Yuan
bioRxiv (2020-05-30) https://doi.org/gg84qf
DOI: 10.1101/701680

11. **Spatial reconstruction of single-cell gene expression data**
Rahul Satija, Jeffrey A Farrell, David Gennert, Alexander F Schier, Aviv Regev
Nature Biotechnology (2015-04-13) https://doi.org/f7bmck
DOI: 10.1038/nbt.3192 · PMID: 25867923 · PMCID: PMC4430369

12. **Single-Cell Multi-omic Integration Compares and Contrasts Features of Brain Cell Identity**
Joshua D. Welch, Velina Kozareva, Ashley Ferreira, Charles Vanderburg, Carly Martin, Evan Z. Macosko
Cell (2019-06) https://doi.org/gf3m3v
DOI: 10.1016/j.cell.2019.05.006 · PMID: 31178122 · PMCID: PMC6716797

13. **Cluster Validation by Prediction Strength**
Robert Tibshirani, Guenther Walther
Journal of Computational and Graphical Statistics (2005-09) https://doi.org/fvtcf4
DOI: 10.1198/106186005x59243

14. **Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming**
Geoffrey Schiebinger, Jian Shu, Marcin Tabaka, Brian Cleary, Vidya Subramanian, Aryeh Solomon, Joshua Gould, Siyan Liu, Stacie Lin, Peter Berube, … Eric S. Lander
Cell (2019-03) https://doi.org/gfwk5n
DOI: 10.1016/j.cell.2019.02.026 · PMID: 30849376 · PMCID: PMC6615720

15. **Inferring spatial and signaling relationships between cells from single cell transcriptomic data**
Zixuan Cang, Qing Nie
Nature Communications (2020-04-29) https://doi.org/gg9pf7
DOI: 10.1038/s41467-020-15968-5 · PMID: 32350282 · PMCID: PMC7190659

16. **Spatial proteomics: a powerful discovery tool for cell biology**
Emma Lundberg, Georg H. H. Borner
Nature Reviews Molecular Cell Biology (2019-01-18) https://doi.org/gft39v
DOI: 10.1038/s41580-018-0094-y · PMID: 30659282

17. **Matching species traits to environmental variables: a new three-table ordination method**
S. Dolédec, D. Chessel, C. J. F. ter Braak, S. Champely
Environmental and Ecological Statistics (1996-06) https://doi.org/fhwz55
DOI: 10.1007/bf02427859

18. **Using single-cell genomics to understand developmental processes and cell fate decisions**
Jonathan A Griffiths, Antonio Scialdone, John C Marioni
Molecular Systems Biology (2018-04-16) https://doi.org/gdgbtq
DOI: 10.15252/msb.20178046 · PMID: 29661792 · PMCID: PMC5900446

19. **Reprogramming the Methylome: Erasing Memory and Creating Diversity**
Heather J. Lee, Timothy A. Hore, Wolf Reik
Cell Stem Cell (2014-06) https://doi.org/f6f83c
DOI: 10.1016/j.stem.2014.05.008 · PMID: 24905162 · PMCID: PMC4051243

20. **scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells**
Stephen J. Clark, Ricard Argelaguet, Chantriolnt-Andreas Kapourani, Thomas M. Stubbs, Heather J. Lee, Celia Alda-Catalinas, Felix Krueger, Guido Sanguinetti, Gavin Kelsey, John C. Marioni, … Wolf Reik
Nature Communications (2018-02-22) https://doi.org/gc4q72
DOI: 10.1038/s41467-018-03149-4 · PMID: 29472610 · PMCID: PMC5823944

21. **Multi-omics profiling of mouse gastrulation at single-cell resolution**
Ricard Argelaguet, Stephen J. Clark, Hisham Mohammed, L. Carine Stapel, Christel Krueger, Chantriolnt-Andreas Kapourani, Ivan Imaz-Rosshandler, Tim Lohoff, Yunlong Xiang, Courtney W. Hanna, … Wolf Reik
Nature (2019-12-11) https://doi.org/ggfrnn
DOI: 10.1038/s41586-019-1825-8 · PMID: 31827285 · PMCID: PMC6924995

22. **Pan-cancer identification of clinically relevant genomic subtypes using outcome-weighted integrative clustering**
Arshi Arora, Adam B. Olshen, Venkatraman E. Seshan, Ronglai Shen
bioRxiv (2020-05-12) https://doi.org/gg8np9
DOI: 10.1101/2020.05.11.084798

23. **Variable selection for generalized canonical correlation analysis**
A. Tenenhaus, C. Philippe, V. Guillemot, K.-A. Le Cao, J. Grill, V. Frouin
Biostatistics (2014-02-17) https://doi.org/gg583d
DOI: 10.1093/biostatistics/kxu001 · PMID: 24550197

24. **mixOmics: An R package for ‘omics feature selection and multiple data integration**
Florian Rohart, Benoît Gautier, Amrit Singh, Kim-Anh Lê Cao
PLOS Computational Biology (2017-11-03) https://doi.org/gcj84s
DOI: 10.1371/journal.pcbi.1005752 · PMID: 29099853 · PMCID: PMC5687754

25. **impute**
Robert Tibshirani Trevor Hastie
Bioconductor (2017) https://doi.org/gg9dds
DOI: 10.18129/b9.bioc.impute

26. **MOFA+: a statistical framework for comprehensive integration of multi-modal single-cell data**
Ricard Argelaguet, Damien Arnol, Danila Bredikhin, Yonatan Deloro, Britta Velten, John C. Marioni, Oliver Stegle
Genome Biology (2020-05-11) https://doi.org/ggvwsr
DOI: https://doi.org/10.1186/s13059-020-02015-1

27. **Adjusting batch effects in microarray expression data using empirical Bayes methods**
W. Evan Johnson, Cheng Li, Ariel Rabinovic
Biostatistics (2007-01) https://doi.org/dsf386
DOI: 10.1093/biostatistics/kxj037 · PMID: 16632515

28. **Eleven grand challenges in single-cell data science**
David Lähnemann, Johannes Köster, Ewa Szczurek, Davis J. McCarthy, Stephanie C. Hicks, Mark D. Robinson, Catalina A. Vallejos, Kieran R. Campbell, Niko Beerenwinkel, Ahmed Mahfouz, … Alexander Schönhuth
Genome Biology (2020-02-07) https://doi.org/ggkkr4
DOI: 10.1186/s13059-020-1926-6 · PMID: 32033589 · PMCID: PMC7007675

29. **Variance stabilization applied to microarray data calibration and to the quantification of differential expression**
W. Huber, A. von Heydebreck, H. Sultmann, A. Poustka, M. Vingron
Bioinformatics (2002-07-01) https://doi.org/dbb6xx
DOI: 10.1093/bioinformatics/18.suppl_1.s96 · PMID: 12169536

30. **Integrative inference of brain cell similarities and differences from single-cell genomics**
Joshua Welch, Velina Kozareva, Ashley Ferreira, Charles Vanderburg, Carly Martin, Evan Macosko
bioRxiv (2018-11-02) https://doi.org/gfgr7b
DOI: 10.1101/459891

31. **mogsa**
Chen Meng
Bioconductor (2017) https://doi.org/gg583f
DOI: 10.18129/b9.bioc.mogsa

32. **Combining the fourth-corner and the RLQ methods for assessing trait responses to environmental variation**
Stéphane Dray, Philippe Choler, Sylvain Dolédec, Pedro R. Peres-Neto, Wilfried Thuiller, Sandrine Pavoine, Cajo J. F. ter Braak
Ecology (2014-01) https://doi.org/gdsf9z
DOI: 10.1890/13-0196.1 · PMID: 24649641

33. **What Is Your Conceptual Definition of "Cell Type" in the Context of a Mature Organism?**
Cell Systems
(2017-03) https://doi.org/d38b
DOI: 10.1016/j.cels.2017.03.006 · PMID: 28334573

34. **Multiple factor analysis.**
L. L. Thurstone
Psychological Review (1931) https://doi.org/dq4k9p
DOI: 10.1037/h0069792

35. **The ACT (STATIS method)**
Christine Lavit, Yves Escoufier, Robert Sabatier, Pierre Traissac
Computational Statistics & Data Analysis (1994-08) https://doi.org/c8xttz
DOI: 10.1016/0167-9473(94)90134-1

36. **Multivariate data analysis: The French way**
Susan Holmes
Institute of Mathematical Statistics (2008) https://doi.org/cmnf7j
DOI: 10.1214/193940307000000455

37. **Multitable Methods for Microbiome Data Integration**
Kris Sankaran, Susan P. Holmes

Frontiers in Genetics (2019-08-28) https://doi.org/gf8dqn
DOI: 10.3389/fgene.2019.00627 · PMID: 31555316 · PMCID: PMC6724662

38. **Mapping identifiers for the integration of genomic datasets with the R/Bioconductor package biomaRt**
Steffen Durinck, Paul T Spellman, Ewan Birney, Wolfgang Huber
Nature Protocols (2009-07-23) https://doi.org/c4b7dd
DOI: 10.1038/nprot.2009.97 · PMID: 19617889 · PMCID: PMC3159387

39. **Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry**
Thanmayi Ranganath, Laura J. Simpson, Anne-Maud Ferreira, Christof Seiler, Elena Vendrame, Nancy Zhao, Jason D. Fontenot, Susan Holmes, Catherine A. Blish
Frontiers in Immunology (2020-04-24) https://doi.org/gg5jcr
DOI: 10.3389/fimmu.2020.00714 · PMID: 32391016 · PMCID: PMC7194113

40. **DIABLO: an integrative approach for identifying key molecular drivers from multi-omics assays**
Amrit Singh, Casey P Shannon, Benoît Gautier, Florian Rohart, Michaël Vacher, Scott J Tebbutt, Kim-Anh Lê Cao
Bioinformatics (2019-09-01) https://doi.org/ggpt9c
DOI: 10.1093/bioinformatics/bty1054 · PMID: 30657866 · PMCID: PMC6735831

41. **Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments**
Luyi Tian, Xueyi Dong, Saskia Freytag, Kim-Anh Lê Cao, Shian Su, Abolfazl JalalAbadi, Daniela Amann-Zalcenstein, Tom S. Weber, Azadeh Seidi, Jafar S. Jabbari, … Matthew E. Ritchie
Nature Methods (2019-05-27) https://doi.org/gf3jhp
DOI: 10.1038/s41592-019-0425-8 · PMID: 31133762

42. **Benchmarking single-cell RNA-sequencing protocols for cell atlas projects**
Elisabetta Mereu, Atefeh Lafzi, Catia Moutinho, Christoph Ziegenhain, Davis J. McCarthy, Adrián Álvarez-Varela, Eduard Batlle, Sagar, Dominic Grün, Julia K. Lau, … Holger Heyn
Nature Biotechnology (2020-04-06) https://doi.org/ggrbbh
DOI: 10.1038/s41587-020-0469-4 · PMID: 32518403

43. **Systematic comparison of single-cell and single-nucleus RNA-sequencing methods**
Jiarui Ding, Xian Adiconis, Sean K. Simmons, Monika S. Kowalczyk, Cynthia C. Hession, Nemanja D. Marjanovic, Travis K. Hughes, Marc H. Wadsworth, Tyler Burks, Lan T. Nguyen, … Joshua Z. Levin
Nature Biotechnology (2020-04-06) https://doi.org/ggrksw
DOI: 10.1038/s41587-020-0465-8 · PMID: 32341560 · PMCID: PMC7289686

44. **Accounting for technical noise in single-cell RNA-seq experiments**
Philip Brennecke, Simon Anders, Jong Kyoung Kim, Aleksandra A Kołodziejczyk, Xiuwei Zhang, Valentina Proserpio, Bianka Baying, Vladimir Benes, Sarah A Teichmann, John C Marioni, Marcus G Heisler
Nature Methods (2013-09-22) https://doi.org/gbd3mc
DOI: 10.1038/nmeth.2645 · PMID: 24056876

45. **Splatter: simulation of single-cell RNA sequencing data**
Luke Zappia, Belinda Phipson, Alicia Oshlack
Genome Biology (2017-09-12) https://doi.org/gc3h3g
DOI: 10.1186/s13059-017-1305-0 · PMID: 28899397 · PMCID: PMC5596896

46. **A Sparse PLS for Variable Selection when Integrating Omics Data**
Kim-Anh Lê Cao, Debra Rossouw, Christèle Robert-Granié, Philippe Besse
Statistical Applications in Genetics and Molecular Biology (2008-01-18) https://doi.org/cw7zft
DOI: 10.2202/1544-6115.1390 · PMID: 19049491

47. **Sparse principal component analysis via regularized low rank matrix approximation**
Haipeng Shen, Jianhua Z. Huang
Journal of Multivariate Analysis (2008-07) https://doi.org/b7x3cc
DOI: 10.1016/j.jmva.2007.06.007

48. **Quantifying the Association between Gene Expressions and DNA-Markers by Penalized Canonical Correlation Analysis**
Sandra Waaijenborg, Philip C. Verselewel de Witt Hamer, Aeilko H Zwinderman
Statistical Applications in Genetics and Molecular Biology (2008-01-23) https://doi.org/bpzb68
DOI: 10.2202/1544-6115.1329 · PMID: 18241193

49. CCA **: An *R* Package to Extend Canonical Correlation Analysis**
Ignacio Gonzalez, Sébastien Déjean, Pascal Martin, Alain Baccini
Journal of Statistical Software (2008) https://doi.org/gf4f5m
DOI: 10.18637/jss.v023.i12

50. **HIGHLIGHTING RELATIONSHIPS BETWEEN HETEROGENEOUS BIOLOGICAL DATA THROUGH GRAPHICAL DISPLAYS BASED ON REGULARIZED CANONICAL CORRELATION ANALYSIS**
I. GONZÁLEZ, S. DÉJEAN, P. G. P. MARTIN, O. GONÇALVES, P. BESSE, A. BACCINI
Journal of Biological Systems (2011-11-21) https://doi.org/bmbjf5
DOI: 10.1142/s0218339009002831

51. **A penalized matrix decomposition, with applications to sparse principal components and canonical correlation analysis**
D. M. Witten, R. Tibshirani, T. Hastie
Biostatistics (2009-04-17) https://doi.org/fd4g54
DOI: 10.1093/biostatistics/kxp008 · PMID: 19377034 · PMCID: PMC2697346

52. **Sparse Canonical Correlation Analysis with Application to Genomic Data Integration**
Elena Parkhomenko, David Tritchler, Joseph Beyene
Statistical Applications in Genetics and Molecular Biology (2009-01-06) https://doi.org/b7x4jb
DOI: 10.2202/1544-6115.1406 · PMID: 19222376

53. **Integrative analysis of gene expression and copy number alterations using canonical correlation analysis**
Charlotte Soneson, Henrik Lilljebjörn, Thoas Fioretos, Magnus Fontes
BMC Bioinformatics (2010-04-15) https://doi.org/dtxhsx
DOI: 10.1186/1471-2105-11-191 · PMID: 20398334 · PMCID: PMC2873536

54. **Gene expression signatures modulated by epidermal growth factor receptor activation and their relationship to cetuximab resistance in head and neck squamous cell carcinoma**
Elana J Fertig, Qing Ren, Haixia Cheng, Hiromitsu Hatakeyama, Adam P Dicker, Ulrich Rodeck, Michael Considine, Michael F Ochs, Christine H Chung
BMC Genomics (2012) https://doi.org/gb3fgp
DOI: 10.1186/1471-2164-13-160 · PMID: 22549044 · PMCID: PMC3460736

55. **Identifying multi-layer gene regulatory modules from multi-dimensional genomic data**
W. Li, S. Zhang, C.-C. Liu, X. J. Zhou

Bioinformatics (2012-08-03) https://doi.org/f4d488
DOI: 10.1093/bioinformatics/bts476 · PMID: 22863767 · PMCID: PMC3463121

56. **Cross-platform comparison and visualisation of gene expression data using co-inertia analysis**
Aedín C. Culhane, Guy Perrière, Desmond G. Higgins
BMC bioinformatics (2003-11-21)
DOI: 10.1186/1471-2105-4-59 · PMCID: PMC317282

57. **Extensions of Sparse Canonical Correlation Analysis with Applications to Genomic Data**
Daniela M Witten, Robert J. Tibshirani
Statistical Applications in Genetics and Molecular Biology (2009-01-09) https://doi.org/b45jtg
DOI: 10.2202/1544-6115.1470 · PMID: 19572827 · PMCID: PMC2861323

58. **MOGSA: Integrative Single Sample Gene-set Analysis of Multiple Omics Data**
Chen Meng, Azfar Basunia, Bjoern Peters, Amin Moghaddas Gholami, Bernhard Kuster, Aedín C. Culhane
Molecular & Cellular Proteomics (2019-08-09) https://doi.org/ggf3j3
DOI: 10.1074/mcp.tir118.001251 · PMID: 31243065 · PMCID: PMC6692785

59. **Consistency and overfitting of multi-omics methods on experimental data**
Sean D McCabe, Dan-Yu Lin, Michael I Love
Briefings in Bioinformatics (2020-07) https://doi.org/gghpmf
DOI: 10.1093/bib/bbz070 · PMID: 31281919 · PMCID: PMC7373174

60. **Bootstrapping cluster analysis: Assessing the reliability of conclusions from microarray experiments**
M. K. Kerr, G. A. Churchill
Proceedings of the National Academy of Sciences (2001-07-24) https://doi.org/cgpp6p
DOI: 10.1073/pnas.161273698 · PMID: 11470909 · PMCID: PMC55356

61. **A prediction-based resampling method for estimating the number of clusters in a dataset**
Sandrine Dudoit, Jane Fridlyand
Genome Biology (2002-06-25)
DOI: 10.1186/gb-2002-3-7-research0036 · PMCID: PMC126241

62. **A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes**
Benjamin Haibe-Kains, Christine Desmedt, Sherene Loi, Aedin C. Culhane, Gianluca Bontempi, John Quackenbush, Christos Sotiriou
JNCI: Journal of the National Cancer Institute (2012-02-22) https://doi.org/fzb27r
DOI: 10.1093/jnci/djr545 · PMID: 22262870 · PMCID: PMC3283537

63. **A simple, scalable approach to building a cross-platform transcriptome atlas**
Paul W Angel, Nadia Rajab, Yidi Deng, Chris M Pacheco, Tyrone Chen, Kim-Anh Lê Cao, Jarny Choi, Christine A Wells
bioRxiv (2020-03-11) https://doi.org/gg898g
DOI: 10.1101/2020.03.09.984468

64. **A federated ecosystem for sharing genomic, clinical data**
The Global Alliance for Genomics and Health
Science (2016-06-09) https://doi.org/ggctm3
DOI: 10.1126/science.aaf6162 · PMID: 27284183

65. **GrimoireLab - Software Development and Community Analytics platform**
https://chaoss.github.io/grimoirelab/

66. http://ceur-ws.org/Vol-987/3.pdf

67. **Bioconductor - Home** https://bioconductor.org/

68. **Bioconductor build/check results** https://bioconductor.org/checkResults/

69. https://bioconductor.org/support

70. **MultiAssayExperiment**
Marcel Ramos [Aut, Cre], Levi Waldron [Aut], MultiAssay SIG[Ctb]
Bioconductor (2017) https://doi.org/gg6p3d
DOI: 10.18129/b9.bioc.multiassayexperiment

71. **Software for the Integration of Multiomics Experiments in Bioconductor**
Marcel Ramos, Lucas Schiffer, Angela Re, Rimsha Azhar, Azfar Basunia, Carmen Rodriguez, Tiffany Chan, Phil Chapman, Sean R. Davis, David Gomez-Cabrero, … Levi Waldron
Cancer Research (2017-10-31) https://doi.org/gcj278
DOI: 10.1158/0008-5472.can-17-0344 · PMID: 29092936 · PMCID: PMC5679241

72. **ExperimentHub**
Bioconductor Package Maintainer
Bioconductor (2017) https://doi.org/gg6p3c
DOI: 10.18129/b9.bioc.experimenthub

73. **DelayedArray**
Hervé Pagès
Bioconductor (2017) https://doi.org/gg5tw4
DOI: 10.18129/b9.bioc.delayedarray

74. **rhdf5**
Bernd Fischer [Aut], Gregoire Pau [Aut], Mike Smith [Aut, Cre]
Bioconductor (2017) https://doi.org/gg5tw6
DOI: 10.18129/b9.bioc.rhdf5

75. **mbkmeans: fast clustering for single cell data using mini-batch *k*-means**
Stephanie C. Hicks, Ruoxi Liu, Yuwei Ni, Elizabeth Purdom, Davide Risso
bioRxiv (2020-05-27) https://doi.org/gg5tw3
DOI: 10.1101/2020.05.27.119438

76. **mbkmeans**
Yuwei Ni, Davide Risso, Stephanie Hicks, Elizabeth Purdom
Bioconductor https://doi.org/gg5tw5
DOI: 10.18129/b9.bioc.mbkmeans

77. **SCANPY: large-scale single-cell gene expression data analysis**
F. Alexander Wolf, Philipp Angerer, Fabian J. Theis
Genome Biology (2018-02-06) https://doi.org/gc22s9
DOI: 10.1186/s13059-017-1382-0 · PMID: 29409532 · PMCID: PMC5802054

78. **SingleCellExperiment**
Aaron Lun [Aut, Cph], Davide Risso [Aut, Cre, Cph]
Bioconductor (2017) https://doi.org/gg5wfr
DOI: 10.18129/b9.bioc.singlecellexperiment

79. **SingleCellMultiModal**
Marcel Ramos, Kelly Eckenrode, Levi Waldron, Dario Righelli
Bioconductor https://doi.org/gg95x5
DOI: 10.18129/b9.bioc.singlecellmultimodal

80. **GenomicRanges**
H. Pagès P. Aboyoun
Bioconductor (2017) https://doi.org/gg6rfz
DOI: 10.18129/b9.bioc.genomicranges

81. **SPOTlight: Seeded NMF regression to Deconvolute Spatial Transcriptomics Spots with Single-Cell Transcriptomes**
Marc Elosua, Paula Nieto, Elisabetta Mereu, Ivo Gut, Holger Heyn
bioRxiv (2020-06-04) https://doi.org/gg6rfx
DOI: 10.1101/2020.06.03.131334

82. **Points of view: Color blindness**
Bang Wong
Nature Methods (2011-06-01) https://www.nature.com/articles/nmeth.1618
DOI: 10.1038/nmeth.1618

83. **Color coding**
Bang Wong
Nature Methods (2010-08) https://doi.org/dhm3mz
DOI: 10.1038/nmeth0810-573 · PMID: 20704014

84. **The viridis color palettes** https://cran.r-project.org/web/packages/viridis/vignettes/intro-to-viridis.html

85. **dittoSeq**
Daniel Bunis, Jared Andrews
Bioconductor https://doi.org/gg95x4
DOI: 10.18129/b9.bioc.dittoseq

86. **Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution**
Samuel G. Rodriques, Robert R. Stickels, Aleksandrina Goeva, Carly A. Martin, Evan Murray, Charles R. Vanderburg, Joshua Welch, Linlin M. Chen, Fei Chen, Evan Z. Macosko
Science (2019-03-29) https://doi.org/gfxpjk
DOI: 10.1126/science.aaw1219 · PMID: 30923225 · PMCID: PMC6927209

87. **Highly multiplexed molecular and cellular mapping of breast cancer tissue in three dimensions using mass tomography**
Raúl Catena, Alaz Özcan, Laura Kütt, Alex Plüss, Peter Schraml, Holger Moch, Bernd Bodenmiller, IMAXT Consortium
Cold Spring Harbor Laboratory (2020-05-25) https://doi.org/gg87jf
DOI: 10.1101/2020.05.24.113571

88. **ZipSeq: barcoding for real-time mapping of single cell transcriptomes**
Kenneth H. Hu, John P. Eichorst, Chris S. McGinnis, David M. Patterson, Eric D. Chow, Kelly Kersten, Stephen C. Jameson, Zev J. Gartner, Arjun A. Rao, Matthew F. Krummel
Nature Methods (2020-07-06) https://doi.org/gg87jd
DOI: 10.1038/s41592-020-0880-2 · PMID: 32632238

89. **Orchestrating single-cell analysis with Bioconductor**
Robert A. Amezquita, Aaron T. L. Lun, Etienne Becht, Vince J. Carey, Lindsay N. Carpp, Ludwig Geistlinger, Federico Marini, Kevin Rue-Albrecht, Davide Risso, Charlotte Soneson, … Stephanie C. Hicks
Nature Methods (2019-12-02) https://doi.org/ggdxgx
DOI: 10.1038/s41592-019-0654-x · PMID: 31792435 · PMCID: PMC7358058

90. **Integrating single-cell transcriptomic data across different conditions, technologies, and species**
Andrew Butler, Paul Hoffman, Peter Smibert, Efthymia Papalexi, Rahul Satija
Nature Biotechnology (2018-04-02) https://doi.org/gc87v6
DOI: 10.1038/nbt.4096 · PMID: 29608179 · PMCID: PMC6700744

91. **The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution**
Orit Rozenblatt-Rosen, Aviv Regev, Philipp Oberdoerffer, Tal Nawy, Anna Hupalowska, Jennifer E. Rood, Orr Ashenberg, Ethan Cerami, Robert J. Coffey, Emek Demir, … Xiaowei Zhuang
Cell (2020-04) https://doi.org/ggtkzd
DOI: 10.1016/j.cell.2020.03.053 · PMID: 32302568 · PMCID: PMC7376497

92. **The Human Cell Atlas**
Aviv Regev, Sarah A Teichmann, Eric S Lander, Ido Amit, Christophe Benoist, Ewan Birney, Bernd Bodenmiller, Peter Campbell, Piero Carninci, Menna Clatworthy, … Human Cell Atlas Meeting Participants
eLife (2017-12-05) https://doi.org/gcnzcv
DOI: 10.7554/elife.27041 · PMID: 29206104 · PMCID: PMC5762154

93. **The Human Cell Atlas: from vision to reality**
Orit Rozenblatt-Rosen, Michael J. T. Stubbington, Aviv Regev, Sarah A. Teichmann
Nature (2017-10-26) https://doi.org/gfgkr8
DOI: 10.1038/550451a · PMID: 29072289

94. **Modern statistics for modern biology**
Susan Holmes, Wolfgang Huber
Cambridge University Press (2018)
ISBN: 9781108705295

95. **Multi-Omics Data Integration and Mapping of Altered Kinases to Pathways Reveal Gonadotropin Hormone Signaling in Glioblastoma**
Savita Jayaram, Manoj Kumar Gupta, Rajesh Raju, Poonam Gautam, Ravi Sirdeshmukh
OMICS: A Journal of Integrative Biology (2016-12) https://doi.org/f9h7sd
DOI: 10.1089/omi.2016.0142 · PMID: 27930095

96. **A multivariate approach to the integration of multi-omics datasets**
Chen Meng, Bernhard Kuster, Aedín C Culhane, Amin Gholami
BMC Bioinformatics (2014) https://doi.org/f6btpk
DOI: 10.1186/1471-2105-15-162 · PMID: 24884486 · PMCID: PMC4053266

97. **Multivariate analysis of multiblock and multigroup data**
A. Eslami, E. M. Qannari, A. Kohler, S. Bougeard
Chemometrics and Intelligent Laboratory Systems (2014-04) https://doi.org/f52wrr
DOI: 10.1016/j.chemolab.2014.01.016

98. **Dimension reduction techniques for the integrative analysis of multi-omics data**
Chen Meng, Oana A. Zeleznik, Gerhard G. Thallinger, Bernhard Kuster, Amin M. Gholami, Aedín C. Culhane
Briefings in Bioinformatics (2016-07) https://doi.org/f83qvd
DOI: 10.1093/bib/bbv108 · PMID: 26969681 · PMCID: PMC4945831

99. **Robust meta-analysis of gene expression using the elastic net**
Jacob J. Hughey, Atul J. Butte
Nucleic Acids Research (2015-07-13) https://doi.org/f7nnbm
DOI: 10.1093/nar/gkv229 · PMID: 25829177 · PMCID: PMC4499117

100. **Biomarker definitions and their applications**
Robert M Califf
Experimental Biology and Medicine (2018-02-06) https://doi.org/gcxh8n
DOI: 10.1177/1535370217750088 · PMID: 29405771 · PMCID: PMC5813875

101. **Biomarker signatures of aging**
Paola Sebastiani, Bharat Thyagarajan, Fangui Sun, Nicole Schupf, Anne B. Newman, Monty Montano, Thomas T. Perls
Aging Cell (2017-04) https://doi.org/d2cm
DOI: 10.1111/acel.12557 · PMID: 28058805 · PMCID: PMC5334528

102. **Biomarker Panels in Critical Care**
Susan R. Conway, Hector R. Wong
Critical Care Clinics (2020-01) https://doi.org/d2cn
DOI: 10.1016/j.ccc.2019.08.007 · PMID: 31733684

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Chapter 9

Mathematical Models in Biology: from Information Theory to Thermodynamics (20w5074)

July 27 - 29, 2020

Organizer(s): Peter J. Thomas (Case Western Reserve University), Michael Hinczewski (Case Western Reserve University), Andrew Eckford (York University)

Overview of the Field

All living things, from the simplest bacteria to human beings, are made of cells. Fundamental understanding of living systems, both in health and in disease, depends on understanding the complex interactions among and within living cells. Multiple scientific disciplines have separately shed light on the problems of communication and organization in living systems. Biochemistry, bioinformatics and systems biology describe the basic ingredients of cells: DNA, RNA, proteins, lipids, and their interactions. Information theory, founded by Claude Shannon, provides a framework for quantifying the flow of information through any communications system, whether living or engineered (or both, as in the rapidly growing field of synthetic biology). Statistical thermodynamics, the branch of physics concerned with transformations among different forms of energy as well as with the physics of information, sets fundamental limits on the energetic price cells must pay for the information they sense (from each other, from the environment, and from their own DNA).

In the last five years, significant advances in statistical thermodynamics and the information theory of biological systems have set the stage for a deeper understanding of how cells process and organize information, make decisions, predict the future, and learn from the past. An essential link between these traditionally disparate fields is the language of mathematics, which provides a common framework within which researchers can understand each other across disciplines. The workshop on Mathematical Models in Biology: from Information Theory to Thermodynamics was planned to bring together leading experts and aspiring junior researchers from systems biology, statistical physics, information theory, and applied mathematics to develop the fundamental, linking ideas, to compare recent advances in their fields, and to establish new collaborations.

Stochastic Thermodynamics. The principles of classical thermodynamics have been established since the 19th century, including foundational notions such as the conservation of energy in its many forms (kinetic energy; gravitational and electrical potential energy; enthalpy U of chemical reactions; work), absolute temperature T, Boltzmann's entropy S, and Gibb's free energy $G = U - TS$. Boltzmann famously had his entropy formula

$S = k \log W$ engraved as his epitaph, where k is Boltzmann's constant and W denotes *Wahrscheinlichkeit*, or probability. Decades later, Claude Shannon put the theory of communication systems on a firm mathematical basis by establishing the entropy $H = -\sum_i p_i \log p_i$ as the quantitative measure of *information* of a source producing the ith symbol with probability p_i. The formal similarity between the physical entropy S and Shannon's information measure H has spurred volumes of research aiming to elucidate their shared significance (if any). Particularly within theoretical biology, at the cellular or subcellular level, one confronts processes that are naturally described one the one hand by the laws of chemistry, physics, and thermodynamics, and at the same time appear to function as teleological systems performing information-processing functions, e.g. communication, sensing, learning, or decision-making. The goal of the workshop was to advance interdisciplinary communication in this area.

Recent Developments and Open Problems

The last fifteen years have seen rapid advancement in the area of *stochastic thermodynamics*, led by the work of U. Seifert, cf. [Seifert (2008), Seifert (2019)], which provides the most promising intellectual framework yet for the analysis of information processing at cellular and subcellular scales within biology. Stochastic thermodynamics provides two conceptual advantages that are particularly relevant to biology: (i) It allows for a self-consistent thermodynamic description of arbitrarily small systems coupled to a thermal environment, for example individual biomolecules in solution. This is in contrast to conventional thermodynamics, which typically assumes both system and environment are macroscopic. (ii) It assigns thermodynamic quantities like entropy, work, and energy to individual time trajectories of a system. These trajectory-based definitions agree with the traditional ensemble-based definitions in the macroscopic limit, but they also reveal new physics: a variety of so-called "fluctuation theorems" that have been discovered over the last two decades. These theorems, which have been experimentally validated in biophysical systems, effectively generalize the second law of thermodynamics. They represent the most significant addition to our understanding of classical thermodynamics since the work of Boltzmann, Gibbs, and Maxwell in the 19th century. However the full implications of this novel physics for biological function, particularly information processing, are still being explored. The workshop provided a broad overview of the topic (through the opening talk of Udo Seifert), and in the subsequent talks illustrated the diverse applications of these ideas in biological systems.

Presentation Highlights

The workshop schedule, abbreviated to accommodate the online format, comprised five scientific talks (followed by ample time for discussion) and a virtual poster session.

Talk 1. Udo Seifert: From Stochastic Thermodynamics to Thermodynamic Inference

Udo Seifert (Univ. Stuttgart) set the stage by introducing stochastic thermodynamics, which apply to systems in which non-equilibrium is caused by mechanical or chemical forces, ambient solution provides a thermal bath of well-defined temperature T and chemical potential μ_i, and fluctuations are relevant due to small numbers of involved molecules [Collin et al (2005)]. He asked whether the same principles of thermodynamics that apply to the heat engines of the 19th century apply to molecular motors such as the F_1-ATPase rotor. The main idea, Seifert urged, is to take energy conservation and entropy production seriously along the individual trajectories [Seifert (2008)].

The setting for stochastic thermodynamics, reviewed in [Seifert (2012)], begins with a closed equilibrium system in contact with a thermal reservoir at fixed temperature $T \equiv \beta^{-1}$, nominally described by an ensemble of microstates ξ with energy $H(\xi)$. At equilibrium, state ξ occurs with probability $p_{\text{eq}}(\xi) = e^{-\beta H(\xi)}/Z$, normalized by the partition function $Z = \sum_\xi e^{-\beta H(\xi)}$. The (mean) internal energy $U = \sum_\xi p_{\text{eq}}(\xi) H(\xi)$, the entropy $S = \sum_\xi p_{\text{eq}}(\xi) \ln(1/p_{\text{eq}})$, and the free energy $F = U - TS$ are given by the classic thermodynamic relations $F = -\beta^{-1} \ln Z$, $U = \partial_\beta(\beta F)$, and $S = \beta^2 \partial_\beta F$. Thus $p_{\text{eq}}(\xi) = \exp(-\beta(H(\xi) - F))$.

One typically does not observe the system in a way that resolves individual microstates, but rather makes coarse-grained observations of an observable giving an ensemble of mesoscopic states $\{I\}$, with each microstate belonging to exactly one mesostate, $\xi \in I$. One can define the free energy $F(I)$, internal energy $U(I)$ and entropy $S(I)$ for mesoscopic states in terms of the conditional probabilities $p_{\text{eq}}(\xi \mid I)$. By observing long trajectories $I(t;\beta)$ at slightly different inverse temperatures β, one can estimate thermodynamic quantities associated with particular mesoscopic observables from experimental data. If the equilibration of the microstates within each mesostate is fast compared to the transition times between mesostates, then one can recover an effective thermodynamics (first and second law) at the mesoscopic level. Along a stochastic mesoscopic trajectory $I(t)$ one has (stochastically) fluctuating quantities e.g. $U(I(t))$. Starting from an out-of-equilibrium initial probability distribution, $p_0(I) \neq p_{\text{eq}}(I)$, one can compute the total entropy production, the heat dissipation, and the stochastic entropy production by comparing forward and (fictitious) backward-in-time trajectories. In order to consider driven systems, such as chemically driven molecular motors performing work against an applied load, one embeds the system of interest in a closed "supersystem" which is then partitioned into a core system and a connected reservoir. In this setting one may describe a nonequilibrium steady-state (NESS) for which the probability distribution of total entropy production obeys a detailed fluctuation theorem. One can further coarse grain the mesostates into functionally distinct macrostates, equipped under certain conditions with a notion of nonequilibrium entropy production [Seifert (2019)]. Thermodynamic *inference* then refers to extracting information about hidden states from the observable trajectories that would otherwise remain inaccessible, without application of the stochastic thermodynamic framework. Finally, thermodynamic uncertainty relations established within the stochastic thermodynamic framework allow one to put bounds on the energetic cost necessary for accurate timekeeping at the molecular level [Barato and Seifert (2016)].

Talk 2. Sarah Harvey: An Energy-Accuracy Tradeoff in Nonequilibrium Cellular Sensing

Building on the framework reviewed in Seifert's talk, Sarah Harvey addressed the question of the relationship between entropy production and measurement precision in chemical networks, when the network functions to estimate the concentration of a chemical signal [Harvey et al (2020)]. This question goes back to classical work of [Berg and Purcell (1977)] that was revisited in an ideal observer framework in [Endres and Wingreen (2009)], and studied as an information theoretic problem in [Thomas and Eckford (2016)]. Exploiting the stochastic thermodynamics framework and large deviation theory, Harvey derived two theoretical bounds on the uncertainty of a sensor modeled as a continuous-time Markov process, in different limits of what is observable about the process. The Cramèr-Rao bound for an ideal observer gives $\text{var}(\hat{c})/c^2 \geq 1/\overline{N}$, where $\overline{N}$ is the expected number of binding events in a fixed observation time T_{obs}, c is the concentration that is to be estimated, and $\hat{c}$ is the estimate. In contrast, the "coarse-grained" bound for a simple observer gives $\text{var}(\hat{c})/c^2 \geq 8/(T_{\text{obs}}\Sigma^{\pi} + 4\overline{N})$, where Σ^{π} is the entropy production rate. In particular, Harvey showed there is no advantage to endowing the signal transduction network with additional states beyond "bound" and "unbound".

Talk 3. Massimiliano Esposito: Thermodynamics of Biochemical Reaction Networks: Information, Accuracy and Speed

Massimiliano Esposito began by reviewing deterministic aspects of open chemical reaction networks (CRNs). As in Seifert's description of a "supersystem" in which a "core system" and a "reservoir" are embedded, an open CRN allows for exchange of energy and matter with its surroundings. Objects used in network analysis of chemical reaction systems such as the stoichiometry matrix naturally partition into components defined by the core/reservoir distinction, leading to versions of the first and second law of thermodynamics adapted to this setting [Rao and Esposito (2016)]. The topology of the CRN and any resulting conservation laws impact the entropy production, thus even for models of *deterministic* chemical reaction systems, thermodynamics and information are fundamentally related to one another. These observations lead to a relation between the relative entropy and the minimum work needed to generate a nonequilibrium distribution, starting from equilibrium (which equals the maximum work that could be extracted from that nonequilibrium distribution as the system approaches equilibrium) [Falasco et al (2018)]. One can analyze open chemical systems as thermodynamic machines and design systems for self-assembly [Penocchio et al (2019)]. This framework allows one to assess the cost, accuracy and speed of various cellular operations, such as energy transduction from molecular motors to metabolism, and the cost of cellular information processing and computation.

Bridging from the deterministic to the stochastic thermodynamic setting, Esposito observed that the underlying structure of thermodynamics carries over unchanged, with thermodynamic entropy becoming the Shannon entropy of the probability of species abundances, and with entropy production satisfying a fluctuation relation [Rao and Esposito (2018)]. In some cases the stochastic and deterministic descriptions are equivalent, for instance when the CRN is linear, or when a CRN with a network deficiency is at steady state. In general, however, strict equivalence is not satisfied. Finally, in order to rigorously treat energetic and information processing constraints on biological systems beyond the subcellular level, detailed accounting of energetic would be required, which remains a daunting challenge [Esposito (2020)].

Talk 4. Thomas Ouldridge: Non-Equilibrium Thermodynamics of Catalytic Information Processing

A catalytic information processing system (as introduced in Seifert's talk) is a communication system in which the state of a receiver (e.g. a receptor protein) is "copied" to the state of a readout molecule, without consuming or altering the receiver. Examples include cell surface receptors, but also DNA (the DNA molecule is not consumed or altered in the process of transcription) and RNA (RNA's involvedment in translation may be considered catalytic). As a hallmark of catalytic information processing, the effect of the input persists beyond the timescale of the substrate/catalyst interaction. This extended persistence effect can be exploited for signal amplification, signal splitting, time integration, and modularity. [Ouldridge (2018)]

However, catalytic molecular systems are challenging to design and build. In thermodynamic terms, one considers two distinct macrostates m and m' (as in Seifert's formulation) each containing several microstates $y \in m$, $y' \in m'$. The probability of the microstate $p(m)$, which indicates how far m is removed from equilibrium, is the key quantity to consider, along with the generalized free energy $G[p(m)] = U[p(m)] - TS[p(m)]$. Information transfer from the input signal to the output signal requires occupation of macrostates far from equilibrium. In contrast to recent feats of nanoengineering involving specification of *equilibrium* states (e.g. self-assembly of molecular structures), producing specific non-equilibrium states remains remarkably difficult. As Ouldridge explained: the reason there are very few examples of synthetically engineered catalytic information processing systems (despite the nanoengineering field's track record of success with self-assembly) is that in principle they require strong, selectively-attractive interactions that can be disrupted later, when no longer needed. To address these problems, Ouldridge and colleagues have investigated ways to optimize enzymatic catalysts for rapid turnover of substrates, with low enzyme sequestration; results were published in [Deshpande and Ouldridge (2020)].

Talk 5. Ilka Bischofs: Information Processing by Bacterial Quorum Sensing Systems

Signal transduction in bacteria provides important examples of communications systems at the level of single cells and, in the case of quorum sensing, populations of cells. Quorum sensing allows the bacteria in a colony to communicate, via secretion and detection of autoinducer molecules, in order to undertake collective actions that individual bacteria could not accomplish alone. Examples include production of bioluminescence that provides a symbiotic advantage to a multicellular host organism such as the angler fish [Nealson and Hastings (1979)], formation of biofilms, induction of virulence factors, initiation of sporulation, production of antibiotics to suppress competing, and many other actions [Miller and Bassler (2001), Mukherjee and Bassler (2019)].

Bischoffs described the commonly observed one-component signaling systems, of which the lac operon is a canonical example, and the less common two-component system, of which histidine kinase signaling or cheA signaling in chemotaxis are well studied examples, provide instances of "catalytic information processing" in the sense discussed by Ouldridge earlier in the workshop. Auto-inducer systems involved in quorum sensing provide another class of examples. Auto-inducer systems are commonly thought to be detecting population density, triggering a population-level response when the density exceeds some threshold. Specific examples of have been reported as early as 1964 in gram-positive pneumococcus bacteria (an activator-inhibitor system regulating competence for genetic transfer [Tomasz and Hotchkiss (1964)]) and 1970 in gram-negative bacteria [Nealson et al. (1970)].

Quorum sensing systems exhibit a variety of network architectures, often (but not always) involving positive feedback loops. Recent work has emphasized the importance of adopting a modular view of quorum sensing systems, representing encoding and decoding as two distinct aspects [Drees et al (2014)]. In the majority of previous work in quorum sensing, bacterial populations are conceived as homogeneous, and synchronized in their response to changes in population density. In contrast, Bischof's recent work has emphasized heterogeneous and heterochronous aspects of quorum-sensing populations and responses [Bettenworth et al (2019)] as well as a novel pump-probe model of ratiometric population sensing [Babel et al (2020)].

Scientific Progress Made

Given the reduced scope of the workshop, and the lack of opportunities for informal face-to-face conversations (on the trail up Tunnel Mountain, for example) the organizers did not expect to report immediate significant scientific advances. However, as one of the few conferences devoted solely to exploring the implications of stochastic thermodynamics in biological systems, the workshop served as a meeting ground for researchers in this area, and started new conversations. Several participants reported following up with new contacts initiated through the workshop. As one participant (V. Klika) wrote "taking part in the workshop has finally pushed me to carry out an idea I had for many years now – the effect of kinetic energy density on reaction-diffusion model when derived via non-equilibrium thermodynamics."

Outcome of the Meeting

The original organizers of 20w5074 planned to coordinate a special issue of the journal *Biological Cybernetics* on the topic of "Information Theory and Thermodynamics in Biology" in conjunction with the BIRS workshop.

Following the onset of the coronavirus pandemic, two of the original three co-organizers resigned from organization of the conference, and were replaced with new co-organizers. The workshop was reorganized on a smaller scale with five talks and a poster session spread over three days. The planned special issue attracted only four submissions; as of the submission of this report one paper was published as part of a regular issue of the journal [Deshpande and Ouldridge (2020)], one paper was rejected, one is being revised by its authors, and one remains under review.

On the positive side, the online format allowed for greater participation in the workshop than the in-person format would have allowed. Over 60 participants attended each session of the online workshop. One of the speakers (Seifert, a leading figure in the field) had previously declined to participate because of being unable to travel, but was able to give the keynote talk remotely.

Participants

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Bibliography

[Babel et al (2020)] H. Babel, P. Naranjo-Meneses, S. Trauth, S. Schulmeister, G. Malengo, V. Sourjik and I.B. Bischofs, Ratiometric population sensing by a pump-probe signaling system in Bacillus subtilis. *Nature communications* **11**.1 (2020), 1–13.

[Barato and Seifert (2016)] A.C. Barato and U. Seifert, Cost and precision of Brownian clocks, *Physical Review X* **6**.4 (2016), 041053.

[Berg and Purcell (1977)] H.C. Berg and E.M. Purcell, Physics of chemoreception, *Biophysical journal* **20**.2, (1977) 193–219.

[Bettenworth et al (2019)] V. Bettenworth, B. Steinfeld, H. Duin, K. Petersen, W.R. Streit, I. Bischofs and A. Becker, Phenotypic heterogeneity in bacterial quorum sensing systems, *Journal of molecular biology*, **431**.23 (2019), 4530–4546.

[Collin et al (2005)] D. Collin, F. Ritort, C. Jarzynski, S.B. Smith, I. Tinoco and C. Bustamante, Verification of the Crooks fluctuation theorem and recovery of RNA folding free energies, *Nature* **437**.7056 (2005), 231–234.

[Deshpande and Ouldridge (2020)] A. Deshpande and T.E. Ouldridge, Optimizing enzymatic catalysts for rapid turnover of substrates with low enzyme sequestration, *Biological Cybernetics* **114**.6 (2020), 653–668.

[Drees et al (2014)] B. Drees, M. Reiger, K. Jung and I.B. Bischofs, A modular view of the diversity of cell-density-encoding schemes in bacterial quorum-sensing systems, *Biophysical journal* **107**.1 (2014), 266–277.

[Endres and Wingreen (2009)] R.G. Endres and N.S. Wingreen, Maximum likelihood and the single receptor, *Physical review letters* **103**.15 (2009), 158101.

[Esposito (2020)] M. Esposito, Open questions on nonequilibrium thermodynamics of chemical reaction networks, *Communications Chemistry* **3**.1 (2020), 1–3.

[Falasco et al (2018)] G. Falasco, R. Rao and M. Esposito, Information thermodynamics of turing patterns, *Physical Review Letters* **121**.10 (2018), 108301.

[Harvey et al (2020)] S. Harvey, S. Lahiri and S. Ganguli, An Energy-Accuracy Tradeoff for Nonequilibrium Receptors, *Bulletin of the American Physical Society* **65** (2020).

[Horowitz and Esposito (2014)] J.M. Horowitz and M. Esposito, Thermodynamics with continuous information flow, *Physical Review X* **4**.3 (2014), 031015.

[Miller and Bassler (2001)] M.B. Miller and B.L. Bassler, Quorum sensing in bacteria, *Annual Reviews in Microbiology*, **55**.1 (2001), 165–199.

[Mukherjee and Bassler (2019)] S. Mukherjee and B.L. Bassler, Bacterial quorum sensing in complex and dynamically changing environments, *Nature Reviews Microbiology* **17**.6 (2019), 371–382.

[Nealson et al. (1970)] K.H. Nealson, T. Platt and J. W. Hastings, The cellular control of the synthesis and activity of the bacterial luminescent system, *J. Bacteriol.* **104** (1970), 313–322.

[Nealson and Hastings (1979)] K.H. Nealson and J.W. Hastings, Bacterial bioluminescence: its control and ecological significance, *Microbiological reviews* **43**.4 (1979), 496–518.

[Ouldridge (2018)] T.E. Ouldridge, The importance of thermodynamics for molecular systems, and the importance of molecular systems for thermodynamics, *Natural computing* **17**.1 (2018), 3–29.

[Penocchio et al (2019)] E. Penocchio, R. Rao, and M. Esposito, Thermodynamic efficiency in dissipative chemistry, *Nature communications* **10**.1 (2019), 1–5.

[Rao and Esposito (2016)] R. Rao and M. Esposito, Nonequilibrium thermodynamics of chemical reaction networks: wisdom from stochastic thermodynamics, *Physical Review X* **6**.4 (2016), 041064.

[Rao and Esposito (2018)] R, Rao, and M. Esposito, Conservation laws and work fluctuation relations in chemical reaction networks, *The Journal of Chemical Physics* **149**.24 (2018), 245101.

[Seifert (2008)] U. Seifert, Stochastic thermodynamics: principles and perspectives, *The European Physical Journal B* **64**.3-4 (2008), 423–431.

[Seifert (2012)] U. Seifert, Stochastic thermodynamics, fluctuation theorems and molecular machines, *Reports on progress in physics* **75**.12 (2012).

[Seifert (2019)] U. Seifert, From stochastic thermodynamics to thermodynamic inference, *Annual Review of Condensed Matter Physics* **10** (2019), 171–192.

[Thomas and Eckford (2016)] P.J. Thomas and A.W. Eckford, Capacity of a simple intercellular signal transduction channel, *IEEE Transactions on Information Theory* **62**.12 (2016), 7358–7382.

[Tomasz and Hotchkiss (1964)] A. Tomasz and R.D. Hotchkiss, Regulation of the transformability of pneumococcal cultures by macromolecular cell products, *Proceedings of the National Academy of Sciences of the United States of America* **51**.3 (1964), 480–487.

Chapter 10

Modern Breakthroughs in Diophantine Problems (20w5005)

August 30 - September 4, 2020

Organizer(s): Michael Bennett (University of British Columbia), Nils Bruin (Simon Fraser University), Samir Siksek (Warwick University), Bianca Viray (University of Washington)

Overview of the Field and Recent Developments

The subject of Diophantine equations is currently experiencing a rapid succession of breakthroughs. These include:

(i) The work of Rafael von Känel, Benjamin Matschke, Hector Pasten, and others, proving powerful results on classical Diophantine equations by associating solutions to points on modular or Shimura curves.

(ii) Recent successes in making the Chabauty-Kim method effective, explicit and practical, due to Balakrishnan, Dogra, Müller, and others.

(iii) Progress on Manin's conjecture and other quantitative questions by a new generation of analytic number theorists, including Browning, Loughran, Schindler, Tanimoto and many others.

(iv) The introduction of the notion of Campana points which interpolate between rational and integral points, and which give rise to a host of new Diophantine problems.

(iv) Applications of modularity over number fields to the asymptotic Fermat conjecture and other Diophantine problems due to Bennett, Dahmen, Freitas, Kraus, Sengun, Siksek and others.

Whilst these and other successes constitute dramatic progress on problems of tremendous historical importance, there has also been a divergence of methods and approaches, and the subject is undergoing a period of fragmentation. A primary objective of the workshop was to reverse this fragmentation by bringing together researchers belonging to disparate Diophantine traditions, and who would otherwise rarely interact.

Presentation Highlights

Benjamin Matschke: A general S-unit equation solver and tables of elliptic curves over number fields

Many Diophantine problems can be algorithmically reduced to solving unit and S-unit equations, including the determination of integral points on elliptic and hyperelliptic curves, the resolution of Thue and Thue–Mahler equations, and the enumeration elliptic and hyperelliptic curves of good reduction outside a given finite set of primes. Matschke presented work in progress on a new highly optimized solver for general and constraint S-unit equations over number fields. He previewed some impressive applications to computing tables of elliptic curves over number fields which involve improvements to the method of Koutsianas (Parshin, Shafarevich, Elkies). For example, Matschke has computed all elliptic curves with everywhere good reduction over all number fields K with absolute discriminants ≤ 20000.

Josha Box: Modularity of elliptic curves over totally real quartic fields not containing $\sqrt{5}$

The proof by Wiles, Breuil, Conrad, Diamond and Taylor that elliptic curves over the rationals are modular was one of the highlights of 20th century mathematics. More recently, modularity of elliptic curves over totally real fields of degree 2 and 3 has been proved by Freitas, Le Hung and Siksek, and Derickx, Najman and Siksek respectively. In fact, the strategy involves reducing the problem to the determination of low degree points on some collection of complicated modular curves. Box tackles the problem for totally real quadratic fields. Recent strong results of Thorne and Kalyanswami allow him to eliminate some of the modular curves, subject to the assumption that $\sqrt{5}$ is not contained in the field. For the remaining modular curves, Box used Chabauty's method and sieving to describe the quartic points. This allowed him to prove the following theorem.

Theorem 10.0.1 (Box)**.** *Let K be a totally real quartic fields not containing $\sqrt{5}$. Let E be an elliptic curve defined over K. Then E is modular. More precisely, there is a Hilbert eigenform $\mathfrak{f}$ over K with parallel weight 2 and rational Hecke eigenvalues such that $L(E, s) = L(\mathfrak{f}, s)$.*

Hector Pasten: A Chabauty–Coleman bound for surfaces in cubic threefolds

Let $C/\mathbb{Q}$ be a curve of genus $g \geq 2$, and write J for the Jacobian of C. Let $r = \operatorname{rank}(J(\mathbb{Q}))$ and suppose $r < g$. Let $p > 2g$ be a prime of good reduction for C. A famous theorem of Coleman assert that

$$\#C(\mathbb{Q}) \leq \#C(\mathbb{F}_p) + (2g - 2). \tag{10.0.1}$$

The method of Chabauty–Coleman can often be refined to determine the rational points $C(\mathbb{Q})$ provided the condition $r < g$ holds, and this is the most popular method for determining rational points on curves. There are extensions to Chabauty–Coleman higher dimension, which apply to symmetric powers of curves, or to Weil restrictions of curves defined over number fields, but these have yet to yield an analogue of Coleman's elegant bound (10.0.1).

Pasten sketched a proof of the following elegant theorem, which is the first instance of a Coleman-style bound in higher dimension.

Theorem 10.0.2 (Caro and Pasten)**.** *Let $A/\mathbb{Q}$ be an elliptic variety of dimension 3 such that $\operatorname{rank}(A(\mathbb{Q})) = 1$. Let $X/\mathbb{Q}$ be a smooth projective hyperbolic surface contained in A. Write $c_1^2(X) = (K_X, K_X)$ (this is the first Chern number of X). Let p be a prime $> 15c_1^2(X)^2$ of good reduction such that $X \otimes \overline{\mathbb{F}}_p$ does not contain elliptic curves. Then*

$$\#X(\mathbb{Q}) \leq \#X(\mathbb{F}_p) + (p + 4\sqrt{p} + 8) \cdot c_1^2(X).$$

Open Problems

Adam Logan: Quicksand K3s

Define a K3 surface X to be 'quicksand' if there is no map of finite degree from X to a nonisomorphic K3 surface Y. (In characteristic p I exclude supersingular K3 surfaces on both sides. I do not require every finite-degree map from X to itself to be an isomorphism.) Obviously a K3 surface is not quicksand if it has an elliptic fibration with an isogeny of degree greater than 1, or if it has a genus 1 fibration without a section.

If a K3 does not have one of these types of fibration, should it be expected to be quicksand? In particular, what about:

- X of Picard number 1;
- X with Picard lattice $U + E_6 + E_8$, where U is the hyperbolic lattice generated by x, y with $x^2 = y^2 = 0$, $(x, y) = 1$?

Probably easy: prove that there are no examples with rank greater than 16.

Lajos Hajdu: Arithmetic Progressions of Powers

Problem 1: Is it true that the length of any non-constant arithmetic progression of perfect powers (possibly with different exponents) with initial term 1 or -1 is bounded by an absolute constant?

Problem 2: More generally, is it true that the length of any primitive non-constant arithmetic progression of perfect powers (possibly with different exponents) is bounded by an absolute constant? (An arithmetic progression $a + td$ $(t = 0, 1, 2, \dots)$ is primitive if $\gcd(a, d) = 1$.)

Remarks by Lajos Hajdu: Both problems are open. Note that the cases where the exponents of the perfect powers are the same, immediately follow from results of Darmon and Merel [1].

- If in Problem 1, the first term of the progression is a with $|a| \geq 2$, then the length of the progression can be bounded in terms of a. If $a = 0$, then the length of the progression cannot be bounded. For details, see [2].
- The question in Problem 2 was answered affirmatively in [3], assuming the abc conjecture.

Benjamin Matschke: Szpiro Ratio

How large can you make $\frac{\log|\Delta_E|}{\log \operatorname{rad}(N_E)}$ for elliptic curves $E/\mathbb{Q}$? Here,

- Δ_E is the minimal discriminant of E, and
- $\operatorname{rad}(N_E)$ is the radical of the conductor of E, that is, the product of all primes of bad reduction.

Remarks:

- The limsup over all $E/\mathbb{Q}$ might be 6.
- $E : y^2 = x^3 - 54540x + 9958896$ yields $21.2187\dots$.
- Any uniform upper bound would yield a strengthening of the best currently known bounds for the *abc* conjecture.

Outcome of the Meeting

We were initially overwhelmed by the idea of running an online workshop, but the BIRS staff were really supportive and guided us through the process. The combination of using Zoom for the lectures and Zulip for the discussions worked unexpectedly well, and most talks generated good feedback and interactions. With the cancellation of many workshops and local seminar series, there are fewer opportunities for young mathematicians to shine, and so we made a choice to have as many talks by younger participants as possible. Whilst the online format lacked many of the informal exchanges that are integral to a face-to-face workshop, it has allowed us to welcome a much larger number of participants. We are particularly pleased that many PhD students and postdocs were able to join the workshop, and also with the surprising geographical spread of the participants.

Participants

Akhtari, Shabnam (Pennsylvania State University)
Alpoge, Levent (Harvard University)
Anni, Samuele (Aix-Marseille Université)
Balakrishnan, Jennifer (Boston University)
Balestieri, Francesca (The American University of Paris)
Banwait, Barinder (Ruprecht-Karls-Universität Heidelberg)
Bennett, Michael (University of British Columbia)
Best, Alexander (Vrije Universiteit Amsterdam)
Bianchi, Francesca (Groningen)
Bourdon, Abbey (Wake Forest University)
Box, Josha (University of Warwick)
Browning, Tim (Institute of Science and Technology Austria)
Bruin, Nils (Simon Fraser Univeristy)
Brumer, Armand (Fordham University)
Cantoral Farfán, Victoria (Georg-August-Universität Göttingen)
Capuano, Laura (Università degli Studi Roma Tre)
Carr, Thomas (University of Washington)
Çelik, Türkü Özlüm (Boğaziçi University)
Chan, Stephanie (University of Michigan)
Chen, Imin (Simon Fraser University)
Corpuz, Raiza (University of the Philippines Diliman)
Cremona, John (University of Warwick)
Dahmen, Sander (Vrije Universiteit Amsterdam)
Daw, Chris (University of Reading)
Dogra, Netan (King's College London)
Ejder, Ozlem (Bogazici University)
Freitas, Nuno (University of Barcelona)
Fuentes, Eliezer (Pontificia Universidad Católica de Chile)
Gallegos-Ruiz, Homero (DNA)
Garcia-Fritz, Natalia (Pontificia Universidad Católica de Chile)
Gherga, Adela (University of Warwick)
Hajdu, Lajos (University of Debrecen)
Hast, Daniel (Boston University)
Huang, Keping (Michigan State University)
Javanpeykar, Ariyan (Universitat Mainz)
Kim, Seoyoung (University of Goettingen)
Kulkarni, Avinash (Dartmouth College)
Laishram, Shanta (Indian Statistical Institute New Delhi)

Lawrence, Brian (UCLA)
Le Fourn, Samuel (Université Grenoble Alpes)
Levin, Aaron (Michigan State University)
Li, Wanlin (Washington University in St. Louis)
Logan, Adam (Government of Canada)
Loughran, Daniel (University of Bath)
Lyczak, Julian (Institute of Science and Technology Austria)
Macedo, André (University of Reading)
Malmskog, Beth * (Colorado College)
Matschke, Benjamin (Boston University)
Michaud-Jacobs, Philippe (University of Warwick)
Miller, Victor (IDA)
Müller, Steffen (University of Groningen)
Najman, Filip (University of Zagreb)
Nakahara, Masahiro (University of Washington)
Newton, Rachel (King's College London)
Ozman, Ekin (Bogazici University)
Park, Jennifer (Ohio State University)
Pasten, Hector (Pontificia Universidad Catolica de Chile)
Paucar Rojas, Rina Roxana (Instituto de Matemáticas y Ciencias Afines)
Pieropan, Marta (Utrecht University)
Plante, Thomas (Michigan State University)
Poonen, Bjorn (MIT)
Pries, Rachel (Colorado State University)
Rebolledo, Marusia (Université Clermont Auvergne)
Rivera, Carlos (University of Washington)
Roven, Sam (University of Washington)
Salgado, Cecília (Universidade Federal do Rio de Janeiro)
Schindler, Damaris (Goettingen University)
Seguel, Tomas (Pontificia Universidad Catolica de Chile)
Shankar, Arul (University of Toronto)
Shnidman, Ari (Hebrew University of Jerusalem)
Shute, Alec (Institute of Science and Technology Austria)
Siksek, Samir (University of Warwick)
Silverberg, Alice (University of California - Irvine)
Stoll, Michael (Universität Bayreuth)
Streeter, Sam (University of Bath)
Sutherland, Andrew (Massachusetts Institute of Technology)
Tanimoto, Sho (Nagoya University)
Tawfik, Mohamed (University of Reading)
Trbović, Antonela (University of Zagreb)
Turcas, George (Institute of Mathematics of the Romanian Academy)
Várilly-Alvarado, Anthony (Rice University)
Viray, Bianca (University of Washington)
Vogt, Isabel (Brown University)
Voight, John (Dartmouth College)
von Känel, Rafael (IAS Tsinghua University)
Vukovic, Andrej (University of Waterloo)
Wang, Jerry (University of Waterloo)
Watson, Lori (Wake Forest University)
Wilsch, Florian (Institute of Science and Technology Austria)
Winter, Rosa (Leiden University)

Yoo, Hwajong (Seoul National University)
Youell, Zack (University of Reading)

Bibliography

[1] H. Darmon and L. Merel, Winding quotients and some variants of Fermat's Last Theorem, *J. Reine Angew. Math.* **490** (1997), 81–100.

[2] L. Hajdu, Powerful arithmetic progressions, *Indag. Math.* **19** (2008), 547–561.

[3] L. Hajdu, Perfect powers in arithmetic progression. A note on the inhomogeneous case, *Acta Arith.* **113** (2004), 343–349.

Chapter 11

Arithmetic Aspects of Algebraic Groups 20w5133 (20w5133)

September 8 - 9, 2020

Organizer(s): Mikhail Ershov (University of Virginia), Alex Lubotzky (Hebrew University of Jerusalem), Dave Morris (University of Lethbridge), Gopal Prasad (University of Michigan)

The theory of arithmetic aspects of algebraic groups is rooted in the study of algebraic groups over global fields. (This is described in the classic monograph of V. Platonov and A. Rapinchuk [3].) A few of the major topics are finiteness theorems, rigidity theorems, the Congruence Subgroup Property, and the Kneser-Tits Conjecture. However, the field has expanded to include analogous results about algebraic groups over more general fields of arithmetic nature.

A typical finiteness theorem establishes that only finitely many algebraic groups have certain specified natural properties. For example, it was known classically that there are only finitely many connected, semisimple algebraic $\mathbf{R}$-groups of any given dimension. Such finiteness results over global fields can often be interpreted as the finiteness of the kernel of a homomorphism between certain Galois cohomology groups (cf. [3, Chap. 6]).

Rigidity theorems come in many forms, but an interesting special class of results show (roughly speaking), for certain interesting subgroups H of G, that every homomorphism defined on H can be extended to be defined on all of G. (See, for example [4].)

If G is an algebraic $\mathbf{Q}$-group, then the group $\Gamma = G_{\mathbf{Z}}$ of all integer points of G has a family of natural finite-index subgroups, called *principal congruence subgroups*. Roughly speaking, the *Congruence Subgroup Property* is the assertion that every finite-index subgroup of Γ contains at least one of these principal congruence subgroups [5]. It is still an open problem to determine which arithmetic groups have this property, and this problem has been generalized to certain other situations in which a group has a natural collection of finite-index subgroups. (See, for example, [1].)

It was conjectured more than 60 years ago that if G is an isotropic, simply-connected, almost-simple algebraic group over a field K, then the central quotient $G_K/Z(G_K)$ is simple as an abstract group. This is known to be true if K is a local field or global field, but counterexamples over certain other fields are known, and many cases remain open. This is known as the Kneser-Tits Conjecture [2].

The research area of the workshop has close connections to the theory of division algebras. (See, for example, [6].) Slightly more than a third of the talks in the workshop were specifically devoted to Brauer groups or other aspects of this fundamental area: "SK_1 triviality for l-torsion algebras over p-adic curves — a proof sketch" by Nivedita Bhaskhar (University of Southern California), "Polynomials over central division algebras" by Eli Matzri (Bar-Ilan University, Israel), "The unramified Brauer group" by Raman Parimala (Emory University), and "The generic Clifford algebra and its Brauer class" by Charlotte Ure (University of Virginia).

Half of the other talks discussed recent results on finiteness or rigidity: “Rigidity for unirational groups” by Zev Rosengarten (Hebrew University, Israel), “A finiteness theorem for special unitary groups of quaternionic skew-hermitian forms with good reduction” by Srimathy Srinivasan (University of Colorado), and “Superrigidity in rank one” by Matthew Stover (Temple University).

The remaining three talks discussed the Congruence Subgroup Problem, the Kneser-Tits Conjecture, and connections with mathematical logic: “The Congruence Subgroup Problem for automorphism groups” by David El-Chai Ben-Ezra (Hebrew University, Israel), “On the Tits-Weiss conjecture on U-operators and the Kneser-Tits conjecture for some groups of type E_7 and E_8” by Vladimir Chernousov (University of Alberta), and “Mathematical logic and its applications in arithmetics of algebraic groups and beyond” by Jinbo Ren (University of Virginia).

The workshop provided an opportunity for the community to learn about interesting recent work of strong young researchers who might not have had another outlet to obtain international exposure during the pandemic. There was also one keynote address by a leading senior researcher each day (Vladimir Chernousov and Raman Parimala). Each talk was followed by a question period, which was often quite active, and chat rooms were provided for other discussions. Even so, the level of interaction was much less than at a typical workshop, so we are very much looking forward to the in-person workshop that is scheduled to run at BIRS in 2022.

Participants

Abels, Herbert (Bielefeld University)
Abramenko, Peter (University of Virginia)
Acciarri, Cristina (University of Modena and Reggio Emilia)
Avni, Nir (Northwestern University)
Awawdeh, Areej (Hebrew University of Jerusalem)
Barlow, Jack (Emory University)
Bayer-Fluckiger, Eva (Ecole Polytechnique Federale de Lausanne (EPFL))
Belolipetsky, Mikhail (IMPA)
Ben-Ezra, David El-Chai (Soreq NRC)
Bhaskhar, Nivedita (Sisu)
Bhattacharya, Shomrik (Central Michigan University)
Bingöl, Fatma Kader (Galatasaray University)
Bitan, Rony (Afeka Academic College)
Borovoi, Mikhail (Tel Aviv University)
Braun, Amiram (University of Haifa)
Brion, Michel (Institut Fourier, Université de Grenoble)
Calmes, Baptiste (Université d’Artois)
Cao, Yang (Leibniz Universitat Hannover)
Castillo, Victor (Pontificia Universidad Católica de Chile)
Chapman, Adam (Tel-Aviv-Yaffo Academic College)
Chernousov, Vladimir (University of Alberta)
Colliot-Thélène, Jean-Louis (Université Paris-Saclay)
Ershov, Mikhail (University of Virginia)
First, Uriya (University of Haifa)
Garge, Shripad (IIT Bombay)
Gazaki, Evangelia (University of Virginia)
Gille, Philippe (Université Lyon 1)
Glubokov, Andrey (Purdue University)
Greenfeld, Beeri (Univeristy of California in San Diego)
Grimm, David * (Universidad de Santiago de Chile)
Guhan, Jayanth (Emory University)
Guo, Ning (Université Paris-Sud)

Gupta, Parul (IISER Pune (India))
Guralnick, Robert (University of Southern California)
Hawtin, Daniel (Memorial University of Newfoundland)
Hoffmann, Detlev (TU Dortmund)
Hu, Yong (Southern University of Science and Technology)
Jaikin, Andrei (Universidad Autonoma de Madrid)
Kamber, Amitay (University of Cambridge)
Karpenko, Nikita (University of Alberta)
Kassabov, Martin (Cornell University)
Katoch, Vikas (Raj Kumar Goel Institute of Technology Ghaziabad)
Kionke, Steffen (University of Hagen)
Krashen, Daniel (University of Pennsylvania)
Kulshrestha, Amit (IISER Mohali (India))
Kunyavskii, Boris (Bar-Ilan University)
Lapid, Erez (Weizmann Institute of Science)
Lifschitz, Lucy (University of Oklahoma (USA))
Lohan, Tejbir (Indian Institute of Science Education and Research Mohali , India)
Lourdeaux, Alexandre (University of Alberta)
Lubotzky, Alex (Hebrew University of Jerusalem)
Lucchini Arteche, Giancarlo (Universidad de Chile)
Malinin, Dmitry (University of Florence)
Matzri, Eli (Bar Ilan University)
McGuirk, Zachary (The Hebrew University of Jerusalem)
McInroy, Justin (University of Bristol)
McReynolds, Ben (Purdue University)
Meiri, Chen (Technion)
Merkurjev, Alexander (University of California at Los Angeles)
Morris, Dave (University of Lethbridge)
Obus, Andrew (Baruch College / CUNY Graduate Center)
Orr, Martin (University of Warwick)
Ozturk, Semra (Middle East Technical Univ. Ankara)
Parimala, Raman (Emory University)
Pei, Zitong (Emory University)
Petrov, Victor (Saint Petersburg State University)
Pham, Lam (Brandeis University)
Plotkin, Eugene (Bar-Ilan University)
Popov, Vladimir (Steklov Mathematical Institute, Moscow)
Prasad, Gopal (University of Michigan, Ann Arbor. MI)
Quéguiner-Mathieu, Anne (Université Sorbonne Paris Nord)
Raghunathan, Madabusi S. (Centre of Excellence in Basic Sciences)
Rangarajan, Bharatram (Hebrew University Of Jerusalem)
Rapinchuk, Andrei (University of Virginia)
Rapinchuk, Igor (Michigan State University)
Reichstein, Zinovy (University of British Columbia)
Rémy, Bertrand (Ecole polytechnique and CMLS)
Ren, Jinbo (Institute for Advanced Study)
Rosengarten, Zev (Hebrew University of Jerusalem)
Rowen, Louis (Bar Ilan University)
Roy, Avinash (IISER Pune, India)
Salehi Golsefidy, Alireza (University of California - San Diego)
Saltman, David (Institute for Defense Analyses/Center for Communications Research Princeton)
Santos Rego, Yuri (Otto von Guericke University Magdeburg)

Schein, Michael (Bar-Ilan University)
Schillewaert, Jeroen (University of Auckland)
Segev, Yoav (Ben Gurion University)
Shalom, Yehuda (Tel Aviv University)
Shpectorov, Sergey (University of Birmingham)
Singh, Anupam (IISER Pune, India)
Srinivasan, Srimathy (Tata Institute of Fundamental Research)
Stavrova, Anastasia (PDMI RAS)
Stover, Matthew (Temple University)
Suresh, Venapally (Emory university)
Sury, B. (Indian Statistical Institute (India))
Tignol, Jean-Pierre (UCLouvain)
Tikhonov, Sergey (Belarusian State University)
Tralle, Aleksy (University of Warmia and Mazury)
Tralle, Wojciech (University of Virginia)
Trost, Alexander (University of Aberdeen)
Ure, Charlotte (University of Virginia)
Vavilov, Nikolai (St. Petersburg State University)
Wei, Dasheng * (Chinese Academy of Science - Beijing)
Xu, Fei * (Capital Normal University, China)
Zalesskii, Pavel (University of Brasilia)
Zaynullin, Kirill (University of Ottawa)

Bibliography

[1] G. A. Fernández-Alcober, A. Garrido, and J. Uria-Albizuri, On the congruence subgroup property for GGS-groups. *Proc. Amer. Math. Soc.* **145** (2017), 3311–3322.

[2] P. Gille, Le problème de Kneser-Tits. Séminaire Bourbaki #983 (2007/2008), 39–81.

[3] V. Platonov and A. Rapinchuk, *Algebraic groups and number theory*. Academic Press, Inc., Boston, MA, 1994.

[4] I. Rapinchuk, On abstract homomorphisms of Chevalley groups over the coordinate rings of affine curves, *Transform. Groups* **24** (2019), 1241–1259.

[5] B. Sury, *The congruence subgroup problem*. Texts and Readings in Mathematics, Hindustan Book Agency, New Delhi, 2003.

[6] A. Weil, Algebras with involutions and the classical groups. *J. Indian Math. Soc.* **24** (1960), 589–623.

Chapter 12

Women in Mathematical Physics (20w5170)

September 20th-25th, 2020

Organizer(s): Nezhla Aghaei (MPIM Bonn, Germany), Ana Ros Camacho (Cardiff University, Wales)

This is a summary of activities for the virtual workshop 20w5170 "Women in Mathematical Physics" (from here on "WoMaP").

Reformulation of the WoMaP workshop for online version

Given the impossibility of a meeting in the standard Banff format, we met with the WoMaP group leaders (Katrina Barron, Gail Yamskulna, Daniela Cadamuro, Sylvie Paycha, Kasia Rejzner, Carla Cederbaum, Melanie Graf, Antonella Grassi, Elham Izadi, Ljudmila Kamenova, Julia Plavnik, Colleen Delaney, Claudia Scheimbauer, Ulrike Tillmann, Anne Taormina and Katrin Wendland) on June 29th and brainstormed together over Zoom. This was a very productive session, where we got some powerful ideas for our workshop and some important points were made. After reflecting on this feedback, collecting some extra input from the leaders via some forms, and taking into account our own considerations, the organizing team decided to have a 2-days virtual meeting on September 21st and 22nd, with only two activities per day:

- on Monday September 21st: a poster session and a (Corona) Q&A session, and
- on Tuesday September 22nd : a tribute session to work and life of Prof. Maryam Mirzakhani and a 1-to-1 mentoring session.

A summary of the principles we followed to organize the virtual meeting is:

- **Short:** we intended to keep screen-time to a minimum, and so we scheduled only four activitie in two days, which was a doable amount even for those participants overloaded with work at home.
- **Concise:** we programmed one activity a day where the participants had to be active, and another more passive, listening-type. This would produce some engagement from the participants, without a deep sensation of commitment. [1]

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[1] In our case: for day one, we had a poster session (active) and a Q&A session on work-life balance at the Corona times (passive) and for day two we had a tribute session to Maryam Mirzakhani (passive) and a 1-to-1 mentoring session (active).

- **Maximize benefit:** if it is either a more passive or active activity, we made it so the participants could get something (the most if possible) out of everything they did.[2] We offered something unique/special: at the Mirzakhani session we presented things that were never discussed before about her, like e.g. some not-so-well-known around remarks on the Mathematics education and community in Iran.

- **Minimize effort**: we had very clear communication via email of crucial details with the participants, while minimizing the amount of mails. We pointed to Zulip for extra details on anything mentioned in the emails. We kept everything optional for everybody, so they can adjust to the schedule the best they could.

- **Keep it social**: we allowed time for informal discussions, which we deemed still important to plan and have. In our case, we had "coffee breaks" with "moderators" who kept the chat alive, and according to our feedback everybody enjoyed that and requested more for next time.

- **Everybody in**: we teamed up with our group leaders for making every step. It was important to make it successful and getting everybody involved as much as we could. We chose a time frame for our activities optimal for accommodating everybody (we had a time difference of 16h between our earliest and latest participants).

Besides the 43 already invited participants, we invited 8 more (who were in our back-up list of participants or had been suggested straight away by the group leaders).

Details on the activities performed

Four activities were scheduled:

Poster session (Monday September 21st 15:15-16:15 CEST): prior to the start of the workshop, we sent a form to the participants requesting who would like to present a poster. 7 posters were presented during this session:

- Zhongshan An (University of Connecticut, USA) on "Geometric boundary conditions for the vacuum Einstein equations",
- Lisa Glaser (University of Vienna, Austria) on "Recovering geometry from spectral triples",
- Ana Kontrec (University of Zagreb, Croatia) on "Representation theory of the Bershadsky-Polyakov vertex algebra at certain levels",
- Flor Orosz Hunziker (University of Colorado, USA) on "Tensor categories arising from the Virasoro algebra",
- Veronika Pedic Tomic (University of Zagreb, Croatia) on "Fusion rules for the Beta-gamma system and Lie superalgebra gl(1,1)",
- Maria Schimpf (TU-Wien, Austria) on "Moonshine", and
- Mara Ungureanu (University of Freiburg, Germany) on "Universal polynomials for counts of secant varieties".

Corona Q&A (Monday September 21st 16:45-18:00 CEST): we had a discussion on work-life balance as a female/non-binary mathematician with a focus on the academic aftermaths of the Covid-19 pandemic. Our panel members were Katrina Barron (University of Notre Dame, USA), Stacey Harris (University of St Louis, USA), Carolina Neira (Universidad Nacional at Bogotá, Colombia) and Melanie Graf (University of Washington, USA).

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[2] In our case: those displaying a poster could get this as an extra point to their CV and get extra networking. According to our feedback, the mentoring sessions helped a lot to everybody participating.

Mirzakhani session (Tuesday September 22nd 15:00-16:15): this session included two introductory talks to the mathematical work of Maryam Mirzakhani by Jenya Shapir (former PhD student of Prof. Mirzakhani) and Elba García Faílde. The titles of the talks were "Another direction: Mirzakhani's counting theorem" and "An overview on some of the beautiful work of Maryam Mirzakhani" respectively. They were followed by a third talk by Nezhla Aghaei on the mathematics education in Iran.

During the whole week of our conference the participants had access to watch the movie "Secrets of surface: the mathematical vision of Maryam Mirzakhani", a documentary by George Csicsery on the life and mathematics of Prof. Mirzakhani. The discussion lead by Nezhla Aghaei was planned to be complementary to the documentary, trying to explain several unclear points shortly mentioned in it.

1-to-1 Mentoring session (Tuesday September 22nd 16:45-18:00): we organized private mentoring meetings between 16 participants and 13 team leaders, matching them by their preference. In the same form where we asked participants about whether they were interested on presenting at the poster session, we also asked who wanted a mentoring session and with whom. We deliberately made participants meet leaders out of their research area and optimized the requests to keep to a minimum the amount of meetings for the leaders.

Other activities: in addition to these, we had a virtual gong-show over Zulip, where everybody could introduce themselves and their research by either writing or by preparing a short video and upload it. We kept a thread in our joint Zulip on job opportunities, which we called "Hire and Seek".

Furthermore, we made available working rooms to each team to meet during the whole week (at their own discretion and choice of time). We had a brief Welcome session right before the Poster session, and "coffee breaks" between activities (moderated by four volunteers: Karina Batistelli, Yajnaseni Dutta, Flor Orosz Hunziker and Corina Keller) and a short Farewell session at the end.

Scientific Progress Made

To our knowledge, most of the WoMaP teams are currently working on their suggested research projects and expect to get publications out of them. In addition, we are aware that some extra research collaborations have started out of our workshop. It is a bit early to see the mathematical fruits of our workshop, but we expect them to start popping up soon.

Outcomes of the meeting and future plans

Besides that of BIRS, we asked to our participants for feedback on our workshop. Here's a summary of impressions:

- Many requested extra time to meet informally other participants, with e.g. longer coffee breaks or joint online lunches/dinners.
- The Poster session, the Mirzakhani session and the 1-to-1 Mentoring session were really appreciated. The Corona Q&A and Hire and Seek not so much.
- Many declared to have enjoyed lots the online version, and looked forward to the in-person version.

We plan to have an in-person version in 2022 at BIRS, once circumstances allow. We plan to give participation priority to the research groups that were on board in 2020, and open applications for whatever remaining spots. Given their success, we plan to repeat several of the activities we had in the online version.

Participants

Adamo, Maria Stella (University of Rome ”Tor Vergata”)
Addabbo, Darlayne (University of Notre Dame)
Aghaei, Nezhla (South Denmark University (SDU, QM center) and University of Geneva)
An, Zhongshan (University of Connecticut)
Barron, Katrina (University of Notre Dame)
Batistelli, Karina (Universidad de Chile)
Budzik, Kasia ()
Cadamuro, Daniela (Universität Leipzig)
Cederbaum, Carla (University of Tübingen)
Cepek, Anna (IBS-CGP)
Cogo, Albachiara (Universität Tübingen)
De Clercq, Hadewijch (Ghent University)
Delaney, Colleen (UC Berkeley)
Dutta, Yajnaseni (Universität Bonn)
Frabetti, Alessandra (University Lyon 1)
Garcia-Failde, Elba (Université Paris-Saclay)
Glaser, Lisa (University of Vienna)
Graf, Melanie (University of Washington)
Grassi, Antonella (Universita di Bologna)
Harris, Stacey (Saint Louis University)
Hoekzema, Renee (VU Amsterdam)
Iseppi, Roberta (QGM, Aarhus University)
Izadi, Elham (University of California San Diego)
Jabiri, Fatima Ezzahra (Sorbonne Universités)
Kamenova, Ljudmila (Stony Brook University)
Keller, Corina (University of Montpellier)
Kontrec, Ana (RIMS Kyoto)
Mejía Castaño, Adriana (Universidad del Norte)
Neira Jimenez, Carolina (Universidad Nacional de Colombia)
Ninad, Urmi (University of Bonn)
Orosz Hunziker, Flor (Harvard University)
Paycha, Sylvie (Potsdam University)
Pedic Tomic, Veronika (University of Zagreb)
Perales, Raquel (CIMAT)
Plavnik, Julia (Indiana University)
Rejzner, Kasia (University of York)
Ros Camacho, Ana (Cardiff University)
Sancassani, Anna (University of Tübingen)
Scheimbauer, Claudia (TU Munich)
Schimpf, Maria (TU Wien)
Taormina, Anne (Durham University)
Tillmann, Ulrike (Oxford University)
Torzewska, Fiona (University of Leeds)
Ungureanu, Mara (University of Freiburg)
Urresta, Lyda (University of Notre Dame)
Valcu, Maria Caterina (École Polytechnique)
van Gemst, Karoline (University of Sheffield)
Vičánek Martínez, Olivia (Universität Tübingen)
Wendland, Katrin (Albert-Ludwigs-Universität Freiburg)
Yamskulna, Gaywalee (Illinois State University)

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Zhang, Qing (University of California, Santa Barbara)

Chapter 13

Combinatorial and Geometric Discrepancy (20w5141)

September 30 - October 2, 2020

Organizer(s): Aleksandar Nikolov (University of Toronto), Christoph Aistleitner (Graz University of Technology), Nicole Tomczak-Jaegermann (University of Alberta), Christian Weiss (Hochschule Ruhr West)

General Information

The workshop on Combinatorial and Geometric Discrepancy was intended as a one-week workshop held at BIRS. Because of the international covid crisis, the workshop could not be held as originally planned, and will hopefully take place as an in-presence workshop at BIRS in 2021 or 2022 instead. We decided against holding the full workshop as an online event; however, to give some of the young (potential) participants an opportunity to present themselves and their research work, we organized two half-day session with online talks. All the talks were held by young researchers (typically early-stage PostDocs). Additionally, there was an open problem and discussion session.

Overview of the Field

Discrepancy theory deals with problems concerning the existence and the construction of configurations exhibiting a very high degree of regularity, usually tested with respect to a supremum norm or other norm over a large class of test objects. A classical situation are finite point sets in the d-dimensional unit cube $[0,1]^d$, with the class of test sets being the class of all axis-parallel boxes contained in $[0,1]^d$: the relative number of elements of the point set in a test box is compared with the volume, and then a supremum over all boxes in the class of test sets is taken. There are also notions of discrepancy which are of a much more combinatorial flavor, such as for example red-blue colorings of points sets. Many interesting questions concerning the smallest possible value of the discrepancy in a particular setup remain unsolved, but it is a difficult and important challenge to find (algorithmically efficient) constructions of low-discrepancy sets. Discrepancy theory is closely connected with many mathematical areas, including harmonic analysis, number theory, numerical analysis, ergodic theory, combinatorics, to name just a few. The main idea of our workshop was to bring together researchers from different mathematical areas, who are linked by their common interest in discrepancy-related topics, but who often are not closely following the developments and the methods used by other researchers working on related problems but using the language of another mathematical discipline.

Presentations

As noted above, the main idea of our online mini-workshop was to give young researchers a possibility to introduce themselves and their research area to other members of the discrepancy theory community. In total we had 9 speakers, and around 75 persons in the audience. The duration of the talks was 25 minutes each, and the speakers were asked to give non-technical and accessible talks, considering the diverse mathematical background of the members of the audience. From members of the audience we heard that the event was very entertaining and pleasant to follow. At the end of the workshop we held an open problem and discussion session, which was well attended and which some young researchers used (in the spirit of the event) to indicate that their working contracts were about to expire and that they were looking for a new (PostDoc) position.

The following talks were given during the online-workshop:

- Ryan Alweiss (Princeton University): Discrepancy Minimization via a Self-Balancing Walk
- Samantha Fairchild (University of Washington): Families of Well-approximable Measures
- Sebastian Neumayer (TU Berlin): Curve Based Approximation of Images on Manifolds
- Tetiana Stepaniuk (Universität Lübeck): Hyperuniformity of Point Set Sequences
- Hendrik Pasing (Hochschule Ruhr West): Improved Discrepancy Bounds and Estimates
- Ujue Etayo (TU Graz): A Deterministic Set of Spherical Points with Small Discrepancy
- Mathias Sonnleitner (JKU Linz): (Non-)optimal Point Sets for Numerical Integration
- Victor Reis (University of Washington): Vector Balancing in Lebesgue Spaces
- Lily Li (University of Toronto): On the Computational Complexity of Linear Discrepancy

Participants

Adamo, Maria Stella (The University of Tokyo)
Ahn, Hee-Kap (Pohang University of Science and Technology (POSTECH))
Aistleitner, Christoph (Graz University of Technology)
Alweiss, Ryan (Princeton University)
Athreya, Jayadev (University of Washington)
Bansal, Nikhil (CWI)
Barrera, Gerardo (University of Helsinki)
Beltran, Carlos * (Universidad de Cantabria)
Bilyk, Dmitriy (University of Minnesota)
Blagojevic, Pavle * (Freie Universität)
Blumenthal, Alex * (Georgia Institute of Technology)
Borda, Bence (Graz University of Technology)
Briceño, Raimundo (Pontificia Universidad Católica de Chile)
Brown, Louis (Yale University Math Department)
Brunner, Jim (Mayo Clinic)
Dadush, Daniel (Centrum Wiskunde & Informatica)
De Courcy-Ireland, Matthew (EPFL)
Defant, Colin (Harvard University)
Doerr, Benjamin (École Polytechnique)
Drmota, Michael (Technische Universitaet Wien)
Drutu, Cornelia * (Oxford University)

Dueñez, Eduardo (University of Texas at San Antonio)
El-Baz, Daniel (TU Graz)
Eren Gokmen, Buket (TU Graz)
Etayo, Ujue (TU Graz)
Fairchild, Samantha (University of Washington)
Feldheim, Ohad Noy (Hebrew University of Jerusalem)
Ferenczi, Sebastien (Institut de Mathematiques de Marseille)
Franks, Cole (MIT)
García-Lirola, Luis C. (Universidad de Zaragoza)
García-Ramos, Felipe (Universidad Autonoma de San Luis Potosi)
Ge, Yan (City University of Hong Kong)
Gnewuch, Michael (Universität Osnabrück)
Goering, Max (University of Washington)
Grepstad, Sigrid (Norwegian University of Science and Technology)
Gurel-Gurevich, Ori (Hebrew University of Jerusalem)
Hauke, Manuel (TU Graz)
Hinrichs, Aicke (Johannes Kepler Universität Linz)
Hofer, Roswitha (Johannes Kepler Universität)
Huicochea, Mario (CONACyT/UAZ)
Jaquette, Jonathan (Boston University)
Jiménez de Santiago, Valentín (Instituto de Matemáticas UNAM)
Kolountzakis, Mihalis (University of Crete)
Kovac, Vjekoslav (University of Zagreb)
Kritzer, Peter (Austrian Academy of Sciences)
Kwietniak, Dominik (Jagiellonian University)
Lapkova, Kostadinka (TU Graz)
Larcher, Gerhard (Johannes Kepler Universitat)
Latala, Rafal (University of Warsaw)
Leobacher, Gunther (KFU Graz)
Li, Lily (University of Toronto)
Lipnik, Gabriel (TU Graz)
Litvak, Alexander (University of Alberta)
Liu, Yang (Stanford University)
Lovett, Shachar (University of California San Diego)
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Mastrianni, Michelle (University of Minnesota - Twin Cities)
Matzke, Ryan (University of Minnesota)
Meka, Raghu (UCLA)
Munsch, Marc (TU Graz)
Myroshnychenko, Sergii (University of Alberta)
Neumayer, Sebastian (TU Berlin)
Newman, Alantha (CNRS and Université Grenoble-Alpes)
Nikolov, Aleksandar (University of Toronto)
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Ortega Moreno, Oscar Adrian (Technische Universität Wien)
Park, Josiah (Texas A & M University)
Pasing, Hendrik (Ruhr West University of Applied Sciences)
Pausinger, Florian (Queen's University Belfast)
Petersen, Karl (University of North Carolina)
Petrache, Mircea (Pontificia Universidad Católica de Chile)
Pillichshammer, Friedrich (Johannes Kepler Universität)

Pohl, Anke (Universität Bremen)
Putterman, Eli (Tel Aviv University)
Ramachandran, Akshay (University of Waterloo)
Reis, Victor (IAS)
Roysdon, Michael (Brown University)
Rubin, Natan (Ben-Gurion University)
Sadhu, Susmita * (Georgia College and State University)
Sawhney, Mehtaab (Massachusetts Institute of Technology)
Singh, Mohit (Georgia Institute of Technology)
Skill, Thomas (Hochschule Bochum)
Sonnleitner, Mathias (JKU Linz)
Sourmelidis, Athanasios (TU Graz)
Steinerberger, Stefan (University of Washington)
Stepaniuk, Tetiana (Universität zu Lübeck)
Szarek, Stanislaw (Case Western Reserve University)
Taha, Diaaeldin (American University in Cairo)
Technau, Marc (TU Graz)
Tomczak-Jaegermann, Nicole (University of Alberta)
Travaglini, Giancarlo (Università di Milano-Bicocca)
Treviño, Rodrigo (University of Maryland)
Ullrich, Mario (JKU Linz)
Verjovsky, Alberto (UNAM Mexico)
Vlasiuk, Oleksandr (Florida State University)
Weiss, Christian (Hochschule Ruhr West)
Xing, Sudan (University of Arkansas at Little Rock.)
Yang, Daodao (TU Graz)
Yoo, Jisang (Sungkyunkwan University)

Chapter 14

Dynamical Algebraic Combinatorics (20w5164)

October 19 - 30 2020

Organizer(s): Tom Roby (University of Connecticut), James Propp (University of Massachusetts-Lowell), Jessica Striker (North Dakota State University), Nathan Williams (University of Texas at Dallas)

Overview of the Field

Rowmotion and Homomesy. *Rowmotion* was introduced by Duchet in [Duc74]; studied for the Boolean lattice (and the product of two chains) by Brouwer and Schrijver [BS74, Bro75]; and (still for the Boolean lattice) related to matroid theory by Deza and Fukuda [DF90]. Cameron and Fon-der-Flaass considered rowmotion on the product of two and then three chains [Fon93, CF95]. Because the orbit structure of rowmotion on Boolean lattices is so wild, much of the effort in the references above is dedicated to understanding which orbit sizes are realizable.

Its study then apparently lay dormant for over a decade until Panyushev resurrected it in the form of a series of conjectures of the orbit structure of rowmotion on the root posets of Lie algebras [Pan09]. The focus then shifted to finding equivariant bijections to natural combinatorial objects, and Stanley (and, independently, Thomas) completely characterized the orbit structure of rowmotion on the product of two chains combinatorially (using the Stanley-Thomas word) [Sta09]. Armstrong, Stump, and Thomas [AST13] resolved Panyushev's conjectures using an equivariant bijection to noncrossing partitions under the Kreweras complement, while Striker and Williams unified and extended various results by relating rowmotion to *jeu-de-taquin* and made terminological innovations to the theory [SW12]. Influentially, Propp and Roby returned to the product of two chains and introduced the notion of *homomesy* [PR15]. This popularization of rowmotion led to a swell of related work falling under Propp's heading of *dynamical algebraic combinatorics*.

K-Theoretic Promotion and Resonance. Work of Dilks, Pechenik, Striker, and later Vorland connected rowmotion to Thomas and Yong's K-theoretic *jeu-de-taquin*, developed to compute structure coefficients in K-theoretic Schubert calculus [DPS17, DSV19]. The quasi-periodicity (under the name *resonance*) of K-theoretic promotion of rectangular tableau was studied by Dilks, Pechenik, and Stiker using the relationship to rowmotion on plane partitions [DPS17]; this relationship was exploited in the other direction by Patrias and Pechenik to resolve a long-standing conjecture of Cameron and Fon-Der-Flaass [PP20]. The relationship to K-theoretic slides was later picked up by Dao, Wellman, Yost-Wolff, and Zhang [DWYWZ20] via a bijection of Hamaker, Patrias, Pechenik, and Williams between plane partitions of trapezoidal and rectangular posets [HPPW20].

Piecewise-Linear Rowmotion and Promotion of Semistandard Tableaux. Motivated by Berenstein and Kirillov's piecewise-linear Bender-Knuth involutions on Gelfand-Tsetlin patterns [KB95], Einstein and Propp considered a piecewise-linear lifting of rowmotion to the order polytope of a poset [EP13+, EP14]. Einstein and Propp [EP14] (and Hopkins [Hop20, Appendix A], as well as Propp [1]) elucidated the connection between piecewise-linear rowmotion on rectangular plane partitions and promotion of rectangular semistandard Young tableaux, further solidifying the representation-theoretic connections. With Bernstein and Vorland, Striker generalized semistandard tableaux and promotion to P-strict labelings under promotion, establishing a more general correspondence between PL-rowmotion on plane partitions and promotion on (flagged and symplectic) tableaux [BSV20]. Thus, rowmotion on plane partitions recovers K-theoretic promotion on increasing tableaux, while PL-rowmotion on plane partitions recovers promotion of semistandard tableaux.

Birational Rowmotion Einstein and Propp further lifted rowmotion to the birational setting (from which tropicalization recovers the piecewise-linear definition) [EP13+, EP14]. Birational rowmotion on rectangles and shifted staircases was studied by Grinberg and Roby [GR15, GR16]; Glick and Grinberg later showed in unpublished work that one of the Grinberg-Roby results was equivalent to an instance of Zamolodchikov periodicity. Building on the Grinberg-Roby result, Musiker and Roby gave a precise description using families of non-intersecting lattice paths for powers of birational rowmotion on rectangles, giving an independent proof of periodicity and homomesy [MR19].

Joseph and Roby have continued in this birational direction with a generalization of the Stanley-Thomas word [JR20b], as well as a definition of birational toggles on antichains and a generalization to the noncommutative (skew field) setting [JR20a].

Minuscule Posets and Representation Theory. Rush and Shi placed rowmotion in a natural representation-theoretic setting, which gives a partial explanation for the reappearance in the theory of certain posets with preferred properties [RS13]. Using the Striker-Williams conjugacy result, they obtained a uniform and conceptual explanation for the periodicity of rowmotion on combinatorial models of bases for minuscule representations V_λ (notably, all weight-spaces have dimension one), by connecting rowmotion to the action of a Coxeter element of W. Rush later built on this machinery in [RW15+, Rus16+] to establish homomesy results. Through the connection with Bender-Knuth involutions in type A, piecewise-linear rowmotion corresponds to the action of the cactus group on $V_{m\lambda}$, although this connection remains mysterious in general. Certain homomesies were established by Bloom, Pechenik, and Saracino in [BPS16].

At the piecewise-linear level, using the reflection functors of quiver representation theory (and embedding minuscule posets inside the Auslander-Reiten quiver of the root category), Garver, Patrias, and Thomas gave a uniform proof of periodicity of piecewise-linear rowmotion on minuscule posets [GPT18]. They further show that the RSK and Hillman-Grassl correspondence are recovered as special cases of their constructions via certain compositions of PL-toggles.

At the birational level, Okada checked the remaining E_7 case by computer to complete the proof of periodicity of birational rowmotion for minuscule posets (the other cases were essentially dealt with above by Grinberg and Roby) [Oka20]. Okada also established homomesies via a case-by-case check.

Rowmotion in other Settings. Striker extended the definition of rowmotion by concentrating on generalizing the concept of toggle [Str15, Str16]. Joseph completed one branch of this program by establishing the relationship between toggles on antichains and toggles on order ideals [Jos19], and other variants of toggles on more varied combinatorial objects appeared in [STWW17, CHHM17, EFG16].

Joseph and Roby studied the structure of rowmotion on order ideals in a zigzag poset, with the interpretation as independent sets of a path graph [JR18]. Motivated by this, lattice theory, Catalan combinatorics, and quiver representation theory, Thomas and Williams worked on independent sets of directed acyclic graphs, giving their independent sets a partial order from which rowmotion could be computed in several different ways [TW19b, TW19a]. Galashin and Pylyavskyy's R-systems give a different generalization (of birational rowmotion) to strongly connected directed graphs [GP19].

Recent Developments and Open Problems

- It is still open to show that PL-rowmotion on general trapezoidal posets and Hopkins' V poset has the predicted order (a good survey is given in [Hop20b]).
- Cyclic sieving phenomena (CSP) for plane partitions in minuscule and coincidental root posets under PL-rowmotion remain unproven. There is no equivariant correspondence between minuscule and their coincidental doppelgängers (beyond height one).
- There is no representation-theoretic interpretation of birational toggles. Such an interpretation could lead directly to a proof of the CSPs above using the representation-theoretic paradigm for proving the CSPs above [RSW04, Lemma 2.4].
- It would be good to generalize the relationship in type A between the cactus group and Bender-Knuth involutions should generalize to other types. This is being currently studied by Dranowski, Elek, Kamnitzer, Libman, and Morton-Ferguson.
- Williams and his student Kraushal are developing piecewise-linear and birational analogues of independence posets.

Further open problems were presented in the problem session on the last day of the conference, and are available on Zulip.

Presentation Highlights

All talks were given remotely, using Zoom.

Monday, October 19. Striker gave the first talk of the workshop, giving a historical overview of dynamical algebraic combinatoics (DAC) through her work extending notions of rowmotion and promotion to increasingly broad classes of objects [SW12, Str16, DPS17, DSV19]. Striker's student Vorland gave the second talk, introducing the notion of homomesy and illustrating several examples of the phenomenon. The day concluded with Garver speaker on his joint work with Patrias and Thomas on PL-rowmotion on minuscule posets, interpreting the problem using the language of quiver representation theory [GPT18].

Wednesday, October 21. Pechenik spoke of his recent work with Patrias [PP20] resolving a conjecture of Cameron and Fon-der-Flaass regarding the orbit lengths of rowmotion on the product of three chains by using his previous work connecting this problem to K-theoretic promotion [DPS17, BPS16, Pec17]. Patrias spoke of her work in generalizing promotion on webs (invariant tensors in $V^{\otimes n}$ for V the first fundamental representation of $\mathfrak{sl}_2$) to webs with two colors (now invariant tensors using factors V and V^*). Gunawan gave an expository talk on classical friezes, building to cluster algebras.

Friday, October 23. Roby's talk "Let's birational" explained his continuing work extending "classical" homomesy and periodicity results from the combinatorial to piecewise-linear and birational levels. Okada followed with his recent proof of homomesy results for all minuscule posets at the birational level of generality. The day concluded with 14 posters, given via breakout rooms; participants were free to roam the breakout rooms, or stay in the main room to chat. A moderator stayed in the room to help direct participants with an older version of Zoom.

1. Carlos Alejandro Alfaro - The sandpile groups of outerplanar graphs (joint work with Ralihe Raúl Villagrán)
2. Joseph Bernstein - P-strict promotion and piecewise-linear rowmotion (joint work with Jessica Striker and Corey Vorland)
3. Colin Defant - Promotion Sorting (joint work with Noah Kravitz)
4. Ben Drucker, Eli Garcia, and Rose Silver - RSK algorithm and the box-ball system (joint work with Aubrey Rumbolt)
5. Noah Kravitz - Friends and strangers walking on graphs (joint work with Noga Alon and Colin Defant)

6. Matthew Macauley - Abstract Algebra through Cayley diagrams, actions, and lattices
7. Rene Marczinzik - Distributive lattices and Auslander regular algebras (joint work with Osamu Iyama)
8. Jaeseong Oh - Cyclic sieving and orbit harmonics (joint work with Brendon Rhoades)
9. GaYee Park - Naruse Hook length formula for linear extensions of mobile posets
10. Matthew Plante - Periodicity and Homomesy for the $V \times [n]$ poset and center-seeking snakes
11. Samu Potka - Refined Catalan and Narayana Cyclic Sieving (joint work with Per Alexandersson, Svante Linusson, and Joakim Uhlin)
12. James Propp - A Spectral Theory for Combinatorial Dynamics
13. Bruce Sagan - Fences, unimodality, and rowmotion (includes joint work with Thomas McConville and Clifford Smyth)
14. Hugh Thomas - Independence posets (joint work with Nathan Williams).

Monday, October 26. Williams spoke on his joint work “Independence Posets” with Thomas (also presented as an interactive poster); independence posets are a generalization of distributive lattices, eliminating the lattice requirement and allowing for several definitions of rowmotion. Barnard then followed with her related representation-theoretic work on generalizing the Kreweras complement (or rowmotion) to semidistributive lattices. Yıldırım discussed her thesis work on the Coxeter transformation on cominuscule posets, discussing the similarities of this transformation to rowmotion.

Wednesday, October 28. Grinberg spoke about Littlewood-Richardson coefficients and birational combinatorics. Following this, Joseph discussed recent work on a birational lifting of the Lalanne–Kreweras involution on Dyck paths and Hopkins spoke on rowvacuation of root posets. This topic relates to work of Panyushev, whose work initiated a lot of the recent activity in DAC. Hopkins noted the open problem he discussed could serve to “bring DAC full circle.”

Friday, October 30. The last day was dedicated to a moderated open problem session, with participants then joining breakout rooms to work on their preferred problem, also using the Zulip platform. Problems were presented by Sagan and Gunawan, Joseph, Pechenik, Hopkins, and Propp.

- **Sagan and Gunawan.** A fence is a poset induced by an orientation of a path graph — its distributive lattice of order ideals has many interpretations, including as certain perfect matchings and certain weak order intervals in the symmetric group. What can be said about rowmotion orbits on fences with more than two segments?
- **Pechenik.**
  1. Give a direct proof that the order of K-promotion on $\mathrm{Inc}^{a+b}(a\times b)$ is $a+b$, and similarly for $\mathrm{Inc}^{a+b+1}(a\times b)$ and $a+b+1$.
  2. Is there a Cameron/Fon-Der-Flaass theorem for products of 4 chains/other “nice” posets?
- **Joseph.** The trapezoid poset $T(a,b) = \{(i,j) : 1 \leq i \leq a \text{ and } i \leq j \leq a+b-i\}$, defined for $a < b$, is a “doppelganger” of the poset $[a] \times [b]$, and the two posets have some similar behavior under rowmotion.
  1. For $T(2,b) \times [c]$, antichain cardinality appears to be homomesic for rowmotion.
  2. Orbit structure on $T(2,b) \times [c]$ appears to be the same as that of $[2] \times [b] \times [c]$.
  3. For $T(a,b) \times [2]$ with $3 \leq a \leq b$, the order of rowmotion appears to be $2(a+b+1)$, which is twice that of $[a] \times [b] \times [2]$.
  4. Find a birational lifting of the OY (Oksana Yakimova) invariant of [Pan04].
  5. There are several interesting problems regarding toggling independent sets of a cycle graph.

- **Hopkins.** Prove Narayana symmetry for W-nonnesting partitions under the antichain cardinality (slides at `http://www.birs.ca/workshops/2020/20w5164/files/Hopkins_talk.pdf`).
- **Propp.** Prove that the antichain cardinality statistic is homomesic under Propp's q-generalization of rowmotion, described in `http://jamespropp.org/q-rowmotion.pdf`.

Scientific Progress Made

A team of (mostly young) researchers who attended the workshop has solved a problem raised by organizer Jim Propp during the open problem session. Colin Defant, Sam Hopkins, Svetlana Poznanovik, and others participating in a shared Zulip thread have shown that organizer Jessica Striker's toggleability statistic and its generalizations, and the "rooks" technique developed by Hopkins and his collaborators, are the key to obtaining both proofs of new results in the field (specifically, the desired homomesy result for q-rowmotion) and streamlined proofs of already-known results. One or more articles are expected to result from this burst of effort.

Hopkins and Joseph have already posted a preprint to the arXiv (https://arxiv.org/abs/2101.02329) studying a PL and birational generalization of the Lalanne–Kreweras involution on Dyck paths. In particular, they prove that the number of valleys and major index symmetry properties of the Lalanne–Kreweras involution extend to these lifts.

Defant and Hopkins used the work of Armstrong, Stump, and Thomas [AST13] to find an explicit map on nonnesting partitions of classical type that proves Narayana symmetry. This work has been posted to the arXiv (https://arxiv.org/abs/2012.15795)

The group considering Sagan and Gunawan's problem on fence posets (Elizalde, Gunawan, Plante, Roby, Sagan, Serhiyenko, and Yıldırım) has proven a number of results characterizing orbit structures and proving homomesic statistics for rowmotion acting on fence posets with specific parameters. These could be turned into a preprint at any time, but the group is currently trying to explore the wide range of possibilities further.

After engaging in some computer exploration, a team consisting of Karen Collins, Oliver Pechenik, Anne Schilling, and Jessica Striker concluded that the Cameron/Fon-Der-Flaass theorem does not extend to products of 4 chains (counterexample in $[2] \times [2] \times [2] \times [3]$) or the simplest "bird" poset from Proctor's d-complete posets.

Outcome of the Meeting

Although the community was disappointed to have to postpone our face-to-face meeting due to the coronavirus pandemic, we felt that the online meeting went very well. We made a point of emphasizing early-career mathematicians among our invited speakers. The overall quality of the presentations was excellent.

A number of open problems were presented at the end of the meeting, and continue to be actively pursued by subgroups of the participants (some on the Zulip thread, others via email and Overleaf).

The video lectures make a valuable permanent record of the state of dynamical algebraic combinatorics in Fall 2021, and will be useful to other young researchers who wish to become involved.

We think the meeting generated a lot of enthusiasm for the subfield, and created interpersonal connections between researchers at various levels of their professional careers, which will stand us in good stead for having a successful in-person meeting at Banff when the pandemic permits.

Participants

Adin, Ron (Bar-Ilan university)
Alexandersson, Per (Stockholm University)
Alfaro Montufar, Carlos Alejandro (Bank of Mexico)
Alhajjar, Elie (United States Military Academy)
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Arreche, Carlos (The University of Texas at Dallas)

Banaian, Esther (Aarhus University)
Barkley, Grant (Harvard University)
Barnard, Emily (DePaul University)
Berenstein, Arkady (University of Oregon)
Bergeron, François (Université du Québec à Montréal)
Bernstein, Joe (North Dakota State University)
Billey, Sara (University of Washington)
Biswal, Rekha (National Institute of Science Education and Research - Bhubaneswar)
Brauner, Sarah (University of Minnesota)
Burcroff, Amanda (Harvard University)
Buskirk, Adam * (North Dakota State University)
Byun, Seok Hyun (Indiana University Bloomington)
Cameron, Peter (University of St Andrews)
Chen, Angela (University of Minnesota)
Collins, Karen (Wesleyan University)
Colmenarejo, Laura (North Carolina State University)
Commins, Patty (University of Minnesota)
Condon, Daniel (Indiana University)
David, Laurent-Marc (University of Texas-Dallas)
Defant, Colin (Harvard University)
Desai, Deep (University of Texas at Dallas)
Drucker, Ben (Swarthmore College)
Elizalde, Sergi (Dartmouth College)
Eu, Sen-Peng (National Taiwan Normal University)
Farrell, Libby (University of Minnesota)
Feinberg, Robert (self)
Forsman, Joey (NDSU Math Graduate Student)
Franckowiak, Spencer (University of Texas at Dallas)
Fraser, Chris (Michigan State University)
Gaetz, Christian (UC Berkeley)
Galashin, Pavel * (UCLA)
Gao, Yibo (MIT)
Garver, Alexander (University of Michigan)
Gaudin, Solal (Universitat Wien)
Gessel, Ira (Brandeis University)
Glubokov, Andrey (Purdue University)
Greene, Curtis (Haverford College)
Greenwood, Torin (North Dakota State University)
Grinberg, Darij (Drexel University)
Gunawan, Emily (University of Oklahoma)
Haglund, Jim (University of Pennsylvania)
Hamaker, Zachary (University of Florida)
Heuer, Dylan (North Dakota State University)
Höngesberg, Hans (University of Vienna)
Hopkins, Sam (Howard University)
Hopkins, Brian (Saint Peter's University)
Hossain, Chetak (Texas State University)
Hwang, Byung-Hak (Sungkyunkwan University)
Johnson, Joe (North Carolina State University)
Joseph, Michael (Dalton State College)
Jung, Woo-Seok (Sogang University)
Karn, Trevor (University of Minnesota)

Kelley, Elizabeth (University of Illinois Urbana-Champaign)
Kim, Jang Soo (Sungkyunkwan University)
Krattenthaler, Christian (University of Vienna)
Küstner, Josef (University of Vienna)
Lai, Tri (University of Nebraska)
Lakshmanadoss, Karthikeyan * (University of Texas at Dallas)
Lazar, Alexander (KTH Royal Institute of Technology)
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Lee, Yi-Lin (Indiana University)
Lee, Kang-Ju (Seoul National University)
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Liu, Ricky (University of Washington)
Lo, Yuan-Hsun (National Pingtung University)
Macauley, Matthew (Clemson University)
Majumder, Pritam (Indian Statistical Institute - Kolkata)
Mandelshtam, Olya (University of Waterloo)
Marczinzik, Rene (University of Stuttgart)
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McConville, Thomas (Kennesaw State University)
McDonough, Alex (University of California - Davis)
Meunier, Paul (École normale supérieure de Lyon)
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Moore, Katherine (Wake Forest University)
Musiker, Gregg (University of Minnesota)
Nadeau, Philippe (CNRS & University Lyon 1)
Nenashev, Gleb (Brandeis University)
Nguyen, khanh (Otto-von-Guericke- Universität Magdeburg)
Oh, Jaeseong (Seoul National University)
Okada, Soichi (Nagoya University)
Panova, Greta (University of Southern California)
Park, GaYee (UMass Amherst)
Patrias, Rebecca (University of Michigan)
Pechenik, Oliver (University of Waterloo)
Perkinson, David (Reed College)
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Plante, Matthew (University of Connecticut)
Potka, Samu (KTH Royal Institute of Technology)
Poznanovic, Svetlana (Clemson University)
Propp, James (University of Massachusetts - Lowell)
Pylyavskyy, Pavlo (University of Minnesota - Twin Cities)
Rashid, Mushfiq (University of Texas at Dallas)
Reiner, Victor (University of Minnesota, Minneapolis)
Rhoades, Brendon (UC San Diego)
Roby, Tom (University of Connecticut)
Sadhukhan, Arghya * (University of Maryland)
Sagan, Bruce (Michigan State University)
Saikia, Manjil (Cardiff University)
Schiffler, Ralf (University of Connecticut)
Schilling, Anne (University of California, Davis)
Scott, Jeanne (Universidad de los Andes)

Scrimshaw, Travis (University of Queensland)
Serhiyenko, Khrystyna (University of Kentucky)
Sferrazza, Michelle (The University of Texas at Dallas)
Shakir, Qays (Middle Technical University)
Sherman-Bennett, Melissa (MIT)
Silver, Rose (Northeastern University)
Smirnov, Evgeny (National Research University Higher School of Economics)
Solhjem, Sara (Minnesota State University Moorhead)
Stanley, Richard (University of Miami)
Stephens, Riley (The University of Texas at Dallas)
Striker, Jessica (North Dakota State University)
Sundaram, Sheila (University of Minnesota)
Swanson, Joshua (University of Southern California)
Terada, Itaru (University of Tokyo)
Tewari, Vasu (University of Pennsylvania)
Thomas, Hugh (Université du Québec à Montréal)
Van Willigenburg, Stephanie (UBC)
Vargas, Yannic (Graz University of Technology)
Vindas Meléndez, Andrés (University of Kentucky)
von Bell, Matias * (University of Kentucky)
Vorland, Corey (Marian University)
Williams, Lauren * (Harvard)
Williams, Nathan (University of Texas at Dallas)
Williams, Austin (University of Texas at Dallas)
Wilson, Andy (Kennesaw State University)
Winkler, Peter (Dartmouth College)
Winter, Matthew (The University of Texas at Dallas)
Yip, Martha (University of Kentucky)
Yıldırım, Emine (Queen’s University)
Yoo, Meesue (Chungbuk National University)
Young, Benjamin (University of Oregon)
Zhang, Sylvester (University of Minnesota - Twin Cities)

Bibliography

[AST13] Drew Armstrong, Christian Stump, and Hugh Thomas, A uniform bijection between nonnesting and noncrossing partitions, *Transactions of the American Mathematical Society* **365** (2013), no. 8, 4121–4151.

[BSV20] Joseph Bernstein, Jessica Striker, and Corey Vorland, P-strict promotion and piecewise-linear rowmotion, with applications to tableaux of many flavors, arXiv preprint arXiv:2012.12219 (2020).

[BPS16] Jonathan Bloom, Oliver Pechenik, and Dan Saracino, Proofs and generalizations of a homomesy conjecture of Propp and Roby, *Discrete Mathematics* **339** (2016), no. 1, 194–206.

[Bro75] Andries Brouwer, On dual pairs of antichains, *Stichting Mathematisch Centrum. Zuivere Wiskunde* (1975), no. ZW 40/75, 1–8.

[BS74] Andries Brouwer and Alexander Schrijver, On the period of an operator, defined on antichains, *Stichting Mathematisch Centrum. Zuivere Wiskunde* (1974), no. ZW 24/74.

[CF95] Peter J Cameron and Dmitry G Fon-der-Flaass, Orbits of antichains revisited, *European Journal of Combinatorics* **16** (1995), no. 6, 545–554.

[CHHM17] Melody Chan, Shahrzad Haddadan, Sam Hopkins, and Luca Moci, The expected jaggedness of order ideals, *Forum of Mathematics, Sigma* **5** (2017).

[CGP16] Michael Chmutov, Max Glick, and Pavlo Pylyavskyy, The Berenstein-Kirillov group and cactus groups, arXiv preprint arXiv:1609.02046 (2016).

[DWYWZ20] Quang Vu Dao, Julian Wellman, Calvin Yost-Wolff, and Sylvester W Zhang, Rowmotion orbits of trapezoid posets, arXiv preprint arXiv:2002.04810 (2020).

[DF90] Michel Marie Deza and Komei Fukuda, Loops of clutters, *Coding Theory and Design Theory*, Springer, 1990, 72–92.

[DPS17] Kevin Dilks, Oliver Pechenik, and Jessica Striker, Resonance in orbits of plane partitions and increasing tableaux, *Journal of Combinatorial Theory, Series A* **148** (2017), 244–274.

[DSV19] Kevin Dilks, Jessica Striker, Corey Vorland, Rowmotion and Increasing Labeling Promotion. *J. Combin. Theory Ser. A*, **164** (2019), 72–108.

[Duc74] Pierre Duchet, Sur les hypergraphes invariants, *Discrete Math.* **8** (1974), no. 3, 269–280.

[EFG16] David Einstein, Miriam Farber, Emily Gunawan, Michael Joseph, Matthew Macauley, James Propp, and Simon Rubinstein-Salzedo, Noncrossing partitions, toggles, and homomesies, *The Electronic Journal of Combinatorics* **23** (2016), no. 3, P3–52.

[EP14] David Einstein and James Propp, Piecewise-linear and birational toggling. *26th International Conference on Formal Power Series and Algebraic Combinatorics (FPSAC 2014)*, *Discrete Math. Theor. Comput. Sci. Proc.* **AT**, 513–524.

[EP13+] David Einstein and James Propp, Combinatorial, piecewise-linear, and birational homomesy for products of two chains, arXiv preprint arXiv:1310.5294 (2013).

[Fon93] Dmitry G Fon-der-Flaass, Orbits of antichains in ranked posets, *European journal of combinatorics* **14** (1993), no. 1, 17–22.

[GP19] Pavel Galashin and Pavlo Pylyavskyy, R-systems, *Selecta Math. (N.S.)* **25** (2019), no. 2, Paper No. 22, 63 pp.

[GPT18] Alexander Garver, Rebecca Patrias, and Hugh Thomas, Minuscule reverse plane partitions via quiver representations, arXiv preprint arXiv:1812.08345 (2018).

[GR15] Darij Grinberg and Tom Roby, Iterative properties of birational rowmotion II: rectangles and triangles. *Elec. J. Combin.* **22**(3), #P3.40, 2015.

[GR16] Darij Grinberg and Tom Roby, Iterative properties of birational rowmotion I: generalities and skeletal posets, *Elec. J. Combin.* **23**(1), #P1.33, 2016.

[HPPW20] Zachary Hamaker, Rebecca Patrias, Oliver Pechenik, and Nathan Williams, Doppelgängers: Bijections of Plane Partitions, *Int. Math. Res. Not. IMRN 2020*, no. 2, 487–540.

[Hop20] Sam Hopkins, Cyclic sieving for plane partitions and symmetry, *SIGMA Symmetry, Integrability and Geometry: Methods and Applications* **16** (2020), 130.

[Hop20b] Sam Hopkins, Order polynomial product formulas and poset dynamics, arXiv preprint arXiv:2006.01568 (2020).

[HPPW20] Zachary Hamaker, Rebecca Patrias, Oliver Pechenik, and Nathan Williams, Doppelgängers: bijections of plane partitions, *International Mathematics Research Notices* **2020** (2020), no. 2, 487–540.

[Jos19] Michael Joseph, Antichain toggling and rowmotion, *Electron. J. Combin.* **26** (2019), no. 1, Paper No. 1.29, 43 pp.

[JR18] Michael Joseph and Tom Roby, Toggling independent sets of a path graph. *Electron. J. Combin.* **25** (2018), no. 1, Research Paper P1.18.

[JR20a] Michael Joseph and Tom Roby, Birational and noncommutative lifts of antichain toggling and rowmotion, *Algebraic Combinatorics* **3** (2020), no. 4, 955–984.

[JR20b] Michael Joseph and Tom Roby, A birational lifting of the Stanley–Thomas word on products of two chains, arXiv preprint arXiv:2001.03811 (2020).

[KB95] Anatolii Nikolaevich Kirillov and Arkady D Berenstein, Groups generated by involutions, Gelfand–Tsetlin patterns, and combinatorics of Young tableaux, **7** (1995), no. 1, 92–152.

[Oka20] Soichi Okada, *Birational rowmotion and Coxeter-motion on minuscule posets*, arXiv preprint arXiv:2004.05364 (2020).

[MR19] Gregg Musiker and Tom Roby, Paths to understanding birational rowmotion on products of two chains. *Algebr. Comb.* **2** (2019), no. 2, 275–304.

[Pan09] Dmitri Panyushev, On orbits of antichains of positive roots, *European Journal of Combinatorics* **30** (2009), no. 2, 586–594.

[Pan04] Dmitri Panyushev, ad-nilpotent ideals of a Borel subalgebra: generators and duality, *Journal of Algebra* 274(2):822–846, 2004.

[PP20] Rebecca Patrias and Oliver Pechenik, Dynamics of plane partitions: Proof of the Cameron–Fon-der-Flaass conjecture, *Forum of Mathematics, Sigma*, Vol. 8, Cambridge University Press, 2020.

[Pec14] Oliver Pechenik, Cyclic sieving of increasing tableaux and small Schröder paths, *J. Combin. Theory Ser. A*, **125** 357–378, (2014).

[Pec17] Oliver Pechenik, Promotion of increasing tableaux: Frames and homomesies, *Electron. J. Combin.* **24**(3) (2017), #P3.50.

[1] James Propp, *Young tableaux as lattice points in order cones: promotion, fiber-flipping and cyclic sieving*, MIT Combinatorics Seminar given March 11, 2015, notes available at `http://faculty.uml.edu/jpropp/gtt-promotion.txt`

[PR15] James Propp and Tom Roby, Homomesy in products of two chains. *Elec. J. Combin.* **22** (2015), no. 3.

[RSW04] Victor Reiner, Dennis Stanton, and Dennis White, The cyclic sieving phenomenon. *J. Combin. Theory Ser. A* **108** (2004), no. 1, 17–50.

[Rob16] Tom Roby, Dynamical algebraic combinatorics and the homomesy phenomenon, in A. Beveridge, J. Griggs, L. Hogben, G. Musiker, P. Tetali, eds., *Recent Trends in Combinatorics, IMA Vol. Math. Appl., 159*, Springer, [Cham], 2016, 619–652

[RS13] David B Rush and XiaoLin Shi, On orbits of order ideals of minuscule posets, Journal of Algebraic Combinatorics **37** (2013), no. 3, 545–569.

[RW15+] David B Rush and Kelvin Wang, On orbits of order ideals of minuscule posets II: homomesy, arXiv preprint arXiv:1509.08047 (2015).

[Rus16+] David B Rush, On order ideals of minuscule posets III: The CDE property, arXiv preprint arXiv:1607.08018 (2016).

[Sag11] Bruce Sagan, The cyclic sieving phenomenon: a survey. *Surveys in combinatorics 2011*, 183–233, London Math. Soc. Lecture Note Ser., **392**, *Cambridge Univ. Press, Cambridge* (2011).

[STWW17] Anne Schilling, Nicolas M. Thiéry, Graham White, and Nathan Williams, Braid moves in commutation classes of the symmetric group, *European Journal of Combinatorics* **62** (2017), 15–34.

[Sta09] Richard P. Stanley, Promotion and evacuation, *Electronic Journal of Combinatorics* **16** (2009), no. 2, R9.

[SW12] Jessica Striker and Nathan Williams, Promotion and rowmotion. Eur. J. Combin. 33 (2012), no. 8, 1919–1942.

[Str15] Jessica Striker, The toggle group, homomesy, and the Razumov-Stroganov correspondence, *Electron. J. Combin.* **22** (2015), no. 2, Paper 2.57, 17 pp.

[Str16] Jessica Striker, Rowmotion and generalized toggle groups, *Discrete Math. Theor. Comput. Sci.* **20** (2018), no. 1, Paper No. 17, 26 pp.

[Str17] Jessica Striker, Dynamical algebraic combinatorics: Promotion, rowmotion, and resonance, *AMS Notices*, June/July 2017, 543–549.

[TW19a] Hugh Thomas and Nathan Williams, Independence posets, *Journal of Combinatorics* 10 (2019), no. 3, 545–578.

[TW19b] Hugh Thomas and Nathan Williams, Rowmotion in slow motion, *Proceedings of the London Mathematical Society* **119** (2019), no. 5, 1149–1178.

[Vor19] Corey Vorland, Homomesy in products of three chains and multidimensional recombination, *Electron. J. Combin.* **26** (2019), no. 4, Paper No. 4.30, 26 pp.

Chapter 15

Algebraic Dynamics and its Connections to Difference and Differential Equations (20w5206)

November 9 - 14, 2020

Organizer(s): Jason P. Bell (University of Waterloo), Dang-Khoa Nguyen (University of Calgary), Thomas Scanlon (UC Berkeley)

First of all, we wish to thank BIRS for supporting this 5-day workshop which had to be done in an online format due to travel restrictions caused by the pandemic.

Overview of the Workshop

This workshop brings together (in an online setting) researchers in Algebraic Dynamics and Algebraic Differential and Difference Equations. Each is a highly interesting area in its own and an important connection between them lies in the model theory of difference fields. There have been several significant results in both sides recently. One the one hand, we have results involving the classification of periodic subvarieties of split polynomial maps, canonical heights, equidistribution, and unlikely intersections. On the other hand, we have results on difference Galois theory, algebraic independence of Mahler functions, and Painlevé irreducibility of certain Schwarzian equations. This workshop comes at the right time to further the exchange of ideas, collaboration, and advancement of both areas.

There are 12 talks in total featuring a wide range of topics. All the talks are done through Zoom. We strive to commit to diversity and inclusion: at least one third of the talks is given by members of underrepresented groups is mathematics. Although the number of talks is only around 60% the number in a “normal” BIRS 5-day workshop in order to accommodate speakers and participants from different time zones, many of the talks attract more participants than the typical capacity of 40 people in the BIRS lecture hall at Banff. After each talk, many participants choose to remain in the “main room” to continue the discussion with the speaker. Many other participants can also join the “breakout room” in which they have casual chats about life at different parts of the world during this challenging time.

Presentation Highlights

Unlike a normal workshop in which participants would travel to the Banff Centre and devote the whole week for the workshop activities, this time everyone still needs to continue with duties at his/her home institution as well as familial responsibilities. In spite of this, each talk is prepared carefully and delivered in the most engaging way possible. For this reason, we feel that every single talk has to be part of the highlight of this workshop. In chronological order, these talks are:

- “Difference equations over fields of elliptic functions” by Ehud Deshalit (Einstein Institute of Mathematics).
- “Billiards and the arithmetic of non-arithmetic groups ” by Curtis McMullen (Harvard).
- “On the Zariski dense orbit conjecture” by Junyi Xie (IRMAR - Université de Rennes 1).
- “Schwarzian equation, automorphic functions and functional transcendence” by Joel Nagloo (CUNY).
- “Elliptic surfaces and R-divisors ” by Laura DeMarco (Harvard).
- “Equivariant currents and heights on the boundary of the ample cone of a K3 surface” by Simion Filip (Chicago).
- “A couple of conjectures in arithmetic dynamics over fields of positive characteristic” by Dragos Ghioca (UBC).
- “Model theory of group actions on fields” by Piotr Kowalski (Uniwersytet Wrocławski).
- “Definable Galois theory and holomorphic vector bundles” by Anand Pillay (Notre Dame).
- “On an arithmetic criterion for holonomicity” by Vesselin Dimitrov (UToronto).
- “Algebraic independence of solutions of linear difference equations” by Charlotte Hardouin (IMT - Université Paul Sabatier.)
- “Finite orbits and canonical heights for large groups of automorphisms” by Serge Cantat (Université de Rennes 1).

Further Comments

Although the main drawback of the online format is that participants cannot devote as much time and energy, there are several notable advantages. The first obvious one is the elimination of carbon footprint and environmental impact of travel. The second is the increase in the number and diversity of participants: while most participants are from Europe and North America due to the more favorable time zones, there are also several participants from China, Japan, and other places.

Dr. Di Vizio at CNRS sent us the following comments after the workshop, “..., it is easier to follow on Zoom than on the live video that are recorded at BIRS usually. So I think that we, all of us, have to think about how to organize hybrid online-in presence events, which should be the norm in the future. I’m digressing...I was skeptical about the whole on line things, but actually it worked nicely for me: I followed the talks better than usual (but I was not jet-lagged and there were less of them, which is good). Mathematically, I liked the talks. There were 4 of 5 of them which were of particular interest for me and that I found outstanding...”

Participants

Adamczewski, Boris (CNRS, Lyon)
Albayrak, Seda (University of Waterloo)
Barroero, Fabrizio (Università degli studi Roma 3)
Bell, Jason (University of Waterloo)
Benedetto, Rob (Amherst College)
Bugeaud, Yann * (Université de Strasbourg)
Cantat, Serge (CNRS, University Rennes 1)
Capuano, Laura (Università degli Studi Roma Tre)
Chatzidakis, Zoé (CNRS)
Chen, Shaoshi (Chinese Academy of Sciences)
Dang, Nguyen-Bac (Stony Brook University)
Delaygue, Eric (Universite de Lyon 1)
DeMarco, Laura (Harvard University)
Deshalit, Ehud (Hebrew University of Jerusalem)
Di Vizio, Lucia (Universite de Versailles-St Quentin)
Diller, Jeffrey (University of Notre Dame)
Dimitrov, Vesselin (University of Toronto)
Dreyfus, Thomas (Universite de Strasbourg)
Dujardin, Romain (Sorbonne Université)
Eterović, Sebastian (UC Berkeley)
Favre, Charles (CNRS)
Feng, Ruyong (Chinese Academy of Sciences)
Fili, Paul (Oklahoma State University)
Filip, Simion (University of Chicago)
Firsova, Tatiana (Kansas State University)
Freitag, James (University of Illinois at Chicago)
Gauthier, Thomas (Ecole Polytechnique)
Ghioca, Dragos (University of British Columbia)
Glubokov, Andrey (Purdue University)
Gunn, Keira (University of Calgary)
Hardouin, Charlotte (Institut de mathematiques de Toulouse)
Henson, Ward (University of Illinois)
Hindes, Wade (Texas State University)
Hrushovski, Ehud (Oxford)
Hu, Fei (University of Oslo)
Ih, Su-ion (University of Colorado at Boulder)
Ingram, Patrick (York University)
Jones, Rafe (Carleton College)
Jones, Gareth (University of Manchester)
Juul, Jamie (Colorado State University)
Kamensky, Moshe (Ben Gurion University)
Kawaguchi, Shu (Doshisha University)
Kowalski, Piotr (Uniwersytet Wrocławski)
Krieger, Holly (University of Cambridge)
Leon Sanchez, Omar (University of Manchester)
Lesieutre, John * (The Pennsylvania State University)
Lind, Douglas (University of Washington)
Looper, Nicole (Brown University)
Mavraki, Myrto (University of Basel)
McMullen, Curtis (Harvard University)

Medvedev, Alice * (City College of New York)
Mello, Jorge (UNSW Sydney)
Meretzky, David (The University of Notre Dame)
Mishna, Marni (Simon Fraser University)
Moosa, Rahim (University of Waterloo)
Mutchnik, Scott (UC Berkeley)
Nagloo, Joel (University of Illinois at Chicago)
Nguyen, Dang Khoa (University of Calgary)
Okuyama, Yusuke (Kyoto institute of technology)
Olechnowicz, Mateusz (University of Toronto)
Ovchinnikov, Alexey (CUNY Queens College)
Padgett, Adele (UC Berkeley)
Pakovich, Fedor (Ben Gurion University)
Pillay, Anand (University of Notre Dame)
Poonen, Bjorn (MIT)
Ramadas, Rohini (Brown University)
Reichstein, Zinovy (University of British Columbia)
Satriano, Matthew (University of Waterloo)
Scanlon, Thomas (University of California, Berkeley)
Schmidt, Harry (University of Basel)
Silverman, Joseph (Brown University)
Singer, Michael (North Carolina State University)
Vicaría, Mariana (UCLA)
Walker, Roland (University of Illinois at Chicago)
Wibmer, Michael (Graz University of Technology)
Wood, Carol (Wesleyan University)
Xie, Junyi (BICMR of Pekin University)
Yasufuku, Yu (Nihon University)
Ye, Hexi (Zhejiang University)
Zannier, Umberto * (Scuola normale superiore, Pisa, Italy)
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Bibliography

[1] E. De Shalit, Elliptic (p, q)-difference modules, to appear in *Algebra & Number Theory*, 2020.

[2] C. McMullen, Billiards, heights, and the arithmetic of non–arithmetic groups, preprint available on the author's website, 2020.

[3] J. Xie, The existence of Zariski dense orbits for endomorphisms of projective surfaces (with an appendix in collaboration with Thomas Tucker), preprint available on the author's website, 2019.

[4] G. Cassale, J. Freitag, and J. Nagloo, Ax-Lindemann-Weierstrass with derivatives and the genus 0 Fuchsian groups, *Annals of Mathematics* **192** (3), 721-765, 2020.

[5] L. DeMarco and N. Mavraki, Elliptic surfaces and arithmetic equidistribution for R-divisors on curves, preprint available on the author's website, 2020.

[6] S. Filip and V. Tosatti, Canonical currents and heights for K3 surfaces, preprint available on the author's website, 2021.

[7] P. Corvaja, D. Ghioca, T. Scanlon, and U. Zannier, The Dynamical Mordell-Lang conjecture for endomorphisms of semiabelian varieties defined over fields of positive characteristic, *J. Inst. Math. Jussieu*, **20** (2), 669-698, 2021.

[8] D. Hoffmann and P. Kowalski, Model theory of fields with finite group scheme actions, preprint available on the author's website, 2020.

[9] B. Adamczewski, T. Dreyfus, C. Hardouin, and M. Wibmer, Algebraic independence and linear difference equations, to appear in *Journal of the European Mathematical Society*, 2021.

[10] S. Cantat and R. Dujardin, Finite orbits for large groups of automorphisms of projective surfaces, preprint available on the author's website, 2020.

Two-day
Workshop
Reports

Chapter 16

Alberta Number Theory Days XII (20w2254)

May 1 - 3, 2020

Organizer(s): Andrew Fiori (University of Lethbridge), Zafer Selcuk Aygin (University of Calgary/University of Lethbridge), Jack Klys (University of Calgary), Eric Primozic (University of Alberta)

Special Circumstances

Due to the COVID crises all in person events where by necessity cancelled and we chose to proceed with our planned conference in a virtual format using online support systems provided by the Banff International Research Station (BIRS).

To honour the memory of the Late Richard Guy this event was dedicated to him.

Objectives achieved:

This was the twelfth edition of Alberta Number Theory Days. Previous conferences took place in Lethbridge (2008), Calgary (2009), and BIRS (2010, 2011, 2013, 2014, 2015, 2016, 2017, 2018, 2019). This meeting gathers the number theorists of the Alberta Universities to interact and exchange ideas. Its purpose is to solidify the relations between Alberta Number Theorists, to motivate local young researchers, and to create ties with out-of-province researchers. Despite the online nature of the event participants did have opportunities to interact socially.

This year, the conference had a total of 13 talks. One was a plenary lecture given by Mike Bennett from the University of British Columbia. Other out-of-province speakers included Allysa Lumley from the CRM (Montreal). There were a total of 5 talks by Faculty Members, 3 by Postdoctoral Researchers and 5 by Graduate Students.

The event included participants from the University of Alberta, the University of Calgary, the University of Lethbridge, Concordia University of Edmonton, King's University in Edmonton, and Mount Royal University in Calgary. One of our aims is to provide early-career researchers with access to a nourishing research environment is reflected in the participant pool in general. To this end our list of participants include both senior undergraduate and graduate students. Do to the online nature of this event there were no limits on participation numbers and invitations to participate were extended to anyone with a connection to number theory in Alberta. There were a total of 44 registered participants, though not all of these attended all the talks we recorded at least 35 unique attendees across all events and the major events enjoyed over 30 participants. Due to the open nature of the invitation to participate the demographics of the event reflect precisely those of the Alberta Number Theory community.

Scientific highlight:

This year, the scientific highlights included the plenary talk given by Michael Bennett from the University of British Columbia as well as several talks with personal connections to the work of Richard Guy.

Particpants:

Aygin, Zafer Selcuk (University of Lethbridge)
Fiori, Andrew (University of Lethbridge)
Klys, Jack (University of Calgary)
Primozic, Eric (University of Alberta)
Akbary, Amir (University of Lethbridge)
Ali, Abid (University of Alberta)
Bennett, Michael (University of British Columbia)
Berger, Arno (University of Alberta)
Broadbent, Sam (University of Lethbridge)
Cameron, Alex (University of Calgary)
Cunningham, Clifton (University of Calgary)
Das, Sourabh (University of Lethbridge)
Fakhari, Milad (University of Lethbridge)
Feaver, Amy (The King's University)
Greenberg, Matthew (University of Calgary)
Gunn, Keira (University of Calgary)
Hamieh, Alia (University of Northern British Columbia)
Hasanalizade, Elchin (University of Lethbridge)
Jacobson, Jr., Michael (University of Calgary)
Joshi, Aniket (University of Alberta)
Kadiri, Habiba (University of Lethbridge)
Leem, Sumin (University of Calgary)
Lumley, Allysa (York University)
MacDonald, Colter (University of Alberta)
Morrill, Ryan (University of Calgary)
Ng, Nathan (University of Lethbridge)
Nguyen, Dang Khoa (University of Calgary)
Pacheco Castan, Edgar (University of Calgary)
Patnaik, Manish (University of Alberta)
Roettger, Eric (Mount Royal University)
Scheidler, Renate (University of Calgary)
Shen, Quanli (University of Lethbridge)
Smolcic, Josip (University of Lethbridge)
Sobrevilla Moreno, Pedro (University of Calgary)
Steele, James (University of Calgary)
Swidinsky, Joshua (University of Lethbridge)
Topaz, Adam (University of Alberta)
Totani, Yash (University of Lethbridge)
Tran, Ha (Concordia University of Edmonton)
Vooys, Geoff (University of Calgary)
Wong, Peng-Jie (University of Lethbridge)
Yee, Randy (University of Waterloo)
Zhang, Qing (University of Calgary)
de Waal, André (University of Calgary)

Titles of talks:

Speaker: Renate Scheidler
Title: Difference Necklaces

Speaker: Randy Yee
Title: Unconditional computation of fundamental units in number fields

Speaker: Peng-Jie Wong
Title: Refinements of Strong Multiplicity One for GL(2)

Speaker: Aniket Joshi
Title: Hecke operators on vector-valued modular forms

Speaker: Allysa Lumley
Title: Distribution of values of L-functions in the critical strip - Function Field version

Speaker: Michael Bennett
Title: Differences Between Perfect Powers (Plenary)

Speaker: Sourabh Das
Title: An explicit version of Chebotarev's density theorem

Speaker: Arno Berger
Title: Digits, dynamics, and Benford's Law

Speaker: Qing Zhang
Title: Arthur packets for sub-regular unipotent representations of G2

Speaker: Eric Roettger
Title: Some Primality Tests Constructed from a Cubic Extension of the Lucas Functions

Speaker: Abid Ali
Title: Gindikin-Karpelevich Finiteness for Local Kac-Moody Groups

Speaker: Quanli Shen
Title: The fourth moment of quadratic Dirichlet L-functions

Speaker: Michael Jacobson, Jr.
Title: Statistical Analysis of Aliquot Sequences

Chapter 17

Canadian Queueing Theorists and Practitioners Conference (20w2253)

August 21 - 22, 2020

Organizer(s): Javad Tavakoli (UBC Okanagan), Yiqiang Zhao (Carleton University)

Overview of the Field

Queueing theory is the mathematical study of various aspects arisen from the congestion and delays of waiting in line, including modelling, performance, control, simulation, computations, approximations, inference, optimization among possible others. Moreover, Queueing Systems involve ”customers” waiting for ”services.” Where, the terms ”customers” and ”servers” are generic. Customers could, for example, be humans waiting in a physical line or waiting on hold on telephones, jobs waiting to be processed in a factory, or tasks waiting for processing in a computer or communication system and more of this type of services.

The CanQueue annual conference started from a workshop, organized by Dr. Alfa, at the University of Manitoba in 1999. Since then, twenty (20) CanQueue conferences have been held in Canada, including CanQueue 2002 at U of Saskatchewan; 2004 at UBC Okanagan, 2006 and 2011 at Banff, both sponsored by BIRS. It was a decision at the CanQueue2019, at Fields Institute in Toronto in August 2019 that CanQueue 2020 will be organized by us and held at Banff (based on the feedback from Canadian queueing community people). It turned out a very special and very successful event of this Canqueue, despite the pandemic of COVID-19.

Queueing theory started with the work of Danish mathematician A. K. Erlang in 1909, which was motivated by the problem of designing telephone exchanges. The field has grown to include the application of a variety of mathematical methods to the study of waiting lines in many different contexts. The mathematical methods include Markov processes, linear algebra, transform theory, and asymptotic methods, to name a few. The areas of application include computer and communication systems, manufacturing systems, and health care systems. Many recent developments in queueing theory have been driven in large part by a greater interest in applications that involve human customers, for example in the rapidly growing call centre sector. Humans behave in less predictable ways than, say, jobs in a factory or tasks in a computer system. For example, they may renege (abandon the queue), and retry later. The needs of human customers are likely to be heterogeneous (motivating the use of skills-based routing to connect different customers to different servers) and to vary with time (sometimes requiring transient rather than steady state solutions).

In CanQueue2020, which sponsored by BIRS, more than 40 participants attended, most of whom are from Canada and some of whom are from USA, Australia and Europe. Two prominent professors: Prof. Peter Taylor of the University of Melbourne and Winfried K. Grassmann of the University of Saskatchewan provided plenary (one-hour) speeches at the event.

The plenary talk by Prof. Taylor addressed admission policies for complex resource allocation problems, and the talk by Prof. Grassmann emphasised that queueing theory is in a world where most queueing problems are solved by simulation.

There were 16 other research talks given at the conference within the two days (August 21-22). Seven of these talks were delivered by graduate students or post-docs, covering a broad spectrum of topics such as: block-structured queues, double-sided queues, GI/G/1 queues, queues with time-varying periodic transition rates, statistical queues, admission policies, allocation problems, copulas, error estimation, matrix-analytic methods (MAM), mean-field approximations, random walks, simulation, optimal joining strategies, Markov chain decomposition method, health care applications.

Overall, on the feedbacks of participants, this conference was very successful and useful mostly for graduate students. Moreover, it was a great idea that the whole talks have been recorded by BIRS facilities and availability of talks for public. In fact, this technology first used in this conference, by the fact that the conference was virtual, which was successful.

Participants

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