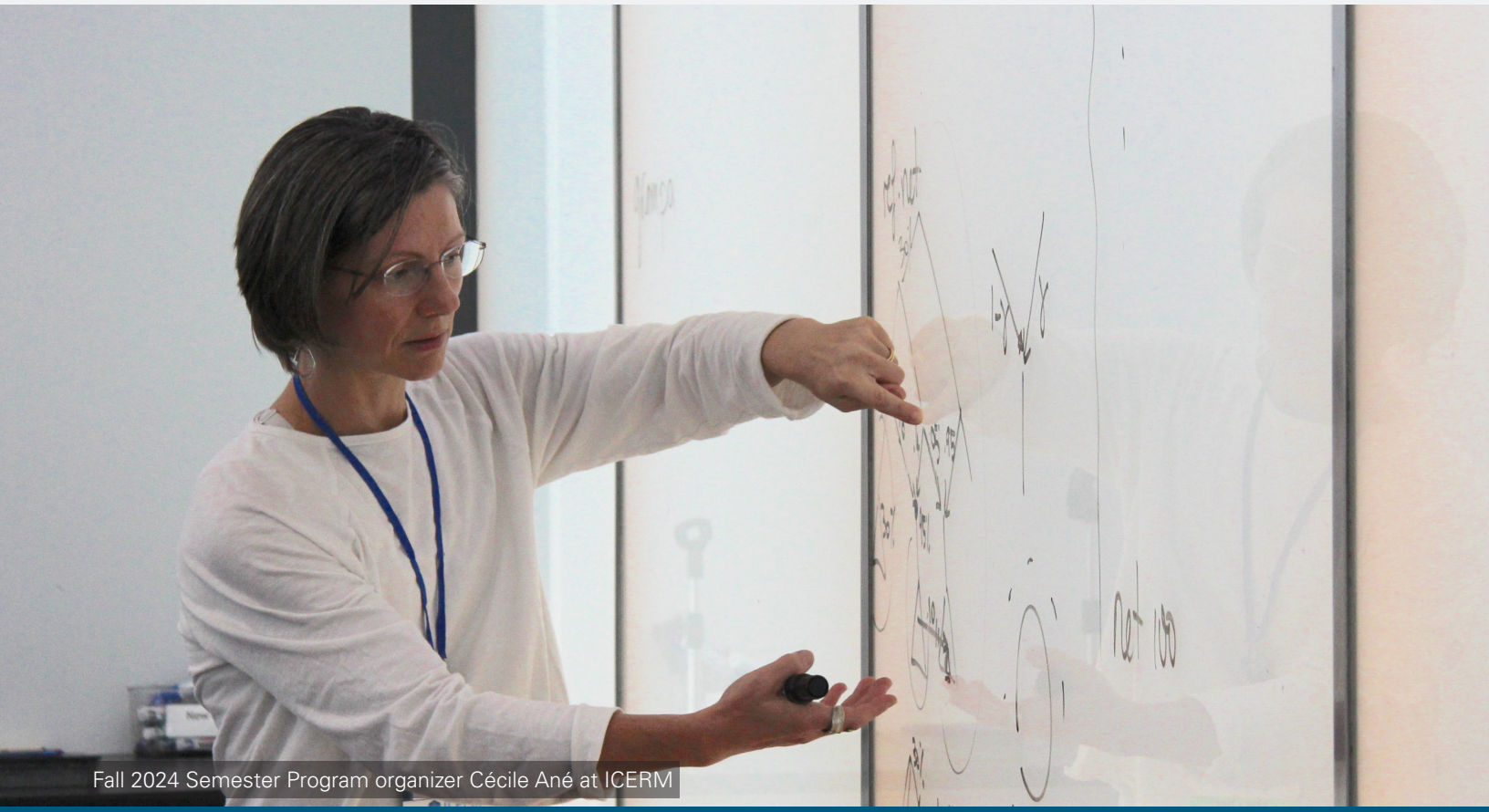
Fall 2024 Newsletter



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Newsletter Editor/Layout and Design: Halle Bryant

UPDATES FROM DIRECTOR BRENDAN HASSETT

Greetings!

This semester, ICERM has the pleasure of hosting the Fall Semester Program Theory, Methods, and Applications of Quantitative Phylogenomics. Researchers in residence at ICERM have been immersed in their work, developing new methods to bridge information about evolutionary relationships with ever-increasing genomic data. The program is co-organized by Elizabeth Allman (University of Alaska Fairbanks), Cécile Ané (University of Wisconsin - Madison), Elizabeth Gross (University of Hawai'i at Manoa), Barbara Holland (University of Tasmania), Laura Kubatko (The Ohio State University), Simone Linz (University of Auckland), Siavash Mirarab (UCSD), John Rhodes (University of Alaska Fairbanks), Sebastien Roch (University of Wisconsin-Madison), and Leo Van Lersel (Delft University of Technology).

Since September, over 130 experimental biologists, computer scientists, mathematicians, and statisticians have visited ICERM for three major workshops addressing mathematical and statistical challenges in phylogenetics, many of which are related to the need for advanced computational tools. We expect participants' work related to gene flow modeling, anomalous phylogenetic networks, inference problems on gene orders, and other timely subjects to encourage new directions in mathematical and biological research for years to come.

ICERM has hosted two Hot Topics Workshops this Fall – Modeling and Simulations in Fluids and Robust Optimization and Simulation of Complex Stochastic Systems. During Modeling and Simulations in Fluids, participants came together to advance the study of turbulent mixing and combustion and honor the work of James Glimm, who received a 2002 National Medal of Science for his outstanding research in computational fluid dynamics. Robust Optimization and Simulation of Complex Stochastic Systems explored different perspectives on uncertainty quantification, efficient simulation, and analysis of complex stochastic systems. The workshop paid special attention to the work of Brown University's IBM Professor of Applied Mathematics Paul Dupuis, whose contributions to the study of large deviations, stochastic control, and numerical methods have been extremely influential.

More recently, we were pleased to welcome the 2024 Blackwell-Tapia Conference, held November 15–16. The biennial conference honors Dr. David Blackwell and Dr. Richard Tapia, two groundbreaking figures who have inspired generations of Black, Latinx, and Indigenous students and researchers in the mathematical sciences. Each time ICERM hosts Blackwell-Tapia, we are excited by the range of mathematical topics covered in a short amount of time, from computational biology to trace ideals. This year, we were honored to hear from Richard Tapia himself and celebrate Illya Hicks, the recipient of the 2024 Blackwell-Tapia Prize. We are grateful to the Mathematical Sciences Institutes Diversity Initiative, the Alfred P. Sloan Foundation, the Brown University Department of Mathematics, and the Brown University Office of Institutional Equity and Diversity for making this year's Blackwell-Tapia Conference possible.

I would also like to congratulate ICERM Co-founder Björn Sandstede and ICERM Principal Investigator Benoît Pausader on their appointments to the American Mathematical Society's 2025 Class of Fellows! AMS Fellows are elected by their peers for their exceptional contributions to mathematics, both through scholarship and service. Those of us at ICERM who have worked closely with Björn and Benoît know just how well-deserved this honor is. We are proud to have them on our leadership team and look forward to seeing what this new chapter brings.

To our alumni and friends, I am grateful for your support and participation in ICERM's mission to broaden the relationship between mathematics and computation. The end of 2024 provides an opportunity to reflect on the past year of scientific inquiry and exploration at the institute. Since January, we have hosted programs and events across the mathematical spectrum, from algebraic cycles to phylogenetics, machine learning to astrophysics, and mathematical databases to optimization. Across the board, these programs have led to new collaborations and relationships that will steer our participants' work and benefit their research communities for years to come. In 2025, we look forward to another year of programs that are just as far-reaching and — we hope — just as fruitful for our visitors!

See you at your next workshop!

Sincerely,



Brendan Hassett

UPCOMING PROGRAMS

Semester Programs

Spring 2025: Geometry of Materials, Packings, and Rigid Frameworks

Feb 10 - 12: Circle Packings, Minimal Surfaces, and Discrete Differential Geometry

Mar 17 - 21: Matroids, Rigidity, and Algebraic Statistics

Apr 7 - 11: Geometry of Materials

Fall 2025: Categorification and Computation in Algebraic Combinatorics

Sep 15 - 19: Category Theory, Combinatorics, and Machine Learning

Oct 20 - 24: Diagrammatic Categorification

Nov 10 - 14: Computation in Representation Theory

Spring 2026: Stochastic and Randomized Algorithms in Scientific Computing: Foundations and Applications

Fall 2026: Computations on K3 Surfaces and Related Varieties

Topical Workshops

Dec 9 - 13, 2024: Harmonic Analysis and Convexity

Jan 6 - 10, 2025: Computational Learning for Model Reduction

Jan 13 - 17, 2025: Women in Mathematical Computational Biology

Jan 21 - 24, 2025: Patterns, Dynamics, and Data in Complex Systems

May 12 - 16, 2025: Links in Dimensions 3 and 4

Jun 2 - 6, 2025: Scientific Machine Learning for Gravitational Wave Astronomy

Jun 23 - 27, 2025: Algebraic Points on Curves

Jul 7 - 11, 2025: LMFDB, Computation, and Number Theory (LuCaNT) 2025

Jul 21 - 25, 2025: Innovative and Efficient Strategies for Stiff Differential Equations

Aug 11 - 15, 2025: Illustrating Math: Reunion & Expansion

MEET ICERM'S FALL 2024 EARLY-CAREER FELLOWS*

Maize Curiel

Fall 2024 Semester Postdoc



Maize Curiel received their Ph.D. in 2024 from the University of Hawai'i at Manoa under the supervision of Elizabeth Gross. Their doctoral dissertation is titled "Algebraic and Combinatorial Applications in Systems and Evolutionary Biology." Maize joined ICERM in Fall 2024 for the Semester Program Theory, Methods, and Applications of Quantitative Phylogenomics. Their research interests are in applied algebraic geometry and combinatorics.

ICERM: What most excites you about what you're researching right now?

Curiel: So I really like computing things. I compute a lot of ideals, varieties, mixed volumes, and those kinds of things. Anything that has ties to geometry and algebra - those are things I really like to compute.

ICERM: How do you describe your work to people who aren't experts in your field?

Curiel: I do a lot of algebraic geometry stuff, so at its core it's something that we're pretty familiar with. If you're thinking of your high school algebra class, you solve linear equations or quadratic equations, and that's just a line in the plane or a quadratic in the plane. I think that's something people can understand or have seen before. And so I tell them I solve equations, but that I'm also interested in the geometry of them. That's usually an entry point that I like to use.

ICERM: What first inspired you to pursue mathematics and computational biology and what keeps you engaged?

Curiel: I think I've always been interested in math but I think when I first learned there was math beyond calculus… When I was in undergrad I took my first intro to proofs class. That's when I really learned that there was math beyond calculus and I think that was really exciting for me. It felt endless, and it kind of is, right? So I think that was really exciting and then I just continued to keep learning and building after that. When I was in undergrad, actually with Joe Rusinko, who's also here [at ICERM], we did a project that was phylogenetics-related. It was very combinatorial and it was a really difficult problem, but it was really interesting.

What keeps me motivated? I think just learning new things. That's really good fuel and is really exciting, but also finding new projects where I can use the things that I've learned and apply them. I [also] think meeting new people and traveling to new places is really fun, just learning more about what's really out there in math and what I can do. This is my first postdoc so learning about the field and what it means to be a mathematician at this stage is scary, but also exciting.

ICERM: What are you looking forward to in the semester at ICERM?

Curiel: I guess that's what I'm looking forward to. I'm looking forward to learning new problems, more computations. I'm going to be applying to jobs this semester and I guess I'm looking forward to meeting people and figuring out what that might mean for me in terms of jobs. I'm also just really excited that there are a lot of people here who I've met before. Like Joe [Rusinko], I think I haven't seen him since I graduated undergrad so it's nice to see people I've met before but still get to know people I haven't and their work. ■

**Transcripts have been lightly edited for clarity.*

Dimitrios Diamantidis

2024- 2025 Institute Research Associate



Dimitrios Diamantidis received his Ph.D. in 2024 from the Mathematics Department at Indiana University under the supervision of Wai Tong (Louis) Fan. In the academic year 2024-2025, he joins ICERM as a Postdoctoral Fellow, participating in the Fall Semester Program Theory, Methods, and Applications of Quantitative Phylogenomics. His research interests lie at the intersection of probability theory, population genetics, and coalescent theory. In particular, he is working on conditional coalescent theory and is interested in its applications to genomic data under various independence structures as theoretically captured by matroids.

ICERM: What most excites you about what you're researching right now?

Diamantidis: There are a few things. One is that the study of random trees just seems fun to me and interesting. And also there are connections with actual problems and genetic data that could potentially be better analyzed through theoretical work at the intersection of biology broadly speaking and mathematics is encouraging.

ICERM: How do you describe your work to people who aren't experts in your field?

Diamantidis: I would say that during my Ph.D., the most recent work that I did was on coalescent theory and populations and ethics. We were trying to model the evolutionary relationships of different versions of genes within a population through the use of trees.

ICERM: What first inspired you to pursue mathematics and computational biology and what keeps you engaged?

Diamantidis: The thing that interests me about math is essentially the ability to solve puzzles, come up with creative solutions, and there is this feeling of persisting on a problem until it finally starts to click that feels very rewarding to me. And computationally biology or, more broadly speaking, biology, I think that's thanks to my PhD advisor Wai Tong (Louis) Fan, who was a good figure to introduce me to the mathematics that are being used in biology.

ICERM: What are you looking forward to in the year at ICERM?

Diamantidis: Some good research. Hopefully that will produce interesting outcomes. ■

Apply to be a 2025-2026 ICERM Postdoctoral Fellow

ICERM is accepting applications for postdoctoral fellowship positions in the 2025-2026 academic year. These positions are intended for mathematical scientists at an early stage of their career, specifically those who have completed their Ph.D. within three years of the start of the appointment.

Applications are open for 9-month Institute Postdoc positions and 4-month Semester Postdoc positions. Appointed postdocs will join ICERM's Fall 2025 or Spring 2026 Semester Programs: Categorification and Computation in Algebraic Combinatorics (Fall 2025) or Stochastic and Randomized Algorithms in Scientific Computing: Foundations and Applications (Spring 2026). **Apply via MathJobs.org**.

Marina Garotte López

Fall 2024 Semester Postdoc



Marina Garrote-López received her Ph.D. in 2021 from the Universitat Politècnica de Catalunya under the supervision of Marta Casanellas and Jesús Fernández Sánchez. Her doctoral thesis is titled "Algebraic and Semi-algebraic Phylogenetic Reconstruction." She joined ICERM in September 2024, participating in the Theory, Methods, and Applications of Quantitative Phylogenomics Semester Program. Previously, she was a postdoctoral researcher at the Max Planck Institute for Mathematics in the Sciences and the University of British Columbia. She also spent a short period as a postdoctoral fellow at the University of Alaska, working with Elizabeth S. Allman and John A. Rhodes. Her research focuses on integrating theoretical and computational algebraic tools to comprehensively analyze the geometric and algebraic structure of statistical models derived from problems in evolutionary biology, and graphical models or machine learning to address questions related to identifiability, parameter estimation, and causal inference.

ICERM: What most excites you about what you're researching right now?

Garotte López: I work on phylogenetics, which is the topic of the semester, but from an algebraic perspective. So we use algebra and algebraic tools to understand the phylogenetic models. This can be [placed] inside a bigger topic called algebraic statistics, which is using algebra to understand different statistical models. And now I'm transitioning a little bit from working only on phylogenetics to other statistical models. So I'm working on some things more applied to machine learning and data science, and I'm excited to see how these algebraic tools can be used to really understand a lot of different models with many many applications.

ICERM: How do you describe your work to people who aren't experts in your field?

Garotte López: So I would try to explain to people what algebra is, which is basically polynomials. I think everyone has seen polynomials at some point in their life. So using these polynomials, these equations, to understand how the real world works. So you can somehow model how things work like phylogenetics, for instance. You can somehow make a mathematical model that is described by some polynomial equations. Then we decide on these polynomials and try to take some insights.

ICERM: What first inspired you to pursue mathematics and computational biology and what keeps you engaged?

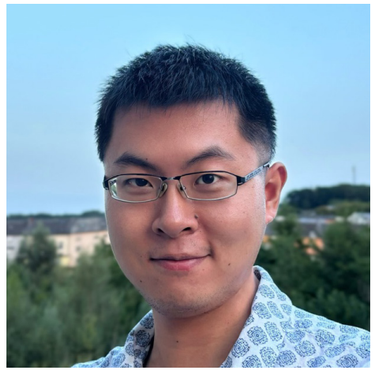
Garotte López: I always wanted to do science. The first thing I remember I wanted to do was some kind of biology. And then I was thinking of biology or medicine, but I wasn't really sure. I got into math a little bit randomly because I knew some people who did math, they said it was cool. I was good at math, and then at some point I thought it was going to be more challenging that doing biology and then I just started studying math. And then during my second year of my bachelor, I figured out that my PhD advisor (she was my professor at the time) and she was applying algebra and so on in phylogenetics. And then I thought it was very very cool, you know, that math that I didn't know the applications for could be applied to biology, which is something I've always been really interested in. And I think what keeps me very motivated is seeing how many applications this has. Like, the math itself is cool but sometimes it's hard to see they can be really useful in many many different fields.

ICERM: What are you looking forward to in the semester at ICERM?

Garotte López: Mostly learning. I think there are a lot of people here whose papers I've read and names I know but I've never met, and they're very very good experts in the field doing work from many different perspectives. So I'm very happy to learn as much as I can from all of them. ■

Zeyuan He

2024-2025 Institute Postdoc



Zeyuan He received his B.Eng. from Tsinghua University in 2017 and Ph.D. from the University of Cambridge in 2021. After a year in the metallurgy industry, he pursued postdoctoral research at Kyoto University, the University of Toronto, and the University of Cambridge. In 2024-2025, he joins ICERM as an Institute Postdoc for the program Geometry of Materials, Packings, and Rigid Frameworks. His research sits in between the mathematical and engineering research on geometrically constrained systems, focusing on the continuous isometric deformation of surfaces and the development of novel engineering mechanisms inspired by such deformation.

ICERM: What most excites you about what you're researching right now?

He: My research sits in between the mathematical and engineering research on geometrically constrained systems, focusing on the continuous isometric deformation (flex) of surfaces and the development of novel engineering mechanisms inspired by such deformation. One exciting research project is on the generalization of flexible closed polyhedral surfaces. While it may seem counterintuitive that polyhedral surfaces with the topology of a cube can fold, such surfaces do exist. I have developed a novel construction method that has led to the discovery of new families of these variations.

ICERM: How do you describe your work to people who aren't experts in your field?

He: Have you ever tried paper folding? It turns out that you can fold a sheet of paper into not only simple shapes, like stars or airplanes, but also complex 3D geometries, such as a dragon with intricate details. For polyhedral surfaces with various topologies (sphere, tube, torus, plane, etc.), a comprehensive theory addressing their existence, possible configurations, and range of folding motions is still largely incomplete. Notably, the relationship between folding polyhedral surfaces and smooth surfaces is particularly fascinating.

ICERM: What first inspired you to pursue mathematics and computational biology and what keeps you engaged?

He: During my Ph.D., I developed a strong interest in the flexibility of surfaces, a topic I am eager to pursue throughout my academic career. One of the key reasons for my sustained engagement in this field is the tangible nature of the research outcomes, which can be physically realized as dynamic models in 3D space, offering significant potential for engineering design.

ICERM: What are you looking forward to in the semester at ICERM?

He: In addition to completing the proposed research during my stay, I see this as an excellent opportunity to expand my professional network, gain insights from discussions on the latest and unpublished work, and contribute to organizing workshop events. I am also excited about my first long-time visit to America. ■

Max Hill

Fall 2024 Semester Postdoc

Max Hill received his Ph.D. in 2024 from the University of Wisconsin-Madison under the supervision of Sebastien Roch. His dissertation work involved probabilistic analyses of evolution models with applications to phylogenetic inference. After earning his doctorate, he was a postdoc at the University of California Riverside. He joins ICERM as a Semester Postdoc in the Fall 2024 Semester Program Theory, Methods, and Applications of Quantitative Phylogenomics. In Spring 2025, he will be a researcher at the University of Hawai'i at Manoa working with Elizabeth Gross. His research interests include phylogenetic network models, maximum likelihood estimation, and understanding the impact of biological phenomena such as recombination, gene duplication, and variable mutation rates on phylogenetic inference.

ICERM: What most excites you about what you're researching right now?

Hill: There are a lot of things to think about. So I really like the area of application, I think the questions with some sort of biological questions are interesting. My work is really at the intersection of algebraic statistics and probability, so often these problems in phylogenetics have a component you can look at from two different perspectives. That's one thing I like - I think it's very beautiful when you see the intersection of mathematical fields. Also, I just like working with people. I collaborate with people who I like and so it's fun to meet up with them and work on things.

ICERM: How do you describe your work to people who aren't experts in your field?

Hill: I try to say as little as possible, so I'll say, "I study mathematical models of evolution." And then if they press me, I'll say a little bit more. But usually, if I say more than two or three sentences people's eyes kind of glaze over. I don't know, sometimes people do press me and I'll explain a little bit more and I'll draw some phylogenetic trees to say, "Okay, this describes an evolutionary history. We want to try to recover this and infer it from genetic data." And then it's a statistical problem and it's got randomness and that's what I do.

ICERM: What first motivated you to pursue mathematics and computational biology and what keeps you engaged?

Hill: I got involved in math in college. I took an intro Stats 101 course and it really changed the way I saw things. It gave me a new perspective on looking at phenomena in the world. So I was like, "Okay, I have to take the math statistics course." And then I had to take a bunch of math prereqs to do that, and then by the time I got there, I was basically done with the math major and ready to go to grad school.

So [my entrance to] computational biology is actually more interesting, I think. I was taking an applied math course in graduate school and we had to do a final project where we could just pick some math paper and give a presentation on it. I ended up picking a paper where the authors looked at the question, "When did people start making and wearing clothing?" They came up with an estimate of like 70 to 180 thousand years ago by looking at louse DNA. There are head lice and clothing lice, and you can't have the emergence of clothing lice until people start wearing clothes. So if you can estimate how long ago that speciation event took place, you get a lower bound for how long ago people started wearing clothes. So I was like, "This is a really cool topic." And my professor at the time, Professor Sebastian Roch, who eventually became my advisor and is here now, directed me to the field.

ICERM: What are you looking forward to in the semester at ICERM?

Hill: So I'm looking forward to both starting projects and finishing projects. It's much easier to start projects than to finish them, but so far I'm really enjoying meeting people and working with collaborators who I've been Zooming with for the last year. I think that the social aspect is probably the thing that most animates me and excites me for the semester. Is having people who are experts who I can actually meet and interact with on a day-to-day basis. ■

Joshua Justison

Fall 2024 Semester Postdoc



Joshua Justison graduated from the University of Minnesota Twin Cities in 2018 and completed his Ph.D. from Iowa State in 2024 under the supervision of Tracy Heath. His dissertation work primarily focused on modeling gene flow processes and how they affect patterns in macroevolution. As part of this work, he developed tools for phylogenetic network simulation and trait evolution software that can account for reticulate histories. Joshua joined ICERM in the Fall of 2024 as a Semester Postdoctoral Fellow. His research interests primarily lie in inferring reticulate phylogenetic histories and their use in understanding patterns of diversification.

ICERM: What most excites you about what you're researching right now?

Justison: I guess for me, with the stuff I'm researching, we can use it to understand patterns and processes kind of across the tree of life and use these types of methods in things that I'm working on to learn more about the natural world around us and the kinds of biological processes that are important for shaping some of these patterns.

ICERM: How do you describe your work to people who aren't experts in your field?

Justison: The stuff I work on is developing methods to understand how organisms are related to one another historically. And specifically on methods that account for things like hybridization, when it's not just species branching off and splitting from one another. You have some species coming back and exchanging genetic material.

ICERM: What first inspired you to pursue mathematics and computational biology and what keeps you engaged?

Justison: I guess my background is in biology and I guess I just took a computer science course kind of on a whim and I really enjoyed that. And we did a homework assignment where we had to model how grocery lines would change over time. So I really liked the idea of using computers to model the real world. And I gues I was looking for an outlet in that in the realm of biology and came across phylogenetics and it to me is the perfect crossroads of biology, computer science, and stats.

ICERM: What are you looking forward to in the semester at ICERM?

Justison: Just meeting with a bunch of really math-savvy folks and being able to nerd out about phylogenetics. ■

Sungsik Kong

Fall 2024 Semester Postdoc



Sungsik (Kevin) Kong is a computational evolutionary biologist who focuses on developing methods to address questions in evolutionary biology using techniques and concepts from statistics, mathematics, and computer science. He is particularly interested in developing scalable methods that infer phylogenetic networks to understand the role of reticulate evolution (e.g., hybridization) in shaping today's biodiversity by utilizing information embedded in genomic data. Sungsik holds a Ph.D. in Evolution, Ecology, and Organismal Biology from Ohio State University, where he was advised by Dr. Laura Kubatko. Following his graduation, he joined the Wisconsin Institute for Discovery at the University of Wisconsin-Madison as a Research Associate, working with Dr. Claudia Solís-Lemus. He earned his M.Sc. and B.Sc. in Ecology and Evolutionary Biology and Zoology from the University of Toronto.

ICERM: What most excites you about what you're researching right now?

Kong: So I'm originally trained as a biologist. So my undergrad, master's, and Ph.D. are all in ecology and evolutionary biology. And originally I was fascinated by the diversity of different plants and different animals. And this is from my experience of working in the Royal Ontario Museum in Toronto through my undergraduate institution. So I worked with different organisms in the museum's collection and just thought, "Oh my god, there's so much diversity here. Everybody is so different, collected from different parts of the world."

The next thing I got interested in was what the relationships are between these different animals. The field of understanding how different species are related to each other and what kind of biological processes resulted in creating that diversity is called phylogenetics. So I have been interested in phylogenetics since then. Mostly in the early stages of my career, I worked on using methods that analyze phylogenetic signals from the data and their results – basically a tree-like structure called a phylogeny that shows the relationship between different species. But during my Ph.D., I got interested more in how to develop these models or these computational tools and methods. Right now, a lot of my work involves inferring phylogenies. There are two different types: phylogenetic trees and phylogenetic networks. Trees have some assumptions that different animals arise through speciation events, whereas networks include speciation and hybridization events. So right now I'm mostly working [to understand], given some sort of biological data, how can we infer or estimate these phylogenetic trees or networks in ways that are statistically sound and computationally efficient? So we can use that for more practical use.

ICERM: What first motivated you to pursue mathematics and computational biology and what keeps you engaged?

Kong: For any scientific research, one thing that one really needs to be cautious about is being objective. And especially for taxonomy, historically people look at different specimens and say, "Oh, I think that this is this species or that species," which involves subjectivity. So what really fascinates me about using mathematics for this kind of research is you can be objective, it can be model-based, and it can be evaluated statistically. That's what engages me to stay in this more statistical and mathematical side of biology. But of course, another important thing is the people here working in this field. It's a very narrow field, but everybody here is great people. As an international student, I don't have a family in the U.S. or anywhere nearby. Having these great senior people around me is really a big thing, rather than being surrounded by competitors, for example. ■

ICERM: What are you looking forward to in the semester at ICERM?

Kong: For a more life-related answer, it's my first time in New England so I want to experience and explore different parts, try different food, and try to see the historical places around this area. But more on the academic side, this is a great and rare opportunity where all these experts from around the world are in the same place spending the entire semester together. So I would like to build a network and come up with as many research ideas as I can with other people, and work on those research problems for many coming years in my career. And ICERM has a really great environment for working. Everything is offered, so all of us have been spending many hours every day working. So working hard and enjoying hard are what I'm looking forward to. ■

EIGHT DISCRETE OPTIMIZATION PROGRAM ALUMNI RECOGNIZED BY GLOBAL RESEARCH COMMUNITY

An impressive number of researchers who attended ICERM's Spring 2023 Discrete Optimization: Mathematics, Algorithms, and Computation Semester Program have been recognized by the international discrete optimization research community.



Participants in ICERM's August 2024 Discrete Optimization Reunion Workshop

At the 2024 Conference on Integer Programming and Combinatorial Optimization, program alumni Gérard Cornuéjols and Siyue Liu (both at Carnegie Mellon University) received the conference's Best Paper Award for their paper "Approximately Packing Dijoins via Nowhere-Zero Flows." A separate research collaboration with Samuel Fiorini (Université Libre de Bruxelles) and Sebastian Pokutta (Zuse Institute Berlin) was awarded a 2023 Gödel Prize for outstanding papers in the area of theoretical computer science; the other 2023 Gödel Prize was awarded to Thomas Rothvoss (University of Washington), who also attended the Spring 2023 program. Discrete Optimization program Research Fellow Luze Xu (University of California, Davis) was part of the research team that received the INFORMS Optimization Society's 2024 Young Researchers Paper Prize. Finally, program alumni Alberto del Pia (University of Wisconsin-Madison) and Aida Khajavirad's (Lehigh University) paper series on convexification of mixed-integer polynomial optimization problems earned them the 2023 INFORMS Computing Society Prize.

The Spring 2023 Semester Program was co-organized by Jesús De Loera (University of California, Davis), Antoine Deza (McMaster University), Marcia Fampa (Federal University of Rio de Janeiro), Volker Kaibel (Otto-von-Guericke Universität Magdeburg), Jon Lee (University of Michigan), and Laura Sanità (Bocconi University of Milan). According to De Loera, the secret to the program's success was its unique group of researchers. "Make sure the organizers always look for a broad, diverse set of talented individuals, not just an inner circle of old colleagues," he advised.

In August 2024, many Discrete Optimization program alumni returned to ICERM for a weeklong reunion workshop. Recorded talks and posters from Cornuéjols, Khajavirad, and other honorees are available on the program website. ■

RESEARCH SPOTLIGHT: SIJING LIU

Sijing Liu (Worcester Polytechnic Institute) was an Institute Postdoctoral Fellow at ICERM from Fall 2023-Spring 2024, participating in the Spring 2024 Semester Program Numerical PDEs: Analysis, Algorithms, and Data Challenges. The following research highlight is based on Liu's collaboration with Spring 2024 program co-organizer Johnny Guzmán (Brown University) and program alumni Erik Burman (University College London), Miguel A. Fernandez (Inria Paris), and Rebecca Durst (University of Pittsburgh).

A SECOND-ORDER METHOD FOR A PARABOLIC-PARABOLIC INTERFACE PROBLEM

SIJING LIU

BASED ON JOINT WORK WITH ERIK BURMAN, MIGUEL A. FERNÁNDEZ, REBECCA DURST AND JOHNNY GUZMÁN

Fluid-structure interaction (FSI) problems involve the study of how fluids and solid structures interact with each other. These problems are important in many engineering and scientific applications, such as in aeronautics, aeroelasticity, aerodynamics, biomechanics, civil engineering, and mechanical engineering.

The computational solution of fluid-structure interaction problems remains a challenging problem, especially how to computationally couple the two sub problems. One popular approach is the so-called loosely coupled scheme where the solid and fluid systems are solved sequentially. Using this method, information is passed across the coupling interface at discrete time levels with no iteration between the sub-systems within one time-step. See Figure 1 for an illustration of a loosely coupled scheme. Here Ω_s and Ω_f represent two subdomains that interact through an interface Σ. A solid problem is defined in Ω_s, while a fluid problem is defined in Ω_f, with the interaction governed by coupling conditions at Σ.

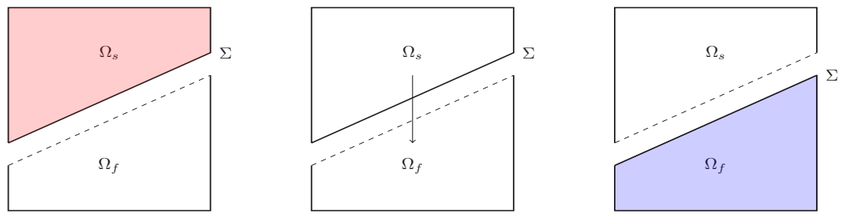


FIGURE 1. Loosely Coupled Scheme

Numerous studies in the literature focus on loosely coupled schemes for incompressible FSI with thick-walled solids. In particular, Robin-Robin loosely coupled schemes have recently been proposed and analyzed [3, 5], demonstrating unconditional stability and, for the first time, a spatially uniform splitting error. The term Robin-Robin refers to the use of Robin-type boundary conditions applied at the interface for both subproblems.

In our recent paper "Estimates of discrete time derivatives for the parabolic-parabolic Robin-Robin coupling method," we consider a parabolic-parabolic interface problem, a simplified version of FSI. See Figure 2 for an illustration. In each subdomain, a simple heat equation is defined, with the two problems coupled by boundary conditions at the interface Σ. It is known that Robin-Robin loosely coupled schemes for parabolic-parabolic interface problems exhibit first-order convergence in time [8, 5]. However, there seems to be a lack of analysis on high-order methods for FSI problems or parabolic-parabolic problems. To the best of our knowledge, there are no existing proofs of second-order accuracy for the defect-correction method applied to PDE interface problems. Our goal is to address this gap by proving second-order convergence of a prediction-correction method with a single correction step (see [6]). This opens the door to more high-order convergent methods and provides insights into the analysis of FSI and other real-world applications.

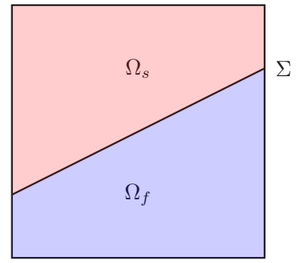


FIGURE 2. The domains Ω_f and Ω_s with non-horizontal interface Σ.

By leveraging the good stability properties and spatially uniform splitting error of the method in [5, 7], we aim to construct a higher-order scheme in time by building on the prediction-correction methodology [1], with the Robin-Robin loosely coupled method as the prediction step. The guiding principle of our correction method is to have discrete time differences of the prediction step error appearing in the right-hand side of the correction step error equations. Then, one uses the fact that these discrete time differences converge with second-order accuracy (see [4]). Let us describe the steps of the prediction-correction method at time t_{n+1}:

- Solve the prediction step to obtain the defect solutions u_0^{n+1}, w_0^{n+1} and λ_0^{n+1}.
- Modify the right-hand side of the prediction step using the solutions u_0^{n+1}, w_0^{n+1} and λ_0^{n+1}, while keeping the left-hand side of the prediction step unchanged.
- The modification of the right-hand sides is designed in such a way that the right-hand sides of the error equations of the correction step consists of the term $U_0^{n+1} - U_0^n$, $W_0^{n+1} - W_0^n$, $\Lambda_0^{n+1} - \Lambda_0^n$ and their gradients.
- Solve the new system with the modified right-hand side to obtain the correction solutions u_1^{n+1}, w_1^{n+1} and λ_1^{n+1}.

where u_0 (resp. w_0) represents the solution in Ω_f (resp. Ω_s) for the prediction step, and λ_0 denotes the Lagrange multiplier for the prediction step. The terms U_0^n, W_0^n and Λ_0^n are the corresponding error terms of the variables u_0^n, w_0^n and λ_0^n at time t_n. As mentioned above, it has been observed numerically that $U_0^{n+1} - U_0^n$, $W_0^{n+1} - W_0^n$, and $\Lambda_0^{n+1} - \Lambda_0^n$ converge with rate $\mathcal{O}((\Delta t)^2)$ in the L^2-norm in general. We have rigorously proved that our defect-correction methods achieve second-order accuracy in time for a specific case with a horizontal interface. Additionally, numerical results indicate second-order convergence in more general scenarios. We refer to [6, 4] for more details.

Sijing Liu was an Institute Postdoctoral Fellow at ICERM during the Fall 2023 semester and the Spring 2024 "Numerical PDEs: Analysis, Algorithms, and Data Challenges" program. He focused on this problem during his fellowship, collaborating with Prof. Burman, Prof. Fernández, Dr. Durst, and Prof. Guzmán. Additionally, he worked on other projects concerning convection-dominated problems and optimal control problems, leading to the submission of four manuscripts [4, 9, 2, 6].

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UPCOMING OPPORTUNITIES

ICERM Mixer at JMM 2025

at Jefferson, Sheraton Grand Seattle
Friday, January 10 from 6:00-7:30 pm
We hope to see you there!

Research Experiences for Undergraduate Faculty

The next Research Experiences for Undergraduate Faculty (REUF) workshop will take place June 9-13, 2025 at ICERM. The annual REUF workshops are a formal collaboration between ICERM and the American Institute of Mathematics (AIM). REUF brings together leading research mathematicians and faculty based at primarily undergraduate institutions to investigate open questions in the mathematical sciences and to equip participants with tools to engage in research with undergraduate students.

Latinx in the Mathematical Sciences Conference (LatMath) 2025

The Institute for Pure and Applied Mathematics (IPAM) will host LatMath 2025, conference showcasing the achievements of Latinx mathematicians. The goals of the conference are to encourage Latinx students to pursue careers in the mathematical sciences, to promote the advancement of Latinx researchers currently in the discipline, to showcase research being conducted by Latinx mathematicians at the forefront of their fields, and to build a community around shared academic interests. The conference will be held on the UCLA campus in Los Angeles, CA from March 6-8, 2025.

Infinite Possibilities Conference 2025

The Institute for Mathematical and Statistical Innovation (IMSI) will host the 2025 Infinite Possibilities Conference (IPC). IPC is a national conference designed to broaden participation in the mathematical sciences. IPC aims to foster a sense of community in mathematics among women from underserved populations and welcomes all mathematicians who feel they may contribute to or benefit from this event. The conference will take place in Chicago, IL from April 11-12, 2025.

PROPOSE A PROGRAM

ICERM is accepting proposals for the following program types:

Semester Programs

ICERM hosts a Spring and Fall Semester Program every year. Each has organizers and long-term participants who are expected to be in-residence for the majority of the semester. Semester programs typically incorporate three week-long associated workshops. For a typical program, ICERM provides travel and lodging support for 5-10 organizers (at least a month in residence, with some for the full semester); 20-30 long-term participants (4+ weeks); 1 Institute and 5 Semester postdoctoral fellows (salaried); 60 short-term participants (1-4 weeks); 10-15 graduate students (6+ weeks); and workshop attendees. ICERM helps essential long-term participants negotiate sabbatical leaves or teaching releases to foster their participation.

Summer@ICERM

Summer@ICERM is a Research Experience for Undergraduates led by faculty organizers who develop a variety of topical research projects that are interdisciplinary in nature. Throughout the eight-week program, students work on their assigned projects in groups of two-to-four, mentored by faculty advisors and teaching assistants. Summer@ICERM is not your typical REU, in that ICERM provides comprehensive start-to-finish logistical support to the faculty organizers, including assistance recruiting TAs. In addition, faculty and TAs are paid summer salary with lodging support, and the average faculty/TA-to-student ratio is 1:3.

Topical Workshops

Topical Workshops run over 5 weekdays and focus on a topical theme that aligns with the Institute's mission of supporting and broadening the relationship between mathematics and computation. ICERM hosts 5-7 topical workshops each year. They are typically scheduled in December, January, and May through August (around the dates of the semester programs). ICERM covers travel and lodging expenses of the organizers and 20-25 invited speakers/lead participants; some participants (applicants) to the workshop may also be supported.

Graduate Training Workshops

Graduate Training Workshops are 1-3 week events on a timely and exciting mathematical or computational theme, with a focus on training graduate students, recent PhDs, and researchers new to the field. They are typically scheduled in December, January, and May through August (around the dates of the semester programs). ICERM covers travel and lodging expenses of the organizers, invited speakers, TAs, and early-career participants.

Collaborate@ICERM

Collaborate@ICERM offers teams of 3-6 researchers the opportunity to spend five days at the Institute during the summer (May-August) or during the month of January. The team research project should have a computational or experimental component. ICERM provides access to a variety of software packages and high performance computing through Brown's Center for Computation and Visualization. Proposals involving research projects initiated at past ICERM programs are encouraged. This program provides limited funding for travel to the Institute and local accommodations for six nights.

Hot Topics Workshops

Hot Topics Workshops are designed to allow ICERM to move quickly in order to start the public exploration of breakthroughs and emerging mathematical areas. They run 2-3 days and are organized on a few months' notice. They can originate through suggestions from ICERM boards or the community.

Deadlines and Review Process

The next target deadline for Hot Topics Workshop suggestions is **February 1, 2025**. The next target deadline for all other proposal types is **May 1, 2025**. Submissions and inquiries should be sent to ICERM's Director. ICERM's Directorate and the Scientific Advisory Board (SAB) review all proposals. Proposers will receive feedback within a month of the SAB meeting.

For more information, visit icerm.brown.edu/proposals.

PRACTICAL INFERENCE ALGORITHMS FOR SPECIES NETWORKS

by Hector Baños

Hector Baños is a long-term participant in ICERM's Theory, Methods, and Applications of Quantitative Phylogenomics Semester Program and a U.S. National Science Foundation Partnerships for Research Innovation in the Mathematical Sciences (PRIMES) awardee. The PRIMES program seeks to support relationships between NSF Division of Mathematical Sciences-supported institutes such as ICERM and faculty at minority-serving institutions. Baños is an Assistant Professor in the Department of Mathematics at California State University, San Bernardino, a designated Hispanic-serving institution and one of the most diverse public universities in the state of California. Before joining ICERM in September, Baños used support from the PRIMES program to develop and lead a weeklong program for undergraduate and graduate students at CSUSB, introducing them to current topics in mathematical phylogenetics. His research interests lie in coalescent theory, hybridization, profile mixture models, and combinatorial phylogenetics.

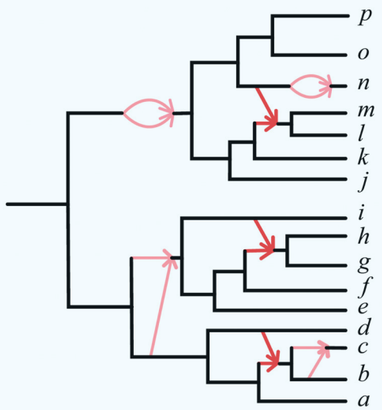


Figure 1. Species network illustrating hybridization events with colored arrows

Phylogenetics is a field of evolutionary biology dedicated to understanding the evolutionary relationships among species. Inferring these relationships is essential for diverse applications, including conservation efforts, tracking infectious disease dynamics, and improving agricultural practices.

Hybrid speciation, or hybridization, occurs when two distinct populations merge genetically to form a new population. Recent advances in genome sequencing and phylogenetic analysis have shown the significant role of hybridization in the tree of life across a wide variety of species, from orchids to leopards. As a result, there is a need for effective methods to infer hybridization, using realistic models of biological processes to better understand species' evolutionary relationships.

My research and the scope of my PRIMES grant focus on developing practical algorithms to uncover complex evolutionary relationships in the presence of hybridization. Traditionally, species networks are the objects used to depict evolutionary relationships when hybridization is involved (see Figure 1). A major challenge in inferring these networks is known as gene tree incongruence, where the evolutionary history of individual genes (gene trees) may not reflect that of the species. Gene tree incongruence is a central issue in modern phylogenetics and can result from naturally occurring factors such as incomplete lineage sorting, gene duplication and loss, horizontal gene transfer, and hybridization, as well as methodological errors in gene tree inference.

The theoretical foundation for my research is the Network Multispecies Coalescent (NMSC) model [1], a standard stochastic model describing the differing evolutionary histories of gene trees in the presence of both incomplete lineage sorting and hybridization. Current methods for inferring species network features under the NMSC are restricted to a rather simple class of "level-1" networks, or networks with no interlocking cycles. A goal of my research includes developing algorithms that infer statistically consistent estimators of species networks, focusing on supporting a wider range of networks and utilizing individual gene trees or genomic sequences composed of many genes as input. Our work also involves implementing these algorithms in user-friendly, reliable, and efficient software, capable of handling large datasets within practical timeframes while requiring reasonable computational resources. My research team and I have developed the R package MSCquartets for this purpose [2].

Specifically, we developed the Network inference Algorithm via NeighborNet Using Quartet distance (NANUQ), implemented in MSCquartets. NANUQ is a statistically consistent algorithm that offers a significant speed advantage over other algorithms because it eliminates the need for network search entirely, instead using combinatorial techniques to construct the network. This efficiency enables researchers to analyze large datasets whose size may be impractical for other methods. Additionally, NANUQ can detect model violations, such as when data does not originate from a level-1 network under the NMSC. Another key advantage is that NANUQ does not require prior knowledge of the number of hybridization events in a network, unlike other approaches.

Before developing NANUQ, it was crucial to first determine which features of species networks are identifiable from biological data under the NMSC. Building on the work of Solís-Lemus and Ané [3], we demonstrated that most features of level-1 networks can indeed be inferred from gene trees. This result required borrowing techniques from algebraic statistics, combinatorics, and probability. Using a similar framework, my collaborators and I extended these identifiability results to level-1 networks inferred from genomic sequences, thus bypassing the need for gene tree inference. As part of my research objectives, I aim to extend these identifiability results to a broader range of network classes. This includes identifying more general families of networks that can be inferred from biological data and establishing identifiability results for these classes using both genomic sequences and individual gene trees.

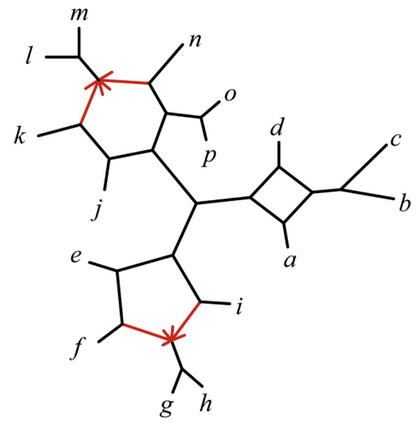


Figure 2. Network features inferable from quartet concordance factors, obtained from NANUQ for data generated by the network in Figure 1 under the NMSC events with colored arrows

We have made significant progress in identifying more general families of networks that can be inferred from data, as well as in developing algorithms for statistically consistent estimation of species network features. This progress, along with new research directions, has accelerated notably since the start of the ICERM Semester Program. For instance, my officemate Vu Dihn (University of Delaware), whom I met at ICERM, and I began investigating the pitfalls of various inference methods under model misspecification. This research will raise evolutionary biologists' awareness of these issues and encourage caution in their analyses.

In summary, by expanding the range of identifiable network classes, addressing the limitations of existing methods, and enhancing the reliability and scalability of species network inference techniques, our work provides biologists with the tools and insights necessary for more accurate and comprehensive investigations of evolutionary relationships. ■

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CLIMATE CONSCIOUS COMPUTING: EXPLOITING DATA SPARSITY FOR MODEL PERFORMANCE AND SUSTAINABILITY

by David Keyes

A climate emulator exploiting data sparsity to produce unprecedented resolution in space and time – and minimize its own carbon footprint – was one of many applications featured at Modeling and Simulations in Fluids, a September Hot Topics Workshop. On behalf of a research team of twelve climate modelers, mathematicians, statisticians, and computer scientists, Professor David Keyes shared the method behind the model, which was recently nominated for the Association of Computer Machinery's (ACM) 2024 Gordon Bell Prize in Climate Modelling. Since 2022, Keyes has been a member of four research teams that have been finalists for the ACM Bell Prize and the recently instituted Bell Climate Prize. The prizes are awarded annually at the International Conference for High Performance Computing, Networking, Storage, and Analysis.

From 2011-2020, Keyes served as a member of ICERM's Board of Trustees. Currently, he is a Professor of Applied Mathematics and Computational Science and Director of the Extreme Computing Research Center at the King Abdullah University of Science and Technology (KAUST) in Saudi Arabia.

The Gordon Bell Prize bears the name of the founding head of the U.S. National Science Foundation's Computing and Information Science and Engineering (CISE) Directorate. A renowned computing systems engineer himself, Bell endowed the award in 1988 to challenge the high-performance computing community to deliver performance on real-world applications and reach beyond previous benchmarks concerned with supercomputer hardware design. Over the past two years, our team has competed for the prize with four different applications that promote the same "renaissance" in computational linear algebra, motivated by the need to compute with greater energy efficiency. Current exascale supercomputers draw upwards of 20 MegaWatts in continuous operation, suggesting an annual carbon footprint comparable to that of 20,000 average cars in the USA.

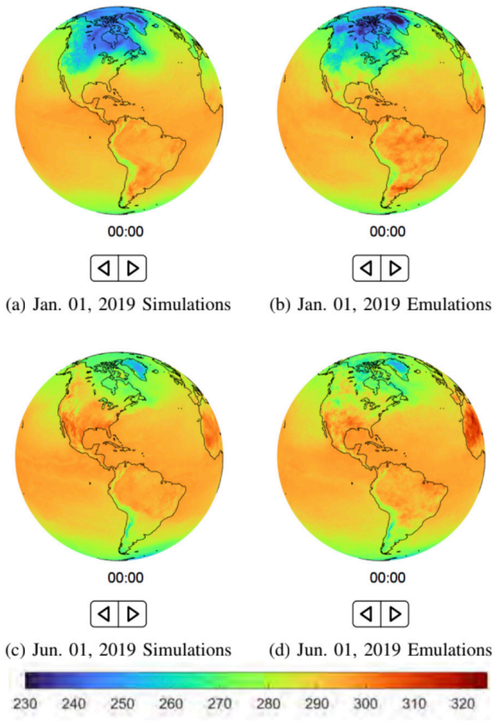


Photo courtesy of David Keyes. Figures show consistency between climate simulations and the less "expensive" climate emulator designed by Keyes and his collaborators.

The highly scalable climate emulator described at ICERM offers faster, high-resolution simulations without the need for massive data storage. Instead of storing many simulations, it stores their statistical parameters, allowing it to generate an arbitrary number of emulations with the same statistics as the simulations. In the words of my frequent collaborator Marc Genton (KAUST), "PDE-based climate models are complex and can take weeks or months to run, even on the fastest supercomputers. They generate massive amounts of data that become nearly impossible to store, and this is increasingly a problem as climate scientists are constantly pushing for higher resolution." Genton has been designing the emulator's algorithm for nearly a decade, steering the overall reduction of computational time and storage requirements.

During our process, our team ran our emulator on four of the world's top ten supercomputers: Frontier and Summit at Oak Ridge National Laboratory, ALPS at the Swiss National Computing Centre (CSCS), and Leonardo at the Italian CINECA. These runs demonstrated portability over four GPU processors: AMD's MI250X, and NVIDIA's V100, A100, and H100. By running on 9,025 nodes of Frontier, the climate emulator offers a remarkable resolution of 3.5 kilometers and can replicate local conditions on a timescale from days down to hours. The emulator uses a fast spherical harmonic transform (SHT) method that converts elements such as temperature, wind, and pressure into simple frequency amplitudes that describe how they change over time in more than 54 million locations around the globe. We have found that the keys to our performance accomplishments and to bringing down the carbon footprint of numerous applications are exploiting data sparsity in algebraic rank and floating point precision in fine-grained blocks of matrix operators. As I said during my ICERM talk, "Do Linear Algebra; see the world!" Or, better yet, "Do Linear Algebra; see many worlds."



Participants in ICERM's September 2024 Modeling and Simulations in Fluids Workshop

A vast number of computationally demanding applications are amenable to the use of our team's Hierarchical Computations on Manycore Architectures (HiCMA) software package, which has powered our climate emulator and our three additional Bell Prize finalist nominations. Specifically, HiCMA can be utilized for problems expressable as integral equations with smooth kernels or fractional differential operators, covariances in spatial distributions, Schur complements of elliptic discretizations, Hessians of PDE-constrained optimization, radial basis function discretizations, and many types of kernel matrices from Gaussian and other processes. Applications range from climate and weather modeling to seismic imaging, from wireless signal decoding to atmospheric turbulence mitigation in telescopy, to genome-wide association studies in adapting agriculture to climate stress. Indeed, HiCMA has been applied in all of these domains at KAUST.

I am encouraged by the supercomputing research community's growing interest in computations that are designed to reduce, not increase, floating point operations per second (flop/s), the rate by which methods have traditionally been evaluated. By strategically squeezing out operations unnecessary for obtaining a sufficiently accurate result, our team appeals to time to solution, reduction of memory footprint, and other metrics of merit that may be more appropriate going forward in supercomputing. Indeed, my talk emphasized using mathematics and computer architecture considerations to get the job done while minimizing computational requirements.

I believe that the late Gordon Bell would approve of the selection committee's decision to give podium attention to our data sparsity campaign at the last three ACM Supercomputing conferences. Indeed, he adapted the topics of "special prizes" several times in the early years as parallel computing evolved. There are traditionally six Gordon Bell Prize finalists per year from around the globe and three Climate Prize finalists. Our team from KAUST are the first finalists from the Middle East in the prize's thirty-seven year history. Perhaps this year will be the year! ■

SIMULATING eXTREME SPACETIMES COLLABORATION VISITS ICERM

by Halle Bryant



Photo and description courtesy of Nils Deppe. A rendering of two black holes similar to those from the first gravitational wave event, GW150914. The camera is located approximately 900 miles away from the center between the two black holes. Each black hole is about 30 times more massive than the Sun. Visible near each black hole is a small shadow called an "eyebrow," which is an image of the rear of the companion black hole. This is visible because the extremely strong gravity near a black hole bends (or "lenses") light around it. A so-called "Einstein ring" is visible as a darker circle roughly halfway between the left/right edges and the center of the image.

In 2016, scientists at the Laser Interferometer Gravitational-Wave Observatory (LIGO) made the first-ever detection of gravitational waves from a binary black hole system, marking a shift in the study of astrophysics comparable to the advent of Galileo's telescope. The detection provided the first direct evidence that black holes exist, opening the door to a new realm of astrophysics and astronomy beyond light- and electromagnetism-based observation. During the Simulating Extreme Spacetimes with SpEC and SpECTRE workshop at ICERM, leaders of the Simulating eXtreme Spacetimes (SXS) collaboration gathered with fellow astrophysicists to share code designed to support an anticipated flood of gravitational wave research in the coming decades. The SXS collaboration is a joint research effort across multiple institutions in the U.S. and Canada studying the motion of black holes and other extreme spacetimes. These objects are fundamental to the study of relativity, first theorized by Albert Einstein in the early 1900s.

Since the early 2000s, the SXS collaboration team has worked to develop numerical simulations for gravitational wave systems. "It started as a collaboration between Caltech and Cornell, doing the kinds of calculations or working towards learning how to do colliding black holes and colliding neutron stars, things like that," explained Geoffrey Lovelace (California State University, Fullerton), a SXS researcher and co-organizer of the Simulating Extreme Spacetimes workshop. Now, their simulations allow researchers to perform data analysis on ripples in space-time created by two orbiting astronomical objects – typically black holes or neutron stars – and determine properties such as the objects' masses and orbital trajectories. In response to the groundbreaking wave detection in 2016, the team is especially focused on developing an open-source successor to their Spectral Einstein Code (SpEC), the original codebase for the project.

The upgraded code, named SpECTRE, is being designed with an eye toward new user accessibility and adaptability to future supercomputer hardware. "The hope is that, with modern software engineering practices, [SpECTRE's] twenty-year lifetime or thirty-year lifetime can actually be extended indefinitely if the code is easy enough to change," explained SXS collaborator Nils Deppe (Cornell University). "The big thing there is to write code that is very modular and flexible and try to disentangle and keep separate differences in how the computations are done from how they would map onto the hardware," he added. By separating code layers that perform computations on data from those that communicate with supercomputer processing units, SpECTRE's developers will be able to quickly respond to advances in exascale computer architecture. As an added benefit, meticulous documentation of the new model has helped the team train researchers outside of the collaboration group to use and contribute to SpECTRE.

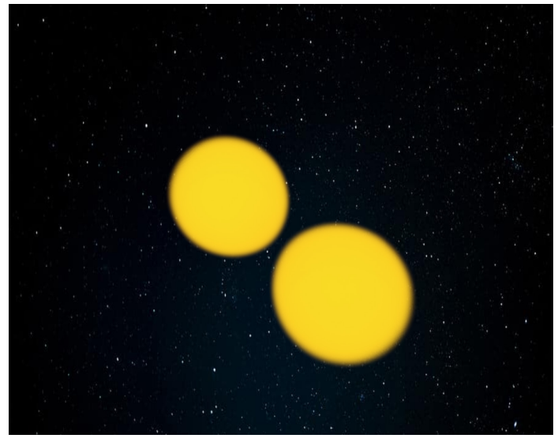


Photo and description courtesy of Nils Deppe. A rendering from a simulation of two neutron stars orbiting each other approximately 12 milliseconds before they collide. Each star is about 1.4 times more massive than our Sun. The stars will undergo three more orbits before colliding. In order to achieve three orbits in such a short amount of time they move at about 10% the speed of light, or 67 million miles per hour.

The development and dissemination of SpECTRE were central goals of the Simulating Extreme Spacetimes gathering at ICERM, where the organizers split their time between small group developers' meetings and a tutorial-based workshop for first-time users. "Overall, it worked really well," said Deppe. "[We] made a lot of progress, probably months' worth of progress in three hours that otherwise is very difficult when it's broken into short telecons." For SXS team, progress means improving computational accuracy to keep up with state-of-the-art detectors in several newly-planned gravitational wave observatories. "Our calculations are accurate enough for these detectors today," Lovelace explained. "But for these new detectors that are going to push our vision, there's a lot less wiggle room because they will be so much more sensitive."

To meet the precision requirements of modern wave detectors, the group is pushing for a tenfold increase in computational accuracy. "We've been working toward [getting] our new code where it can merge black holes to spiral together for the first time," said Lovelace. "And really, we got unstuck through these in-person discussions [at ICERM]." ■

MAKE A GIFT TO ICERM

Through our Semester Programs, Topical and Hot Topics Workshops, Collaborate@ICERM awards, Summer@ICERM undergraduate research programs, and GirlsGetMath@ICERM, we bring researchers at all career stages to Providence, from around the world.

Individual donations to ICERM help us maintain a fund specifically dedicated to meeting the needs of every visitor. This fund enables us to support mathematicians with families, provide assistance to visitors with emergency expenses, and offer free and low-cost community-engaged programs such as GirlsGetMath@ICERM.

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