EXPLORATORY WORKSHOP ON MATH, THEORY, AND CANCER BIOLOGY

MARCH 11-12, 2024

PARTICIPANT LIST

Raul Rabadan

Gerald and Janet Carrus Professor in the Departments of Systems Biology, Biomedical Informatics and Surgery, Columbia University

Raul Rabadan is the Gerald and Janet Carrus Professor in the Departments of Systems Biology, Biomedical Informatics and Surgery at Columbia University. He is the director of the Program for Mathematical Genomics (PMG) and the Center for Topology of Cancer Evolution and Heterogeneity. Dr. Rabadan's current interest focuses on uncovering patterns of evolution in biological systems—in particular, RNA viruses and cancer.

Shmuel Weinberger

Andrew MacLeish Distinguished Service Professor of Mathematics, University of Chicago

Most of my research is concerned with understanding things geometrically or understanding geometric things. I have been interested in manifolds, stratified spaces, homology manifolds, their invariants, the large scale geometry of discrete groups and other natural large scale metric spaces such as function spaces. In recent years my focus has been on quantitative topology, i.e. understanding the sizes of topological constructions, and on geometric problems suggested by scientific applications.

Sandy Anderson

Chair of the Integrated Mathematical Oncology (IMO) department and Senior member, Moffitt Cancer Center

Dr. Anderson performed his doctoral work on hybrid mathematical models of nematode movement in heterogeneous environments at the Scottish Crop Research Institute in Dundee, UK. His postdoctoral work was on hybrid models of tumor-induced angiogenesis with Prof. Mark Chaplain at Bath University, UK. He moved back to Dundee in 1996 where he worked for the next 12 years on developing mathematical models of many different aspects of tumor progression and treatment, including anti-angiogenesis, radiotherapy, tumor invasion, evolution of aggressive phenotypes and the role of the microenvironment. He is widely recognized as one of only a handful of mathematical oncologists that develop truly integrative models that directly impact upon biological experimentation. His pioneering work using evolutionary hybrid cellular automata models has led to new insights into the role of the tumor microenvironment in driving tumor progression. Due to his belief in the crucial role of mathematical models in cancer research he moved his group to the Moffitt Cancer Center in 2008 to establish the Integrated Mathematical Oncology department.

Antonio (Tuca) Auffinger

Professor, Department of Mathematics, Northwestern University

Auffinger completed his PhD at New York University in 2011. He was an L.E. Dickson Instructor at the University of Chicago before joining the faculty of Northwestern in 2014. Auffinger's research is on probability theory, more specifically sub-additive processes, spin glasses, gaussian fields and random matrices. He explores connections with partial differential equations and dynamical systems, mathematical physics and theoretical biology. A theme of his work is the complexity of disordered systems and universal aspects of their long-time behavior.

Andrew Blumberg

Herbert and Florence Irving Professor of Cancer Data Research (in the Herbert and Florence Irving Institute of Cancer Dynamics and Herbert Irving Comprehensive Cancer Center) and Professor of Mathematics and Computer Science, Columbia University

Andrew has broad research interests in mathematics and computer science. His research includes work in algebraic topology, topological data analysis, and computer security and privacy. He is particularly interested in the applications of geometry and topology to the analysis of genomic data. Andrew is an editor for the Journal of Topology, an associate editor for Advances in Mathematics, and an editor for the Journal of Applied and Computational Topology. He is a member of the Center for topology of cancer evolution and heterogeneity based at Columbia University. He is also part of the Pepper project at NYU on verifiable outsourced computing.

Curt Callan

James S. McDonnell Distinguished University Professor of Physics, Princeton University

For most of my career, I focused on understanding the workings of the quantum field theories that underlie the phenomena of particle physics. This led me to study issues in string theory (the construction of conformal field theories corresponding to solitons of various kinds) and in quantum gravity (the problem of Hawking radiation and the endpoint of black hole evaporation). A side interest in the application of field theory techniques to condensed matter problems led to work on dissipative quantum mechanics and the (quantum) fracture of materials. Over the past decade, however, my interest has shifted to theoretical problems in cellular biology. Modern biology increasingly has the ability to generate data (DNA sequence data, for one) in quantities that threaten to outrun our ability to comprehend it and use it for predictive purposes. I believe that the modeling and statistical inference approaches that are the stock in trade of physics are part of the answer to this growing problem, and I have been developing concrete examples of how this might work in problems ranging from gene regulation in bacteria to the functioning of the immune system in humans. In the process, I have become closely involved with the design and analysis of novel experiments, designed to answer unconventional, theoretically motivated, questions in biology.

Pablo Cámara

Assistant Professor of Genetics, University of Pennsylvania

Pablo G. Cámara is an Assistant Professor of Genetics at the University of Pennsylvania and a faculty member of the Penn Institute for Biomedical Informatics and the Center for AI and Data Science for Integrated Diagnostics. He received a Ph.D. in Theoretical Physics in 2006 from Universidad Autónoma de Madrid. He performed research in string theory for several years, with postdoctoral appointments at Ecole Polytechnique, the European Organization for Nuclear Research (CERN), and the University of Barcelona. Fascinated by the extremely interesting and fundamental open questions in biology, in 2014 he shifted his research focus into problems in quantitative biology, and joined the groups of Dr. Rabadan, at Columbia University, and Dr. Levine, at the Institute for Advanced Study (Princeton). Building upon techniques from applied topology and statistics, he has devised novel approaches to the inference of ancestral recombination, human recombination mapping, the study of cancer heterogeneity, and the analysis of single-cell RNA-sequencing data from dynamic and heterogeneous cellular populations.

Gunnar Carlsson

Professor Emeritus in the Department of Mathematics, Stanford University

Gunnar E. Carlsson (born August 22, 1952 in Stockholm, Sweden) is an American mathematician, working in algebraic topology. He is known for his work on the Segal conjecture, and for his work on applied algebraic topology, especially topological data analysis. He is a Professor Emeritus in the Department of Mathematics at Stanford University. He is the founder and president of the predictive technology company Ayasdi.

Ben Greenbaum

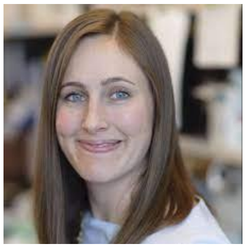
Associate attending computational oncologist, Memorial Sloan Kettering Cancer Center

Dr. Greenbaum's main research interests have long centered around the fundamental question of self vs non-self discrimination: How does the immune system recognize and target particular molecular patterns and sequences as 'foreign', and how does this affect the evolution of tumors and viruses? As the director of Computational Immuno-Oncology within the Computational Oncology Service, Dr. Greenbaum combines statistical physics and information theory with evolutionary biology. After a PhD in theoretical physics from Columbia University he focused on the effect of the innate immune system on viral evolution: his models predicted how the 1918 influenza virus evolved after the pandemic and continued to be cited during Covid-19. His next step took him from virally transcribed RNA to viral mimics: RNA produced from genomic repeat elements in cancer cells. He applied methods from statistical physics to quantify how the immune system recognizes these aberrantly transcribed self-RNAs. Dr. Greenbaum developed the first models to quantify this 'viral mimicry', molecular patterns reminiscent of pathogens that can activate the innate immune system. Within the last few years Dr. Greenbaum's group and his collaborators also created models to predict the role of neoantigens in tumor evolution, and they established the concept of 'neoantigen quality' to assess the likelihood that a neoantigen will induce an immune response. His team discovered an immune tradeoff in cancer evolution: oncogenic mutations with lower fitness present poorly to the immune system, while mutations with high fitness generate potent neoantigens.

Smita Krishnaswamy

Associate Professor of Genetics and of Computer Science, Yale University

Smita Krishnaswamy is an Associate professor in Genetics and Computer Science. She is affiliated with the applied math program, computational biology program, Yale Center for Biomedical Data Science and Yale Cancer Center. Her lab works on the development of machine learning techniques to analyze high dimensional high throughput biomedical data. Her focus is on unsupervised machine learning methods, specifically manifold learning and deep learning techniques for detecting structure and patterns in data. She has developed algorithms for non-linear dimensionality reduction and visualization, learning data geometry, denoising, imputation, inference of multi-granular structure, and inference of feature networks from big data. Her group has applied these techniques to many data types such as single cell RNA-sequencing, mass cytometry, electronic health record, and connectomic data from a variety of systems. Specific application areas include immunology, immunotherapy, cancer, neuroscience, developmental biology and health outcomes. Smita has a Ph.D. in Computer Science and Engineering from the University of Michigan.



Ashley Laughney

Assistant Professor, Institute for Computational Biomedicine, Department of Physiology and Biophysics, Weill Cornell Medicine

Initially trained as an engineer and in systems biology, Ashley developed functional spectroscopy (Dartmouth College) and single cell imaging and genomics methods in cancer biology (Harvard Medical School and Memorial Sloan Kettering) to quantify functional diversity in individual tumor cells. Combining high-throughput single cell transcriptional profiling with development of innovative computational tools and recruited expertise in synthetic biology, her laboratory aims to understand how the same protein can adapt multiple functions during an evolutionary, multi-cellular process like cancer progression.

Carlos Lopez

Lead, Multiscale Modeling Group (CIH), Principal Scientist, CIPHeR Group, Altos Laboratories

Carlos F. Lopez received his BSc and BLA degrees from University of Miami, his PhD in Physical Chemistry from University of Pennsylvania, had a postdoctoral position at UT-Austin, and was the HW Pierce/King Trust Research Fellow at Harvard Medical School. Dr. Lopez has received multiple prestigious appointments and awards, including serving as the Vanderbilt University-Oak Ridge National Lab Liaison (2017-2019) and re-cently attaining an NSF CAREER Award (2019) and a member of the Maximizing Access Committee in AS-BMB. His work employs novel theoretical, computational and modeling approaches, in combination with ex-perimental data, to explain and predict cellular dynamic processes across multiple scales.

Konstantin Mischaikow

Professor, Department Mathematics and BioMaPS Institute, Rutgers University

Konstantin Mischaikow received a B.A. in mathematics from Reed College in 1979, and an M.A and Ph.D. in mathematics from the University of Wisconsin, Madison in 1983 and 1985, respectively. He was a Visiting Assistant Professor (Research) in the Division of Applied Mathematics at Brown University from 1985-1987. He spent 1987-1989 at Michigan State University and then moved to Georgia Tech from 1989 - 2006 and is currently a Distinguished Professor at Rutgers University in the Department of Mathematics. In addition, he holds Visiting Professorship in the Mathematics Department of the VU Amsterdam and is a Fellow of the American Mathematical Society.

Mischaikow's research is driven by the goal of understanding nonlinear dynamics. More precisely, he works on developing homological invariants that can be used to prove existence and structure of invariant sets. He is developing computational tools to extract information about global dynamics in the settings of continuous maps, differential equations, and time series data. He is applying these techniques in the context of systems biology, control theory, bioengineering, and ecological models.

Elchanan Mossel

Professor of Mathematics, MIT

Elchanan Mossel works in probability, combinatorics and inference. His interests include combinatorical statistics, discrete Fourier analysis, randomized algorithms, computational complexity, Markov random fields, social choice, game theory, evolution, and the mathematical foundations of deep learning. His research in discrete function inequalities, isoperimetry, and hypercontractiviting led to the proof that Majority is Stablest and confirmed that optimality of the Goemans-Williamson MAX-CUT algorithm under the unique games conjecture from computational complexity. His work on the reconstruction problem on trees provides optimal algorithms and bounds for phylogenetic reconstruction in molecular biology and has led to sharp results in the analysis of Gibbs samplers from statistical physics and inference problems on graphs. His research has resolved open problems in computational biology, machine learning, social choice theory, and economics.

Sylvia Plevritis

Professor of Biomedical Data Science and of Radiology and Chair of Biomedical Data Science, Stanford University

Dr. Sylvia K. Plevritis is Professor of Biomedical Data Science, and of Radiology at Stanford University, and Chair of Biomedical Data Science. She leads a systems biology cancer research program that bridges genomics, biocomputation, imaging and population sciences to decipher properties of cancer progression to guide advances in early detection and treatment response. Dr. Plevritis received her Ph.D. in Electrical Engineering and M.S. in Health Services Research, both from Stanford University, with a focus on cancer imaging physics and modeling cancer outcomes, respectively.

Padmini Rangamani

Professor in Mechanical and Aerospace Engineering, University of California, San Diego

Padmini Rangamani is a Professor in Mechanical and Aerospace Engineering at the University of California, San Diego. She joined the department in July 2014. Her research focuses on mathematical and computational biophysics with an emphasis on modeling different aspects cellular mechanotransductiion. Earlier, she was a UC Berkeley Chancellor’s Postdoctoral Fellow, where she worked on lipid bilayer mechanics. She obtained her Ph.D. in biological sciences from the Icahn School of Medicine at Mount Sinai. She received her B.S. and M.S. in Chemical Engineering from Osmania University (Hyderabad, India) and Georgia Institute of Technology respectively. She is the recipient of the PECASE, ARO, AFOSR, and ONR Young Investigator Awards, and a Sloan Research Fellowship for Computational and Molecular Evolutionary Biology. She is also the lead PI for a MURI award on Bioinspired low energy information processing from the AFOSR. She was recently elected as a fellow of the American Institute for Biological and Medical Engineers.Professor Rangamani's research is focused on understanding the design principles of biological systems. Her long-term research goal is to understand the control of cell shape by analyzing biological membranes and their interaction with proteins and the cytoskeleton using principles from transport phenomena. This is a unifying framework that brings together, mechanics of the membrane, membrane-bound proteins, and their coupled interactions. Her work uses a combination of novel mechanical theories and computational approaches to simulate many aspects of cellular membranes, in collaboration with experimentalists.

Tatiana Toro

Professor, Director of the Simons Laufer Mathematical Sciences Institute

Tatiana Toro is a mathematician working at the interface of geometric measure theory, harmonic analysis and partial differential equations. The interaction between these three areas has been one of the pillars of her research. Her work focuses on understanding mathematical questions that arise in an environment where the known data is very rough. In particular she studies the properties of interfaces arising in “noisy" minimization problems. The main premise of her work is that under the right lens, objects, which at first glance might appear to be very irregular, do exhibit quantifiable regular characteristics. With C. Kenig she introduced the notion of chord arc domains, setting a new framework to study boundary regularity questions for second order partial differential operators. They laid the foundation of what has become a new, rapidly developing area within PDEs. Her work with C. Kenig and D. Preiss brought tools from geometric measure theory to study basic questions about the structure of harmonic measure.

Bei Wang

Associate Professor in the School of Computing and a faculty member in the Scientific Computing and Imaging (SCI) Institute, University of Utah

Dr. Bei Wang Phillips is an Associate Professor in the School of Computing and a faculty member in the Scientific Computing and Imaging (SCI) Institute, University of Utah. She obtained her Ph.D. in Computer Science from Duke University. Her research focuses on topological data analysis, data visualization, and computational topology. She works on combining topological, geometric, statistical, data mining, and machine learning techniques with visualization to study large and complex data for information exploration and scientific discovery. Some of her current research activities involve the analysis and visualization of high-dimensional point clouds, scalar fields, vector fields, tensor fields, networks, and multivariate ensembles. Dr. Phillips is a DOE Early Career Research Program (ECRP) awardee in 2020 and an NSF CAREER awardee in 2022. Her research has been supported by multiple awards from NSF, NIH, and DOE.

Itai Yanai

Professor in the Department of Biochemistry and Molecular Pharmacology, NYU Grossman School of Medicine

Itai Yanai is a Professor at the NYU Grossman School of Medicine, Department of Biochemistry and Molecular Pharmacology. He received his undergraduate degrees in Computer Engineering and the Philosophy of Science and his PhD in Bioinformatics from Boston University. His lab is a pioneer of the single-cell RNA-Seq approach and its application to the functional study of development, host-pathogen interactions, and cancer cell states. The Yanai lab has used computational and experimental approaches to make contributions to diverse fields including the evolution of developmental gene expression programs, cellular plasticity and developmental constraint in tumor progression and drug resistance, and bacterial genome regulation. Yanai is also committed to communicating science to a popular audience. He recently co-authored a popular science book, entitled “The Society of Genes”, along with Dr. Martin Lercher from Heinrich-Heine University in Düsseldorf. With Dr. Lercher, he is currently publishing editorials, podcasting, and leading workshops on the topic of ‘Night Science’, the scientific creative process.