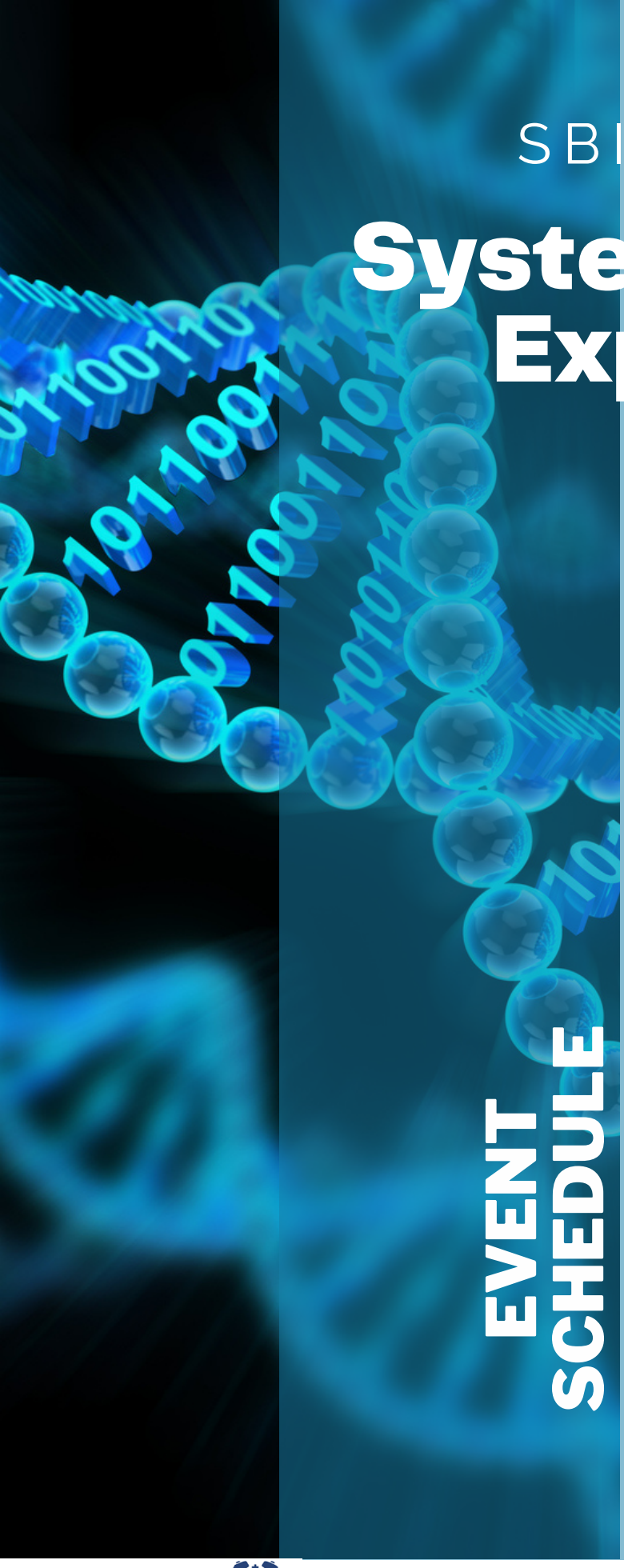

SBI PRESENTS

# Systems Biology Expo 2020

NOVEMBER 13TH
4PM-9PM

Learn about research in systems biology | Connect with professors | Participate in computational biology workshops

## EVENT SCHEDULE

**4:00 - 5:00 Workshop: Intro RNA-Seq**
**5:00 - 5:25 Prof. Cory Abate-Shen**
**5:25 - 5:50 Prof. David Knowles**
**5:50 - 6:15 Prof. Andrea Califano**
**6:15 - 6:40 Prof. Simon Tavaré**
**6:40 - 7:05 Prof. Dana Pe'er**
**7:05 - 7:20 Intermission**
**7:20 - 7:45 Prof. Itsik Pe'er**
**7:45 - 8:10 Aleksandar Obradovic (Califano Lab)**
**8:10 - 8:35 Dr. Sima Lao (Leong Lab)**
**8:35 - 9:35 Workshop: COVID TCR Analysis**

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# Presentors

## Lab Introductions

**Prof. Cory Abate-Shen**
Topics: Prostate cancer, cancer, metastasis

**Prof. David Knowles**
Topics: Predictive models of RNA splicing, Convex dimensionality reduction for sparse data, Causal network inference

**Prof. Andrea Califano**
Topics: Regulatory Architecture of Cancer Cell

**Prof. Simon Tavaré**
Topics: Computational Molecular Biology

**Prof. Dana Pe'er**
Topics: Learning dynamics from single cell data

## Research Presentations

**Prof. Itsik Pe'er**
Topics: Microbial dynamics, Inference of longitudinal count data

**Aleksandar Obradovic (Califano Lab)**
Topics: Single-cell RNA profiling of kidney tumor immune microenvironment

**Dr. Sima Lao (Leong Lab)**
Topics Covered: CRISPR technology and somatic genome editing

## Computational Bio Workshops

**Theodore Nelson**
Introduction to RNA-Sequencing Data Analysis

**Joshua Fuller**
Analyzing T-cell receptor data for COVID-19

# Prof. Cory Abate-Shen

Michael and Stella Chernow Professor of Urologic Sciences (in Urology)
Professor of Pathology and Cell Biology (in the Herbert Irving Comprehensive Cancer Center)

**Research presented:**
Prostate cancer, cancer, metastasis

Dr. Abate-Shen joined Columbia University Medical School in 2007 - She was an Associate Director of the Cancer Center from 2008-2017, and served as its Interim Director from 2011-2012 and in 2017-2018. Recently, she was appointed as Chair of the Department of Pharmacology and the Robert Sonneborn Professor of Pharmacology at Columbia University Vagelos College of Physicians and Surgeons.Dr. Abate-Shen is an internationally-recognized leader in genitourinary malignancies. Her innovative studies of genetically-engineered mouse models of prostate and bladder cancer have led to the discovery of new biomarkers for early detection, as well as advances in cancer prevention and treatment. In recognition of her achievements, Dr. Abate-Shen has been the recipient of numerous awards, including a Sinsheimer Scholar Award, an NSF Young Investigator Award, and an American Cancer Society Research Professorship, which was the first to be awarded at Columbia University Irving Medical Center. Recently, she was elected as a fellow of the American Association for the Advancement of Science.As a teacher and mentor, Dr. Abate-Shen has trained eight PhD students, more than thirty five postdoctoral fellows and numerous medical and undergraduate students. Most of her trainees have been successful in receiving grant funding and obtaining independent positions in academia or industry, and have been the recipients of numerous awards and fellowships.

# Prof. David Knowles

Assistant Professor, Department of Computer Science
Core Member, New York Genome Center

**Research presented:**
Predictive models of RNA splicing, Convex dimensionality reduction for sparse data, Causal network inference

David Knowles is an Assistant Professor in Computer Science, an Interdisciplinary Appointee in Systems Biology (both at Columbia), and a Core Faculty Member at the New York Genome Center. His research focuses on the development of novel machine learning methods and their application to data analysis challenges in genomics with the aim to better understand the role of transcriptomic dysregulation across the spectrum from rare to common genetic disease. Another key area of study is better characterization of the genetic and environmental factors contributing to mRNA expression and splicing variation. The lab works with diverse research groups in collecting large-scale genomics datasets in the context of neurological disease and developing novel genomic technologies including single cell methods, forward genetic screens and long-read transcriptomics. Dr. Knowles studied Natural Sciences and Information Engineering at the University of Cambridge before obtaining an MSc in Bioinformatics and Systems Biology at Imperial College London. During his PhD studies in the Cambridge University Engineering Department Machine Learning Group under Zoubin Ghahramani he worked on Bayesian nonparametric models for factor analysis, hierarchical clustering and network analysis, as well as on variational inference. He was a postdoctoral researcher at Stanford University with Daphne Koller (Computer Science), Sylvia Plevritis (Center for Computational Systems Biology/Radiology) and Jonathan Pritchard (Genetics/Biology).

# Prof. Andrea Califano

Clyde and Helen Wu Professor of Chemical and Systems Biology
Chair, Department of Systems Biology
Director, JP Sulzberger Columbia Genome Center

**Research presented:**
Regulatory Architecture of Cancer Cell

Andrea Califano, Dr., is a pioneer in the field of systems biology and founding chair of the Department of Systems Biology at Columbia University Irving Medical Center. A physicist by training, Dr. Califano has taken innovative, systematic approaches to identify the molecular factors that lead to cancer progression and to the emergence of drug resistance at the single-cell level. Directing the conversation about cancer research away from focusing solely on gene mutations, Dr. Califano examines the complex and tumor-specific molecular interaction networks that determine cancer cell behavior. Using information theoretic approaches, analysis of these networks can precisely pinpoint master regulator proteins that are mechanistically responsible for supporting tumorigenesis and for implementing tumor cell homeostasis. Dr. Califano and his lab have shown that master regulators represent critical drivers and tumor dependencies, despite the fact that they are rarely mutated or differentially expressed, thus establishing them as a bona fide new class of therapeutic targets.

# Prof. Simon Tavaré

Professor, Biological Sciences and Statistics
Director, Irving Institute for Cancer Dynamics

**Research presented:**
Computational molecular biology

Simon Tavaré joined Columbia University in 2018 as the Herbert and Florence Irving Director of the Irving Institute for Cancer Dynamics and a professor in the Departments of Statistics and Biological Sciences. From 2003 to 2018, he was a professor in the Department of Applied Mathematics and Theoretical Physics and the Department of Oncology at the University of Cambridge, England. Simon was director of the Cancer Research UK Cambridge Institute from 2013 to 2018. His research focuses on statistics, computational biology and genetics, particularly evolutionary approaches to understanding cancer biology. Dr. Tavaré is an elected fellow of the Academy of Medical Sciences and of the Royal Society, and a member of the European Molecular Biology Organization. He was president of the London Mathematical Society from 2015 to 2017 and was elected a fellow of the American Mathematical Society and an International Member of the U.S. National Academy of Sciences in 2018.

# Prof. Dana Pe'er

Adjunct Professor of Biological Sciences
Chair, Computational and Systems Biology Program, SKI
Scientific Director, Alan and Sandra Gerry Metastasis and Tumor Ecosystems Center

**Research presented:**
Learning dynamics from single cell data

Dana Pe'er is an adjunct professor in the Departments of Biological Sciences at Columbia University. She received a Ph.D in Computer Science from the Hebrew University of Jerusalem and continued her post-doctoral studies with George Church at Harvard Medical School. In particular, we study how genetic variation alters regulatory network function, subsequently phenotype in health and disease. This path has led her to explore how systems biology approaches can be used to personalize cancer care, by developing models that predict how individual tumors will respond to certain drug and drug combinations. Dana is recipient of the Burroughs Wellcome Fund Career Award, NIH Directors New Innovator Award, NSF CAREER award, Stand Up To Cancer Innovative Research Grant and a Packard Fellow in Science and Engineering.

# Prof. Itsik Pe'er

Associate Professor, Department of Computer Science

**Research presented:**
Microbial dynamics, Inference of longitudinal count data

Itsik Pe’er is an associate professor in the Department of Computer Science. His laboratory develops and applies computational methods for the analysis of high-throughput data in germline human genetics. Specifically, he has a strong interest in isolated populations such as Pacific Islanders and Ashkenazi Jews. The Pe’er Lab has developed methodology to identify hidden relatives — primarily in such isolated populations — that involves inferring their past demography, detecting associations between phenotypes and genetic segments co-inherited from the joint ancestors of hidden relatives, and establishing the exceptional utility of whole-genome sequencing in population genetics. With the arrival of high-throughput sequencing methods, Pe’er has focused on characterizing genetic variation that is unique to isolated populations, including the effects of such variation on phenotype.

# Aleksandar Obradovic (Califano Lab)

MD/PhD Candidate
CC '17

**Research presented:**
Single-cell RNA profiling of kidney tumor immune microenvironment

MD/PhD Student jointly co-mentored in the Department of Systems Biology and Center for Translational Immunology. Actively researching tumor immunology and cancer immunotherapy in human clinical trial data profiled at the single-cell level. Expertise in high-throughput TCR-sequencing analysis, master regulator inference from gene expression data, and analysis of single-cell RNASeq datasets, with experience in immunology bench techniques and in clinical practice.

# Dr. Sima Lao (Leong Lab)

Ph.D. in Biomedical Engineering, Columbia University

**Research presented:**
CRISPR technology and somatic genome editing

Sima received his PhD last year and is currently a postdoctoral fellow in Prof Kam Leong's lab in the BME department. His research expertise and focuses are on CRISPR technology, somatic genome editing and babysitting. Besides doing research, he likes reading, and his favorite book is Corduroy.

# Computational Biology Workshops

Presentation 1:
4:00-5:00

***Introduction to RNA-Sequencing Data Analysis***

by Theodore Nelson

What genes are altered across different samples? How do we interpret these to draw biologically relevant conclusions? How do we choose between all of the different software packages out there? As the number of available RNAseq samples increases exponentially there is more work to be done in this field than ever before. This workshop will include two parts: a brief introductory presentation explaining RNA sequencing from a biological context and then an interactive programming session.

Presentation 2:
8:35-9:35

***Analyzing T-cell receptor data for COVID-19***

by Joshua Fuller

In this intermediate level python workshop, we will be working with several large databases of sequenced t-cell receptors from patients who were diagnosed with COVID-19. Participants only need basic python skills.

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