

**2<sup>nd</sup> International Symposium on Mathematical and  
Computational Oncology (ISMCO'20)**

October 8-10, 2020, Virtual (Pacific Standard Time – PST)



**ISMCO 2020**

# Contents

THURSDAY, OCTOBER 8 <sup>th</sup> .....	3
FRIDAY, OCTOBER 9 <sup>th</sup> .....	4
SATURDAY, OCTOBER 10 <sup>th</sup> .....	5
Keynote Speakers .....	6
Steering Committee/Program Chairs .....	12
International Program Committee .....	13
Special Tracks / Tutorials .....	17

Registration Desk Hours: N/A



# Thursday, October 8<sup>th</sup>

8:50–9:00	<i>Welcome – <u>George Bebis</u>, University of Nevada, Reno</i>	
9:00–10:00	<i>Keynote: <u>Doron Levy</u>, University of Maryland at College Park, USA</i> Moderator: <u>George Bebis</u>	
10:10-11:10	<b>Statistical and Machine Learning Methods for Cancer Research I</b> Chair: <u>George Bebis</u>	
	10:10	<b>Cristian Axenie and Daria Kurz.</b> CHIMERA: Combining Mechanistic Models and Machine Learning for Personalized Chemotherapy and Surgery Sequencing in Breast Cancer
	10:30	<b>Roshan Welikala, Paolo Remagnino, Jian Han Lim, Chee Seng Chan, Senthilmani Rajendran, Thomas Kallarakkal, Rosnah Zain, Ruwan Jayasinghe, Jyotsna Rimal, Alexander Kerr, Rahmi Amtha, Karthikeya Patil, Wanninayake Tilakaratne, John Gibson, Sok Ching Cheong and Sarah Barman.</b> Fine-Tuning Deep Learning Architectures for Early Detection of Oral Cancer
	10:50	<b>Sokratis Makrogiannis, Chelsea Harris and Keni Zheng.</b> Discriminative Localized Sparse Representations for Breast Cancer Screening
11:10-11:30	Coffee Break	
11:30-12:30	<b>Poster Session I</b> (pre-recorded poster presentations will start at 12:00) Chair: <u>Dinler Antunes</u>	
	<b>Koichi Saeki and Hiroshi Haeno.</b> A Mathematical Model of Cancer Immune Escape <b>Gurvan Hermange, Amandine Tisserand, François Girodon, William Vainchenker, Isabelle Plo and Paul-Henry Cournède.</b> Model of hematopoiesis dynamics under IFN alpha therapy in Myeloproliferative Neoplasms (pre-recorded) <b>Takuya Moriyama, Seiya Imoto, Satoru Miyano and Rui Yamaguchi.</b> Theoretical Foundation of the Performance of Phylogeny-Based Somatic Variant Detection (pre-recorded) <b>Leonard Harris, Samantha Beik, Carlos Lopez and Vito Quaranta.</b> Modulating tumor composition in a cell-cell interaction model of SCLC	
12:30-1:30	Lunch Break	
1:30-2:30	<i>Keynote: <u>Sridhar Hannenhalli</u>, National Cancer Institute, USA</i> Moderator: <u>Mircea Nicolescu</u>	
2:40-3:00	<b>Spatio-temporal tumor modeling and simulation</b> Chair: <u>Jana Gevertz</u>	
	2:40	<b>Robert Noble, Dominik Burri, John T. Burley, Cécile Le Sueur, Jeanne Lemant, Yannick Viossat, Jakob Nikolas Kather, Michael E. Hochberg and Niko Beerenwinkel.</b> Characterizing and forecasting tumour evolution
3:00-3:20	Coffee Break	
3:20-5:00	<b>Panel Discussion I</b> Moderator: <u>Oliver Bogler</u> (Director, Center for Cancer Training, NCI)	
	<b>Topic:</b> Training of Computational Scientists in Cancer <b>Panelists:</b> Anne Deslattes Mays, Ken Chen, Dorin Levy, Jean Clairambault	

# Friday, October 9<sup>th</sup>

9:00–10:00	<p><i>Keynote:</i> <b><u>Jean Clairambault</u></b>, Inria and Sorbonne University, Paris, France  Moderator: <u>Dorin Levy</u></p>	
10:10-11:10	<p><b>Mathematical Modeling for Cancer Research</b>  Chair: <u>Ernesto Lima</u></p>	
	10:10	<b>Iurii Nagornov, Jo Nishino and Mamoru Kato.</b> tugHall: a tool to reproduce Darwinian evolution of cancer cells for simulation-based personalized medicine
	10:30	<b>Hiroshi Haeno.</b> Mathematical modeling of clonal evolution in hematopoietic tissue
	10:50	<b>Jeroen H.A. Creemers, Niven Mehra, Winald R. Gerritsen, I. Jolanda M. De Vries and Johannes Textor.</b> Better immunotherapy trials with higher power using mechanistic microsimulations
11:10-11:30	Coffee Break	
11:30-12:30	<p><b>Poster Session II</b>  Chair: <u>George Bebis</u></p>	
	<p><b>Dinler Antunes, Jayvee Abella, Sarah Hall-Swan, Didier Devaurs, Anja Conev, Mark Moll, Gregory Lizeé and Lydia Kavraki.</b> Virtual screening of peptide-targets for cancer immunotherapy using HLA-Arena  <b>Phillip Nicol.</b> Detecting subclones from spatially resolved RNA-seq data  <b>Ofek Shami-Schnitzer, Zohar Zafrir and Tamir Tuller.</b> Novel driver synonymous mutations in the coding regions of GCB lymphoma patients improve the transcription levels of BCL2  <b>Alec Kacew, Garth Strohhenn, Loren Saulsberry, Neda Laiteerapong, Jakob Kather and Alexander Pearson.</b> Financial and clinical impact of artificial intelligence for colorectal cancer genotyping  <b>Tanishq Abraham, Andrew Shaw, Daniel O'Connor, Austin Todd and Richard Levenson.</b> Ex-vivo slide-free microscopy with H&amp;E color-mapping via unpaired image-to-image translation</p>	
12:30-1:30	Lunch Break	
1:30-2:30	<p><i>Keynote:</i> <b><u>Ken Chen</u></b>, MD Anderson, USA  Moderator: <u>Sokratis Makrogiannis</u></p>	
2:40-3:40	<p><b>Statistical and Machine Learning Methods for Cancer Research II</b>  Chair: <u>Sokratis Makrogiannis</u></p>	
	2:40	<b>Elliot Gray, Young Hwan Chang, Shannon Liudahl, Shamilene Sivagnanam, Courtney Betts, Jason Link, Dove Keith, Brett Sheppard, Rosalie Sears, Guillaume Thibault, Joe W. Gray and Lisa M. Coussens.</b> Activation vs. Organization: Prognostic Implications of T and B cell Features of the PDAC Microenvironment
	3:00	<b>James Dolezal, Anna Trzcinska, Chih-Yi Liao, Sara Kochanny, Elizabeth Blair, Nishant Agrawal, Peter Angelos, Nicole Cipriani and Alexander Pearson.</b> Deep learning prediction of BRAF-RAS gene expression signature identifies noninvasive follicular thyroid neoplasms with papillary-like nuclear features
	3:20	<b>Elvire Roblin, Stefan Michiels and Paul-Henry Cournède.</b> On the use of neural networks with censored time-to-event data
3:40-4:00	Coffee Break	
4:00-5:30	<p><b>Panel Discussion II</b>  Moderators: <u>Ernesto Lima</u> &amp; <u>Chengyue Wu</u> (University of Texas at Austin)</p>	
	<p><b>Topic:</b> Incorporating patient-data into mathematical modeling of cancer: What data do we have and how can we use it?  <b>Panelists:</b> Russell Rockne, Vishaka Gopalan, Vakul Mohanty, Frederick Howard, Harsh Jain</p>	

# Saturday, October 10<sup>th</sup>

9:00–10:00	<p><i>Keynote:</i> <b>Alexander Pearson</b>, UChicago Medicine, USA  Moderator: <u>Trachette Jackson</u></p>	
10:10-11:10	<p><b>General cancer computational biology</b>  Chair: <u>Dinler Antunes</u></p>	
	10:10	<b>Matthew Hayes, Angela Nguyen, Ethan Tran, Derrick Mullins and Chindo Hicks.</b> Leveraging Hi-C and Whole Genome Shotgun Sequencing for Double Minute Chromosome Discovery
	10:30	<b>Sarah Hall-Swan, Dinler Antunes and Lydia Kavraki.</b> Scoring class I peptide-HLA complexes
	10:50	<b>Kirill Medvedev, Anna Savelyeva, Aditya Bagrodia and Nick Grishin.</b> The potential of single cell RNA-sequencing data for the prediction of gastric cancer serum biomarkers
11:10-11:30	Coffee Break	
11:30-1:00	<b>Workshop</b>	
	<p><b>Title:</b> Advice for the Novice Investigator: Grant writing for the NIH and other agencies  <b>Presenter:</b> Nicholas Stergiou, University of Nebraska at Omaha</p> <p>Dr. Nick Stergiou is the Distinguished Community Research Chair in Biomechanics and Professor as well as the Director of the Biomechanics Research Building and the Center for Research in Human Movement Variability at the University of Nebraska at Omaha. He is the Founding Chair of the first ever academic Department of Biomechanics which offers a BS degree in Biomechanics. His research focuses on understanding variability inherent in human movement and he is an international authority in the study of Nonlinear Dynamics. He has published more than 200 peer-reviewed papers and have been inducted to the National Academy of Kinesiology and as a Fellow to the American Institute for Medical and Biological Engineering and the American Society of Biomechanics. He has received more \$40M in funding from NIH, NASA, NSF, the US Department of Education, and many other agencies and foundations. He is the author of the book “<b>Advice for the Novice Investigator: Examples Taken from Movement Sciences</b>” which was recently published by CRC Press</p> <p><a href="https://www.routledge.com/Advice-for-the-Novice-Investigator-Examples-Taken-from-Movement-Sciences/Stergiou/p/book/9781138626188">https://www.routledge.com/Advice-for-the-Novice-Investigator-Examples-Taken-from-Movement-Sciences/Stergiou/p/book/9781138626188</a></p>	
1:00-1:30	Lunch Break	
1:30-2:30	<p><i>Keynote:</i> <b>Jennifer Couch</b>, National Cancer Institute, USA  Moderator: <u>Russell Rockne</u></p>	
2:30-3:00	Coffee Break	
3:00-7:00	<p><b>Tutorial</b>  Moderator: <u>Dinler Antunes</u></p>	
	<p><b>Current methods and open challenges for structural modeling in cancer immunotherapy</b>  <b>Instructors:</b> Antunes Dinler, Maurício M. Rigo, Sarah Hall-Swan, Lydia Kavraki</p>	

# KEYNOTE TALK

Thursday, October 8, 2020 at 9:00am

## Fighting Drug Resistance with Math

Doron Levy  
University of Maryland at College Park  
USA

**Abstract:** The emergence of drug-resistance is a major challenge in chemotherapy. In this talk we will overview some of our recent mathematical models for describing the dynamics of drug-resistance in solid tumors. These models follow the dynamics of the tumor, assuming that the cancer cell population depends on a phenotype variable that corresponds to the resistance level to a cytotoxic drug. Under certain conditions, our models predict that multiple resistant traits emerge at different locations within the tumor, corresponding to heterogeneous tumors. We show that a higher drug dosage may delay a relapse, yet, when this happens, a more resistant trait emerges. We will show how mathematics can be used to propose an efficient drug schedule aiming at minimizing the growth rate of the most resistant trait, and how such resistant cells can be eliminated.



**Speaker Bio-Sketch:** Doron Levy is a Professor of Mathematics and the Department Chair at the University of Maryland, College Park. He is also a member of the Center for Scientific Computation and Mathematical Modeling, and the Maryland BioPhysics Program. Previously he held positions at Stanford University, UC Berkeley, Lawrence Berkeley National Lab, the University of Paris 6, and the Ecole Normale Supérieure (ENS) Paris. In 2013 Dr. Levy was named a Distinguished Scholar-Teacher by the University of Maryland, and in 2014 he was named a Fellow of the John Simon Guggenheim Memorial Foundation. He is also a Pauli Fellow at the Wolfgang Pauli Institute in Vienna. His research focuses on biomedical applications of mathematics: cancer dynamics, drug resistance, immunology, imaging, and cell motility. He is a member of ten editorial boards of mathematical and biomath journals. Dr. Levy has been a plenary and keynote speaker in many national and international conferences, including the keynote speaker in the American Mathematical Society briefing to the US

Congress, and the SIAM representative in the Coalition for National Science Funding Meeting on Capitol Hill.

# KEYNOTE TALK

Thursday, October 8, 2020 at 1:30pm

## To Function or Not to Function

Sridhar Hannenhalli  
National Cancer Institute  
USA

**Abstract:** The functions of only a minority of genes in any species is known. And even in those cases the functional annotation is highly incomplete and largely devoid of context. At an even more fundamental level, how can we know whether a gene serves any relevant biological function in a given context? In this informal presentation we will discuss a few vignettes related to the broad questions of context-specific functions of genes, in a variety of contexts from bacterial response to drugs, normal tissues, and cancer.



**Speaker Bio-Sketch:** Dr. Hannenhalli obtained a B. Tech from the Indian Institute of Technology (1990) and his Ph.D. in Computer Science from the Pennsylvania State University (1995). After a postdoctoral fellowship at the University of California-San Diego (1996-1997), he worked as a Senior Scientist at Glaxo Smith-Kline (1997-2000) and then at Celera Genomics (2000-2003), where he was involved in the work reporting the first human genome sequence. He was a faculty member in the Department of Genetics at the University of Pennsylvania (2003-2010), and then at the University of Maryland (UMD) with joint appointments in the Department of Cell Biology and Molecular Genetics, and the University of Maryland Institute for Advanced Computer Studies (2010-2019). Dr. Hannenhalli served as Interim Director of the Center for Bioinformatics and Computational Biology at UMD (2012-2013) and was a Fulbright Scholar and Visiting Professor at the Indian Institute of Sciences and the

National Center for Biological Sciences, Bengaluru (2017-2018). The Hannenhalli lab is broadly interested in developing computational and statistical approaches to harness the huge amount of biological data to ultimately answer specific biological questions pertaining to gene regulation and evolution, both from the basic science as well as translational perspective, with specific applications to development and diseases, with an emphasis on cancer.

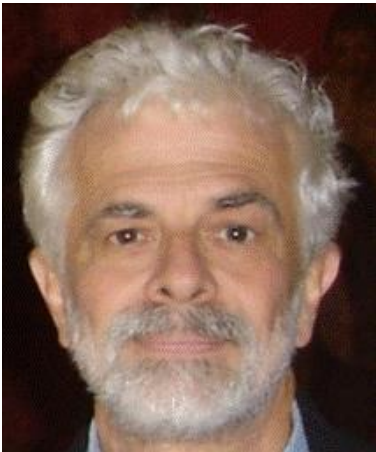
# KEYNOTE TALK

Friday, October 9, 2020 at 9:00am

## From Mathematical Modelling of Cancer Cell Plasticity to Philosophy of Cancer

Jean Clairambault  
INRIA and Sorbonne University, Paris  
France

**Abstract:** In this talk, I will suggest that cancer is fundamentally a disease of the control of cell differentiation in multicellular organisms, uncontrolled cell proliferation being a mere consequence of blockade, or unbalance, of cell differentiations. Cancer cell populations, that can reverse the sense of differentiations, are extremely plastic and able to adapt without mutations their phenotypes to transiently resist drug insults, which is likely due to the reactivation of ancient, normally silenced, genes. Stepping from mathematical models of non genetic plasticity in cancer cell populations and questions they raise, I will propose an evolutionary biology approach to shed light on this problem both from a theoretical viewpoint by a description of multicellular organisms in terms of multi-level structures, which integrate function and matter from lower to upper levels, and from a practical point of view oriented towards cancer therapeutics, as cancer is primarily a failure of multicellularity in animals and humans. This approach resorts to the emergent field of knowledge named philosophy of cancer.



**Speaker Bio-Sketch:** Jean Clairambault, PhD, MD, is an emeritus research director (senior scientist) at Inria Paris, France. He is also a member of Jacques-Louis Lions Lab at Sorbonne University (which now includes the former Paris VI, Pierre-et-Marie-Curie University) in Paris. After studies in mathematics until French 'agrégation' and PhD in geometry, he switched to medical studies until MD (thesis on heart rate variability in sleeping newborns), and then accomplished his research career at INRIA teaching mathematics and modelling biomedical topics by means of multidimensional statistics and differential equations. Having started from autonomic control on cardiovascular dynamics and later circadian clock control on the division cycle in healthy and cancer cells, he devotes himself to therapeutic optimization for cancer therapeutics, in particular with respect to reversible, drug-induced, anticancer drug resistance. Related to evolution towards drug resistance in cancer cell populations, he is also interested in understanding cancer as a disease of differentiation control in multicellular organisms, seen in a billion-year evolutionary perspective.



# KEYNOTE TALK

Friday, October 9, 2020 at 1:30pm

## Quantitative Molecular Dissection of Cancer Evolution

Ken Chen  
MD Anderson Cancer Center  
USA

**Abstract:** A cancer initiates, grows and metastasizes over time and space. It often involves dynamic, genotypical and phenotypical evolution and interaction of millions of cells, belonging to hundreds of cell types. Successful cancer prevention and treatment require quantitative approaches that can identify key factors that are causal to cancer evolution and can be therapeutically intervened. Achieving such a goal has been challenging, due partly to limitations in data collection, analysis and interpretation. In this talk, I will highlight ongoing efforts that involve various aspects of experimental design, application of high-throughput multiomics technologies such as single-cell DNA, RNA and ATAC sequencing, and statistical computational approaches to tackle such an important challenge.



**Speaker Bio-Sketch:** Dr. Chen is currently a tenured associate professor in the Department of Bioinformatics and Computational Biology at the University of Texas MD Anderson Cancer Center. He received his quantitative science training from Tsinghua University (Beijing), University of Illinois at Urbana-Champaign, and University of California at San Diego. He also worked at Washington University School of Medicine in St. Louis as a senior scientist and a research faculty, before starting his lab in 2011. Having a background in machine learning, statistical signal processing, and cancer omics, his primary interest is to develop computational approaches to analyze and interpret human molecular and clinical data towards the realization of cancer precision medicine. He has developed numerous computational tools such as BreakDancer and VarScan that have been widely applied to perform molecular characterization in various large-scale scientific investigations such as the 1000 Genomes project, TCGA, and the Human Cell Atlas. He is particularly interested in comprehensively and

accurately constructing the genomes and the transcriptomes of various cancer cell populations towards understanding the heterogeneity and the evolution of cancer as a consequence of genetics and environment, and identify targets that are useful for cancer diagnosis and treatment.

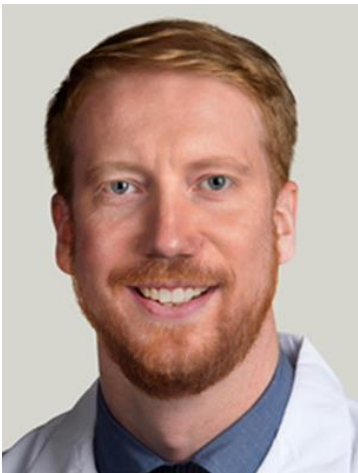
## KEYNOTE TALK

Saturday, October 10, 2020 at 9:00am

### Deep Learning for Clinically Actionable Cancer Pathology Feature Detection

Alexander Pearson  
UChicago Medicine  
USA

**Abstract:** An immense amount of information is stored in the spatial information of tumor histology. Access to contemporary neural network architecture, the decreasing cost of hardware, and the immense amount of available pathologic and genomic data have contributed to rapid innovation in digital pathology analysis. We will describe the basics of deep learning and how it can readily be applied to histology data. We will further describe specific applications to clinical oncology, including defining molecular treatment targets directly from histology. Finally we will discuss the state of the field, and barriers and opportunities for wide deployment of deep learning in our healthcare system.



**Speaker Bio-Sketch:** Dr. Alexander Pearson is a quantitative scientist, medical oncologist, and director of the head/neck cancer program at the University of Chicago. Dr. Pearson completed a combined MD and PhD program at the University of Rochester, where he won the American Statistical Association Computational Award for his statistics PhD dissertation work. He then completed his clinical training in the University of Michigan Physician Scientist Training Program where he completed a combined a post doc with mathematician Dr. Trachette Jackson and Cancer Biologist Dr. Jacques Nor. Dr. Pearson joined the University of Chicago to establish his laboratory in 2017. Dr. Pearson's lab at the University of Chicago has a combined focus on integrating cancer biology techniques into mathematical modeling frameworks as well as using machine learning for head/neck cancer characterization. In 2019 Dr. Pearson was named a HemOnc Today Next Gen Innovator, a 40 under 40 Chicago Scientist, and was awarded the ACCRF Kara Gelb Memorial Award for early-career investigators.

# KEYNOTE TALK

Saturday, October 10, 2020 at 1:30pm

## Enriching Cancer Research Through Unconventional Collaborations

Jennifer Couch  
National Cancer Institute  
USA

**Abstract:** Cancer is complicated and complex, arising in multiple cell types and tissue of origin, initiating and progressing differently in different individuals or under different conditions, with effects crossing multiple biological scales. It is also adaptive, evolving at both the molecular and cellular scales during treatment. Because of this, cancer researchers are often early adopters of new technologies, methods and approaches and they routinely adopt tools and methods originally developed in other, very different fields for use in modeling, understanding, and combating cancer. Systems biology, with its combination of experimental biology and mathematical modeling, plays an increasingly important role in cancer research. Advances in data science, high performance computing, and artificial intelligence have led to increasingly creative adoption of these tools and approaches in cancer research. But high-dimensional data, complicated problems, and collaborative problem solving also exist in areas such as entertainment video games and virtual and augmented reality. And cancer data and its contextual information can come from a variety of sources including patients and the public through citizen science and crowdsourcing. This talk will explore this broader collaborative and creative space and high-light both on-going and new programs supported by the National Cancer Institute to create opportunities for cross-field interactions and to accelerate new collaborations and new interdisciplinary approaches to cancer research.



**Speaker Bio-Sketch:** Jennifer Couch, Ph.D., is the Chief of the Structural Biology and Molecular Applications Branch, Division of Cancer Biology, NCI, NIH. Dr. Couch's branch supports research and development of enabling technologies, models and methodologies including structural biology and biophysical characterization; bioinformatics, computational biology, mathematical modeling, data science, systems biology, citizen science and crowdsourcing methods; and bioengineering, biomimetics and biotechnology. Dr. Couch co-leads the NIH Citizen Science Working Group and acts as the NIH Citizen Science and Crowdsourcing Coordinator. She co-leads the Technology Development Implementation Team for the Cancer Moonshot Initiative and the NCI Artificial Intelligence Working Group. And she participates in trans-NIH and trans-agency efforts in a variety of areas including big data, single cell, inter-disciplinary research, systems pharmacology, AI, and interactive digital media.

## **Steering Committee**

- Anastasiadis Panagiotis, Mayo Clinic
- Bebis George, University of Nevada, Reno (chair)
- Jackson Trachette, University of Michigan
- Levy Doron, University of Maryland, College Park
- Rockne Russell, City of Hope
- Vasmataz George, Mayo Clinic
- Yankeelov Thomas, University of Texas, Austin

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- Cho Heyrim, University of California, Riverside
- Gevertz Jana, The College of New Jersey
- Martinez Maria Rodriguez, IBM, Zurich Research Laboratory

## **Publicity Chairs**

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- Petereit Juli, University of Nevada, Reno

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- Scalzo Fabien, University of California at Los Angeles

## **Web Master**

- Isayas Berhe Adhanom, University of Nevada, Reno

## International Program Committee

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- Harris Leonard , University of Arkansas
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- Hubert Florence , Aix-Marseille universite
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- Jain Harsh , Florida State University
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- Liu Jiajian , Merck-KGaA
- Lorenzo Guillermo , University of Texas at Austin & University of Pavia
- Loss Leandro , QuantaVerse, ITU, ESSCA
- Lou Shaoke , Yale University
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- Müller Henning , University of Applied Sciences Western Switzerland, Sierre (HES-SO)
- Münzner Ulrike , Osaka University
- Murad Neha , Calico Labs

- Nagornov Iurii , National Cancer Center Japan
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- Pirkl Martin , ETH Zurich
- Pisco Angela , Chan Zuckerberg Biohub
- Pognard Clair , INRIA Bordeaux-Sud Ouest-Team MC2
- Posada David , University of Vigo
- Powathil Gibin , Swansea University
- Przulj Natasa , University College London
- Radunskaya Ami , Pomona College
- Raphael Ben , Princeton University
- Renard Bernhard , Robert Koch Institute
- Rigo Mauricio , Universidade Federal do Rio Grande do Sul
- Rigoutsos Isidore , IBM Thomas J Watson Research Center
- Rockne Russell , City of Hope National Medical Center
- Sadanandam Anguraj , Institute of Cancer Research (ICR)
- Satagopam Venkata Pardhasaradhi , University of Luxembourg and ELIXIR-Luxembourg
- Scalzo Fabien , University of California, Los Angeles
- Schaefer Martin H , Centre for Genomic Regulation
- Schissler Alfred , Lussier Lab
- Schoenhuth Alexander , Vrije Universiteit Amsterdam
- Schwartz Russell , Carnegie Mellon University
- Schwarz Roland , Max Delbrueck Center for Molecular Medicine
- Scott Jacob , Cleveland Clinic
- Shen Feichen , Mayo Clinic
- Shen Yang , Texas A&M University
- Shi Xinghua , Temple University
- Sohn Sunghwan , Mayo Clinic
- Sorribes Inmaculada , Duke University
- Stegle Oliver , German Cancer Research Center & European Molecular Biology Laboratory
- Stephanou Angelique , TIMC-IMAG - CNRS
- Stevens Rick , University of Chicago & Argonne National Laboratory
- Sykacek Peter , Boku University
- Tafti Ahmad , Mayo Clinic
- Tang Haixu , Indiana University Bloomington
- Topaloglu Umit , Wfbmc
- Tuller Tamir , Tel Aviv University

- Tuszynski Jack , University of Alberta
- Ushizima Daniela , Lawrence Berkeley National Laboratory
- Vasmatzis George , Mayo Clinic
- Vilar-Sanchez Eduardo , MD Anderson Cancer Center
- Viossat Yannick , Université Paris-Dauphine
- Wang Yanshan , Mayo Clinic
- Wang Li-San , University of Pennsylvania
- Wass Mark , University of Kent
- Williams Matt , Imperial College
- Xu Yanji , NIH
- Yamaguchi Rui , Aichi Cancer Center Research Institute
- Zacharakis Nikos , NCI/NIH
- Zehavi Meirav , Ben-Gurion University
- Zelikovsky Alex , Georgia State University
- Zolnoori Maryam , Mayo Clinic



## Discussion Panels

### (1) Training of Computational Scientists in Cancer

#### **Moderator**

- Bogler Oliver, Director, Center for Cancer Training, NCI

#### **Panelists**

- Deslattes Mays Anne, Science and Technology Consulting, LLC
- Chen Ken, MD Anderson
- Levy Dorin, University of Maryland at College Park
- Clairambault Jean, INRIA and Sorbonne University, Paris

### (2) Incorporating patient-data into mathematical modeling of cancer: What data do we have and how can we use it?

#### **Moderators**

- Wu Chengyue, University of Texas at Austin
- Lima Ernesto, University of Texas at Austin

#### **Panelists**

- Russell Rockne, City of Hope
- Vishaka Gopalan, NCI
- Vakul Mohanty, MD Anderson
- Frederick Howard, University of Chicago
- Harsh Jain, University of Minnesota

## Workshop

Advice for the Novice Investigator: Grant writing for the NIH and other agencies

#### **Persenter**

- Stergiou Nicholas, University of Nebraska at Omaha

## Tutorial

Current methods and open challenges for structural modeling in cancer immunotherapy

#### **Instructors:**

- Antunes Dinler, Rice University, USA
- Hall-Swan Sarah, Rice University, USA
- Lydia Kavradi, Rice University, USA
- Rigo Mauricio, Pontifical Catholic University of Rio Grande do Sul, Brazil