

SUNDAY, SEPT 9

09:00 - 19:30
17:45 - 18:10
18:10 - 19:00

Registration - Entrance		
Opening Conference ECCB 2018		
Keynote speaker: John Ioannidis - Professor of Medicine, Stanford University - Reproducibility with small and big data - Main stage		
Welcome reception at the Light house (Stavros Niarchos Foundation Cultural Center)		

19:30 - 21:30

MONDAY, SEPT 10

07:30 - 18:00
08:15 - 08:30
08:30 - 9:20

Registration open (all day)		
Welcome and announcements		
Keynote speaker: Janet Thornton - Director Emeritus of EMBL-EBI - Integrating heterogenous molecular data to repurpose drugs to improve human health during ageing - Main stage		
Invited speaker: Niklas Blomberg - ELIXIR Director - ELIXIR: A Common European Infrastructure for Bioinformatics Research. - Main stage		
theme: Genes Main stage	theme: Data Hall 5A	track: Applications Alternative stage
<p>PT01: "Discovering epistatic feature interactions from neural network models of regulatory DNA sequences" <u>Payton Greenside</u>, Tyler Shimko, Polly Fordyce and Anshul Kundaje</p> <p>PT02: "A Deep Neural Network Approach for Learning Intrinsic Protein-RNA Binding Preferences" <u>Ilan Ben-Bassat</u>, Benny Chor and Yaron Orenstein</p> <p>HT03: "Differential gene expression in disease: a comparison between high-throughput studies and the literature" <u>Raul Rodriguez-Esteban</u> and Xiaoyu Jiang</p>	<p>HT02: "SourceData: a semantic platform to make data and figures discoverable" Robin Liechti, Lou Gotz, <u>Anastasia Chasapi</u>, Nancy George, Sara El-Gebali, Isaac Crespo, Ioannis Xenarios and Thomas Lemberger</p> <p>PT03: "Ontology-based validation and identification of regulatory phenotypes" <u>Maxat Kulmanov</u>, Paul Schofield, Georgios Gkoutos and Robert Hoehndorf</p> <p>PT04: "An ontology-based method for assessing batch effect adjustment approaches in heterogeneous data sets" <u>Florian Schmidt</u>, Markus List, Engin Cukuroglu, Sebastian Köhler, Jonathan Göke and Marcel Schulz</p>	<p>AT01: "Mechanism-Based Biomarker Discovery" <u>Asier Antoranz</u>, Theodoros Sakellariopoulos, Julio Saez-Rodriguez and Leonidas Alexopoulos</p> <p>AT02: "Re-inventing Pairwise Sequence Alignment Using Fully Differentiable Deep Recurrent Neural Network" <u>Zhizhuo Zhang</u>, Minh Duc Cao, Umut Eser and Jonathan Rothberg</p> <p>AT03: "Deep learning model to improve speed and accuracy of genome assembly" <u>Minh Duc Cao</u>, Umut Eser, Michael Meyer, Zhizhuo Zhang and Jonathan Rothberg</p>
coffee break & exhibition		
theme: Genomes Main stage	theme: Proteins Hall 5A	track: ELIXIR Alternative Stage
<p>PT05: "SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error" <u>Mohammed El-Kebr</u></p> <p>PT06: "Accurate and Adaptive Imputation of Summary Statistics in Mixed-Ethnicity Cohorts" <u>Matteo Togninalli</u>, Damian Roqueiro, Copdgene Investigators and Karsten Borgwardt</p> <p>HT03: "Module Analysis Captures Pancancer Genetically and Epigenetically Deregulated Cancer Driver Genes for Smoking and Antiviral Response" Kevin Brennan, Nathalie Pochet and <u>Olivier Gevaert</u></p>	<p>HT04: "A comprehensive assessment of long intrinsic protein disorder from the DisProt database" Marco Necci, Damiano Piovesan, Zsuzsanna Dosztányi, Peter Tompa and <u>Silvio Ce Tosatto</u></p> <p>PT07: "DeepDTA: Deep Drug-Target Binding Affinity Prediction" <u>Hakime Öztürk</u>, Arzucan Ozgur and Elif Ozkirimli</p> <p>PT08: "Predicting protein-protein interactions through sequence-based deep learning" <u>Somaye Sadat Hashemifar</u>, Behnam Neyshabur, Aly Khan and Jinbo Xu</p>	<p>ET01: "ELIXIR Beacon - A Driver Project for the Global Alliance for Genomics and Health" <u>Michael Baudis</u></p> <p>ET02: "EGA - new and future functionality" <u>Audald Lloret-Villas</u>, Jordi Rambla de Argila, Thomas Keane and Dylan Spalding</p> <p>ET03: "Secure e-infrastructure services supporting cross-border genomic and register studies" <u>Joel Hedlund</u>, Yi Lu, Patrick Sullivan, Niclas Jareborg, Ali Syed, Abdurrahman Azab and Antti Pursula</p>
lunch break, exhibition & poster viewing		
theme: Genes Main stage	theme: Systems Hall 5A	track: Applications Alternative Stage
<p>PT09: "CisPi: an RNA-based score for disclosing disease-associated lincRNAs" Zhehen Wang, John Cunningham and <u>Xinan Yang</u></p> <p>PT10: "iRSOM, a reliable identifier of ncRNAs based on supervised Self-Organizing Maps with rejection" <u>Ludovic Platon</u>, Farida Zehraoui, Abdelhafid Bendahmane and Fariza Tahri</p> <p>HT05: "Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes" <u>Tomas Tokar</u>, Chiara Pastrello, Varune Ramnarine, Chang-Qi Zhu, Kenneth Craddock, Larrisa Pikor, Emily Vucic, Simon Vary, Frances Shepherd, Ming-Sound Tsao, Wan Lam, Igor Jurisica</p>	<p>HT06: "A Compendium of Co-regulated Protein Complexes in Breast Cancer Reveals Collateral Loss Events" <u>Colm Ryan</u>, Susan Kennedy, Ilirjana Bajrami, David Matallanas and Christopher J. Lord</p> <p>PT11: "Scalable and exhaustive screening of metabolic junctions carried out by microbial consortia" <u>Clémence Frioux</u>, Enora Fremy, Camille Trotter and Anne Siegel</p> <p>PT12: "FLYCPD: metabolic modeling-based analysis and engineering microbial communities" <u>Beatriz García-Jiménez</u>, José Luis García and Juan Nogales</p>	<p>AT04: "Live analysis of Illumina data while the sequencer is still running for time-critical applications and enhanced privacy protection" Tobias P. Loka, Simon H. Tausch, Martin S. Lindner, Piotr W. Dabrowski, Benjamin Strauch, Jakob M. Schulze, Aleksandar Radonić, Andreas Nitsche and <u>Bernhard Y. Renard</u></p> <p>AT05: "Application of MEGACLUST Infrastructure-As-A-Service for multi-parameters CYTOMETRY-based clinical studies" <u>Martial Sankar</u>, Petra Baumgartner, Julien Faget, Julien Dorier, George Coukos, Ioannis Xenarios, Miguel Garcia and Nicolas Gueux</p> <p>AT06: "Automated MicroRNA NGS Analysis Pipeline: From pre-process to quantification" <u>Athanasios Alexiou</u>, Dimitrios Zisis, Antonis Koussounadis, Ioannis Kavakiotis, Dimitra Karagkouni and Artemis Hatzigeorgiou</p>
coffee break & exhibition		
theme: Genomes Main stage	theme: Data Hall 5A	track: ELIXIR Alternative Stage
<p>PT13: "An accurate and rapid continuous wavelet dynamic time warping algorithm for end-to-end mapping in ultra-long nanopore sequencing" <u>Renmin Han</u>, Yu Li, Xin Gao and Sheng Wang</p> <p>PT14: "DREAM-Yara: An exact read mapper for very large databases with short update time" <u>Temesgen Hailemariam Dadi</u>, Enrico Siragusa, Vitor C. Piro, Andreas Andrusch, Enrico Seller, Bernhard Y. Renard and Knut Reinert</p> <p>HT07: "Alternative Splicing May Not Be the Key to Proteome Complexity/Most Alternative Isoforms Are Not Functionally Important" <u>Michael Tress</u>, Alfonso Valencia and Federico Abascal</p>	<p>HT08: "Multiple hot-deck imputation for network inference from RNA sequencing data" <u>Alyssa Imbert</u>, Armand Valsesia, Claudia Armenise, Gregory Lefebvre, Pierre-Antoine Gourraud, Nathalie Viguerie and Nathalie Villa-Vialaneix</p> <p>PT15: "Computational enhancement of single-cell sequences for inferring tumor evolution" <u>Savaka Miura</u>, Sudhir Kumar, Louise Huuki, Tiffany Buturla, Tracy Vu and Karen Gomez</p> <p>PT16: "fastp: an ultra-fast all-in-one FASTQ preprocessor" <u>Shifu Chen</u>, Yanqing Zhou, Yaru Chen and Jia Gu</p>	<p>ET04: "Help yourself, and your community. Software reproducibility with BioContainers" <u>Olivier Sallou</u>, Bjørn Gruening and Yasset Perez</p> <p>ET05: "Galaxy integration with DIANA-tools" Dimitris Papadimitriou, Maria Paraskevopoulou, <u>Dimitra Karagkouni</u> and Artemis Hatzigeorgiou</p> <p>ET06: "Automated workflow composition in mass spectrometry based proteomics" Magnus Palmblad, Anna-Lena Lamprecht, Jon Ison and <u>Veit Schwämmle</u></p>
Keynote speaker: Manolis Kellis - Associate Professor of Computer Science, MIT - From Genomics To Therapeutics: Uncovering And Manipulating The Genomic Circuitry of Human Disease - Main stage		
poster session 1, exhibition & drinks posters with odd numbers: 17:30 to 18:30 - posters with even numbers: 18:30 to 19:30		
Athens by night		
20:00 - ...		

TUESDAY, SEPT 11

7:00 - 8:00
08:00 - 18:00
08:45 - 09:00
09:00 - 9:50

ECCB 2018 morning run		
Registration open (all day)		
Welcome and announcements		
Keynote speaker: Eleftheria Zeggini - Institute of Translational Genomics Helmholtz Zentrum München German Research Center for Environmental Health (GmbH) - The genomic aetiology of osteoarthritis - Main stage		
theme: Genomes	theme: Systems	track: Applications
Main stage	Hall 5A	Alternative Stage
<p>10:00 - 11:00</p> <p>PT17: "Fast Characterization of Segmental Duplications in Genome Assemblies" <u>Ibrahim Numanaqidi</u>, Alim Ş. Gökkaya, Lillian Zhang, Bonnie Berger, Can Alkan and Faraz Hach</p>	<p>HT10: "Ribothrypsin, a novel process of canonical mRNA decay, mediates ribosome-phased mRNA endonucleolysis" Fadia Ibrahim, <u>Manolis Maragkakis</u>, Panagiotis Alexiou and Zissimos Mourelatos</p>	<p>AT07: "Expression Atlas: Analysis and display of expression data across multiple species" <u>Irene Papaioannidou</u>, Nuno Fonseca, Laura Huerta, Alfonso Muñoz-Pomer Fuentes, Suhaib Mohammed, Anja Füllgrabe, Elisabet Barrera, Wojciech Bazant, Nancy George, Jonathan Manning, Robert Petryszak and Alvis Brazma</p>
<p>10:20 - 10:40</p> <p>PT18: "A Fast Adaptive Algorithm for Computing Whole-Genome Homology Maps" <u>Chirag Jain</u>, Sergey Koren, Alexander Dilthey, Adam Phillippy and Srinivas Aluru</p>	<p>PT19: "TIP: Inferring the Topology of Omics Data" Nanne Aben, Johan Westerhuis, Yipeng Song, Henk Kiers, Magali Michaut, Age Smilde and Lodewyk Wessels</p>	<p>AT08: "AQUA-DUCT: a solvent and ligands tracking tool" <u>Tomasz Magdziarz</u>, Karolina Mitusińska, Maria Bzówka, Agata Raczynska and Artur Góra</p>
<p>10:40 - 11:00</p> <p>HT09: "MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets" Martin Steinegger and <u>Johannes Soedling</u></p>	<p>PT20: "A Boolean Network Inference from Time-Series Gene Expression Data Using a Genetic Algorithm" <u>Shohag Barman</u> and Yung-Keun Kwon</p>	<p>AT09: "NAVIGATOR: Scalable Network Visualization and Analysis in Translational Research" <u>Anne-Christin Hauschild</u>, Chiara Pastrello, Renatas Minkstimas and Igor Jurisica</p>
theme: Proteins	theme: Data	track: ELIXIR
Main stage	Hall 5A	Alternative Stage
<p>11:30 - 11:50</p> <p>PT21: "Insights on the alteration of functionality of a Tyrosine kinase 2 variant. A Molecular Dynamics Study." Nastazia Lesgidou, Elias Eliopoulos, George Goulelmos and <u>Metaxia Vlassi</u></p>	<p>HT12: "Repurposing High-Throughput Image Assays Enables Biological Activity Prediction for Drug Discovery" Jaak Simm, Gunter Klambauer, <u>Adam Arany</u>, Marvin Steijaert, Jörg Kurt Wegner, Emmanuel Gustin, Vladimir Chupakhin, Yolanda T. Chong, Jorge Vialard, Peter Buijnsters, Ingrid Velter, Alexander Vapirev, Shantanu Singh, Anne E. Carpenter, Roel Wuyts, Sepp Hochreiter, Yves Moreau and Hupso Ceulemans</p>	<p>ET07: "cpPredictor: Webservice for template-based prediction of RNA secondary structure" <u>Jan Jelínek</u> and Josef Panek</p>
<p>11:50 - 12:10</p> <p>PT22: "Protein Pocket Detection via Convex Hull Surface Evolution and Associated Reeb Graph" <u>Rundong Zhao</u>, Zixuan Cang, Yiyang Tong and Guo-Wei Wei</p>	<p>PT23: "piMGM: Incorporating Multi-Source Priors in Mixed Graphical Models for Learning Disease Networks" Dimitris Manatakis, <u>Vineet Raghun</u> and Panayiotis Benos</p>	<p>ET08: "nextProt, a FAIR human protein resource working with the scientific community: Two use cases" <u>Monique Zahn</u>, Pascale Gaudet, Valérie Hinard, Aurore Britan, Anne Gleizes, Valentine Rech de Laval, Mathieu Schaeffer, Daniel Teixeira, Frederic Niklitsin, Alain Gateau, Paula Duek Roggli, Pierre-André Michel, Amos Baroach and Lydie Lane</p>
<p>12:10 - 12:30</p> <p>HT11: "Unraveling the Motions behind Enterovirus 71 Uncoating" <u>Ali Rana Atilgan</u>, Caroline Ross, Ozlem Bishop and Canan Atilgan</p>	<p>PT24: "Conditional Generative Adversarial Network for Gene Expression Inference" Xiaoqian Wang, Kamran Ghasedi and <u>Heng Huang</u></p>	<p>ET09: "3DBIONOTES crossing genomics, proteomics and interactomics" <u>Joan Segura</u>, Ruben Sanchez-Garcia, Carlos Oscar Sánchez Sorzano and Jose Maria Carazo</p>
<p>12:30 - 13:00</p> <p>Invited speaker: Farzana Rahman - ISCB Student Council- The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide.</p>	<p>lunch break, exhibition & poster viewing</p>	<p>Sponsored talk: Rossen Apostolov - KTH Royal Institute of Technology - BioExcel CoE - Driving and Supporting Computational Biomolecular Research in Europe</p>
<p>13:00 - 14:00</p>		
theme: Genes	theme: Systems	track: Applications
Main stage	Hall 5A	Alternative Stage
<p>14:00 - 14:20</p> <p>PT25: "Off-target predictions in CRISPR-Cas9 gene editing using deep learning" <u>Jiecong Lin</u> and Ka-Chun Wong</p>	<p>HT14: "Cell type-specific signalling network maps help to reveal signatures of cell heterogeneity and polarization in tumor microenvironment" Maria Kondratova, Ana Costa, Yann Kieffer, Urszula Czerwinska, Fatima Mechta-Grigoriou, Andrei Zinoviyev, Emmanuel Barillot and <u>Inna Kuperstein</u></p>	<p>AT10: "Seven Bridges - Actionable Informatics for Biomedical Research" <u>Vaibhav Bhardwaj</u>, Ricarda Gaentzsch and Jack Digiovanna</p>
<p>14:20 - 14:40</p> <p>PT26: "Bayesian inference on stochastic gene transcription from flow cytometry data" <u>Simone Tiberi</u>, Mark Walsh, Massimo Cavallaro, Daniel Hebenstreit and Bärbel Finkenstädt</p>	<p>PT27: "Single cell network analysis with a mixture of Nested Effects Models" <u>Martin Pirkl</u> and Niko Beerewinkel</p>	<p>AT11: "Streamlined, unsupervised biomarker signature derivation with the e-NIOS BioInfoMiner 2.0 integrative -omics data analysis and interpretation platform" <u>Eleftherios Pilialis</u>, Theodoros Koutsandreas and Aristotelis Chatziloannou</p>
<p>14:40 - 15:00</p> <p>HT13: "SQANTI: extensive characterization of long-read transcript sequences for quality control in full-length transcriptome identification and quantification" <u>Ana Conesa</u>, Lorena de La Fuente Lorente, Manuel Tardaguila, Hector Del Risco, Cécile Pereira, Cristina Marti, Marissa Macchietto, Maravillas Mellado, Victoria Moreno, Ali Mortazavi, Susana Rodriguez, Francisco José Pardo-Palacios, Marc Ferrer, Kenneth Verheggen, Iakes Ezkurdia, Jesus Vazquez, Michael Tress, Lennart Martens and Mariola Edelman</p>	<p>PT28: "Branch-recombinant Gaussian processes for analysis of perturbations in biological time series" <u>Christopher Penfold</u>, Anastasiya Sybirna, John Reid, Yun Huang, Lorenz Wernisch, Zoubin Ghahramani, Murray Grant and Azim Surani</p>	<p>AT12: "Functional Annotation of Genes Through Integration of Disparate Data Sources with Deep Learning" <u>Umut Eser</u>, Zhizhou Zhang, Michael Meyer and Jonathan Rothberg</p>
theme: Genomes	theme: Data	track: ELIXIR
Main stage	Hall 5A	Alternative Stage
<p>15:00 - 15:30</p> <p>PT29: "Recognition of CRISPR/Cas9 off-target sites through ensemble learning of uneven mismatch distributions" <u>Hui Peng</u>, Yi Zheng, Zhixun Zhao, Tao Liu and Jinyan Li</p>	<p>HT16: "CellCycleTRACER accounts for cell cycle and volume in mass cytometry data" <u>Maria Anna Rapsomaniki</u>, Xiaokang Lun, Stefan Woerner, Marco Laumanns, Bernd Bodenmiller and Maria Rodriguez Martinez</p>	<p>ET10: "GA4GH Compatible Analysis Platform & Reference Dataset Distribution Services" Ania Niewielska, Jinny Chien, Erik van den Bergh, Pau Ruiz Safont, Gianni Dalla Torre, Olli Tourunen, Risto Laurikainen, Juha Törnroos, Shubham Kapoor, <u>Sushheel Varma</u>, Tommi Nyronen and Steven Newhouse</p>
<p>15:30 - 16:30</p> <p>PT30: "CNEFinder: Finding Conserved Non-Coding Elements in Genomes" <u>Lorraine Avad</u>, Solon Pissis and Dimitris Polychronopoulos</p>	<p>PT31: "DeepDiff: Deep-learning for predicting Differential gene expression from histone modifications" <u>Arshdeep Sekhon</u>, Ritambhara Singh and Yanjun Qi</p>	<p>ET11: "Training as a service - empowering scientists to provide high quality training" <u>Patricia M. Palagi</u>, Gabriella Rustici and Celia van Gelder</p>
<p>16:10 - 16:30</p> <p>HT15: "ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues" <u>Sergei Manjula</u></p>	<p>PT32: "Liquid-Chromatography Retention Order Prediction for Metabolite Identification" <u>Eric Bach</u>, Céline Brouard, Juho Rousu, Sandor Szedmak and Sebastian Böcker</p>	<p>ET12: "The role of public bioinformatics infrastructures in supporting innovation in the life sciences" <u>Katharina Lauer</u> and Andrew Smith</p>
<p>16:40 - 17:30</p> <p>Keynote speaker: Christos Davatzikos - Wallace T. Miller Sr. Professor of Radiology at the University of Pennsylvania School of Medicine - Machine learning in Neuroimaging and links to Genomics: Application to clinical Neuroscience - Main stage</p>		
<p>17:30 - 19:30</p> <p>poster session 2, exhibition & drinks <i>posters with odd numbers: 17:30 to 18:30 - posters with even numbers: 18:30 to 19:30</i></p>		
<p>20:00 - 23:30</p> <p>Conference dinner</p>		

WEDNESDAY, SEPT 12

7:00 - 8:00
07:30 - 18:00
08:45 - 09:00
09:00 - 9:50

ECCB 2018 morning run		
Registration open (all day)		
Welcome and announcements		
Keynote speaker: Jose Onuchic - Harry C & Olga K Wiess Professor of Physics, Rice University- Exploring the Energy Landscape for Protein Folding and Function: The Convergences of Structural Models and Sequence Coevolution Information - Main stage		
theme: Genomes	theme: Data	theme: Proteins
Main stage	Hall 5A	Alternative Stage
<p>10:00 - 11:00</p> <p>PT33: "Towards an Accurate and Efficient Heuristic for Species/Gene Tree Co-estimation" <u>Yaxuan Wang</u> and Luay Nakhlleh</p>	<p>HT18: "Quantitative Comparison of Abundance Structures of Generalized Communities: From B-Cell Receptor Repertoires to Microbiomes" <u>Mohammadkarim Saeedghalati</u>, Farnoush Farahpour, Bettina Budeus, Anja Lange, Astrid M. Westendorf, Marc Seifert, Ralf Küppers and Daniel Hoffmann</p>	<p>PT37: "Topology independent structural matching discovers novel templates for protein interfaces" <u>Claudio Mirabella</u> and Björn Wallner</p>

10:20 - 10:40	<p>PT34: "S-Cluster++: A Fast Program for Solving the Cluster Containment Problem for Phylogenetic Networks"</p> <p>Hongwei Yan, Andreas Dwi Maryanto Gunawan and Louxin Zhang</p>	<p>PT35: "Semantic Disease Gene Embeddings (SmdGE): phenotype-based disease gene prioritization without phenotypes"</p> <p>Mona Alshahrani and Robert Hoehndorf</p>	<p>HT19: "DARC: Mapping Surface Topography by Ray-Casting for Effective Virtual Screening at Protein Interaction Sites"</p> <p>Ragul Gowthaman and John Karanickolas</p>
10:40 - 11:00	<p>HT17: "Complex evolutionary footprints revealed in an analysis of reused protein segments of diverse lengths"</p> <p>Sergey Nepomnyachiy, Nir Ben-Tal and Rachel Kolodny</p>	<p>PT36: "MDPbiome: microbiome engineering through prescriptive perturbations"</p> <p>Beatriz García-Jiménez, Tomas de la Rosa and Mark Wilkinson</p>	<p>PT38: "Analysis of single amino acid variations in singlet hot spots of protein-protein interfaces"</p> <p>Ozlem Keskin, Emine Sila Ozdemir and Attila Gursoy</p>
11:00 - 11:30	coffe break & exhibition		
11:30 - 12:30	theme: Genomes Main stage	theme: Systems Hall 5A	theme: Proteins Alternative Stage
11:30 - 11:50	<p>PT39: "Approximate, simultaneous comparison of microbial genome architectures via syntentic anchoring of quiver representations"</p> <p>Alex Salazar and Thomas Abeel</p>	<p>HT21: "Alignment of dynamic networks"</p> <p>Vipin Vijayan, Dominic Critchlow and Tijana Milenkovic</p>	<p>PT43: "Learning structural motif representations for efficient protein structure search"</p> <p>Yang Liu, Qing Ye, Liwei Wang and Jian Peng</p>
11:50 - 12:10	<p>PT40: "PAIPlane: Pathogen identification in metagenomic and clinical next generation sequencing samples"</p> <p>Andreas Andrusch, Piotr W Dabrowski, Jeanette Klenner, Simon H Tausch, Claudia Kohl, Abdalla A Osman, Bernhard Y Renard and Andreas Nitsche</p>	<p>PT41: "Higher order molecular organisation as a source of biological function"</p> <p>Thomas Gaudelot, Noel Malod-Dognin and Natasza Przulj</p>	<p>HT22: "Unraveling the determinants of chaperonin GroEL dependence"</p> <p>Tridib Mondal and Amnon Horovitz</p>
12:10 - 12:30	<p>HT20: "Generalist species drive microbial dispersion and evolution."</p> <p>Sira Sriswasdi, Ching-Chia Yang and Wataru Iwasaki</p>	<p>PT42: "Hierarchical HotNet: identifying hierarchies of altered subnetworks"</p> <p>Matthew Revyns, Mark Leiserson and Benjamin Raphael</p>	<p>PT44: "iCFN: an efficient exact algorithm for multistate protein design"</p> <p>Mostafa Karimi and Yang Shen</p>
12:30 - 13:15	<p>Invited speaker: John Seiradakis - Department of Physics, Section Astrophysics, Aristotle University of Thessaloniki - The Antikythera Mechanism: Decoding an astonishing 2000 years old astronomical computer</p> <p style="text-align: right;">lunch break, exhibition & poster viewing</p>		
13:15 - 14:00	coffe break & exhibition		
14:00 - 15:00	theme: Genes Main stage	theme: Systems Hall 5A	track: Applications Alternative Stage
14:00 - 14:20	<p>PT45: "Prioritising Candidate Genes Causing QTL using Hierarchical Orthologous Groups"</p> <p>Alex Warwick Vesztrocy, Christophe Dessimoz and Henning Redestig</p>	<p>HT24: "Personalized adaptation to stress and physiological trade-offs in the circadian regulation of the HPA axis: A systems biology approach."</p> <p>Rohit Rao and Ioannis Androulakis</p>	<p>AT13: "A privacy-preserving analysis of environmental and clinical samples with Nephel"</p> <p>Rachid Ounit, Niamh O'Hara, Stefano Lonardi and Christopher Mason</p>
14:20 - 14:40	<p>PT46: "Quantitative Trait Loci Identification for Brain Endophenotypes via New Additive Model with Random Networks"</p> <p>Xiaoqian Wang, Hong Chen, Jingwen Yan, Kwangsik Nho, Shannon Risacher, Andrew Saykin, Li Shen and Heng Huang</p>	<p>PT47: "Understanding the evolution of functional redundancy in metabolic networks"</p> <p>Gayathri Sambamoorthy and Karthik Raman</p>	<p>AT14: "Implementation of communication technologies in tandem with bioinformatics for the assessment of food quality and safety"</p> <p>George Nychas, Emma Sims, Stathis Panagou and Fady Mohareb</p>
14:40 - 15:00	<p>HT23: "Prediction and interpretation of deleterious coding variants in terms of protein structural stability."</p> <p>François Ancien, Fabrizio Pucci, Maxime Godfroid and Marianne Rooman</p>	<p>PT48: "Comparative Network Reconstruction using Mixed Integer Programming"</p> <p>Evert Bosdriesz, Anirudh Prahallad, Bertram Klinger, Anja Sieber, Astrid Bosma, Rene Bernards, Nils Blüthgen and Lodewyk Wessels</p>	<p>AT15: "Carnelian: alignment-free functional binning and abundance estimation of metagenomic reads"</p> <p>Sumaiya Nazeen and Bonnie Berger</p>
15:00 - 15:30	coffe break & exhibition		
15:30 - 16:40	Presentation of ISMB/ECCB 2019		
15:40 - 16:30	<p>Keynote speaker: Bonnie Berger - Simons Professor of Mathematics at MIT - Biomedical data sharing with privacy - Main stage</p>		
16:30 - 16:50	Awards & closing remarks		
18:30 - 22:00	Farewell cocktail party @ Sounion		