ECCB 2016

SUNDAY, SEPT 4

08:15 - 19:30	registration desk open all day
	opening conference
17:45 - 19:00	**keynote speaker: Hans Clevers, Princess Maxima Center for Pediatric Oncology & Hubrecht Institute, Netherlands** Lgr5 stem cell based organoids and their applications
19:30 - 21:00	welcome reception combined with visit to Gemeentemuseum The Hague

MONDAY, SEPT 5

07:00 - 08:00	ECCB 2016 morning run
07:30 - 18:00	registration desk open all day
08:45 - 09:00	**welcome & announcements**
09:00 - 09:50	**keynote speaker: Amos Tanay, Weizmann Institute of Science, Israel** Studying epigenetic memory at single cell resolution

	Theater (plenary hall)	Mississippi	Amazon
10:00 - 11:00	**theme: Genomes**	**theme: Systems**	**track: Applications**
10:00 - 10:20	Highlight talk 01 - Coding Exon-Structure Aware Realigner (CESAR) utilizes genome alignments for accurate comparative gene annotation Authors: Virag Sharma, Anas Elghafari and Michael Hiller	Proceeding talk 03 - Genome wide predictions of miRNA regulation by transcription factors Authors: Matthew Ruffalo and Ziv Bar-Joseph	Application talk 01 - The ISB Cancer Genomics Cloud Authors: Theo Knijnenburg, Ilya Shmulevich, Sheila Reynolds, Phyliss Lee, Michael Miller, Kelly Iverson, Abigail Hahn, Zack Rodebaugh, Kalle Leinonen, Dave Gibbs, Varsha Dhankani, Jonathan Bingham, Nicole Deflaux, Matt Bookman and David Pot
10:20 - 10:40	Proceeding talk 01 - Information-Optimal Genome Assembly via Sparse Read-Overlap Graphs Authors: Ilan Shomorony, Samuel Kim, Thomas Courtade and David Tse	Highlight talk 02 - Cross-tissue regulatory gene networks in coronary artery disease Authors: Tom Michoel, Husain Talukdar, Hassan Foroughi Asl, Rajeev Jain, Raili Ermel, Arno Ruusalepp, Oscar Franzen, Brian Kidd, Ben Redhead, Chiara Giannarelli, Torbjorn Ivert, Joel Dudley, Mete Civelek, Aldons Lusis, Eric Schadt, Josefin Skogsberg and Johan Bjorkegren	Application talk 02 - A drug-centric view of drug development: How drugs spread from disease to disease Author: Raul Rodriguez-Esteban
10:40 - 11:00	Proceeding talk 02 - CoLoRMap: Correcting Long Reads by Mapping short reads Authors: Ehsan Haghshenas, Faraz Hach, S. Cenk Sahinalp and Cedric Chauve	Proceeding talk 04 - Logical model specification aided by model-checking techniques: application to the mammalian cell cycle regulation Authors: Pauline Traynard, Adrien Fauré, François Fage and Denis Thieffry	Application talk 03 - Interactive visualisation of large macromolecular structures like ribosomes and viruses in real-time? Authors: David Sehnal, Radka Svobodová Vařeková, Karel Berka, Sameer Velankar, Mandar Deshpande, Lukáš Pravda and Jaroslav Koča

11:00 - 11:30	coffee & exhibition

	Theater (plenary hall)	Mississippi	Amazon
11:30 - 12:30	**theme: Data**	**theme: Genes**	**track: ELIXIR - Human genomics and translational data**
11:30 - 11:50	Proceeding talk 05 - Estimating real cell size distribution from cross section microscopy imaging Authors: Michael Lenz, Nadia J. T. Roumans, Roel G. Vink, Marleen Van Baak, Edwin Mariman, Ilja C.W. Art, Theo M. de Kok and Gokhan Ertaylan	Highlight talk 04 - A landscape of pharmacogenomic interactions in cancer Authors: Francesco Iorio, Theo Knijnenburg, Daniel Vis, Graham Bignell, Michael Menden, Nanne Aben, Lodewyk Wessels, Julio Saez-Rodriguez, Ultan McDermott and Mathew Garnett	ELIXIR talk 01 - Services for the use of human data in cross-border research collaborations Authors: Antti Pursula, Maria Francesca Iozzi, Niclas Jareborg and Ali Syed
11:50 - 12:10	Highlight talk 03 - Entropy-Scaling Search of Massive Biological Data Authors: Y. William Yu, Noah Daniels, David Christian Danko and Bonnie Berger	Proceeding talk 07 - Gene-Set Association Tests for Next-Generation Sequencing Data Authors: Jaehoon Lee, Young Jin Kim, Juyoung Lee, Bong-Jo Kim, Seungyeoun Lee and Taesung Park	ELIXIR talk 02 - Integrating Oncotrack and TraIT workflows with EGA to store and reference Human Data Authors: J. Dylan Spalding, David Henderson, Reha Yildirimman, Sanne Abeln, Susanna Repo, Niklas Blomberg, Alexander Senf, Jeff Almeida-King, Jordi Rambla, Audald Lloret I Villas, Chao Zhang, Jochem Bijlard, Youri Hoogstrate, Remond Fijneman, Andrew P. Stubbs, Jan-Willem Boiten, Gerrit Meijer and Helen Parkinson
12:10 - 12:30	Proceeding talk 06 - The Network Library: A Framework to Rapidly Integrate Network Biology Resources Authors: Georg Summer, Thomas Kelder, Marijana Radonjic, Marc van Bilsen, Suzan Wopereis and Stephane Heymans	Proceeding talk 08 - XGSA: A statistical method for cross-species gene set analysis Authors: Djordje Djordjevic, Kenro Kusumi and Joshua Ho	ELIXIR talk 03 - NGS-Logistics: federated analysis of NGS sequence variants across multiple locations Authors: Amin Ardeshirdavani, Erika Souche, Luc Dehaspe, Jeroen Van Houdt, Joris Vermeesch and Yves Moreau

12:30 - 14:00	lunch, exhibition & poster viewing

	Theater (plenary hall)	Mississippi	Amazon
14:00 - 15:00	**theme: Genomes**	**theme: Proteins**	**track: Application**
14:00 - 14:20	Proceeding talk 09 - Improve homology search sensitivity of PacBio data by correcting frameshifts Authors: Nan Du and Yanni Sun	Highlight talk 06: Large-Scale Analysis Exploring Evolution of Catalytic Machineries and Mechanisms in Enzyme Superfamilies Authors: Nicholas Furnham, Natalie Dawson, Syed Rahman, Janet M. Thornton and Christine Orengo	Application talk 04 - Scalable, Accelerated and Secure NGS Analysis Platform for the Clinical Environment Authors: Zaid Al-Ars, Vlad-Mihai Sima and Kurt Florus
14:20 - 14:40	Proceeding talk 10 - PanTools: representation, storage, and exploration of pan-genomic data Authors: Siavash Sheikhizadeh Anari, Eric Schranz, Mehmet Akdel, Dick de Ridder and Sandra Smit	Proceeding talk 11 - Patterns of amino acid conservation in human and animal immunodeficiency viruses Authors: Olga Voitenko, Andi Dhroso, Anna Feldmann, Dmitry Korkin and Olga Kalinina	Application talk 05 - TopAnat: GO-like enrichment of anatomical terms mapped to genes by expression patterns Authors: Frederic B. Bastian, Julien Roux, Mathieu Seppey, Komal Sanjeev, Valentine Rech de Laval, Philippe Moret, Panu Artimo, Séverine Duvaud, Vassilios Ioannidis, Heinz Stockinger and Marc Robinson-Rechavi
14:40 - 15:00	Highlight talk 05 - Pangenome-based computational metagenomic profiling enables strain-level culture-free epidemiology and population genomics studies Authors: Matthias Scholz, Doyle V. Ward, Edoardo Pasolli, Thomas Tolio, Moreno Zolfo, Francesco Asnicar, Duy Tin Truong, Adrian Tett, Ardythe L. Morrow and Nicola Segata	Proceeding talk 12 - A probabilistic model for detecting rigid domains in protein structures Authors: Thach Nguyen and Michael Habeck	Sponsored talk 01 - The Hyve - Open source communities for analyzing healthcare data: OHDSI, tranSMART and cBioPortal

Time	Theater (plenary hall)	Mississippi	Amazon
15:00 - 15:30	coffee, exhibition & poster viewing		
15:30 - 16:30	theme: Genes	theme: Systems	track: ELIXIR - Data resources
15:30 - 15:50	Highlight talk 07 - MicroRNA–mRNA interactions underlying colorectal cancer molecular subtypes Authors: Laura Cantini, Claudio Isella, Consalvo Petti, Gabriele Picco, Simone Chiola, Elisa Ficarra, Michele Caselle and Enzo Medico	Proceeding talk 15 - Edge-based sensitivity analysis of signaling networks by using Boolean dynamics Authors: Hung-Cuong Trinh and Yung-Keun Kwon	ELIXIR talk 04 - Marine metagenomics infrastructure as driver for research and industrial innovation Authors: Nils Peder Willassen, Robert D. Finn, Guy Cochrane, Lars Ailo Bongo and Petra Ten Hoopen
15:50 - 16:10	Proceeding talk 13 - Pathway-based approach using hierarchical components of collapsed rare variants Authors: Sungyoung Lee, Sungkyoung Choi, Young Jin Kim, Bong-Jo Kim, Tiidgenes Consortium, Heungsun Hwang and Taesung Park	Proceeding talk 16 - On cross-conditional and fluctuation correlations in competitive RNA networks Authors: Daniel Sanchez-Taltavull, Matthew MacLeod and Theodore Perkins	ELIXIR talk 05 - Reference Proteomes,Pan Proteomes and Redundant Proteomes: concepts that define protein space in UniProtKB Authors: Benoit Bely, Ramona Britto, Borisas Bursteinas, Alan Wilter Sousa Da Silva, Andrea Auchincloss, Chuming Chen, Maria Martin and Uniprot Consortium
16:10 - 16:30	Proceeding talk 14 - A unified model-based multifactor dimensionality reduction framework for detecting gene-gene interactions Authors: Wenbao Yu, Seungyeoun Lee and Taesung Park	Highlight talk 08 - Inferring causal molecular networks: empirical assessment through a community-based effort Authors: Steven M. Hill, Laura M. Heiser, Thomas Cokelaer, Michael Unger, Nicole K. Nesser, Daniel E. Carlin, Yang Zhang, Artem Sokolov, Evan O. Paull, Chris K. Wong, Kiley Graim, Adrian Bivol, Haizhou Wang, Fan Zhu, Bahman Afsari, Ludmila V. Danilova, Alexander V. Favorov, Wai Shing Lee, Dane Taylor, Chenyue W. Hu, Byron L. Long, David P. Noren, Alexander J. Bisberg, Gordon B. Mills, Joe W. Gray, Michael Kellen, Thea Norman, Stephen Friend, Amina A. Qutub, Elana J. Fertig, Yuanfang Guan, Mingzhou Song, Joshua M. Stuart, Paul T. Spellman, Heinz Koeppl, Gustavo Stolovitzky, Julio Saez-Rodriguez and Sach Mukherjee	ELIXIR talk 06 - Identifying ELIXIR Core Data Resources Authors: Christine Durinx, Jo McEntyre, Ron Appel, Rolf Apweiler, Mary Barlow, Niklas Blomberg, Chuck Cook, Elisabeth Gasteiger, Vassilios Ioannidis, Jee-Hyub Kim, Rodrigo Lopez, Nicole Redaschi, Heinz Stockinger, Daniel Teixeira and Alfonso Valencia
16:40 - 17:30	keynote speaker: John Marioni, EMBL-EBI, UK Using single-cell transcriptomics to understand cellular heterogeneity		
17:30 - 19:30	poster session 1, exhibition & drinks posters with odd numbers: 17h30 to 18h30 - posters with even numbers: 18h30 to 19h30		
20:00 - ….	The Hague @ Night		

ECCB 2016

TUESDAY, SEPT 6

Time	Theater (plenary hall)	Mississippi	Amazon
08:00 - 18:00	registration desk open all day		
08:45 - 09:00	welcome & announcements		
09:00 - 09:50	keynote speaker: Nuria Lopez-Bigas, Universitat Pompeu Fabra, Spain Tumour genomes shed light into mutational processes and cancer vulnerabilities		
10:00 - 11:00	theme: Data	theme: Systems	track: Applications
10:00 - 10:20	Proceeding talk 17 - Causality Modeling for Directed Disease Network Authors: Sunjoo Bang, Hyunjung Shin and Jae-Hoon Kim	Highlight talk 10 - Network-based approaches for drug response prediction and drug combinations in cancer Authors: Inna Kuperstein, Eric Bonnet, Maria Kondratova, Mathurin Dorel, Wael Jdey, David Cohen, Eric Viara, Luca Grieco, Hien-Anh Nguyen, Laurence Calzone, Christophe Russo, Marie Dutreix, Emmanuel Barillot and Andrei Zinovyev	Application talk 06 - Predictive analytics for therapeutic target discovery backed by more than 100 public databases Authors: Aram Krol, Arie Baak, Onno Becker Hof and Kristina Hettne
10:20 - 10:40	Highlight talk 09 - Searching molecular structure databases with tandem mass spectra using CSI:FingerID, Kai Dührkop, Huibin Shen, Marvin Meusel, Céline Brouard, Sebastian Böcker and Juho Rousu	Proceeding talk 19 - A Weighted Exact Test for Mutually Exclusive Mutations in Cancer Authors: Mark Leiserson, Matthew Reyna and Benjamin Raphael	Application talk 07 - Visualization methods for spatial and temporal evolution analysis in cancer Authors: Maia Smith, Cydney Nielsen, Fong Chun Chan, Andrew Roth, Andrew McPherson, Daniel Machev and Sohrab Shah
10:40 - 11:00	Proceeding talk 18 - Complementary Feature Selection from Alternative Splicing Events and Gene Expression for Phenotype Prediction Authors: Charles Labuzzetta, Margaret Antonio, Patricia Watson, Robert Wilson, Lauren Laboissonniere, Jeffrey Trimarchi, Baris Genc, P. Hande Ozdinler, Dennis Watson and Paul Anderson	Proceeding talk 20 - Bayesian parameter estimation for the Wnt pathway: An infinite mixture models approach Authors: Konstantinos Koutroumpas, Paolo Ballarini, Irene Votsi and Paul-Henry Cournède	Sponsored talk 02 - Keygene - CropPedia – the integrated database and software platform for lead discovery and accelerated breeding Authors: Jan van Oeveren, Rudi L. van Bavel, Lian W. Wiggers-Perebolte, Rob E. Spee, Maarten Hekkelman, Roeland C.H.J. van Ham
11:00 - 11:30	coffee, exhibition & poster viewing		
	Theater (plenary hall)	Mississippi	Amazon
11:30 - 12:30	theme: Genomes	theme: Data	track: ELIXIR – Tools for data analysis
11:30 - 11:50	Proceeding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histone modifications Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi	Proceeding talk 23 - Combining Dependent P-values with an Empirical Adaptation of Brown's Method Authors: William Poole, David Gibbs, Ilya Shmulevich, Brady Bernard and Theo Knijnenburg	ELIXIR talk 07 - The Genomic HyperBrowser Authors: Boris Simovski, Finn Drabløs, Sveinung Gundersen, Morten Johansen, Diana Domanska, Abdulrahman Azab, Geir Kjetil Sandve and Eivind Hovig
11:50 - 12:10	Proceeding talk 22 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Äijö, Harri Lähdesmäki, Anjana Rao and Xiaojing Yue	Highlight talk 12 - Halvade: scalable sequence analysis with MapReduce Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostier	ELIXIR talk 08 - Chipster - comprehensive package of NGS data analysis tools and reference data, with an intuitive GUI Authors: Eija Korpelainen, Taavi Hupponen, Petri Klemelä, Maria Lehtivaara, Kimmo Mattila, Ari-Matti Saren and Aleksi Kallio
12:10 - 12:30	Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko	Proceeding talk 24 - Drug response prediction by inferring pathway-response associations with Kernelized Bayesian Matrix Factorization Authors: Muhammad Ammad-Ud-Din, Suleiman A.Khan, Disha Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski	ELIXIR talk 09 - An application suite based on the IFB Container as a Service platform Authors: François Moreews, Olivier Sallou and Olivier Collin
12:30 - 14:00	lunch, exhibition & poster viewing		
	Theater (plenary hall)	Mississippi	Amazon
14:00 - 15:00	theme: Genes	theme: Proteins	track: Applications

Time	Theater (plenary hall)	Mississippi	Amazon
14:00 - 14:20	Highlight talk 13 - A widespread role of the motif environment in transcription factor binding across diverse protein families Authors: Yael Mandel-Gutfreund, Iris Dror, Tamar Golan, Carmit Levy and Remo Rohs	Proceeding talk 27 - AUCpreD: proteome-level protein disorder prediction by AUC-maximized Deep Convolutional Neural Fields Authors: Sheng Wang, Jianzhu Ma and Jinbo Xu	Application talk 08 - MOLGENIS Diagnostic Platform for Clinical Genomics Authors: Joeri van der Velde, Bart Charbon, Dennis Hendriksen, Mark de Haan, Cisca Wijmenga, Tom de Koning, Rolf Sijmons, Richard Sinke and Morris Swertz
14:20 - 14:40	Proceeding talk 25 - Detecting Horizontal Gene Transfer by Mapping Sequencing Reads Across Species Boundaries Authors: Kathrin Trappe, Tobias Marschall and Bernhard Renard	Proceeding talk 28 - PRED-TMBB2: Improved topology prediction and detection of beta-barrel outer membrane proteins Authors: Konstantinos D. Tsirigos, Arne Elofsson and Pantelis G. Bagos	Sponsored talk 03 - DataComputing - Bringing it all together: universal secure (research) data storage, data sharing and open source data science software in the near future
14:40 - 15:00	Proceeding talk 26 - PeakXus: Comprehensive Transcription Factor Binding Site Discovery From ChIP-Nexus and ChIP-exo Experiments Authors: Tuomo Hartonen, Biswajyoti Sahu, Kashyap Dave, Teemu Kivioja and Jussi Taipale	Highlight talk 14 - Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs Authors: David Juan, Juliane Perner, Enrique Carrillo-De Santa Pau, Simone Marsili, David Ochoa, Ho-Ryun Chung, Martin Vingron, Daniel Rico and Alfonso Valencia	Application talk 9 - The THOR project: Integrating persistent identifiers such as ORCIDs in life sciences data resources Authors: Johanna McEntyre, Guilherme Formaggio de Mello, Florian Graf, Josh Brown, Tom Demeranville and Maaike Duine
15:00 - 15:30	coffee, exhibition & poster viewing		
	Theater (plenary hall)	Mississippi	Amazon
15:30 - 16:30	theme: Genomes	theme: Systems	track: ELIXIR - National collaborations, international standards
15:30 - 15:50	Proceeding talk 29 - Fast genotyping of known SNPs through approximate k-mer matching Authors: Ariya Shajii, Deniz Yorukoglu, Y. William Yu and Bonnie Berger	Highlight talk 16 - Revisiting drug discovery through integrative network pharmacology in the era of precision medicine Authors: Emre Guney, Jorg Menche, Marc Vidal and Albert-Laszlo Barabasi	ELIXIR talk 10 - Fostering excellence in data science to support progress in biological research and health at the SIB Swiss Institute of Bioinformatics, the Swiss Node of ELIXIR Authors: Ioannis Xenarios, Christine Durinx and Ron Appel
15:50 - 16:10	Highlight talk 15 - DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo Authors: Anthony Mathelier, Beibei Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman	Proceeding talk 31 -TANDEM: a Two-stage Approach to Maximize Interpretability of Drug Response Models Based on Multiple Molecular Data Types Authors: Nanne Aben, Daniel J. Vis, Magali Michaut and Lodewyk F. A. Wessels	ELIXIR talk 11 - The BioSharing Registry: mapping the landscape of standards and database resources in the life sciences Authors: Peter Mcquilton, Alejandra Gonzalez-Beltran, Massimiliano Izzo, Allyson Lister, Eamonn Maguire, Philippe Rocca-Serra, Milo Thurston and Susanna-Assunta Sansone
16:10 - 16:30	Proceeding talk 30 - Optimization of signal-to-noise ratio for efficient microarray probe design Authors: Svetlana Shabalina, Olga Matveeva, Yury Nechipurenko, Nafisa Nazipova, Aleksey Ogurtsov, Evgeniy Riabenko and Chikako Ragan	Proceeding talk 32 - SWORD - a highly efficient protein database search Authors: Robert Vaser, Dario Pavlović and Mile Šikić	ELIXIR talk 12 - Using FAIR data to solve cross-resource questions in Rare Disease research Authors: Mark Thompson, Rajaram Kaliyaperumal, Pedro Sernadela, Robert Reihs, Davide Piscia, Kees Burger, Andrew Gibson, Claudio Carta, Marco Crimi, Heimo Müller, Arnold Kuzniar, Anand Gavai, Richard Finkers, Sergi Beltran, J. L. Oliveira, Barend Mons, Marco Roos, Mark D. Wilkinson and Luiz Bonino
16:40 - 17:30	keynote speaker: Benedict Paten, University of California, Santa Cruz, US Population assisted genome inference		
17:30 - 19:30	poster session 2, exhibition & drinks posters with even numbers: 17h30 to 18h30 - posters with odd numbers: 18h30 to 19h30		
20:00 - 23:30	Conference dinner @ the beach		

ECCB 2016

WEDNESDAY, SEPT 7			
08:00 - 17:00	registration desk open all day		
08:45 - 09:00	welcome & announcements		
09:00 - 09:50	keynote speaker: Paulien Hogeweg, Utrecht University, Netherlands Long term information integration: evolution of evolution		
	Theater (plenary hall)	Mississippi	Amazon
10:00 - 11:00	theme: Genomes	theme: Systems	theme: Proteins
10:00 - 10:20	Proceeding talk 33 - A program for verification of phylogenetic network models Authors: Andreas Dwi Maryanto Gunawan, Bingxin Lu and Louxin Zhang	Highlight talk 18 - Sparse and Compositionally Robust Inference of Microbial Ecological Networks Authors: Richard Bonneau, Zach Kurtz, Christian Müller and Emily Miraldi	Proceeding talk 37 - PEPSI-Dock: A Detailed Data-Driven Protein-Protein Interaction Potential Accelerated By Polar Fourier Correlation Authors: Emilie Neveu, David Ritchie, Petr Popov and Sergei Grudinin
10:20 - 10:40	Highlight talk 17 - Automated filtering of multiple sequence alignments frequently worsen phylogenetic inference Authors: Ge Tan, Matthieu Muffato, Christian Ledergerber, Javier Herrero, Nick Goldman, Manuel Gil and Christophe Dessimoz	Proceeding talk 35 - L1 regularization facilitates detection of cell type-specific parameters in dynamical systems Authors: Bernhard Steiert, Jens Timmer and Clemens Kreutz	Proceeding talk 38 - Simulated linear test applied to quantitative proteomics Authors: T.V. Pham and C.R. Jimenez
10:40 - 11:00	Proceeding talk 34 - Extending partial haplotypes to full genome haplotypes using chromosome conformation capture data Authors: Shay Ben-Elazar, Benny Chor and Zohar Yakhini	Proceeding talk 36 - Large-scale inference of Conjunctive Bayesian Networks Authors: Hesam Montazeri, Jack Kuipers, Roger Kouyos, Jürg Böni, Sabine Yerly, Thomas Klimkait, Vincent Aubert, Huldrych Günthard and Niko Beerenwinkel	Highlight talk 19 - Data-driven Image Fusion between Mass Spectrometry and Microscopy: Linking Histology to Spatial Proteomics and Lipidomics Authors: Raf Van de Plas, Junhai Yang, Jeffrey Spraggins and Richard M. Caprioli
11:00 - 11:30	coffee, exhibition & poster viewing		
	Theater (plenary hall)	Mississippi	Amazon
11:30 - 12:30	theme: Data	theme: Systems	theme: Genes

Time	Theater (plenary hall)	Mississippi	Amazon
11:30 - 11:50	**Highlight talk 20** - Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota Authors: Kristoffer Forslund, Falk Hildebrand, Trine Nielsen, Gwen Falony, Emmanuelle Le Chatelier, Shinichi Sunagawa, Edi Prifti, Sara Vieira-Silva, Valborg Gudmundsdottir, Helle Krogh Pedersen, Manimozhiyan Arumugam, Karsten Kristiansen, Anita Yvonne Voigt, Henrik Vestergaard, Rajna Hercog, Paul Igor Costea, Jens Roat Kultima, Junhua Li, Torgen Jorgensen, Florence Levenez, Joel Dore, Henrik Bjorn Nielsen, Soren Brunak, Jeroen Raes, Torben Hansen, Wang Jun, Dusko Ehrlich, Peer Bork and Oluf Pedersen	**Proceeding talk 41** - ModuleAlign: Module-based global alignment of protein-protein interaction networks Authors: Somaye Hashemifar, Jianzhu Ma, Hammad Naveed, Stefan Canzar, Jinbo Xu and Sheng Wang	**Proceeding talk 43** - MetaProb: Accurate Metagenomic Reads Binning based on Probabilistic Sequence Signatures Authors: Samuele Girotto, Cinzia Pizzi and Matteo Comin
11:50 - 12:10	**Proceeding talk 39** - Mutual enrichment in aggregated ranked lists with applications to gene expression regulation Authors: Dalia Cohn-Alperovich, Alona Rabner, Ilona Kifer, Yael Mandel-Gutfreund and Zohar Yakhini	**Proceeding talk 42** - iReMet-Flux: Constraint-based approach for integrating relative metabolite levels into a stoichiometric metabolic models Authors: Max Sajitz-Hermstein, Nadine Töpfer, Sabrina Kleessen, Alisdair Fernie and Zoran Nikoloski, Kevin Schwahn	**Highlight talk 22** - Widespread disruption of host transcription termination in HSV-1 infection Authors: Caroline C. Friedel, Andrzej Rutkowski, Florian Erhard, Anne L'Hernault, Thomas Bonfert, Markus Schilhabel, Colin Crump, Philip Rosenstiel, Stacey Efstathiou, Ralf Zimmer and Lars Dölken
12:10 - 12:30	**Proceeding talk 40** - GTRAC: Fast retrieval from compressed collections of genomic variants Authors: Kedar Tatwawadi, Mikel Hernaez, Idoia Ochoa and Tsachy Weissman	**Highlight talk 21** - A map of directional genetic interactions in a metazoan cell Authors: Bernd Fischer, Thomas Sandmann, Thomas Horn, Maximilian Billmann, Varun Chaudhary, Wolfgang Huber and Michael Boutros	**Proceeding talk 44** - Snowball: Strain aware gene assembly of metagenomes Authors: Ivan Gregor, Alexander Schoenhuth and Alice C. McHardy
12:30 - 14:00	*lunch,* **exhibition & poster viewing**		
	Theater (plenary hall)	Mississippi	Amazon
14:00 - 15:00	**theme: Genomes**	**theme: Data**	**track: Applications**
14:00 - 14:20	**Proceeding talk 45** - Characterizing leader sequences of CRISPR loci Authors: Omer S. Alkhnbashi, Shiraz A. Shah, Roger A. Garrett, Sita J. Saunders, Fabrizio Costa and Rolf Backofen	**Proceeding talk 47** - Higher order methylation features for clustering and prediction in epigenomic studies Authors: Chantriolnt-Andreas Kapourani and Guido Sanguinetti	**Application talk 10** - Cross-industry collaboration via Open Source Development: Contributions to cBioPortal Authors: Pieter Lukasse, Sjoerd van Hagen, Sander de Ridder, Fedde Schaeffer, James Lindsay, Jianjiong Gao, Benjamin Gross, Zachary Heins, Priti Kumari, Adam Abeshouse, Hongxin Zhang, Robert Sheridan, Onur Sumer, Stuart Watt, Chris Sander, Nikolaus Schultz, Ethan Cerami and Yichao Sun
14:20 - 14:40	**Proceeding talk 46** - Assemble CRISPRs from metagenomic sequencing data Authors: Jikai Lei and Yanni Sun	**Highlight talk 24** - Exploring the variant combinations in the digenic diseases database DIDA Authors: Tom Lenaerts, Andrea Gazzo, Dorien Daneels, Elisa Cilia, Maryse Bonduelle, Marc Abramowicz, Sonia Van Dooren and Guillaume Smits	**Application talk 11** - Search! Authors: Young Mi Park, Andrew Cowley, Weizhong Li, Nicola Buso, Szymon Chojnacki, Tamer Gur, Silvano Squizzato and Rodrigo Lopez
14:40 - 15:00	**Highlight talk 23** - Investigating molecular determinants of Ebola virus pathogenicity Authors: Mark Wass, Miguel Juliá, Mark Howard, Jeremy Rossman, Martin Michaelis and Morena Pappalardo	**Proceeding talk 48** - Simultaneous discovery of cancer subtypes and subtype features by molecular data integration Authors: Thanh Le Van, Matthijs van Leeuwen, Ana Carolina Fierro, Dries De Maeyer, Jimmy Van den Eynden, Lieven Verbeke, Luc De Raedt, Kathleen Marchal and Siegfried Nijssen	**Application talk 12** - Structured Data for Life Science using Schema.org Authors: Martin Cook, Aleksandra Nenadic, Carole Goble, Rafael Jimenez, Teresa Attwood, Norman Morrison, Niall Beard, Celia van Gelder, Frederik Coppens, Brane Leskosek, Jon Ison, Peter McQuilton, Alejandra Gonzalez-Beltran, Susanna-Assunta Sansone, Christof De Bo, Alexander Botzki, John Darrell Van Horn, Jose-Luis Ambite, Kristina Lerman, Rochelle Tractenberg, Carlos Horro, Roberto Preste, Christa Janko, Claire Johnson, Pavel Dallakian, Robert Pergl
15:00 - 15:30	*coffee* **& exhibition**		
15:30 - 16:40	**presentation of ISMB/ECCB 2017**		
15:40 - 16:30	**keynote speaker: Christina Leslie, Memorial Sloan Kettering Cancer Center, New York, US** Decoding epigenetic programs in cellular differentiation		
16:30 - 16:50	**awards & closing remarks**		