

SUNDAY, SEPT 4			ECCB 2016
08:15 - 19:30		registration desk open all day	
17:45 - 19:00	keynote speaker: Hans	opening conference Clevers, Princess Maxima Center for Pediatric Oncology &	& Hubrecht Institute, Netherlands
		Lgr5 stem cell based organoids and their applications	<u> </u>
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		
10:00 - 11:00	Theater (plenary hall) theme: Genomes	Mississippi theme: Systems	Amazon 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: <u>Theo Kniinenburg</u> , 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		Application talk 02 - A drug-centric view of drug development: How drugs
	Sparse Read-Overlap Graphs Authors: <u>Ilan Shomorony</u> , Samuel Kim, Thomas Courtade and David Tse	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	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: <u>Pauline Traynard</u> , 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, <u>Radka Svobodová Vařeková</u> , 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	Highlight talk 04 - A landscape of pharmacogenomic interactions in cancer	ELIXIR talk 01 - Services for the use of human data in cross-border research collaborations
	Authors: <u>Michael Lenz</u> , Nadia J. T. Roumans, Roel G. Vink, Marleen Van Baak, Edwin Mariman, Ilja C.W. Art, Theo M. de Kok and Gokhan Ertaylan	Authors: Francesco Iorio, Theo Knijnenburg, Daniel Vis, Graham Bignell, Michael Menden, Nanne Aben, Lodewyk Wessels, Julio Saez-Rodriguez, Ultan McDermott and Mathew Garnett	Authors: <u>Antti Pursula</u> , Maria Francesca lozzi, Niclas Jareborg and Ali Syed
11:50 - 12:10	Highlight talk 03 - Entropy-Scaling Search of Massive Biological Data	Proceeding talk 07 - Gene-Set Association Tests for Next- Generation Sequencing Data	ELIXIR talk 02 - Integrating Oncotrack and TraIT workflows with EGA to store and reference Human Data
	Authors: <u>Y. William Yu</u> , Noah Daniels, David Christian Danko and Bonnie Berger	Authors: <u>Jaehoon Lee</u> , Young Jin Kim, Juyoung Lee, Bong-Jo Kim, Seungyeoun Lee and Taesung Park	Authors: <u>J. Dylan Spalding</u> , 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	Proceeding talk 08 - XGSA: A statistical method for cross-species gene set analysis	ELIXIR talk 03 - NGS-Logistics: federated analysis of NGS sequence variants across multiple locations
	Authors: <u>Georg Summer</u> , Thomas Kelder, Marijana Radonjic, Marc van Bilsen, Suzan Wopereis and Stephane Heymans	Authors: <u>Diordie Diordievic,</u> Kenro Kusumi and Joshua Ho	Authors: Amin Ardeshirdavani, Erika Souche, Luc Dehaspe, Jeroen Van Houdt, Joris Vermeesch and <u>Yves Moreau</u>
12:30 - 14:00		lunch, exhibition & poster viewing	
14:00 45:00	Theater (plenary hall)	Mississippi	Amazon
14:00 - 15:00 14:00 - 14:20	theme: Genomes Proceeding talk 09 - Improve homology search sensitivity of PacBio data by correcting frameshifts	theme: Proteins Highlight talk 06: Large-Scale Analysis Exploring Evolution of Catalytic Machineries and Mechanisms in Enzyme Superfamilies	track: Application Application talk 04 - Scalable, Accelerated and Secure NGS Analysis Platform for the Clinical Environment
	Authors: <u>Nan Du</u> and Yanni Sun	Authors: <u>Nicholas Furnham</u> , Natalie Dawson, Syed Rahman, Janet M. Thornton and Christine Orengo	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	Proceeding talk 11 - Patterns of amino acid conservation in human and animal immunodeficiency viruses	Application talk 05 - TopAnat: GO-like enrichment of anatomical terms mapped to genes by expression patterns
	Authors: <u>Siavash Sheikhizadeh Anari</u> , Eric Schranz, Mehmet Akdel, Dick de Ridder and Sandra Smit	Authors: <u>Olga Voitenko</u> , Andi Dhroso, Anna Feldmann, Dmitry Korkin and Olga Kalinina	Authors: <u>Frederic B. Bastian</u> , Julien Roux, Mathieu Seppey, Komal Sanjeev, Valentine Rech de Laval, Philippe Moret, Panu Artimo, Séverin 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	Proceeding talk 12 - A probabilistic model for detecting rigid domains in protein structures	Sponsored talk 01 - The Hyve - Open source communities for analyzing healthcare data: OHDSI, tranSMART and cBioPortal
	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	Authors: <u>Thach Nquyen</u> and Michael Habeck	

15:00 - 15:30		coffee, exhibition & poster viewing	
	Theater (plenary hall)	Mississippi	Amazon
15:30 - 16:30	theme: Genes	theme: Systems	track: ELIXIR - Data resources
		Proceeding talk 15 - Edge-based sensitivity analysis of signaling networks by using Boolean dynamics	ELIXIR talk 04 - Marine metagenomics infrastructure as driver for research and industrial innovation
	Authors: <u>Laura Cantini</u> , Claudio Isella, Consalvo Petti, Gabriele Picco, Simone Chiola, Elisa Ficarra, Michele Caselle and Enzo Medico	Authors: <u>Hung-Cuong Trinh</u> and Yung-Keun Kwon	Authors: Nils Peder Willassen, Robert D. Finn, Guy Cochrane, Lars Ailo Bongo and Petra Ten Hoopen
	Proceeding talk 13 - Pathway-based approach using hierarchical components of collapsed rare variants	Proceeding talk 16 - On cross-conditional and fluctuation correlations in competitive RNA networks	ELIXIR talk 05 - Reference Proteomes, Pan Proteomes and Redundant Proteomes: concepts that define protein space in UniProtKB
	Authors: Sunqvoung Lee, Sungkyoung Choi, Young Jin Kim, Bong-Jo Kim, Tiidgenes Consortium, Heungsun Hwang and Taesung Park	Authors: <u>Daniel Sanchez-Taltavull</u> , Matthew MacLeod and Theodore Perkins	Authors: <u>Benoit Bely</u> , Ramona Britto, Borisas Bursteinas, Alan Wilter Sousa Da Silva, Andrea Auchincloss, Chuming Chen, Maria Martin and Uniprot Consortium
	Authors: Wenbao Yu, Seungyeoun Lee and <u>Taesung Park</u>	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		geneity
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		

Perceeding talk 18 - Complementary Feature Selection from Alternotive States Laburzetta Margaret Antonic, Particle Water, Branch States Complementary Feature Selection from Alternotive States Laburzetta Margaret Antonic, Particle Water, Timester (Jenary National College) Proceeding talk 21 - DeepChromoc Deep-learning for predicting gene expression from histone modifications with complex experimental designs Authors: Ritambara Sinch, Jack Lanchantin, Gabrier Robins Authors: Water (Jenary National) Proceeding talk 22 - Lux CLM: A probabilistic covariate model Tipo - 12:30 Proceeding talk 22 - Lux CLM: A probabilistic covariate model Authors: Shan Li and Juck Lanchantin, Gabrier Robins Authors: Water (Jenary National) Proceeding talk 21 - DeepChromor Dedications with complex experimental designs Authors: Shan Li and Juck Lanchantin, Gabrier Robins Authors: Water (Jenary National) Proceeding talk 22 - Lux CLM: A probabilistic covariate model Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Shan Li and Juan Orycharerko Theater (plenary hall) Authors: Theater (plenary hall) Authors: The Complementary or producting plenary or produ				ECCB 2016
New York September Septe	TUESDAY, SEPT 6			
Theater (plenary hall) Mississipp Tamour genomes shed light to mulational processes and cancer vulnerabilities	08:00 - 18:00	registration desk open all day		
Trunour genomes the light into mutational processes and cancer vulnerabilities Theorie (planory half) Theorie (planory half)	08:45 - 09:00	welcome & announcements		
1000 - 10 20 Proceeding talk 17 - Causality Modeling for Directed Disease Network Authors: Sunico Barry, Hyunjung Shin and Jae-Hoon Kim Authors: Sunico Barry, Hyunjung Shin Authors: Sunico Barry, Hyunjung Shin Authors: Sunico Barry, Hyunjung Shin Jae-Hoon Kima Shin Jae-Hoon	09:00 - 09:50			
Proceeding lalk 17 - Causality Modeling for Directed Disease Protection and Application talk 68 - Predictive analysis for therapeutic larget discove predictions and drug combinations in cancer value of the protection of the prot		Theater (plenary hall)	Mississippi	Amazon
Network Authors: Sunico Bang, Hyunjung Shin and Jae-Hoon Kim Authors: Sunico Bang, Hyunjung Shin and Jae-Hoon Kim Authors: Ina Kuperatein, Eric Bonnet, Maria Kondiratova, Mathurin Dorel, Wass Joby, David Cottent, Eric Viana, Luca Ginco, Hein- Emmanuel Barillot and Andrei Zimoyov Multiplight talk 09 - Searching molecular structure delablases with tandem mass spectra using GSI-FingerID, Kal Duhrkop, Hulbin Shen, Marvin Meusel, Celline Brouard, Sebastian Bocker and Juho Rooss Proceeding talk 19 - A Vergiphed Exact Test for Mutually Exclusive Authors: Mark Leserson, Matthew Revng and Benjamin Raphael Authors: Charles Labuzzetta Margaret Annoino, Patricia Watson, Robert Wisson, Lauren Laboissominere, Jeffery Timanchi, Baris Genc, P. Hande Ozdnier, Dennis Watson and Proceeding talk 21 - DeepChronec Deep-learning for producing gene expression from histone modifications with copflex expression from histone modifications with copflex expression from histone modifications with complex experimental designs Authors: Ritambaras Sharth, Jack Lanchartini, Gatriel Robins Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Bernard and Thee Kulturengas. Pavio Bernard Alvanos. Proceeding talk 22 - Lux CLM: A probabilistic covariate model Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Authors: Brand Jack Jack Lanchartini, Gatriel Robins Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Authors: William Poole, David Gibbs, Ilys Shmulevich, Brady Authors: William Poole, David Gibbs, Ilys Shmulevich,	10:00 - 11:00	theme: Data	theme: Systems	track: Applications
Dorel, Was Joep, David Cohen, Eric Vara, Luca Grieco, Phirishoph Ruse. Anh Nguyen, Lucence Calcine, Christophe Ruse, Marie Dutreix, Emmanuel Barillot and Andrei Zmovyev Highlight talk 09 - Searching molecular structure databases with tandem mass spectra using CSI-FingeriD, Kai Dührkop, Hubin Shen, Marvin Museul, Celline Brouard, Sebastian Böcker and Juho Rousu Proceeding talk 19 - Complementary Feature Selection from Alternative Splicing Events and Gene Expression for Phenotype Prediction Authors: Mark Leiserson, Matthew Revng and Benjamin Raphael Andrew McPhenson, Damei Machev and Schrata Shah Authors: Mark Leiserson, Matthew Revng and Benjamin Raphael Andrew McPhenson, Damei Machev and Schrata Shah Authors: Mark Leiserson, Matthew Revng and Benjamin Raphael Andrew McPhenson, Damei Machev and Schrata Shah Authors: Mark Leiserson, Matthew Revng and Benjamin Raphael Andrew McPhenson, Damei Machev and Schrata Shah Authors: Charles Labuzzetta, Maggerd Antonio, Patricia Watson, Robet Wilson, Lucer Labissomerie, Jeffer by Timarchi, Baris Gene, P. Hande Ozdinler, Dennis Watson and Paul Anderson Theater (plenary hall) Theater (plenary hall) Theater (plenary hall) Theater (plenary hall) Authors: Riambhara Singh, Jack Lanchantin, Gabriel Robins and Varigin Ori Authors: Riambhara Singh, Jack Lanchantin, Gabriel Robins and Varigin Ori Authors: Tarmo Aljo, Harri Labdesmaki, Anjana Rao and Xiaojing Yue Thoogeding talk 21 - DeepChrome-Deep-learning for predicting gene expression from histore monficiations Authors: Tarmo Aljo, Harri Labdesmaki, Anjana Rao and Xiaojing Yue Thoogeding talk 22 - Lux GLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Aljo, Harri Labdesmaki, Anjana Rao and Xiaojing Yue Thooged Talk Agent Andrew Rown and Andrew Revnig and Benjamin Raphael Andrew Rown and Rown Andrew Rown Andrew Rown Andrew Rown Andrew Rown Andrew Rown Andrew Rown A	10:00 - 10:20			Application talk 06 - Predictive analytics for therapeutic target discovery backed by more than 100 public databases
tandem mass spectra using CSI-FingerID, Kai Dührkop, Hubin Mattanors in Cancer Authors: Mark Leiserson, Matthew Reyna and Benjamin Raphaa Muthors: Mark Leiserson, Matthew Reyna and Benjamin Raphaa Authors: Mark Leiserson, Matthew Reyna and Benjamin Raphaa Muthors: Mark Leiserson, Matthew Reyna and Benjamin Raphaa Muthors: Mark Leiserson, Matthew Reyna and Benjamin Raphaa Muthors: Mails Smith, Cydney Nielsen, Fong Chun Chan, 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 11:00 - 11:30 Theater (plenary hall) Theater (plenary hall) Theater (plenary hall) Theater (plenary hall) Mississippi Mississippi Mississippi Mississippi Mississippi Mississippi Track: ELIXIR -Tools for data analysis LIXIR talk 07 - Keygene - CropPedia - the integrated database of vivare platform for lead discovery and accelerated breeding and Paul Henry Cournède Authors: Vanisham Reynam All Paul Henry Cournède Coffee, exhibition & poster viewing Mississippi Mississippi Mississippi Mississippi Mississippi Marcon Authors: Blain Mississipsi and Special Mississipsi and Mississipsi and Special Mississipsi and Special Mississipsi and Special Mississipsi and Mississipsi and Mississipsi and Mississipsi and Mississipsi and Mississipsi		Authors: <u>Sunjoo Banq</u> , Hyunjung Shin and Jae-Hoon Kim	Dorel, Wael Jdey, David Cohen, Eric Viara, Luca Grieco, Hien- Anh Nguyen, Laurence Calzone, Christophe Russo, Marie Dutreix,	Authors: <u>Aram Krol</u> , Arie Baak, Onno Becker Hof and Kristina Hettne
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 **Coffee, exhibition & poster viewing** Theater (plenary hall) Theater (plenary hall) Mississippi 11:30 - 11:50 Proceeding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histome modifications Authors: Ritambhara Singh. Jack Lanchantin, Gabriel Robins and Vanjun Qi 11:50 - 12:10 Proceeding talk 22 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Ājlō, Harri Lähdesmäki, Anjana Rao and Xisojing Yue 11:50 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Authors: Margaret Antonio, Patricia wathors: Variable Security Trimarchi, Barbier (plenary hall) Authors: Proceeding talk 22 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostian: Authors: Blak (31 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Theater (plenary hall) Authors: Margaret Antonio, Patricia Watsons Authors: Blak (31 - LixGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostian: Authors: Mulammad Anmad-VIL-Din. Suleiman A Khan, Disha Malani, Asrid Murumagi, Olli Kaliloniemi, Tero Attockalio and Sa	10:20 - 10:40	tandem mass spectra using CSI:FingerID, Kai Dührkop, Huibin Shen, Marvin Meusel, Céline Brouard, Sebastian Böcker and	Mutations in Cancer	
Atthors: Charles Labuzzetta. Margaret Antonio, Patricia Watson, Robert Wilson, Lauren Laboissonniere, Jeffrey Trimarchi, Baris Gene, P. Hande Ozdinler, Dennis Watson and Paul Anderson 11:00 - 11:30 Theater (plenary hall) Theater (plenary hall) Theater (plenary hall) Theorems: Stambhara Singh, Jack Lanchantin, Gabriel Robins and Yarijun Ol Proceeding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histone modifications with complex experimental designs Authors: Tarmo Aljö, Harri Lahdesmäki. Anjana Rao and Xiaojing Yue Tition - 12:30 Theater (plenary hall) Theater (Andrew McPherson, Daniel Machev and Sohrab Shah
Authors: Charles Labuzzetta, Margaret Antonio, Patricia Watson, Robert Wilson, Lauren Labiossonniere, Jeffrey Trimarchi, Baris Genc, P. Hande Ozdinler, Dennis Watson and Paul Anderson Theater (plenary hall) Theater (plenary hall	10:40 - 11:00	Alternative Splicing Events and Gene Expression for Phenotype	pathway: An infinite mixture models approach	software platform for lead discovery and accelerated breeding
Theater (plenary hall) theme: Genomes Thoseding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histone modifications Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi 11:50 - 12:10 Proceeding talk 22 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Aijo, Harri Lahdesmäki, Anjana Rao and Xiaojing Yue 12:10 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Mississippi Mistince: E		Watson, Robert Wilson, Lauren Laboissonniere, Jeffrey Trimarchi, Baris Genc, P. Hande Ozdinler, Dennis Watson and		
11:30 - 12:30 11:30 Theme: Genomes Theme: Data Track: ELXIR - Tools for data analysis 11:30 - 11:50 Proceeding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histone modifications Proceeding talk 23 - Combining Dependent P-values with an Empirical Adaptation of Brown's Method Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi Proceeding talk 22 - LuxGLM: A probabilistic covariate model for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Aijō, Harri Lähdesmäki, Anjana Rao and Xiaojing Yue Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) The Action of DNA methylation modifications with complex expressions and Yanjun Qi Theater (plenary hall) The Action proceeding talk 23 - Combining Dependent P-values with an Empirical Adaptation of Brown's Method ELIXIR talk 07 - The Genomic HyperBrowser Authors: ElixIR talk 10 - The Genomic HyperBrowser Authors: ElixIR talk 10 - The Genomic HyperBrowser Authors: Carbon Spris Simovski, Finn Drables, Sveirung Gundersen, Mo	11:00 - 11:30		coffee, exhibition & poster viewing	
Proceeding talk 21 - DeepChrome: Deep-learning for predicting gene expression from histone modifications Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi 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 12:10 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) 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 Proceeding talk 24 - Drug response prediction by inferring pathway-response associations with Kernelized Bayesian Matrix Factorization Authors: Shan Li and Ivan Ovcharenko Iunch, exhibition & poster viewing 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 Knjilmenburg Authors: Boris Simovski, Finn Drables, Sveinung Gundersen, Morten Johansen, Diana Domanska, Abdulrahman Azab, Geir Kjetil Sandve a ELIXIR talk 08 - Chipster - comprehensive package of NGS data analysis with MapReduce Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostler. Authors: Ejia Korpelainen, Taavi Hupponen, Petri Klemelä, Maria Lehtivaara, Kimmo Mattia, Ari-Matti Saren and Aleksi Kailio Authors: Muhammad Ammad-Ud-Din, Suleiman A Khan, Disha Malani, Astrid Murnagi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski Ninnch, exhibition & poster viewing Theater (plenary hall) Mississippi Amazon		Theater (plenary hall)	Mississippi	Amazon
gene expression from histone modifications Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi 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 12:10 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Teston - 14:00 Manufaction of DNA methylation modifications with complex experimental designs Authors: Tarmo Äijö, Harri Lähdesmäki. Anjana Rao and Xiaojing Yue Lizio - 14:00 Manufaction of DNA methylation modifications with complex experimental designs Authors: Tarmo Äijö, Harri Lähdesmäki. Anjana Rao and Xiaojing Yue Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostier. 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 Aitokallio and Samuel Kaski Mississippi Mississippi Amazon	11:30 - 12:30	theme: Genomes	theme: Data	track: ELIXIR – Tools for data analysis
Authors: Ritambhara Singh, Jack Lanchantin, Gabriel Robins and Yanjun Qi 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 Authors: Tarmo Äijö, Harri Lähdesmäki, Anjana Rao and Xiaojing Yue Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Authors: Muhammad Ammad-Ud-Din, Suleiman A.Khan, Disha Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski Amazon Authors: Proceeding talk 24 - Drug response prediction by inferring pathway-response associations with Kernelized Bayesian Matrix Factorization Authors: Shan Li and Ivan Ovcharenko Lizao - 14:00 Theater (plenary hall) Amazon	11:30 - 11:50		Empirical Adaptation of Brown's Method	<i>"</i>
for quantification of DNA methylation modifications with complex experimental designs Authors: Tarmo Äijö, Harri Lähdesmäki, Anjana Rao and Xiaojing Yue 12:10 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Authors: Shan Li and Ivan Ovcharenko 12:30 - 14:00 Theater (plenary hall) MapReduce Authors: Dries Decap, Joke Reumers, Charlotte Herzeel, Pascal Costanza and Jan Fostier. Authors: Elia Korpelainen, Taavi Hupponen, Petri Klemelä, Maria Lehtivaara, Kimmo Mattila, Ari-Matti Saren and Aleksi Kallio Proceeding talk 24 - Drug response prediction by inferring pathway-response associations with Kernelized Bayesian Matrix Factorization Authors: Shan Li and Ivan Ovcharenko Authors: Muhammad Ammad-Ud-Din, Suleiman A.Khan, Disha Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski Theater (plenary hall) Mississippi Amazon			Authors: William Poole, David Gibbs, Ilya Shmulevich, Brady	Johansen, Diana Domanska, Abdulrahman Azab, Geir Kjetil Sandve and
Authors: Tarmo Äijö, Harri Lähdesmäki, Anjana Rao and Xiaojing Yue 12:10 - 12:30 Highlight talk 11 - Human Enhancers Are Fragile and Prone to Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko 12:30 - 14:00 Authors: Shan Li and Ivan Ovcharenko Theater (plenary hall) Costanza and Jan Fostier. Lehtivaara, Kimmo Mattila, Ari-Matti Saren and Aleksi Kallio Lehtivaara, Kimmo Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mattila, Ari-Mat	11:50 - 12:10	for quantification of DNA methylation modifications with	MapReduce	
Deactivating Mutations Authors: Shan Li and Ivan Ovcharenko Authors: Shan Li and Ivan Ovcharenko Authors: Muhammad Ammad-Ud-Din, Suleiman A.Khan, Disha Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski 12:30 - 14:00 Theater (plenary hall) Tresponse 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 12:30 - 14:00 Authors: François Moreews, Olivier Sallou and Olivier Collin				
Authors: <u>Muhammad Ammad-Ud-Din,</u> Suleiman A.Khan, Disha Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and Samuel Kaski 12:30 - 14:00 Theater (plenary hall) Amazon	12:10 - 12:30	Deactivating Mutations	response associations with Kernelized Bayesian Matrix	
Theater (plenary hall) Mississippi Amazon		Authors: Shan Li and <u>Ivan Ovcharenko</u>	Malani, Astrid Murumägi, Olli Kallioniemi, Tero Aittokallio and	Authors: François Moreews, <u>Olivier Sallou</u> and Olivier Collin
Theater (plenary hall) Mississippi Amazon	12:30 - 14:00		lunch, exhibition & poster viewing	
		Theater (plenary hall)		Amazon
	14:00 - 15:00	" ,	theme: Proteins	track: Applications

transcription factor binding across deverse protein families Authors: Yand Mandel Gatheurul, Ins Dror, Tamar Golan, Carmil Authors: Sheme Wang, Jianhu Ma and Jinbo Xu Proceeding table 25. Detecting better protein for the foliance and Manging Sequencing Reads Across Spooles Boundaries Authors: September Boundaries Authors: Tomor Hartosta Biowayor Shu, Keshyap Dave, Teemin Kiviga and Justa Taipate Theater (plensy hall) Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Boundaries kerner matching Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Boundaries kerner matching Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Bounde Robert States Biological Robert Views in the read precision in New Systems Theater (plensy) hall) Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Bounde Robert States Biological Robert Views in the read precision medicine Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Bounde Robert States Biological Robert Views in the read precision medicine Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Bounde States Biological Robert Views in the read precision medicine Authors: Anno Shall, Denitz Yorukoglu, Y. William Yu and Bounde States Biome States Biome States Biome States Biological Robert Views in the Robert	14:00 - 14:20	Highlight talk 13 - A widespread role of the motif environment in	Proceeding talk 27 - Al ICpreD: proteome-level protein disorder	Application talk 08 - MOLGENIS Diagnostic Platform for Clinical
Levy and Remo Rohs Levy and Remo Rohs Haan, Cisca Wilmenga, Tom de Koning, Rolf Simons, Richard Sinke and Morris Swetz: Authors: Kathen Trappe, Tobias Manschall and Bernhard Remand Remain Remainder Manschall and Bernhard Remand Remainder Kathen State Remand Remainder Kathen State Remainder Manschall and Chena Helphight talk 14 - Epigenomic Co-localization and Co-evolution Record in the Presidence data resources and Record Remainder Remand Remainder R				
Mapping Sequencing Reads Across Species Boundaries Authors: <u>Solitrin Traces</u> . Tobias Marchall and Bernhard Rends Authors: <u>Solitrin Traces</u> . Tobias Marchall and Bernhard Rends Authors: <u>Solitrin Traces</u> . Actions Marchall and Bernhard Rends Authors: <u>Solitrin Traces</u> . Proceeding talk 28 - PeakVus. Comprehensive Transcription Factor Binding Ste Bioscovery From Chil-Nexus and Chil-Peop. Revent als Key Refer for Stort. as Communication and Coverolation Authors: <u>Traces Hartores</u> . Bioswylof Sahu, Kashyap Dave, Authors: <u>Proceeding talk 29 - Feat genotyping</u> of Known SNPs through Theater (plenary hall) Solitrin S			Authors: <u>Sheng Wang</u> , Jianzhu Ma and Jinbo Xu	Haan, Cisca Wijmenga, Tom de Koning, Rolf Sijmons, Richard Sinke and
Authors: Kalthrin Trappe, Tobias Marschall and Bernhard Renard Authors: Genetatines D. Tairiops. Ame Eloisson and Paintelis G. Bagos Proceeding talk 26 - PeaXus: Comprehensive Transcription Factor Binding Site Discovery From CNP-Nexus and CNP-exe Experiments Authors: Tuomo Hartones, Blewshord Saltus, Kashyap Dave, Teemu Kiviroja and Juses Taipale Theater (plenary hall) Authors: Aris Shalli, Deniz Yorukoglu, Y. William Yu and Bonnie Berger Authors: Aris Shalli, Deniz Yorukoglu, Y. William Yu and Bonnie Berger Teemu Kiviroja and Massis Perdictions in Vivo Authors: Aris Shalli, Deniz Yorukoglu, Y. William Yu and Bonnie Berger Theater (plenary hall) Authors: Aris Shalli, Deniz Yorukoglu, Y. William Yu and Bonnie Berger The Highlight talk 15 - DNA Shape Features Improve Transcription Proceeding talk 29 - Fast genotyping of known SNPs through Integrating Proceeding talk 29 - Fast genotyping of known SNPs through Planmacology in the era of precision medicine Authors: Aris Shalli, Deniz Yorukoglu, Y. William Yu and Bonnie Berger The Highlight talk 15 - DNA Shape Features Improve Transcription Proceeding talk 29 - The BioSharing Registry: mapping the landacape of Shacked Data Types Authors: James Agent Data Types Authors: James Agent Data Types Authors: Maria Sile Predictions in Vivo Authors: Systems Shalling, Gelbei Xin, Tau-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman The Control of Sile Predictions in Vivo Authors: Systems Shalling, Olga Matveeva, Yury Raterion And Shalling, Olga Matveeva, Vegenity Risterion and Chikako Ragan Authors: Systems Shalling, Olga Matveeva, Vegenity Risterion and Chikako Ragan Authors: Systems Shalling, Olga Matveeva, Vegenity Risterion and Chikako Ragan Authors: Systems Shalling, Olga Matveeva, Vegenity Risterion and Chikako Ragan Authors: Systems Shalling, Olga Matveeva, Vegenity Risterion and Chikako Ragan Authors: Systems Shalling, Olga				secure (research) data storage, data sharing and open source data science
Feator Binding Site Discovery From ChiP-Nexus and ChiP-sex Experiments Experiments Authors: Tumon Hartonen, Biswajyofi Sahu, Kashyap Dave, Teenu Kivioja and Jusai Taipale Theater (plenary hall) Authors: Sandymate k-mer matching Authors: Arthory Kryn Shall, Denic Rico and Afforsio Valencia Authors: Arthory Matheliae Authors: Arthory Matheliae Berger Tis. 30 - 16:30 Proceeding talk 29 - Fast genotyping of known SNPs through approximate k-mer matching Authors: Arthory Matheliae Authors: Arthory Matheliae Berger Authors: Arthory Matheliae Berger Proceeding talk 15 - DNA Shape Features Improve Transcription Facior Binding Site Predictions in Vivo Authors: Arthory Matheliae Berger Berger Authors: Arthory Matheliae Proceeding talk 30 - Optimization of signal-to-noise ratio for efficient microarray probe design Authors: Authory Matheliae Authors: Anthory Matheliae Authors: Anthory Matheliae Berger Berger Authors: Arthory Matheliae Authors: Anthory Matheliae Berger Berger Berger Authors: Anthory Matheliae Proceeding talk 30 - Optimization of signal-to-noise ratio for efficient microarray probe design Authors: Anthory Matheliae Authors: Anthory Matheliae Berger Be				
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Theater (plenary hall) Theate		Teemu Kivioja and Jussi Taipale	Pau, Simone Marsili, David Ochoa, Ho-Ryun Chung, Martin	
15:30 - 16:30 Theme: Genomes Theme: Systems Track: ELIXIR - National collaborations, international standards ELIXIR talk 10 - Fostering excellence in data science to support progress in biological research and health at the SIB Swiss Institute of Barabasi Authors: Anthors: Anthory Mathelier, Beibei Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman Track: ELIXIR - National collaborations, international standards ELIXIR talk 10 - Fostering excellence in data science to support progress in biological research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Bioling Gain research and health at the SIB Swiss Institute of Biolin	15:00 - 15:30		coffee, exhibition & poster viewing	
15:30 - 15:50 Proceeding talk 29 - Fast genotyping of known SNPs through approximate k-mer matching Authors: Ariva Shaiji, Deniz Yorukoglu, Y. William Yu and Bonnie Berger 15:50 - 16:10 Highlight talk 15 - DNA Shape Features Improve Transcription Factor Binding Site Predictions in Vivo Authors: Anthors: Ant		Theater (plenary hall)	Mississippi	Amazon
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Authors: Ariva Shaili. Deniz Yorukoglu, Y. William Yu and Bonnie Berger Authors: Emre Guney, Jorg Menche, Marc Vidal and Albert-Laszlo Barabasi 15:50 - 16:10 Highlight talk 15 - DNA Shape Features Improve Transcription Factor Binding Site Predictions In Vivo Authors: Anthony Mathelier, Beibel Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman Proceeding talk 30 - Optimization of signal-to-noise ratio for efficient microarray probe design Authors: Svellana Shabalina, Olga Matveeva, Yury Nechipurenko, Nafisa Nazipova, Aleksey Ogurtsov, Evgeniy Riabenko and Chikako Ragan Authors: Robert Vaser, Dario Pavlović and Mile Šikić Authors: Wanne Aben, Daniel J. Vis, Magali Michaut and Lodewyk F. A. Wessels BLIXIR talk 11 - The BioSharing Registry: mapping the landscape of standards and database resources in the life sciences Molecular Data Types Authors: Nanne Aben, Daniel J. Vis, Magali Michaut and Lodewyk F. A. Wessels BLIXIR talk 12 - Using FAIR data to solve cross-resource questions in Rare Disease research Authors: Svellana Shabalina, Olga Matveeva, Yury Nechipurenko, Nafisa Nazipova, Aleksey Ogurtsov, Evgeniy Riabenko and Chikako Ragan Authors: Robert Vaser, Dario Pavlović and Mile Šikić Authors: Mark Thompson, Rajaram Kaliyaperumal, Pedro Sernadela, Robert Reihs, Davide Piscia, Kees Burger, Andrew Gibson, Claudio Carta, Marco Crim, Heims Müller, Arnoid Kuzniar, Anand Gaval, Richard Finkers, Sergi Bertin, J. L. Oliveira, Barend Mons, Marco Roos, Mark D. Wilkinson and Lutz Bonino keynote speaker: Benedict Paten, University of California, Santa Cruz, US Population assisted genome inference poster session 2, exhibition & drinks				in biological research and health at the SIB Swiss Institute of
Factor Binding Site Predictions In Vivo Authors: Anthony Mathelier, Beibel Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman 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 Nathors: Robert Vaser, Dario Pavlović and Mile Šikić keynote speaker: Benedict Paten, University of California, Santa Cruz, US Poster session 2, exhibition & drinks Interpretability of Drug Response Models Based on Multiple Molecular Data Types Authors: Anthony Mathelier, Beibel Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman Interpretability of Drug Response Models Based on Multiple Molecular Data Types Authors: Anthony Mathelier, Beibel Xin, Tsu-Pei Chiu, Lin Yang, Remo Rohs, and Wyeth W. Wasserman Interpretability of Drug Response Models Based on Multiple Molecular Data Types Authors: Peter Mcguilton, Alejandra Gonzalez-Beltran, Massimiliano Izzo, Authors: Peter Mcguilton, Alejandra Gonzalez-Beltran, University and Lodewyk F. A. Wuthors: Peter Mcguilton, Alejandra Gonzalez-Beltran, University of California, Santa Cruz, US Population assisted genome inference				
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Population assisted genome inference poster session 2, exhibition & drinks		Nechipurenko, Nafisa Nazipova, Aleksey Ogurtsov, Evgeniy	Authors: <u>Robert Vaser</u> , Dario Pavlović and Mile Šikić	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.
	16:40 - 17:30	key		nta Cruz, US
posicio mai ovoi nambolo. Trito to 10100 - posicio mai ode nambolo. Totto to 10100	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	20:00 - 23:30		Conference dinner @ the beach	

WEDNESDAY, SEPT			ECCB 2016
7 08:00 - 17:00		registration desk open all day	
08:45 - 09:00		welcome & announcements	
09:00 - 09:50	1	keynote speaker: Paulien Hogeweg, Utrecht University, Ne Long term information integration: evolution of evolution	therlands
	Theater (plenary hall)	Mississippi	Amazon
10:00 - 11:00	theme: Genomes	theme: Systems	theme: Proteins
			Proceeding talk 37 - PEPSI-Dock: A Detailed Data-Driven Protein-Protein Interaction Potential Accelerated By Polar Fourier Correlation
	Authors: Andreas Dwi Maryanto Gunawan, <u>Bingxin Lu</u> and Louxin Zhang	Authors: <u>Richard Bonneau</u> , Zach Kurtz, Christian Müller and Emily Miraldi	Authors: Emilie Neveu, David Ritchie, Petr Popov and Sergei Grudinin
	Highlight talk 17 - Automated filtering of multiple sequence alignments frequently worsen phylogenetic inference		Proceeding talk 38 - Simulated linear test applied to quantitative proteomics
	Authors: Ge Tan, Matthieu Muffato, Christian Ledergerber, Javier Herrero, Nick Goldman, Manuel Gil and <u>Christophe</u> <u>Dessimoz</u>	Authors: <u>Bernhard Steiert</u> , Jens Timmer and Clemens Kreutz	Authors: <u>T.V. Pham</u> and C.R. Jimenez
			Highlight talk 19 - Data-driven Image Fusion between Mass Spectrometry and Microscopy: Linking Histology to Spatial Proteomics and Lipidomics
			Authors: <u>Raf Van de Plas,</u> 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

Authors: Somage Hashendar, Janchu Ma, Harnmad Naveed, Green Falory, Emmanuelle Le Cheatelet, Ohnord Sungapan, Korgen Green, Anthors: Control Patrice, Maning January, Anthors: Maning Patrice, Maning January, Anthors: Maning Patrice, Anthors: Somage Hashendar, January Anthors: Maning Patrice, Anthors: Control Patrice, Anthors: Control Patrice, Anthors: Maning January, An	11:30 - 11:50	Highlight talk 20 - Disentangling type 2 diabetes and metformin		Proceeding talk 43 - MetaProb: Accurate Metagenomic Reads Binning
Soften Carzar, Jinto Xu and Schear Wang Fire Mills, Sar Visins-Sar Visitory, Charmodoric Holes Kindamann, Anian Yvonne Vorgi, Henrik Verlag part Rapia Jargement, Frantice Leverat, Lodo Chris, Henrik Span Needer Jargement, Frantice Leverat, Lodo Chris, Man application to gene expression regulation Intelligence of the Will application to gene expression regulation Intelligence of the William Span Span Needer Amende Cultifured and Zobar Yashini		treatment signatures in the human gut microbiota	of protein-protein interaction networks	based on Probabilistic Sequence Signatures
Lists with applications to gene expression regulation Authors. <u>Patic Anthory Order, Nature Reports</u> Authors. <u>Patic Anthory Order, Nature Reports</u> Authors. <u>Patic Anthory Order, Nature Reports</u> Authors. <u>Cautin Comments</u> Authors. <u>Cautin Comments</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Ferrie and Zoran Nikoloski, <u>Kevin Schwahn</u> Authors. <u>Read Tatewards</u> Mischier Jate Mischier Man Spitch Late 21 - A map of direction in a material metaperioms in a material metaperioms. The active (plenary half) The active (plenary half) The active (plenary half) Mississippi Authors: <u>Carents</u> Authors: <u>Mississippi</u> Mississippi Authors: <u>Mississippi</u> Author		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	Stefan Canzar, Jinbo Xu and <u>Sheng Wang</u>	Authors: Samuele Girotto, Cinzia Pizzi and <u>Matteo Comin</u>
Authors: Dalla Cohn Algeorytic, Mona Raber, Ilona Kofer, Yaek Mandel-Guffeund and Zohar Yakhini. Allows: Max Saljitz-Hermstein, Nadine Topfer, Sabrina Keessen, Allodair Fornia and Zohan Nikoloski, Keyin Schrashin. Rosenside, Stacey Efisiathiou, Rall Zimmer and Lars Dokton Proceeding task 40 - GTRAC: Feat retrieval from compressed collections of genomic variants. Authors: Keder Tatwawad, Mikel Hernaez, Idois Ochos and Fasety Weissman. Authors: Beand Flischer, Thomas Sandmann, Thomas Horn, Maximilan Billmann, Varun Chaudhary, Wolfgang Huber and Michael Botton. Authors: Beand Flischer, Thomas Sandmann, Thomas Horn, Maximilan Billmann, Varun Chaudhary, Wolfgang Huber and Michael Botton. **Top Continue Top Continu	11:50 - 12:10		integrating relative metabolite levels into a stoichiometric	
metazoan cell Authors: Keder Tatwawedi, Mikel Hernaez, Idoia Ochoa and Taschy Weissman Michael Boutos Munch, exhibition & poster viewing Theater (plenary hall) Mississippi Mississippi Mississippi Mississippi Mississippi Amazon Trocceding talk 45 - Characterizing leader sequences of CRISPR (col. CRISP		Authors: <u>Dalia Cohn-Alperovich</u> , Alona Rabner, Ilona Kifer, Yael Mandel-Gutfreund and Zohar Yakhini	Authors: Max Sajitz-Hermstein, Nadine Töpfer, Sabrina Kleessen,	L'Hernault, Thomas Bonfert, Markus Schilhabel, Colin Crump, Philip
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