19th European Conference on Computational Biology

Planetary Health and Biodiversity

31st August - 8th September 2020

eccb20.org

#ECCB2020

WEST	EEST	CDT	CEST	MONDAY, 7 September			TUESDAY, 8 September		CEST
08.00 - 08.10	10.00 - 10.10	02.00 - 02.10	09.00 - 09.10	**ECCB2020 - Virtual Opening**			**Announcements**		09.00 - 09.10
08.10 - 09.00	10.10 - 11.00	02.10 - 03.00	09.10 - 10.00	Keynote by **Modesto Orozco** on **Simulation of DNA. from the atom to the chromatin** Chaired by **Alfonso Valencia**			Keynote by **Fabian Theis** on **Modeling cellular state and dynamics in single cell genomics** Chaired by **Marc Martí-Renom**		09.10 - 10.00
09.00 - 10.00	11.00 - 12.00	03.00 - 04.00	10.00 - 11.00	**Parallel Track #01 Genomes** Chaired by **Stephane Rombauts** **Huan Shi** | A general near-exact k-mer counting method with low memory consumption enables de novo assembly of 106x human sequence data in 2.7 hours **Maor Asif** | DeepSELEX: Inferring DNA-binding preferences from HT-SELEX data using multi- class CNNs **Emilio Dorigatti** | Joint epitope selection and spacer design for string-of-beads vaccines **Adelme Bazin** | panRGP: a pangenome-based method to predict genomic islands and explore their diversity	**Parallel Track #02 Systems** Chaired by **Patrick Aloy** **Shohag Barman** | A Neuro-Evolution Approach to Infer a Boolean Network from Time-Series Gene Expressions **Taiki Fuji** | Feasible-Metabolic-Pathway-Exploration Technique using Chemical Latent Space **Yahui Long** | Ensembling graph attention networks for human microbe-drug association prediction **Gian Marco Messa** | A Siamese Neural Network model for theprioritization of metabolic disorders by integratingreal and simulated data	**Parallel Track #03 Data** Chaired by **Josep Lluís Gelpí** **Dong-gi Lee** | Dementia Key Gene Identification with Multi- Layered SNP-Gene-Disease Network **Thomas Gumbsch** | Enhancing statistical power in temporal biomarker discovery through representative shapelet mining **Tamim Abdelaal** | SCHNEL: Scalable clustering of high dimensional single-cell data **Derrick Blakely** | FastSK: Fast Sequence Analysis with Gapped String Kernels	**Parallel Track #07** - Chaired by **Toni Gabaldón** **Data** **PhD. Qiao Liu** | DeepCDR: a hybrid graph convolutional network for predicting cancer drug response **Joanna Ficek** | SCIM: Universal Single-Cell Matching with Unpaired Feature Sets **Genomes** **Marleen Nieboer** | svMIL: Predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants through multiple instance learning **Luca Nanni** | Exploring Chromatin Conformation and Gene Co-Expression through Graph Embedding	**Parallel Track #08** - Chaired by **Ana Conesa** **Genes** **Ayse Dincer** | Adversarial Deconfounding Autoencoder for Learning Robust Gene Expression Embeddings **Vu Viet Hoang Pham** | DriverGroup: A novel method for identifying driver gene groups **Protein** **Wenjing Xuan** | CLPred: A sequence-based protein crystallization predictor using BLSTM neural network **Janani Durairaj** | Geometricus Represents Protein Structures as Shape-mers Derived from Moment Invariants	10.00 - 11.00
10.00 - 10.20	12.00 - 12.20	04.00 - 04.20	11.00 - 11.20	BioBreak			BioBreak		11.00 - 11.20
10.20 - 11.10	12.20 - 13.10	04.20 - 05.10	11.20 - 12.10	Keynote by **Geneviève Almouzni** on **Chromatin plasticity, cell fate and identity** Chaired by **Christine Orengo**			Keynote by **Bissan Al-Lazikani** on **More than the sum of parts: Multidiciplinary big data in cancer therapy** Chaired by **Patrick Aloy**		11.20 - 12.10
11.10 - 12.10	13.10 - 14.10	05.10 - 06.10	12.10 - 13.10	**Parallel Track #04 Genomes** Chaired by **Toni Gabaldón** **Jack Lanchantin** | Graph Convolutional Networks for Epigenetic State Prediction Using Both Sequence and 3D Genome Data **Huy Nguyen** | Finding Orthologous Gene Blocks in Bacteria: The Computational Hardness of the Problem and Novel Methods to Address it **Sayaka Miura** | PathFinder: Bayesian inference of clone migration histories in cancer **Sarah Christensen** | Detecting Evolutionary Patterns of Cancers using Consensus Trees	**Parallel Track #05 Systems** Chaired by **Patrick Aloy** **Salvador Casani** | Padhoc: A computational pipeline for Pathway Reconstruction On the Fly **Sergio Doria-Belenguer** | Probabilistic Graphlets Capture Biological Function in Probabilistic Molecular Networks **Alina Renz** | FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2 **David Merrell** | Inferring Signaling Pathways with Probabilistic Programming	**Parallel Track #06 Data** Chaired by **Josep Lluís Gelpí** **Jason Fan** | Matrix (Factorization) Reloaded: Flexible Methods for Imputing Genetic Interactions with Cross-Species and Side Information **Wesley Qian** | Batch Equalization with a Generative Adversarial Network **Jose Barba** | Using a GTR+Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated **Elliot Layne** | Supervised learning on phylogenetically distributed data **Kerem Ayoz** | The Effect of Kinship in Re-identification Attacks Against Genomic Data Sharing Beacons	**Parallel Track #09 Genes** Chaired by **Artemis Hatzigeorgiou** **Milad Mokhtaridoost** | An efficient framework to identify key miRNA-mRNA regulatory modules in cancer **Joske Ubels** | RAINFOREST: A random forest approach to predict treatment benefit in data from (failed) clinical drug trials **Mohammad Lotfollahi** | Conditional out-of-sample generation for un-paired data using transfer VAE **Guillem Ylla** | MirCure: A tool for quality control, filter, and cu-ration of microRNAs of animals and plants	**Parallel Track #10 Proteins** Chaired by **Mark Wass** **Sabrina de Azevedo Silveira** | GRaSP: a graph-based residue neighborhood strategy to predict binding sites **Lukasz Kurgan** | PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictor selection **Yisu Peng** | New mixture models for decoy-free false discovery rate estimation in mass-spectrometry proteomics **Zhenling Peng** | APOD: accurate sequence-based predictor of disordered flexible linkers	12.10 - 13.10
12.10 - 12.30	14.10 - 14.30	06.10 - 06.30	13.10 - 13.30	**EMBL-EBI** **European Bioinformatics Institute**			**RES** **Spanish Supercomputing Network**		13.10 - 13.30
12.30 - 14.00	14.30 - 16.00	06.30 - 08.00	13.30 - 15.00	Break			Break		13.30 - 15.00
14.00 - 15.20	16.00 - 17.20	08.00 - 09.20	15.00 - 16.20	**A glimpse into Global Bioinformatics Communities: Latin America - SolBio** Chaired by **Javier De Las Rivas** **Benilton Carvalho** | The Brazilian Initiative on Precision Medicine: Strategies and Findings **Gregorio Iraola** | Building city-scale genomic cartographies for improved response to emerging infectious diseases **Wendy González Diaz** | Molecular Modeling of Ion Channels-Associated Diseases **Alejandra Medina Rivera** | Logical modeling of dendritic cells in vitro differentiation from human monocytes unravels novel transcriptional regulatory interactions			**A glimpse into Global Bioinformatics Communities: ELIXIR** Chaired by **Jennifer Harrow** **Sameer Velankar |** 3D-Beacons: An integrative, distributed platform for FAIR access to experimental and predicted macromolecular structures **Jose Ramon Macias Gonzalez |** 3DBionotes-COVID19 Edition: bringing together structural and functional information on SARS-CoV-2 proteome **Deborah Caucheteur | COVoc:** a COVID-19 ontology to support literature triage **Bjoern Gruening |** The ELIXIR Tools Platform - solutions for COVID-19 research **Azab Abdulrahman |** Nordic development on federating the EGA **Flora D'Anna |** FAIR data by design		15.00 - 16.20
15.20 - 15.30	17.20 - 17.30	09.20 - 09.30	16.20 - 16.30	BioBreak			BioBreak		16.20 - 16.30
15.30 - 16.20	17.30 - 18.20	09.30 - 10.20	16.30 - 17.20	Keynote by **Deborah Marks** on **Prediction and design of biological sequences with neural machines** Chaired by **Baldo Oliva**			Keynote by **Londa Schiebinger** on **Gendered Innovations in Biomedicine, Machine Learning, and Robotics** Chaired by **Niklas Blomberg**		16.30 - 17.20
16.20 - 16.30	18.20 - 18.30	10.20 - 10.30	17.20 - 17.30	**Announcements**			**ECCB2020 - Virtual Closing**		17.20 - 17.30
16.30 - 18.00	18.30 - 20.00	10.30 - 12.00	17.30 - 19.00	Network & Connect					