19th European Conference on Computational Biology

Planetary Health and Biodiversity

31st August - 8th September 2020

eccb20.org

ECCB 2020 Virtual!

#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**	**Parallel Track #02 Systems** Chaired by **Patrick Aloy**	**Parallel Track #03 Data** Chaired by **Josep Lluís Gelpi**	**Parallel Track #07 - Chaired by Toni Gabaldón** Data / Genomes	**Parallel Track #08 - Chaired by Ana Conesa** Genes / Protein	10.00 - 11.00
				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	**Shohag Barman** | A Neuro-Evolution Approach to Infer a Boolean Network from Time-Series Gene Expressions	**Dong-gi Lee** | Dementia Key Gene Identification with Multi- Layered SNP-Gene-Disease Network	**PhD. Qiao Liu** | DeepCDR: a hybrid graph convolutional network for predicting cancer drug response	**Ayse Dincer** | Adversarial Deconfounding Autoencoder for Learning Robust Gene Expression Embeddings	
				Maor Asif | DeepSELEX: Inferring DNA-binding preferences from HT-SELEX data using multi- class CNNs	**Taiki Fuji** | Feasible-Metabolic-Pathway-Exploration Technique using Chemical Latent Space	**Thomas Gumbsch** | Enhancing statistical power in temporal biomarker discovery through representative shapelet mining	**Joanna Ficek** | SCIM: Universal Single-Cell Matching with Unpaired Feature Sets	**Vu Viet Hoang Pham** | DriverGroup: A novel method for identifying driver gene groups	
				Emilio Dorigatti | Joint epitope selection and spacer design for string-of-beads vaccines	**Yahui Long** | Ensembling graph attention networks for human microbe-drug association prediction	**Tamim Abdelaal** | SCHNEL: Scalable clustering of high dimensional single-cell data	**Marleen Nieboer** | svMIL: Predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants through multiple instance learning	**Wenjing Xuan** | CLPred: A sequence-based protein crystallization predictor using BLSTM neural network	
				Adelme Bazin | panRGP: a pangenome-based method to predict genomic islands and explore their diversity	**Gian Marco Messa** | A Siamese Neural Network model for the prioritization of metabolic disorders by integrating real and simulated data	**Derrick Blakely** | FastSK: Fast Sequence Analysis with Gapped String Kernels	**Luca Nanni** | Exploring Chromatin Conformation and Gene Co-Expression through Graph Embedding	**Janani Durairaj** | Geometricus Represents Protein Structures as Shape-mers Derived from Moment Invariants	
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**	**Parallel Track #05 Systems** Chaired by **Patrick Aloy**	**Parallel Track #06 Data** Chaired by **Josep Lluís Gelpi**	**Parallel Track #09 Genes** Chaired by **Artemis Hatzigeorgiou**	**Parallel Track #10 Proteins** Chaired by **Mark Wass**	12.10 - 13.10
				Jack Lanchantin | Graph Convolutional Networks for Epigenetic State Prediction Using Both Sequence and 3D Genome Data	**Salvador Casani** | Padhoc: A computational pipeline for Pathway Reconstruction On the Fly	**Jason Fan** | Matrix (Factorization) Reloaded: Flexible Methods for Imputing Genetic Interactions with Cross-Species and Side Information	**Milad Mokhtaridoost** | An efficient framework to identify key miRNA-mRNA regulatory modules in cancer	**Sabrina de Azevedo Silveira** | GRaSP: a graph-based residue neighborhood strategy to predict binding sites	
				Huy Nguyen | Finding Orthologous Gene Blocks in Bacteria: The Computational Hardness of the Problem and Novel Methods to Address it	**Sergio Doria-Belenguer** | Probabilistic Graphlets Capture Biological Function in Probabilistic Molecular Networks	**Wesley Qian** | Batch Equalization with a Generative Adversarial Network	**Joske Ubels** | RAINFOREST: A random forest approach to predict treatment benefit in data from (failed) clinical drug trials	**Lukasz Kurgan** | PROBselect: accurate prediction of protein- binding residues from proteins sequences via dynamic predictor selection	
				Sayaka Miura | PathFinder: Bayesian inference of clone migration histories in cancer	**Alina Renz** | FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2	**Jose Barba** | Using a GTR+Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated	**Mohammad Lotfollahi** | Conditional out-of-sample generation for un-paired data using transfer VAE	**Yisu Peng** | New mixture models for decoy-free false discovery rate estimation in mass-spectrometry proteomics	
				Sarah Christensen | Detecting Evolutionary Patterns of Cancers using Consensus Trees	**David Merrell** | Inferring Signaling Pathways with Probabilistic Programming	**Elliot Layne** | Supervised learning on phylogenetically distributed data	**Guillem Ylla** | MirCure: A tool for quality control, filter, and cu-ration of microRNAs of animals and plants	**Zhenling Peng** | APOD: accurate sequence-based predictor of disordered flexible linkers	
						Kerem Ayoz | The Effect of Kinship in Re-identification Attacks Against Genomic Data Sharing Beacons			
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**			**A glimpse into Global Bioinformatics Communities: ELIXIR** Chaired by **Jennifer Harrow**		15.00 - 16.20
				Benilton Carvalho | The Brazilian Initiative on Precision Medicine: Strategies and Findings			**Sameer Velankar** | 3D-Beacons: An integrative, distributed platform for FAIR access to experimental and predicted macromolecular structures		
				Gregorio Iraola | Building city-scale genomic cartographies for improved response to emerging infectious diseases			**Jose Ramon Macias Gonzalez** | 3DBionotes-COVID19 Edition: bringing together structural and functional information on SARS-CoV-2 proteome		
				Wendy González Diaz | Molecular Modeling of Ion Channels-Associated Diseases			**Deborah Caucheteur** | COVoc: a COVID-19 ontology to support literature triage		
				Alejandra Medina Rivera | Logical modeling of dendritic cells in vitro differentiation from human monocytes unravels novel transcriptional regulatory interactions			**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		
15.20 - 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					