ECCB 2020
Virtual!

19th
European Conference on Computational Biology
Planetary Health and Biodiversity

SCIENTIFIC PROGRAMME

31st August - 8th September, 2020

Barcelona Supercomputing Center
Centro Nacional de Supercomputación

INB Spanish National Bioinformatics Institute

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eccb20.org

FEDER

19th European Conference on Computational Biology

Planetary Health and Biodiversity

31st August - 8th September 2020

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ECCB2020 SCIENTIFIC PROGRAMME

Time indicated in CEST

Monday, September 7, 2020

09:00 - 10:00

ECCB2020 - Virtual Opening || Keynote speaker - Modesto Orozco

Chaired by Alfonso Valencia

Barcelona Supercomputing Center (BSC), Spain

09:10 - 10:00 Simulation of DNA. from the atom to the chromatin

Presenter Modesto Orozco
Institute for Research in Biomedicine (IRB Barcelona), Spain

10:00 - 11:00

Parallel Track #01

Chaired by Stephane Rombauts

Center for Plant System Biology, VIB-UGent, Belgium

10:00 - 10:15 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

Presenter Christina Huan Shi
The Chinese University of Hong Kong, Hong Kong

10:15 - 10:30 DeepSELEX: Inferring DNA-binding preferences from HT-SELEX data using multi-class CNNs

Presenter Maor Asif
Ben-Gurion University, Israel

10:30 - 10:45 Joint epitope selection and spacer design for string-of-beads vaccines

Presenter Emilio Dorigatti
Ludwig Maximilian Universitaet Muenchen, Germany

10:45 - 11:00 panRGP: a pangenome-based method to predict genomic islands and explore their diversity

Presenter Adelme BAZIN
LABGeM - UMR8030, Genoscope, France

Monday, September 7, 2020

Parallel Track #02

Chaired by Patrick Aloy

Institute for Research in Biomedicine (IRB Barcelona), Spain

10:00 - 10:15 A Neuro-Evolution Approach to Infer a Boolean Network from Time-Series Gene Expressions

Presenter Shohag Barman
American International University-Bangladesh, Bangladesh

10:15 - 10:30 Feasible-Metabolic-Pathway-Exploration Technique using Chemical Latent Space

Presenter Taiki Fuji
Hitachi Ltd., Japan

10:30 - 10:45 Ensembling graph attention networks for human microbe-drug association prediction

Presenter Yahui Long
Nanyang Technological University, China

10:45 - 11:00 A Siamese Neural Network model for theprioritization of metabolic disorders by integratingreal and simulated data

Presenter Gian Marco Messa
King Abdullah University of Science and Technology (KAUST), Saudi Arabia

Parallel Track #03

Chaired by Josep Ll. Gelpi

University of Barcelona - Barcelona Supercomputing Center (BSC), Spain

10:00 - 10:15 Dementia Key Gene Identification with Multi-Layered SNP-Gene-Disease Network

Presenter Dong-gi Lee
Ajou University, South Korea

10:15 - 10:30 Enhancing statistical power in temporal biomarker discovery through representative shapelet mining

Presenter Thomas Gumbsch
ETH Zürich, Switzerland

10:30 - 10:45 SCHNEL: Scalable clustering of high dimensional single-cell data

Presenter Tamim Abdelaal
Delft University of Technology, Netherlands

10:45 - 11:00 FastSK: Fast Sequence Analysis with Gapped String Kernels

Presenter Yanjun Qi
University of Virginia, United States

11:00 - 11:20

BioBreak

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Monday, September 7, 2020

11:20 - 12:10

Keynote speaker - Geneviève Almouzni

Chaired by Christine Orengo

University College London, United Kingdom

11:20 - 12:10 Chromatin plasticity, cell fate and identity

Presenter Geneviève Almouzni
Chromatin Dynamics team at Institut Curie, Science Academy in France, LifeTime Initiative, France

12:10 - 13:30

Parallel Track #04

Chaired by Toni Gabaldón

Barcelona Supercomputing Center (BSC), Spain

12:10 - 12:25 Graph Convolutional Networks for Epigenetic State Prediction Using Both Sequence and 3D Genome Data

Presenter Jack Lanchantin

University of Virginia, United States

12:25 - 12:40 Finding Orthologous Gene Blocks in Bacteria: The Computational Hardness of the Problem and Novel Methods to Address it

Presenter Huy Nguyen

Iowa State University, United States

12:40 - 12:55 PathFinder: Bayesian inference of clone migration histories in cancer

Presenter Sayaka Miura

Temple University, United States

12:55 - 13:10 Detecting Evolutionary Patterns of Cancers using Consensus Trees

Presenter Sarah Christensen

University of Illinois at Urbana-Champaign, United States

Parallel Track #05

Chaired by Patrick Aloy

Institute for Research in Biomedicine (IRB Barcelona), Spain

12:10 - 12:25 Padhoc: A computational pipeline for Pathway Reconstruction On the Fly

Presenter Salvador Casani

BioBam Bioinformatics, Spain

12:25 - 12:40 Probabilistic Graphlets Capture Biological Function in Probabilistic Molecular Networks

Presenter Sergio Doria-Belenguer

Barcelona Supercomputing Center (BSC), Spain

Monday, September 7, 2020

12:40 - 12:55 FBA reveals guanylate kinase as a potential target for antiviral therapies against SARS-CoV-2

Presenter Alina Renz
Computational Systems Biology, University of Tübingen, Germany

12:55 - 13:10 Inferring Signaling Pathways with Probabilistic Programming

Presenter David Merrell
University of Wisconsin - Madison, United States

Parallel Track #06

Chaired by Josep Ll. Gelpi

University of Barcelona - Barcelona Supercomputing Center (BSC), Spain

12:10 - 12:25 Matrix (Factorization) Reloaded: Flexible Methods for Imputing Genetic Interactions with Cross-Species and Side Information

Presenter Jason Fan
University of Maryland, United States

12:25 - 12:40 Batch Equalization with a Generative Adversarial Network

Presenter Wesley Qian
University of Illinois at Urbana-Champaign, United States

12:40 - 12:55 Using a GTR+Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated

Presenter Jose Barba-Montoya
Temple University, United States

12:55 - 13:10 Supervised learning on phylogenetically distributed data

Presenter Elliot Layne
McGill University, Canada

13:10 - 13:25 The Effect of Kinship in Re-identification Attacks Against Genomic Data Sharing Beacons

Presenter Kerem Ayoz
Bilkent University, Turkey

13:10 - 13:30

Meet our sponsor: EMBL-EBI- European Bioinformatics Institute

13:10 - 13:30 What's new at EMBL-EBI?

Presenter Amonida Zadissa
EMBL-EBI - European Bioinformatics Institute, United Kingdom

Presenter Sarah Morgan
EMBL-EBI - European Bioinformatics Institute, United Kingdom

13:30 - 15:00

Break || Meet our exhibitors

Monday, September 7, 2020

15:00 - 16:20

A glimpse into Global Bioinformatics Communities: Latin America - SolBio

Chaired by Javier De Las Rivas

Spanish National Research Council (CSIC), Universtity of Salamanca (USAL), Spain

15:00 - 15:20 The Brazilian Initiative on Precision Medicine: Strategies and Findings

Presenter Benilton Carvalho
University of Campinas, Brazil

15:20 - 15:40 Building city-scale genomic cartographies for improved response to emerging infectious diseases

Presenter Gregorio Iraola
Microbial Genomics Laboratory, Institut Pasteur de Montevideo, Uruguay

15:40 - 16:00 Molecular Modeling of Ion Channels-Associated Diseases

Presenter Wendy González Diaz
Center for Bioinformatics and Molecular Simulations (CBSM), University of Talca, Chile

16:00 - 16:20 Logical modeling of dendritic cells in vitro differentiation from human monocytes unravels novel transcriptional regulatory interactions

Presenter Alejandra Medina Rivera
Universidad Nacional Autonoma de Mexico, Mexico

16:20 - 16:30

BioBreak

16:30 - 17:30

Keynote speaker - Debora Marks || Announcements

Chaired by Baldo Oliva

Pompeu Fabra University, Spain

16:30 - 17:20 Prediction and design of biological sequences with neural machines

Presenter Debora Marks
Department of Systems Biology, Harvard Medical School, United States

17:30 - 19:00

Network & Connect || Meet our exhibitors

Tuesday, September 8, 2020

09:00 - 10:00

Announcements || Keynote speaker - Fabian Theis

Chaired by Marc Marti-Renom

CNAG-CRG, Spain

09:10 - 10:00 Modeling cellular state and dynamics in single cell genomics

Presenter Fabian Theis
Institute of Computational Biology, Helmholtz Zentrum München, Germany

10:00 - 11:00

Parallel Track #07

Chaired by Toni Gabaldón

Barcelona Supercomputing Center (BSC), Spain

10:00 - 10:15 DeepCDR: a hybrid graph convolutional network for predicting cancer drug response

Presenter Qiao Liu
Tsinghua University, China

10:15 - 10:30 SCIM: Universal Single-Cell Matching with Unpaired Feature Sets

Presenter Joanna Ficek
ETH Zürich, Switzerland

10:30 - 10:45 svMIL: Predicting the pathogenic effect of TAD boundary-disrupting somatic structural variants through multiple instance learning

Presenter Marleen Nieboer
UMC Utrecht, Netherlands

10:45 - 11:00 Exploring Chromatin Conformation and Gene Co-Expression through Graph Embedding

Presenter Luca Nanni
Politecnico di Milano, Italy

Parallel Track #08

Chaired by Ana Conesa

University of Florida, United States

10:00 - 10:15 Adversarial Deconfounding Autoencoder for Learning Robust Gene Expression Embeddings

Presenter Ayse Dincer
University of Washington, United States

10:15 - 10:30 DriverGroup: A novel method for identifying driver gene groups

Presenter Vu Viet Hoang Pham
University of South Australia, Australia

Tuesday, September 8, 2020

10:30 - 10:45 CLPred: A sequence-based protein crystallization predictor using BLSTM neural network

Presenter Wenjing Xuan
Central South University, China

10:45 - 11:00 Geometricus Represents Protein Structures as Shape-mers Derived from Moment Invariants

Presenter Janani Durairaj
Wageningen University, Netherlands

11:00 - 11:20

BioBreak

11:20 - 12:10

Keynote speaker - Bissan Al-Lazikani

Chaired by Patrick Aloy

Institute for Research in Biomedicine (IRB Barcelona), Spain

11:20 - 12:10 More than the sum of parts: Multidiciplinary big data in cancer therapy

Presenter Bissan Al-Lazikani
The Institute of Cancer Research, United Kingdom

12:10 - 13:10

Parallel Track #09

Chaired by Artemis Hatzigeorgiou

University of Thessaly, Hellenic Pasteur Institute, Greece

12:10 - 12:25 An efficient framework to identify key miRNA-mRNA regulatory modules in cancer

Presenter Milad Mokhtaridoost
Koç University, Turkey

12:25 - 12:40 RAINFOREST: A random forest approach to predict treatment benefit in data from (failed) clinical drug trials

Presenter Joske Ubels
UMC Utrecht, Netherlands

12:40 - 12:55 Conditional out-of-sample generation for un-paired data using transfer VAE

Presenter Mohammad Lotfollahi
Helmholtz Zentrum München, Germany

12:55 - 13:10 MirCure: A tool for quality control, filter, and cu-ration of microRNAs of animals and plants

Presenter Guillem Ylla
Harvard University, United States

Tuesday, September 8, 2020

Parallel Track #10

Chaired by Mark Wass

University of Kent, United Kingdom

12:10 - 12:25 GRaSP: a graph-based residue neighborhood strategy to predict binding sites

Presenter Sabrina de Azevedo Silveira
Universidade Federal de Viçosa, Brazil

12:25 - 12:40 PROBselect: accurate prediction of protein-binding residues from proteins sequences via dynamic predictor selection

Presenter Lukasz Kurgan
Virginia Commonwealth University, United States

12:40 - 12:55 New mixture models for decoy-free false discovery rate estimation in mass-spectrometry proteomics

Presenter Yisu Peng
Northeastern University, United States

12:55 - 13:10 APOD: accurate sequence-based predictor of disordered flexible linkers

Presenter Zhenling Peng
Tianjin University, China

13:10 - 13:30

Meet our sponsor: RES - Spanish Supercomputing Network

13:10 - 13:30 The Spanish Supercomputing Network offers HPC resources to the scientific community

Presenter Jordi Mas
Spanish Supercomputing Network (Red Española de Supercomputación RES), Spain

13:30 - 15:00

Break || Meet our exhibitors

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Tuesday, September 8, 2020

15:00 - 16:20

A glimpse into Global Bioinformatics Communities: Europe - ELIXIR

Chaired by Jen Harrow

ELIXIR, United Kingdom

15:00 - 15:13 3D-Beacons: An integrative, distributed platform for FAIR access to experimental and predicted macromolecular structures

Presenter Sameer Velankar
Protein Data Bank In Europe, EMBL-EBI, United Kingdom

15:13 - 15:26 3DBionotes-COVID19 Edition: bringing together structural and functional information on SARS-CoV-2 proteome

Presenter Jose Ramon Macias Gonzalez
Biocomputing Unit, CNB-CSIC, Spain

15:26 - 15:39 COVoc: a COVID-19 ontology to support literature triage

Presenter Déborah Caucheteur
HES-SO Genève / Swiss Institute of Bioinformatics (SIB), Switzerland

15:39 - 15:52 The ELIXIR Tools Platform - solutions for COVID-19 research

Presenter Bjoern Gruening
University of Freiburg, Germany

15:52 - 16:05 Nordic development on federating the EGA

Presenter Abdulrahman Azab Mohamed
University Center for Information Technology, University of Oslo, Norway

16:05 - 16:18 FAIR data by design

Presenter Flora D'Anna
VIB, Belgium

16:20 - 16:30

BioBreak

16:30 - 17:30

Keynote speaker - Londa Schiebinger || ECCB2020-Virtual Closing

Chaired by Niklas Blomberg

ELIXIR, United Kingdom

16:30 - 17:20 Gendered Innovations in Biomedicine, Machine Learning, and Robotics

Presenter Londa Schiebinger
Stanford University, United States