Day 1 - Monday, September 16th

9:30   OPENING REMARKS

Session: GENOMES (i) – Chair: Haiyan Huang

9:45   **Mario Caceres** (Hospital del Mar Research Institute)
Towards a complete characterization of inversions and other complex variants in the human genome

10:00   **Gil Ast** (TAU)
Shaping splicing: the role of nuclear 3D genome organization

10:15   **Marc Marti-Renom** (CRG)
Structure-based genome editing to characterize the spatio-temporal regulatory landscape of sex-determination

10:30   **Noam Shomron** (TAU)
Genomics throughout life

10:45   **Roderic Guigo** (CRG)
Annotating the human and all eukariotic genomes

11:00   BREAK

Session: METAGENOMICS and METABOLISM - Chair: Roderic Guigo

11:45   **Uri Gophna** (TAU)
Within-host bacterial strain dynamics revealed by genomics and metagenomics

12:00   **Elhanan Borenstein** (TAU)
A tale of two omics: Computational multi-omic methods for studying host-microbiome interactions

12:15   **Ashley Wolf** (UCB)
Bacterial competition and metabolism in the mammalian gut

12:35   **David Burstein** (TAU)
Exploring the language of microbial genomes

12:50   LUNCH

Session: DISEASES (i) - Chair: Martin Vingron

14:20   **Mihaela Zavolan** (University of Basel)
Measuring and modelling the translation landscape of cancers

14:40   **Rani Elkon** (TAU)
GWAS: from genetic research discoveries to clinical utility

14:55   **Cenk Sahinalp** (NIH)
Profiles of expressed mutations in single cells reveal subclonal expansion patterns and therapeutic impact of intratumor heterogeneity

15:15   **Amit Huppert** (TAU)
Estimating the endemic risk of severe disease from COVID-19

15:30   **Soren Brunak** (University of Copenhagen)
Analysis of population-wide disease trajectories and their heritability

15:50   **Karen Avraham** (TAU)
Tackling rare diseases: understanding mechanisms and implementing therapy

16:05   BREAK

Session: PHYLOGENY and EVOLUTION - Chair: Karen Avraham

17:00   **Teresa Przytycka** (NIH)
Gene expression evolution in species and cancer evolution

17:20   **Itay Mayrose** (TAU)
Phylogeny reconstruction as an artificial intelligence game

17:35   **Cedric Notredame** (CRG)
Re-powering phylogeny in a changing data landscape

17:50   **Tal Pupko** (TAU)
A machine-learning based alternative to phylogenetic bootstrap

18:05   END OF DAY

**18:15   Bus pick up for dinner at the Fabra Observatory – Meeting point: PRBB lobby
"Dinner with Stars" combines stargazing with a delightful gastronomic experience at one of the city's most scenic viewpoints. Exclusive for conference participants.**

Day 2 - Tuesday, September 17th

Session: THEORY/METHODS (i) - Chair: Ron Shamir

9:00   **Martin Vingron** (Max Planck Institute for Molecular Genetics)
Visual biclustering of transcriptomics data

9:20   **Orr Spiegel** (TAU)
Computational tools for processing, analyzing and modeling high-resolution animal movement data

9:35   **Donate Weghorn** (CRG)
Probabilistic modeling of mutational processes in cancer and the human germline

9:50   **Denis Titov** (UCB)
Using math and experiments to study cellular metabolism regulation

10:10   **Jian Ma** (Carnegie Mellon School of Computer Science)
Machine learning for single-cell spatial epigenome

10:30   **Roded Sharan** (TAU)
Data integration in a network context

10:45   BREAK

Session: GENOMES (ii) - Chair: Ashley Wolf

11:45   **Steven Brenner** (UCB)
Genome sequence for screening and diagnosis

12:05   **Ben Lehner** (CRG)
Mutate everything

12:20   **Eli Eisenberg** (TAU)
A-to-I editing generates combinatorial complexity in the neural proteome of cephalopods

12:35   **Lars Velten** (CRG)
Synthetic enhancers reveal design principles of cell state specific regulatory elements in hematopoiesis

12:50   **Juan Valcarcel** (CRG)
Networks or alternative splicing regulation in cancer

13:05   LUNCH

Session: PROTEINS - Chair: Cedric Notredame

14:30   **Christine Orengo** (University College London)
Deep learning and AlphaFold expand our understanding of protein structure and function space

14:50   **Baldo Oliva** (Universitat Pompeu Fabra)
Using structures to predict and model protein-DNA binding in cis-regulatory elements

15:05   **Jérôme Tubiana** (TAU)
Harnessing machine learning generative models for peptide binder design

15:20   **Nir Ben-Tal** (TAU)
On the emergence of a rudimentary enzyme from a binding module

15:35   **Luis Serrano** (CRG)
Computer protein design using a structural based software (FoldX, ModelX) of cytokines and antibodies

15:50   **Rotem Rubinstein** (TAU)
Following the evolutionary paths of highly specific homophilic adhesion proteins

16:05   END OF DAY

Day 3 - Wednesday, September 18th

Session: THEORY/METHODS (ii) – Chair: Elhanan Borenstein

9:00 **Anders Krogh** (University of Copenhagen)
Gene expression analysis using a deep generative model instead of control samples

9:20 **Haiyan Huang** (UCB)
Integrative deep multi-learning for biclustering and predicting cancer drug responses: leveraging omics and drug molecular data

9:40 **Saharon Rosset** (TAU)
Using classical algorithms for modern applications: MCMC for tail calculations, EM for PET reconstruction

9:55 **Joseph Lewnard** (UCB)
Modeling the preventable burden of antimicrobial resistance

10:15 BREAK

Session: DISEASES (ii) - Chair: Steven Brenner

10:45 **Asaf Madi** (TAU)
Immune niches | the pre-printed version

11:00 **Tzachi Hagai** (TAU)
The evolutionary paradox of host-virus interactions

11:15 **Mafalda Dias and/or Jonathan Frazer** (CRG)
What can the diversity of life on Earth teach us about severely pathogenic variants?

11:30 **Ron Shamir** (TAU)
Multi-omics and EMRs in disease analysis

11:45 CLOSING REMARKS

12:00 LUNCH