

Morning session I (9.00 - 10:00)

- 08:55-09:00 Introduction
- 9:00-9:45 **Keynote** - Brendan Frey. *Learning deep biological architectures for genomic medicine.*
- 9:45-10:05 **Talk** - Christof Angermueller and Oliver Stegle. *Multi-task deep neural network to predict CpG methylation profiles from low-coverage sequencing data.*
- 10:05-10:10 **Spotlight** - Melanie F. Pradier, Stefan Stark, Stephanie Hyland, Julia E. Vogt, Gunnar Rätsch and Fernando Perez-Cruz. *Large-Scale Sentence Clustering from Electronic Health Records for Genetic Associations in Cancer.*
- 10:10-10:15 **Spotlight** - Oren Kraus, Lei Jimmy Ba and Brendan Frey. *Classifying Microscopy Images Using Convolutional Multiple Instance Learning.*

Morning coffee break (10.15 - 10.30)

- 10:30-10:50 **Talk** - David Kelley, Jasper Snoek and John Rinn. *Basset: Learning the regulatory code of the accessible genome with deep convolutional neural networks*
- 10:50-11:10 **Talk** - Viivi Halla-Aho, Henrik Mannerstrom and Harri Lähdesmäki. *A probabilistic method for quantifying chromatin interactions*
- 11:10-11:30 **Talk** - Scott Lundberg, William Tu, Brian Raught, Linda Penn, Michael Hoffman and Su-In Lee. *ChromNet: Learning the chromatin network from all ENCODE data.*
- 11:30-11:35 **Spotlight** - Mohammad Javad Hosseini and Su-In Lee. *Learning Gaussian Graphical Models with Overlapping Blocks.*
- 11:35-11:40 **Spotlight** - Felipe Llinares-López, Laetitia Papaxanthos, Dean Bodenham and Karsten Borgwardt. *Detecting significant higher-order associations between genotype and phenotype while conditioning on covariates.*
- 11:40-11:45 **Spotlight** - Antti Honkela, Jaakko Peltonen, Hande Topa, Iryna Charapitsa, Filomena Matarese, Korbinian Grote, Hendrik G. Stunnenberg, George Reid, Neil Lawrence and Magnus Rattray. *Genome-wide modelling of transcription kinetics reveals patterns of RNA production delays.*
- 11:45-11:50 **Spotlight** - Victoria Hore, Andy Dahl, Ana Vinuela, Alfonso Buil, Julian Knight, Mark I McCarthy, Kerrin Small and Jonathan Marchini. *Tensor decomposition and causal inference for multi-tissue gene expression experiments.*
- 11:50-11:55 **Spotlight** - Aziz M. Mezlini, Fabio Fuligni, Adam Shlien and Anna Goldenberg. *Disease mechanism discovery by integrating exome and gene expression datasets in one graphical model of disease.*

12-1 Posters/snacks

Lunch break/Posters (1 - 14.30)

Afternoon session I (14.30 - 16.00)

- 14:30-15:15 **Keynote** - Dana Pe'er - *A geometric approach to cellular phenotypes.*
- 15:15-15:35 **Talk** - Kieran Campbell and Chris Yau. *Bayesian Gaussian Process latent variable models for pseudotime inference in single-cell RNA-seq data.*
- 15:35-15:55 **Talk** - Javier Gonzalez, Joseph Longworth, Joselin Noirel, Paul Dobson, Mark Dickman, David James and Neil Lawrence - *In Silico Design of Synthetic Genes for Total Cell Translation Control: a Multi-output Gaussian Processes approach.*

Afternoon coffee break (16.00 - 16.30)

- 16:30-17:15 **Keynote** - Barbara Engelhardt - *Bayesian structured sparsity using Gaussian fields.*
- 17:15-17:35 **Talk** - Dinu Kaufmann, Sebastian Keller and Volker Roth. *Copula Archetypal Analysis*
- 17:35-17:55 **Talk** - Adam Arany, Jaak Simm, Pooya Zakeri, Tom Haber, Jörg K. Wegner, Vladimir Chupakhin, Hugo Ceulemans and Yves Moreau. *Highly Scalable Tensor Factorization for Prediction of Drug-Protein Binding Modes.*
- 17:55-18:15 **Talk** - Tzu-Yu Liu and Yun Song. *Prediction of Ribosome Footprint Distributions from Transcript Sequences via Multiresolution Analysis.*
- 18:15-18:30 **Panel discussion** - Announcement of the new "DREAM Idea Challenge".