CDCS CENTER FOR DATA AND COMPUTING IN NATURAL SCIENCES

## **OPENING SYMPOSIUM 2022**







Contribution ID: 61

Type: Poster

## De-novo reconstruction and identification of transcriptional gene regulatory network modules differentiating single-cell clusters

Single-cell RNA sequencing (scRNA-seq) technology provides an unprecedented opportunity to understand gene functions and interactions at single-cell resolution. Various computational methods have been developed for differential expression and co-expression analysis in scRNA-seq data. However, little attention has been paid to differential co-expression analysis that potentially holds valuable insights that facilitate understanding disease mechanisms and underlying regulatory dynamics. Here we propose a new de novo reconstruction and identification of transcriptional gene regulatory network modules differentiating cell clusters (DiNiro) to accurately identify gene modules that exhibit varying regulatory patterns across cell clusters in single-cell RNA-sequencing data by capturing the variation in co-expression patterns based on gene expression profiles. Our method can determine small regulatory mechanisms underlying diseases or cellular programs that govern disease progression. Consequently, DiNiro is closing the gap between single-cell expression analysis and systems medicine by providing a tool for the reconstruction of predictive gene regulatory disease programs de novo directly from scRNAseq data. DiNiro is available at https://exbio.wzw.tum.de/diniro/.

**Primary author:** Mr OUBOUNYT, Mhaned (Chair of Computational Systems Biology, University of Hamburg, Hamburg, Germany)

**Co-author:** Prof. BAUMBACH, Jan (Chair of Computational Systems Biology, University of Hamburg, Hamburg, Germany)

**Presenter:** Mr OUBOUNYT, Mhaned (Chair of Computational Systems Biology, University of Hamburg, Hamburg, Germany)

Session Classification: Poster session with buffet

Track Classification: CDL3 (Systems Biology)