







Online Symposium Minerva-Gentner Symposium 2020

Single Cell Analysis: from Development to Disease

Sunday May 31, 2020

10:00-14:25, German time (break 12:10-12:40) 11:00-15:25, Israel time (break 13:10-13:40)

Introduction: Karen B. Avraham, Tel Aviv University

Plenary speaker: **Eileen Furlong**, EMBL, Heidelberg: *Regulatory changes during embryogenesis as single cell resolution*

Session 1: Development Deciphered by Single Cell Analysis

Jan Philipp Junker, Max Delbrück Center for Molecular Medicine, Berlin: Simultaneous lineage tracing and transcriptome profiling in single cells

Shalev Itzkovitz, Weizmann Institute: *Spatial transcriptomics* of mammalian tissues

Dominic Grun, Max Planck Institute of Immunology and Epigenetics, Freiburg: A human liver cell atlas: revealing cell type heterogeneity and adult liver progenitors by single-cell RNA-sequencing

Simon Haas, Heidelberg Institute for Stem Cell Technology and Experimental Medicine: *Mapping blood stem cell commitment at the single cell level*

Ron Shamir, Tel Aviv University: Proliferation and differentiation in early embryonic lineages

Session 2: Genomics in Single Cell Analysis and Technologies

Shai Shen-Orr, Technion: Modeling biological processes as

Monday June 1, 2020

10:00-14:20, German time (break 12:05-12:35) 11:00-15:20, Israel time (break 13:05-13:35)

Introduction: Omri Wurtzel, Tel Aviv University

Session 3: From Populations to Cellular Dynamics

Naomi Habib, Hebrew University: Deciphering the cellular landscape of the Alzheimer's brain by single nucleus RNA-seq

Oren Ram, Hebrew University: Code of early differentiation using high sensitive single cell assays

Efrat Shema, Weizmann Institute: Single-cell and singlemolecule epigenomics: genome-regulation at unprecedented resolution

Gerd Meyer zu Horste, Westfälische Wilhems-University, Münster: Applying single cell transcriptomics to cerebrospinal fluid cells in neurological disorders

Asaf Madi, Tel Aviv University: Single cell T-cell exhaustion and checkpoint blockade immunotherapy

Itay Tirosh, Weizmann Institute: Charting human tumors by single cell RNA sequencing

Session 4: Disease Mechanisms by Single Cell Analysis

Nir Friedman, Hebrew University: Single cell genomics of single cell organisms

Naama Geva-Zatorsky, Technion: The undisclosed interactions with our tiniest gut residents

quantifiable units

Tal Shay, Ben-Gurion University: Splicing bias of single immune cells

Martin Vingron, Max Planck Institute for Molecular Genetics: Looking at high-dimensional data using correspondence analysis

Micha Drukker, Helmholtz Zentrum München: *BART-seq*: cost-effective massively parallel targeted sequencing for genomics and transcriptomics

Ran Elkon, Tel Aviv University: Inference of cell types involved in the pathology of complex diseases using single-cell transcriptomes

Closing for the day: Omri Wurtzel, Tel Aviv University

Daniel Lipka, DFKZ German Cancer Research Center, Heidelberg: Single cell transcriptomics and epigenomics allow

the dissection of cellular hierarchies and disease mechanisms in hematopoiesis

Merav Cohen, Weizmann Institute, Tel Aviv University: Molecular insight into cellular crosstalk during development and disease

Tomer Kalisky. Bar-Ilan University: Cellular heterogeneity and splice isoform switching in kidney development and tumorigenesis

Closing the symposium: **Karen Avraham**, Tel Aviv University





For more details

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