

Genomics - One Cell at A Time

Opening of the Single Cell Analysis Core

October 22-23, 2017

Symposium: Sunday, October 22

Yaglom Senate Hall

10:00 - 10:45

Special seminar

Oliver Hobert, Columbia University & HHMI:
Organizational principles of *C. elegans* nervous
system development

11:00 – 15:30

Plenary speaker

Sarah Teichmann, European Bioinformatics
Institute, EMBL-EBI:
Immunogenomics one cell at a time

Hila Sharim (Ebenstein lab), TAU: Single-
molecule genome mapping of
5-hydroxymethylcytosine allows single cell like
population clustering

Amos Tanay, WIS:
Single cell epigenomics and epigenetic memory

Franziska Paul (Amit lab), WIS:
Single cell genomic analysis of hematopoietic
progenitors: Towards a refined model of
hematopoiesis

Oren Ram (HUJI):
From single cells to clones: Advances in droplet-
based microfluidics

Workshop: Monday, October 23

Workshop on scRNA-seq
Katzir Hall – Green building,
Faculty of Life Sciences

9:15 – 13:00

PRE-REGISTRATION REQUIRED, space limited

Aaron Lun, European Bioinformatics Institute,
EMBL-EBI:

Computational analysis of single-cell RNA-seq data:
challenges, solutions and opportunities

Aaron Lun:

Technical details of single-cell RNA-seq data
(practical session)

Yael Steurman, (Gat-Viks lab), TAU:

In silico cell annotation of single-cell RNA-seq
data (practical session)

Irit Gat-Viks, TAU:

Deconvolution analysis with single cell RNA-seq
data

Registration for workshop only: [https://en-
med.tau.ac.il/biomed_tau/register](https://en-med.tau.ac.il/biomed_tau/register)

Organizers: Karen Avraham, Yuval Ebenstein,
Irit Gat-Viks, Lior Mayo, Anat Moshayov,
Naomi Caplan, Oded Rechavi