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
Sackler School of Medicine building,
Floor 9, room 936

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 Steuerman, (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

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