

# 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** (Yuval 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** (Ido 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

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