

Wednesday  
March 11, 2022  
15.00 (GMT+1)

The seminar will be held on line. Please register at <https://bit.ly/3BZcq2l>

You will receive an invite with the link to the seminar.  
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## Computational and Quantitative Biology Lecture Series



**Itay Tirosh**

Dept. of Molecular Cell Biology,  
Weizmann Institute of Science

### Dissecting glioblastoma by single cell RNA-seq

Cellular heterogeneity is a fundamental property of glioblastoma that represents a central barrier for effective therapies. I will present our studies of glioblastoma by single cell RNA-seq, in which we focus on the malignant cells, define their diversity of cellular states and explore the mechanisms that generate heterogeneity and its functional significance. We find that glioblastoma tumors consistently contain cells in four cellular state and that all four are proliferative and have previously been proposed to reflect glioma stem cells. These four states recapitulate expression programs from neural development as well as a mesenchymal-like state. We demonstrate a high degree of cellular plasticity, in which cells rapidly transition between those states and we further examine the role of macrophages in driving transitions towards the mesenchymal state through secretion of Oncostatin M. These results revise our understanding of glioblastoma, explain the basis for previously defined subtypes, and suggest that future therapies will have to co-target multiple cellular states in order to improve patient survival.

**Itay Tirosh** obtained his PhD from the Weizmann Institute of Science in the area of computational biology. From 2012 to 2017 he was a postdoctoral fellow at the Regev and Golub labs at the Broad Institute of MIT and Harvard, and since August 2017 he is a Senior Scientist at the Weizmann Institute of Science. The Tirosh lab is combining computational approaches and experimental single cell methods to understand the diversity of cells within human tumors, with a focus on glioma.

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