Wednesday
March 23, 2022
15.00 (GMT+1)

Computational and Quantitative Biology Lecture Series

The seminar will be held on line. Please register at https://bit.ly/3u53chQ

You will receive an invite with the link to the seminar.
Visit https://cqb.dieti.unina.it/index.php/events for the event series.

Oliver Stegle
German Cancer Research Center (DKFZ) Germany

Computational single-cell biology - from one to many cells

Technological advances have enabled assaying molecular variation at the single-cell level, both at the RNA level but increasingly across a growing range of molecular layers and most recently in spatial contexts. In this talk, I will provide an overview of recent advances in single-cell biology, where I describe novel assays and computational methods for unravelling molecular changes across multiple omics layers in the same cells. In the second part of the talk I will highlight novel opportunities for the application of single-cell technologies for assaying regulatory effects of human disease variants with single-cell resolution.

Oliver Stegle is the Head of the Computational Genomics and Systems Genetics Division at the German Cancer Research Center (DKFZ) and group leader at EMBL in Heidelberg, Germany.
His group's main interest lies in computational methods to unravel the genotype–phenotype map on a genome-wide scale. To address this question, the team carries out research at the interface of statistical inference, machine learning and computational biology, pioneering computational methods for integrating large and heterogeneous datasets across individual and at the single-cell level. The methods and models they develop allow for tying together molecular changes with genetic variation and disease phenotypes and are applied in the context of important studies. Their most recent advances are in the area of single-cell genomics, deriving approaches both for interpreting conventional single-cell RNA-seq variability as well for the analysis of data from spatial technologies. A current direction in the lab is to extend the boundaries of single-cell analysis to integrate single-cell RNA-seq with somatic mutations and clonal substructure in tissues. Oliver obtained his PhD from the University of Cambridge in Physics in 2009 and worked as a postdoc at the Max Planck Institute for Intelligent Systems in Tübingen. He was a group leader at the EMBL European Bioinformatics before moving to Heidelberg in 2018, where he obtained a full professorship (W3) at Heidelberg University in 2020. He has received several recognitions, coordinates the ELLIS Health program and is an ERC investigator.

With the contribution of:

Hosted by: