Robust differential composition and variability analysis for multisample cell omics

A seminar by Stefano Mangiola

WEHI – Walter Eliza Hall Institute of Medical Research – Australia

Thursday 21 Apr 2022 | 12:30 p.m.
Room SC60 and live Zoom
Department of Statistical Sciences

Cell omics such as single-cell genomics, proteomics and microbiomics allow the characterisation of tissue and microbial community composition, which can be compared between conditions to identify biological drivers. This strategy has been critical to unveiling markers of disease progression such as cancer and pathogen infection. For cell omic data, no method for differential variability analysis exists, and methods for differential composition analysis only take a few fundamental data properties into account. Here we introduce sccomp, a generalised method for differential composition and variability analyses able to jointly model data count distribution, compositionality, group-specific variability and proportion mean-variability association, with awareness against outliers. Sccomp is an extensive analysis framework that also allows realistic data simulation and cross-study knowledge transfer.

8OO
1222·2022
ANNI

UNIVERSITÀ
DEGLI STUDI
DI PADOVA

DIPARTIMENTO
DI SCIENZE
STATISTICHE