Contribution ID : **34** Type : **not specified**

A fast variational algorithm to detect the clonal copy number substructure of tumors from single-cell data

lunedì 28 febbraio 2022 15:10 (10)

Understanding intratumor heterogeneity and the interactions between tumor cells and the immune system is the critical step in the study of tumor growth and evolution. Typically in these studies a large number of unsorted cells from tumor biopsies are subject to Single-cell RNA sequencing (scRNA-seq) and then classified as malignant cells, stromal cells, and immune cells.

The distinction of malignant from non-malignant cells is a key step in the follow-up analysis of scRNA-seq tumo

The main drawback is that the clusters of reference non-malignant cells require manual identification, and rece

We have developed Single CEll Variational ANeuploidy analysis (SCEVAN). It uses a multichannel segmentation al

We apply SCEVAN to several datasets encompassing 106 samples and 93,322 cells from different tumors types and t

SCEVAN is available in open source as an R package at the following address \textbackslash{}href\{https://gi

Department

DIETI

Primary author(s) : Mr. DE FALCO, Antonio (University of Naples Federico II (DIETI) & BIOGEM Institute of Molecular Biology and Genetics, 83031 Ariano Irpino, Italy); Mr. IAVARONE, Antonio (Institute for Cancer Genetics, Columbia University, 1130 St Nicholas Ave, New York, NY 10032, USA); Ms. CARUSO, Francesca (Department of Electrical Engineering and Information Technology (DIETI) & BIOGEM Institute of Molecular Biology and Genetics, 83031 Ariano Irpino, Italy); Prof. CECCARELLI, Michele (University of Naples, Federico II); Mr. SU, Xiao-Dong (Biomedical Pioneering Innovation Center (BIOPIC), School of Life Sciences, Peking University, 5 Yiheyuan Rd, Haidian District, 100871 Beijing, China)

Presenter(s) : Mr. DE FALCO, Antonio (University of Naples Federico II (DIETI) & BIOGEM Institute of Molecular Biology and Genetics, 83031 Ariano Irpino, Italy)