

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

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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 tumors.

The main drawback is that the clusters of reference non-malignant cells require manual identification, and recent methods are not able to handle large datasets.

We have developed Single Cell Variational ANeuploidy analysis (SCEVAN). It uses a multichannel segmentation algorithm to identify malignant cells.

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

SCEVAN is available in open source as an R package at the following address [\textbackslash{}href\{\{https://github.com/antoniofalco/scevan\}](https://github.com/antoniofalco/scevan)

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