The TAVNIT1.0 pipeline (Hebrew *tavnit* – pattern) is dedicated to cancer subtyping and subsequent subtype signature extracting. The pipeline compares cancer and non-cancer samples to extract quantified signatures that strictly detach cancer subtypes from all non-cancer cells. The signatures describe shifts in transcription levels in different cancers. The goal is to use these signatures as targets for cancer drugs.

The pipeline is based on two algorithms: the Constrained–Divisive algorithm for hierarchical clustering and Tjala (an Ant Colony Optimization [ACO] algorithm) for extracting signatures of hierarchical clusters. The Constrained–Divisive algorithm was developed by Kestler et al. [1]. Tjala is inspired by the ℎ𝑚AntMinerorder [2] and Ant-Miner [3] algorithms.

The clustering package consumes transcriptomic data from cancer and non-cancer samples. Notably, cancer and non-cancer samples can be prelabeled to cluster them apart. The clustering output is the input for signature extraction. The signatures describe the transcription levels of a number of genes to outline a number of samples. The signatures can be extracted for whole cells or for surfaceome only. An advantageous strategy is “sufaceome-only signatures from all-genes-included clustering.” The surfaceome signatures can be used as targets for surface-recognizing gated drugs (e.g., CR-cells).

Future prospects include the following:

- the implementation of specific omic distance metrics [4,5]

- the assessment of clustering quality

- the implementation of more options for term selection [6]

(N.B. “Term” is a “brick” for building signatures.)

- the assessment of the applicability of the signatures for real-world drug design.

In addition to the people whose ideas directly served as the foundation for this pipeline, Dr. Marco Dorigo, the creator of ACO [7], and those who developed the applications of ACO and hierarchical multilabel classification in biology [for a review, see 8], are deeply appreciated.

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