Platform enables comparative research on cancerous tumors

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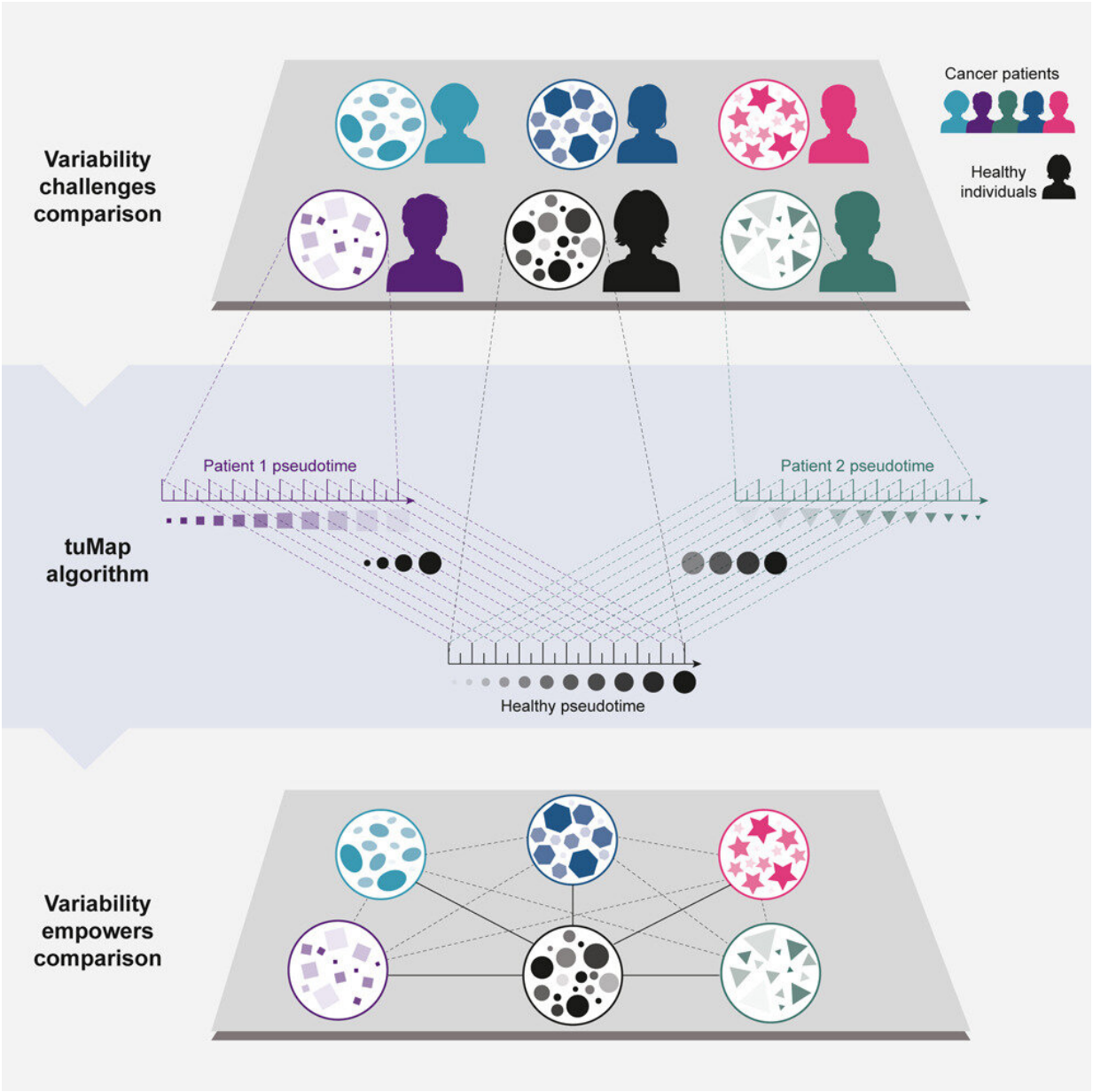

Graphical abstract. Credit: DOI: 10.1016/j.cels.2021.09.003

Researchers at the Technion-Israel Institute of Technology's Rappaport Faculty of Medicine have developed an innovative algorithm that detects an uninterrupted common denominator in multidimensional data gathered from tumors of different patients. The study, which was published in *Cell Systems*, was led by Professor Shai Shen-Orr, Dr. Yishai Ofran, and Dr. Ayelet Alpert, and conducted in collaboration between researchers at the Technion, the Rambam Health Care Campus, the Shaare Zedek Medical Center, and the University of Texas.

In recent years, cancer research has undergone a series of significant revolutions, including the introduction of single-cell high-resolution characterization capabilities, or, more specifically, simultaneous high-throughput profiling of cancer samples using single-cell RNA sequencing and proteomics analysis. This has led to the generation of vast quantities of multidimensional data on a huge number of cells, allowing for the characterization of both the healthy tissue and malignant tissues. This high amount of data has revealed the great variability between tumors of different patients, where cellular characterization that is derived from the patient's genetic background is unique to each patient.

Despite the substantial advantage that is derived from such an accurate characterization of the specific patient, this development hinders comparison of different patients: in the absence of a common denominator, the comparison, which is essential for identifying prognostic markers (e.g. mortality or severity of illness), becomes impossible.

The tuMap algorithm developed by the Technion researchers provides a

solution to this complex challenge by means of a "variance-based comparison." The innovative algorithm delivers the possibility to place numerous different tumors on a uniform scale that provides a benchmark for comparison. In this way, the tumors of different patients can be meaningfully compared, as well as tumors of the same patient over the disease course (for example, on diagnosis and after treatment). The resolution provided by the algorithm can be leveraged for clinical applications such as prediction of various clinical indices with a very high accuracy, outperforming traditional tools. Although the researchers tested the algorithm on leukemia tumors, they believe that it will also be relevant for other cancer types.

More information: Ayelet Alpert et al, Alignment of single-cell trajectories by tuMap enables high-resolution quantitative comparison of cancer samples, *Cell Systems* (2021). DOI: 10.1016/j.cels.2021.09.003

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