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^{OA}Open Access paper



Cover Central questions in human biology and medicine are questions about the human cell lineage tree: its structure, dynamics, and variance during development, aging, disease progression, and in response to therapy. In this issue, a new study presents a platform for generic single-cell lineage analysis that is cost-effective, scalable and, being retrospective, applicable to human analysis. It consists of an integrated biochemical-computational pipeline that inputs individual cells, produces targeted single-cell sequencing data, and uses it to reconstruct the lineage tree of the input cells. The illustration presents an artistic abstraction of the presented platform as a low-tech machine that inputs cells and outputs their corresponding lineage. (Cover illustration by Mayan Vigelman, Design, Photography and Printing branch, Weizmann Institute of Science, 2016. [For details, see Biezuner et al., pp. 1588–1599.])