CellTrans: An R package to quantify stochastic cell state transitions

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Many normal and cancerous cell lines exhibit a stable composition of cells in distinct states. There is evidence that such an equilibrium is associated with stochastic transitions between the distinct states. Quantifying these transitions has the potential to better understand cell lineage compositions. We introduce CellTrans, an R package to quantify stochastic cell state transitions from fluorescence activated cell sorting (FACS) and flow cytometry experiments. The key assumption of the mathematical model underlying CellTrans is that cell state alterations are caused by stochastic transitions between distinct cell states which only depend on the current state of a cell. We explain how CellTrans deals with analytical challenges in the quantification of these cell transitions. The applicability of CellTrans is demonstrated on publicly available data of the evolution of cell state compositions in cancer cell lines. We show that CellTrans can be utilized to (i) infer the transition probabilities between different cell states, (ii) predict cell line compositions at a certain time, (iii) predict equilibrium cell state compositions, and (iv) estimate the time needed to reach this equilibrium.