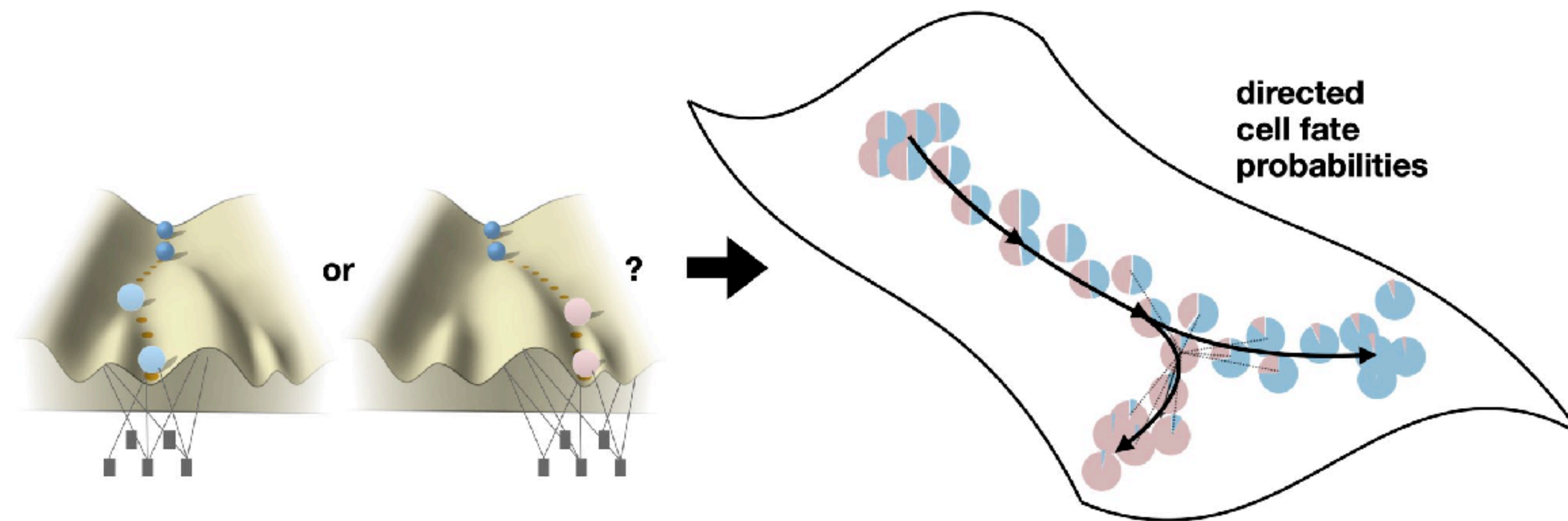


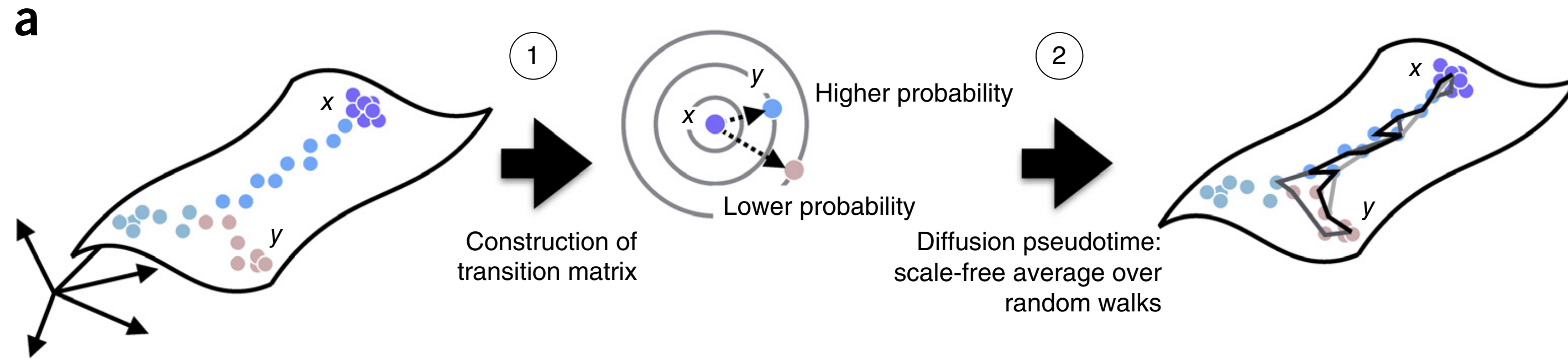
CellRank for directed single-cell fate mapping

Marius Lange^{1,2}, Volker Bergen^{1,2}, Michal Klein¹, Manu Setty³, Bernhard Reuter^{4,5}, Mostafa Bakhti^{6,7}, Heiko Lickert^{6,7}, Meshal Ansari^{1,8}, Janine Schniering⁸, Herbert B. Schiller⁸, Dana Pe'er^{3*}, Fabian J. Theis^{1,2,9*}

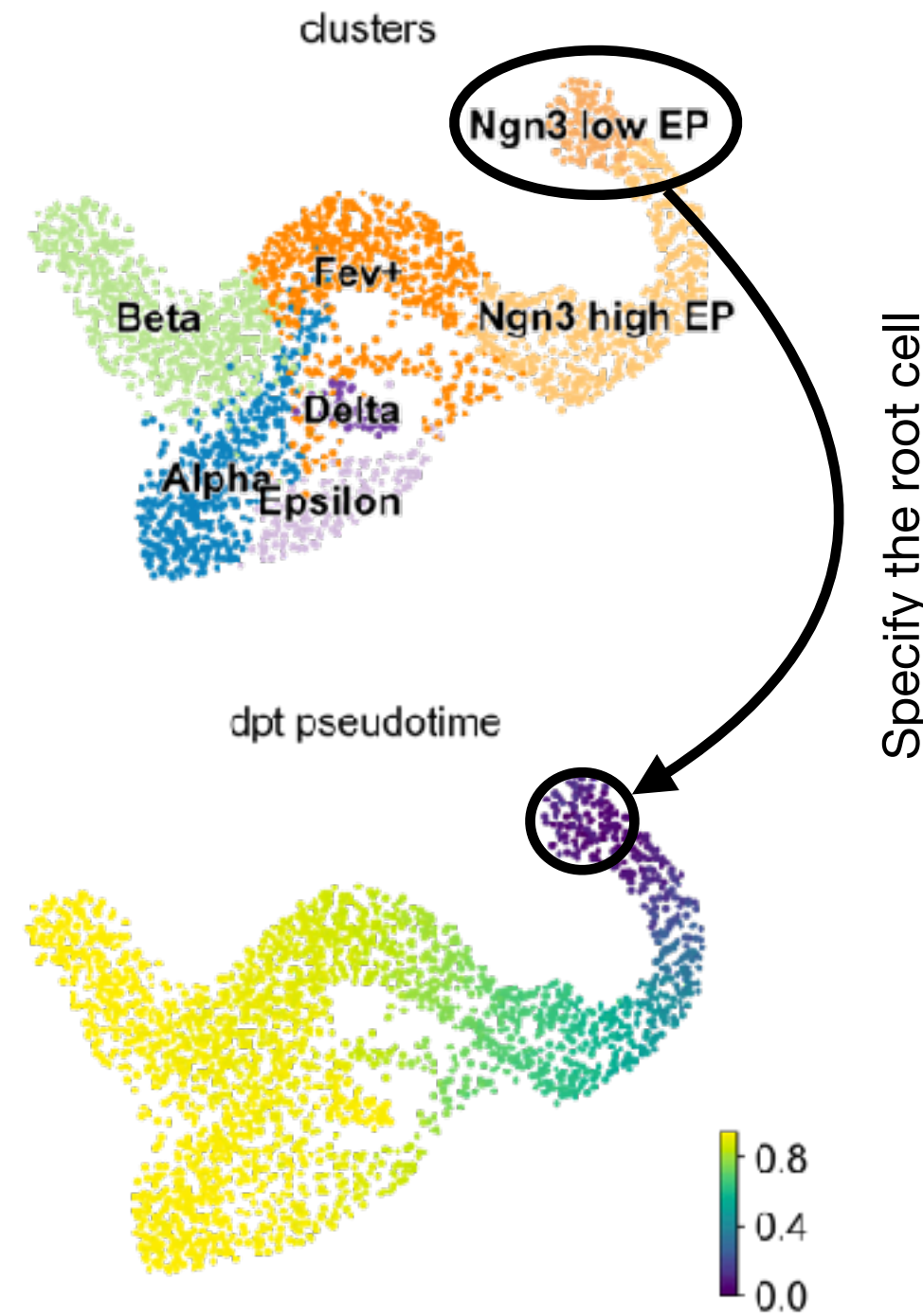
Institute of Computational Biology, Institute of Diabetes and Regeneration Research and Institute of Lung Biology and Disease @ Helmholtz Munich, Program for Computational and Systems Biology @ MSKCC New York, Department of Computer Science @ University of Tübingen



Single cell RNA-seq and computational tools uncover lineage relationships



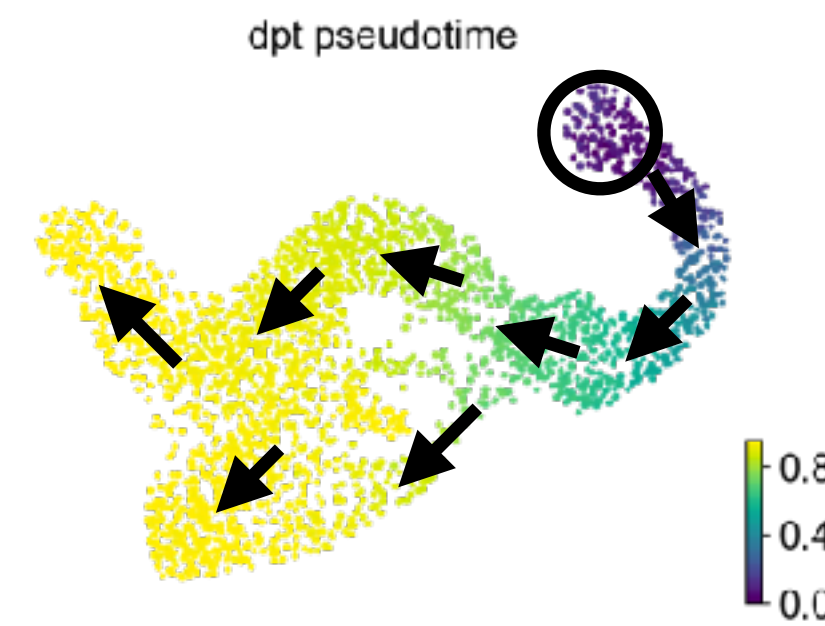
Works **really** well for normal development



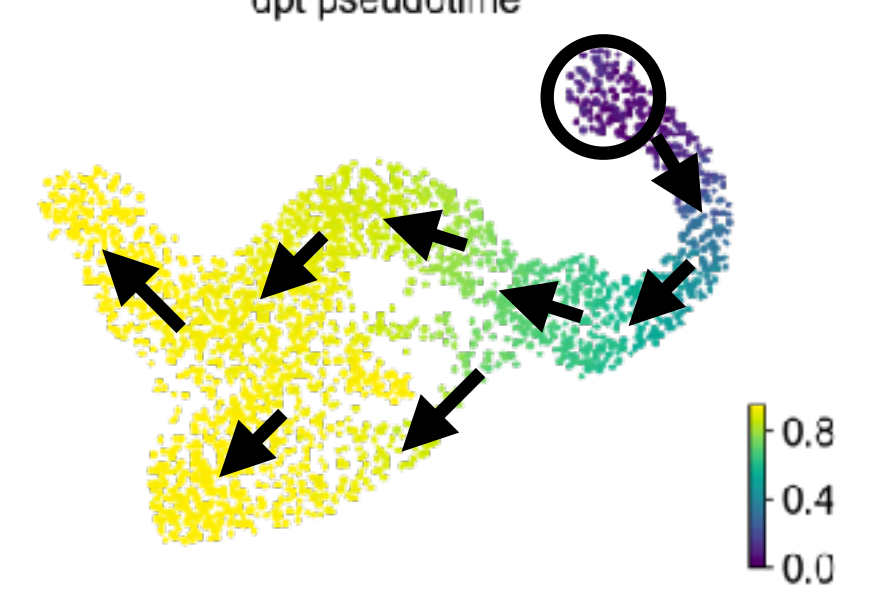
perturbed conditions
regeneration, reprogramming, etc

Challenges under **perturbed** conditions

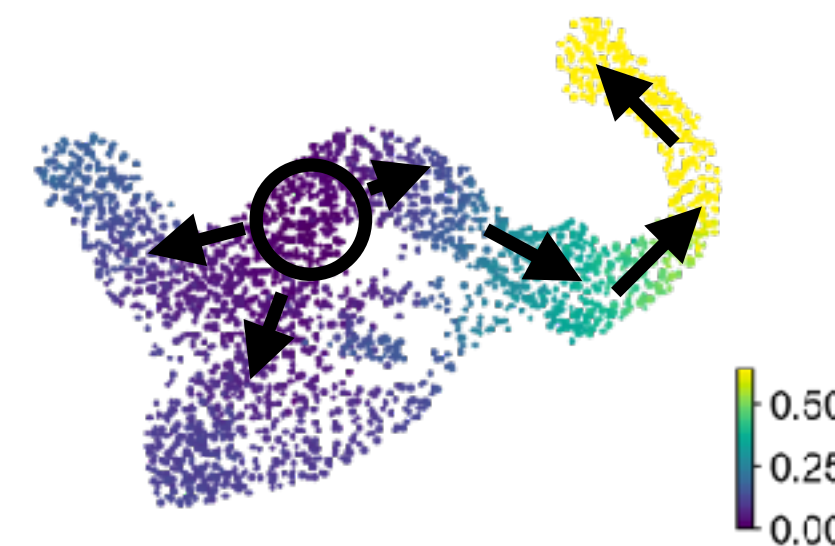
Uncertain initial/terminal states



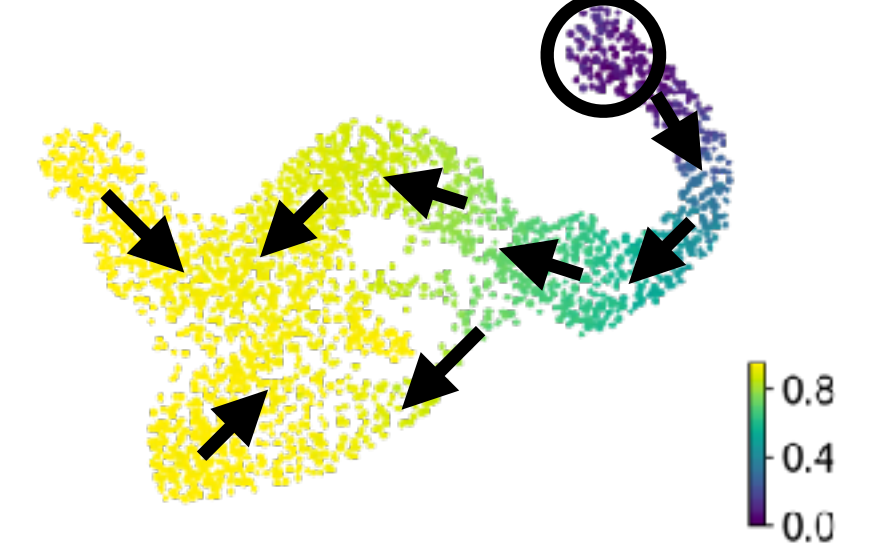
Uncertain directions



or



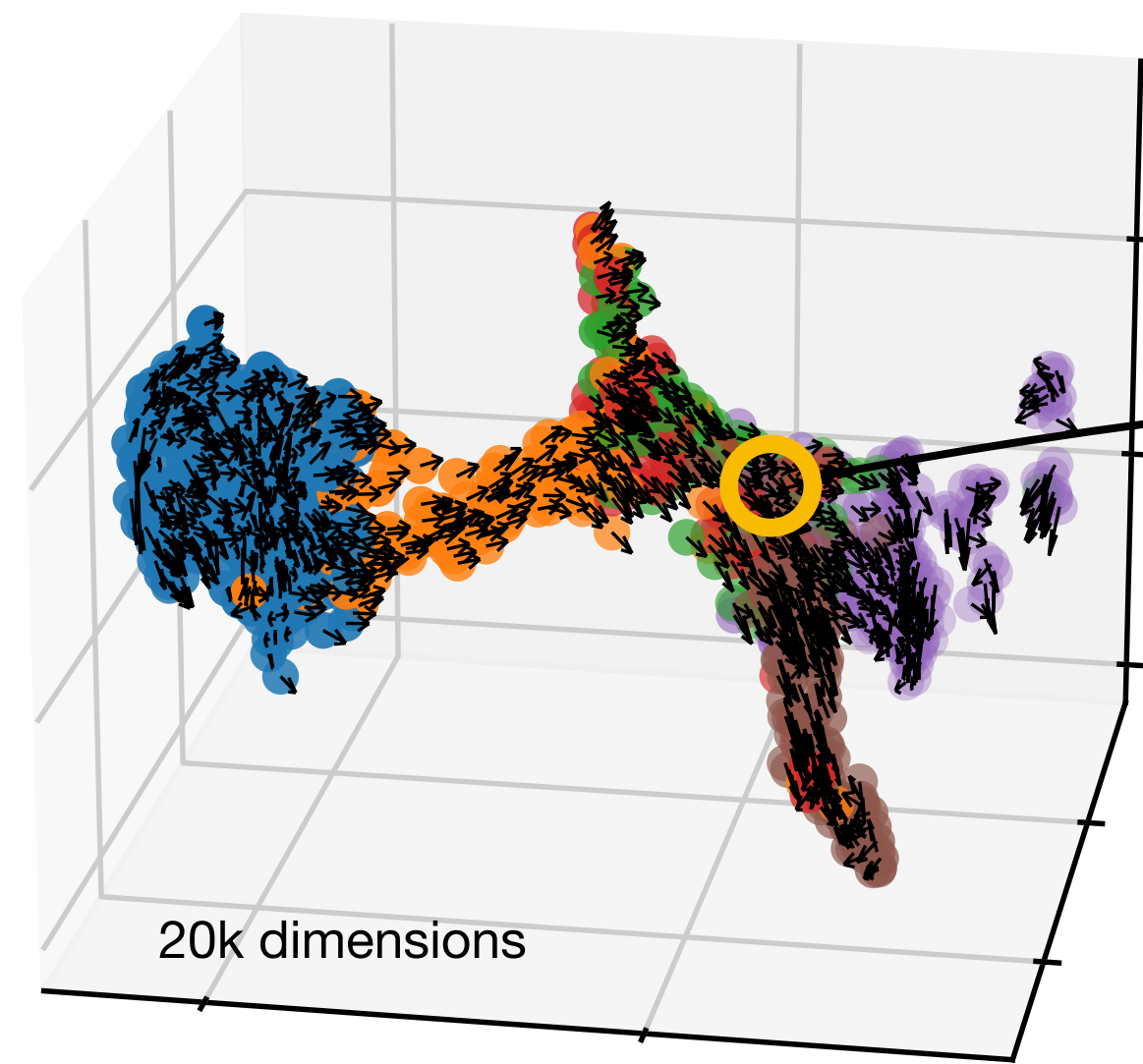
or



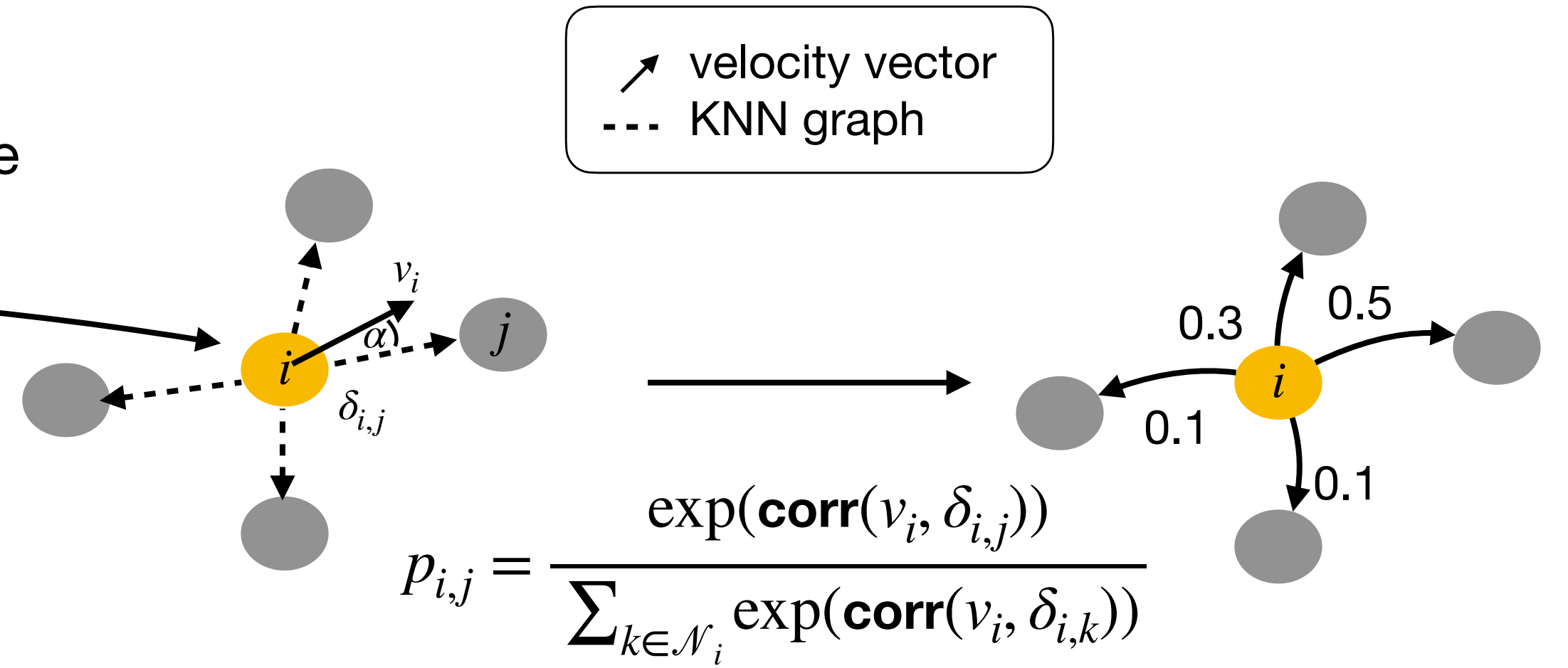
Top panel taken from Haghverdi et al., Nature Methods (2016)

Data from Bastidas-Ponce et al., Development (2019)

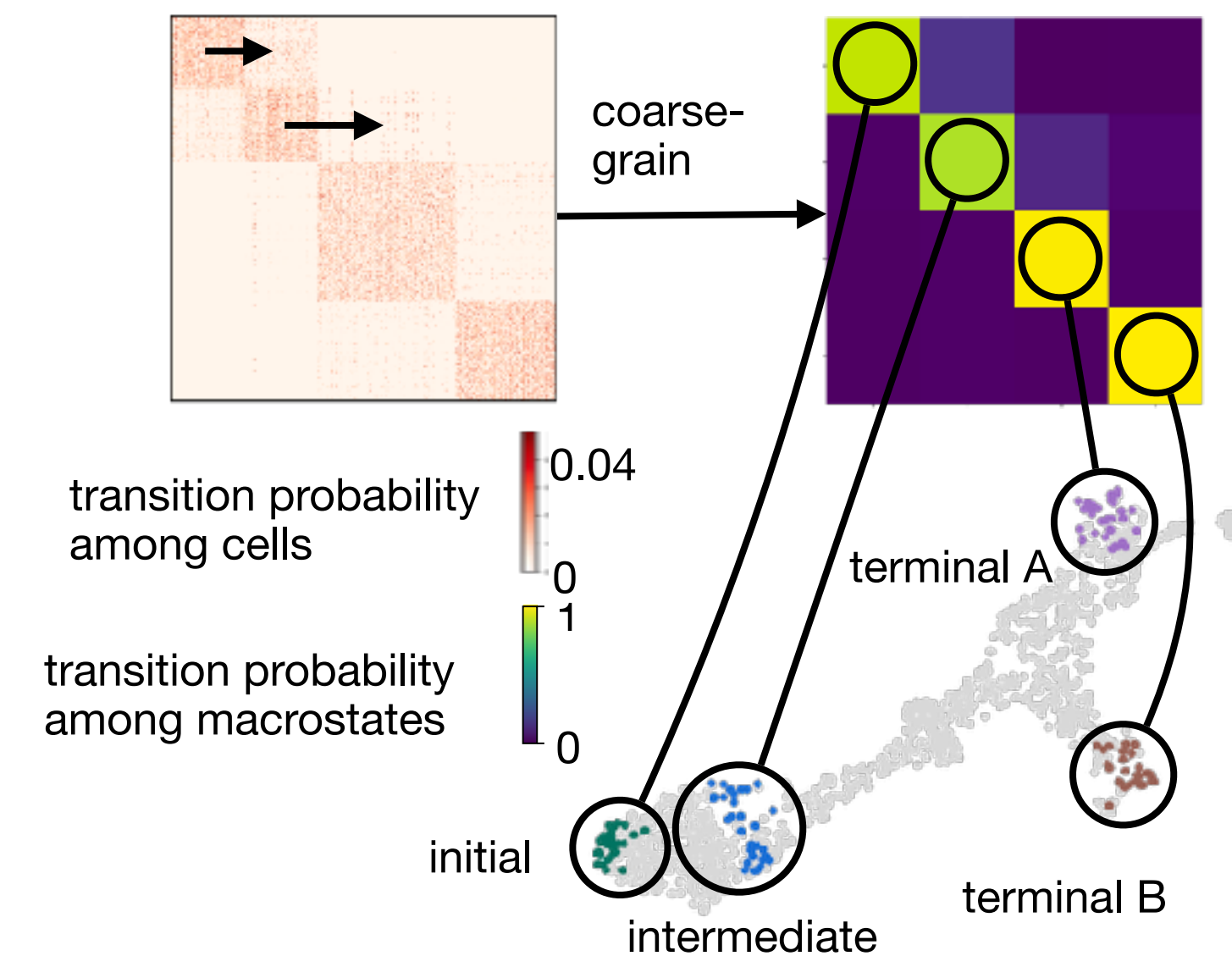
CellRank combines RNA Velocity with transcriptomic similarity to robustly model cellular fate establishment



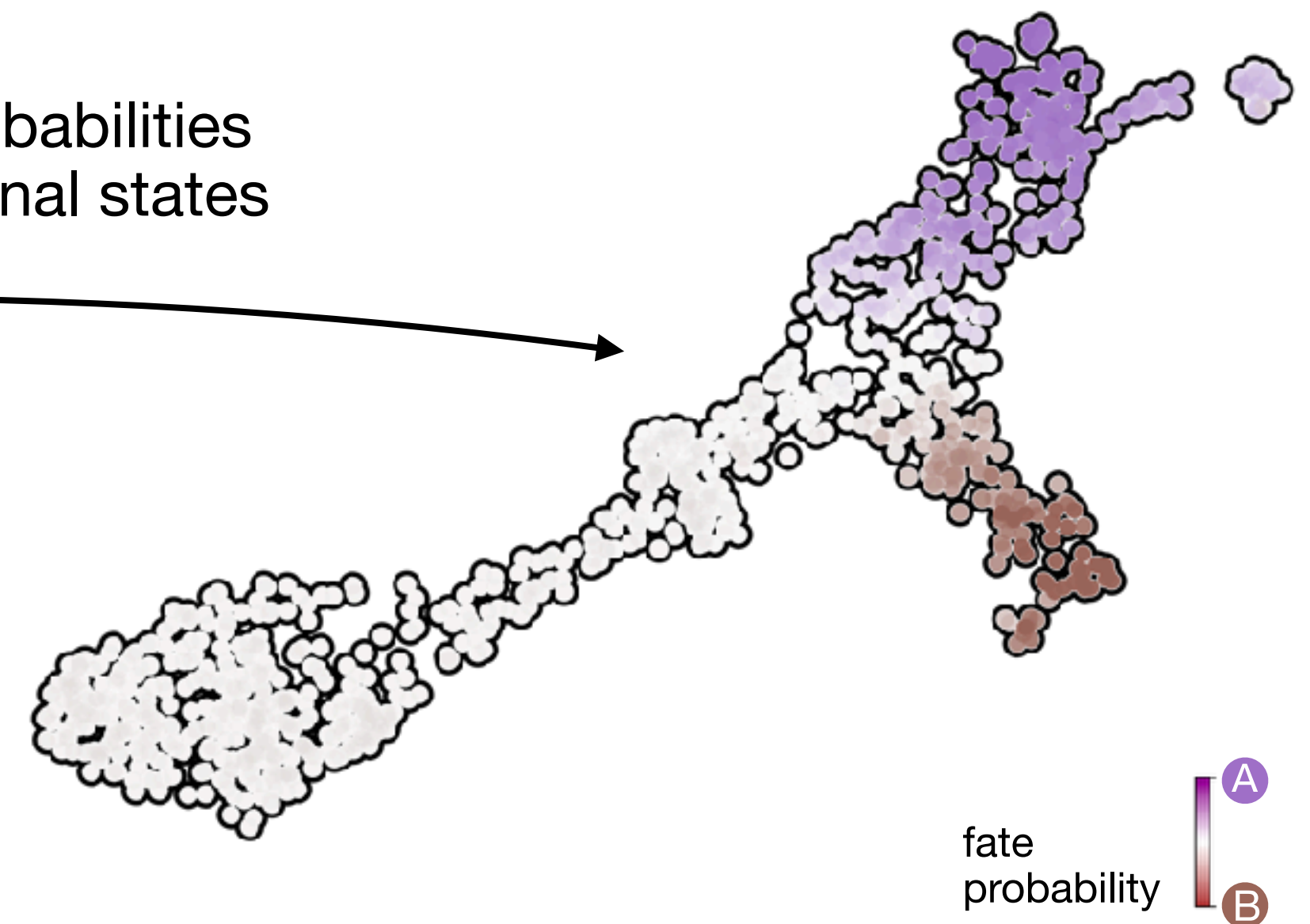
for each cell i , combine velocity with similarity to define transition probabilities



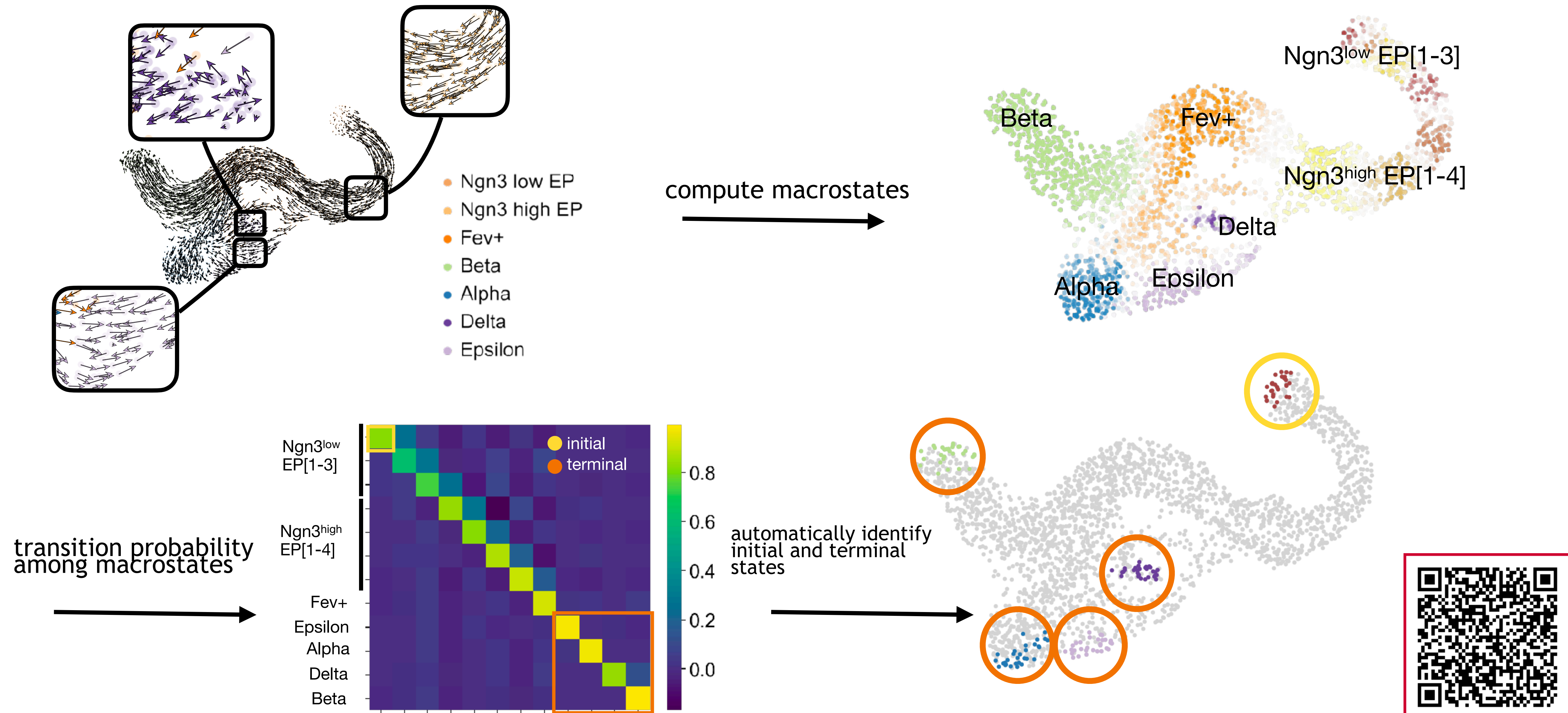
Coarse-grain the large transition matrix to reduce the system to its essence



Compute fate probabilities towards the terminal states



CellRank delineates fate choice in pancreatic development



Please see our manuscript for the full story!



10.1101/2020.10.19.3

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