## Nested Stochastic Block Models Applied to the Analysis of Single Cell Data

Leonardo Morelli<sup>1,2</sup>, Valentina Giansanti<sup>1,3</sup>, and Davide Cittaro<sup>1</sup>

<sup>1</sup>Center for Omics Sciences, IRCCS San Raffaele Institute, Milan, Italy
<sup>2</sup>Università Vita-Salute San Raffaele, Milan, Italy
<sup>3</sup>Department of Informatics, Systems and Communication, University of Milano-Bicocca, Milan, Italy

April 15, 2021

## Supplementary figures

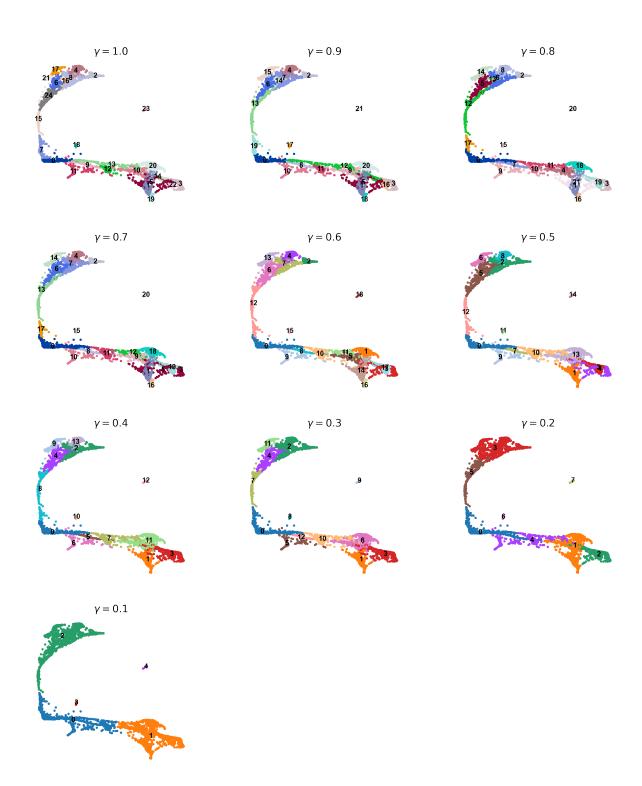


FIGURE S1: Low dimension embedding of single cells for hematopoietic differentiation colored according to Leiden clustering at decreasing resolution, from 1.0 to 0.1. Lowering the distribution does not grant that cells are grouped in a hierarchical way, e.g. in the Erythroid branch groups 7 and 15 at resolution r=1 are merged or split at coarser resolutions ( $\gamma=0.6$  and  $\gamma=0.3$ )

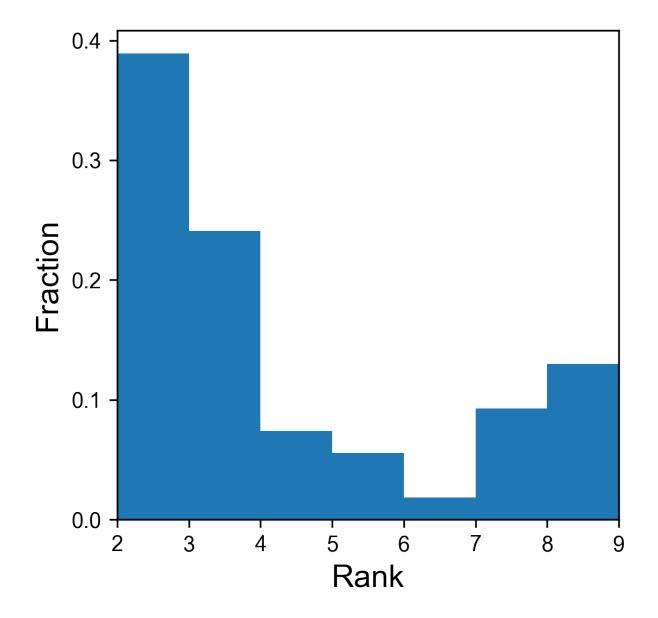


FIGURE S2: TO BE WRITTEN