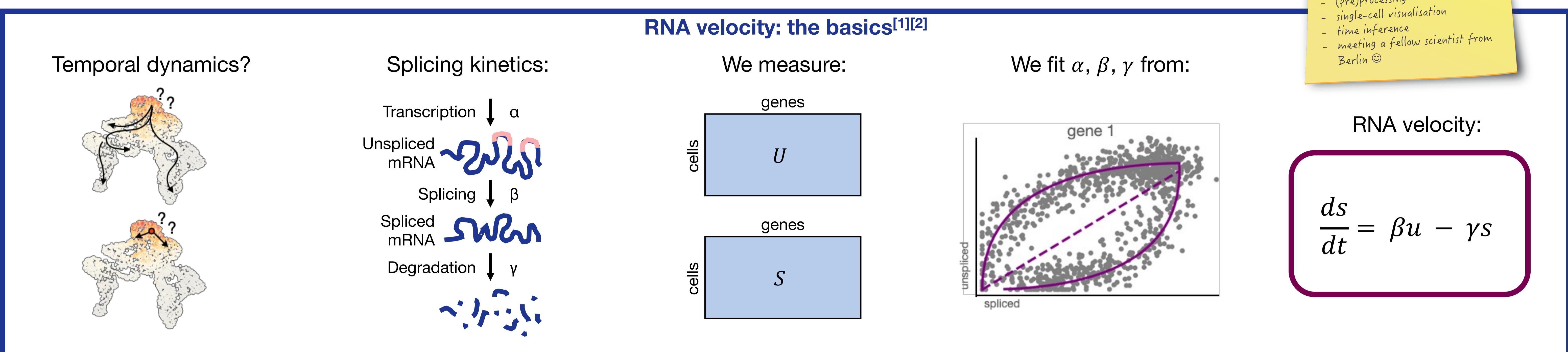


# K-velo improves single-cell RNA-velocity estimation

Brigitte Joanne Bouman<sup>1,2,\*</sup>, Valérie Marot-Lassauzaie<sup>1,3,\*</sup>, Fearghal Declan Donaghy<sup>1</sup>, Yasmin Demerdash<sup>4</sup>, Marieke Alida Gertruda Essers<sup>4</sup> and Laleh Haghverdi<sup>1</sup>

\*These authors contributed equally to this work.  
 1 Berlin Institute for Medical Systems Biology, Max Delbrück Center in the Helmholtz Association, Berlin, Germany  
 2 Humboldt Universität zu Berlin, Institute for Biology, Berlin, Germany  
 3 Charité – Universitätsmedizin Berlin, Berlin, Germany  
 4 Division Inflammatory Stress in Stem Cells, German Cancer Research Center (DKFZ), Heidelberg, Germany

This poster could be interesting for you if you like:  
 - RNA velocity  
 - dynamics in single-cell datasets  
 - (pre)processing  
 - single-cell visualisation  
 - time inference  
 - meeting a fellow scientist from Berlin ☺



## Scale invariance

Solution  $(\alpha, \beta, \gamma)$  is not unique:  $(\kappa\alpha, \kappa\beta, \kappa\gamma)$  is a solution for any  $\kappa$ . We need to find real scaling parameter  $\kappa$ .

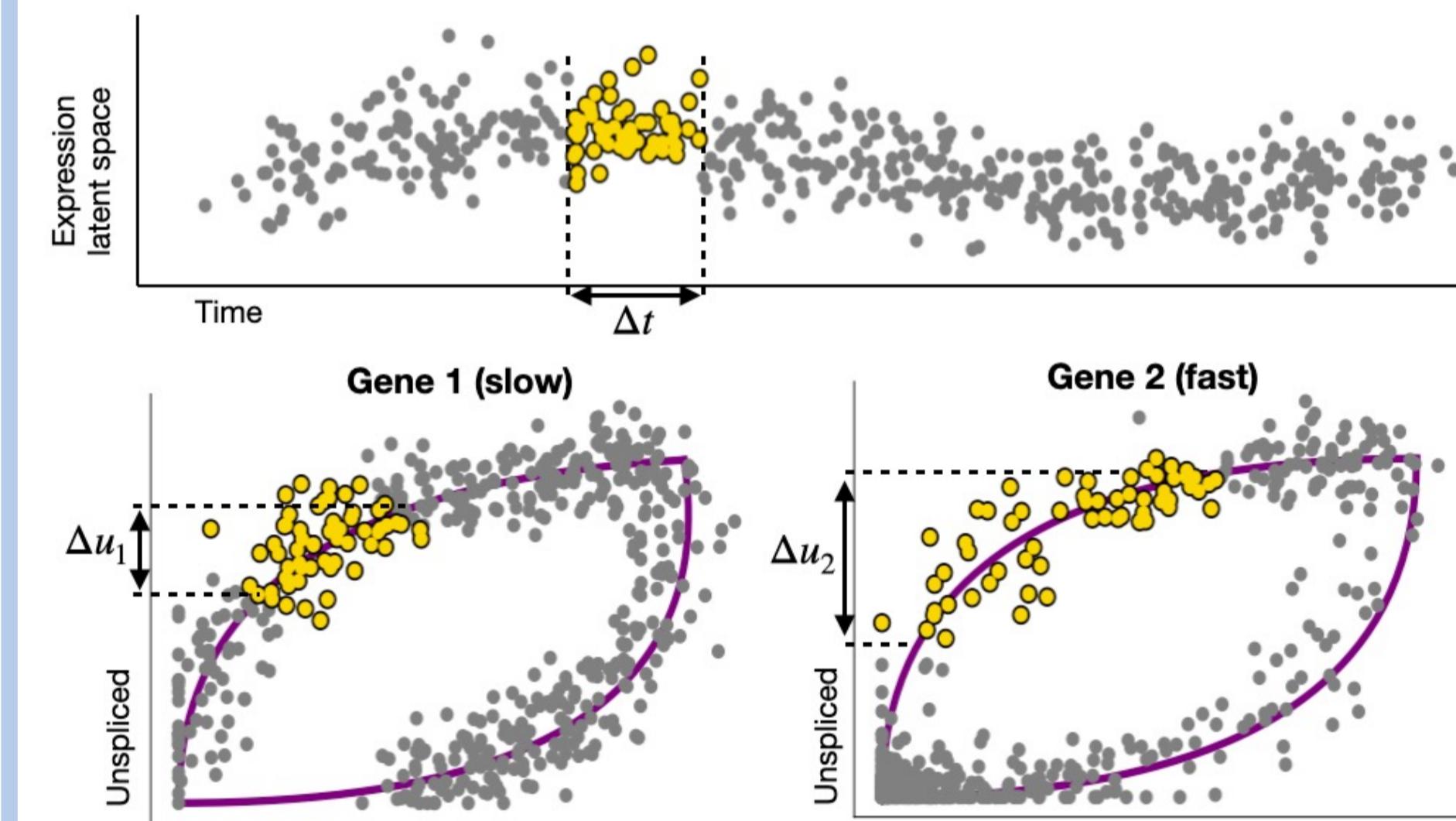
### Solution:

Given  $\Delta t$  a measure of time between states  $i, j$ .

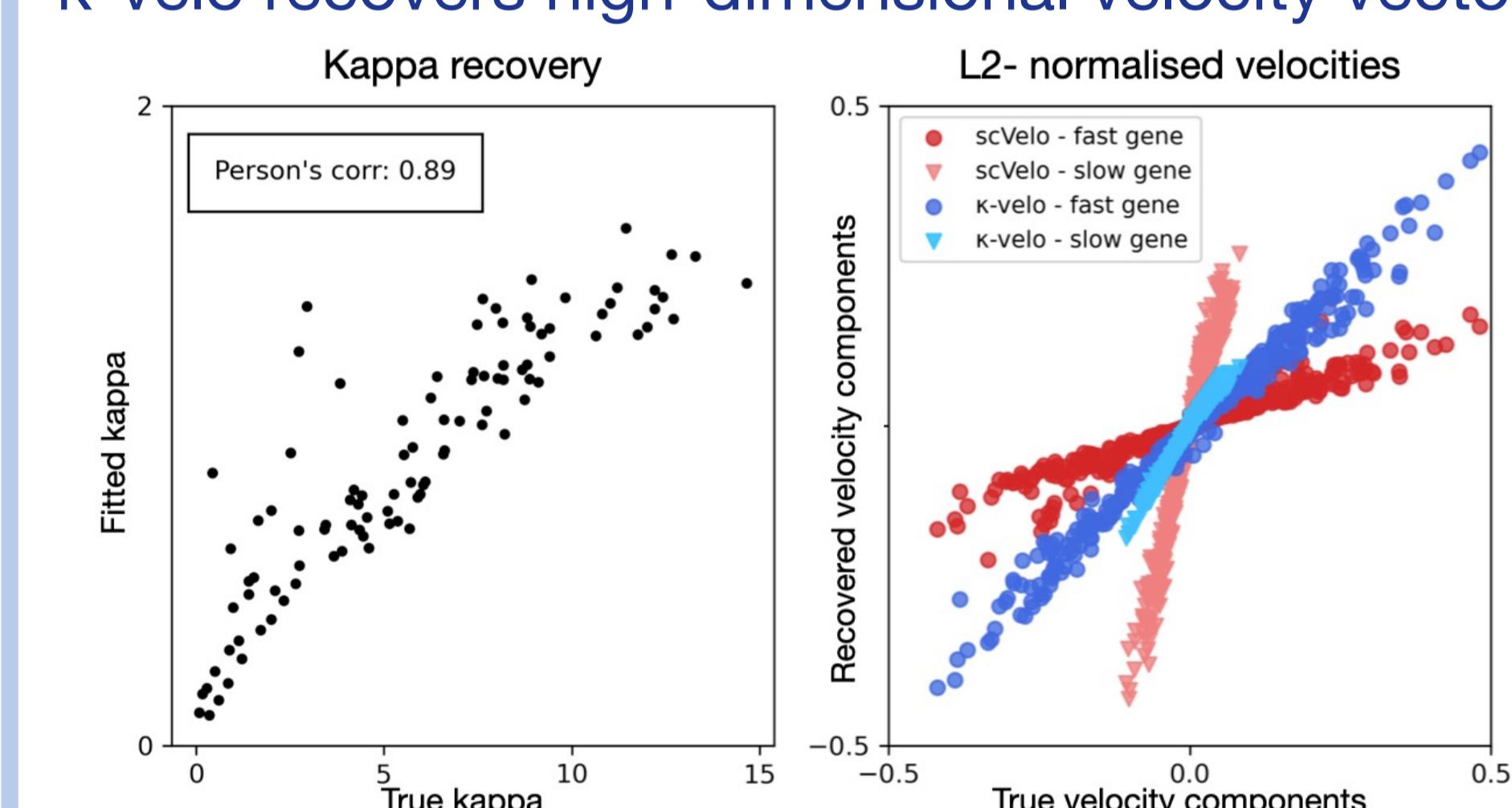
$$\kappa \Delta t = -\frac{1}{\beta} \log \frac{u_i - \alpha/\beta}{u_j - \alpha/\beta}$$

Given a measure of  $\Delta t$  we can solve for gene-specific  $\kappa$ .

## Density of cells can be used as a proxy of time



## k-velo recovers high-dimensional velocity vector



## Visualisation

Low-dimensional representation of velocity should preserve:

- the direction of the vectors
- the magnitude (speed of change) of the vectors
- local variations (representing fluctuations of the dynamics & cell plasticities)

## Nyström projection accurately represents variance and magnitude on non-linear embedding



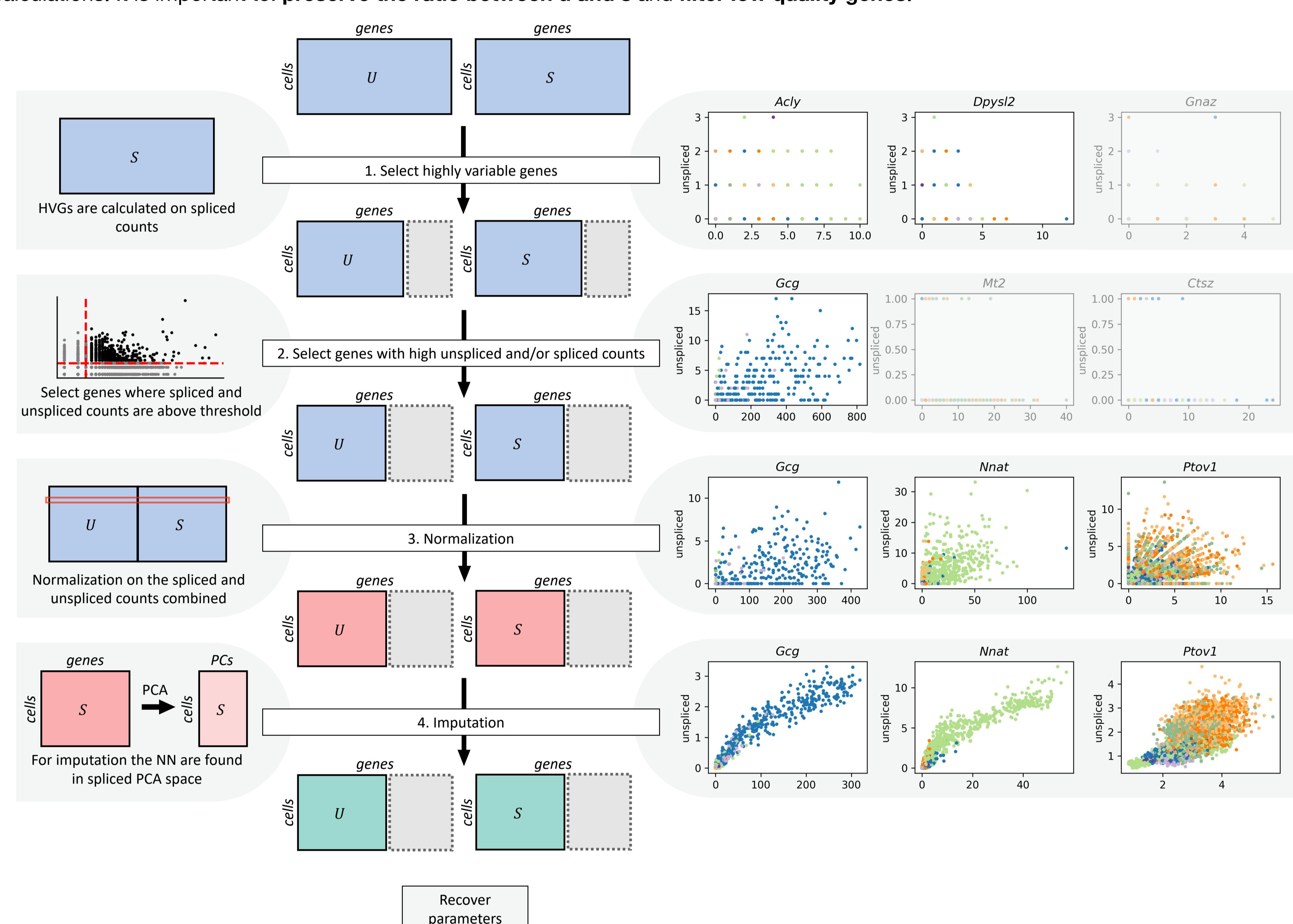
Valérie and me (Brigitte) are always happy with feedback, questions, discussions and collaborations. So feel free to reach out to us!

email: brigitte.joanne.bouman@mdc-berlin.de

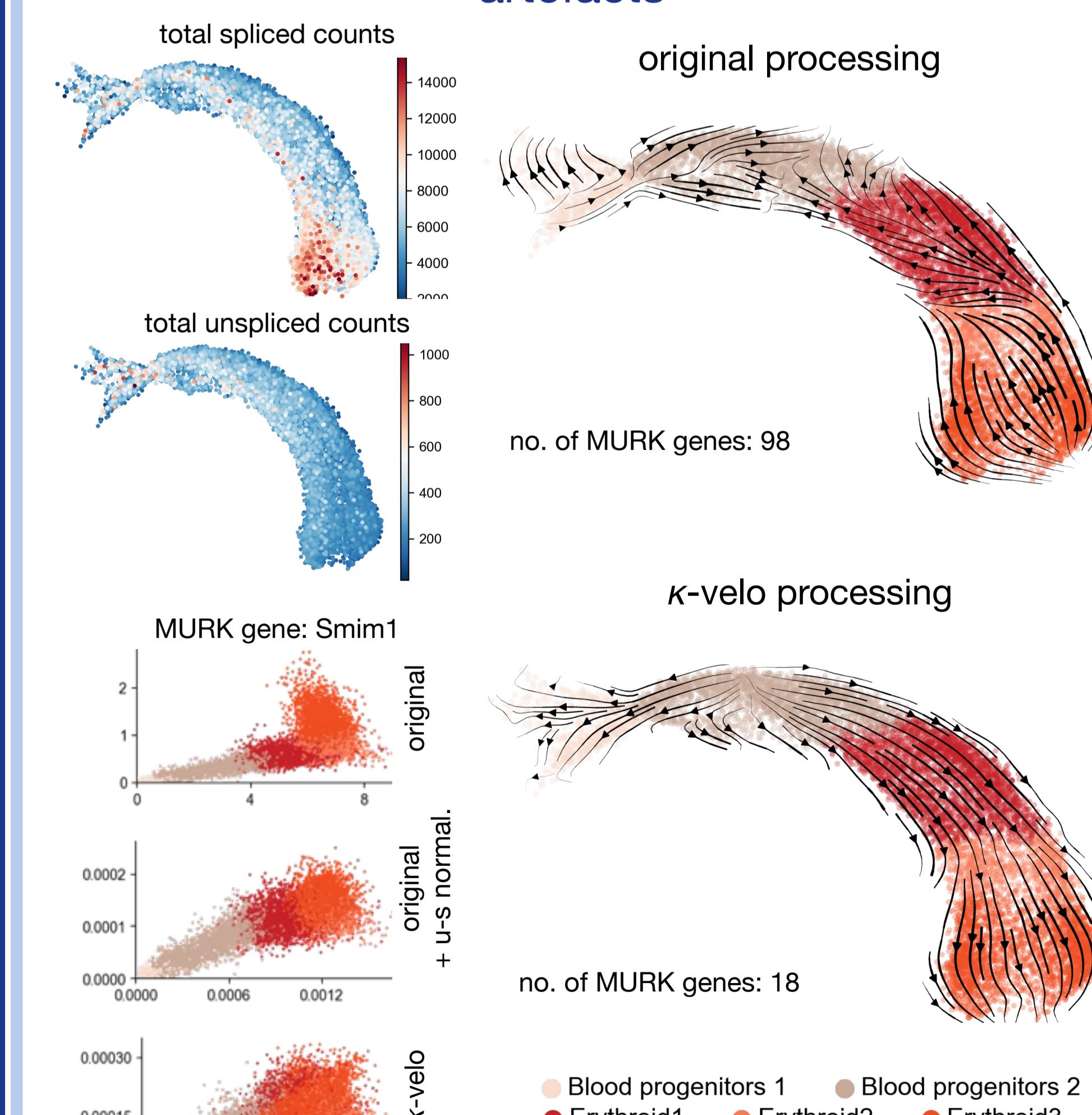
Or meet us for a cup of coffee in Berlin!

## Processing

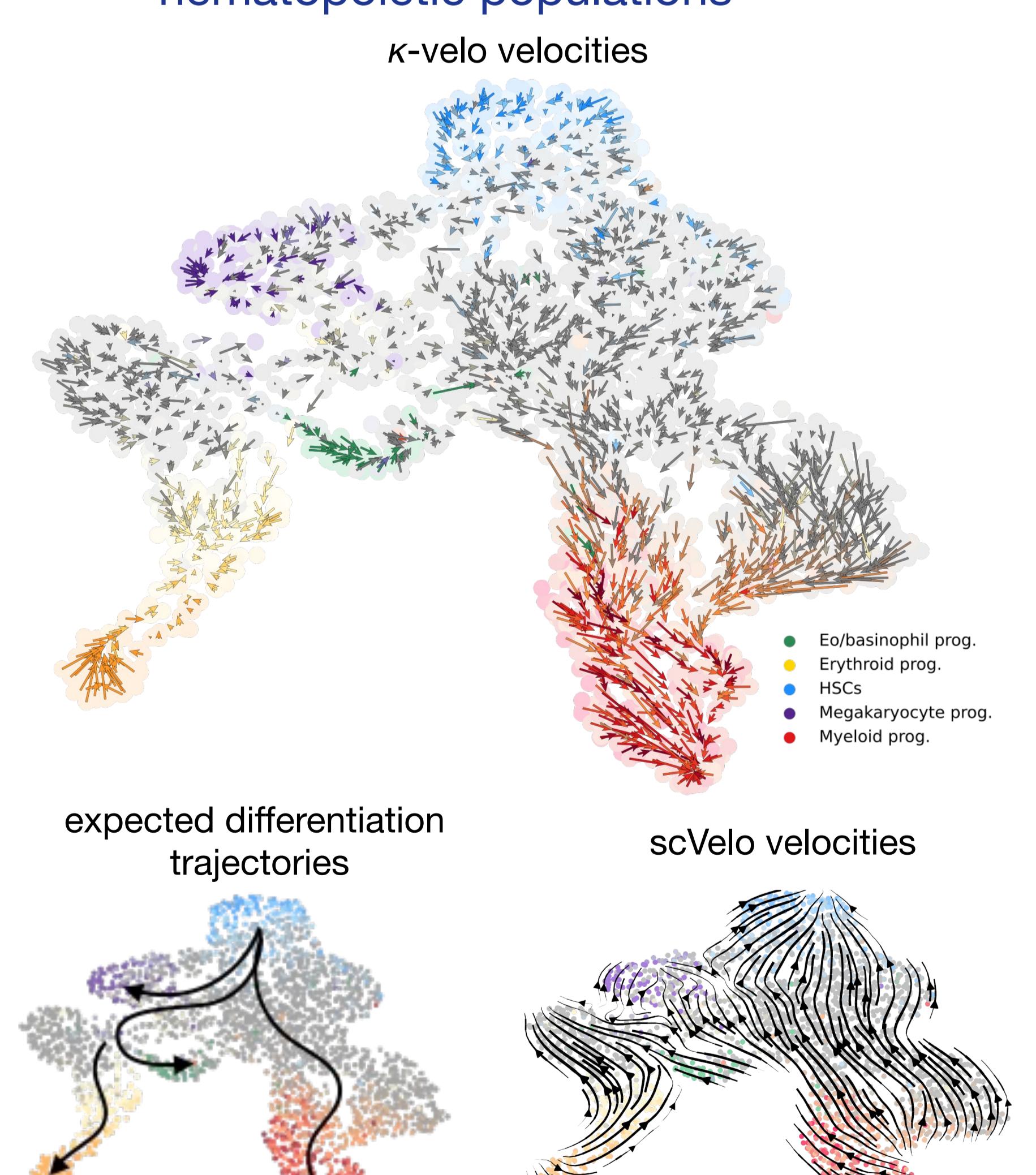
After counting the unspliced and spliced reads (read alignment), both matrices ( $U$  and  $S$ ) are processed. It is important to: **preserve the ratio between  $u$  and  $s$  and filter low quality genes**.



## Careful processing prevents introduction of artefacts<sup>[3]</sup>



## k-velo recovers differentiation trajectory in hematopoietic populations<sup>[2][4]</sup>



## References:

- [1] La Manno et al. (2018) RNA velocity of single cells. *Nature*.
- [2] Bergen et al. (2020), Generalizing RNA velocity to transient cell states through dynamical modeling, *Nature Biotech.*
- [3] Barile, M. et al. (2021) Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. *Genome Bio.*
- [4] Yasmin Demerdash, et. al. (2019) Inflammatory Stress in Stem Cells. International Symposium FOR 2033: The Hematopoietic Niches

## The paper:

Marot-Lassauzaie and Bouman et al. (2022) Towards reliable quantification of cell state velocities. *BioRxiv*.

## Find out more:

- k-velo package
- k-velo tutorials
- the paper
- the Haghverdi lab

