\( \kappa \)-velo improves single-cell RNA-velocity estimation

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**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 plasticity)

**Scale invariance**

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

Solution:
Given a measure of time between states \(u\),
\[ \kappa \Delta t = \frac{1}{\beta} \log \left( \frac{u(t) - u(t-\Delta t)}{u(t) - u(t+\Delta t)} \right) \]
Given a measure of \(\Delta t\) we can solve for gene-specific \(\kappa\).

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

**\( \kappa \)-velo recovers high-dimensional velocity vector**

**Careful processing prevents introduction of artefacts**

**\( \kappa \)-velo recovers differentiation trajectory in hematopoietic populations**

**Processing**

After counting the unspliced and spliced reads (read alignment), both matrices \((U\) and \(S)\) are processed. For the downstream velocity calculations, it is important to:
- preserve the ratio between \(u\) and \(s\)
- filter low quality genes.

**References:**

**Find out more:**
- BioRxiv tutorials
- the paper
- the hashtag lab