scVelo

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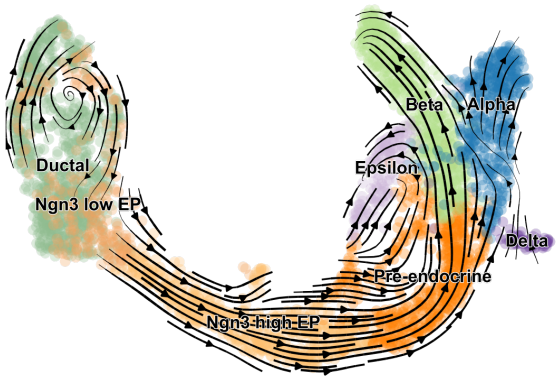
Main



scVelo is a scalable toolkit for RNA velocity analysis in single cells. The methods are based on our preprint Bergen et al. (2019).

RNA velocity enables the recovery of directed dynamic information by leveraging splicing information. scVelo generalizes the concept of RNA velocity (La Manno et al., 2018) by relaxing previously made assumptions with a stochastic and a dynamical model that solves the full transcriptional dynamics. It thereby adapts RNA velocity to widely varying specifications such as non-stationary populations.

scVelo is compatible with scanpy and hosts efficient implementations of all RNA velocity models.

CHAPTER 1

scVelo's key applications

- estimate RNA velocity to study cellular dynamics.
- identify putative driver genes and regimes of regulatory changes.
- infer a latent time to reconstruct the temporal sequence of transcriptomic events.
- estimate reaction rates of transcription, splicing and degradation.
- use statistical tests, e.g., to detect different kinetics regimes.

CHAPTER 2

Reference

Bergen et al. (2019), *Generalizing RNA velocity to transient cell states through dynamical modeling*, biorxiv.

CHAPTER 3

Support

Feel free to submit an issue or send us an email. Your help to improve scVelo is highly appreciated.