Table 1. Summary of three categories RNA velocity computational methods.

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| **Category** | **Methods** | **Modeling Approach** | **Advantages** | **Limitations** |
| Steady-state Methods | *Velocyto*, *scVelo* (deterministic and stochastic model), *MultiVelo* (deterministic and stochastic model), *VeloAE*, *TopicVelo* | Analytical or stochastic models assuming constant splicing rate and transcriptional equilibrium. Typically use least-squares regression on steady-state cells. | 1. Simple, fast, and interpretable; 2. Effective in capturing clear steady-state differentiation processes. | 1. Assumes constant splicing rate; 2. Assumptions often violated in heterogeneous populations or when dynamics are incomplete; 3. Inaccurate for complex kinetic patterns and non-steady states. |
| Trajectory Methods | *scVelo* (dynamical model), *MultiVelo* (dynamical model), *UniTVelo*, *Dynamo*, *veloVI*, *VeloVAE*, *LatentVelo*, *Pyro-Velocity*, *cell2fate* | Fit full transcriptional dynamics by constructing phase trajectories using ODEs; often involve latent time and EM or VAE frameworks. | 1. Flexible modeling of complex, nonlinear dynamics; 2. Generate biologically meaningful latent variables during inference; 3. Often include uncertainty estimates. | 1. Sensitive to incomplete trajectories; 2. Kinetics inference is restricted by ODE formulation; 3. Complex optimization. |
| State Extrapolation Methods | *cellDancer*, *DeepVelo*, *SymVelo* | Local modeling of cell-specific kinetics via nearest neighbors; learn velocity by extrapolating expression states over time in high-dimensional space. | 1. Superior ability to capture lineage heterogeneity and subtle kinetic variations; 2. Provide cell-specific kinetic parameters. | 1. Limited practical validation in biological settings; 2. Sensitive to local neighboring cells identification; 3. Computationally intensive. |