Table 2. Summarization of RNA Velocity models.

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| **Category** | | **Models** | **Multi-Omics** | **Discrete Raw Count Use** | **Gene-specific Kinetic Parameter** | **Gene-specific Transcription Rate** | **Gene-specific Splicing Rate** | **Gene-specific Degradation Rate** | **Latent Time in Parameter Estimation** | **Transcriptional Dynamics Modeling** | **Parameter Estimation Framework** | **Ref** |
| **Steady-state methods** | **Linear regression** | *Velocyto*  *(scVelo - Deterministic)* | No | No | Yes | Yes | Global constant | Yes | No | Linear ODE | Linear least-squares | [8, 10] |
| *scVelo (Stochastic)* | No | No | Yes | Yes | Global constant | Yes | No | Linear ODE with second-order moments | Linear least-squares | [10] |
| *MultVelo (Stochastic)* | ATAC-seq | No | Yes | Yes | Global constant | Yes | No | Linear ODE with second-order moments | Linear least-squares | [13] |
| *veloAE* | No | No | Yes (Latent space) | Yes (Latent space) | Global constant | Yes (Latent space) | No | Linear ODE in latent space | Autoencoder | [14] |
| **KL divergence** | *TopicVelo* | No | Yes | Process-specific | Process-specific | Global constant | Process-specific | No | Chemical master equation | Backpropagation | [15] |
| **Trajectory methods** | **Cell-shared trajectory** | *scVelo (Dynamical)* | No | No | Yes | Yes | Yes | Yes | Gene-specific | Linear ODE | Expectation maximization | [10] |
| *MultiVelo (Dynamical)* | ATAC-seq | No | Cell-specific | Cell-specific | Yes | Yes | Gene-specific | Linear ODE with chromatin accessibility | Expectation maximization | [13] |
| *UniTVelo* | No | No | Yes | No TR | Yes | Yes | Gene-specific or shared | RBF-based ODE | Expectation maximization | [16] |
| *Dynamo* | Metabolic Labeling | No | Yes | Yes | Yes | Yes | Gene-specific labeling time | Linear ODE | Non-linear least-squares | [17] |
| *Pyro-Velocity* | No | Yes | Yes | Yes | Yes | Yes | Gene-shared | Linear ODE | Stochastic variational inference | [21] |
| **Cell-specific trajectory** | *veloVI* | No | No | Cell-specific\* | Cell-specific\* | Yes | Yes | Gene-specific | Linear ODE with transcription regulation | Variational autoencoder | [18] |
| *veloVAE* | No | No | Cell- & lineage-specific | Cell-specific | Lineage-specific | Lineage-specific | Gene-shared | Linear ODE with transcription regulation | Variational autoencoder | [19] |
| *LatentVelo* | ATAC-seq\* | No | Cell-specific (Latent Space) | No TR | No SR | No DR | Gene-shared | Neuro ODE with transcription regulation in latent space | Variational autoencoder | [20] |
| *cell2fate* | No | Yes | Cell-specific | Cell-specific | Cell-specific\* | Cell-specific\* | Gene-shared | Linear ODE with transcription regulation | Stochastic variational inference | [21] |
| **State extrapolation method** | **Cosine similarity** | *cellDancer* | No | No | Cell-specific | Cell-specific | Cell-specific | Cell-specific | No | Linear ODE | Backpropagation | [23] |
| **State distance** | *DeepVelo* | No | No | Cell-specific | Cell-specific | Cell-specific | Cell-specific | No | Linear ODE | Backpropagation | [24] |
| *SymVelo* | ATAC-seq\* | No | Cell-specific | No TR | No SR | No DR | No | Neuro ODE | Mutual learning (State extrapolation module & Steady-state module) | [25] |
| Yes (Latent space) | Yes (Latent space) | Global constant | Yes (Latent space) | No | Linear ODE in latent space |

Abbreviation: No TR, No SR, and No DR indicate transcription rate, splicing rate, and degradation rate are not explicitly modeled in the ODE system (e.g. hyper kinetic parameters in neuro ODE system). Descriptions with *stars* (\*) refer to features in model extension.