Table 3. Summarization of RNA velocity applications across biological scenarios.

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| Categories | Tissue/Cells | Biological Implications | Algorithms | Key findings | Ref. |
| Differentiation and development | Mouse embryonic cells | Asynchronous emergence; Multiple subpopulations | *scVelo* (deterministic) | Identified three neural crest cell subpopulations and validated cellular trajectories from E3.5 to E13.5. | [56] |
| Human forebrain | Rare population identification; Temporal sequence; Multiple developmental states | *scVelo* (dynamical) | Revealed temporal sequence of OPC specification and identified two distinct EGFR+ populations as OPC sources. | [53] |
| Zebrafish neural stem cells | scRNA-Seq and scSLAM-Seq dual validation; Alternative pathways; Spatiotemporal diversity | *scVelo* (stochastic) *Dynamo* | Validated direct and proliferative differentiation trajectories. | [57] |
| Zebrafish enteric nervous system | Neuronal subtype specification; Spatiotemporal emergence patterns | scVelo (dynamical); UniTVelo | Identified distinct neuron subtypes with spatiotemporal emergence patterns. | [Spatiotemporal dynamics of the developing zebrafish enteric nervous system at the wholeorgan level] |
| Human retina | Bidirectional development; Multi-omic integration; Temporal progression | *scVelo* (dynamical) *Multivelo* (dynamical) | Revealed bidirectional developmental trajectories of retinal progenitor cells. | [55] |
| Mouse medullary thymic epithelial cells | Branching development; Precursor validation; Experimental verification | *scVelo* (stochastic & dynamical) | Identified TAC-TECs as precursors to major mTEC subpopulations and predicted branching developmental model. | [58] |
| Human bone marrow stromal cells | Hierarchical organization; Multiple directions; Driver gene identification | *scVelo* (stochastic) | Revealed two main developmental directions from MSSCs and identified key driver genes. | [59] |
| Human Bone marrow | Lineage commitment; Transitional progenitor states; NK cell ontogeny | *scVelo* (no model specified); *TopicVelo* | Identified transitional NK progenitors bridging HPCs and NK cells. | [51] |
| Human B cells from multiple organs | Peripheral origin of thymic B cells;Spatiotemporal B cell subset relationships | *UniTVelo* | Peripheral origin of thymic B cells confirmed by trajectory. | [B cells orchestrate tolerance to the  neuromyelitis optica autoantigen AQP4] |
| Human subcutaneous adipose tissue | Active transitions; Multiple sample types; scRNA-Seq and snRNA-seq analysis | *scVelo* (dynamical) | Validated adipocyte differentiation trajectories in WAT and SVF samples. | [60] |
| Human small intestine | Sequential differentiation; Unidirectional progression; Stepwise maturation | *scVelo* (dynamical) | Mapped unidirectional cellular trajectory from stem cells to mature absorptive enterocytes. | [61] |
| Human intestinal  cells | Lineage differentiation; Secretory cell specification; Intra-cryptal maturation | *CellDancer* | Traced origin of differentiated intestinal cell types from intestinal stem cells. | [Intestinal secretory differentiation reflects nichedriven phenotypic and epigenetic plasticity of a common signal-responsive terminal cell] |
| Human endometrial tissue | Epithelial-to-stromal transition | *scVelo*  (dynamical), *CellDancer* | Revealed disrupted epithelial-mesenchymal transition in preeclampsia patients. | [Multi-omics-based mapping of decidualization resistance in patients with a history of severe preeclampsia] |
| Human endometrial tissue | Luminal-to-glandular differentiation;  Endometrial regeneration | *UniTVelo* | Luminal cells show high differentiation potential toward glandular cells. | [Time-series single-cell transcriptomic profiling of luteal-phase endometrium uncovers dynamic characteristics and its dysregulation in recurrent implantation failures] |
| Human fetal lung tissue | Progenitor differentiation | *LatentVelo* | Uncover unexpected cell lineage transitions in developing epithelium. | [Early human fetal lung atlas reveals the temporal dynamics of epithelial cell plasticity] |
| Mouse testis (spermatocytes) | Meiotic progression; Transcriptional dynamics in spermatogenesis | *scVelo* (dynamical),  *UniTVelo* | Revealed stage-specific regulators guiding pachytene progression in spermatogenesis. | [62] |
| Mouse visual cortex neurons | Stimulus-dependent transcriptional dynamics;Vision-dependent circuit refinement during development | *UniTVelo* | Immediate early gene vs late response gene waves identified. | [A single-cell transcriptomic atlas of sensory-dependent gene expression in developing mouse visual cortex] |
| Tomato callus | Sequential states; Developmental relationships | *scVelo* (dynamical); *Dynamo* | Elucidated developmental trajectory among three shoot primordia subtypes. | [63] |
| Diseases and injured microenvironments | Human & mouse monocytes | Early fate decision; Alternative pathways; Distinct lineages | *scVelo* (stochastic) | Revealed early bifurcation of monocytes into mo-DC and mo-Mac lineages. | [64] |
| Human peripheral blood mononuclear cells | Population heterogeneity; SLE Patient variation; Disease correlation | *scVelo* (no model specified) | Examined transcriptional heterogeneity in SLE patients. | [65] |
| Human placentas | State transitions; Disease-specific populations; Developmental divergence | *scVelo* (dynamical) | Showed developmental stalling of preeclamptic trophoblasts. | [66] |
| Mouse and Human Lung Alveolar Epithelium | Treatment response; State redirection; Therapeutic mechanism | *scVelo* (dynamical) | Revealed how HIF2 inhibition alters cell fate decisions. | [67] |
| Human postmortem prefrontal cortex | Synaptic dysregulation; Cell cycle acceleration; Neurodegenerative trajectory | *scVelo* (stochastic); *veloVI* | Revealed accelerated synaptic and developmental disruptions in Alzheimer’s cortex. | [68] |
| Mouse cardiac cells | Sequential transitions; Multiple population dynamics | *scVelo* (stochastic & dynamical) | Mapped transitions in fibroblast and macrophage populations post- myocardial infarction. | [69] |
| Human diabetic foot ulcers keratinocytes | Healing dynamics; State fluidity; Comparative analysis | *scVelo* (dynamical) | Revealed differences in cellular dynamics between healing and non-healing DFUs. | [70] |
| Human lung epithelial cells | Bidirectional trajectory; Infection response; Temporal stages | *scVelo* (no model specified) | Identified bidirectional differentiation between IS cells and BC during infection. | [71] |
| Murine skin | Driver gene identification; Phase transitions; Developmental potential | *scVelo* (dynamical) | Identified Lef1 as critical driver gene in papillary fibroblasts development. | [72] |
| Tumor microenvironments | Mouse T cells | Temporal hierarchy; Stage-specific effects; T cell fate transition | *scVelo* (stochastic) | Revealed temporal hierarchy of epigenetic regulation during T cell differentiation. | [49] |
| Human non-small cell lung cancer cells | Dual origins; Treatment response; Immune dynamics | *scVelo* (stochastic) | Validated two distinct origins of cytotoxic T cells in tumor microenvironment. | [50] |
| Mouse tumor-infiltrating lymphocytes | T cell exhaustion trajectory; Spatial trajectory; Origin identification; | *scVelo* (stochastic) | Demonstrated developmental trajectory from lymph nodes to tumors. | [73] |
| Human non-small cell lung cancer cells (NSCLC) | State evolution; Multiple transitions; Microenvironment influence | *scVelo* (dynamical) | Uncovered evolution pattern of neutrophil subtypes in NSCLC. | [74] |
| Human prostate cancer epithelial cells | Tumor heterogeneity; Directional transformation；Origin resolution | *scVelo* (dynamical) | Demonstrated NEPC cells originate exclusively from luminal-like malignant cells. | [75] |
| Human colorectal polyps cells | Contrasting trajectories; Pre-cancerous dynamics | *scVelo* (no model specified) | Validated distinct cellular origins of different polyp types. | [76] |
| Human chronic lymphocytic leukemia peripheral blood mononuclear cells | Unidirectional progression; State transition; Irreversible fate | *scVelo* (no model specified) | Revealed unidirectional fate progression in lymph node microenvironment. | [54] |
| Human and mouse pancreatic ductal adenocarcinoma cells | PI3Kδ inhibition mechanism; Development disruption; Side effect explanation | *scVelo* (no model specified) | Revealed how PI3Kδ inhibition affects Treg development. | [77] |
| Human primary central nervous system lymphoma cells | Clonal heterogeneity; Developmental diversity; Subclone evolution | *scVelo* (dynamical) | Identified developmental paths between malignant B cell clusters. | [78] |
|  | Human glioma stem cells | Hypoxia-induced cell state transitions; Epigenomic and transcriptomic remodeling | *MultiVelo* | Revealed hypoxia-induced reversal of cell state trajectories in multiple clusters, identified regulatory mechanisms through gene models of activation/repression. | [Multiomic profiling of hypoxic glioblastoma stem cells reveals expansion of subpopulations with distinct epigenetic and CNV profiles] |
|  | Human myeloid and T lymphocytes | Immune cell fate determination | *Dynamo* | Revealed distinct lineage commitment pathways across immune archetypes. | [Single cell profiling of bone metastasis ecosystems from multiple cancer types reveals convergent and divergent mechanisms of bone colonization.] |