Flowchart Known Data scTrip Predicted Trajectory Inference Perturbation Analysis Recovery Prediction Compatible Modalities Gene Expression Chromatin Accessibility **DNA Methylation** Developmental Trajectory Perturbation and Progression Spatial Measurements Electrophysiological Other matrix data scTRIP $\xrightarrow{\pi}$ scTRIP Model Training **Multimodal Single Cell Data Environmental Reward** $[R_B^t]_i = \begin{cases} -1 & \max(\vec{x}_i) = 1 \\ 0 & \text{else} \end{cases}, \quad \begin{aligned} \text{Velocity Penalty} & \text{Action Penalty} \\ [R_V^t]_i = -||\vec{v}_i^t||^2, & [R_A^t]_i = -||\Delta \vec{v}_i^t||^2, \end{aligned}$ $M^{(1)}$ pistance Reward $[R_D^{t+1}]_i = \delta_i^{t+1} - \delta_i^t, \quad \delta_i^t = \sum_{k=1}^{n_m} \sum_{j=1 \neq i}^{n_c} (D_{ij}^{(k)} - D_{ij}^t)^2,$ Modal features (e.g. chromatin regions) $M^{(k)}$ Total Reward $R^t = R_D^t + R_B^t + R_V^t + R_A^t \label{eq:reward}$ $ec{x}_i, ec{v}_i$ Cell position and velocity $M^{(k)}$ Modal data $\vec{X}^{t_0}, \vec{V}^{t_0}$ \uparrow $\downarrow R^{t_0}$ $t = t_0$ $t = t_1$ **Inter-Cell Distances** Random Initialization $D^{(k)}, D_{ij}$ Distance for modality and latent space $ec{X}^{t_0},ec{V}^{t_0}igg|\int_{\Deltaec{V}^{t_0}}$ **Development and Perturbation Analysis Disease Trajectory** and Feature Reconstruction **Prioritization Per-Cell Action Loop** $\vec{a}_i = E_a\left(\left[\vec{x}_i, \vec{v}_i, E^{(1)}(M_i^{(1)}), \dots, E^{(k)}(M_i^{(k)})\right]\right)$ \vec{x}_i \vec{v}_j $\vec{b}_{ij} = E_b\left(\left[\vec{x}_j, \vec{v}_j, E^{(1)}(M_j^{(1)}), \dots, E^{(k)}(M_j^{(k)}), \vec{a}_i\right]\right)$ Residual Self-Attention $ec{a}_i, \dot{b_{ij}}$ Cell and neighbor embeddings $E^{(k)}$ Encoder for modality k

 $ec{s}_i, \Delta ec{v}_i$ State and action vectors

 π Trained policy

 E_a, E_b, E_s Cell, neighbor, and state encoders