## Visualization Cell type identification sparse encoder Marker gene annotation with weight matrix **B** decoder Inspection of developmental patterns with parameters $\theta$ reconstructed data $\hat{\boldsymbol{X}}^{\dagger}$ original data $\boldsymbol{X}^{\top}$ original data $\boldsymbol{X}^{\top}$ genes latent space cells $Z = BX^{\top}$ $loss(X, Z, \theta)$ pseudo target $\nabla_{\theta} loss(\boldsymbol{X}, \boldsymbol{Z}, \boldsymbol{\theta}) \longleftarrow = \|\boldsymbol{X} - decoder(\boldsymbol{Z}, \boldsymbol{\theta})\|_{2}^{2}$ to update $B \longleftarrow \nabla_{\boldsymbol{z}} loss(\boldsymbol{X}, \boldsymbol{Z}, \boldsymbol{\theta}) \longleftarrow = \|\boldsymbol{X} - decoder(\boldsymbol{X}^{\top}\boldsymbol{B}, \boldsymbol{\theta})\|_{2}^{2}$ 7 constraint for learning **o** cellular heterogeneity constraint for learning temporal structure Learning disentangled dimensions 3) B Coupling time points $\widetilde{\boldsymbol{B}}^{(1)} = \boldsymbol{B}^{(0)} := \mathbf{0}_{\mathbb{R}^{p \times d}}$ data from $t_1$ : data from $t_2$ : data from $t_3$ :

Integrating boosting in an autoencoder

after training is done:  $\mathbf{B} := (\widetilde{\mathbf{B}}^{(2)}, \dots, \widetilde{\mathbf{B}}^{(N+1)}), f_{\text{enc}}^{\text{timeBAE}}(\mathbf{x}; \mathbf{B}) := \mathbf{B}^{\top} \mathbf{x}$