# Visualizing RNA velocity

**Genomic Data Visualization** 

Lyla Atta 03/07/2022

## **Visualizing RNA Velocity**

RNA velocity recap
Visualizing RNA velocity - previous approaches
VeloViz: RNA velocity-informed low dimensional embeddings
Try it out!

## **Visualizing RNA Velocity**

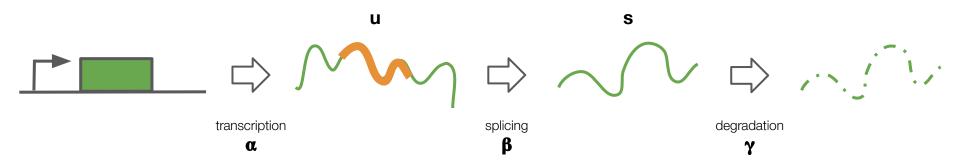
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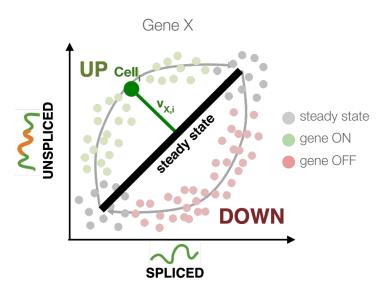
#### RNA velocity recap

Assign directionality to transcriptomic states

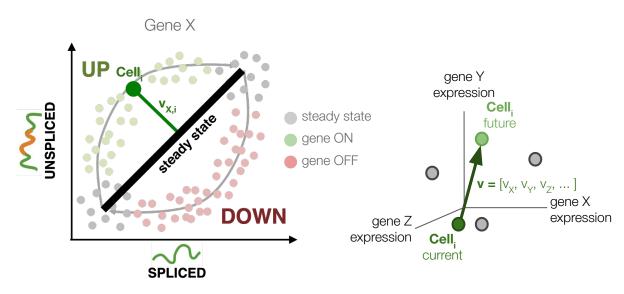
Relative quantities of spliced and unspliced

Rate at which genes are being expressed

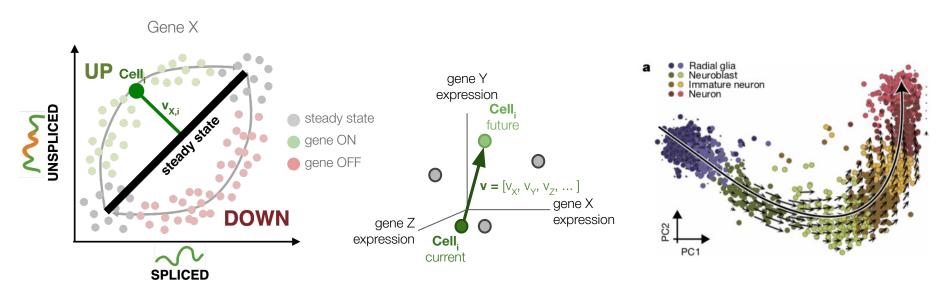




 $\mathbf{v}_{\mathbf{X},\mathbf{i}} = \mathbf{velocity}$  for gene X in cell i



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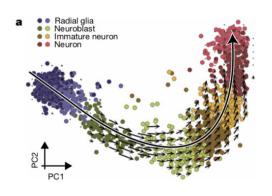
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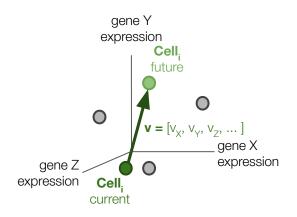
#### **Visualizing RNA velocity trends**

#### Goals:

- Encode direction, predicted states
- Differentiation, general cell state transitions, origin of rare cell types

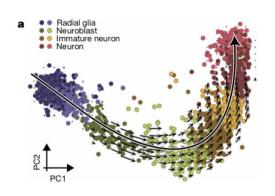
### Visualizing RNA velocity trends - PCA

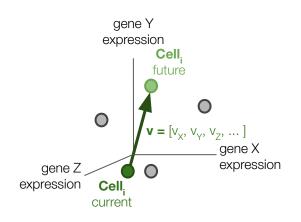




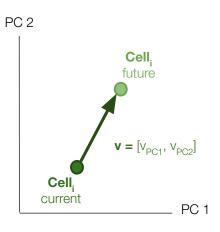
PC1 = 3X - 7YPC2 = 0.5X + 5Y

### Visualizing RNA velocity trends - PCA



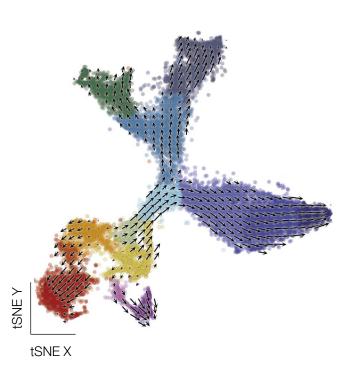


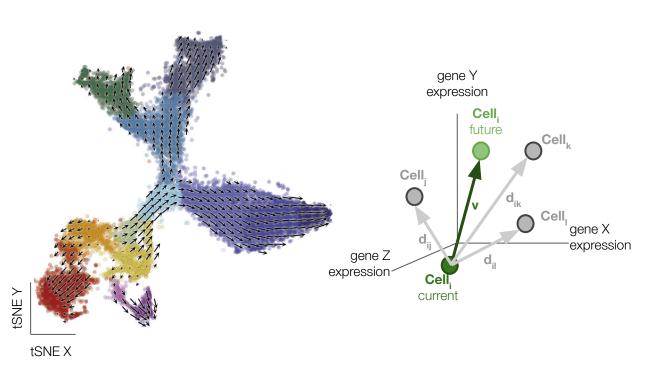
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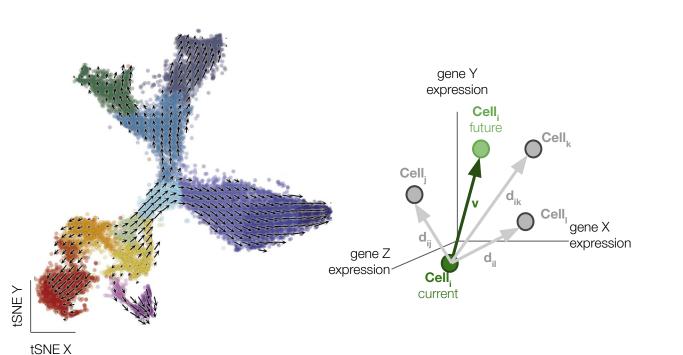


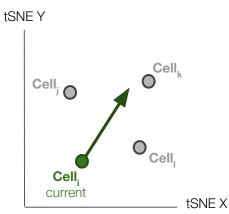
$$V_{PC1} = 3V_X - 7V_Y$$

$$V_{PC2} = 0.5V_{X} - 5V_{Y}$$



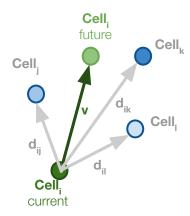






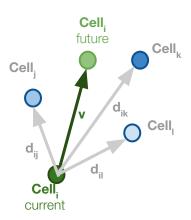
Transition probability:

$$P_{ix} \sim corr(v_{ix}, d_{ix})$$



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Given an embedding **X** of n cells:

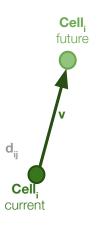
$$X = [x_1, x_2, ..., x_{n-1}, x_n]$$

Velocity displacement of a cell in embedding:

$$\mathbf{v}_{tSNE} \sim \mathbf{\Sigma}_{j} \mathbf{P}_{ij} \frac{(\mathbf{x}_{j} - \mathbf{x}_{i})}{\|\mathbf{x}_{j} - \mathbf{x}_{i}\|}$$

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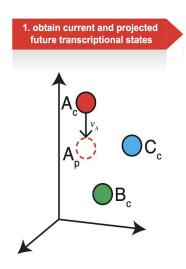
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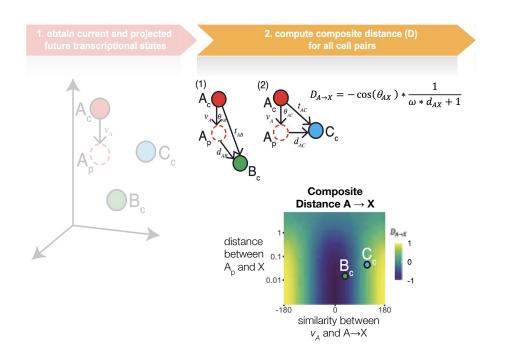
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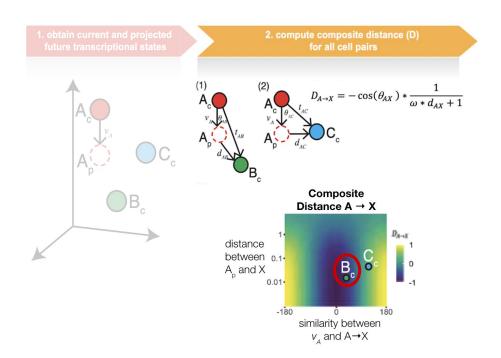
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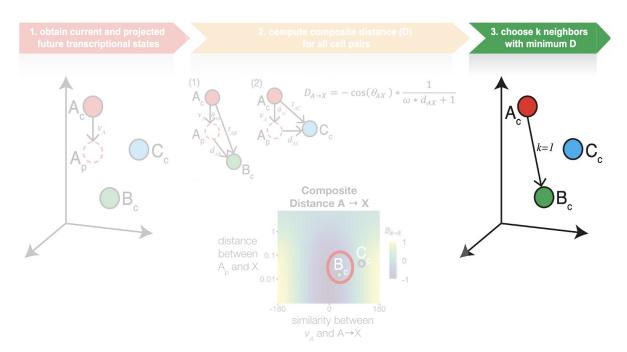


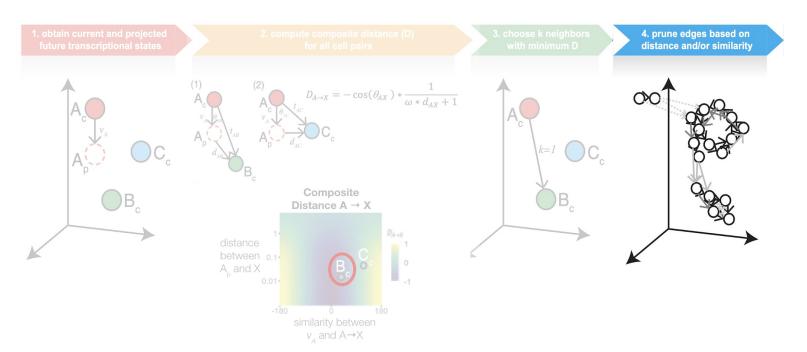
X<sub>c</sub> = observed current transcriptional state

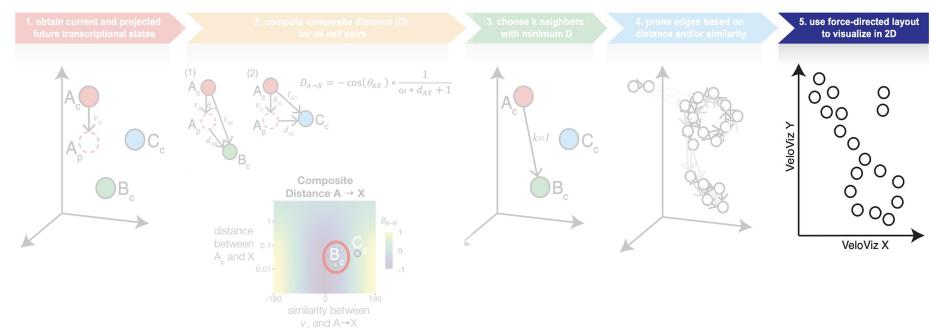
 $X_p^c$  = predicted future transcriptional state  $v_x$  = RNA velocity for cell X





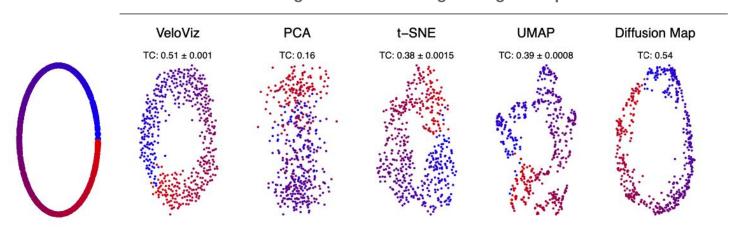






# VeloViz embeddings: simulated cycling and branching trajectories

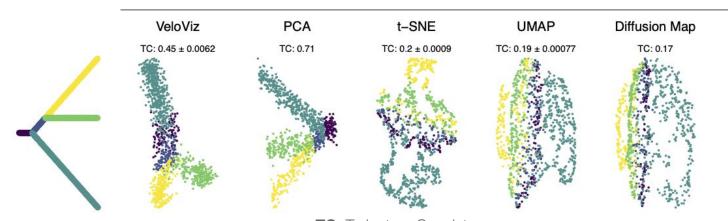
#### 2D embeddings of simulated single cell gene expression



TC: Trajectory Consistency
TC = 1: perfect representation of ground truth trajectory
error over random seeds

### VeloViz embeddings: simulated cycling and branching trajectories

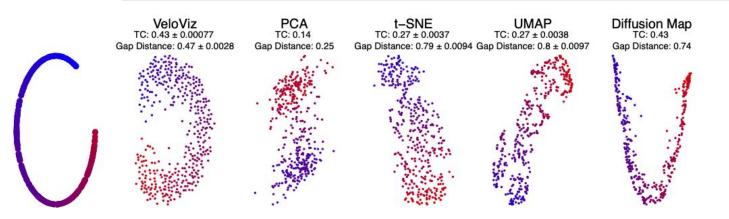
#### 2D embeddings of simulated single cell gene expression



**TC:** Trajectory Consistency TC = 1: perfect representation of ground truth trajectory error over random seeds

# VeloViz embeddings: simulated trajectories with missing intermediates

#### 2D embeddings of simulated single cell gene expression



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TC = 1: perfect representation of ground truth trajectory

Gap Distance: distance in embedding between cells before and after trajectory gap

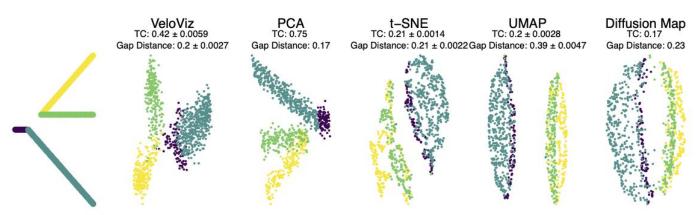
error over random seeds

Bioinformatics, 2021: tinyurl.com/veloviz Software + tutorials: jef.works/veloviz



#### VeloViz embeddings: simulated trajectories with missing intermediates

#### 2D embeddings of simulated single cell gene expression



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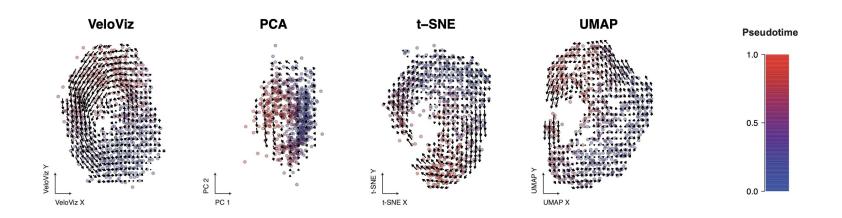
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# VeloViz embeddings: spatial single-cell transcriptomics cycling cultured cells



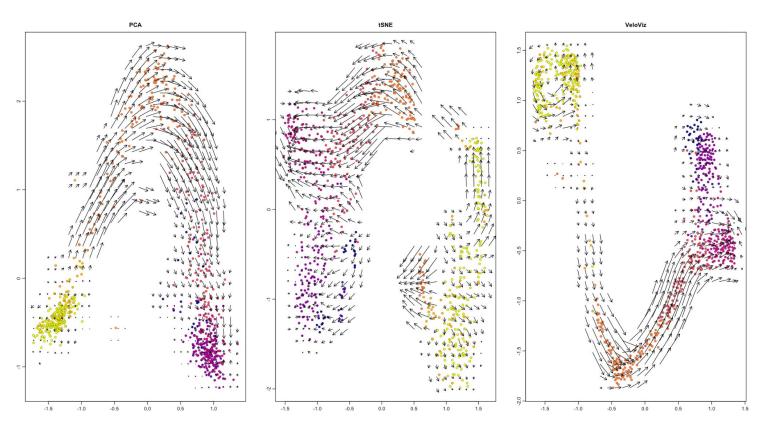
### **Questions?**

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#### VeloViz: RNA velocity-informed low dimensional embeddings

