Clustering of Embryonic scRNA-seq Data

Reveal Potential Heterogeneity in Germ

Layer Development

Understanding Gastrulation in Early Embryonic Development through Neural Networks



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INTRODUCTION

- Gastrulation is the stage in early embryonic development where the three germ layers (endoderm, mesoderm, ectoderm) form
- How can graphical representations of our scRNA-seq data coupled with typical time series forecasting networks help us understand germ layer differentiation and heterogeneity?

RESULTS



Source human and	Use adjacency matrix
gastruloid data and	to create pruned
calculate adjacency matrix	KNN graph

METHODS

- 1. Determine top 3000 genes with variable expression
- 2. Compare diffusion maps and UMAPs of in vivo human embryo scRNA-seq data (Tyser et. al) with in vitro gastruloid data (Minn et. al) so as to determine developmental trajectories
- 3. Run pseudotime inference
 - models to determine cell lineages
- 4. Determine how graphical neural network and other network implementations can improve on

Figure 1: Distribution of Human and Gastruloid Cell Clustering along DC3 and DC4 components reveal potential mesoderm heterogeneity

DISCUSSION

 These cell diffusion maps could reveal further tissue heterogeneity and could

FURTHER WORK

Diffusion maps and other simple clustering techniques like MAGIC and Phenotype generally carry imputation biases, so using graphical neural networks to learn embeddings could illuminate latent



lend insights into the transitional stages of embryonic development

cell-cell relationships

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