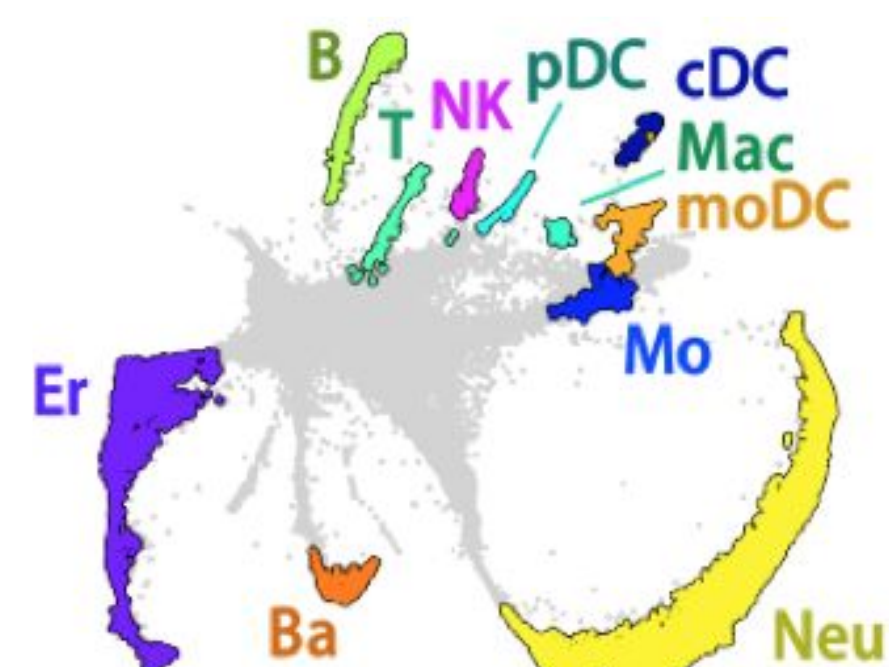


Current Methods for Lineage Tracing

Lineage Tracing: determining ancestors and descendants of individual cells in a population observed over time.

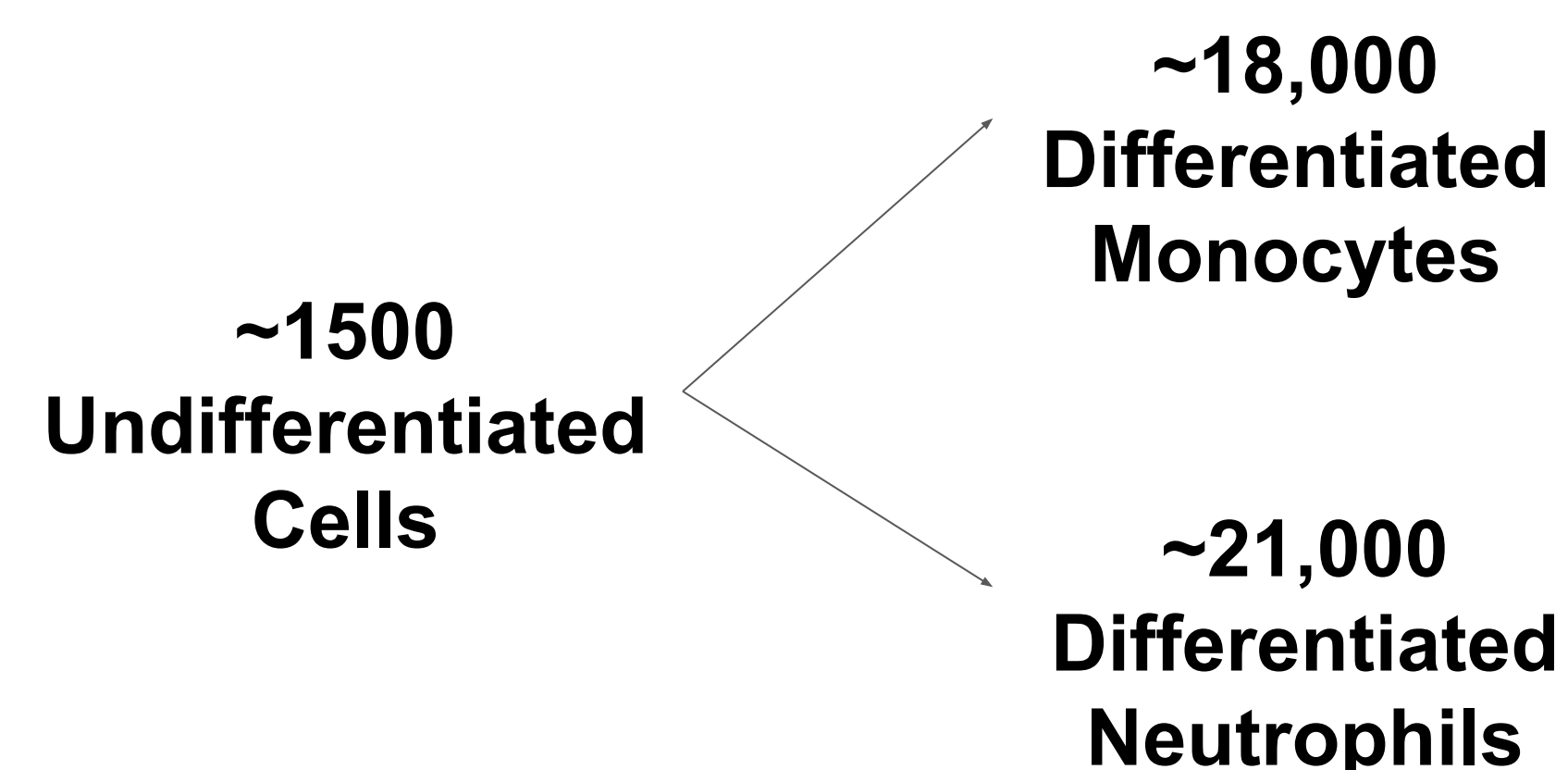


Source: Weinreb et al., American Association for the Advancement of Science, 2020

Current methods are **unsupervised** and rely on cell clones being close in gene expression space, which does not necessarily reflect experimental trajectories

Evaluation

Goal: Evaluate different lineage tracing methods based on how well they predict the transformation of undifferentiated cells into **Neutrophils** or **Monocytes**



Prediction Accuracies of Super-OT vs. Baseline Unsupervised and Fully Supervised Models

SETTING	ACCURACY
WOT: PREDICTED LABELS	0.6535
WOT: REAL LABELS	0.6531
CONDITIONAL GAN	0.5982
GAN-BASED OT	0.6219
SUPER-OT: 300	0.6731
SUPER-OT: 600	0.6856
SUPER-OT: 900	0.7188
SUPERVISED	0.7534

Unsupervised Models

Super-OT with 300, 600, 900 paired labels

Supervised Model

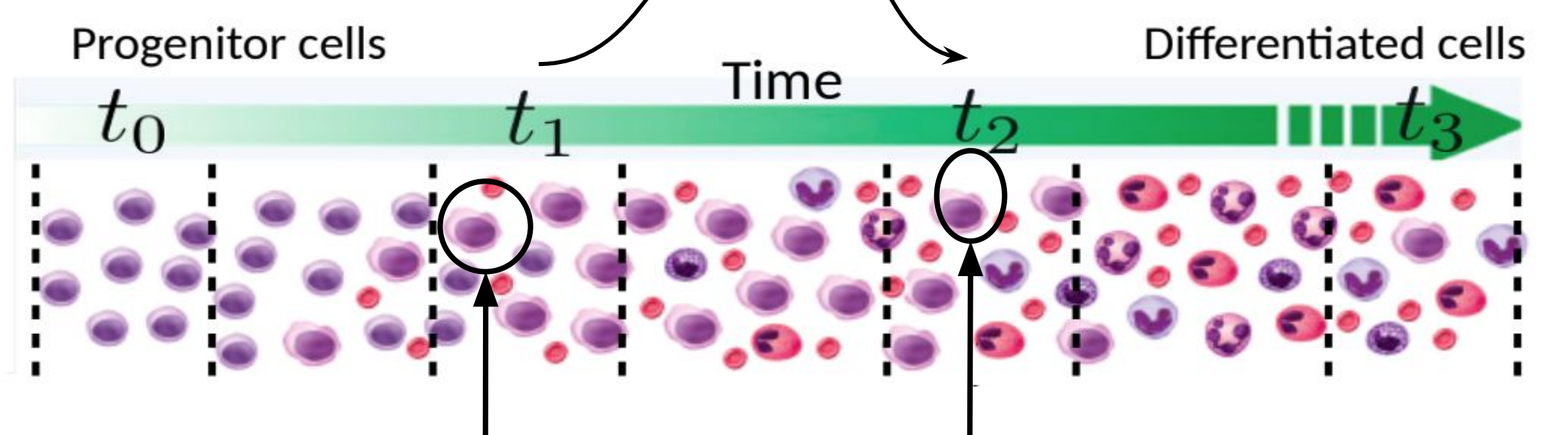
Super-OT models show improvement over unsupervised baseline and approach fully supervised accuracy

Super-OT: Components of the Loss Function

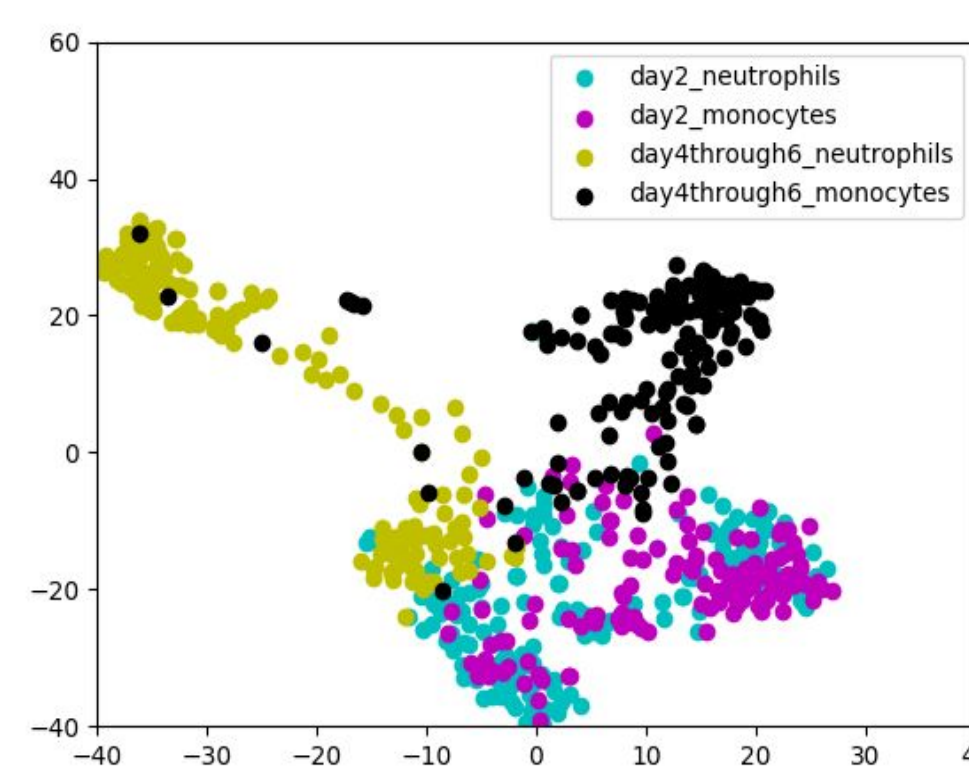
Loss Function

GAN Loss + Transport Cost + Supervised Cost

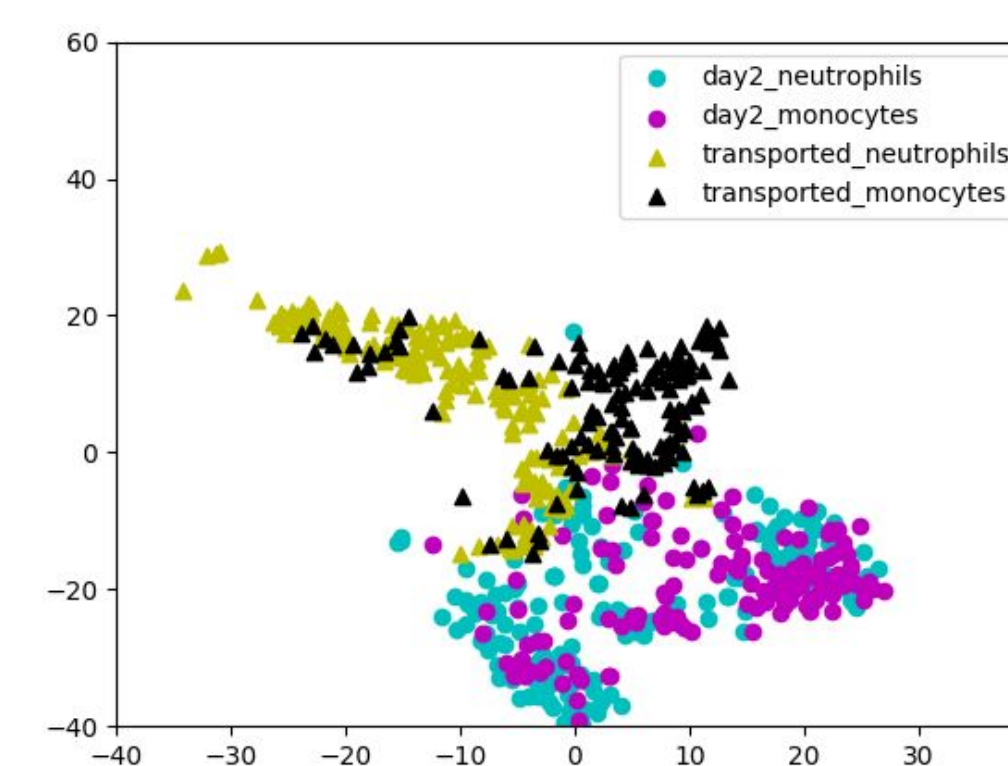
Transport Map



Visualizing Predicted Cell Differentiation Trajectories



Actual



Predicted (Super-OT: 600)

Super-OT separates the Neutrophil/Monocyte distributions correctly and there is considerable overlap between the transported cell distribution and ground truth as shown in the t-SNE plots.

Conclusions

- Super-OT is a new framework for computational lineage tracing that combines a supervised learning framework with Optimal Transport based on GANs
- Super-OT achieves gains over conventional lineage tracing methods by integrating additional information during training

References

Yang, K. D. and Uhler, C. Scalable unbalanced optimal transport using generative adversarial networks. International Conference on Learning Representations, 2019.

Weinreb, C., Rodriguez-Fraticelli, A., Camargo, F. D., and Klein, A. M. Lineage tracing on transcriptional landscapes links state to fate during differentiation. Science, 367(6479), 2020