ACE: Explaining single-cell cluster from an adversarial perspective

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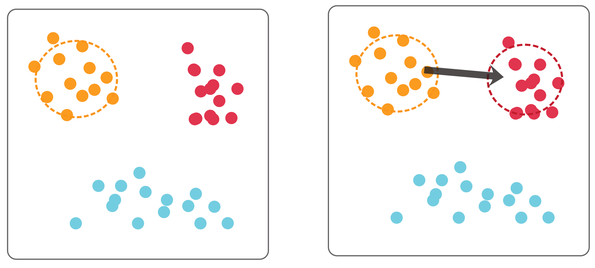
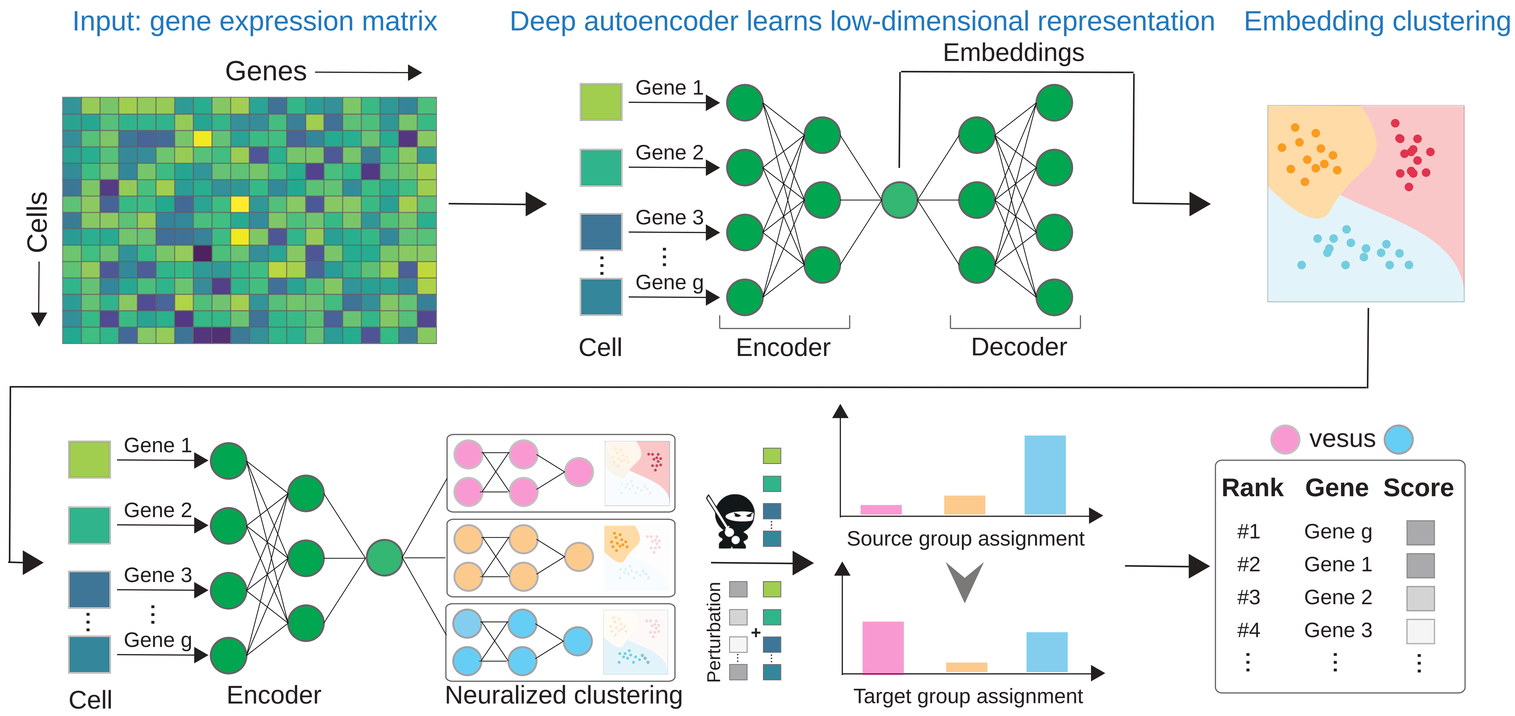
Overview

ACE (Adversarial Clustering Explanation) aims to identify differential genes in scRNA-seq data by joingly modelling:

- The uncertainty in nonlinear embedding of scRNA-seq data.
- The stochasticity in cluster assignments.
- The dependency among genes.
- Both enriched and depleted genes relative to other cell types.

ACE supports the following setups



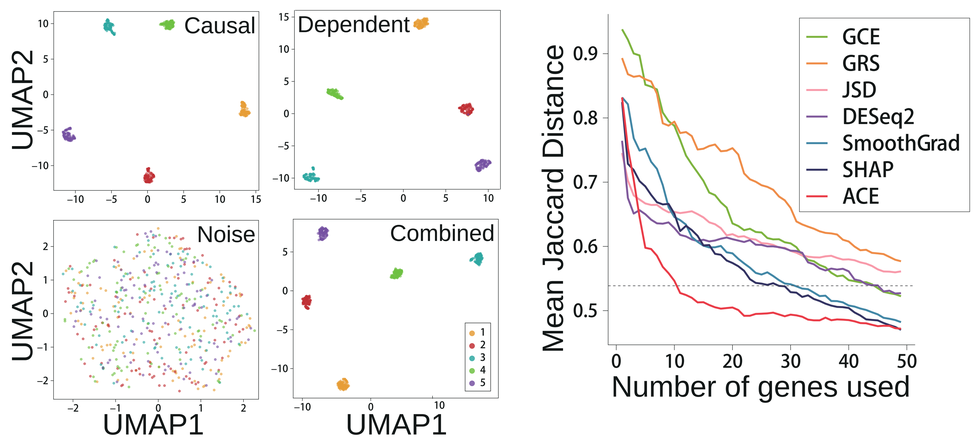


Performance on simulated data

We use SymSim [1] to simulate causal and noise genes for 500 cells

- 20 causal genes, 100 noise genes
- 100 dependent genes are weighted sums of random causal genes with noises

We use Mean Jaccard Distance to quantify how well the top k genes in the ranking capture the clustering structure

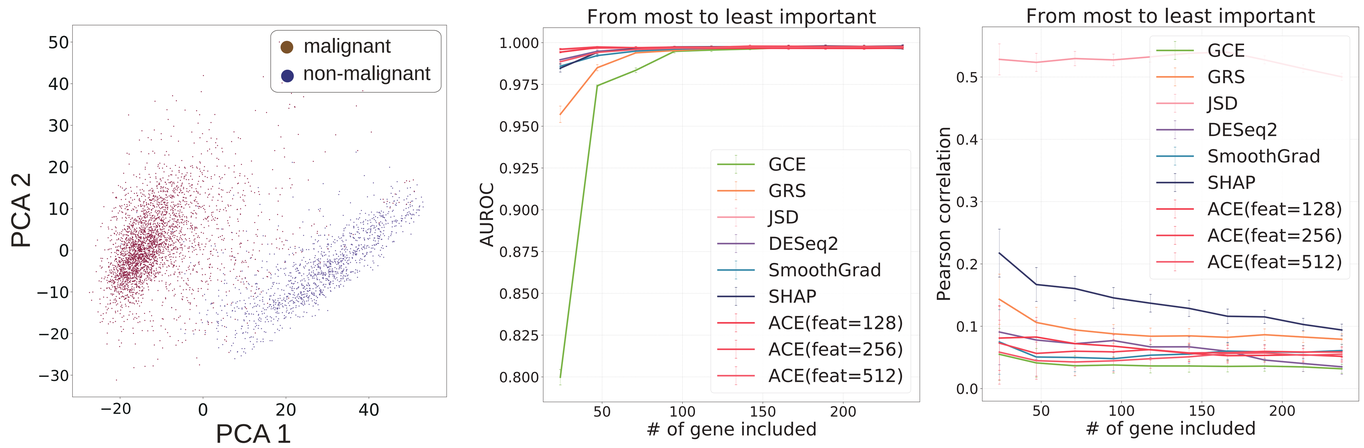


Performance on melanoma dataset [2]

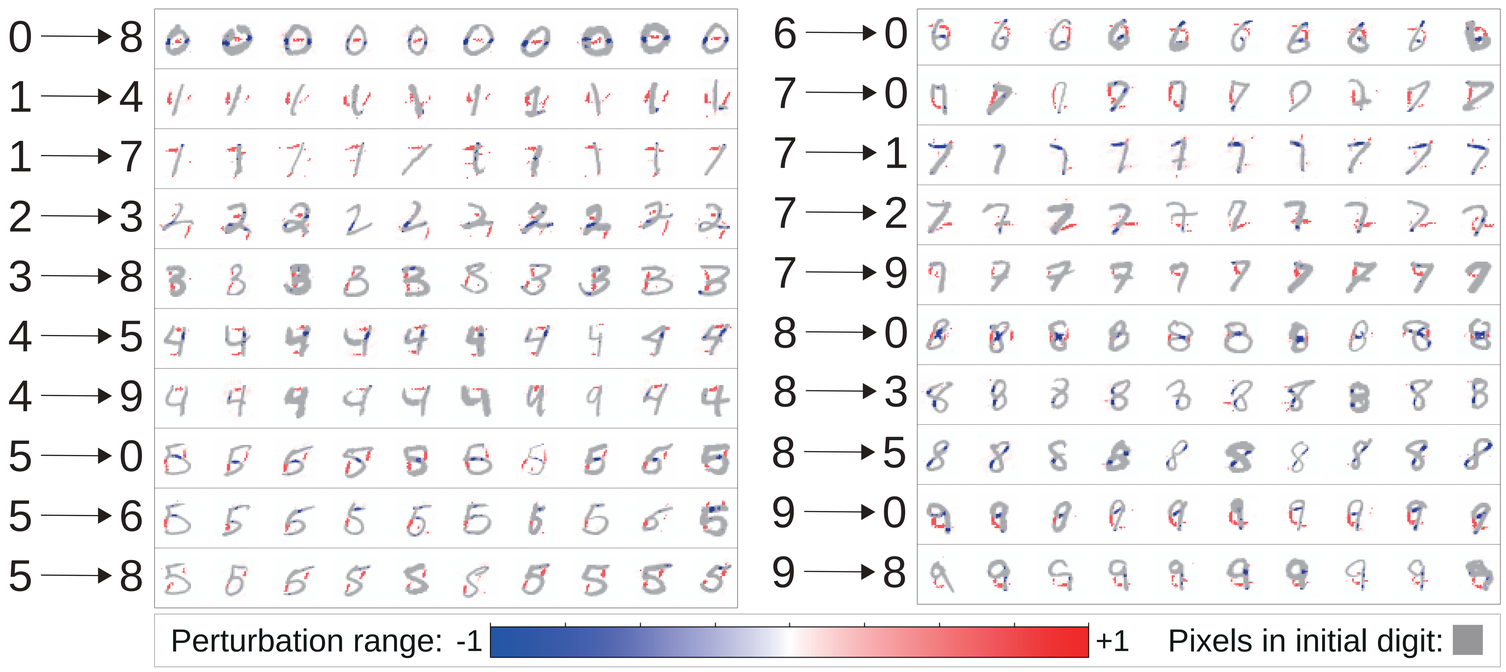
The cell labels are determined by copy number variation instead of data-driven

- Two cell types: malignant vs. non-malignant
- 4513 cells (1257 malignant and 3256 non-malignant), 23686 genes

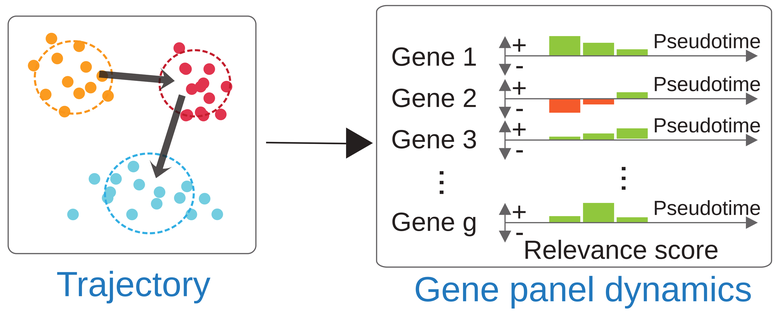
We want the top k genes in the ranking to be both highly discriminative and lowly redundant



Performance on MNIST dataset



Future work



Reference

[1] Zhang, et al. "Simulating multiple faceted variability in single cell RNA sequencing." Nature Communications 10.1 (2019): 1-16.

[2] Tirosh, et al. "Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq." Science 352.6282 (2016): 189-196.