SCREEN: predicting single-cell gene expression perturbation responses via optimal transport

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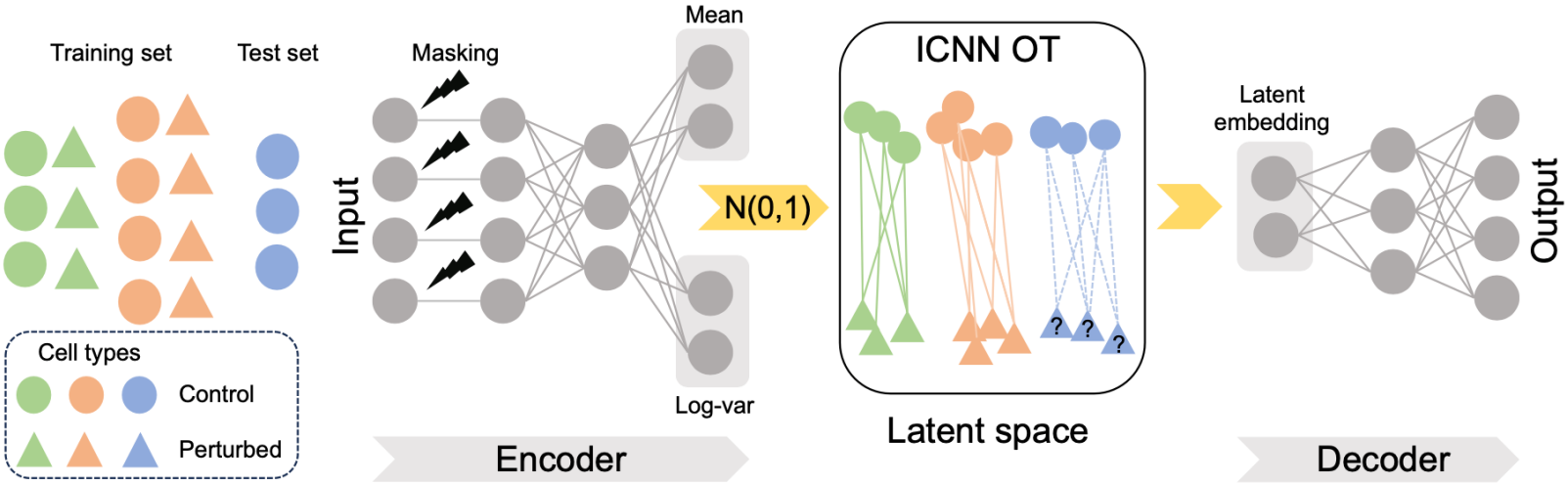
Problems & Ideas

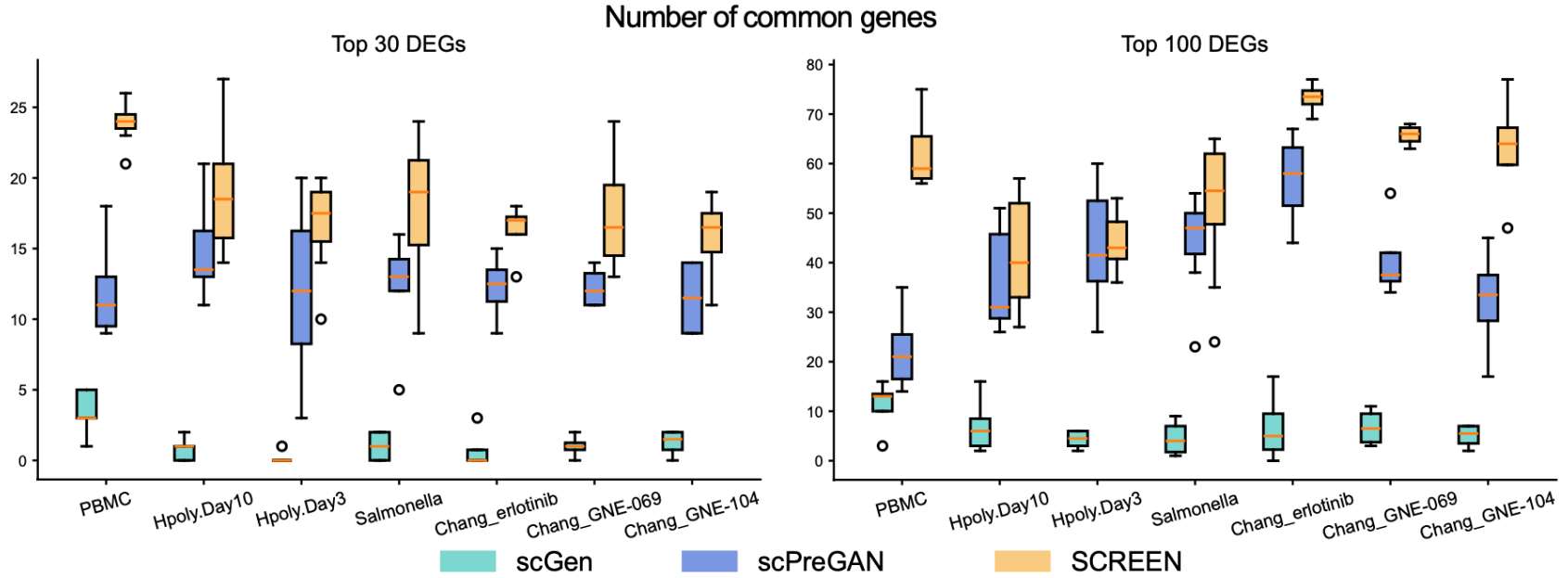
- Problems of single-cell perturbation analysis:
  - Obtaining perturbed samples can be challenging in some cases.
  - The high cost associated with sequencing limits the feasibility of large-scale experiments.
  - There is still room for further improving the prediction accuracy of computational methods.
- Ideas: A generative model based on masked variational autoencoder and optimal transport mapping



The graphical illustration of our proposed SCREEN model. SCREEN is based on masked variational autoencoder (MVAE) and input convex neural network optimal transport (ICNN OT).

Main Contributions

- Contributions:
  - SCREEN predicts single-cell gene expression perturbation responses more accurately than baseline methods.
  - The results of SCREEN can preserve the inherent biological implication, offering valuable support for downstream analyses.
  - SCREEN shows advantages in various scenarios with superior robustness to noise/sparsity degree, number of cell types, and cell type imbalance.



Performance of different methods on various datasets evaluated by the number of common genes between the two sets of differentially expressed genes (DEGs) derived from true and predicted responses, respectively.