scSSL-Bench: Benchmarking Self-Supervised Learning for Single-Cell Data



Florian Barkmann

Philip Toma

Imant Daunhawer

Julia Vogt Sebastian Schelter

Valentina Boeva







Motivation

- Why is genomics analysis an important research direction?
 - Profile cells at different resolutions and modalities
 - Understand diseases, develop personalized treatments, trace origins of conditions like cancer and autoimmune disorders
- What is single-cell data?
 - High-dimensional gene expression (GEX) levels in individual cells
 - Additional molecular features measured together with GEX
 - Protein levels
 - Open chromatin accessibility

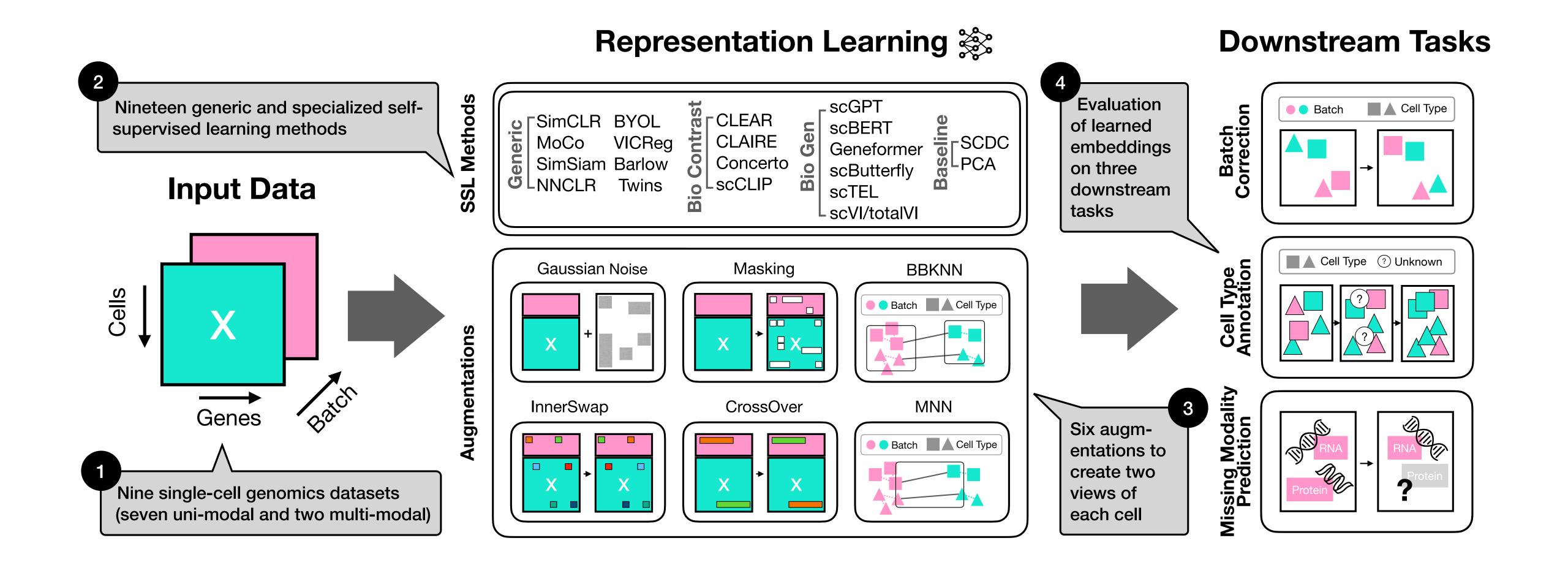
Why is a Benchmark Needed?

 Self-supervised learning (SSL) is a powerful approach for the representation extraction from single-cell data

Research questions:

- Benchmark if specialized single-cell SSL methods outperform generic methods
- Assess hyperparameters and augmentation techniques of generic SSL approaches
- Evaluate if genomics benefit from techniques proposed for images

scSSL-Bench Design



Downstream Tasks on Learned Cell Representations

Batch effect correction

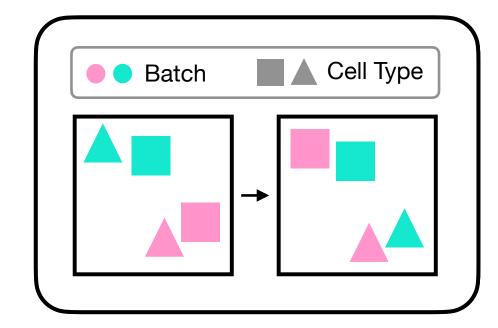
- Reduce technical biases introduced while sequencing
- Preserve true biological signal

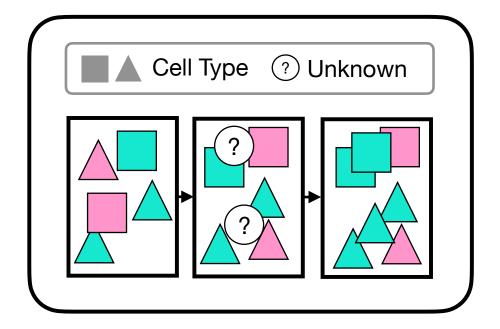
Cell typing

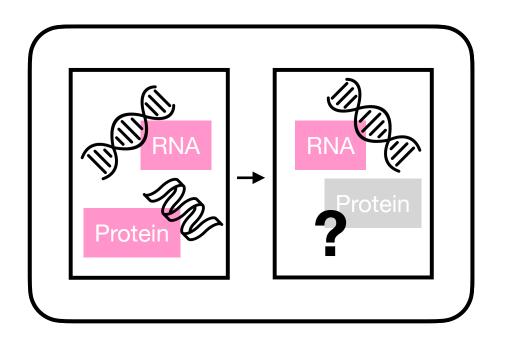
 Annotate cells of hold-out dataset by mapping them to seen cells

Missing modality prediction

Infer unmeasured modalities for the hold-out dataset



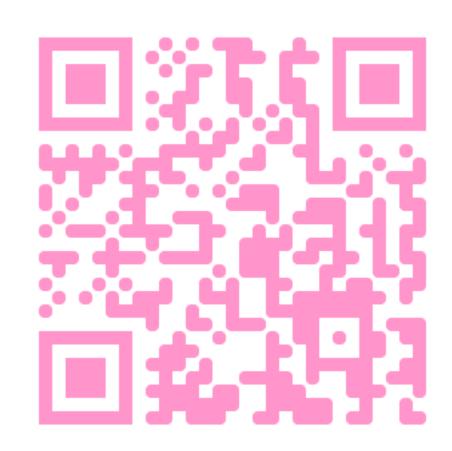




Conclusions

- Specialized single-cell SSL methods work better for uni-modal data
 - scVI, CLAIRE, fine-tuned scGPT
- Generic SSL methods succeed in multi-modal single-cell data integration
 - SimCLR, VICReg
- Masking is the best augmentation technique
- Moderately-sized embeddings lead to better results

scSSL-Bench: Benchmarking Self-Supervised Learning for Single-Cell Data



Code



Paper



Contact Me





