

Learning cell identities and (post-)transcriptional regulation using single-cell data

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Citation

Michielsen, L. C. M. (2024, June 13). *Learning cell identities and (post-)transcriptional regulation using single-cell data*. Retrieved from https://hdl.handle.net/1887/3763527

Version:	Publisher's Version
License:	Licence agreement concerning inclusion of doctoral thesis in the Institutional Repository of the University of Leiden
Downloaded from:	https://hdl.handle.net/1887/3763527

Note: To cite this publication please use the final published version (if applicable).

Stellingen behorend bij het proefschrift getiteld

Learning cell identities and (post-) transcriptional regulation using single-cell data

- 1. Rare or diseased cell types in single-cell RNA sequencing data cannot be detected using the posterior probability as a rejection option (this thesis).
- 2. Researchers' trust in manual annotations obtained using clustering instead of classification is unjustified since the former has more mistakes and lacks consistency (this thesis).
- 3. We need sequence-based models trained on single-cell RNA sequencing data to understand transcriptional regulation in heterogeneous tissues (this thesis).
- 4. Sequence-based models must be trained on individual genomes and perturbation data to increase the variation in the training data (this thesis).
- 5. Using popular, trending terms, such as foundation models, distracts users and reviewers from a model's actual functionalities and performance and hinders scientific progress.
- 6. Cells form a continuum, but discrete cell types are needed to facilitate downstream analysis.
- 7. The human cell atlas will always be incomplete so a correctly working rejection option will remain necessary for classification methods.
- 8. Single-cell reference atlases are better built per tissue than organismwide.
- 9. Men must take the same time of paternity leave as women to enforce equal career opportunities.
- 10. Generative models such as ChatGPT and Dall-E must show users their carbon footprint.