



FACULTY OF VETERINARY MEDICINE
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Studying dynamic processes with networks and trajectories

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Doctor in Computer Science, 2019

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Acknowledgements

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CHAPTER 1

Introduction

Abstract: Recent developments in single-cell transcriptomics have opened new opportunities for studying dynamic processes in immunology in a high-throughput and unbiased manner. Starting from a mixture of cells in different stages of a developmental process, unsupervised trajectory inference algorithms aim to automatically reconstruct the underlying developmental path that cells are following. In this review, we break down the strategies used by this novel class of methods, and organize their components into a common framework, highlighting several practical advantages and disadvantages of the individual methods. We also give an overview of new insights these methods have already provided regarding the wiring and gene regulation of cell differentiation. As the trajectory inference field is still in its infancy, we propose several future developments which will ultimately lead to a global and data-driven way of studying immune cell differentiation.

Adapted from:

Cannoodt, R.*, Saelens, W.*, and Saeys, Y. Computational methods for trajectory inference from single-cell transcriptomics. *European Journal of Immunology* 46, 11 (2016), 2496–2506. doi:10.1002/eji.201646347.

* Equal contribution

1.1 Single cell biology

1.1.1 Dynamic processes

1.1.2 Gene regulation

1.1.3 Single cell transcriptomics

1.2 Machine learning

1.2.1 Supervised learning

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A comparison of single-cell trajectory inference methods

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Adapted from:

Saelens, W.*, **Cannoodt, R.***, Todorov, H., and Saeys, Y. A comparison of single-cell trajectory inference methods. *Nature Biotechnology* 37, 5 (2019), 547–554. doi:10.1038/s41587-019-0071-9.

* Equal contribution

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Fast, accurate, and robust single-cell pseudotime

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Adapted from:

Cannoodt, R., . . . , De Preter, K., and Saeys, Y. SCORPIUS improves trajectory inference and identifies novel modules in dendritic cell development. *Journal* vol, issue (2019), page–page. doi:10.1101/079509v2.

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A toolkit for inferring and interpreting trajectories

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Inferring single cell regulatory networks

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Adapted from:

Cannoodt, R., Saelens, W., and Saeys, Y. Inferring Single Cell Regulatory Networks. *Journal* vol, issue (2019), page–page. doi.

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Optimising regulatory networks

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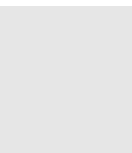
Cannoodt, R., Ruyssinck, J., Ramon, J., De Preter, K., and Saeys, Y. IncGraph: Incremental graphlet counting for topology optimisation. *PLOS ONE* 13, 4 (2018), e0195997. doi:10.1371/journal.pone.0195997.

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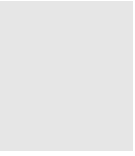
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7.1 Overview and conclusions of the presented work

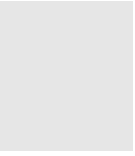
7.2 Future research directions



Samenvatting



Summary



List of Publications
