



# Robrecht Cannoodt

SOFTWARE ENGINEER · DATA SCIENTIST

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## Hello! This is me.

- I'm a software engineer specialised in data science. I'm a father-of-one, and a very lucky man.
- I enjoy the company of weird people, but even more so the company of people who are true to themselves.
- I (try to) approach problems from multiple perspectives. Some people believe I'm just a slow thinker.

## Education

### VIB – Ghent University

Ghent, Belgium

PHD IN COMPUTER SCIENCE

Sep 2013 - Dec 2019

- Dissertation: "Modelling single-cell dynamics with trajectories and gene regulatory networks"
- Science Communication skills: Academic Writing, Presenting, and Data Visualisation
- Bioinformatics skills: Single-Cell Omics, Gene Regulatory Network Inference, Trajectory Inference,
- Data Science skills: Data Analysis, Data Wrangling, Benchmarking, (Co-)authored 24 R Software Packages
- Soft skills: Mentor for 6 Master Thesis Students, Teaching Assistant 6 times, Intense collaborations with PhD students

### Ghent University

Ghent, Belgium

MASTER OF SCIENCE IN COMPUTER SCIENCE ENGINEERING: SOFTWARE ENGINEERING

Sep 2011 - Jun 2013

- Master Thesis: "Network inference by integrating biclustering and feature selection"
- Programming courses: Programming Languages, Functional Programming
- Engineering courses: Software Architecture, Advanced Computer Architecture, Distributed Software, High Performance Computing
- Other courses: Philosophy and Science, Robotics, Computational Biology

### Ghent University

Ghent, Belgium

BACHELOR OF SCIENCE IN INFORMATICS

Sep 2008 - Jun 2011

- Engineering courses: Software Development, Programming, Scripting, Operating Systems, Computer Architecture, Network Management
- Computer Science courses: Machine Learning, Algorithms and Data Structures, Formal Logic
- Math courses: Statistics, Linear Algebra, Geometry, Discrete Math, Calculus

### International School of Berne

Berne, Switzerland

INTERNATIONAL BACCALAUREATE

Sep 2003 - Jul 2007

- Taught in English
- Main courses: Math, Physics, Philosophy, Visual Arts

## Skills

### Research Domains

Data Science, Machine Learning, Software Engineering, Bioinformatics

### Communication

Effective Data Visualisation, Academic Writing, Presentations (Technical and Non-technical)

### Programming

R, Scala, Java, C++, bash, awk, sed, MySQL, RMarkdown,  $\text{\LaTeX}$

### Software Development

Git, Docker, Singularity, Travis CI, UML, Agile/Scrum

### Languages

Dutch (Native), English (Fluent), French (If-need-be), Hindi (None at all)

## Software

Below is a selection of software projects. Visit [cannoodt.dev/software](https://cannoodt.dev/software) for a full list of software I've (co-)authored.

1. Watanabe K and **Cannoodt R**. proxyC: Computes Proximity in Large Sparse Matrices. Role: Contributor. <https://CRAN.R-project.org/package=proxyC>
2. Hastie T, Weingessel A, Hornik K, Bengtsson H and **Cannoodt R**. princurve: Fits a Principal Curve in Arbitrary Dimension. Role: Maintainer. <https://CRAN.R-project.org/package=princurve>
3. **Cannoodt R** and Saelens W. GillespieSSA2: Gillespie's Stochastic Simulation Algorithm for Impatient People. Role: Lead Developer. <https://CRAN.R-project.org/package=GillespieSSA2>
4. **Cannoodt R** and Saelens W. dyno: Inferring, interpreting and visualising trajectories using a streamlined set of packages. Role: Lead Developer. <https://github.com/dynverse/dyno>
5. **Cannoodt R** and Saelens W. lmds: Landmark Multi-Dimensional Scaling. Role: Lead Developer. <https://CRAN.R-project.org/package=lmds>
6. **Cannoodt R** and Saelens W. SCORPIUS: Inferring Developmental Chronologies from Single-Cell RNA Sequencing Data. Role: Lead Developer. <https://CRAN.R-project.org/package=SCORPIUS>
7. **Cannoodt R** and Saelens W. babelwhale: Talking to Docker and Singularity Containers. Role: Lead Developer. <https://CRAN.R-project.org/package=babelwhale>

## Publications

Below is a selection of publications. Visit [cannoodt.dev/publication](https://cannoodt.dev/publication) or my ORCID profile for a full list of publications.

1. Saelens W\*, **Cannoodt R**\*, Todorov H, Saeys Y. A comparison of single-cell trajectory inference methods. *Nature Biotechnology*. 2019 Apr 1;37(5):547–54. doi:10.1038/s41587-019-0071-9
2. Todorov H, **Cannoodt R**, Saelens W, Saeys Y. Network Inference from Single-Cell Transcriptomic Data. *Gene Regulatory Networks*. 2018 Dec 14;235–49. doi:10.1007/978-1-4939-8882-2\_10
3. Weber LM, Saelens W, **Cannoodt R**, Sonesson C, Hapfelmeier A, Gardner PP, et al. Essential guidelines for computational method benchmarking. *Genome Biology*. 2019 Jun 20;20(1). doi:10.1186/s13059-019-1738-8
4. Saelens W, **Cannoodt R**, Saeys Y. A comprehensive evaluation of module detection methods for gene expression data. *Nature Communications*. 2018 Mar 15;9(1). doi:10.1038/s41467-018-03424-4
5. **Cannoodt R**, Saelens W, Sichien D, Tavernier S, Janssens S, Guillems M, et al. SCORPIUS improves trajectory inference and identifies novel modules in dendritic cell development. *bioRxiv*; 2016 Oct 6; doi:10.1101/079509
6. **Cannoodt R**\*, Saelens W\*, Saeys Y. Computational methods for trajectory inference from single-cell transcriptomics. *European Journal of Immunology*. 2016 Oct 19;46(11):2496–506. doi:10.1002/eji.201646347

\*: Equal contribution

## Teaching

### TEACHING ASSISTANT

2014	Bioinformatics: lessons in R	<i>Biomedical sciences</i>
2015	Bioinformatics: lessons in R	<i>Biomedical sciences</i>
2016	Bioinformatics: lessons in R	<i>Biomedical sciences</i>
2017	Bioinformatics: lessons in R	<i>Biomedical sciences</i>
2018	Bioinformatics: lessons in R	<i>Biomedical sciences</i>
2019	Bioinformatics: lessons in R	<i>Biomedical sciences</i>

### MASTER THESIS GUIDANCE

2013-2014	Identificatie van nieuwe kankergenen voor neuroblastoomonderzoek met machine learning	<i>Leen De Baets</i>
2013-2014	Locale cel-type specifieke genexpressie in het myeloïde transcriptoom	<i>Wouter Saelens</i>
2015-2016	Quantitative evaluation of network inference methods for single-cell cancer regulomes	<i>Charlotte De Vogelaere</i>
2015-2016	Comparative review of dimensionality reduction methods for high-throughput single-cell transcriptomics	<i>Sofie Veys</i>
2016-2017	Het afleiden van dynamische grafen op basis van snapshot data	<i>Chloë Guidi</i>
2018-2019	Inferentie van cellontwikkelingstrajecten met machine learning	<i>Jarre Knockaert</i>

## Conferences and workshops

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### ACCEPTED TALKS

2013	Network inference by integrating biclustering and feature selection, BeNeLux Bioinformatics Conference	Brussels, Belgium
2015	Differential module analysis in neuroblastoma regulatory networks, Oncopoint	Ghent, Belgium
2015	Inferring developmental chronologies from single cell RNA, BeNeLux Bioinformatics Conference	Antwerp, Belgium
2016	SCORPIUS: Inferring trajectories along dynamic processes from single-cell RNA-seq data, Single Cell Biology Workshop	Ghent, Belgium
2016	Improving marker gene discovery from high-dimensional single-cell snapshot data, CYTO	Seattle, USA
2016	Unbiased modelling of dynamic processes with single-cell RNA-sequencing, BENELEARN	Kortrijk, Belgium
2017	Unbiased modelling of dynamic processes identifies novel modules in dendritic cell development, VIB Seminar	Veldhoven, Netherlands
2019	Automated building and unit testing, Docker and Singularity, VIB Developers Meeting	Ghent, Belgium
2019	Assessing Accuracy, Robustness and Usability of Single-Cell Trajectory Inference methods, Keystone Symposia: Single Cell Biology	Colorado, USA

### ACCEPTED POSTERS

2014	Network Inference by Integrating Biclustering and Feature Selection, N2N Annual Symposium	Ghent, Belgium
2014	Differential Module Analysis in Neuroblastoma Regulatory Networks, BeNeLux Bioinformatics Conference	Luxembourg, Belgium
2015	Differential Module Analysis in Neuroblastoma Regulatory Networks, BIG N2N symposium	Ghent, Belgium
2016	Unbiased modelling of dynamic processes with single-cell RNA-sequencing, Single Cell Biology	Hinxton, United Kingdom
2016	Unbiased modelling of dynamic processes with single-cell RNA-sequencing, BIG N2N symposium	Ghent, Belgium
2016	Improving marker gene discovery from high-dimensional single-cell snapshot data, CYTO	Seattle, USA
2016	Unbiased modelling of dynamic processes with single-cell RNA-sequencing, BENELEARN	Kortrijk, Belgium
2016	Unbiased modelling of dynamic processes with single-cell RNA-sequencing, Single Cell Genomics	Hinxton, United Kingdom
2017	Unbiased modelling of dynamic processes with SCORPIUS identifies novel modules in dendritic cell development, VIB Seminar	Veldhoven, Netherlands
2017	True single cell network inference: Modelling gene regulation of individual cells, Keystone Symposia: Single Cell Omics	Stockholm, Sweden
2017	Generalised framework for and comparison of 24 trajectory inference methods, BeNeLux Bioinformatics Conference	Louvain, Belgium
2018	A comparison of single-cell trajectory inference methods: towards more accurate and robust tools, Single Cell Biology	Hinxton, United Kingdom
2019	Assessing Accuracy, Robustness and Usability of Single-Cell Trajectory Inference methods, Keystone Symposia: Single Cell Biology	Colorado, USA