# Robrecht **Cannoodt**

SOFTWARE ENGINEER · DATA SCIENTIST

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## **Hel**lo! 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.

## **Edu**cation

### **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: Mentored 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

## **Ski**lls

| | |
|---|---|
| **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, 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 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 Deverloper. `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 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**, Soneson 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, Guilliams 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 | *Biomedical sciences* |
| 2015 | Bioinformatics: lessons in R | *Biomedical sciences* |
| 2016 | Bioinformatics: lessons in R | *Biomedical sciences* |
| 2017 | Bioinformatics: lessons in R | *Biomedical sciences* |
| 2018 | Bioinformatics: lessons in R | *Biomedical sciences* |
| 2019 | Bioinformatics: lessons in R | *Biomedical sciences* |

## MASTER THESIS GUIDANCE

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

# Conferences and workshops

## 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* |