

Curriculum vitae

➤ PERSONAL INFORMATION

Family name: Gilis

First name: Jeroen

Nationality: Belgian

Date of birth: 28/07/1994

Personal website: <https://jqilis.github.io>

Researcher unique identifier (ORCID): 0000-0001-8415-0943

➤ Experience

- 2024-current *Postdoctoral researcher, Chalmers University of Technology, Sweden*
Supervisor: Docent Eduard Kerkhoven
- 2018-2024 *PhD candidate in data science, Ghent university, Belgium*
Supervisors: Prof. Lieven Clement, Prof. Yvan Saeys and Dr. Koen Van den Berge
- 2017-2019 *Master of science in bioinformatics - summa cum laude - Ghent university, Belgium*
Master thesis: Scalable differential transcript usage analysis for single-cell applications, under supervision of Prof. Lieven Clement and Dr. Koen Van den Berge
- 2015-2017 *Master of science in biochemistry & biotechnology - magna cum laude - Leuven university, Belgium*
Master thesis: Modification of TPS1 for increased acetic acid tolerance in second generation bioethanol fermentations, under supervision of Prof. Johan Thevelein
- 2012-2015 *Bachelor of science in biochemistry and biotechnology, Leuven university, Belgium*

➤ FELLOWSHIPS AND AWARDS

- 2019-2023 *Scholarship from Research Foundation Flanders, competitive fund for 4-year research PhD research grants*

➤ PUBLICATIONS (before November 2024)

1. Malfait M, Gilis J*, Van den Berge K, Takele Assefa A, Verbist B, and Clement L. (2024) Strategies for addressing pseudoreplication in multi-patient scRNA-seq data, bioRxiv
2. Gilis J*, Perin L, Malfait M, Van den Berge K, Takele Assefa A, Verbist B, Risso D and Clement L. (2023) Differential detection workflows for multi-sample single-cell RNA-seq data, bioRxiv

3. Browaeys R, Gilis J*, Sang-Aram C, De Bleser P, Hoste L, Tavernier SJ, Lambrechts D, Seurinck R and Saeys Y. (2023) MultiNicheNet: a flexible framework for differential cell-cell communication analysis from multi-sample multi-condition single-cell transcriptomics data, bioRxiv
4. Segers A, Gilis J*, Van Heetvelde M, De Baere E and Clement L. (2023) Juggling offsets unlocks RNA-seq tools for fast scalable differential usage, aberrant splicing and expression analyses, bioRxiv
5. Sonrel A, Luetge A, Soneson C, Mallona Gonzalez I, Germain PL, Knyazev S, Gilis J*, Gerber R, Seurinck R, Paul D, Sonder E, Crowell HL, Fanaswala I, Al Ajami A, Heidari E, Schmeing S, Milosavljevic S, Saeys Y, Mangul S and Robinson MD. (2023) Meta-analysis of (single-cell method) benchmarks reveals the need for extensibility and interoperability, Genome Biology 24, 1
6. Gilis J*, Vitting-Seerup K, Van den Berge K and Clement L. (2022) satuRn: Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications. F1000Research 10, 374
7. Gilis J*, Taelman S, Davey L, Martens L and Clement L. (2020) Pitfalls in re-analysis of observational omics studies: a post-mortem of the human pathology atlas, bioRxiv

➤ **INTERSHIPS**

2016 *Beer laboratory Delvaux* – Topic: Characterization of phenolic acids and enzyme activity in barley varieties used for beer production, under supervision of Dr. Filip Delvaux

➤ **SUPERVISION OF GRADUATE STUDENTS**

2022-2023 *Laura Perin, master thesis student, Padova University, Italy*
 Thesis title: Differential detection and differential expression in single-cell RNA-seq data
 Joint supervision with Prof. Lieven Clement (Ghent University) and Prof. Davide Risso (Padova University)

2021-2022 *Tim Meese, master thesis student, Ghent University, Belgium*
 Thesis title: Sub-gene level differential expression analysis for droplet single-cell RNA-seq data
 Joint supervision with Prof. Lieven Clement (Ghent University)

2021-2022 *Dingrongruo Yu, master thesis student, Ghent University, Belgium*
 Thesis title: Differential transcript usage along single-cell gene expression trajectories
 Joint supervision with Prof. Lieven Clement (Ghent University)

➤ **TEACHING ACTIVITIES**

2018-2023 *Teaching assistant* – Statistics, semester course, taught to BSc. students in chemistry, biochemistry, biology, geology and biomedical sciences, Ghent University, Belgium

2022 *Instructor* – Single-cell transcriptomics data analysis, specialist short course, taught to PhD candidates, post-docs and researchers from the life sciences industry, Ghent University,

Belgium

2020-2021 *Co-instructor* – Practical statistics for the life sciences, crash course, taught to graduate students and PhD candidates, Gulbenkian institute, Oeiras, Portugal

➤ **SOFTWARE**

Author *satuRn* – Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications, R, Bioconductor

Contributor *isoformSwitchAnalyzeR* – Identifying, annotating, and visualizing alternative splicing and isoform switches with functional consequences from both short- and long-read RNA-seq data, added a new functionality to the package to support differential expression tests with *satuRn*, written in R, available from Bioconductor

Contributor *fishpond* – Contains methods for differential transcript and gene expression analysis of RNA-seq data using inferential replicates for uncertainty of abundance quantification, as generated by Gibbs sampling or bootstrap sampling, added a new functionality to the package to support working with Salmon and Alevin quantification files, written in R, available from Bioconductor

Contributor *TENxPBMCDData* – Data package that allows for easy access to single-cell RNA-seq data generated with the 10X Genomics technology on PBMC cells, added new a CITE-seq dataset to the package, written in R, available from Bioconductor

➤ **RESEARCH VISITS**

2023 Visited the group of Prof. Davide Risso, 3 weeks, Padova University, Italy

2022 Visited the group of Prof. Mark Robinson, group hackathon event, 3 days, Zurich University, Switzerland