Curriculum vitae

➢ *PERSONAL INFORMATION*

Family name: Gilis

First name: Jeroen

Nationality: Belgian

Date of birth: 28/07/1994

Personal website: https://jgilis.github.io

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

➢ *EDUCATION*

2018-current *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*

➢ *Internships*

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

➢ *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	*TENxPBMCData* – Data package that allows for easy acces 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

➢ *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

➢ *Research visits*

2023 *Research group of Prof. Davide Risso, 3 weeks, Padova University, Italy*

2022 *Research group of Prof. Mark Robinson, group hackathon event, 3 days, Zurich University, Switzerland*