Curriculum Vitae

Koen Van den Berge

March 21, 2021

Personal Data

Place and Date of Birth: Ghent, Belgium | 21 October 1990
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Professional Experience

Current | Postdoctoral Researcher, University of California, Berkeley and Ghent University
Nov 2019 | Supervisors: Prof. Dr. Sandrine Dudoit & Prof. Dr. Lieven Clement

In my postodoctoral research, I am developing statistical methods to interpret single-cell RNA-seq and ATAC-seq datasets. My projects include statistical analysis of networks, including gene regulatory networks, estimation of transcription factor activity, multi-patient differential expression analysis in single-cell RNA-seq data.

Oct 2019 | PhD student, Ghent University, Belgium
Oct 2014 | Supervisor: Prof. Dr. Lieven Clement

My PhD research, situated in the field of statistical genomics, focussed on the development and implementation of statistical methods for high-throughput biological data. In particular, I have developed powerful multiple testing strategies and novel differential expression analysis tools for bulk RNA-seq and single cell RNA-seq data, in addition to the development of normalization procedures for ATAC-seq data. All procedures were implemented as open-source software in the form of R packages.

June 2018 | Visiting Scholar, University of California, Berkeley, USA
April 2018 | Supervisor: Prof. Dr. Sandrine Dudoit

During my research visit to the Dudoit lab at UC Berkeley, I have developed normalization procedures for ATAC-seq data, and statistical methods for assessing differential expression based on single-cell developmental trajectories.

December 2016, and May 2016 | Visiting Scholar, University of Zurich, Zurich, Switzerland
Supervisor: Prof. Dr. Mark Robinson

During my research visit (two weeks) to the Robinson lab at the University of Zurich, I have worked on developing stage-wise testing procedures and unlocking bulk RNA-seq methods to deal with zero inflation.

Education

2013-2014 Master of Science in Statistical Data Analysis, **Ghent University**, Belgium
Graduated with Great Distinction
Thesis title: " Temporal expression divergence of homeologous genes during seed development in *Arabidopsis thaliana"*
Thesis Advisor: Prof. Dr. Lieven Clement
Awarded Quetelet Prize from the International Biometric Society for outstanding Master thesis in the field of Biometrics

2011-2013 Master of Science in Biology , **Ghent University**, Belgium
Graduated with Great Distinction
Thesis title: "Habitat features affecting the Marsh harrier's (*Circus aeruginosus*) breeding success in intensively cultivated landscapes: a multi-scale approach"
Thesis Advisors: Dr. Anny Anselin, Prof. Dr. Luc Lens

2008-2011 Bachelor of Science in Biology, **Ghent University**, Belgium

Awards and Scholarships

- Postdoctoral fellowship (three years) from the Research Foundation Flanders, 2019, €166000.
- Fellowship for Post-doctoral research in the U.S.A. from the Belgian American Educational Foundation (BAEF), 2019, $45000.
- Bursary travel grant from the Genome Research Institute - Wellcome Genome Campus to attend the Genome Informatics Conference in Hinxton, UK, 2018, £ 181.
- Travel grant from the Research Foundation Flanders for a long research visit to the group of Prof. Sandrine Dudoit at the University of California, Berkeley, 2018, €3366.
- Award for best poster presentation at the International Biometric Conference, Vancouver, Canada, 2016.
- PhD grant from the Research Foundation Flanders, 2015, €168000.
- Quetelet prize from the International Biometric Society for an outstanding Master thesis in Biometrics, 2015, €250.

Publications

Co-first-authored publications are marked with a star (*).
Co-last-author publications are marked with a dagger (†).

- E. Bonneure, A. De Baets, S. De Decker, **K. Van den Berge**, L. Clement, W. Vyverman, S. Mangelinckx. Altering the sex pheromone Cyclo (I-Pro I-Pro) of the diatom Seminavis robusta towards a chemical probe. *International journal of molecular sciences* 22(3): 1037, 2021.
- F. Stock, G. Bilcke, S. De Decker, C.M. Osuna-Cruz, **K. Van den Berge**, E. Vancaester, L. De Veylder, K. Vandepoele, S. Mangelinckx. Distinctive growth and transcriptional changes of the diatom Seminavis robusta in response to quorum sensing related compounds. *Frontiers in Microbiology* 11:1240, 2020.
- T. Li, L. Lei, S. Bhattacharyya, **K. Van den Berge**, P. Sarkar, P. J. Bickel, E. Levina. Hierarchical community detection by recursive partitioning. *Journal of the American Statistical Association* (in print), 2020.
- Gust Bilcke*, **Koen Van den Berge***, Sam De Decker, Eli Bonneure, Nicole Poulsen, Petra Bulankova, Cristina Maria Osuna-Cruz, Jack Dickenson, Koen Sabbe, Georg Pohnert, Klaas Vandepoele, Sven Mangelinckx, Lieven Clement, Lieven De Veylder, Wim

Vyverman. Mating type specific transcriptomic response to sex inducing pheromone in the pennate diatom Seminavis robusta. *The ISME Journal*, 2020.

- D. H. Brann*, T. Tsukahara*, C. Weinreb*, M. Lipovsek, **K. Van den Berge**, B. Gong, R. Chance, I. C. Macaulay, H. Chou, R. Fletcher, D. Das, K. Street, H. Roux de Bezieux, Y. Choi, D. Risso, S. Dudoit, E. Purdom, J. S. Mill, R. A. Hachem, H. Matsunami, D. W. Logan, B. J. Goldstein, M. S. Grubb, J. Ngai, S. Robert Datta. Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. *Science Advances* 6:31, 2020.
  Featured in the Harvard Gazette: https://news.harvard.edu/gazette/story/2020/07/how-to-understand-covid-19-related-loss-of-smell/.
- **K. Van den Berge**, H. Roux de Bézieux, K. Street, W. Saelens, R. Cannoodt, Y. Saeys, S. Dudoit, L. Clement. Trajectory-based differential expression analysis for single-cell sequencing data. *Nature Communications* 11:1201, 2020.
  Top 50 read papers in 2020: This paper was included in the top 50 (out of 6400+) published papers of 2020, in the category 'Life and Biological Sciences' at *Nature Communications*.
- **K. Van den Berge***, K. Hembach*, C. Soneson*, S. Tiberi*, L. Clement, M. I. Love, R. Patro, M. D. Robinson. RNA sequencing data: hitchhiker's guide to expression analysis. *Annual Reviews in Biomedical Data Science* 2:139-173, 2019.
- M. Cougnon, **K. Van den Berge**, T. D'Hose, L. Clement, D. Reheul. Effect of management and age of ploughed out grass-clover on forage maize yield and residual soil nitrogen. *The Journal of Agricultural Science* 1-10, 2018.
- **K. Van den Berge***, F. Perraudeau*, C. Soneson, M. I. Love, D. Risso, J. P. Vert, M. D. Robinson, S. Dudoit, and L. Clement. Observation weights unlock bulk RNA-seq tools for zero inflation and single-cell applications. *Genome Biology* 19:24, 2018.
- S. Derycke, L. Kéver, K. Herten, **K. Van den Berge**, M. Van Steenberge, J. Van Houdt, L. Clement, P. Poncin, E. Parmentier, and E. Verheyen. Neurogenomic Profiling Reveals Distinct Gene Expression Profiles Between Brain Parts That Are Consistent in Ophthalmotilapia Cichlids. *Frontiers in Neuroscience* 12:136, 2018.
- **K. Van den Berge**, C. Soneson, M. D. Robinson, and L. Clement. stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. *Genome Biology* 18:151, 2017.
- S. Moeys, J. Frenkel, C. Lembke, J. T. F. Gillard, V. Devos, **K. Van den Berge**, B. Bouillon, M. J. J. Huysman, S. De Decker, J. Scharf, A. Bones, T. Brembu, P. Winge, K. Sabbe, M. Vuylsteke, L. Clement, L. De Veylder, G. Pohnert, and W. Vyverman. A sex-inducing pheromone triggers cell cycle arrest and mate attraction in the diatom Seminavis robusta. *Scientific Reports* 6:19252, 2016.

Preprints

- Z. Yao*, H. Liu*, F. Xie*, S. Fischer*, ... , **K. Van den Berge**, ... , H. Zeng*, E. Mukamel*. An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types. *bioRxiv,* doi: 10.1101/2020.02.29.970558.
- H. Roux de Bezieux, K. Street, S. Fischer, **K. Van den Berge**, R. Chance, D. Risso, J. Gillis, J. Ngai, E. Purdom, S. Dudoit. Improving replicability in single-cell RNA-Seq cell type discovery with Dune. *bioRxiv*, doi: 10.1101/2020.03.03.974220.
- **Brain Initiative Cell Census Network (BICCN)**. A multimodal cell census and atlas of the mammalian primary motor cortex. *bioRxiv*, doi: 10.1101/2020.10.19.343129.

- T.K.H. Nguyen, **K. Van den Berge**, M. Chiogna, D. Risso. Structure learning for zero-inflated counts, with an application to single-cell RNA-sequencing data. arXiv, doi: 2011.12044v1.
- J. Gilis, K. Vitting-Seerup, **K. Van den Berge**†, L. Clement†. satuRn: Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications. *bioRxiv*, doi: 10.1101/2021.01.14.426636.
- **K. Van den Berge**, H. Chou, H. Roux de Bézieux, K. Street, D. Risso, J. Ngai, S. Dudoit. Normalization benchmark of ATAC-seq datasets shows the importance of accounting for GC-content effects. *bioRxiv*, doi: 10.1101/2021.01.26.428252.

Software Packages

Authored packages

- tradeSeq: trajectory-based differential expression analysis for sequencing data (https://bioconductor.org/packages/release/bioc/html/tradeSeq.html)
- zingeR: zero inflated negative binomial gene expression in R (https://github.com/statOmics/zingeR).
- stageR: stage-wise analysis of high throughput gene expression data in R (http://bioconductor.org/packages/stageR/).

Contributions to

- slingshot: Identifying and characterizing continuous developmental trajectories in single-cell data (https://github.com/kstreet13/slingshot).
- zinbwave: Zero-Inflated Negative Binomial Model for RNA-Seq Data (https://bioconductor.org/packages/release/bioc/html/zinbwave.html).
- DESeq2: Differential gene expression analysis based on the negative binomial distribution (https://bioconductor.org/packages/release/bioc/html/DESeq2.html).

Teaching and mentoring

Fall 2020 **Co-lecturer**.
Statistical Genomics, Master in Statistical Data Analysis and Master in Bioinformatics.
Co-lecturer responsible for topics on single-cell data analysis and project supervision.

2014-2019 **Teaching assistant**.
Statistics, Second Bachelor year in Biology; Biochemistry & Biotechnology.
Responsible teaching assistant for all written and PC labs in a basic statistics course.

Workshops

- *Trajectory inference across conditions: differential expression and differential progression.* European Bioconductor Conference 2020 (virtual).
- *Trajectory inference across conditions: differential expression and differential progression.* Bioconductor Conference 2020, Boston (virtual).
- Bioinformatics Summer School 2019, Louvain-La-Neuve, July 1-5, 2019 (https://uclouvain-cbio.github.io/BSS2019/). Taught experimental design, bulk RNA-seq and single-cell RNA-seq together with Charlotte Soneson.
- R Bootcamp, Department of Statistics, University of California, Berkeley, August 10-13, 2020.

Mentored students

- Gust Bilcke, Master thesis student in Biology, Ghent University, 2015-2016. Project title: Molecular characterization of sex signalling in diatoms.
- Lana Goeminne, Master thesis student in Biochemistry and Biotechnology, Ghent University, 2015-2016. Project title: The origin of species: Cryptic genomic speciation in the pennate diatom Seminavis robusta.
- Tine Descamps, Master thesis student in Statistical Data Analysis, Ghent University, 2015-2016. Project title: Metagenomics Data Analysis with edgeR: using weights to unlock zero-inflation.
- Tim Meese, Master thesis student in Bioinformatics, Ghent University, 2017-2018. Project title: Filtering and data-driven hypothesis weighting for transcript-level RNA-seq data analysis.
- Jeroen Gilis, Master thesis student in Bioinformatics, Ghent University, 2018-2019. Project title: Simulation and differential analysis for transcript-level single-cell RNA-sequencing data.
- Ameek Bindra, Undergraduate research project, Department of Statistics, University of California, Berkeley, 2020. Project title: Normalization of DNA chromatin conformation (ATAC-seq) datasets.
- David Lyu and Star Liu, Undergraduate research project, Department of Statistics, University of California, Berkeley, 2020. Project title: Recovering datasets' true dimensionality, evaluating initialization and hyperparameters in non-linear dimensionality reduction.
- Svetlana Afanaseva, Master project, Department of Statistics, University of California, Berkeley, 2020. Project title: GC-content normalization of single-cell ATAC-seq datasets.
- Jeroen Gilis, PhD student, Department of Applied Mathematics, Computer Science and Statistics, Ghent University, 2019-current. Project title: Methods for differential expression analysis in single-cell transcriptomics at the gene and transcript level.

Reviews

Reviewed for following journals: Bioinformatics, Biometrics, Genome Biology, Nature Communications, Statistical Applications in Genetics and Molecular Biology, PNAS.
Editorial advice provided for: Nature Communications.

Presentations

Invited Presentations

- Why R? Foundation, February 2021.
  Interpretation of single-cell RNA-seq trajectories using additive models for differential expression analysis.
- Single-Cell Sequencing Virtual Symposium - Bay Area, October 2020.
  Interpretation of single-cell RNA-seq trajectories using differential expression and differential progression analysis.
- Statistics in Genomics Seminar Series, University of California, Berkeley. May 2018.
  Stage-wise testing for differential expression analysis in sequencing studies.
- Annual Meeting of the Belgian Statistical Society, Leuven, Belgium. October 2015.
  Quantifying expression divergence of duplicated genes with microarrays.

Contributed Presentations

- Bioconductor conference 2020, Boston (virtual), USA, July 2020.
  Interpretation of single-cell RNA-seq trajectories using differential expression and differential progression analysis.

- f-Tales, Ghent, Belgium. September 2018.
  Continuous differential expression analysis for single-cell RNA-seq data.
- Genome Informatics, Hinxton, UK. September 2018.
  Discrete and continuous differential expression analysis for single-cell RNA-seq data.
- European Bioconductor Conference, Cambridge, UK. December 2017.
  Unlocking RNA-seq tools for zero inflation and single cell applications using ZINB-WaVE observation weights.
- Internal Biostatistics Seminar, group of Mark Van de Wiel, Vrije Universiteit Amsterdam, Amsterdam, Netherlands. June 2017.
  A general and powerful stage-wise testing procedure for differential expression and differential transcript usage.
- International Biometric Society Channel Conference, Hasselt, Belgium. April, 2017.
  A general and powerful stage-wise testing procedure for differential expression and differential transcript usage.
- Bioinformatics Seminar, University of Zurich, Zurich, Switzerland. May 2016.
  Unlocking edgeR for zero inflation.

Languages

Dutch:	Mothertongue
English:	Fluent
French:	Good
German:	Basic knowledge

Other

- September-October 2017: Volunteer at Batumi Raptor Count (BRC). The BRC project monitors populations of migrating raptor species in order to provide useful data for conservation and population trends. I was a volunteer at the counting station in Batumi, Georgia.
- Fall 2020: Member of anti-racism reading group in the Department of Statistics at University of California, Berkeley.