

Curriculum Vitae

Koen Van den Berge

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PERSONAL DATA

PLACE AND DATE OF BIRTH: Ghent, Belgium | 21 October 1990
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PROFESSIONAL EXPERIENCE

<i>Current</i> FEB 2022	Principal Statistician, Janssen R&D, Belgium Leading single-cell projects in drug discovery across several therapeutic areas.
<i>Feb 2022</i> SEP 2020	(Co-)Lecturer of Statistical Genomics, Ghent University, Belgium In the academic years 2021-2022 I was the responsible lecturer of Statistical Genomics, an advanced course for Master students in Bioinformatics and Statistical Data Analysis. In 2020-2021, I was a co-lecturer for the course.
<i>Feb 2022</i> NOV 2019	Postdoctoral Researcher, University of California, Berkeley, USA and Ghent University, Belgium Supervisors: Prof. Dr. Sandrine Dudoit & Prof. Dr. Lieven Clement In my postdoctoral 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 OCT 2014	PhD student, Ghent University, Belgium 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.
JUN 2018 APR 2018	Visiting Scholar, University of California, Berkeley, USA 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.
DEC 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

- Award for best poster presentation at the International Biometric Conference, Vancouver, Canada, 2016.

SCHOLARSHIPS

- Travel grant from the Research Foundation Flanders for a long research visit to the group of Prof. Sandrine Dudoit and Prof. Peter Bickel, at the University of California, Berkeley, 2021, €2310.
- 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.
- 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 (†).

For citation metrics, please see my [Google Scholar Profile](#).

- B. Tytgat, E. Verleyen, M. Sweetlove, **K. Van den Berge**, E. Pinseel, D.A. Hodgson, S.L. Chown, K. Sabbe, A. Wilmotte, A. Willems, Polar Lake Sampling Consortium, W. Vyverman. Polar lake microbiomes have distinct evolutionary histories. *Science Advances* 9(46): eade7130, 2023.
- E. Pinseel, T. Nakov, **K. Van den Berge**, K.M. Downey, K.J. Judy, O. Kourtchenko, A. Kremp, E.C. Ruck, C. Sjöqvist, M. Töpel, A. Godhe, A.J. Alverson. Strain-specific transcriptional responses overshadow salinity effects in a marine diatom sampled along the Baltic Sea salinity cline. *The ISME Journal* 16:7 176-1787, 2023.

- 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. *Annals of Applied Statistics* 17(3): 2555-2573, 2023.
- **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. *Cell Reports Methods* 2:11 100321, 2022.
- **Brain Initiative Cell Census Network**. A multimodal cell census and atlas of the mammalian primary motor cortex. *Nature* 598: 86–102, 2021.
- 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. *Nature* 598: 103–110, 2021.
- 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. *F1000Research*, doi: 10.1101/2021.01.14.426636.
- 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 Bézieux, 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*. It has been accessed over 40,000 times.
Our software, tradeSeq, has been downloaded by over 4,000 distinct IP addresses.
- **K. Van den Berge***, K. Hembach*, C. Sonesson*, 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

- **K. Van den Berge**, H. Chou, D. Kunda, D. Risso, K. Street, E. Purdom, S. Dudoit, J. Ngai, W. Heavner. A Latent Activated Olfactory Stem Cell State Revealed by Single Cell Transcriptomic and Epigenomic Profiling. *bioRxiv*, doi: 10.1101/2023.10.26.564041.
- N. Conceição-Neto Q. Han, Z. Yao, W. Pierson, Q. Wu, K. Docx, L. Aerts, D. De Maeyer, **K. Van den Berge**, C. Li, G. Kukolj, R. Zhu, O. Podlaha, I. Nájera, E. Van Gulck. AAV-HBV mouse model replicates immune exhaustion patterns of chronic HBV patients at single-cell level. *bioRxiv*, doi: 10.1101/2023.08.07.552328.
- H. Roux de Bezieux, **K. Van den Berge**, K. Street[†], S. Dudoit[†]. Trajectory inference across multiple conditions with condiments: differential topology, progression, differentiation, and expression. *bioRxiv*, doi: 10.1101/2021.03.09.433671.
- 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.

SOFTWARE PACKAGES

Authored packages

- traviz: Utility functions for trajectory inference in single-cell sequencing data. <https://bioconductor.org/packages/release/bioc/html/traviz.html>
- 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

- condiments: Trajectory inference and interpretation across multiple conditions. <https://github.com/HectorRDB/condiments>

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

TEACHING AND MENTORING

- 2020-2021 **(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. Taught experimental design, bulk RNA-seq and single-cell RNA-seq together with Charlotte Sonesson. <https://uclouvain-cbio.github.io/BSS2019/>
- R Bootcamp, Department of Statistics, University of California, Berkeley, August 10-13, 2020.

Mentored students

- Alexandre Segers, PhD Student, Department of Applied Mathematics, Computer Science and Statistics, Ghent University, and Center for Medical Genetics, University Hospital Ghent. Project title: Identification of aberrant splicing and gene expression in rare retinal diseases.
- 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.
- Svetlana Afanaseva, Master project, Department of Statistics, University of California, Berkeley, 2020. Project title: GC-content normalization of single-cell 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.
- Ameet Bindra, Undergraduate research project, Department of Statistics, University of California, Berkeley, 2020. Project title: Normalization of DNA chromatin conformation (ATAC-seq) datasets.
- 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.

- 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.
- 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.
- 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*.
- Gust Bilcke, Master thesis student in Biology, Ghent University, 2015-2016. Project title: Molecular characterization of sex signalling in diatoms.

REVIEWS

Reviewed for following journals: Bioinformatics, Biometrics, Cell Reports Methods, F1000 Research, 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.
- Nov 10 2015
- 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 Prof. 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.
- RNA-seq symposium, Janssen Pharmaceutica, Beerse, Belgium. Nov 2015.
Testing for interactions between multiple variables in RNA-seq experiments.

SPOKEN LANGUAGES

DUTCH: Mothertongue
 ENGLISH: Fluent
 FRENCH: Good
 GERMAN: Basic knowledge

PROGRAMMING LANGUAGES

R: Expert
 MARKDOWN: Expert
 LATEX: Expert
 GIT: Expert
 UNIX: Good
 PYTHON: Good
 SAS: Moderate
 C++: Basic knowledge

SOCIAL VOLUNTEERING

- Fall 2020: Member of anti-racism reading group in the Department of Statistics at University of California, Berkeley.
- 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, where we counted over 1 million individual birds during the entire migration season.