

Curriculum Vitae

Koen Van den Berge

November 9, 2019

PERSONAL DATA

PLACE AND DATE OF BIRTH: Ghent, Belgium | 21 October 1990
EMAIL: koen.vandenberge@ugent.be

PROFESSIONAL EXPERIENCE

<i>Current</i> Nov 2019	Postdoctoral Researcher, University of California, Berkeley Supervisor: Prof. Dr. Sandrine Dudoit
OCT 2019 OCT 2014	PhD student, Ghent University, Belgium Supervisor: Prof. Dr. Lieven Clement My research, situated in the field of statistical genomics, focusses 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 APRIL 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.
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 best Master thesis in the field of Biometrics across Flanders
- 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 (*).

- **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.

REVIEWS

Reviewed for following journals: Bioinformatics.

SOFTWARE PACKAGES

Authored packages

- tradeSeq: trajectory-based differential expression analysis for sequencing data (<https://github.com/statOmics/tradeSeq>)
- 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/slinsshot>).
- 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>).

PRESENTATIONS

Invited Presentations

- 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

- 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.

TEACHING

2014-Current **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

- 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.

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.