

Sebastiaan Vanuytven

Curriculum Vitae

Leuvenseweg 1 Bus 6

3020 Herent, Belgium

☎ +32 (498) 371 962

✉ Sebastiaan.vanuytven@gmail.com

📄 <https://svanuytven.github.io/>

🌐 [svanuytven](#)

🐦 [Svanuytven](#)

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Belgian

Research Interests

- Single-Cell (Multi-)Omics
- Oncobiology
- Gene Therapy
- Ageing
- Bayesian Statistics
- Nuclear Architecture
- HIV
- Bioinformatics

Experience

- 2017–Present **PhD Student Computational Biology**,
Laboratory of Reproductive Genomics, KU Leuven, Belgium.
Studying for the first time the complete phenotype of a single cancer cell in its natural environment by combining single-cell multi-omics techniques and spatial transcriptomics
- 2017–Present **Visiting Scientist**,
Cancer Genomics Laboratory, Francis Crick Institute, United Kingdom.
- 2013–2014 **Research Rotations**,
KU Leuven, Belgium.
Internships in the research groups of Prof. Zeger Debyser, Prof. Stein Aerts and Prof. Johan Neyts

Education

- 2015–2017 **Master of Science Bioinformatics**, *KU Leuven*, *Magna cum laude*.
- 2013–2015 **Master of Science Biomedical Sciences**, *KU Leuven*, *Magna cum laude*.
- 2010–2013 **Bachelor of Science Biomedical Sciences**, *KU Leuven*, *Cum laude*.

Master thesis

Master of Science Bioinformatics

- Title *Single-cell sequencing to understand the biology of cellular heterogeneity in cancer*
- Supervisors Prof. Thierry Voet, Prof. Stein Aerts, Dr. Alejandro Sifrim, Dr. Daniel Brown
- Description Development of novel analysis methods and robust pipelines for single-cell multi-omics experiments and analysis of large-scale single-cell sequencing datasets of primary breast cancers

Master of Science Biomedical Sciences

Title	<i>Development of safer MLV-based gene therapy vectors: studying BET protein-chromatin occupation and generation of p12-fusions</i>	
Supervisors	Prof. Zeger Debyser, Prof. Rik Gijssbers, Dr. Jonas Demeulemeester	
Description	Analysis of BET protein ChIP-seq data and generation of p12-fusions to understand the genotoxicity of MLV-based gene therapy vectors	

Grants

2020	EACR travel fellowship	<i>Travel grant to visit Crick Institute</i>
2018-2022	FWO Strategic basic research grant	<i>Personal Funding for PhD research</i>
2015	BBC2015 Student Fellowship	<i>Travel grant to attend BBC2015 conference</i>

Publications

Journal Articles

- [1] Maria Xydia*, Raheleh Rahbari*, Eliana Ruggiero*, Iain Macaulay, Maxime Tarabichi, Robert Lohmayer, Stefan Wilkening, Tillmann Michels, Daniel Brown, **Sebastiaan Vanuytven**, Svetlana Mastitskaya, Sean Laidlaw, Niels Grabe, Maria Pritsch, Raffaele Fronza, Klaus Hexel, Steffen Schmitt, Michael Müller-Steinhardt, Niels Halama, Christoph Domschke, Manfred Schmidt, Christof von Kalle, Florian Schütz, Thierry Voet, and Philipp Beckhove. Common clonal origin of conventional t cells and induced regulatory t cells in breast cancer patients. *Nature Communications*, 12(1), feb 2021.
- [2] Jordi Camps, Natacha Breuls, Alejandro Sifrim, Nefele Giarratana, Marlies Corvelyn, Laura Danti, Hanne Grosemans, **Vanuytven Sebastiaan**, Irina Thiry, Marzia Belicchi, et al. Interstitial cell remodeling promotes aberrant adipogenesis in dystrophic muscles. *Cell Reports*, 31(5):107597, 2020.
- [3] Anna-Marei Böhm*, Naomi Dirckx*, Robert J. Tower*, Nicolas Peredo, **Vanuytven Sebastiaan**, Koen Theunis, Elena Nefyodova, Ruben Cardoen, Volkhard Lindner, Thierry Voet, Matthias Van Hul, and Christa Maes. Activation of skeletal stem and progenitor cells for bone regeneration is driven by pdgfrb signaling. *Developmental Cell*, 2019.

Conference Posters

- [1] **Vanuytven Sebastiaan**, Koen Theunis, Jean-Christophe Marine, and Thierry Voet. Single cell Genome-and-Transcriptome sequencing without upfront whole-genome amplification reveals cell state plasticity of melanoma subclones. In *Single Cell Biology / EK26 2021*, Leuven, Belgium, Mar. 2021.
- [2] **Vanuytven Sebastiaan**, Koen Theunis, Jean-Christophe Marine, and Thierry Voet. Single cell Genome-and-Transcriptome sequencing without upfront whole-genome amplification reveals cell state plasticity of melanoma subclones. In *Genome Informatics 2020*, Cambridge, UK, Oct. 2020.
- [3] **Vanuytven Sebastiaan**, Koen Theunis, Jean-Christophe Marine, and Thierry Voet.

Single cell Genome-and-Transcriptome sequencing without upfront whole-genome amplification reveals cell state plasticity of melanoma subclones. In *Emerging Technologies in Single Cell Research 2020*, Leuven, Belgium, Nov. 2020.

- [4] **Vanuytven Sebastiaan**, Koen Theunis, Jean-Christophe Marine, and Thierry Voet. Single-cell genome-plus-transcriptome sequencing without upfront preamplification reveals genomic and transcriptomic heterogeneity in a human melanoma PDX model. In *Somatic Evolution and Tumour Microenvironment Symposium 2020*, London, UK, Dec. 2019.
- [5] **Vanuytven Sebastiaan**, Koen Theunis, Sarah Geurs, Peter Van Loo, Giuseppe Floris, and Thierry Voet. Single-Cell Multi-Omics Sequencing to Understand the Nature, Extent and Biology of Cellular Heterogeneity in Six Special Breast Cancer Cases. In *EACR Cancer Genomics 2019*, Cambridge, UK, June 2019.
- [6] **Vanuytven Sebastiaan**, Alejandro Sifirm, Mabel T Teng, Laura Mora Bitria, Daniel Brown, Elia Fernandez Gallardo, Koen Theunis, Sarah Geurs, Samira Majjaj, Hughes Duvilliers, Michail Ignatiadis, Francoisea Rothe, Christos Sotiriou, Peter Van Loo, Christine Desmedt, and Thierry Voet. Single-cell multi-omics sequencing to understand the nature, extent and biology of cellular heterogeneity in breast cancer. In *Single Cell Biology Confernece*, Wellcome Genome Campus, Hinxton, UK, Mar. 2018.
- [7] **Vanuytven Sebastiaan**, Alejandro Sifirm, Mabel T Teng, Laura Mora Bitria, Daniel Brown, Elia Fernandez Gallardo, Koen Theunis, Sarah Geurs, Samira Majjaj, Hughes Duvilliers, Michail Ignatiadis, Francoisea Rothe, Christos Sotiriou, Peter Van Loo, Christine Desmedt, and Thierry Voet. Single-cell multi-omics sequencing to understand the nature, extent and biology of cellular heterogeneity in breast cancer. In *Benelux Bioinformatics Conference*, Leuven, Belgium, Dec. 2017.
- [8] **Vanuytven Sebastiaan**, Jonas Demeulemeester, Zeger Debyser, and Gijsbers Rik. Studying BET protein-chromatin occupation to understand genotoxicity of MLV-based gene therapy vectors. In *Benelux Bioinformatics Conference*, Antwerp, Belgium, Dec. 2015.

Talks

- 02/2021 **Introduction To Single-Cell Sequencing And Computational Analysis Symposium 2021**, *Leuven*, Belgium, Invited Speaker.
The magic behind Genomics and Transcriptomics Sequencing
- 10/2020 **Crick Cancer Research Symposium 2020**, *London*, United Kingdom, Selected Speaker.
Single cell Genome-and-Transcriptome sequencing without upfront whole-genome amplification reveals cell state plasticity of melanoma subclones
- 05/2019 **EMBO Single-cell Biology**, *Tokyo*, Japan, Selected Speaker.
Single-Cell Multi-Omics Sequencing to Understand the Nature, Extent and Biology of Cellular Heterogeneity in Six Special Breast Cancer Cases

- 11/2018 **Genomics for diagnostics of Rare Diseases TRAINMALTA meeting**, *Leuven*, Belgium, Invited Speaker.
Single-cell multi-omics to detect genetic variants in cancer and development
- 06/2018 **European Human Genetics Conference 2018**, *Milan*, Italy, Selected speaker.
Single-cell multi-omics sequencing to understand the nature, extent and biology of cellular heterogeneity in breast cancer
- 05/2018 **Bioinformatics Student Symposium 2018**, *Antwerp*, Belgium, Selected speaker.
Single-cell multi-omics sequencing to understand the nature, extent and biology of cellular heterogeneity in breast cancer
- 02/2018 **Belgian Human Genetics Conference 2018**, *Ghent*, Belgium, Selected speaker.
Single-cell multi-omics sequencing to understand the nature, extent and biology of cellular heterogeneity in breast cancer
- 12/2015 **BBC2015 Student Conference**, *Antwerp*, Belgium, Selected speaker.
Studying BET protein-chromatin occupation to understand genotoxicity of MLV-based gene therapy vectors

Reviewing activities

- Journals Cell (junior reviewer), Genome Biology
- Conferences ESHG 2018-2020

Scientific leadership experiences

- Organiser RGS Belgium student symposium 2019
- Representative Board of the Department of Human Genetics 2018-...
- Representative University Council 2020-...
- Representative Academic Council 2020-...
- Representative Research Policy Council 2020-...
- Representative Executive Committee Biomedical Sciences 2020-...

Teaching

- 2019-2021 Computational Practical Human Genetics KU Leuven

Languages

- Dutch Native language
- English Extensive Knowledge
- French Good knowledge
- German Basic knowledge
- Swedish Basic knowledge

Bioinformatic skills

Programming	Python, Bash, Java, SQL, Git, Snakemake
Statistics	R, Bioconductor, Stan, Matlab
Single-Cell	Seurat, Scater, SingleCellExperiment, Scanpy, SC3, SCENIC, MOFA+, Slingshot
Alignment	BWA, Kallisto, STAR, Bowtie2, Samtools, bedtools, RSEM, HTseq, Featurecounts, Cutadapt, GATK
Cancer	ASCAT, MuTect2, Delly, VarScan, Sequenza, SomaticSignature, FreeBayes
ATAC	MACS2, cisTopic, snapATAC
General	IGV, Picard, Multiqc, BEAST, PLINK

Interests

2020-Present	Scientific Blogger , https://svanuytven.github.io/ .
2018-Present	Volunteer and KU Leuven representative. ISCB Regional Student Group Belgium
2017-Present	Instructor. Teaching (single-cell) RNA-seq analysis to starting PhD students
2010-Present	Passionate mountaineer and runner.
2015-2017	Student representative and member of the education committee Bioinformatics KU Leuven. Organiser buddy system first year students

References

Thierry Voet, Prof.

Laboratory of Reproductive Genomics, KU Leuven
Thierry.Voet@kuleuven.be, +32 16 33 08 41

Peter Van Loo, Prof.

Cancer Genomics Laboratory, The Francis Crick Institute
Peter.Vanloo@crick.ac.uk +44 (0)20 3796 1719

Alejandro Sifrim, Prof.

Laboratory of Multi-Omic Integrative Bioinformatics, KU Leuven
Alejandro.Sifrim@kuleuven.be

Jonas Demeulemeester, PhD.

Laboratory of Reproductive Genomics, KU Leuven
Jonas.Demeulemeester@kuleuven.be