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Sebastiaan Vanuytven

Curriculum Vitae

Research Interests

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

Experience

2017–Present **PhD Student Computational Biology**,
Labratory 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 *Development of safer MLV-based gene therapy vectors: studying BET protein-chromatin occupation and generation of p12-fusions*

Supervisors Prof. Zeger Debyser, Prof. Rik Gijsbers, 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 — *Travel grant to visit Crick Institute*

2018-2022 FWO Strategic basic research grant — *Personal Funding for PhD research*

2015 BBC2015 Student Fellowship — *Travel grant to attend BBC2015 conference*

Publications

Journal Articles

[1] 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.

[2] 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-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.

[2] **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.

[3] **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.

[4] **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.

[5] **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

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)

Conferences ESHG 2018-2020

Scientific leadership experiences

Organiser RGS Belgium student symposium 2019

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
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Peter Van Loo, Prof.
Cancer Genomics Laboratory, The Francis Crick Institute
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Alejandro Sifrim, Prof.
Laboratory of Multi-Omic Integrative Bioinformatics, KU Leuven
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Jonas Demeulemeester, PhD.
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