



Seppe De Winter

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Recent PhD in Biomedical Sciences with strong analytical and computational skills. Experienced in data science, software design, and deep learning, developed through high-impact academic research projects. Adept at translating complex problems into data-driven solutions and eager to apply these skills in a data science role.

Experience

Postdoctoral Scientist

Laboratory of Computational Biology, VIB.AI - KU Leuven Leuven
Jan. 2026 - Present

PhD Biomedical Sciences

Laboratory of Computational Biology, VIB.AI - KU Leuven Leuven
Aug. 2020 - Dec. 2025

Tutor of Biology, Physics, Chemistry and Mathematics

Student Belgium
Sep. 2017 - Aug. 2020

Student Researcher (LVSO)

Department of Imaging & Pathology, KU Leuven Leuven
Jul. 2016

Education

PhD Biomedical Sciences

University of Leuven (KU Leuven) Leuven
2020-2025

Msc and BSc Biomedical Sciences

University of Leuven (KU Leuven) Leuven
2015-2020

ASO Wetenschappen Wiskunde

Heilig-Hart College Heist-op-den-Berg
2009-2015

Skills

- Software development (Python & Rust).
- Continuous integration and delivery (Git).
- Data Science (Pandas/Polars, Numpy, Scipy, ...).
- Machine learning (Scikit-learn) and Artificial Intelligence (Tensorflow, Keras)
- Soft skills: Project management, Problem analysis and solving, Critical thinking, Attention to detail, Innovation, Enthusiasm, Learning agility.

Projects

SCENIC+: Gene regulatory network inference.

Python, Scikit-Learn, NumPy, Pandas, Snakemake, topic modelling

Built a statistical framework for inferring gene regulatory networks from high-dimensional multi-modal genomic datasets, now widely adopted in the computational genomics community with 500+ citations (Nature Methods) and used by researchers worldwide.

<https://github.com/aertslab/scenicplus>

scATAC Fragment Tools: Command line-utility to work with big genomic datasets.

Rust

Developed an open-source command-line tool for efficient processing of single-cell genomic data files, handling billions of records with minimal memory footprint through optimized I/O operations and multi-threading.

https://github.com/aertslab/scatac_fragment_tools

CREsted: Training and analyzing genomic deep learning models.

Python, Keras, Tensorflow, PyTorch

Co-developed and maintained a flexible deep learning library for training and analyzing CNN models on genomic sequences, focusing on model interpretation tools and sequence design capabilities to help researchers understand neural network predictions (55 GitHub stars and 13,000+ PyPI downloads).

<https://github.com/aertslab/CREsted>

TF-MINDI: Explainable AI for genomic deep learning.

Python, Scikit-Learn, NumPy, Pandas, topic modelling

Developed and explainable AI framework to extract interpretable sequence motifs from trained deep learning models, translating black-box neural network predictions into understandable gene regulatory patterns.

<https://github.com/aertslab/TF-MINDI>

Publications

De Winter S., Mannens C., Christiaens V., Vandepoel R., Hu L., Linnarsson S., Aerts S. (2026). System-wide extraction of cis-regulatory rules from sequence-to-function models in human neural development. *BioRxiv*.

Kempynck N. & **De Winter S.**, Blaauw C. H., Konstantakos V., Dieltiens S., Can Ekşi E., Bercier V., Taskiran I. I., Hulselmans G., Spanier K., Christiaens V., Van Den Bosch L., Mahieu L., Aerts S. (2025). CREsted: modeling genomic and synthetic cell type-specific enhancers across tissues and species. *BioRxiv*.

De Winter S., Konstantakos V., Aerts S. (2025). Modelling and design of transcriptional enhancers. *Nature Reviews Bioengineering*.

Johansen N. J., Kempynck N., Zemke N. R., Somasundaram S., **De Winter S.**, Hooper M., Dwivedi D., Lohia R., Wehbe F., Li B., Abaffyová D., Armand E. J., De Man J., Can Eksi E., Hecker N., Hulselmans G., Konstantakos V., Mauduit D., Mich J. K., Partel G., Daigle T. L., Levi B. P., Zhang K., Tanaka Y., Gillis J., Ting J. T., Ben-Simon Y., Miller J., Ecker J. R., Ren B., Aerts S., Lein E. S., Tasic B., Bakken T. E. (2024). Evaluating Methods for the Prediction of Cell Type-Specific Enhancers in the Mammalian Cortex. *Cell Genomics*.

Bravo González-Blas C. & **De Winter S.**, Hulselmans G. J., Hecker N., Matetovici I., Christiaens V., Poovathingal S., Wouters J., Aibar S., Aerts S. (2023). SCENIC+: single-cell multiomic inference of enhancers and gene regulatory networks. *Nature Methods*.

Floc'hlay S., Balaji R., Stanković D., M Christiaens V., Bravo González-Blas C., **De Winter S.**, Hulselmans G. J., De Waegeneer M., Quan X., Koldere D., Atkins M., Halder G., Uhlirova M., Classen A., Aerts S. (2023). Shared enhancer gene regulatory networks between wound and oncogenic programs. *eLife*.

Styfals R., Zolotarov G., Hulselmans G., Spanier K. I., Poovathingal S., Elagoz A. M., **De Winter S.**, Deryckere A., Rajewsky N., Ponte G., Fiorito G., Aerts S., Seuntjens E. (2022). Cell type diversity in a developing octopus brain. *Nature Communications*.
