

Thomas Chris Smits

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Passionate bioinformatics graduate with a focus on data visualization and development of analysis tools, especially in the realms of genomic and spatial data. Eager to leverage my skills in Python, R, and JavaScript/TypeScript to bring innovative and visually captivating solutions to complex biological datasets.

Education

- 2021 - 2023 **Master in Biomedical Informatics**
Harvard Medical School
- Relevant coursework: Genomic Data Manipulation, Deep Learning for Biomedical Data, Cancer Genome Data Science, Biomedical Data Visualization, Computing for Big Data, Biological Systems Modeling [MIT]
- 2020 - 2021 **Transfer program in Computer Science**
Delft University of Technology
- Relevant coursework: Object-Oriented Programming, Logic, Algorithms, Web- and Database Structures, and Microservices Software Engineering
- 2017 - 2020 **Bachelor of Science in Life Science & Technology** (*Honors & Summa cum Laude*)
Delft University of Technology & Leiden University (joint degree)
- Relevant coursework: Bioinformatics, Life Sciences, Calculus, Statistics
 - Honors program Beta & Life Sciences at *Leiden University*
 - Study abroad at the *University of British Columbia*

Research Experience

- 2023 – present **Associate in Biomedical Informatics**
Harvard Medical School | Department of Biomedical Informatics | dr. Nils Gehlenborg
- Lead projects:
 - ❖ Creating automatic text generation for accessibility of genome-mapped data visualization with TypeScript, using genome-mapped visualization tool Gosling ([AltGosling](#)).
 - ❖ Development of web-based interactive visualization for single-cell data with TypeScript and D3.js ([CellPop](#)).
 - ❖ Creating integrated analyses of spatial and single-cell data in the HuBMAP consortium Data Portal with Python ([Workspace templates](#)).
 - ❖ Comparison of different techniques of introducing genomics visualization to a blind individual.
 - Contributing projects:
 - ❖ State of the art overview of spatial omics visualizations
 - ❖ Multimodel search engine for genomics visualizations
 - ❖ Accessibility of life science resources
 - ❖ Keyboard navigation of visualizations
 - Mentored intern from HuBMAP Underrepresented Student Internship program (2023) and intern from Summer Institute in Biomedical Informatics (2024)
- 2022 **Graduate Student**
Harvard Medical School | Department of Biomedical Informatics | dr. Nils Gehlenborg
- Lead project: Development of automatic feature extraction in JavaScript for written descriptions of visualization in grammar-based genomic visualization tool Gosling
- 2021 – 2022 **Graduate Student**
Dana-Farber Cancer Institute | Department of Data Science | dr. Mehmet Samur
- Lead project: mutational burdens and signature analysis of hyperdiploidy in multiple myeloma.
 - Contributing projects: investigation of ChIP-seq, ATAC-seq, CLIP-seq and RNAs-seq data with differential analyses in R with Bioconductor, including conversion and peak calling from raw data.
- 2020 **Undergraduate Researcher**
Delft Bioinformatics Lab | dr. Thomas Abeel & dr. ir. Robert Mans
- Lead project: Developing various models in Python for prediction of potential hosts of SARS-CoV-2 by analyzing ACE2 receptor sequences

Teaching Experience

2023	Harvard Medical School <ul style="list-style-type: none">Teaching assistant for Deep Learning for Biomedical Data for Master in Biomedical Informatics.Teaching assistant for Computationally-Enabled Medicine for Doctor of Medicine.
2021	Delft University of Technology <ul style="list-style-type: none">Teaching assistant for Biotechnology in BSc Life Science & Technology.
2018 - 2020	Leiden University <ul style="list-style-type: none">Teaching/laboratory assistant for Biochemistry 1 at BSc Bio-Pharmaceutical Sciences.Teaching assistant for Calculus 2 in BSc Life Science & Technology.Student coach at BSc Life Science & Technology.Teaching assistant for Biotechnology summer school in BSc Life Science & Technology.

Awards

2022	American Society of Hematology Abstract Achievement Award	659 out of ~25 000 participants
2022	International Myeloma Society Young Investigator Award	25 out of ~200 participants
2020	Summa cum laude jurisdiction for BSc. Life Science & Technology	top 1 out of 100 students
2019	HOLLAND scholarship 2019 for exchange at the University of British Columbia	top ~10%
2018	Royal Holland Society of Sciences and Humanities (KHMW) Young Talent Award in the discipline Chemistry of Life	67 out of ~100 000 1st year university of the Netherlands
2018	Summa cum laude jurisdiction for 'propedeuse' (first year) for BSc. Life Science & Technology	top 2 out of 150 students

Skills

- Programming & Tools:** Python (Pandas, Scikit-learn, Matplotlib, Seaborn, TensorFlow, Keras), R (tidyverse, Bioconductor (e.g., DiffBind), RCPP), JavaScript/TypeScript (Web development, React, Vite), Data visualization (D3.js, Vega-Lite, Altair, Gosling), SQL (MySQL, PostgreSQL), Git, Microsoft Excel
- Biological Data Analysis:** Single-cell (epi)genomics, transcriptomics, and spatial datasets
- Laboratory techniques: PCR, gel analysis, mutagenesis, kinetics, microscopy, mass/fluorescence spectroscopy

Selected Publications

- L'Yi et al. (2025). A comprehensive evaluation of life sciences data resources reveals significant accessibility barriers. *Scientific Reports*, 15, 23676. <https://doi.org/10.1038/s41598-025-08731-7>
- Keller et al. (2025). The State of Single-Cell Atlas Data Visualization in the Biological Literature. *IEEE computer graphics and applications*, PP, Advance online publication. <https://doi.org/10.1109/MCG.2025.3583979>
- Smits et al. (2024). AltGosling: Automatic Generation of Text Descriptions for Accessible Genomics Data Visualization, *Bioinformatics* 40(12), btae670. <https://doi.org/10.1093/bioinformatics/btae670>
- Smits et al. (2022). *Somatic Changes Prior to the Development of Hyperdiploidy Expose Mutation Accumulation Rate and Activated Processes in Multiple Myeloma*. 64th ASH Annual Meeting and Exposition, New Orleans, LA. <https://doi.org/10.1182/blood-2022-168837>

For a full overview of publications, please visit my [website](#), [ORCID](#) or [Google Scholar](#) page.