Philip Hartout

Curriculum Vitæ



15/09/2022- ETH Zürich, PhD student.

Present • PhD student at the Machine Learning and Computational Biology Laboratory of Prof. Dr. Karsten Borgwardt. From 1/2/2023 at the Max Planck Institute of Biochemistry in Munich.

2019–2022 ETH Zürich, MSc in Computational Biology and Bioinformatics GPA: 5.34/6.

- o Computer Science courses: Focus on Machine Learning (course work ☑), Data Mining,
- o *Biology Courses*: Genomics, ImmunoEngineering, Single Cell Data Analysis, Computational Biology, (see example final project ☑, journal club ☑)

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French and Dutch

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- Academic internship completed with the *University of Amsterdam Oncogenomics department*. (code **'**
- Academic internship completed in the *Machine Learning and Computational Biology (MLCB)* research group to design a topological data analysis pipeline to characterise Alzheimer's disease using structural MRI images. (code , report)
- Master's Thesis in the MLCB research group, designing a composable python library that evaluates generative
 protein models using maximum mean discrepancy. Involves working with kernel functions, topological data
 analysis, point clouds and sequence data.

2015–2018 Amsterdam University College, BSc in Liberal Arts & Science GPA: 3.68/4 (Cum Laude).

- Selective honors programme with an interdisciplinary and intercultural focus. Major focus on biomedical sciences and computer science.
- o Bachelor's thesis: Assessment of Cerebrospinal Fluid and Plasma Concentrations of Amyloid Precursor Protein Products and Clusterin as Biomarkers for Prodromal Late-Onset Alzheimer's Disease. (report ☑)
- Editor-in-chief of AUC's Academic Journal Led a team of 10 editors to publish 2 journal volumes. 🗷 🗹.
- **Tutor** Tutoring Syrian refugees in various disciplines (English, Dutch, Statistics, Calculus, Academic Writing) through the Right2Education foundation .

Professional Experience

2021 Computational Biologist, Novartis Institutes of Biomedical Research (NIBR), Switzerland.

Developed an end-to-end transformer-based modeling pipeline predicting peptide presentation by MHCII.
 Deployed within NIBR to guide therapeutic sequence design (monoclonal antibodies, therapeutic peptides).

2018-2019 Data Scientist, Performation, The Netherlands.

- Worked within a data science team to develop a generic hospital-wide occupancy predictor for each department based on admission, length of stay, and routing patterns. Resulted in approximately 300% MSE reduction in occupancy prediction w.r.t previous version of the software. In charge of design, development and testing.
- Helped sell and deploy the aforementioned software to 40 Dutch hospitals by pitching the product to clients.
- Prototyped a platform to allow for the fast, modular, reproducible and scalable development and deployment of multiple data pipelines, one of which was extracting an ICD-10 diagnosis from discharge letters using NLP.

Technical Skills

- Programming languages: proficient in R and Python; intermediate in Javascript (ES2016), Java, Matlab.
- >_ **Productivity tools**: unix-based operating systems, emacs (org mode), LATEX, jira, docker, git (GitHub workflows).
- Other tools: Cloud (GCP), RESTful APIs, Bioconductor, poetry, conda. 🛢 Databases: MongoDB, Spark, SQL.
- External libraries/frameworks: tensorflow, pytorch, pandas, giotto-tda, matplotlib, plotly, dash, nextjs, react.
- ♀ Skills: design and implementation of machine learning pipelines; neurodegenerative diseases, biological sequence analysis & single cell data analyses; technical talks (example); pair programming; Agile/Scrum software development. Maintainance and design of Python libraries (see fastwlk)



Native: French, Dutch

Fluent: English

Conversational: German



Sailing, 10 years of high performance sailing. Coaching sailing teams in international competitions. Hiking, outdoors

Tilking, outdoo