

# David Wissel

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Ph.D. candidate at **ETH Zurich** and the **University of Zurich**, specializing in **survival analysis** and **long-read RNA-seq**. Recognized by **80+ citations** across **five peer-reviewed publications** and four preprints in bioinformatics and machine learning. Bringing deep expertise across the data lifecycle, from **experimental design** to **time-series forecasting** and **tabular ML**. Driven by a passion for **computational reproducibility**, I am highly experienced in building robust **Snakemake** pipelines and writing production-ready code in **Python** and **R**.

## EDUCATION

<b>ETH Zurich</b> <i>Ph.D. Computer Science</i>	Zurich, Switzerland <i>Nov 2021 – Jul 2026</i>
<b>ETH Zurich</b> <i>M.Sc. Statistics (GPA: 5.86/6.0, Top 8%)</i>	Zurich, Switzerland <i>Sep 2019 – Sep 2021</i>
<b>University of Minnesota</b> <i>Direct exchange scholarship (GPA: 4.0/4.0)</i>	Minneapolis, MN, USA <i>Aug 2017 – May 2018</i>
<b>Free University of Berlin</b> <i>B.Sc. Business Administration (GPA: 1.3/1.0, Top 3%)</i>	Berlin, Germany <i>Oct 2015 – Mar 2019</i>
<b>Medford High School</b> <i>High school exchange year</i>	Medford, OK, USA <i>Aug 2011 – Jun 2012</i>
<b>Hanns-Seidel-Gymnasium Hosbach</b> <i>Abitur (GPA: 1.8/1.0)</i>	Hosbach, Germany <i>Sep 2005 – Jun 2014</i>

## SELECTED PUBLICATIONS

\* indicates joint first authorship

- ▷ Botta, G.\*, **Wissel, D.\***, Higgins, S., . . . , Stephenson, W., Robinson, M. D., Schubert, R. (2026) “Benchmarking long-read RNA-seq across modalities, methods, and sequencing depth in iNeurons.” **bioRxiv**.
- ▷ **Wissel, D.**, Mehlferber, M. M., Nguyen, K. M., . . . , Tseng, E., Robinson, M. D., Sheynkman, G. M. (2026) “A systematic benchmark of high-accuracy PacBio long-read RNA sequencing for transcript-level quantification.” **Genome Biology**.
- ▷ **Wissel, D.**, Janakarajan, N.\*, Grover, A., Toniato, E., Martínez, M. R., Boeva, V. (2025) “SurvBoard: standardized benchmarking for multi-omics cancer survival models.” **Briefings in Bioinformatics**.
- ▷ **Wissel, D.**, Rowson, D., Boeva, V. (2023) “Systematic comparison of multi-omics survival models reveals a widespread lack of noise resistance.” **Cell Reports Methods**.

## SKILLS

**Languages:** German (Native), English (Fluent), French (Intermediate)  
**Programming:** Python, R, SQL  
**Packages (general):** pandas, NumPy, SciPy, scikit-learn, XGBoost, CatBoost, Optuna, mlr3  
**Packages (deep learning):** PyTorch, scorch, transformers  
**Packages (time series):** sktime, tsfresh, forecast  
**Infrastructure:** Git, Snakemake, SLURM, LSF

## PROFESSIONAL EXPERIENCE

<b>statworx</b> <i>Data Science intern</i>	Frankfurt, Germany <i>May 2019 – Aug 2019</i>
▷ Architected a time-series forecasting meta-learner in a two-person team to systematically outperform baseline models on client datasets.	
▷ Engineered and containerized end-to-end inference pipelines via Docker for robust on-premise deployment in a three-person team.	
<b>Paua Ventures</b> <i>Data Science intern (part-time)</i>	Berlin, Germany <i>Oct 2018 – Mar 2019</i>
▷ Built automated web-scraping and ETL pipelines to extract alternative data for active investment sourcing.	
▷ Developed and deployed machine learning models to score and prioritize outbound dealflow opportunities.	

## SELECTED SUPERVISION

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### ETH Zurich

Zurich, Switzerland

#### *Student supervision*

2021 – 2026

- ▷ **Julius Schulte** (Master's thesis) – Co-authored (2024) “sparsesurv: a Python package for fitting sparse survival models via knowledge distillation.” **Bioinformatics**.
- ▷ **Xintian Yuan** (Master's project) – Co-authored (2024) “sparsesurv: a Python package for fitting sparse survival models via knowledge distillation.” **Bioinformatics**.

### University of Zurich

Zurich, Switzerland

#### *Student supervision*

2022 – 2026

- ▷ **Gianfranco Botta** (Summer intern) – Co-first-authored (2026) “Benchmarking long-read RNA-seq across modalities, methods, and sequencing depth in iNeurons.” **bioRxiv**.
- ▷ **Alexander Popescu** (Summer intern) – Co-authored (2026) “Benchmarking long-read RNA-seq across modalities, methods, and sequencing depth in iNeurons.” **bioRxiv**.
- ▷ **Khue Nguyen** (Master's project) – Co-authored (2026) “A systematic benchmark of high-accuracy PacBio long-read RNA sequencing for transcript-level quantification.” **Genome Biology**.

## TEACHING

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### ETH Zurich

Zurich, Switzerland

#### *Teaching assistant*

2021 – 2026

- ▷ Natural Language Processing (Fall 2021 – 2022)
- ▷ Machine Learning for Genomics (Spring 2022 – 2023, Fall 2024 – 2025)
- ▷ Computational Intelligence Lab (Spring 2024 – 2026)

## LEADERSHIP AND SERVICE

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### Reviewer

*ICML (2025), Experimental Gerontology (2025), Communications Biology (2026)*

2025 – 2026

### **Analytics Club at ETH**

Zurich, Switzerland

*Board member and head of Hack4Good*

2020 – 2021

### **180 Degrees Consulting**

Minneapolis, USA

*Non-profit consulting team lead and consultant*

Aug 2017 – May 2018

### **Hope for Life**

Chiang Rai, Thailand

*Elementary school volunteer English teacher*

Aug 2014 – Jul 2015

## REFERENCES

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- ▷ **Prof. Dr. Valentina Boeva** (ETH Zurich) | valentina.boeva@inf.ethz.ch
- ▷ **Prof. Dr. Mark Robinson** (University of Zurich) | mark.robinson@mls.uzh.ch
- ▷ **Prof. Dr. Gloria Sheynkman** (University of Virginia) | gs9yr@virginia.edu
- ▷ **Dr. Elizabeth Tseng** (Pacific Biosciences) | etseng@pacificbiosciences.com
- ▷ **Dr. William Stephenson** (Genentech) | stephew3@gene.com