

VIVIAN B. BRANDENBURG

Dr. rer. nat. Biologie

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Bioinformatics

VivianBrandenburg



PROFESSIONAL CAREER

Postdoctoral Researcher Bioinformatics Group

- ⌚ since 2023 📍 Ruhr University Bochum
- Development of new deep learning methods in phylogeny
 - Implementation of Explainable AI
 - Supervision of students in lectures, courses and theses

Doctoral Researcher Microbiology & Bioinformatics Group

- ⌚ 2019 – 2023 📍 Ruhr University Bochum
- Development of new deep learning methods for RNA structure prediction
 - Transcriptome analyses
 - Interdisciplinary communication of bioinformatic methods and results

ACADEMIC CAREER

Dr. rer. nat. summa cum laude

- ⌚ 2019 – 2023 📍 Ruhr University Bochum

M. Sc. Biology 1.1

- ⌚ 2017 – 2019 📍 Ruhr University Bochum
- Specialisation in bioinformatics
 - Development of the data processing of a new method for RNA structure mapping in the final thesis
 - Optional subject and teaching assistant in database systems

M. Sc. Biology

- ⌚ 2014 – 2017 📍 Martin Luther Univ. Halle-Witt.
- Specialisation in crop science
 - Research internship in agricultural application research at SKW Piesteritz

B. Sc. Biology 2.2

- ⌚ 2011 – 2014 📍 Leipzig University
- Thesis in crop biology on nitrogen uptake in wheat

B. A. Political Sciences 2.3

- ⌚ 2007 – 2011 📍 Leipzig University
- Research internship in the Science Policy Interface working group at the Helmholtz Centre for Environmental Research

STRENGTHS

Insight-orientated deep learning

Transcriptomics Explainable AI

Innovative Thinking

Familiarisation with new topics

Interdisciplinary communication

LANGUAGES

Python



Bash



R



PUBLICATIONS

- Schmidt*, Remme*, Eisfeld, **Brandenburg**, Bille, Narberhaus, 2024: The LysR-type transcription factor LsrB regulates beta-lactam resistance in Agrobacterium tumefaciens, *Mol Microbiol*, 121(1). doi:10.1111/mmi.15191
- **Brandenburg**, Hack, Mosig, 2023: A quartet-based approach for inferring phylogenetically informative features from genomic and phenomic data, *publiziert in Dissertation*. doi:10.13154/294-10571
- **Brandenburg**, Narberhaus, Mosig, 2022: Inverse folding based pre-training for the reliable identification of intrinsic transcription terminators, *PLOS Comp Biol* 18(7). doi:10.1371/journal.pcbi.1010240
- Eisfeld*, Kraus*, Ronge, Jagst, **Brandenburg**, Narberhaus, 2021: A LysR-type transcriptional regulator controls the expression of numerous small RNAs in Agrobacterium tumefaciens, *Mol Biol* 116(7). doi:10.1111/mmi.14695
- Twittenhoff*, **Brandenburg***, Righetti*, Nuss, Mosig, Dersch, Narberhaus, 2020: Lead-seq: transcriptome-wide structure probing in vivo using lead(II) ions, *NAR* 48(12). doi:10.1093/nar/gkaa404

*shared first authorship