

Dr. Bora Uyar

*Bioinformatics Scientist @
MDC-Berlin*

Hannoversche Str. 28
Berlin 10115
Germany

✉ bora.uyar@mdc-berlin.de
🌐 <https://borauiyar.github.io/>

🔗 [borauiyar](#)

in [bora-uyar-11050425](#)
[arcas.ai](#)



Summary

I am a Bioinformatics Scientist at the Bioinformatics & Omics Data Science platform of the Max-Delbrück-Center for Molecular Medicine. My roles in the platform include research, collaborations with other labs in the institute, and supporting other researchers in the form of consultations, mentorships, workshops, and user-friendly software development for wet-lab researchers. I am also a member of the [arcas.ai](#) team, where my current research is focused on development of deep learning-based multi-modal data integration tools for precision oncology. My work in the last 15 years spanned various categories such as comparative genomics, protein sequence analysis in the context of molecular interactions and disease mechanisms, RNA bioinformatics, and omics data science with a focus on development of reproducible software for the bioinformatics community.

Experience

2015–Present **Bioinformatics Scientist**, *Max-Delbrück-Center for Molecular Medicine*, Berlin, Germany

- Conduct research and collaborations with other labs.
- Support researchers through consultations, mentorships, and workshops.
- Develop user-friendly software for wet-lab researchers.

2014–2015 **Postdoctoral Fellow**, *European Molecular Biology Laboratory*, Heidelberg, Germany

Education

2011–2014 **Ph.D. in Bioinformatics**, *European Molecular Biology Laboratory*, Heidelberg, Germany

2008–2010 **M.Sc. in Bioinformatics**, *Simon Fraser University, BC Cancer Agency*, Vancouver, Canada

2003–2008 **B.Sc. in Biological Sciences**, *Sabanci University*, Istanbul, Turkey

Skills

Programming Languages Python, R, Bash/Shell (*Active*); Perl, C++, SQL (*Familiar/Past*)

Deep Learning Development	PyTorch, PyTorch Lightning, PyTorch Geometric (<i>Active</i>); TensorFlow, Keras (<i>Familiar/Past</i>)
Machine Learning Methods	Random Forests, SVMs, GLMnet
Version Control	Git (<i>Active</i>); Subversion (<i>Familiar/Past</i>)
Workflows	Snakemake (<i>Active</i>); CWL (<i>Familiar/Past</i>)
Package Management	Conda, Guix (<i>Active</i>); Docker (<i>Familiar/Past</i>)
Data Science Toolkits	CRAN/Bioconductor, Python libraries (scikit-learn, NumPy, pandas, Matplotlib)
Keywords	Omic data science for precision oncology, protein language models, causal network analysis, single-cell data analysis (<i>Active</i>); Comparative genomics, short linear motifs (<i>Familiar/Past</i>)

Profiles

Google Scholar	scholar.google.com/YEZr1LUAAAAJ
GitHub	github.com/borauyar
ORCID	orcid.org/0000-0002-3170-4890
LinkedIn	linkedin.com/in/bora-uyar-11050425

News Articles

- New textbook for computational genomics (mdc-berlin.de)
- Searching the sewers for viruses (bionity.com)
- AI identifies cancer cells (bionity.com)
- Parallel Genome Editing in Microscopic Worms Maps Regulatory Genomic Elements to Physiology (genengnews.com)
- Stray proteins cause genetic disorders (sciencedaily.com)
- A genetic chaperone for healthy aging? (bionity.com)

Selected Publications

Genome Biology, 2022	Identifying tumor cells at the single-cell level using machine learning
Cell Reports, 2021	Parallel genetics of regulatory sequences using scalable genome editing in vivo
Aging Research Reviews, 2020	Single-cell analyses of aging, inflammation and senescence

- GigaScience, 2018 PiGx: reproducible genomics analysis pipelines with GNU Guix
- Cell, 2018 Mutations in Disordered Regions Can Cause Disease by Creating Dileucine Motifs
- Nucleic Acids Research, 2017 RCAS: an RNA centric annotation system for transcriptome-wide regions of interest