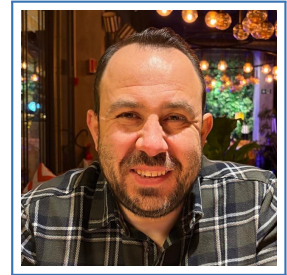


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Summary

I am a Senior Staff Scientist at the Bioinformatics & Omics Data Science platform of the Max-Delbrück-Center for Molecular Medicine. My current research is focused on the development of deep learning-based multi-modal data integration tools for precision oncology. My other roles in the platform include running research collaborations and supporting other researchers in the form of consultations, mentorships, workshops, and user-friendly software development for wet-lab researchers. My work in the last 15 years spanned various topics 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
- 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

Profiles

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

Selected Publications

Nature Communications, 2025 Flexynesis: A deep learning toolkit for bulk multi-omics data integration for precision oncology and beyond

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

My research in the news

- Using deep learning for precision cancer therapy (mdc-berlin.de)
- 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)