Yigit Koray Babal

Postdoctoral Researcher

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Stockholm, Sweden

+46 73 675 4331

yigitbabal.github.io

yigit.koray.babal@ki.se

BabalKoray

yigitbabal

yigitbabal

About me

I am a postdoctoral scholar at Karolinska Institutet focusing on the development and use of computational approaches in the neurobiology field. My research focus is gene regulation of nervous system development and neurodegenerative diseases especially using evolutionary aspects.

Skills

- Full experience with next generation sequencing data analysis with multi-omic approaches (scRNA-seq, scATAC-seq, bulk RNA-seq, ChIP-seq, CUT&RUN)
- Single cell/nuclei sequencing and downstream analysis (clustering, trajectory analysis, reference based machine learning approaches)
- Inference algorithms (Gene regulatory network, cell-to-cell communication, pseudotime inference)
- Single cell DNA barcoding and integrative analysis with single cell transcriptomic (TrackerSeq)
- Highly experience in R and Python.
- Highly experience in Linux (both desktop and server/cloud side), Bash scripting.
- Highly experience Docker/Singularity, HPC clusters and Slurm system.
- Web development (HTML, CSS, Static websites, Shiny application)

Education

2018-2023 PhD in Biotechnology — Gebze Technical University
Kocaeli, Turkey

2016-2018 Master of Molecular Biology and Genetics — Gebze Technical University
Kocaeli, Turkey

2012-2016 Bachelor of Biology — Marmara University
Istanbul, Turkey

2012-2014 Double Major in Mathematics — Marmara University
Istanbul, Turkey

Research Experience

2023- Postdoctoral Researcher — Karolinska Institutet
Stockholm, Sweden

- Single cell multi omic data analysis of brain-vascular cell interaction inALS and MS patient samples.
- Multi-species comparison of neuro-regeneration

2021-2022 Guest Researcher — Max Planck Institute of Biological Intelligence
Munich, Germany

- Single cell multi omic data analysis (scRNAseq, scATACseq, ChIPseq)of inhibitory neuron development including trajectory analysis and genereg-ulatory network inference, motif enrichment and gene oscillatorynetwork analysis.
- Single cell transcriptomic analysis of embryonic development of cortexwith pertubation studies
- Scientific maintenance of Linux-based work-station and HPC clustersincluding reproducible scripting, R and CLI package/tool maintenance

2019-2023 Research Assistant — Gebze Technical University
Kocaeli, Turkey

- Single cell transcriptomic and genomic analyses of nervous systemdevelopment and gene regula-tion during neurogenesis
- Transcriptomic analysis of neurogenesis and brain tumors and analysisof gene regulatory network
- Quantitative kinetic modelling of intra-familial regulation of specifictranscription factor family.
- Molecular investigation of brain tumor cell culture models.

Awards

2023 Awards in Fellowship. Wenner-Gren Fellow Fellowships for Post-doctoral Training

2021 Awards in Grant. Erasmus Grant to be a Guest Researcher in Max Planck Institute of Biological Intelligence

2018 Awards in Scholarship. Council of Higher Education of Turkey 100/2000 PhD Scholarship

2016 Awards in Graduation. As the best student in the programme with high honour degree.

Teaching Experience

2024 PhD course Karolinska Institutet
Stockholm, Sweden
- The Vascular Brain: Evolutionary differences of cell trajectories in developing mammalian cortex

2023 Bachelor course Karolinska Institutet
Stockholm, Sweden
- Cell-, Stem Cell and Developmental Biology

Publications

1. Del-Valle-Anton, L., Amin, S., Cimino, D., Neuhaus, F., Dvoretskova, E., Fernández, V., Babal, Y. K., Garcia-Frigola, C., Prieto-Colomina, A., Murcia-Ramón, R., et al. (2024). Multiple parallel cell lineages in the developing mammalian cerebral cortex. *Science Advances*, *10*(13), eadn9998.
2. Uyar, O. A., Babal, Y. K., Yılmaz, B., & Kurnaz, I. A. (2024). Mitotic kinases aurora-a, Plk1, and Cdk1 interact with elk-1 transcription factor through the n-terminal domain. *International Journal of Cell Biology*, *2024*(1), 6798897.
3. Babal, Y. K., Sonmez, E., & Kurnaz, I. A. (2023). Nervous system-related gene regulatory networks and functional evolution of ETS proteins across species. *Biosystems*, *227*, 104891.
4. Yurduseven, K., Babal, Y. K., Celik, E., Kerman, B. E., & Kurnaz, I. A. (2022). Multiple sclerosis biomarker candidates revealed by cell-type-specific interactome analysis. *Omics: A Journal of Integrative Biology*, *26*(5), 305–317.
5. Babal, Y. K., Kandemir, B., & Kurnaz, I. A. (2021). Gene regulatory network of ETS domain transcription factors in different stages of glioma. *Journal of Personalized Medicine*, *11*(2), 138.