FATMA BETUL DINCASLAN

I am an experimentalist with strong background and solid experience in sequencing data analysis.

🖥 RESEARCH EXPERIENCE

2019 | 2023

NUS Research Scholar (Thesis Defended)
Biomedical Eng., NUS (Supervisor: Lih Feng CHEOW) 📍 Singapore
High-Throughput Total RNA-Sequencing of Single Cells

My PhD project was about the development of single cell high-throughput assay for total RNA sequencing, which could be easily applied on popular platforms like 10X Chromium. Later, I used open-source tools for total RNA-seq data analysis. I validated the assay on different cell lines and Peripheral Blood Mononuclear Cells (PBMCs).

High-Throughput Profiling of Secreting Single Cells

We aimed to develop an assay to profile secreting vs. non-secreting cells of pancreatic islets upon certain stimuli. (Not Completed)

2016 | 2019

Master's Student
MBG, Bilkent University (Supervisor: Ozlen KONU) 📍 Ankara, Turkey
Tissue Specific Transcriptome of Zebrafish in AChE Mutant Embryos

I analyzed tissue specificity (TS) of zebrafish, considering the dynamicity of gene expression, using specific metrics such as Tau, Tsi. Furthermore, I compared the outcome of different normalization methods on TS discovery. Then, I applied the TS analysis on publicly available datasets of mutant zebrafish embryos.

🎓 EDUCATION

2019 | 2023

Ph.D., Biomedical Engineering
Thesis: Development of High-Throughput Total RNA Sequencing of Single Cells
📍 NUS, Singapore

2017 | 2019

M.Sc., Molecular Biology and Genetics
Thesis: Tissue Specific Transcriptome of Zebrafish in AChE Mutant Embryos
📍 Bilkent University, Ankara, Turkey

2011 | 2016

B.Sc., Molecular Biology and Genetics
(First year is English Prep School) 📍 Bilkent University, Ankara, Turkey

CONTACT INFO

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in linkedin.com/fbdincaslan

SKILLS

Dry-Lab

Common bioinformatics databases/tools such as NCBI, Primer3, UCSC Genome Browser, Ensembl, Expression Atlas, STRING, GO/Panther.

Bulk and Single Cell Transcriptomics Data Analysis using Command Line Tools and R.

Wet-Lab

DNA and RNA isolation, q/PCR. Cell Culture and FACS basics. Library Preparation and Illumina Sequencing.

♟ OTHER INTERESTS

- • Playing Basketball and Bullet Chess, Running, Indoor Climbing
- • Reproducibility in Science and Open Science
- • Data Visualization in R and Blogging
- • Learning data science basics via SoloLearn or Kaggle
- • Exploring cultures via languages using Duolingo

📄 PUBLICATIONS AND POSTERS

• High-Throughput Total RNA-Sequencing of Single Cells

Fatma Betul Dincaslan, Lih Feng Cheow

Oral Presentation for jointly hosted CSI-ENS Symposium: Single-Cell Res/volution 2023 (2023, Singapore)

• 1st ASCS: Expanding the ISCB Student Council Symposia to Asia

Aayush Grover, Arsalan Riaz, Syed Muktadir Al Sium, **Fatma B. Dincaslan**, Sanjana Fatema Chowdhury, Gabriel J Olguin-Orellana, R. Gonzalo Parra, Pradeep Eranti

F1000Research, DOI: 10.12688/f1000research.135767.1

• Lessons from a ten-year-long journey: building a student-driven computational biology society across Turkey

Yasin Kaya, Tülay Karakulak, Cemil Can Saylan, E. Ravza Gür, Engin Tatlıdil, Sevilay Güleşen, **Fatma Betül Dinçaslan**, Handan Melike Dönertaş

F1000Research, DOI: 10.12688/f1000research.107886.1

• Functional analysis of co-expression networks of zebrafish ace2 reveals enrichment of pathways associated with development and disease

Ayse Gokce Keskus, Melike Tombaz, Burcin Irem Arici, **Fatma Betul Dincaslan**, Afshan Nabi, Huma Shehwana, and Ozlen Konu

Genome, DOI: 10.1139/gen-2021-0033

• A pipeline for examination of tissue-specificity of differentially expressed genes in zebrafish mutants: Application to AChE mutants

Fatma B. Dincaslan, Afshan Nabi, M. Efe Isilak, Ayse G. Keskus, M. Ender Avci, Michelle M. Adams, Ozlen Konu

Poster for International Symposium on Health Informatics and Bioinformatics (HIBIT) (2018, Antalya, Turkey)