FATMA BETUL DINCASLAN

Molecular Biologist | Bioassay Developer | Bioinformatician

🧠 SELECTED RESEARCH EXPERIENCE

2019 | 2023

NUS Research Scholar

I was leading (design, experiments and analysis) two different bioassay projects.

📍 NUS&iHealthtech, Singapore

High-Throughput Total RNA-Sequencing of Single Cells

- Development of single cell high-throughput one-step (lysis, A-tail modification, reverse transcription and template switching) total RNA sequencing assay
- Optimization in low-bulk format using in-house reaction mixtures
- Modification of the pipelines for total RNA-seq data analysis using open-source tools
- Benchmarking and application of the assay on cell lines and human Peripheral Blood Mononuclear Cells (PBMCs)

The results indicated differentially expressed non-coding RNA biotypes as well as mRNA upon stimulation of PBMCs. It is 10X Chromium compatible as well. Moreover, I developed another single-cell bioassay that captures c-peptide from modified cell surface of human beta cell line upon glucose stimulation.

As a designer and manager of the projects, I have a comprehensive experience of **cell culture**, **bead capture**, compatible **primer design**, **qPCR/Kapa library quantification**, **library preparation**, **miSeq Illumina Sequencing** for the wetlab; **big data management**, **command line tools** for **pre-processing** (i.e., cutadapt), **quality checks** (with FastQC) and **alignment** (with STAR) of the raw data and **Seurat** and downstream bulk and **single cell high-throughput (multi-modal) data analysis** following data visualization using **R/RStudio** for the drylab.

2016 | 2019

Master's Student

I was leading my thesis project as well as assisting a few other KONU Lab projects investigating peridodontis, p53-AChE relationship and role of cholinergic receptors in breast cancer.

📍 Bilkent University, Ankara, Turkey

Tissue Specific Transcriptome of Zebrafish in AChE Mutant Embryos

- Analysis of tissue specificity (TS) of zebrafish
- Comparison of different TS metrics and normalization methods on TS discovery
- Application of the TS analysis on publicly available datasets of mutant zebrafish embryos
- *In vivo* validation of the findings with qPCRs after isolating RNA of model zebrafish embryos

My further investigation of the relationship between acetylcholinesterase (AChE) and TS genes revealed potential non-canonical roles of AChE.

I used **R/RStudio** for **Differential Gene Expression (DEG)** analysis of **bulk RNA-seq data**, TS, **gene set enrichment**, **downstream pathway analysis** (e.g., Gene Ontology) and **data visualization**.

CONTACT INFO

in | ⌂ | ✉

Available for research opportunities

TEACHING

BN2301 Fundamental Biochemistry and Biomaterials for Bioengineers

Teaching Assistant (TA): DNA fingerprinting and tutorships

NUS (2020-2022)

MBG326 Introduction to Bioinformatics

TA: R/RStudio (common databases and tools, case-study data analysis using Bioconductor/CRAN packages)

MBG223 Molecular Genetics & MBG302 Molecular Biology of The Cell-II

TA: molecular cloning experiments (plasmid editing, restriction enzyme digestion, ligation and miniprep) & cell culture experiments (scratch, kinase inhibition and crystal violet assays)

Bilkent (2017-2018)

I also (one-to-one) guided several undergraduate (third/final year) colleagues during M.Sc. and Ph.D.

EDUCATION

2019 | 2023

Ph.D., Biomedical Engineering
Thesis: **(Assay) Development of High-Throughput Total RNA Sequencing of Single Cells**
[*The degree was awarded in December 2023*]
Advisor(s): Lih Feng CHEOW

📍 **National University of Singapore (NUS), Singapore**

2017 | 2019

M.Sc., Molecular Biology and Genetics
Thesis: **Tissue Specific Transcriptome of Zebrafish in AChE Mutant Embryos**
Advisor(s): Ozlen KONU

📍 **Bilkent University, Ankara, Turkey**

2011 | 2016

B.Sc., Molecular Biology and Genetics
(First year is English Prep School)

📍 **Bilkent University, Ankara, Turkey**

AWARDS AND MEMBERSHIPS

2019 | 2023

NUS Research Scholarship
Awarded by Singapore-MOE and NUS for PhD in Biomedical Engineering

📍 Singapore

2022

eLife Ambassador
Short-term trainee of "learning and community-building"

📍 Earth

2018 | 2023

ISCB Student Council & RSG-Turkey Active Member
Various roles in the virtual seminars (webinar) team at ISCB-SC
Organization of the first Asian Student Council Symposium, #ASCS2022
Social media team, symposium organization, and Med&Omics at ISCB-SC-RSG Turkey

📍 World

2011 | 2016

Comprehensive Scholarship
Awarded by Bilkent University (ranked in the top 0.1% among ~1.7×10^6, Turkish University Entrance Exams)

📍 Ankara, Turkey

The education/institutes/projects, group/teams/collaborations and teaching opportunities provided me to build/improve **Independent Researcher**, **Teamwork/Collaboration**, **Analytical Thinking & Problem Solving**, **Resilience**, **Life-long learning attitude**, **Active Communication & Listening** skills.

SELECTED PUBLICATIONS AND POSTERS

2024

Automated high-throughput profiling of single-cell total transcriptome with scComplete-seq
(*Preprint*) DOI: 10.1101/2024.03.12.584729
Fatma Betul Dincaslan, Shaun Wei Yang Ngang, Rui Zhen Tan, Lih Feng Cheow

2023

High-Throughput Total RNA-Sequencing of Single Cells
Oral Presentation for jointly hosted CSI-ENS Symposium: Single-Cell Res/volution 2023

📍 Singapore

Fatma Betul Dincaslan, Lih Feng Cheow

2021

Functional analysis of co-expression networks of zebrafish ace2 reveals enrichment of pathways associated with development and disease
Genome, DOI: 10.1139/gen-2021-0033

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

2018

A pipeline for examination of tissue-specificity of differentially expressed genes in zebrafish mutants: Application to AChE mutants
Poster for International Symposium on Health Informatics and Bioinformatics (HIBIT)

📍 Antalya, Turkey

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