

# Kadir KOCABAŞ

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## ACADEMIC PROJECTS

### March 1, 2021 – Cont.

**Project Title:** Developing Personalized Molecular Interaction Models by using RNA-Seq Data of Alzheimer's Disease and Elucidation of Disease Mechanisms

**Research project funded by The Scientific and Technological Research Council of Turkey**

#### **Project Staff**

Creating Brain-Specific Genome-scale metabolic network (GMN) model consisting of Neuron and glial cells by using generic human GMN with proteome and single-cell RNA-seq data.

### December 2, 2019 – December 15, 2020

**Project Title:** Bioinformatic analysis of transcriptome data and cellular networks for Parkinson's Disease: Identification of novel drug targets and drugs

**Research project funded by The Scientific and Technological Research Council of Turkey**

#### **Project Staff**

The project consists of three parts, wet-lab study, investigation of protein-protein interactions and analysis of the metabolism of Parkinson's disease by constraint-based techniques, and I worked in this last part of the project. A novel brain metabolic model, which is called iBrain671, was created as a result which has not been published yet. Two different constraint-based approaches were used to analyze this model. Firstly, iBrain671 was analysed by standard flux balance analysis (FBA) and MOMA techniques. Secondly, iBrain671 was analysed again by FBA and MOMA but considering molecular crowding that is the main pathological feature of Parkinson's disease. These results have not been published yet, since the paper is still in the process of being written.

### July 23, 2019 – December 1, 2019

**International research project funded by The Scientific and Technological Research Council of Turkey**

**Project Title:** Identification of Potential Drug Targets for *Klebsiella pneumoniae* and *Salmonella enterica*-Induced Deadly Infections by Investigation of Metabolic Pathways with Constraint-Based Modeling Approach

#### **Project Staff**

It was an international joint project between Turkey and Pakistan. The project consists of two parts, identification of drug targets for both *Salmonella enterica* and *Klebsiella*

*pneumonia*, and protein docking analysis to find a suitable molecule that can bind to these targets. My role in the project to identify drug targets for *Salmonella enterica* induced infections. I produced a pathogen-host genome-scale metabolic network by combining human and *Salmonella enterica* genome-scale metabolic networks and further analyzed it by mapping their dual transcriptome data. I performed drug target prioritization analysis to find the most suitable drug targets. Promising results were obtained such that 7 out of 10 identified drug targets were already reported in the literature. The 3 non-reported targets were analysed in Pakistan by using protein docking techniques.

## **EDUCATION**

### **2021 – cont.**

Gebze Technical University | Kocaeli, Turkey

PhD: Bioinformatics and System Biology

### **2018 – 2021**

Gebze Technical University | Kocaeli, Turkey

MSc: Bioinformatics and System Biology

**Thesis Title:** Integrative Analysis of Multi-cellular Genome-scale Metabolic Networks with Cell Type Specific Transcriptome Data Predicted by Deconvolution Algorithms: Application to Parkinson's Disease

I contributed to COBRA Toolbox a tool, that creates interactive metabolite-metabolite interaction network in the scope of my master's thesis (<https://github.com/opencobra/cobratoolbox/pull/1681>, <https://github.com/opencobra/COBRA.tutorials/pull/86>).

### **2012-2016**

Erciyes University | Kayseri, Turkey

BSc: Biomedical Engineering

**Graduation Project:** Development of a diet and nutrition app for the Android platform.

## **SKILLS**

- R programming
- Matlab \*Contributor to The COBRA Toolbox
- Python
- Computational modelling
- Biostatistics
- Machine Learning
- Deep learning
- Natural Language Processing

## **PUBLICATIONS**

- Kocabaş K, Arif A, Uddin R, Çakır T (2022) Dual transcriptome based reconstruction of Salmonella-human integrated metabolic network to screen potential drug targets. PLoS ONE 17(5): e0268889. <https://doi.org/10.1371/journal.pone.0268889>
- Kocabas K., Çakır T. (2020). Integrative Analysis of Multi-cellular Genome-scale Metabolic Networks with Cell Type Specific Transcriptome Data Predicted by Deconvolution Algorithms: Application to Parkinson's Disease. Poster session presented at the annual meeting of international Eurasian conference on biotechnology and biochemistry
- Kocabaş K., Çakır T. (2019). Integrative Analysis of Pathogen Host Metabolic Network of *Salmonella enterica* with Dual RNA-seq data. Poster session presented at the annual meeting of the International Symposium on Health Informatics and Bioinformatics.
- Kocabaş K., Çakır T. (2019). Identification of Drug Target for *Salmonella enterica* induced Infections by Analysis of Integrated Pathogen Host Metabolic Network. Poster session presented at the annual meeting of the Türk Tıp Dünyası Kurultayı.

## **CERTIFICATES**

- Improving Deep Neural Networks: Hyperparameter Tuning, Regularization and Optimization – Coursera - 2021
- Applied Machine Learning in Python – Coursera - 2021
- Neural Networks and Deep Learning – Coursera - 2021
- R Programming – Coursera - 2020
- Getting and Cleaning Data – Coursera – 2020
- The Data Scientist's Toolbox – Coursera – 2020
- The Complete SQL Bootcamp 2020: Go from Zero to Hero Udemy - 2020