

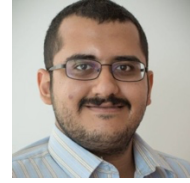
Muhammad Arif

PhD Candidate in Systems and Computational Biology
KTH Royal Institute of Technology | Science for Life Laboratory

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Expertise

Machine Learning, Network
Analysis, Multi-Omics,
Metabolic Modelling, RNA-Seq

Programming

Python, R, MATLAB, C, PHP,
Shell Script, Mathematica

Teaching Experiences

Bioinformatics, Applied
Bioinformatics, Systems Biology,
Thesis Supervision

Languages

English ★★★★★
Swedish ★★☆☆☆
Indonesian ★★★★★

Education

PhD Candidate | KTH Royal Institute of Technology | 2017 – Present
Systems Biology of Human Diseases. Focusing on the usage and development of machine learning and network analysis methods to unveil the underlying mechanism of human diseases.
Supervisors: Prof. Adil Mardinoglu and Prof. Mathias Uhlén

Master of Science | KTH Royal Institute of Technology | 2014 – 2016
European Master of Research on Information and Communication Technologies (MERIT). Double degree program with Universitat Politècnica de Catalunya (UPC), Barcelona.
Supervisors: Dr. Viktoria Fodor (KTH) and Dr. Albert Cabellos (UPC)

Bachelor of Engineering | Institut Teknologi Bandung | 2006 – 2011
Electrical Engineering with concentration track in Computer Engineering.

Key Publications

Zhang C[#], Bjornson E[#], Arif M[#]. (2020) The acute effect of metabolic cofactor supplementation: a potential therapeutic strategy against non-alcoholic fatty liver disease. Molecular Systems Biology.

Uhlen M, et al. (2017) A pathology atlas of the human cancer transcriptome. Science

Lee S[#], Zhang C[#], Arif M[#], et al. (2017) TCSBN: a database of tissue and cancer specific biological networks. Nucleic acids research

Arif M. (2016) Scalable 5-Tuple Packet Classification in Overlay Network. M.Sc. Thesis

Working Experience

Research Assistant | Science for Life Laboratory | 2016 – 2017 | Stockholm, Sweden

Data analysis from exome sequencing data to find predictors for cardiac stress recovery process. Carried on as part of doctoral education in the same research group.

Systems Engineer | Cisco Systems | 2010 – 2014 | Singapore, Singapore

Specializing in Enterprise Networking Technology and subject matter expert on Cisco WAAS and Network Monitoring platforms. Member of Software-Defined Networking (SDN) Tiger Team.

Teaching Experience

KTH Royal Institute of Technology:

Applied Bioinformatics (DD2040) | Teaching Assistant | 2017-2018
Bachelor Degree Project in Biotechnology (BB200X) | Supervisor | 2018
Systems Biology of Human Metabolism and Gut Microbiome | Organizer and Lecturer | 2018, 2020
Bioinformatics (BB24410) | Teaching Assistant | 2019, 2020
Systems Biology (CB2030) | Teaching Assistant | 2019, 2020

King's College London:

Introduction to Programming and Coding (7NNNMHD2) | Lecturer | 2020
Introduction to Linux (7NNNMHD2) | Lecturer | 2020
Statistical Analysis and Probability (7NNNMHD2) | Lecturer | 2020

Sover Academy:

Basic Programming (in Indonesian) | Organizer and Lecturer | 2020

Courses

Single Cell RNA Analysis | Uppsala, SE | NBIS | 2017
Analysis of Data from High-Throughput Molecular Biology Experiments | Stockholm, SE | KTH | 2017
Tools for Reproducible Research | Stockholm, SE | NBIS | 2018
Visualize Your Science | Stockholm, SE | KTH | 2019
Engineering for a Sustainable Society | Stockholm, SE | KTH | 2019
Introduction to Biomedicine | Stockholm, SE | KTH | 2019
Communicating Research beyond the Academy | Stockholm, SE | KTH | 2020

Conferences and Meetings

Integrating Systems Biology: From Networks to Mechanisms to Model | EMBL Heidelberg | 2018
Systems Biology of Mammalian Cells (Poster) | Bremen, DE | 2018
Chan-Zuckerberg Science Retreat (Poster) | Stockholm, SE | 2018

Publications

Published (Peer-Reviewed)

1. Li, X, et al. (2021). Discovery of functional alternatively spliced PKM transcripts in human cancers. *Cancers*.
2. Tebani, A, et al. (2020). Integration of molecular profiles in a longitudinal wellness profiling cohort. *Nature Communications*.
3. Chapman M, et al. (2020) Skeletal muscle transcriptomic comparison between long-term trained and untrained men and women. *Cell Reports*.
4. Zhang C, Bjornson E, **Arif M***. (2020) The acute effect of metabolic cofactor supplementation: a potential therapeutic strategy against non-alcoholic fatty liver disease. *Molecular Systems Biology*.
***Co-first author**
5. Li X, et al. (2020) Classification of clear cell renal cell carcinoma based on PKM alternative splicing. *Heliyon*.
6. Sayitoglu EC, et al. (2020). Boosting Natural Killer Cell-Mediated Targeting of Sarcoma Through DNAM-1 and NKG2D. *Frontiers in Immunology*.
7. Klevstig M, et al. (2019) Cardiac expression of the microsomal triglyceride transport protein protects the heart function during ischemia. *Journal of molecular and cellular cardiology*.

8. Liu Z, et al. (2019) Pyruvate kinase L/R is a regulator of lipid metabolism and mitochondrial function. *Metabolic Engineering*.
9. Benfeitas R, et al. (2019) Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. *eBiomedicine*.
10. Zhang, C, et al. (2019) Elucidating the reprogramming of colorectal cancer metabolism using genome-scale metabolic modeling. *Frontiers in oncology*.
11. Lovric A, et al. (2018) Characterization of different fat depots in NAFLD using inflammation-associated proteome, lipidome and metabolome. *Scientific Reports*.
12. Zhang C, et al. (2018) ESS: a tool for genome-scale quantification of essentiality score for reaction/genes in constraint-based modeling. *Frontiers in Physiology*.
13. Bidkhorji G, et al. (2018) Metabolic network-based identification and prioritization of anti-cancer targets based on expression data in hepatocellular carcinoma. *Frontiers in Physiology*.
14. Lee S, Zhang C, **Arif M**, et al. (2017) TCSBN: a database of tissue and cancer specific biological networks. *Nucleic Acids Research*. **Co-first author**
15. Uhlen M, et al. (2017) A pathology atlas of the human cancer transcriptome. *Science*.

Theses

16. **Arif M**. (2016). Scalable 5-Tuple Packet Classification in Overlay Network-Based SDN. M.Sc. Master Thesis.

Submitted/In-Preparation

17. Mahdessian, D, et al. (2021) Spatiotemporal dissection of the cell cycle with single-cell proteogenomics (Accepted in *Nature*, available in Biorxiv)
18. Van der Kolk, B, et al (2021) Molecular pathways behind acquired obesity: adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI (Accepted in *Cell Reports Medicine*)
19. **Arif M**, et al. Integrative transcriptomic analysis of tissue-specific metabolic crosstalk after myocardial infarction (Submitted to *eLife*, available in Biorxiv).
20. **Arif M**, et al. iNetModels 2.0: an interactive visualization and database of multi-omics data (Under Review in *Nucleic acid Research*, available in Biorxiv).
21. Zeybel M, **Arif M***, et al. Multi-omics analysis reveals the influence of the oral and gut microbiome on host metabolism in non-alcoholic fatty liver disease (Under Review in *Nature Communications*). ***Co-first author**
22. Altay O, **Arif M***, et al. Combined metabolic cofactor supplementation accelerates recovery in mild-to-moderate COVID-19 (Submitted to *Science Advances*). ***Co-first author**
23. Zeybel M, et al. Combined Metabolic Cofactor Supplementation Reduces Liver Fat in Nonalcoholic Fatty Liver Disease (Under Review in *Cell Metabolism*).
24. Karlsson M, Zhang C, et al. A single cell type transcriptomics map of human tissues (Submitted to *Science*).
25. Karlsson M, et al. A Whole-Body Expression Landscape of Pig (Submitted to *Genome Biology*).
26. Klevstig M, **Arif M***, et al. The effect of PCSK9 knockout to heart function during myocardial infarction (In Preparation). ***Co-first author**