Muhammad Arif

PhD in Systems Biology of Human Diseases
KTH Royal Institute of Technology | Science for Life Laboratory
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Expertise

Machine Learning, Network Analysis, Multi-Omics, Metabolic Modelling, Transcriptomics, Proteomics, Metabolomics

Programming

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

Teaching Experiences

Bioinformatics, Applied Bioinformatics, Systems Biology, Statistics, High Performance Computing, Thesis Supervision

Languages

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

Education

PhD | KTH Royal Institute of Technology | 2017 – 2021
Systems Biology of Human Diseases. (Defense Date: 11 June 2021)
Thesis Title: Systems and Network-based Approaches to Complex Metabolic 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 Control Engineering.

Key Publications

Arif M, et al (2021). Integrative transcriptomic analysis of tissue-specific metabolic crosstalk after myocardial infarction. eLife.
Arif M, et al. iNetModels 2.0: an interactive visualization and database of multi-omics data. Nucleic Acids Research.
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.

Total Publication: 27 (Google Scholar, 14 June 2021)
H-index: 10 (Google Scholar, 14 June 2021)

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)

21. **Arif M**, et al (2021). Integrative transcriptomic analysis of tissue-specific metabolic crosstalk after myocardial infarction. eLife. **First Author**
20. **Arif M,** et al (2021). iNetModels 2.0: an interactive visualization and database of multi-omics data. Nucleic Acids Research. **First Author**
19. Smati**,** et al (2021). Arif M, et al (2021). Integrative study of diet-induced mouse models of NAFLD identifies PPARα as a sexually dimorphic drug target. Gut.
18. Kolk, BW, et al (2021) Molecular pathways behind acquired obesity: adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI. Cell Reports Medicine.
17. Doran S., et al. (2021) Multi-omics approaches for revealing the complexity of cardiovascular disease. Briefings in Bioinformatics.
16. Mahdessian, D, et al. (2021) Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. Nature.
15. Li, X, et al. (2021). Discovery of functional alternatively spliced PKM transcripts in human cancers. Cancers.
14. Tebani, A, et al. (2020). Integration of molecular profiles in a longitudinal wellness profiling cohort. Nature Communications.

13. Chapman M, et al. (2020) Skeletal muscle transcriptomic comparison between long-term trained and untrained men and women. Cell Reports.
12. 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**
11. Li X, et al. (2020) Classification of clear cell renal cell carcinoma based on PKM alternative splicing. Heliyon.
10. Sayitoglu EC, et al. (2020). Boosting Natural Killer Cell-Mediated Targeting of Sarcoma Through DNAM-1 and NKG2D. Frontiers in Immunology.
9. 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.
7. Benfeitas R, et al. (2019) Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. eBiomedicine.
6. Zhang, C, et al. (2019) Elucidating the reprograming of colorectal cancer metabolism using genome-scale metabolic modeling. Frontiers in oncology.
5. Lovric A, et al. (2018) Characterization of different fat depots in NAFLD using inflammation-associated proteome, lipidome and metabolome. Scientific Reports.
4. 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.
3. Bidkhori G, et al. (2018) Metabolic network-based identification and prioritization of anti-cancer targets based on expression data in hepatocellular carcinoma. Frontiers in Physiology.
2. 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**
1. Uhlen M, et al. (2017) A pathology atlas of the human cancer transcriptome. Science.

Theses

1. **Arif M**. (2021). Systems and Network-based Approaches to Complex Metabolic Diseases. PhD Thesis.
2. **Arif M.** (2016). Scalable 5-Tuple Packet Classification in Overlay Network-Based SDN. M.Sc. Master Thesis.