

Muhammad Arif

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

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🌐 <http://muharif.net>



Expertise

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

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
Politécnica 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.

Referees:

Dr. Adil Mardinoglu (adilm [at] scilifelab.se)
Prof. Jan Boren (jan.boren [at] wlab.gu.se)

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

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

1. **Arif M**, et al. Multi-Tissue Transcriptomic Profiling of Myocardial Infarction (In Preparation).
2. Klevstig M, **Arif M***, et al. The effect of PCSK9 knockout to heart function during myocardial infarction (In Preparation). ***Co-first author**
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. Benfeitás R, et al. (2019) Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. eBiomedicine.
10. Zhang C, **Arif M***, et al. (2019) MOBN: an interactive database of multi-omics biological networks. (In preparation, preprint in BioRxiv) ***Co-first author**
11. Mahdessian D, et al. (2019) Spatiotemporal dissection of the cell cycle regulated human proteome. Nature. (Under review, preprint in BioRxiv)

12. Lovric A, et al. (2018) Characterization of different fat depots in NAFLD using inflammation-associated proteome, lipidome and metabolome. *Scientific Reports*.
13. 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*.
14. 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*.
15. 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**
16. Uhlen M, et al. (2017) A pathology atlas of the human cancer transcriptome. *Science*.
17. **Arif M**. (2017). Scalable 5-Tuple Packet Classification in Overlay Network-Based SDN. M.Sc. Thesis.