

Curriculum Vitae – Mr. Arash Shahsavari

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Education

- 2016 - 2019 M.S. in Complex Adaptive Systems - Chalmers University of Technology**
Gothenburg, Sweden
Thesis: *An Evaluation of Multi-Step Analyses of Single-Cell RNA Sequencing Data*.
Advisor: Rebecka Jörnsten.
Selected Coursework: Neural Networks, Stochastic Optimization, Information Theory, Dynamical Systems.
- Fall 2017 Exchange Studies - Dongguk University**
Seoul, South Korea
Selected Coursework: Multiple View Geometry, Deep Learning.
- 2013 - 2016 Electrical Engineering - Lund University**
Lund, Sweden
Completed 3 years of a 5-year joint B.S./M.S. program in electrical engineering, equivalent to a B.S. degree.
Selected Coursework: Multivariable Calculus, Control Theory, Mathematical Statistics, Numerical Analysis.

Experience

- 2019- Bioinformatician at Cambridge Stem Cell Institute, University of Cambridge**
Cambridge, UK
- Long-term data science support for multiple biomedical projects (50+ datasets for 10+ different projects).
 - Machine learning and statistics on terabyte-scale datasets
 - Involved in entire recruitment pipeline, from designing recruitment test, to selecting candidates for interviews, interviewing and final recruitment decisions
 - Co-authoring peer-reviewed publications
- 2018-2019 Volunteer at Kodcentrum**
Gothenburg, Sweden
- Teaching coding to children from underprivileged areas
 - Planning and structuring classes, hands-on support to children and other volunteers
 - Long-term development of the learning platforms and curriculum

Selected Research Projects

- 2020-2021 ClustAssess: Tools for scRNA-seq Clustering Assessment - Cambridge**
Cambridge, UK
- Development of R package for data-driven assessment of clustering
 - Profiled code to identify computational bottlenecks and reimplemented performance-critical parts in C++
 - High-resolution quantification of clustering stability
 - Investigation of how cell types inferred from data depend on clustering results
- 2020-2021 Mapping the Biogenesis of Forward Programmed Megakaryocytes - Cambridge**
Cambridge, UK
- Characterization of temporal changes in time-course scRNA-seq data
 - Integration with in-vivo dataset to quantify accuracy of in-vitro system
 - Identification of novel surface markers across multiple flow cytometry datasets
- 2020-2021 Consequences of Splitting 10X scRNA-seq Samples Across Sequencing Lanes - Cambridge**
Cambridge, UK
- Simulation study assessing the downstream consequences of sample splitting, compared to an unsplit sample, throughout the scRNA-seq analysis pipeline
 - Quantification of impact on clustering and cluster marker genes

Spring 2019 Master's Thesis - Dept. of Mathematical Sciences, Chalmers

- Gothenburg, Sweden
 - Benchmarking of scRNA-seq clustering methods across feature selections and datasets
 - Assessing deconvolution methods' robustness to noise in cell type signatures
 - Successful defense of thesis leading to M.S. degree

Fall 2018 HIV Transcription Latency - Dept. of Microtechnology and Nanoscience, Chalmers

- Gothenburg, Sweden
 - Investigation of feedback and noise in mathematical model of HIV transcription
 - Stochastic simulations of biochemical reactions with Gillespie algorithm
 - Quantification of uncertainty of molecular concentrations over time

Spring 2016 Feedback Controller for Ballbot - Dept. of Automatic Control, Lund University

- Lund, Sweden
 - Development of linear state feedback controller for ballbot
 - Evaluating feedback controller and optimizing parameters in simulations with sensor noise
 - Deployment on Arduino microcontroller including interfacing with Inertial Measurement Unit

Mentoring

2021 Andi Munteanu, UAIC Computer Science M.S. student and Cambridge Stem Cell Institute bioinformatics intern

Skills and Development

- **Programming Environments:** Python ([Optimization example](#)), R ([Clustering evaluation package](#), [Random Forest feature selection example](#)), Julia ([Outlier detection example](#), [Optimization example](#)), MATLAB, C++, Bash, \LaTeX , Arduino.
- **Computing Tools:** SLURM, git, Jupyter Notebook ([Example](#)), R Markdown ([Example](#))
- **Software packages:** [ClustAssess](#) - developed from scratch, currently package maintainer [Github](#), [Example](#), [Documentation](#)
- **Professional Courses:** [Python for Bioimage Analysis](#) - week-long course by the Royal Microscopical Society.
- **Self-Studied Books and Courses:** [Intermediate Linear Algebra](#), [Computational Linear Algebra](#), [Real Analysis](#), [Combinatorics & Graph Theory](#), [Reinforcement Learning](#).
- **Blog:** [sharash.github.io](#)

Journal Publications

- [1] **Arash Shahsavari** and I. Mohorianu. "ClustAssess: tools for assessing the robustness of single cell clustering". In preparation (2021).
- [2] J. Chen*, V. Sathiaselvan*, A. Moore, S. Tan, C. S. R. Chilamakuri, **Arash Shahsavari**, C. Jakwerth, S. B. Hake, A. Warren, I. Mohorianu, C. D'Santos, and I. Ringshausen. "[ZAP-70 constitutively regulates gene expression and protein synthesis in chronic lymphocytic leukemia](#)". *Blood* (2021).
- [3] M. Lawrence*, **Arash Shahsavari***, S. Bornelöv*, T. Moreau, K. Kania, M. Paramor, R. McDonald, J. Baye, M. Perrin, M. Steindel, P. Jimenez, C. Penfold, I. Mohorianu, and C. Ghevaert. "[Mapping the biogenesis of forward programmed megakaryocytes from induced pluripotent stem cells](#)". Under review at Science Advances (2021).
- [4] C. M. Morell, S. G. Tilson, R. A. Tomaz, **Arash Shahsavari**, G. Canu, B. T. Wesley, M. Perrin, I. Geti, S. Mukhopadhyay, F. Mazzacova, P. Gissen, J. Garcia-Bernardo, C. A. Rimland, F. Sampaziotis, I. Mohorianu, and L. Vallier. "Novel 3D Approach to Model Non-Alcoholic Fatty Liver Disease using human Pluripotent Stem Cells". In preparation (2021).
- [5] E. Williams*, R. Chazarra-Gil*, **Arash Shahsavari***, and I. Mohorianu. "[The sum of two halves may be different from the whole. Effects of splitting samples across sequencing lanes](#)". Submitted to Cell Reports (2021).

* indicates joint first authorship