Curriculum Vitae – Mr. Arash Shahsavari

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Web	, , webpage

Education

2016 - 2019
Gothenburg, Sweden

M.S. in Complex Adaptive Systems - Chalmers University of Technology
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
Seoul, South Korea

Exchange Studies - Dongguk University
Selected Coursework: Multiple View Geometry, Deep Learning.

2013 - 2016
Lund, Sweden

Electrical Engineering - Lund University
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-
Cambridge, UK

Bioinformatician at Cambridge Stem Cell Institute, University of Cambridge
- 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.
- Mentoring intern to contribute to open-source software and scientific publication.
- Co-authoring peer-reviewed scientific publications.

2018-2019
Gothenburg, Sweden

Volunteer at Kodcentrum
- 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

2020-2022
Cambridge, UK

ClustAssess: Tools for scRNA-seq Clustering Assessment - Cambridge
- 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
Cambridge, UK

Mapping the Biogenesis of Forward Programmed Megakaryocytes - Cambridge
- 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
Cambridge, UK

Consequences of Splitting 10X scRNA-seq Samples Across Sequencing Lanes - Cambridge
- 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.

For an updated version of this CV with hyperlinks, see sharash.github.io/cv.pdf

Spring 2019 Gothenburg, Sweden	**Master's Thesis - Dept. of Mathematical Sciences, Chalmers** • 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 Gothenburg, Sweden	**HIV Transcription Latency - Dept. of Microtechnology and Nanoscience, Chalmers** • 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 Lund, Sweden	**Feedback Controller for Ballbot - Dept. of Automatic Control, Lund University** • 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.

Mentorship

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.
- **Webpage:** sharash.github.io

Journal Publications

[1]   **Arash Shahsavari**, A. Munteanu, and I. Mohorianu. "ClustAssess: tools for assessing the robustness of single cell clustering". Submitted to Nucleic Acids Research (2022).

[2]   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". To appear in Science Advances (2022).

[3]   C. M. Morell, S. G. Tilson, R. A. Tomaz, **Arash Shahsavari**, G. Canu, B. T. Wesley, M. Perrin, I. Geti, S. Mukhopadhyay, F. Mazzacuva, 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 (2022).

[4]   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 (2022).

[5]   J. Chen*, V. Sathiaseelan*, 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), Commentary.

* indicates joint first authorship

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