

# Adrin Jalali

## Curriculum Vitae

Berlin, Germany

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### Experience

- 2018-present **scikit-learn**, *Core Developer*.
- 2020-present **fairlearn**, *Core Developer*.
- 2020-present **Senior Applied Scientist**, *Zalando SE*, Berlin, Germany.
- Center of Excellence for Algorithmic Privacy and Fairness
    - Improve customer trust by incorporating ethical issues in our machine learning practices and increasing transparency about our practices
    - Assess and deploy model cards across the organization
    - Help teams understand and mitigate ethical related risks
    - Audit and review other teams' work to assess potential risks and harms in their models and processes
- 2019-2020 **Open Source Developer**, *Anaconda Inc.*, Berlin, Germany.
- scikit-learn
  - fairlearn: a fairness in ML lib originally by Microsoft
- 2016-2019 **Senior Machine Learning Consultant**, *Ancud IT*, Berlin, Germany.
- Machine Learning (scikit-learn, tensorflow, GPy, etc.)
  - NLU/NLP (intent and entity recognition, conversation context, etc.)
  - NoSQL (Cassandra, Elasticsearch, Solr)
  - MLOps (PipelineIO: kubernetes, weave-scope, AWS, MS-Azure, docker, etc.)
- 2012-2016 **PhD Candidate**, *Max Planck Institute for Informatics*, Saarbrücken, Germany.
- Interpretable Sparse methods for cancer associations using an ensemble of sparse support vector machines (SVMs)
- 2011-2012 **PhD Candidate**, *British Columbia Cancer Research Center*, Vancouver, Canada.
- Automated flow cytometry data analysis and visualization using dynamic programming, clustering, graph algorithms, and SVMs
- 2009-2011 **Team Lead**, *Tosan Intelligent Data Miners*, Tehran, Iran.
- Offline fraud detection and real-time fraud prevention on debit transactions
- 2006-2007 **AI and Statistics Programmer**, *Fidofa Software Group*, Tehran, Iran.
- Automated trading in Future stock market

### Education

- 2012-2021 **PhD (cont.) in Computer Science/Bioinformatics**, *Max Planck Institute for Informatics, Computational Biology and Applied Algorithmics Department*, Saarbrücken, Germany,  
*Dissertation Topic*: Machine Learning in Cancer Diagnosis,  
*Degree anticipated*: 2020.

- 2011-2012 **PhD in Bioinformatics**, *University of British Columbia, British Columbia Cancer Research Center, Terry Fox Laboratory*, Vancouver, Canada,  
*Topic: Automated analysis of flow-cytometry data.*
- 2006-2009 **MSc in Computer Science**, *University of Tehran, School of Mathematics, Statistics, and Computer Science*, Tehran, Iran,  
*Thesis Topic: Finding DNA Motifs Using Bidirectional Recurrent Neural Networks.*
- 2002-2006 **BSc in Computer Science**, *Tehran Polytechnic, Department of Mathematics, and Computer Science*, Tehran, Iran,  
*Thesis Topic: Design and Implementation of a Genetic Algorithm to Solve Time Table Scheduling of a School.*

## Service

- 2017-present **PyData Berlin coorganizer**, NumFocus, Berlin, Germany.
- 2015 **Chemistry, Physics, and Technology Section Representative**, *PhDnet steering group*, Max Planck Society, Germany.
- 2012 **Bioinformatics Representative**, *College for Interdisciplinary Studies Graduate Student Society*, University of British Columbia, Vancouver, Canada.
- 2012 **“Bioinformatics” and “British Columbia Cancer Agency Graduate Student and Post Doctoral Fellow Society” representative**, *Graduate Student Society*, University of British Columbia, Vancouver, Canada.

## Languages

- Persian **Native**
- English **Fluent**
- German **Intermediate (~B2)**

## Publications

1. Handl L, Jalali A, Scherer M, Pfeifer N., *Partially blind domain adaptation for age prediction from DNA methylation data*, arXiv preprint arXiv:1612.06650, 2016.
2. Jalali A., and Pfeifer N., *Interpretable per Case Weighted Ensemble Method for Cancer Associations*, BMC Genomics, volume 17, no. 1, 2016.
3. Courtot M., Meskas J., Diehl A. D., Droumeva R., Gottardo R., Jalali A., Taghiyar M.J., *flowCL: ontology-based cell population labelling in flow cytometry*, Bioinformatics 31, no. 8 (2015): 1337-1339.
4. Jalali A., and Pfeifer N., *Interpretable per Case Weighted Ensemble Method for Cancer Associations*, Algorithms in Bioinformatics, pp. 352-353. Springer Berlin Heidelberg, 2014.
5. O'Neill K.\*, Jalali A.\*, Aghaeepour N.\*, Hoos H.H., and Brinkman R.R., *Enhanced flow-Type/RchyOptimyx: A Bioconductor pipeline for discovery in high-dimensional cytometry data*, Bioinformatics (2014), doi: 10.1093/bioinformatics/btt770.
6. Jalali A.\*, Aghaeepour N.\*, O'Neill K., Chattopadhyay P.K., Roederer M., Hoos H.H., Brinkman R.R., *RchyOptimyx: cellular hierarchy optimization for flow cytometry*, Cytometry Part A 81, no. 12 (2012): 1022-1030.
7. Aghaeepour N., Chattopadhyay P.K., Ganesan A., O'Neill K., Zare H., Jalali A., Hoos H.H.,

Roederer M., and Brinkman R.R., *Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays*, Bioinformatics, 2012: 28(7):1009–1016.

\* co-authors contributed equally