

# Rick Farouni | Curriculum Vitae

Massachusetts General Hospital/Harvard Medical School

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I am currently a post-doctoral research fellow in computational biology, working in the lab of Dr. Pinello at the Massachusetts General Hospital/Harvard Medical School. My research is focused on the application of multivariate statistics, machine learning, and deep learning to epigenomics data in particular, and bioinformatics data, in general. I received a PhD in Quantitative Psychology (statistics applied to modeling psychological and neuroimaging data) and a master's degree in Mathematical Statistics from the Ohio State University. I am dedicated to rigorous science in the public interest and I am passionate about the open access movement in science.

## Experience

### Postdoctoral Research Fellowship

- **Massachusetts General Hospital/Harvard Medical School** **MA, USA**  
*Research Lab of Professor Luca Pinello, Molecular Pathology Unit* 06/2017

### Internship

- **The Department of Biomedical Informatics Summer Internship Program (BMI SIP)**  
*Research Lab of Professor Ewy Mathè, The Ohio State University* 2016  
**Project:** Developing an R package and a Shiny app for the analysis of data generated from genome-wide chromatin accessibility assays such as ATAC-seq and DNase-seq with the goal of identifying regulatory elements involved in the cancer epigenetic landscape.

### Teaching Experience

- **Graduate Teaching Associate** **Ohio, USA**  
*The Ohio State University* 2013–2017  
Served as a Teaching Assistant for three courses: Repeated Measures Models, Covariance Structure Models, and Data Analysis in Psychology.

## Education

### Academic Qualifications

- **The Ohio State University** **Ohio, USA**  
*PhD in Quantitative Psychology* 2015–2017  
Dissertation Topic: 'Application of Deep Latent Generative Models to the Unsupervised Learning of Chromatin States'

- **The Ohio State University** **Ohio, USA**  
*Master of Science in Statistics* *2012-2014*
- **The Ohio State University** **Ohio, USA**  
*Master's Degree in Quantitative Psychology* *2012-2014*  
 Thesis Project: '*Latent Variable Modeling of Categorical Item Responses in a Hierarchical Bayesian Framework*'
- **The Pennsylvania State University** **Pennsylvania, USA**  
*Bachelor's Degree in Psychology with High Distinction* *2011-2012*

## Conference Presentations

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- **Joint Statistical Meetings** **Seattle**  
*Poster Presentation* *2015*  
**Poster Title:** Across-Subject Predictive Modeling of fMRI BOLD Responses to Faces using a sparse Bayesian Group Factor Analysis Model

## Awards and Fellowships

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- **Graduate Student Conference Presentation Award**  
*The Ohio State University* *2015*
- **The Center for Cognitive and Brain Sciences Summer Graduate Fellowship**  
*The Ohio State University* *2015*  
**Project Proposal:** '*Decoding the Pixels of the Face Image from the Voxels of fMRI BOLD Activity Patterns*'
- **The Social and Behavioral Sciences Summer Fellowship**  
*The Ohio State University* *2014*
- **University Fellowship**  
*The Ohio State University* *2012*

## Technical Skill Set

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- **Statistics and Machine Learning**
  - **Scientific Programming Languages:** Proficient in and comfortable transitioning between *R*, *Python* depending on computing goals. Familiar with *Julia*.
  - **Deep Learning Frameworks:** Experienced in using Tensorflow and Keras.
  - **Probabilistic Programming Languages:** Proficient in Stan.
- **Bioinformatics Software**
  - Experienced in analyzing Next Generation Sequencing (NGS) and functional genomics data using R's Bioconductor set of tools, Bowtie2, MACS2, and bedtools.
- **Cluster and High-Performance Computing**

- Good knowledge of running neuroimaging and bioinformatics analysis pipelines on super-computing clusters.
- o **Web and Software Development Tools**
  - L<sup>A</sup>T<sub>E</sub>X, Linux OS, Git, Docker, and Bash. Basic knowledge in website development tools such as HTML, CSS, and Jekyll.

## Publications and Software

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### Journal Papers.....

- o Baskin, E., Farouni, R., and Mathè, E. (2016). ALTRE: workflow for defining ALTered Regulatory Elements using chromatin accessibility data. **Bioinformatics** doi: 10.1093/bioinformatics/btw688. Preprint available at <http://www.biorxiv.org/content/early/2016/10/14/080564.full.pdf+html> (first co-author)
- o Latent variable models: a contemporary overview from a generative probabilistic modeling perspective. (In preparation)

### Software Development.....

- o ALTRE: A Workflow for Identifying ALTered Regulatory Elements using Chromatin Accessibility Data. Github Repo: <https://github.com/Mathelab/ALTRE>.

### Journal Review Service.....

- o **Psychometrika**  
Ad Hoc Reviewer 2015
- o **Psychological Methods**  
Ad Hoc Reviewer 2016