

# Rick Farouni | Curriculum Vitae

McGill University - Génome Québec Innovation Centre

✉ rfarouni@gmail.com • 🌐 <http://rfarouni.github.io/>

I am an applied statistician and computational biologist in the subfield of gene regulation with expertise in the probabilistic modeling and statistical analysis of epigenomics, CRISPR genome editing, and single-cell transcriptomics data.

## Experience

---

### Postdoctoral Researcher.....

- **McGill University-Génome Québec Innovation Centre** **Montreal, Canada**  
*Research Lab of Dr. Najafabadi, Department of Human Genetics* 06/2018-Present
- **Massachusetts General Hospital-Harvard Medical School** **Massachusetts, USA**  
*Research Lab of Dr. Pinello, Molecular Pathology Unit* 06/2017-05/2018  
- The Broad Institute of MIT and Harvard (Affiliated Member)

### Research Intern.....

- **Department of Biomedical Informatics Summer Internship Program** **Ohio, USA**  
*Research Lab of Dr. Ewy Mathè, The Ohio State University* 05/2016-08/2016

### University Teaching Assistant.....

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

## Education

---

### Academic Qualifications.....

- **PhD in Quantitative Psychology (i.e. Applied Statistics)** **Ohio, USA**  
*The Ohio State University* 2015-2017  
Dissertation Topic: 'Application of Deep Latent Generative Models to the Unsupervised Learning of Chromatin States'

- **Master of Science in Mathematical Statistics**  
The Ohio State University
    - **Master's Degree in Psychometrics**  
The Ohio State University
    - **Bachelor's Degree in Psychology**  
The Pennsylvania State University

**Ohio, USA**  
2012-2015

**Ohio, USA**  
2012-2014

**Pennsylvania, USA**  
2011-2012
- Thesis Project: 'Latent Variable Modeling of Categorical Item Responses in a Hierarchical Bayesian Framework'

## Publications

---

### Journal Papers (first author/co-author).....

- **Farouni, R.**, and Najafabadi, H. S. (2019). Statistical modeling, estimation, and remediation of sample index hopping in multiplexed droplet-based single-cell RNA-seq data. (Submitted). BioRxiv preprint available at <https://doi.org/10.1101/617225>.
- Clement, K.<sup>†</sup>, **Farouni, R.**<sup>†</sup>, Bauer, D. E., and Pinello, L. (2018). Design and analysis of unique molecular identifiers for deep amplicon sequencing. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/bty264>. Preprint available at <https://www.biorxiv.org/content/biorxiv/early/2018/03/23/288118.full.pdf>
- Pinello, L.<sup>†</sup>, **Farouni, R.**<sup>†</sup>, and Yuan, G-C. (2018). Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/bty031>. Preprint available at <https://doi.org/10.1101/199067>
- Baskin, E.<sup>†</sup>, **Farouni, R.**<sup>†</sup>, and Mathè, E. (2017). ALTRE: workflow for defining ALTEred Regulatory Elements using chromatin accessibility data. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btx386>. Preprint available at <http://www.biorxiv.org/content/early/2016/10/14/080564.full.pdf+html>

### Journal Papers (middle author).....

- Seruggia, D., Oti, M., Tripathi, P., Canver, M. C., LeBlanc, L., Di Giammartino, D. C., Bullen, M.J., Nefzger C.M., Sun, Y.B.Y., **Farouni, R.**, Polo, J.M., Pinello, L., Apostolou, E., Kim J., Orkin, S.H., and Das, P.P. (2019). TAF5L and TAF6L Maintain Self-Renewal of Embryonic Stem Cells via the MYC Regulatory Network. *Molecular Cell*.
- Clement K., Rees H., Canver, M.C., Gehrke J. M., **Farouni, R.**, Hsu, J.Y., Cole, M., Liu D.R., Joung J.K., Bauer, D.E., Pinello, L. (2019). CRISPResso2 provides accurate and rapid genome editing sequence analysis. *Nature Biotechnology*.
- Hsu, J. Y., Fulco, C.P., Cole, M., Canver, M.C., Pellin D., Sher, F, **Farouni, R.**, Clement K., Biasco L., Engreitz, J.M., Lander, E.S., Joung J.K., Bauer, D.E., Pinello, L. (2018). CRISPR-SURF: Exploratory and interactive software for analyzing CRISPR-based tiling screens. *Nature Methods*.

## Consortium Journal Papers (contributor).....

- Grüning, B., Dale, R., Sjödin, A., Rowe, J., Chapman, B. A., Tomkins-Tinch, C. H., The Bioconda Team, and Köster, J.(2018). Bioconda: A sustainable and comprehensive software distribution for the life sciences. **Nature Methods**. (Bioconda team member contributor, ranked 94 in the consortium author list). .

## Preprints.....

- **Farouni, R.** (2017). A Contemporary Overview of Probabilistic Latent Variable Models. **arXiv preprint**. Preprint available at <https://arxiv.org/abs/1706.08137>

## Dissertation and Thesis.....

- **Farouni, R.** (2017). Application of Deep Latent Generative Models to the Unsupervised Learning of Chromatin States. *PhD Dissertation*. Manuscript available at [https://etd.ohiolink.edu/!etd.send\\_file?accession=osu1492189894812539&disposition=inline](https://etd.ohiolink.edu/!etd.send_file?accession=osu1492189894812539&disposition=inline)
- **Farouni, R.** (2014). Latent Variable Models of Categorical Responses in the Bayesian and Frequentist Frameworks. *Masters Thesis*. Manuscript available at [https://etd.ohiolink.edu/!etd.send\\_file?accession=osu1412374136&disposition=inline](https://etd.ohiolink.edu/!etd.send_file?accession=osu1412374136&disposition=inline)

## Conference Presentations.....

- **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 (available at <https://rfarouni.github.io/assets/posters/jsm2015.pdf>).

## Software Development

---

- Haystack: A Python bioinformatics pipeline for the identification of genomic regions of epigenetic variability across different cell-types, cell-type specific cis-regulatory elements, and their associated transcription factors. GitHub Repo: [https://github.com/pinellolab/haystack\\_bio](https://github.com/pinellolab/haystack_bio).
- ALTRE: A Workflow for Identifying ALTered Regulatory Elements using Chromatin Accessibility Data. GitHub Repo: <https://github.com/Mathelab/ALTRE>.

## Awards and Fellowships

---

- **Graduate Student Conference Presentation Award** *2015*  
*The Ohio State University*
- **The Center for Cognitive and Brain Sciences Summer Graduate Fellowship** *2015*  
*The Ohio State University*  
**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

---

- **Statistics and Machine Learning**
  - **Scientific Programming Languages:** Proficient in and comfortable transitioning between *R* and *Python* depending on computing goals. Familiar with *Julia*.
  - **Deep Learning Frameworks:** Experienced in using Pytorch, Tensorflow, and Keras.
  - **Probabilistic Programming Languages:** Proficient in Stan, familiar with Edward.
- **Bioinformatics Software:** Analysis of next generation sequencing data, R's Bioconductor core packages, Bowtie2, bedtools.
- **Cluster and High-Performance Computing:** Good knowledge of running bioinformatics analysis pipelines on super-computing clusters.
- **Web and Software Development Tools:**  $\text{\LaTeX}$ , Linux OS, Git, Docker, and Bash. Basic knowledge in website development tools such as HTML, CSS, and Jekyll.

## Journal Review Service

---

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

## Personal Details

---

- **Country of Current Residence:** Canada
- **Countries of Previous Residence:** USA, Russia, Jordan
- **Interests and Hobbies:** Theoretical Linguistics, Evolutionary Biology, Experimental Music
- **Languages Spoken:** English, Arabic, Russian, French (intermediate), Spanish (intermediate)