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 and CRISPR 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

- **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

- **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

- **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 supercomputing clusters.

- **Web and Software Development Tools**
  - LaTeX, Linux OS, Git, Docker, and Bash. Basic knowledge in website development tools such as HTML, CSS, and Jekyll.

Publications and Software

Journal Papers

- 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)
- Pinello, L., Farouni, R., and Yuan, G-C. (2017). Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements (under review) doi: 10.1101/199067. Preprint available at `https://doi.org/10.1101/199067` (first co-author)

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`
- 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`

Software Development

- ALTRE: A Workflow for Identifying ALTered Regulatory Elements using Chromatin Accessibility Data. GitHub Repo: `https://github.com/Mathelab/ALTRE`.
- Haystack: systematic analysis of the variation of epigenetic states and cell-type specific regulatory elements. GitHub Repo: `https://github.com/pinellolab/haystack_bio`.

Journal Review Service

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