

Rick Farouni | Curriculum Vitae

ETH Zurich - Department of Biosystems Science and Engineering (D-BSSE)
Basel – Switzerland

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I am an applied statistician and bioinformatics scientist with expertise in the statistical modeling and bioinformatics analysis of genomics, single-cell transcriptomics (scRNA-seq), AAV directed evolution, and CRISPR editing screens data.

Experience

Bioinformatics Scientist.....

- **The Swiss Federal Institute of Technology in Zurich (ETH Zurich)** **Basel, Switzerland**
Research Lab of Dr. Platt, Department of Biosystems Science and Engineering 10/2020-Present
 - Analysis of transcriptional recording data.
 - Analysis of single nucleus RNA-seq in vivo CRISPR perturbation screens.
 - Development of a sequencing databases mining pipeline to discover uncharacterized Cas1-RT fusion proteins.
 - Design and analysis of base and prime editing CRISPR screens.
 - Statistical modeling of in vivo and invitro CRISPRi screens.
 - Development of target sequence extraction pipeline that matches the sequencing read into a given template and partitions it into specified parts. https://github.com/plattlab/quantify_target_sequence (private repo currently)
 - Analysis and modeling of AAV directed evolution (biopanning) experimental data for gene therapy applications.
 - Analysis of Deep Mutational Scans (DMS) screen data.

Postdoctoral Researcher.....

- **McGill University-Génomique Québec Innovation Centre** **Quebec, Canada**
Research Lab of Dr. Najafabadi, Department of Human Genetics 06/2018-09/2020
- **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** **Ohio, USA**
○ *The Ohio State University* **2012–2015**
- **Master's Degree in Psychometrics** **Ohio, USA**
○ *The Ohio State University* **2012–2014**
Thesis Project: '*Latent Variable Modeling of Categorical Item Responses in a Hierarchical Bayesian Framework*'
- **Bachelor's Degree in Psychology** **Pennsylvania, USA**
○ *The Pennsylvania State University* **2011–2012**

Publications

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

- Lazure, F.[†], **Farouni, R.**[†], Sahinyan, K., Blackburn, D.M., Hernández-Corchado, A., Perron, G., Lu, T., Osakwe, A., Ragoussis, J., Crist, C. and Perkins, T.J., Jahani-Asl, A., Najafabadi, H.S., & Soleimani, V.D. (2023). Transcriptional reprogramming of skeletal muscle stem cells by the niche environment. ***Nature Communications***, 14(1), 535. Paper available at <https://www.nature.com/articles/s41467-023-36265-x>. Website: https://csglab.github.io/transcriptional_reprogramming_muscle_cells/.
- **Farouni, R.**, Djambazian, H., Ferri, L. E., Ragoussis, J., & Najafabadi, H. S. (2020). Model-based analysis of sample index hopping reveals its widespread artifacts in multiplexed single-cell RNA-sequencing. ***Nature Communications***. Paper available at <https://www.nature.com/articles/s41467-020-16522-z>. Website: <https://csglab.github.io/PhantomPurgeR/>.
- Clement, K.[†], **Farouni, R.**[†], Bauer, D. E., & 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.[†], **Farouni, R.**[†], & 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.[†], **Farouni, R.**[†], & 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).....

- Belli, O., Karava, K., **Farouni, R.**, & Platt, R. J. (2024). Multimodal mutational scanning with base and prime editing. *Under review*.
- Santinha, A. J., Klingler, E., Kuhn, M., **Farouni, R.**, Lagler, S., Kalamakis, G., Lischetti, U., Jabaudon, D., & Platt, R. J. (2023). Transcriptional linkage analysis with in vivo AAV-Perturb-seq. *Nature*, 622(7982), 367-375. <https://www.nature.com/articles/s41586-023-06570-y>
- Schmidt, F., Zimmermann, J., Tanna, T., **Farouni, R.**, Conway, T., Macpherson, A.J., & Platt, R.J. (2022). Noninvasive assessment of gut function using transcriptional recording sentinel cells. *Science*, 376(6594), p.eabm6038. <https://www.science.org/doi/abs/10.1126/science.abm6038>
- Anderson-Trocmé, L., **Farouni, R.**, Bourgey, M., Kamatani, Y., Higasa, K., Seo, J., Kim, C., Matsuda, F., & Gravel, S. (2019). Legacy Data Confounds Genomics Studies. *Molecular Biology and Evolution*. <https://doi.org/10.1093/molbev/msz201>
- 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., & 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, & 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
- **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

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

- PhantomPurgeR: The optimal purging of phantom molecules by the robust estimation of the sample index hopping rate in multiplexed droplet-based single-cell RNA-seq data. GitHub Repo: <https://csglab.github.io/PhantomPurgeR/>.
- 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/pinello1ab/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**
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**

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:**
 - **Analysis of sequencing data:** scRNAseq, RNAseq, ChIPseq, ATACseq, Deep Mutational Scans (DMS), CRISPR screens, Alternative Splicing, Amplicon Sequencing, PacBio sequencing.
 - **Workflow development:** Development of custom workflows using R's Bioconductor core package, large database protein mining pipelines. Good knowledge of running bioinformatics analysis pipelines on super-computing clusters.
 - **Established tools:** STAR, Bowtie2, bedtools, samtools, PEAR, Prokka, etc.
- **Web and Software Development Tools:** \LaTeX , Linux OS, Git, Docker, and Bash. Basic knowledge in website development tools such as HTML, CSS, and Jekyll.

Personal Details

- **Country of Current Residence:** Switzerland
- **Countries of Previous Residence:** Canada, USA, Russia, Jordan
- **Languages Spoken:** English, Arabic, Russian, French (B1), Spanish (B1), German (A2)