# **RICHARD SHUAI**

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#### **EDUCATION**

**Stanford University** Ph.D. Biophysics

#### University of California, Berkeley

B.A. Computer Science & B.A. Statistics

#### **EMPLOYMENT**

#### Absci, AI Scientist Intern

Built and trained models based on language models and graph neural networks to design and optimize antibodies for binding to a specific target. Wrote pipelines to process PDB files to extract coordinates and torsion angles for training.

#### Amazon, Software Engineering Intern

Developed pricing configuration page for Amazon Pricing Team and external business users for competitive price analysis with Agile development. Expanded backend functionality within Java Spring Framework to add key features. Revamped previous UI with React Redux, supporting 8 month phase-out of previous interface.

#### **RESEARCH EXPERIENCE**

#### Gray Lab, NSF REU Research Fellow, Johns Hopkins University

Jun. 2021 – Sept. 2022 Using generative language modeling to design synthetic antibody libraries. Trained a ~12.8M parameter GPT-based transformer on ~558M antibody sequences. Sampled novel antibody sequences, measured properties for therapeutic developability, and visualized antibody structural predictions with PyMOL. Patent pending.

#### Ioannidis Lab, Research Assistant, UC Berkeley

Using CNN-based deep learning models with scATAC-seq data to prioritize variants affecting chromatin accessibility in kidney tissue. Trained models and evaluated performance on predicting allelic imbalance. Analyzed first-layer convolutional filters and in silico saturation mutagenesis outputs to discover transcription factor binding motifs.

#### **WORKSHOPS & PRESENTATIONS**

- Pooja Kathail, Richard Shuai, Ryan Chung, Chun Jimmie Ye, Gabriel Loeb, Nilah M. Ioannidis. "Assessing the utility of genomic deep learning models for disease-relevant variant effect prediction." ICML Workshop on Computational Biology, spotlight (2022).
- Richard W. Shuai, Jeffrey A. Ruffolo, Jeffrey J. Gray. "Generative Language Modeling for Antibody Design." NeurIPS • Workshop on Machine Learning for Structural Biology, poster (2021).
- Richard W. Shuai, Jeffrey A. Ruffolo, Jeffrey J. Gray. "Generative Language Modeling for Antibody Design." RosettaCON, • poster (2021).

#### **PUBLICATIONS & PRE-PRINTS**

- Amir Shanehsazzadeh\*, Sharrol Bachas\*, George Kasun, John M. Sutton, Andrea K. Steiger, Richard Shuai, ..., Joshua Meier, "Unlocking de novo antibody design with generative artificial intelligence." bioRxiv (2023).
- Richard W. Shuai\*, Jeffrey A. Ruffolo\*, Jeffrey J. Gray. "Generative Language Modeling for Antibody Design." bioRxiv (2022).
- Kyrollos Yanny\*, Kristina Monakhova\*, Richard W. Shuai, Laura Waller. "Deep learning for fast spatially-varying deconvolution." Optica 9, 96-99 (2022).
- Richard W. Shuai\*, Kyrollos Yanny\*, Kristina Monakhova, Laura Waller. "MultiWienerNet: Deep Learning for Fast Shift-Variant Deconvolution." Computational Optical Sensing and Imaging, pages CTh5A-5. Optical Society of America (2021).
- Kathleen M. Yee, Richard W. Shuai, Bin Liu, Christian A. Huynh, Chao Niu, Hailey R. Lee, Min S. Lee, Jirui Wen, Jian Zou, • Jiang Wu, Ke Shuai. "TET1 controls Cxcl1 induction by DNA demethylation and promotes neutrophil recruitment during acute lung injury." bioRxiv (2021).

#### **SKILLS**

#### Programming languages: Python, Java, R, C, Javascript

Libraries: PyTorch, Tensorflow, Keras, HuggingFace, NumPy, pandas, SciPy

Molecular modeling: PyRosetta, PyMOL

Relevant coursework: Machine Learning, Deep Learning, Computational Methods in Genomics and Medicine, Artificial Intelligence, Optimization Models, Probability and Random Processes, Data Structures, Linear Algebra, Linear Modeling

September 2022 - Current GPA: 4.0 / 4.0

Aug 2018 - May 2022

GPA: 3.99 / 4.0

# April 2022 – Sept. 2022

### May 2020 – Aug. 2020

## Jan. 2021 – Current