

# Seyone Chithrananda

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## EDUCATION

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**UC Berkeley** Berkeley, CA Bachelor's in Computer Science (Bioengineering minor)

August 2021-May 2025

- **Coursework:** Discrete Math & Probability Theory, Convex Optimization, Computational Functional Genomics, Structure and Interpretation of Computer Programs, Designing Information Devices and Systems I & II (linear algebra, circuit analysis, ML), Data Structures, Single + Multivariable Calculus. **Activities and societies:** Machine Learning at Berkeley, open source developer for DeepChem project (3K stars).

## EXPERIENCE

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**Broad Institute of MIT and Harvard** *Research Intern*

Cambridge, MA August 2022-present

- Visiting student working with [Eeshit Dhaval Vaishnav](#), advised by [Prof. Eric Lander](#) (Institute founding director, former WH Science Advisor), studying gene expression programs using single-cell data and variational deep learning methods.

**Dyno Therapeutics** *ML Research Intern*

Cambridge, MA May 2022-Sept 2022

- Researching methods for [viral protein AAV capsid design](#), using sequence-to-function graph and sequence-based models (transformers, GNNs, etc). a16z, Google Ventures backed Church Lab startup, with ~\$120M Series A ([blog post](#)).
- Developed generative structure-to-sequence models to propose high-scoring variant sequences, and examined performance at standard protein redesign, handling epistatic interactions, indels, and at predicting binding on experimentally-validated and in silico fitness landscapes. Preprint accepted at [Machine Learning in Structural Biology](#) Workshop, NeurIPS 2022.
- Built and grew internal package containing simulated fitness landscapes for benchmarking models on biological sequence design problems. Implemented statistical models for mapping epistatic interactions in progressively rugged landscapes.

**Nurix Therapeutics** *ML Research Intern*

San Francisco, CA May 2021-September 2021

- Developing computational strategies for DNA-encoded library design, accounting for multiple sources of experimental variation. Developed graph generative models and genetic algorithms for scaffold-based molecular design, using multi-objective optimization.
- Deployed multiple classification and regression models for screening molecules within core DEL-ML platform. Implemented message-passing, graph convolutional neural networks for binding affinity, ADME-tox modeling.

**University of Toronto** *Research Intern - Matter Lab (advised by Alan-Aspuru Guzik)*

Toronto, ON Apr. 2020-May 2021

- Co-developer of [SELFIES v1.0](#), a 100% robust molecular string representation for machine learning models. Developed depth-first graph traversal algorithm and dearomatization code for v1.0 release. Downloaded 9K times to date.
- Published [paper](#) at NeurIPS 2020 [workshop](#) (lead author) on pre-training strategies for large-scale language modeling of molecules. Implemented transformer models and tokenizers, led integration of NLP-style models into library (600,000 model API calls to date).
- Published a [review paper](#), highlighting statistical methods for uncertainty estimation in ML for property prediction.
- Developed pipeline using genetic algorithm, graph-attention ensemble to screen 30,000 small molecules for 3CL-protease binding.

## PUBLICATIONS

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*A Benchmark Framework for Evaluating Structure-to-Sequence Models for Protein Design.* Chan, J., **Chithrananda, S.**, Brookes, D. & Sinai, S., NeurIPS ML for Structural Biology Workshop (2022). Preprint to be released soon.

*ChemBERTa-2: Towards Chemical Foundation Models.* Ahmad, W., Simon, E., **Chithrananda, S.**, Grand, G., & Ramsundar, B., ELLIS ML for Molecules Workshop (December, 2021). [arXiv:2209.01712](#)

*ChemBERTa: Large-Scale Self-Supervised Pre-training for Molecular Property Prediction.* **Chithrananda, S.**, Grand, G., & Ramsundar, B. (NeurIPS 2020 ML for Molecules workshop). [arXiv:2010.09885](#)

*Assigning Confidence to Molecular Property Prediction.* Nigam, A., Pollice, R., Hurley, M.F., Hickman, R.J., Aldeghi, M., Yoshikawa, N., **Chithrananda, S.**, Voelz, V., & Aspuru-Guzik, A. ([Expert Opinions in Drug Discovery](#), Taylor and Francis) 2021.

## SKILLS & INTERESTS

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**Programming:** Python, Tensorflow, Keras, PyTorch, Pandas, RDKit, sklearn, Spark. **Infra:** AWS, Google Cloud, Docker.

**Talks:** Delivered [research talks](#) at CMU, Baylearn, NeurIPS, Royal Society of Chemistry and Re-Work to audiences of 200+.

## AWARDS, GRANTS AND FUNDING

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**Masason Foundation Fellow - Softbank:** Support for my research and education from Masayoshi Son's [foundation](#)

**Emergent Ventures Fellowship:** Recipient of research [fellowship](#), supported by the Thiel Foundation. ([Press Release](#))

**Re-Work Young Researcher:** Delivered [talk](#) at conference in front of over 1000 attendees on independent research in comp. biology

**Tensorflow Research Cloud Fellowship:** [Grant](#) offered by Google to use TPU graphics processing pods for ML research