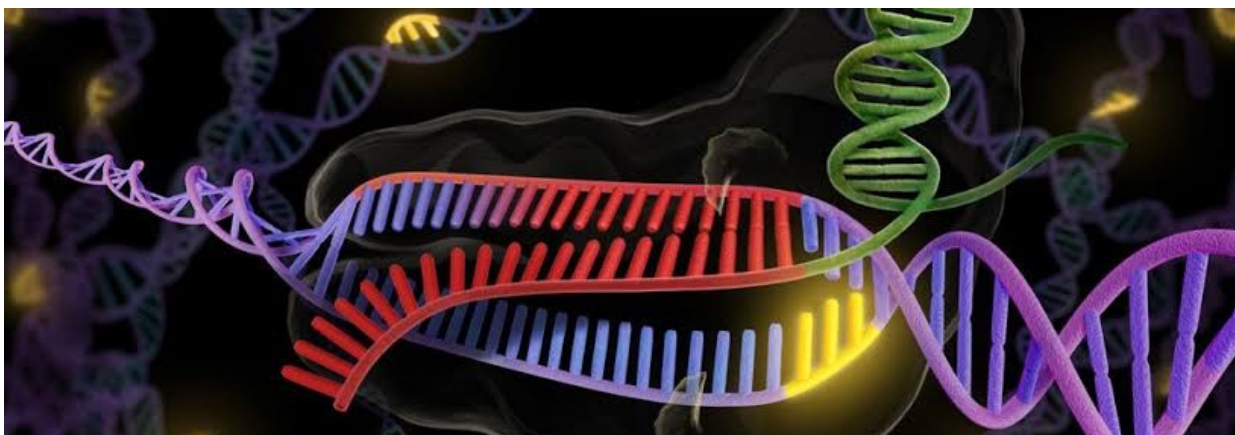




gRNA GPU-Accelerated Analyses

As CRISPR gene-editing applications scale, off-target binding present major challenges in a large search space. This computational genomics and sequence modeling project scales guide RNA (gRNA) evaluation across large genomic datasets using the Delta supercomputer. We deploy machine learning models (e.g., transformers, sequence embeddings) to model binding affinities, detect off-target mutations, and evaluate editing accuracy.

A qualified AI, Bioengineering, Computer Science, Math, or Statistics student will evaluate genomic datasets and apply predictive models to optimize CRISPR gRNA design. The team is led by Dr. Phuong Cao at the National Center for Supercomputing Applications (NCSA) in collaboration with Bioengineering.

Role: Process genomic sequence datasets, build machine learning models for on-target and off-target prediction, and quantify sequence specificity across genomic targets.

Skills: Strong programming background (e.g., Python, C++) and familiarity with machine learning workflows are required. Experience with bioinformatics libraries, sequence modeling frameworks (e.g., PyTorch), or high-performance computing is preferred.

Benefits: Independent study course credit; co-authorship on computational biology and AI publications; direct access to Delta compute allocations and other supercomputers; access (fair-use) to large-scale language models (i.e., both frontier and self-hosted models).

Previous students have successfully transitioned into SpaceX (xAI), Meta, Microsoft AI, Google DeepMind, etc., to continue the collaboration.

Apply: go.illinois.edu/job-grna

About the project & team: Phuong Cao | <https://go.illinois.edu/phuong-cao> | pcao3@illinois.edu

