# Surag Nair

5th Year PhD Student | Stanford University www.stanford.edu/~surag | surag@stanford.edu

# **Research Interests**

Deep Learning for Regulatory Genomics, Single-cell Genomics, Computational Biology, iPSC Reprogramming

# Education

**Stanford University** *PhD in Computer Science* Cumulative Grade Point Average: 4.21

**Stanford University** *MS in Computer Science* 

**Indian Institute of Technology, Delhi** *B.Tech in Electrical Engineering* 

Cumulative Grade Point Average: 9.35/10

# **Relevant Coursework**

Computer Science	:	Artificial Intelligence, Machine Learning, Probabilistic Graphical Models,
		Natural Language Processing, Computer Systems and Organization,
		Databases, Analysis of Networks, Cryptography, Operating Systems
Biology/Biocomputation	:	Deep Learning in Genomics and Biomedicine, Structure of Biomolecules,
		Chromatin Regulation of the Genome

# **Research and Technical Projects**

**Deep Learning Methods for Genomics and Single-cell Epigenomics** *Supervisor: Dr. Anshul Kundaje, Stanford University*  Apr 2018 - Present

## Mitigating spurious feature learning in conventional models of regulatory genomics

- · Demonstrated that conventional machine learning models of regulatory genomics learn spurious features that result in inconsistent predictions, misleading feature interpretation, and erroneous sequence design.
- · Exploring training design decisions that mitigate the learning of spurious sequence features.

## Single-cell dissection of human skin cell reprogramming with DNA sequence models

- · Analyzed single-cell RNA-seq and ATAC-seq of a time course of human skin cell reprogramming to iPSCs.
- · Trained DNA sequence models to predict ATAC-seq at high resolution and performed model interpretation.
- · Linked concentration of transcription factors and their DNA motif sequences to reprogramming progression.
- · Proposed detailed mechanisms for how skin cells lose their identity within the first two days of reprogramming.

## Speeding up In-silico Saturation Mutagenesis (ISM) for convolutional sequence models

- · ISM is an interpretability method for deep learning sequence models in which each position in input sequence is perturbed and propagated through a trained model to measure the effect of the mutation on the output.
- · Developed fastISM, an algorithm that speeds up ISM by over 10x for convolutional neural networks.

# Cis-trans deep learning models for chromatin accessibility

- · Developed models that incorporate DNA sequence with RNA expression data to predict chromatin accessibility.
- · Demonstrated the ability to make predictions in unseen cell types and impute missing chromatin accessibility.
- · Improved state-of-the-art by introducing new features, a ResNet model architecture, and training procedures.

## Timely detection of extreme failure cases for Siri

JUN 2018 - AUG 2018

Summer Internship, Apple Inc. (Siri International team), Cupertino

- · Studied causes for failure in the multi-component machine learning pipeline for Siri, Apple's voice assistant.
- · Devised and implemented an NLP pipeline for real-time detection of failure cases based on usage logs data.
- · Workflow consisted of periodic PySpark and Python scripts running on terabytes of real-time data.

Sep 2019 - Dec 2023 (Expected)

Sep 2017 - Jun 2019

JUL 2013 - JUN 2017

# **Selected Publications and Preprints**

- Transcription factor stoichiometry, motif affinity and syntax regulate single-cell chromatin dynamics during fibroblast reprogramming to pluripotency: Surag Nair\*, Mo Ameen\*, Laksshman Sundaram, Anusri Pampari, Jacob Schreiber, Akshay Balsubramani, Will Wang, David Burns, Helen Blau, Ioannis Karakikes, Kevin Wang, Anshul Kundaje. bioRxiv 2023.
- The dynseq genome browser track displays context-specific sequence features at single-nucleotide resolution: Surag Nair\*, Arjun Barrett\*, Daofeng Li\*, Brian Raney, Brian Lee, Peter Kerpedjiev, Vivek Ramalingam, Anusri Pampari, Fritz Lekschas, Ting Wang, Maximilian Haeussler, Anshul Kundaje. Nature Genetics 2022.
- fastISM: Performant in-silico saturation mutagenesis for convolutional neural networks: Surag Nair, Avanti Shrikumar, Jacob Schreiber, Anshul Kundaje. Bioinformatics 2022.
- Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts: Surag Nair\*, Daniel Kim\*, Jacob Perricone, Anshul Kundaje. Bioinformatics 2019.
- Single-cell multiome of the human retina and deep learning nominate causal variants in complex eye diseases: Sean Wang, Surag Nair, Rui Li, Katerina Kraft, Anusri Pampari, Aman Patel, Joyce Kang, Christy Luoung, Anshul Kundaje, Howard Chang. Cell Genomics 2022.
- Accelerating in silico saturation mutagenesis using compressed sensing: Jacob Schreiber, Surag Nair, Akshay Balsubramani, Anshul Kundaje. Bioinformatics 2022.
- AP-1 is a temporally regulated dual gatekeeper of reprogramming to pluripotency: Glenn Markov, Thach Mai, Surag Nair, Anna Shcherbina, Yu Xin Wang, David Burns, Anshul Kundaje, Helen Blau. PNAS 2021.
- Inferring Temporal Knowledge for Near-Periodic Recurrent Events: Dinesh Raghu\*, Surag Nair\*, Mausam.
  International Joint Conference on Artificial Intelligence (IJCAI) 2018.

\* equal contribution

WINTER 2017-18

WINTER 2017-18

AUTUMN 2017-18

# **Open Source Contributions**

## Multi-framework Alpha Zero 🖓 🗎 [3000+ stars]

• Developed a package for self-play based learning following the Alpha Zero paper by DeepMind. Allows easy addition of new games and works with all major deep learning frameworks (PyTorch, TensorFlow, Keras).

#### Stanford CS230 Deep Learning Starter Code () [2000+ stars]

· Developed starter code for deep learning projects in PyTorch with accompanying tutorials.

# **PyTorch Implementation of seqGAN Algorithm O**[600+ stars]

• Implemented a LSTM based deep learning language model and trained it using a Generative Adversarial Network framework using Policy Gradients, in PyTorch, based on the paper by Lantao Yu et al. 2016.

## **Technical Skills**

Languages:Python, R, C++, SQLSoftwares/Tools:PyTorch, TensorFlow, NumPy, PySpark

## Invited/Selected Talks

- · Invited: IMSc Chennai (Aug 2023): Motif syntax of fibroblast reprogramming
- · Selected (Travel Fellowship): ISMB (France, Jul 2023): Feature leakage in models of regulatory DNA
- · Invited: IGVF Seminar Series (Apr 2023): Motif syntax of fibroblast reprogramming
- · Invited: Bay Area Chromatin Club (Jul 2022): Motif syntax of fibroblast reprogramming
- · Selected: Cold Spring Harbor Systems Biology (Mar 2022): Motif syntax of fibroblast reprogramming
- · Invited: Genentech (Mar 2022): Motif syntax of fibroblast reprogramming
- · Selected: ISMB 2021 (Jul 2021): Motif syntax of fibroblast reprogramming ►
- · Selected: MLCB 2020 (Nov 2020): Speeding up in-silico saturation mutagenesis (fastISM) ▶
- Selected: ISMB 2019 (Switzerland, Jul 2019): Cis-trans deep learning models for chromatin accessibility

# **Professional Activities**

## Journal Reviewer

- · OUP Bioinformatics: 2019, 2023
- · BMC Bioinformatics: 2022, 2023
- · PLOS Computational Biology: 2022, 2023
- · IEEE Transactions on Computational Biology and Bioinformatics: 2023
- · Journal of Open Source Software: 2022, 2023
- · Review Commons: 2021

### **Conference Reviewer**

- · ICML Workshop on Computational Biology: 2023
- · International Conference on Intelligent Systems for Molecular Biology (ISMB): 2023
- · Machine Learning in Computational Biology (MLCB): 2021, 2022

## **External Teaching**

- · Cold Spring Harbor Statistical Analysis of Genome Scale Data, Cold Spring Harbor, USA: 2022
- · Machine Learning in Health and Disease, International Centre for Theoretical Sciences, India: 2023

## **Teaching Experience**

#### CS230: Deep Learning

Course Instructors: Dr. Andrew Ng & Kian Katanforoosh, Stanford University 🔿

WINTER 2017-18

 Project mentor for 14 teams who applied deep learning to domains including space imagery, translation, genomics, and photography. Developed questions for midterm examination. Graded exams and projects for 400+ students.

# **Scholastic Achievements**

- 2017 Department Rank 5 (top 6%) among students of Electrical Engineering Department, Batch of 2017
- 2013 All India Rank 280 in IIT Joint Entrance Exam-Advanced out of over 1 million students
- 2013 National Top 40 in Indian National Chemistry Olympiad

# Mentoring

- · Areeb Gani (Montgomery Blair High School): 2022
- · Arjun Barrett (The Harker School): 2021