

# Aravind Chandrasekaran, Ph. D

Baltimore, MD **US Permanent Resident** [aravindcsn@gmail.com](mailto:aravindcsn@gmail.com) +1-240-281-2241 [LinkedIn](#) [Codes](#)

Biophysicist with expertise in building novel algorithms to study protein dynamics. Currently working on structure-property relationships of liquid protein droplets using minimal physics (mesoscopic) and continuum models. Passionate about leveraging computational frameworks to accelerate research and development.

## Technical Skills

Molecular dynamics, reaction network modeling, agent-based modeling (ABM), Markov models, machine learning (PCA, K-means clustering), optimization (gradient-descent, least-squares, SLSQP)

## Key Accomplishments

- Authored **14** peer-reviewed publications (recognized in prestigious journals such as Nature Physics, Nature Communications, PNAS, and Developmental Cell)
- Lead Developer for a biophysical simulation codebase, guaranteeing consistent project updates (**5 releases**), optimizing performance, and enhancing user experience
- Delivered **20+** talks/posters highlighting research findings (audience size – **50-300**), including 5 platform presentations at leading international conferences

## Research Highlights in Press

- [Graham, Chandrasekaran et. al., Nat. Phys., 2023](#) featured in [Physics Today](#)
- [Chandrasekaran et. al., Mol. Biol. of the Cell, 2022](#) recommended to [H1 Connect](#) (Faculty Opinions)

## Research Experience

### Molecular modeling of cellular signaling (Postdoc and Ph.D.)

- Developed software to study spatial signaling models under both **stochastic** and **continuum frameworks**. Predictions from simulations were experimentally validated
- Devised and delivered automatic actin structure classifier using graph theoretical models, Markov state models, PCA, and machine learning techniques (K-means clustering)
- Developed statistics-driven metrics of protein clustering to understand signaling biophysics through in silico digital twins of experimental systems

### Self-assembly algorithm development (Postdoc and Ph.D.)

- **Lead developer, MEDYAN** ([Github repo](#), C++, **30,000+ lines** over **five releases**) and contributor, **Cytosim** ([GitLab](#) repo C++, forked edits for [constant polymer copy number](#) and [multimerization](#))

### Protein structure-function relationship (Master's)

- Established a non-redundant dataset of DNA-binding proteins incorporating multiple sequence alignment, EC number classification, CATH codes, and crystal structure analysis
- Developed a **docking pose filter**– delivered **2.5-fold** increase in the probability of identifying the protein-DNA structure (tested through bootstrapping)

## Computational Skills

Programming languages	C++, Python, Tcl/Tk, Java
Python Libraries	Scikit-learn, scipy, matplotlib, numpy, pandas, PyTorch
Software development	Jira, Git
Molecular modeling	LAMMPS, Cytosim, MEDYAN, VMD, FTDock
Other	MATLAB, LaTeX, VCell

## Work Experience

Postdoctoral Researcher	University of California San Diego	Aug 2021– Present
Research Fellow	National Institutes of Health, Bethesda	Aug 2018 – Dec 2019
Teaching Assistant	University of Maryland, College Park	Jan 2017– May 2018
Research Scientist.	National Tsing Hua University, Hsinchu Taiwan	Feb. 2014– May 2014

## Education

<b>Ph. D. in Chemistry</b>	University of Maryland, College Park	Aug 2014 – July 2021
<b>M. Sc. Bioinformatics &amp; Structural Biology</b>	National Tsing Hua University, Hsinchu, Taiwan	Feb 2012 – Jan 2014
<b>B. Tech. Chemical Engineering</b>	Anna University, Chennai, India	July 2007 – May 2011

## Leadership and Empowerment

- Led project updates within a multidisciplinary team consisting of over 20 stakeholders
- Mentored **20+** students in science communication and presentation techniques, convened 4 tutorial workshops to introduce new users to cutting-edge research tools (MEDYAN, CytoSim, LAMMPS)
- Led and trained junior developers in software best practices, statistical modeling, and protein simulations, engaged **10** active users
- Organized multi-lab (UC Berkeley, UCSD, and Allen Institute) seminar series to develop novel hypotheses to test through collaborations with experimentalists and computational scientists
- Classroom instruction, Department of Chemistry, UMD for **undergraduate** and **graduate** courses (**9** courses, total students **550+**)

## Honors and Awards

2024	Chosen for the Summer School 2024: Self-Organizing Matter: From Inanimate to the Animate, University of Colorado, Boulder
2023	Chosen for the Rising Stars in Soft and Biological Matter Symposium, University of Chicago
2019, 2015, & 2014	Dean's Fellowship, University of Maryland, College Park
2018	NIH-UMD Partnership Fellowship
2013 & 2012	International Student Scholarship, National Tsing Hua University, Taiwan
2010	Summer Research Fellowship Programme, Indian Academy of Sciences

## Outreach

- 2020 Facilitated panel discussion on addressing imposter syndrome, Grow PoLS workshop
- 2016 US Science & Engineering Festival, Washington D.C.
- 2014 Organized community-building events for the oSTEM UMD chapter

## Publications (selected, 155 citations, total 14, full list [here](#))

1. Walker, C., **Chandrasekaran, A.**, Mansour, D., Graham, K., Torres, A., Wang, L., Lafer, E.M., Rangamani, P., Stachowiak, J.C. (2025). [Liquid-like condensates that bind actin drive filament polymerization and bundling](#), *Developmental Cell (In Press)*
2. **Chandrasekaran, A.**, Graham, G., Stachowiak, J.C., Rangamani, P. (2024). [Kinetic trapping organizes actin filaments within liquid-like protein droplets](#), *Nature Communications*, 15, 3139
3. Graham, G., **Chandrasekaran, A.**, Wang, L., Ladak, A., Lafer, E.M., Rangamani, P., Stachowiak, J.C. (2024). [Liquid-like condensates mediate competition between actin branching and bundling.](#), *PNAS*, 121(3), e2309152121
4. **Chandrasekaran, A.**, Clarke, A., McQueen, P., Fang, H.Y., Papoian, G. A., and Giniger, E. (2022) [Computational simulations reveal that Abl activity controls cohesiveness of actin networks in growth cones](#). *Mol. Biol. of the Cell*, **33:ar92**, 1