Bruno Beltran

BIOPHYSICIST, MATHEMATICIAN, DATA SCIENTIST

Education

Stanford University PhD Biophysics, 2021

Louisiana State University BS Mathematics, 2015

Skills

Programming languages

- **5+ years** of professional experience: C, Fortran, Python
- **2+ years** of professional experience: Bash, C++, Matlab, Javascript
- Strong in Azure, AWS, SQL

Languages

Native fluency in English, Spanish

Side Projects

- Matplotlib developer (commit rights).
- Erebus: a space shooter with immersive, head tracking-based 3D, procedurally generated music, and motionsensor controls.
- The Dish on Science: a science blog for a general audience.
- **pip-cache** maintainer (autocomplete for *pip*!)

Experience

Data Scientist

Crayon, USA / Irvine, CA / 2021–Present

Provided Data Science, Cloud Architecture, and Machine Learning consulting services to clients in diverse sectors including construction, biotechnology, and transportation.

- Contributed pre-sales and solution architecture work leading to multiple engagements from \$50k to \$100k+.
- Gave lectures and provided training on machine learning, cloud computing, and CI/CD best practices to technical and non-technical clients.
- Led a team of data scientists researching, implementing, and optimizing an NLP-based solution for identifying relevant safety issues from raw-text incident reports. Models were trained and deployed using AML.
- Single-handedly designed and implemented a proof-of-concept NLP solution for classifying, sorting, and searching regulatory documents leveraging Azure SQL, Azure Functions, and Azure Cognitive Services on the backend, and Vue.js on the frontend.

Graduate Student Researcher

Spakowitz Lab, Stanford University / Stanford, CA / 2016–2021

Led independent, open-ended research projects in molecular biophysics, cell biology, and the mathematical theory of polymers.

- De facto technical lead guiding the lab's code development, continuous integration, and code review process.
- Pioneered a consistent, stable method for estimating cumulative distribution functions from correlated, censored data (no techniques existed previously).
- Developed the "nucleosome chain" model, a first-principles, bottom-up, analytical model for mesoscale DNA organization *in vivo* that accounts for both geometric heterogeneity due to protein binding and thermal fluctuations.
- Mentored multiple undergraduate researchers.
- Maintained a 25+ node cluster used by multiple labs and a 50k+ line Fortran simulation codebase.

Visiting Student Researcher

Burgess Lab, UC Davis / Davis, CA / 2018–2019

Served as a data science consultant and polymer expert.

- Developed a disruptive model for the progression of homolog pairing in prophase using only the basic polymer physics of meiotic DNA.
- Showing how our model could match experimental data without the need for parameter optimization led to co-first authorship.
- Developed an automated workflow for tracking and segmenting our movies using classical image analysis techniques.
- Assisted in carrying out single-particle tracking experiments, monitoring the diffusion of homologous loci throughout prophase I.

Rotating Student Researcher

Chemical & Systems Biology Department / Stanford, CA / 2015–2016

- Designed and implemented a deep-learning based, automated nuclear segmentation pipeline that was robust to overlapping and dividing cells.
- Pioneered a "stoichiometrically-explicit" approach to bacterial population modeling employing random matrix techniques.

Founder and Manager

Cain Center Tutoring / Baton Rouge, LA / 2011–2014

Founded a learning center targeted at supporting teaching students, using LSU workstudy scholarships to fund undergraduate tutors.

• Connected up to two dozen students a day and six tutors a day.

Linux Administrator

Nandakumar Lab, LSU / Baton Rouge, LA / 2013–2014

Computational consultant for a microfluidics research group.

- Provided support for several dozen shared Red Hat machines.
- Gave regular lectures on advanced Bash usage, including job management, signal handling, and best practices for continuous integration on our cluster.

Research Tech I / EXROP Capstone Fellow

Jacobs Wagner Lab, Yale University / New Haven, CT / 2014–2015

Mathematical consultant for multiple projects in bacterial cell biology.

- In collaboration with Dr. Sangjin Kim, discovered long-range effects of supercoiling on transcription in *E. coli*.
- Constructed analytical and simulation frameworks for reasoning about mRNA transcription initiation, elongation, and degradation.
- Pioneered a model for the mechanism of *parABS* plasmid segregation.
- Co-discovered the "adder" mechanism of bacterial cell size control.

Presentations

Talks

- (session chair): BPS 2018
- Lake Como School of Advanced Studies 2016
 (invited): Humboldt State University 2013 Collo-
- quium Series
- (award): LSU 2012 and 2013 Undergraduate research conference
- SIAM 2013 Mid-Atlantic Meeting
- Brown University 2013 SUMS Conference
- Joint Mathematics Meetings 2013

Publications

Posters

- BPS 2019 Les Houches Meeting
- NSF 2019 Genome Architecture workshop, Varna, Bulgaria.
- Stanford 2019 BioX Symposium
- HHMI 2014 EXROP Meetings
- LSU 2013 and 2014 Honors Colloquia SACNAS 2012
- 1. Beltran B, MacPherson Q, Spakowitz AJ. Waiting Times from Finite Trajectories. (in preparation)
- Newman T*, Beltran B*, McGhehee J, Elnatan D, Cahoon C, Chu D, Spakowitz AJ, Burgess S. Homologous locus pairing is a transient, diffusion-mediated process in meiotic prophase. PNAS. (in review)
- Sandholtz S, Kannan D, Beltran B, Spakowitz AJ. Chromosome Structural Mechanics Dictates the Local Spreading of Epigenetic Marks. Biophysical Journal. (2020)
- MacPherson Q, Beltran B, Spakowitz AJ. Chromatin compaction leads to a preference for peripheral heterochromatin. Biophysical Journal. (2020)
- Beltran B*, Kannan D*, MacPherson Q, Spakowitz AJ. Geometrical heterogeneity dominates thermal fluctuations in facilitating chromatin contacts. Physical Review Letters. (2019)
- Sandholtz S, Beltran B, Spakowitz AJ. Physical modeling of the spreading of epigenetic modifications through transient DNA looping. Journal of Physics A: Mathematical and Theoretical. (2019)
- Kim S, Beltran B, Jacobs-Wagner C. Long-distance cooperative and antagonistic RNA polymerase dynamics via DNA supercoiling. Cell. (2019)
- Ghosh RP, Franklin JM, Draper W, Quanming S, Beltran B, Spakowitz AJ, Liphardt J. A fluorogenic array for temporally unlimited single-molecule tracking. Nature chemical biology. (2019)
- MacPherson (), Beltran B, Spakowitz AJ. Bottom-up modeling of chromatin segregation due to epigenetic modifications. PNAS. (2018)
- Campos M*, Surovtsev IV*, Kato S*, Paintdakhi A, Beltran B, Ebmeier SE, Jacobs-Wagner C. A constant size extension drives bacterial cell size homeostasis. Cell. (2014)
- 11. Lim HC, Surovtsev IV, **Beltran B**, Huang F, Bewersdorf J, Jacobs-Wagner C. Evidence for a DNArelay mechanism in ParABS-mediated chromosome segregation. Elife (2014)

Selected Coursework

Teaching assistantships

Calculus I, II, & III; differential equations.

Graduate classes

Machine learning, molecular bioengineering, stochastic analysis, two-photon imaging, finite element methods, functional analysis, calculus of variations and optimal control, complex analysis, probability theory, differential equations, algebra, advanced numerical linear algebra.

Awards

- NSF GRFP Fellowship
- Goldwater Fellowship
- HHMI EXROP Capstone Fellowship

Fun

Big-wall climber, pianist, guitarist, sushi chef, speedrunner.

Contact

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