

Christopher David Armstrong

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Research Interests: Combinatorics, Data Visualization, Genomics and Epigenetics, Probability and Statistics

Proficiencies (5+ years): Applied Mathematics (statistics, convex optimization, linear regression, simulation); Python (class-based programming, joblib [parallelization library], jsonschema, NumPy); R (base, data.table, doParallel and forEach [parallelization library], ggplot2, plotly); SQL; Japanese (daily-level fluency)

Familiarities (1-3 years): C++; Genomics and Epigenetics; Python (D3); Real Analysis

Experience

Research Associate – Bioinformatics

May 2019 – Present

The University of Pennsylvania – Philadelphia, PA

- Create mathematical models to explore N⁶-methyladenosine (m6A) mRNA modifications in *Arabidopsis thaliana*.
- Develop parallelized data pipelines for high-speed analysis and visualization (R 5000+ lines).
- Collaborate with the Minn lab in the Perelman School of Medical Sciences on analyzing m6A data in *M. musculus* tumor samples.

Research Associate

April 2020 – Present

The George Washington University – Washington, DC

- Develop the JSON/BioCompute Object (BCO) API for the Mazumder lab in the School of Health Sciences.
- Create and edit documentation relating to python packages developed in the lab.
- Develop parallelized pipelines for interacting with NCBI taxonomical databases.
- Teach python and R to other members of the lab.

Graduate Teaching Assistant

May 2019 – August 2019

The Georgia Institute of Technology – Atlanta, GA

- Assisted with teaching the survey probability and statistics course by tutoring students, writing tests, and creating video tutorials; asked to teach separate course on Bayesian statistics.

Developer and Data Analyst

September 2014 – January 2018

Various Clients

- Developed full-stack database interface solution for an HR recruiting firm; automated data pipelines for a political analytics consulting firm.

Mathematics Teacher

August 2008 – September 2014

Various Organizations

- Taught students at all levels and in various areas of mathematics, specializing in the undergraduate engineering calculus sequence; three students went on to become tutors themselves.

Education

Life Sciences Curriculum

Ongoing

Various Institutions

- Relevant Coursework: General Chemistry I, II; Organic Chemistry I; Genetics; Biology; Organic Chemistry II (current semester); Single Cell Biology (Spring '21); Immunology (Spring '21)

M.S., Analytics (Quantitative Modeling Track)

2019

The Georgia Institute of Technology – Atlanta, GA

- Relevant Coursework: Regression Analysis; Simulation; Time Series Analysis; Bayesian Statistics; Deterministic (Convex) Optimization; Data Visualization

B.S., Mechanical Engineering (Thermodynamics Track)

2011

The University of Kansas – Lawrence, KS

- Relevant Coursework: Statistics I; Computational Numerical Analysis; Differential Equations; Engineering Calculus I, II; The Finite Element Method for Stress Analysis; Linear Algebra

Publications

(Preprint) Armstrong, Chris D. “The Anagram Formula Is Uniquely Minimized in the Positive Integers.” 2020. TS. The University of Pennsylvania, Philadelphia. ArXiv. The University of Pennsylvania, 2020. Web. 2020. <<https://arxiv.org>>. ORCID: 0000-0002-9236-472X (Armstrong, Christopher)

Area: Combinatorics

Summary: Armstrong shows that maximizing solutions to the anagram formula exist uniquely in the positive integers. This fact can be applied to characterizing areas of similarity in the genome/transcriptome.

Contribution: All (only author).

(Preprint) Sharma, Bishwas; Armstrong, Chris et al. “The m6A modification as a predictor of stress response in *A. thaliana*.” 2020. TS. The University of Pennsylvania, Philadelphia. Molecular Plant. American Society of Plant Biologists, 2020. Web. 2020. <<http://www.plantcell.org/>>. ORCID: 0000-0002-9236-472X (Armstrong, Christopher)

Area: Plant Genomics

Summary: Sharma et al. show that *A.thaliana* responds to abiotic cold stress conditions with highly selective mRNA expression.

Contribution: Armstrong showed that m6a deposition in *A. thaliana* under abiotic cold stress conditions is highly specific to partitioned sets of genes responsible for cold stress response. In particular, cold-specific m6a sites are shown to be highly selective for the stop codon and downstream positions with a deposition probability of approximately half that of background.

Other Media

BioCompute Object API Source Repository (2020)

Location: Online (https://github.com/biocompute-objects/bco_editor)

Format: Source code and documentation

Summary: Develop source code and documentation for the BioCompute Object API (BCO API)

Additional Information: Languages involved include bash, CSS, JavaScript, HTML, and python.

FDA Scientific Computing Days (2020)

Location: Online (Food and Drug Administration)

Format: Poster

Summary: Contributed technical material to explanatory poster regarding the BioCompute Object (BCO) project in the Mazumder lab.

Preliminary results on methylation in Arabidopsis thaliana (2019)

Location: Gregory Lab (The University of Pennsylvania)

Format: Presentation

Summary: Working off of Anderson et al. and Niu et al., Armstrong showed differentiation in nucleotide diversity between abiotically stressed and non-stress *A. thaliana* specimens.