



Daniel Antonio Negrón

SCIENTIST

+1 (555) 555-5555 | dnegron2@gmu.edu | 0000-0002-6123-2441 | [iEz2FjoAAAAJ](#) | [dnanto](#)

math and programming for art, sport, and research

Education

School of Systems Biology, George Mason University

PHD IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

- Advisor: Dr. Donald Seto

Fairfax, Virginia

Aug 2014 - May 2021

The Zanvyl Krieger School of Arts & Sciences, The Johns Hopkins University

MS IN BIOINFORMATICS

Baltimore, Maryland

Nov 2009 - Dec 2011

College of Arts & Sciences, Boston University

BA IN BIOCHEMISTRY & MOLECULAR BIOLOGY; MINOR IN COMPUTER SCIENCE

Boston, MA

Sep 2005 - May 2009

Skills

Able to quickly learn new skills and refine existing ones on own initiative.

Domain	Summary
Biology	alignment, annotation, homology modeling, network analysis, PCR assay, phylogenetics
Computing	data structures, GPU, HPC, microcontrollers, multithreading, numerical methods, parallel, UI
Programming	Compiled: C, C++, C#, Java; Interpreted: AWK, BASH, JavaScript, perl, python; Coreutils
Mathematics	machine learning (evolutionary/genetic, decision trees), signed-distance functions, stats
Reproducibility	Conda, Docker, Jupyter Notebook, R Markdown, Snakemake
Database	PostgreSQL, SQLite, SQL, ER modeling
Languages	Spanish (Co-native), Japanese (JLPT N5)

Experience

Noblis, Inc.

SCIENTIST

Reston, VA

Aug 2011 - Present

- Build low-resource, low-energy edge-computing devices
- Co-develop BioVelocity® for parallel, reference-based alignment of next-generation sequence reads
- Co-develop PSET (PCR Signature Erosion Tool) for in silico bioinformatic analysis of PCR assays
- Design and supervise internship projects
- Design pipeline to discover subspecies-level sequence fingerprints using probabilistic data structures
- Develop an expert system to recommend environmental remediation methods to reduce well-water contamination
- Develop compression algorithm with application of cellular automata and genetic algorithms
- Develop graph algorithm for traffic congestion prediction
- Develop parallel algorithms using MPI for commodity hardware clusters and compiler directives for the CRAT XMT 2
- Develop statistical models to fingerprint nuclear power plant fuel rods
- Execute laboratory protocols for DNA extraction and sequencing with the MinION
- Investigate criminal activity on the dark web using social network analysis
- Lead developer of a distributed virus scanning system for network traffic based on containerized microservices
- Program as a full-stack developer for web and client applications, such as laboratory and data management software
- Reverse-engineer file formats for forensic analysis
- Visualize large data sets using the R and python programming languages

ON-CALL TECHNICAL INTERN

Aug 2011 - Oct 2011

- Port the program from the research fellowship to run on the CRAY XMT 2 supercomputer
- Run the program to infer co-expression gene networks to identify virulence factors from *P. aeruginosa* microarray data

NOBLIS BIOINFORMATICS INDEPENDENT RESEARCH PROJECT FELLOWSHIP

Jun 2011 - Aug 2011

- Upgrade an existing algorithm for the analysis of host-pathogen interaction networks from microarray data
- Develop an MPI-enabled version of the algorithm for parallel execution
- Run the program to infer a co-expression network and identify network motifs from human-plague microarray data

Infant & Toddler Connection of Fairfax-Falls Church

ADMINISTRATIVE ASSISTANT II / DATA ANALYST

Fairfax, VA

Jun 2011 – Aug 2011

- Interpret for Spanish speaking customers
- Developed VBA macros for use with Microsoft Office applications
- Automate administrative tasks using Windows batch scripts
- Manage all IT support at the Falls Church satellite site

Laboratory for Biocomputing and Informatics, Boston University

UNDERGRADUATE RESEARCHER / DIRECTED STUDY

Boston, MA

2008 – 2009

- Research under the supervision of Dr. Gary Benson
- Implement algorithms for biological data analysis: distance scoring, sequence alignment, and spaced-seed searching
- Develop software to analyze genomic microsatellite junctions and trace tandem repeat evolution

Experimental Condensed Matter Physics, Boston University

UNDERGRADUATE RESEARCHER

Boston, MA

2008 – 2009

- Research under the supervision of Dr. George Ogurek Zimmerman
- Program a type-II superconductor simulator to investigate phenomena related to the Josephson Effect
- Collaborate on the 2D implementation of the simulator and subsequently developed the 3D version

Projects

Capsid Modeling

APPLICATION TO RENDER VIRAL CAPSIDS USING CASPAR-KLUG THEORY

May 2020 - Present

- In the browser with JavaScript to export SVG (democapsid @ <https://dnanto.github.io/democapsid/capsid.html>).
- On the GPU with GLSL for realtime renders (protocapsid @ <https://www.shadertoy.com/view/dlsGRH>).

District Broomball Statistics

DATABASE AND WEBSITE FOR SEASONAL PLAYER STATISTICS

Jun 2019 - Present

- Design ER model and built SQLite database and R-based website generation code.
- <https://github.com/dnanto/broomball>

Publications

PAPERS

Negrón, D. A., Kang, J., Mitchell, S., Holland, M. Y., Wist, S., Voss, J., Brinkac, L., Jennings, K., Guertin, S., Goodwin, B. G., & Sozhamannan, S. (2022). Impact of SARS-CoV-2 Mutations on PCR Assay Sequence Alignment. *Frontiers in Public Health*, 10. <https://doi.org/10.3389/fpubh.2022.889973>

Negrón, D. A. (2021). Molecular Clock Analysis of Human Adenovirus [PhD thesis]. In *ProQuest Dissertations and Theses*. George Mason University.

Wiley, M. R., Fakoli, L., Letizia, A. G., Welch, S. R., Ladner, J. T., Prieto, K., Reyes, D., Espy, N., Chitty, J. A., Pratt, C. B., Paola, N. D., Taweh, F., Williams, D., Saindon, J., Davis, W. G., Patel, K., Holland, M., **Negrón, D.**, Ströher, U., ... Palacios, G. (2019). Lassa virus circulating in Liberia: A retrospective genomic characterisation. *The Lancet Infectious Diseases*, 19(12), 1371–1378. [https://doi.org/10.1016/S1473-3099\(19\)30486-4](https://doi.org/10.1016/S1473-3099(19)30486-4)

Sozhamannan, S., Holland, M. Y., Hall, A. T., **Negrón, D. A.**, Ivancich, M., Koehler, J. W., Minogue, T. D., Campbell, C. E., Berger, W. J., Christopher, G. W., Goodwin, B. G., & Smith, M. A. (2015). Evaluation of Signature Erosion in Ebola Virus Due to Genomic Drift and Its Impact on the Performance of Diagnostic Assays. *Viruses*, 7(6), 3130–3154. <https://doi.org/10.3390/v7062763>

Vasudevan, M., **Negrón, D.**, Feltz, M., Mallette, J., & Wunderlich, K. (2015). Predicting Congestion States from Basic Safety Messages by Using Big-Data Graph Analytics. *Transportation Research Record*, 2500(1), 59–66. <https://doi.org/10.3141/2500-07>

PREPRINTS

Negrón, D. A. (2021). *Vectorized Capsid Rendering in the Browser with Capsid.js*. <https://doi.org/10.1101/2020.12.02.408252>

Holland, M., **Negrón, D.**, Mitchell, S., Dellinger, N., Ivancich, M., Barrus, T., Thomas, S., Jennings, K. W., Goodwin, B., & Sozhamannan, S. (2020). *BioLaboro: A bioinformatics system for detecting molecular assay signature erosion and*

designing new assays in response to emerging and reemerging pathogens. <https://doi.org/10.1101/2020.04.08.031963>

Holland, Mitchell Y., **Negrón, D. A.**, Shane Mitchell, Mychal Ivancich, Katharine W. Jennings, Bruce Goodwin, & Shanmuga Sozhamannan. (2020). *Preliminary in silico assessment of the specificity of published molecular assays and design of new assays using the available whole genome sequences of 2019-nCoV* [Article]. Noblis, Inc.

Negrón, D. A. (2011). *Parallel Algorithm for de novo Co-Expression Networks from Microarray Data* [Article]. The Johns Hopkins University.

Negrón, D. A. (2009). *Microsatellite junction counts are inversely proportional to the size, gap, and edit distance of its constituent units*. Boston University.

PATENTS

Monaco, M. K., **Negrón, D.**, & Satira, B. (2021). *Data loss prevention* (Patent No. US20210165904A1).

Omari, M., Barrus, T. W., Sanders, M., & **Negrón, D.** (2021). *Rapid genomic sequence classification using probabilistic data structures* (Patent No. US11037654B2).

Sanders, M. J., Masi, D. M., McCabe, E. R., Maciejewski, E. J., Dellinger, N. S., & **Negrón, D. A.** (2021). *Network topology discovery* (Patent No. US20210184961A1).

Monaco, M. K., **Negrón, D.**, & Satira, B. (2021). *Data loss prevention* (Patent No. US10915654B2).

Monaco, M. K., **Negrón, D.**, Satira, B., & Collins, M. (2021). *Network security using inflated files for anomaly detection* (Patent No. US10924502B2).

Monaco, M. K., **Negrón, D.**, & Satira, B. (2019). *Data loss prevention* (Patent No. US10331902B2).

POSTERS

Negrón, D. A. (2022, October). Implementation Of Bacilliform Viral Capsid Models. *ASM Microbe 2022*.

Negrón, D. A., Kang, J., Mitchell, S., & Dommaraju, K. (2022, June). A Nextclade dataset for genotyping Human adenovirus. *ASM Microbe 2022*.

Negrón, D. A., Mitchell, S., Holland, M. Y., Ashford, D., & Jennings, K. (2022, June). PCR and LAMP Assays for African Swine Fever Virus and Foot-and-Mouth Disease Virus. *ASM Microbe 2022*.

Negrón, D. A. (2021, April). Elongated Capsid Generation in the Browser. *GMU Spring 2021 SSB Student Research Day*.

Negrón, D. A. (2020, December). Vectorized Capsid Generation in the Browser. *Fall 2020 SSB Student Research Day*.

Thomas, S., Barrus, T., & **Negrón, D. A.** (2020, December). Detection of Engineered E. Coli Reference Genomes within NCBI Using Molecular Clock Analysis. *Sequencing, Finishing, and Analysis in the Future*.

Negrón, D. A., & Sozhamannan, S. (2019, December). Automated Molecular Clock Analysis of the O-PS Gene Cluster of Vibrio cholerae. *54th US-Japan Joint Panel Conference on Cholera and Other Bacterial Enteric Infections*.

Negrón, D. A., Goodwin, B., Smith, M., & Sozhamannan, S. (2016, June). Phylogenetic Analysis of the O-Antigen Biosynthesis Genes in Vibrio cholerae. *Sequencing, Finishing, and Analysis in the Future Meeting*.

Negrón, D. A., & Sozhamannan, S. (2015, June). Functional Unity in Structural Diversity: Genetic Basis of Diversity in O-Antigen Biosynthesis Genes in Vibrio cholerae. *Asm2015 115th General Meeting, Computational Genomics, Databases, and Modeling (Division R)*.

Negrón, D. A. (2013). Perfect Repeats Detection on the CRAY XMT 2. *Noblis, Inc.*

Negrón, D. A., & Thomas, S. (2012, May). Co-Expression Network Generation from Microarray Data on the Cray XMT. *Center for Biotechnology Education 7th Annual Research Symposium*.

Negrón, D. A. (2011, August). Parallel Algorithm for de novo Co-Expression Networks from Microarray Data. *Independent Research Project*.

PRESENTATIONS

Sozhamannan, S., **Negrón, D. A.**, Rajavel, M., & Xie, G. (2018, May). Building A Smart Wall With The Strength Of Diversity - What Can We Learn From Bacteria? *Sequencing, Finishing, and Analysis in the Future*.

Negrón, D. A. (2017, March). Deceptive Defence. *BloomCON 0x02 Forensics and Security Conference*.

Collins, M., & **Negrón, D. A.** (2017, February). Mushrooms Not Honey: Making Deceptive Defenses More Toxic for Attackers. *RSA Conference*.

Baez-Cazull, S., **Negrón, D. A.**, Rak, A., Bruckner, M., Gimon, D., Hayes, P., Jr., James, S., McCabe, E., & Moore, J. (2016, May). Big Data Analysis and Visualization to Identify Best Technology to Meet Remedial Objectives. *Tenth International Conference on Remediation of Chlorinated and Recalcitrant Compounds*.

Thomas, S., **Negrón, D. A.**, Bolipata, A., Barrus, T., Dellinger, N., Holland, M., Tang, J., & Weaver, D. (2013, May). Implementing Fast Sequence Analysis Tools Using a Cray XMT2. *Sequencing, Finishing, and Analysis in the Future*.

Thomas, S., Buthod, J., & **Negrón, D.** (2011, November). Discovering Host-Pathogen Interactions and Pathways Through Data Integration. *Defense Threat Reduction Agency Science and Technology Conference*.

Competitions

Carnegie Mellon Computer Club

Pittsburgh, PA

DEMOSPLASH

2020-2022

- Nov 2022: Freestyle Audio, 4th place, 364pts, "Toccata Crocuta crocuta"
- Nov 2021: Freestyle Audio, 2nd place, 84pts, "demohouse"; Combined Demo, 5th place, 106pts, "democapsid"
- Nov 2020: Freestyle Audio, 4th place, 120pts, "sodium vapor sky"

USA Broomball

Erie, PA

TOURNAMENT

2017; 2022

- Oct 2022: Won the Mid-Atlantic Men's B-bracket as part of the Corruption team representing Washington, D.C.
- Apr 2017: Won the National Men's D division as part of the Regulators team representing Washington, D.C.

Noblis, Inc.

Falls Church, VA

HACKATHON

Jun 2015

- The objective is to reduce the false positive rate of an existing recall management system for healthcare systems.
- Honorable Mention. Participated as a member of the "Ghost in the Shell Script" team.