

Education**George Mason University, School of Systems Biology**

Fairfax, VA

PhD in Bioinformatics & Computational Biology

Aug 2014 – May 2021

Dissertation: Molecular Clock Analysis of Human Adenovirus

Chair: Dr. Donald Seto; Co-Chairs: Dr. Patrick Gillevet & Dr. Sterling Thomas

Johns Hopkins University, Zanvyl Krieger School of Arts & Sciences

Baltimore, MD

MS in Bioinformatics

Nov 2009 – Dec 2011

Capstone: Parallel Algorithm for *de novo* Co-Expression Networks from Microarray Data

Adviser: Dr. Thomas Koval; Supervisors: Dr. Sterling Thomas & Dr. Catherine E. Campbell

Boston University, College of Arts & Sciences

Boston, MA

BA in Biochemistry & Molecular Biology, Minor in Computer Science

Sep 2005 – May 2009

Project: Microsatellite junction counts are inversely proportional to unit size, gap, and edit distance

Adviser: Dr. Gary Benson

Project: Type-II superconductor simulator to investigate magnetic vortex formation

Adviser: Dr. George Ogurek Zimmerman

Skills

| | |
|------------------------|---|
| Biology | alignment, annotation, homology modeling, molecular clock, network analysis, PCR assay, phylogenetics |
| Computing | data structures, GPU, HPC, microcontrollers, multithreading, numerical methods, parallel, UI |
| Programming | AWK, BASH, C, C++, C#, GLSL, HTML, Java, JavaScript, jq, JSON, perl, python, XML |
| Mathematics | calculus, geometry, linear algebra, MCMC, ML, signed-distance functions, statistics |
| Reproducibility | Conda, Docker, Git, L ^A T _E X, pip, R Markdown, Snakemake, Spack, Zotero |
| Database | BLAST+, PostgreSQL, SQLite, SQL, ER modeling |
| Language | Spanish (co-native), Japanese (JLPT 5) |

Experience**Noblis, Inc.**

Reston, VA

Scientist

Oct 2011 – Present

Develop algorithms and program applications for the design and evaluation of assays based on molecular diagnostics such as PCR and LAMP for biosurveillance. Consult on interdisciplinary client work across corporate mission areas, internal R&D, and grant/proposal submissions. Design and supervise internship projects.

On-Call Technical Intern

Aug 2011 – Oct 2011

Port algorithms to run on the CRAY XMT 2 supercomputer using the C programming language and compiler directives.

Analyze *P. aeruginosa* microarray data to identify virulence factors.*Noblis/JHU Independent Research Project Fellowship*

Jun 2011 – Aug 2011

Upgrade an algorithm for the analysis of host-pathogen interaction networks from microarray data. Develop an MPI-enabled version for parallel execution. Analyze human-plague (*Y. pestis*) microarray data to identify network motifs.

Infant & Toddler Connection of Fairfax-Falls Church

Fairfax, VA

Administrative Assistant II / Data Analyst

Sep 2009 – Jun 2011

Develop VBA macros for use with Microsoft Office applications. Automate administrative tasks using Windows batch scripts.

Manage IT support at the Falls Church satellite site.

Boston University

Boston, MA

Laboratory for Biocomputing and Informatics

Sep 2008 – May 2009

Conduct research under the supervision of Dr. Gary Benson. Implement algorithms in Java and python 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

Sep 2008 – May 2009

Conduct research under the supervision of Dr. George Ogurek Zimmerman. Program a type-II superconductor simulator to investigate phenomena related to magnetic field vortices in Java and python. Collaborate on the 2D implementation of the simulator and subsequently developed the 3D version.

Projects**Capsid Modeling***Render viral capsids using Caspar-Klug Theory*

May 2020 – Present

In the browser with JavaScript to export SVG diagrams (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 league statistics*

Jun 2019 – Present

Design ER model, SQLite database, and R code for statistics and website generation (<https://github.com/dnanto/broomball>).**Publications****Papers**

- [1] **D. A. Negrón**, J. Kang, S. Mitchell, M. Y. Holland, S. Wist, J. Voss, L. Brinkac, K. Jennings, S. Guertin, B. G. Goodwin, and S. Sozhamannan. “Impact of SARS-CoV-2 Mutations on PCR Assay Sequence Alignment”. In: *Frontiers in Public Health* 10 (Apr. 2022). ISSN: 2296-2565. DOI: 10.3389/fpubh.2022.889973.
- [2] M. R. Wiley, L. Fakoli, A. G. Letizia, S. R. Welch, J. T. Ladner, K. Prieto, D. Reyes, N. Espy, J. A. Chitty, C. B. Pratt, N. D. Paola, F. Taweh, D. Williams, J. Saindon, W. G. Davis, K. Patel, M. Holland, **D. A. Negrón**, U. Ströher, S. T. Nichol, S. Sozhamannan, P. E. Rollin, J. Dogba, T. Nyenswah, F. Bolay, C. G. Albariño, M. Fallah, and G. Palacios. “Lassa Virus Circulating in Liberia: A Retrospective Genomic Characterisation”. In: *The Lancet Infectious Diseases* 19.12 (Dec. 2019), pp. 1371-1378. ISSN: 1473-3099, 1474-4457. DOI: 10.1016/S1473-3099(19)30486-4.
- [3] S. Sozhamannan, M. Y. Holland, A. T. Hall, **D. A. Negrón**, M. Ivancich, J. W. Koehler, T. D. Minogue, C. E. Campbell, W. J. Berger, G. W. Christopher, B. G. Goodwin, and M. A. Smith. “Evaluation of Signature Erosion in Ebola Virus Due to Genomic Drift and Its Impact on the Performance of Diagnostic Assays”. In: *Viruses* 7.6 (Jun. 2015), pp. 3130-3154. DOI: 10.3390/v7062763.
- [4] M. Vasudevan, **D. A. Negrón**, M. Feltz, J. Mallette, and K. Wunderlich. “Predicting Congestion States from Basic Safety Messages by Using Big-Data Graph Analytics”. In: *Transportation Research Record* 2500.1 (Jan. 2015), pp. 59-66. ISSN: 0361-1981. DOI: 10.3141/2500-07.

Preprints

- [1] **D. A. Negrón**, N. Tolli, S. Guertin, S. Wollen-Roberts, S. Mitchell, J. Haas, C. Pratt, K. Jennings, B. Abramson, L. Brinkac, and D. Ashford. *Clade-Specific MPXV PCR Assays*. Preprint. Apr. 2023. DOI: 10.1101/2023.04.24.538151.
- [2] **D. A. Negrón**. “Molecular Clock Analysis of Human Adenovirus”. PhD thesis. 312 Charles J. Colgan Hall, Science and Tech Campus, Manassas, VA: George Mason University, Sep. 2021.
- [3] **D. A. Negrón**. *Vectorized Capsid Rendering in the Browser with Capsid.js*. Preprint. Apr. 2021. DOI: 10.1101/2020.12.02.408252.
- [4] M. Holland, **D. A. Negrón**, S. Mitchell, N. Dellinger, M. Ivancich, T. Barrus, S. Thomas, K. W. Jennings, B. Goodwin, and S. Sozhamannan. *BioLaboro: A Bioinformatics System for Detecting Molecular Assay Signature Erosion and Designing New Assays in Response to Emerging and Reemerging Pathogens*. Preprint. Apr. 2020. DOI: 10.1101/2020.04.08.031963.
- [5] Holland, Mitchell Y., **D. A. Negrón**, Shane Mitchell, Mychal Ivancich, Katharine W. Jennings, Bruce Goodwin, and Shanmuga Sozhamannan. *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*. Preprint. Noblis, Inc., Jan. 2020.
- [6] J. Kang, **D. A. Negrón**, J. Li, Q. Wang, Q. Zhang, and D. Seto. *Genomic Analysis of a Human Adenovirus Type Strain Associated with an Outbreak*. 312 Charles J. Colgan Hall, Science and Tech Campus, Manassas, VA, 2020.
- [7] **D. A. Negrón**. *Parallel Algorithm for de Novo Co-Expression Networks from Microarray Data*. Report. The Johns Hopkins University, 9601 Medical Center Drive, Rockville, MD: The Johns Hopkins University, Aug. 2011.
- [8] **D. A. Negrón**. *Microsatellite Junction Counts Are Inversely Proportional to the Size, Gap, and Edit Distance of Its Constituent Units*. Report. Laboratory for Biocomputing and Informatics: Boston University, May. 2009.

Patents

- [1] M. K. Monaco, **D. A. Negrón**, and B. Satira. “Data Loss Prevention”. US11580248B2. Feb. 2023.
- [2] M. J. Sanders, D. M. Masi, E. R. McCabe, E. J. Maciejewski, N. S. Dellinger, and **D. A. Negrón**. “Network Topology Discovery”. US11522783B2. Dec. 2022.
- [3] M. K. Monaco, **D. A. Negrón**, and B. Satira. “Data Loss Prevention”. US10915654B2. Feb. 2021.
- [4] M. K. Monaco, **D. A. Negrón**, B. Satira, and M. Collins. “Network Security Using Inflated Files for Anomaly Detection”. US10924502B2. Feb. 2021.

[5] M. Omari, T. W. Barrus, M. Sanders, and **D. A. Negrón**. “Rapid Genomic Sequence Classification Using Probabilistic Data Structures”. US11037654B2. Jun. 2021.

[6] M. K. Monaco, **D. A. Negrón**, and B. Satira. “Data Loss Prevention”. US10331902B2. Jun. 2019.

Posters

[1] **D. A. Negrón**, N. Tolli, B. Abramson, D. Ashford, and K. Jennings. *Novel Clade-specific Monkeypox PCR Assays Validated In Vitro*. Poster. ASM Microbe 2023, Houston, TX, Jun. 2023.

[2] **D. A. Negrón**. *Implementation Of Bacilliform Viral Capsid Models*. Poster. ASM Microbe 2022, Washington, DC, Oct. 2022.

[3] **D. A. Negrón**, J. Kang, S. Mitchell, and K. Dommaraju. *A Nextclade Dataset for Genotyping Human Adenovirus*. Poster. ASM Microbe 2022, Washington, DC, Jun. 2022.

[4] **D. A. Negrón**, S. Mitchell, M. Y. Holland, D. Ashford, and K. Jennings. *PCR and LAMP Assays for African Swine Fever Virus and Foot-and-Mouth Disease Virus*. Poster. ASM Microbe 2022, Washington, DC, Jun. 2022.

[5] **D. A. Negrón**. *Elongated Capsid Generation in the Browser*. Poster. SSB Student Research Day, George Mason University, Apr. 2021.

[6] **D. A. Negrón**. *Vectorized Capsid Generation in the Browser*. Poster. SSB Student Research Day, George Mason University, Dec. 2020.

[7] S. Thomas, T. Barrus, and **D. A. Negrón**. *Detection of Engineered E. Coli Reference Genomes within NCBI Using Molecular Clock Analysis*. Poster. Sequencing, Finishing, and Analysis in the Future, Dec. 2020.

[8] **D. A. Negrón** and S. Sozhamannan. *Automated Molecular Clock Analysis of the O-PS Gene Cluster of Vibrio Cholerae*. Poster. 54th US-Japan Joint Panel Conference on Cholera and Other Bacterial Enteric Infections, Osaka, Japan, Dec. 2019.

[9] **D. A. Negrón**, B. Goodwin, M. Smith, and S. Sozhamannan. *Phylogenetic Analysis of the O-Antigen Biosynthesis Genes in Vibrio Cholerae*. Poster. Sequencing, Finishing, and Analysis in the Future Meeting, Santa Fe, NM, Jun. 2016.

[10] J. Kennedy, D. Montoya, J. Tang, **D. A. Negrón**, and K. Taylor. *Noblis’ BioVelocity Is a Comprehensive and Rapid Post-Sequencing Bioinformatics Tool to Enhance Food Biosecurity, Biosurveillance and Outbreak Investigations through Precise Pathogen Detection*. Poster. Sequencing, Finishing, and Analysis in the Future Meeting, Santa Fe, NM, May. 2015.

[11] **D. A. Negrón** and S. Sozhamannan. *Functional Unity in Structural Diversity: Genetic Basis of Diversity in O-Antigen Biosynthesis Genes in Vibrio Cholerae*. Poster. asm2015, New Orleans, LA, Jun. 2015.

[12] **D. A. Negrón**. *Perfect Repeats Detection on the CRAY XMT 2*. Poster. Noblis, Inc., Falls Church, VA, 2013.

[13] **D. A. Negrón** and S. Thomas. *Co-Expression Network Generation from Microarray Data on the Cray XMT*. Poster. Center for Biotechnology Education 7th Annual Research Symposium, The Johns Hopkins University, Rockville, MD, May. 2012.

[14] **D. A. Negrón**. *Parallel Algorithm for de Novo Co-Expression Networks from Microarray Data*. Poster. The Johns Hopkins University, 9601 Medical Center Drive, Rockville, MD, Aug. 2011.

[15] S. Thomas, J. Buthod, and **D. A. Negrón**. *Discovering Host-Pathogen Interactions and Pathways Through Data Integration*. Poster. Defense Threat Reduction Agency Science and Technology Conference, Las Vegas, NV, Nov. 2011.

Presentations

[1] S. Sozhamannan, **D. A. Negrón**, M. Rajavel, and G. Xie. *Building A Smart Wall With The Strength Of Diversity - What Can We Learn From Bacteria?* Talk. Sequencing, Finishing, and Analysis in the Future, Santa Fe, NM, May. 2018.

[2] M. Collins and **D. A. Negrón**. *Mushrooms Not Honey: Making Deceptive Defenses More Toxic for Attackers*. Talk. RSA Conference, San Francisco, CA, Feb. 2017.

[3] **D. A. Negrón**. *Deceptive Defence*. Talk. BloomCON 0x02 Forensics and Security Conference, Bloomsburg, PA, Mar. 2017.

[4] S. Baez-Cazull, **D. A. Negrón**, A. Rak, M. Bruckner, D. Gimón, P. Hayes Jr., S. James, E. McCabe, and J. Moore. *Big Data Analysis and Visualization to Identify Best Technology to Meet Remedial Objectives*. Talk. Tenth International Conference on Remediation of Chlorinated and Recalcitrant Compounds, Palm Springs, CA, May. 2016.

[5] S. Thomas, **D. A. Negrón**, A. Bolipata, T. Barrus, N. Dellinger, M. Holland, J. Tang, and D. Weaver. *Implementing Fast Sequence Analysis Tools Using a Cray XMT2*. Talk. Sequencing, Finishing, and Analysis in the Future, Santa Fe, NM, May. 2013.