Daniel J. Nasko, Ph.D.
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RESEARCH INTERESTS:	Liquid biopsy, Microbiome, Metagenomics, Bioinformatics, Data Architecture, Analysis Automation, Long read sequencing

EDUCATION:

Doctor of Philosophy, 2017	University of Delaware (Newark, DE)
Major:	Bioinformatics and Systems Biology
Advisors:	Prof. K. Eric Wommack, Ph.D. & Prof. Shawn W. Polson, Ph.D.
Bachelor of Science, 2010	West Chester University (West Chester, PA)
Major:	Pharmaceutical Product Development
Minors:	Chemistry, Biology

APPOINTMENTS:

Jan 2022 - Present **Senior Bioinformatics Scientist**

Pacific Biosciences, Inc.

Role:
- Secondary analysis of HiFi and SBB short read sequence data serving internal and external customers in oncology and microbiome research

Apr 2021 - Dec 2021 **Senior Data Scientist I**

Novozymes, Inc. (Acquired Biota Technology, Inc. in March 2021)

Role:
- Deploying automated and data science-driven infrastructure for microbiome research that integrates shotgun metagenomics, 16S, metabolomics, and metatranscriptomics
- Mining human and animal gut samples for novel bacterial and phage probiotic candidates to treat disease and promote healthy development

Apr 2019 - Mar 2021 **Senior Data Scientist**

Biota Technology, Inc. *Pioneering genomics in the oil and gas industry*

Role:
- Developing automated analysis pipelines and database schemas for metagenomic exploration of environmental samples
- Approaches to profile sulfate reducing prokaryotes from oil reservoir produced fluids

Jul 2018 - Mar 2019: **Assistant Research Scientist**

University of Maryland Institute for Advanced Computer Studies (UMIACS)
Center for Bioinformatics and Computational Biology (CBCB)
University of Maryland, College Park

Research Interests:
- Metagenomic approaches to measure the diversity of influenza A virus and developing strategies to detect transmission events between subjects. DARPA-funded project.
- Improving the taxonomic assignment of unknown sequences.
- Monitoring viruses and bacteria present in pre- and post-processed reclaimed wastewater used for crop irrigation.
- Using CRISPR, marker genes, and assembly graphs to study microbial populations.

Jul 2017 - Jun 2018: **Post-Doctoral Associate**

University of Maryland, College Park
Advisor: Dr. Todd Treangen

Research Interests:
- Functional identification of synthetic DNA molecules. IARPA project successfully funded through phase two.
- Skin and gut microbiome analysis. Specifically, the viral-host interactions during health and disease.
- Bioinformatic workflow development.

Jan 2011 - Jul 2017: **Graduate Research Assistant** (Stipend Supported)

Delaware Biotechnology Institute (DBI)
Center for Bioinformatics and Computational Biology
University of Delaware
Advisor: Drs. K. Eric Wommack and Shawn W. Polson

Research Interests:
- Investigating the utility of single-molecule real time DNA sequencing in viral shotgun metagenomics.
- Exploring the role of viruses in the ecology of bacterial vaginosis.
- Development and maintenance of the bioinformatic analysis pipelines behind the VIROME web application (virome.dbi.udel.edu).
- Assisting researchers from other academic institutions to analyze their metagenomic data using the VIROME end-user web interface.
- Identifying novel CRISPR spacers and exploring their impact on bacteriophage evolution in natural environments.

Dec 2008 - Jan 2011: **Molecular Associate**

Accugenix, Inc. *Environmental Monitoring Lab Serving the Pharmaceutical Industry*

Responsibilities:

- Daily accessioning and processing of customer bacterial and fungal samples in a cGMP laboratory.
- Proficient skills DNA extraction, amplification, 16S rDNA sequencing and alignment, as well as MALDI-TOF mass spectrometry.
- Executed research and development parallel studies exploring differences in current microbial identification methods (sequencing vs. mass spectrometry).
- Designed and created several magnetic plates to improve the extraction and purification of DNA.

AWARDS / HONORS

- Rita Colwell Travel Fellowship (2018)
- University of Delaware Dissertation Fellowship Award (2016-2017)
- International Society for Microbial Ecology Travel Award (2016)
- University of Delaware Professional Development Award (2011, 2012)
- Research and development employee of the month, Accugenix, Inc. (2010)

PROFESSIONAL SOCIETY MEMBERSHIP

- American Society for Human Genetics (2022 - Present)
- American Society for Microbiology (2015 - 2019)
- International Society for Microbial Ecology (2016 - 2019)

PUBLICATIONS

Publication impact (H-index): 13 (Google Scholar); Total citations: 748

Peer-Reviewed Publications:

17. Chopyk, J., **Nasko, D. J.**, Allard, S., Bui, A., Pop, M., Mongodin, E. F., & Sapkota, A. R. *Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond.* Environmental Microbiome, **2020**, 15(1), 1-16.

16. Murray, R., Cruz-Cano, R., **Nasko, D**., Blythe, D., Ryan, P., Boyle, M., ... & Sapkota, A. R. *Association between Private Drinking Water Wells and the Incidence of Campylobacteriosis in Maryland: An Ecological Analysis Using Foodborne Diseases Active Surveillance Network (FoodNet) Data (2007-2016).* Environmental Research, **2020**, 109773.

15. Sapkota, A. R., Kulkarni, P., Olson, N., Bui, A., Bradshaw, R., Del Collo, L., ... & **Nasko, DJ**. *Zero-valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water*. Frontiers in Environmental Science, **2020**. *8*, 203.

14. Chopyk J, **Nasko DJ**, Allard S, Callahan MT, Bui A, Ferelli AMC, Chattopadhyay S, Mongodin EF, Pop M, Micallef SA, Sapkota AR *Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics.* Science of The Total Environment. **2020**; 706, 135395

13. Chopyk J, **Nasko DJ**, Allard S, Bui A, Treangen T, Pop M, Mongodin, EF, Sapkota A. *Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications*. Water Research. **2020**; 169, 115250.

12. Chopyk J, Kulkarni P, **Nasko DJ**, Bradshaw R, Kniel KE, Chiu P, Sharma M, Sapkota AR. *Zero-valent iron sand filtration reduces concentrations of virus-like particles and modifies virome community composition in reclaimed water used for agricultural irrigation.* BMC Res Notes. **2019**; 12 (1), 223.

11. **Nasko DJ**, Ferrell BD, Moore RM, Bhavsar JD, Polson SW, Wommack KE. *CRISPR spacers indicate preferential matching of specific virioplankton genes*. mBio. **2019;** 10(2):e02651-18.

10. **Nasko DJ**, Chopyk J, Sakowski EG, Ferrell BD, Polson SW, Wommack KE. *Family A DNA polymerase phylogeny uncovers diversity and replication gene organization in the virioplankton*. Frontiers in Microbiology. **2018**; 9:3053.

9. **Nasko DJ**, Koren S, Phillippy AM, Treangen TJ. *RefSeq database growth influences the accuracy of k-mer-based lowest common ancestor species identification*. Genome Biology. **2018** Dec;19(1):165. doi: 10.1186/s13059-018-1554-6

8. Chopyk J, Allard S, **Nasko DJ**, Bui A, Mongodin EF, Sapkota AR. *Agricultural freshwater pond supports diverse and dynamic bacterial and viral populations*. Frontiers in Microbiology. **2018** Apr 24;9:792. doi: 10.3389/fmicb.2018.00792

7. Marine R, **Nasko DJ**, Wray J, Polson SW, Wommack KE. *Novel chaperonins are prevalent in the virioplankton and demonstrate links to viral biology and ecology*. ISME J. **2017** Nov;11(11):2479-2491. doi: 10.1038/ismej.2017.102.

6. Johnson TA, Looft R, Severin AJ, Bayles DO, **Nasko DJ**, Wommack KE, Howe A, Allen HK. *The In-Feed Antibiotic Carbadox Induce Phage Gene Transcription in the Swine Gut Microbiome*. mBio. **2017** Aug 8;8(4). pii: e00709-17. doi: 10.1128/mBio.00709-17.

5. Wommack KE, **Nasko DJ**, Chopyk J, Sakowski EG. *Counts and sequences, observations that continue to change our understanding of viruses in nature*. J Microbiol. **2015** Mar;53(3):181-92. doi: 10.1007/s12275-015-5068-6.
4. Sakowski EG, Munsell EV, Hyatt M, Kress W, Williamson SJ, **Nasko DJ**, Polson SW, Wommack KE. *Ribonucleotide reductases reveal novel viral diversity and predict biological and ecological features of unknown marine viruses*. PNAS. **2014** Nov 4;111(44):15786-91. doi: 10.1073/pnas.1401322111.
3. Marine R, McCarren C, Vorrasane V, **Nasko D**, Crowgey E, Polson SW, Wommack KE. *Caught in the middle with multiple displacement amplification: the myth of pooling for avoiding multiple displacement amplification bias in a metagenome*. Microbiome. **2014** Jan 30;2(1):3. doi: 10.1186/2049-2618-2-3.
2. Wommack KE, Bhavsar J, Polson SW, Chen J, Dumas M, Srinivasiah S, Furman M, Jaminder S, **Nasko DJ**. *VIROME: a standard operating procedure for analysis of viral metagenome sequences*. Stand Genomic Sci. **2012** Jul 30;6(3):427-39. doi: 10.4056/sigs.2945050.
1. Wang Q, Arighi CN, King BL, Polson SW, Vincent J, Chen C, Huang H, Kingham BF, Page ST, Rending MF, Thomas WK, Udwary DW, Wu CH, **the North East Bioinformatics Collaborative Curation Team**. *Community annotation and bioinformatics workforce development in concert—Little Skate Genome Annotation Workshops and Jamborees*. Database (Oxford). **2012** Mar 20; 2012:bar064. doi: 10.1093/database/bar064.

SELECTED PRESENTATIONS

Invited Talks:

2. *Uncovering the biological features of unknown viruses using shotgun metagenomic sequence data*. Hebrew University, Rehovot, Israel. January 2019
1. *RefSeq database growth influences the accuracy and sensitivity of species identification from metagenomic samples*. In-Q-Tel, Arlington, VA. February 2018

Oral and Poster Presentations:

11. **Nasko DJ**, Milton DK, Frieman MB, Mongodin EF, Grantham ML, Treangen TJ. *The diversity of influenza A virus differs between body sites within individuals*. International Symposium for Microbial Ecology 17th General Meeting. August, 2018. Leipzig, Germany (Poster).
10. *RefSeq database growth influences species-level metagenomic sequence classification*. Mid-Atlantic Microbiome Meet-up on Biodefense and Pathogen Detection. January 10, 2018. College Park, MD.

9. *Viral informatics resource for metagenome exploration (VIROME)*. Microbiome Analysis in the Cloud Workshop. June 15, 2017. Baltimore, MD.
8. **Nasko DJ**, Sakowski EG, Chopyk J, Wommack KE, Polson SW. *Illuminating population scale variability in viral metagenomic data using De Bruijn graphs.* International Symposium for Microbial Ecology 16th General Meeting. August 2016. Montreal, Canada (Poster).
7. **Nasko DJ**, Chopyk JM, Sakowski EG, Polson SW, Wommack KE. *The long and short of it: Combination of long and short read deep sequencing unveils the evolutionary history and diversity of virioplankton.* American Society for Microbiology 115th General Meeting. May 2015. New Orleans, LA (Poster).
6. **Nasko DJ**, Polson SW, Ma B, Ravel J, Wommack KE, *Assessing CRISPR Spacer Composition in the Vaginal Microbiome.* Human Microbiome Sciences Conference. July 2013. North Bethesda, MD (Poster).
5. Wommack KE, **Nasko DJ**, Polson SW, Radosevich M, DeBruyn J, Tsai YC, Bowman B, Korlach J. *A comparison of two library construction procedures for obtaining long read DNA sequences for use in environmental microbial genomics.* American Society for Microbiology 113th General Meeting. May 2013. San Francisco, CA (Poster).
4. *The bioinformatics behind VIROME*. 2013 Environmental Viruses Workshop. January, 2013. Tucson, AZ.
3. **Nasko DJ**, Wommack KE, Polson SW, Bhavsar JD, *Are certain viral genes more likely to become CRISPR spacers?* International Symposium for Microbial Ecology 14th General Meeting. August 2012. Copenahgen, Denmark (Poster).
2. *Development of a cluster-based sequence compression pipeline*. 2012 Virginia Bioinformatics Institute High Performance Computing Workshop. July 2012. Blacksburg, VA.
1. **Nasko DJ**, Wommack KE, Polson SW, Bhavsar JD, *Are certain viral genes more likely to become CRISPR spacers?* Sixth Aquatic Viral Workshop. November 2011. Texel, The Netherlands (Poster).

TEACHING

Aug 2018	Strategies and Techniques for Analyzing Microbial Population Structure, Marine Biological Laboratory in Woods Hole, MA (teaching assistant).
Jun 2013	University of Delaware EU-US Bioinformatics Training Short Course, Newark, DE (teaching assistant).

May 2012 University of Delaware RNA-Seq Short Course, Newark, DE (teaching assistant).

Students advised:

Andrew Boddicker, currently a Scientist I at Element Biosciences
Nicole Place, currently a Ph.D. student at Yale University
Abbe Miller, currently an undergraduate at University of Maryland
Gilbert Lao, BSc received from the University of Maryland in 2020

EDITORIAL/REVIEW DUTIES

Reviewer for Journals:

Nature Communications, Microbiome, Nucleic Acids Research, BMC Bioinformatics, PLoS ONE, mSphere

Conferences Organized:

Winter 2019 Mid-Atlantic Microbiome Meet-up Taxonomic Identification Workshop (Instructor)

Winter 2018 Mid-Atlantic Microbiome Meet-up Biodefense and Pathogen Detection (Steering committee)

SOFTWARE PACKAGES

1. CASC - CRISPR discovery and validation tool
   https://github.com/dnasko/CASC
2. RUBBLE - BLAST-based pipeline using sequence clusters that improves speed with a minimal reduction in accuracy
   https://github.com/dnasko/rubble

RESEARCH PROJECTS:

Jun 2020 - Present
- Lead developer of Nextflow pipelines, databases (PostgreSQL and MongoDB), and AWS solutions for processing metagenomic sequence data from environmental and human-associated samples sequenced on ONT and Illumina platforms.
- Ideation coordinator with internal stakeholders on lead generation for probiotic discovery

Apr 2019 - Mar 2020

Microbial risk assessment of sulfate reducing bacteria in oil reservoirs using shotgun metagenomics and 16S microbial profiles

Apr 2019 - Mar 2020

Source tracking of microbial communities in oil reservoir produced fluids

Jul 2017 - Mar 2019

Developing a bioinformatic pipeline to determine the threat status of unknown DNA sequences requested to be synthesized at DNA foundries (IARPA funded study).

Aug 2017 - Mar 2019

Using metagenomics to assemble Influenza A genomes from infected students to measure flu diversity and track flu transmission events between infected students (DARPA funded study).

Aug 2017 - Mar 2019

Using shotgun metagenomics to monitor the microbes contained in pre- and post-processed reclaimed wastewater for agricultural use. My role in this study focused on assessing frameworks to study environmental microbes, such as marker genes, assembly graphs, and CRISPR spacers (US Department of Agriculture funded study).

Sep 2011 - Jul 2017

Exploring the utility of single-molecule real time (SMRT) DNA sequencing in viral shotgun metagenomics (Collaboration with Jonas Korlach's team at Pacific Biosciences)

Jun 2011 - Nov 2017

Identifying novel CRISPR spacers in microbial metagenomes to better understand their role as a microbial immune system in natural environments.

Sep 2014 - Sep 2015

Isolation and complete genome sequencing of novel *Bradyrhizobium* spp. and mining for *Bradyrhizobium*-associated bacteriophages.

Jan 2013 - Oct 2016

Studying the role viruses play in the ecology of bacterial vaginosis (NIH R21 funded study).

Feb 2011 - Jul 2017

Maintenance and development of the Viral Informatics Resource fOr Metagenome Exploration (VIROME) bioinformatic analysis pipeline.

Aug 2012 - Dec 2012

In collaboration with AstraZeneca, development of boolean network models for two forms of glutathione depletion in rats exposed to various pharmaceutical compounds.

Jul 17-26 2012

Development of a centroid-based sequence compression program capable of compression rates outperforming conventional gzip and bzip2 applications.

SKILLS:

Computational (2011-present):

- GitHub: github.com/dnasko
- Experience with AWS EC2, IAM, and other AWS services.
- Programming languages: Python, Bash, R, Nextflow, Perl; some experience with Rust, Matlab, Ruby
- Database systems: PostgreSQL, MongoDB, SQLite
- Computational Systems: Experience with HPC environments managed by Slurm, Torque PBS, and SGE. Experience with Singularity and Docker
- Bioinformatics applications: BLAST, BWA, Bowtie, Samtools, QIIME, PacBio® SMRT Analysis Software, CLC Genomics Workbench, MAFFT, MOTHUR, CD-HIT, USEARCH, MetaGene, various de Bruijn graph and overlap consensus assemblers, Anvi'o, PhyML, Phylip, Jellyfish, Kraken, Cytoscape, BLAT, LAST, VarDict
- General applications: Jupyter, LaTeX, Microsoft Word, Excel, Powerpoint, Adobe Illustrator, Omni software

Laboratory (2009-2013):

- ***Microbial Techniques:*** Bacterial and Fungal Culture Isolation and Manipulation. Shotgun viral metagenome sample preparation.
- ***Nucleic Acid Techniques:*** 16S rDNA extraction, amplification, and sequencing
- ***Mass Spectrometry Techniques:*** MALDI-TOF Mass Spectrometry sample preparation and results analysis. Gas Chromatography/Mass Spectroscopy (GC/MS)