

# James Robert White

1529 Lancaster St., Baltimore, MD 21231 | 443 904 6111 | james.dna.white@gmail.com

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## Education

University of Maryland (UMD) – College Park, 2006 – 2010

Ph.D. Applied Mathematics and Scientific Computation – May 2010

Advisor: Mihai Pop, Ph.D. – Department of Computer Science

University of Maryland – College Park, 2002 – 2006

B.S. *summa cum laude*, Mathematics – May 2006

Grade-point average: 4.0

## Skill set

Significant experience with Unix, Perl, Python, R, Matlab, C/C++, office applications, and various software packages for analysis of high-throughput DNA sequence data including BLAST, Bowtie2, CCREPE, Circos, CloVR, Cytoscape, Ergatis, FLASH, Glimmer, HUMAnN, Kraken, Krona, Metaphlan, Metastats, Mothur, MUMMER, QIIME, ShoRAH, SPARCC and UniFrac. Some development experience with PHP, JAVA, MySQL, HTML, CGI, multi-threaded applications, SAS and Fortran 77.

## Experience

January 2014 – Present

Founder | *Resphera Biosciences*

Resphera Biosciences is developing innovative computational and statistical approaches to microbiome sequence analysis that deliver clinically relevant results, enabling doctors and scientists to better identify pathogens and characterize dysbiosis in complex microbial environments.

June 2011 – Present

*Independent contractor*

Research specialist in computational biology and statistical analysis; clients include research groups from the National Institutes of Health, the U.S. Food and Drug Administration, Johns Hopkins University, University of Maryland, and Children's Hospital of Pittsburgh.

June 2010 – April 2013

*Bioinformatics software engineer II – The Institute for Genome Sciences – UMD School of Medicine*

Co-developer of open source software (<http://clovr.org>) that employs cloud computing (e.g. Amazon EC2) for large-scale biological data analysis. Design and implementation of fully automated analysis pipelines for genomic, metagenomic and metatranscriptomic sequence data. Application of novel metagenomic analysis approaches to new fields including immunology, developmental biology and the Human Microbiome Project.

May 2008 – August 2008

*Neural prosthetics algorithms group – Johns Hopkins Applied Physics Lab*

Designed and implemented decision fusion framework (Kalman filtering and artificial neural networks) for multimodal neural prosthetic devices (DARPA-sponsored).

May 2007 – May 2010

*Metagenomics research group – UMD College Park*

Development of novel methods for metagenomic data analysis, statistical modeling of microbial community dynamics in the human gut, comparative metagenomic analysis. Led the computational analysis in multiple metagenomics collaborations including studies of mammalian intestinal tracts, deep ocean sediments, and crop phyllospheres.

## Publications

1. Culkin DJ, Exaire, EJ, Green D, Soloway M, Gross A, Desai M, White JR, Lightner DJ. Anticoagulation and Antiplatelet Therapy in Urologic Practices: ICUD/AUA Review Paper. *The Journal of Urology*. 192, October 2014.
2. Pearle MS, Goldfarb DS, Assimos DG, Curhan G, Denu-Ciocca CJ, Matlaga B, Monga M, Penniston K, Preminger G, Turk T, White JR. Medical Management of Kidney Stones: AUA Guideline. *The Journal of Urology*. 192, August 2014.
3. Hosgood HD, Sapkota AR, Rothman N, Rohan T, Hu W, Xu J, Vermeulen R, He X, White JR, Wu G, Wei F, Mongodin E, Lan Q. The potential role of lung microbiota in lung cancer attributed to household coal burning

exposures. *Environmental and Molecular Mutagenesis*. doi:10.1002/em.21878, June 2014.

4. Ioannidis P, Johnston KL, Riley DR, Kumar N, White JR, Olarte KT, Ott S, Tallon LJ, Foster JM, Taylor MJ, Dunning Hotopp JC. Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial Wolbachia endosymbiont to its host filarial nematode *Brugia malayi*. *BMC Genomics*. 14:639, September 2013.
5. Riley DR, Sieber KB, Robinson KM, White JR, Ganesan A, Nourbakhsh S, Dunning Hotopp JC. Bacteria-Human somatic cell lateral gene transfer is enriched in cancer samples. *PLoS Comp Biol*. 9:6, June 2013.
6. Ottesen AR, González-Peña A, White JR, Pettengill JB, Li C, Allard S, Rideout S, Allard M, Hill T, Evans P, Strain E, Musser S, Knight R, Brown E. Baseline survey of the anatomical microbial ecology of an important food plant: *Solanum lycopersicum* (tomato). *BMC microbiology*. 13:114, June 2013.
7. von Rosenvinge EC, Song Y, White JR, Maddox C, Blanchard T, Fricke WF. Immune status, antibiotic medication and pH are associated with changes in the stomach fluid microbiota. *ISME J*. doi:10.1038/ismej.2013.33, March 2013.
8. White JR, Maddox C, White O, Angiuoli SV, Fricke WF. CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. *Microbiome*. 1:6, February 2013.
9. Lusk T, Ottesen A, White JR, Allard M, Brown E, Kase J. Characterization of microflora in Latin-style cheeses by next-generation sequencing technology. *BMC Microbiology*. 12:254, November 2012.
10. Pettengill JB, McAvoy E, White JR, Allard M, Brown E, Ottesen A. Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. *BMC Research Notes*. 5:378, July 2012.
11. The Human Microbiome Consortium. Structure, function and diversity of the healthy human microbiome. *Nature*. 486, June 2012.
12. The Human Microbiome Consortium. A framework for human microbiome research. *Nature*. 486, June 2012.
13. White JR, Patel J, Ottesen A, Arce G, Blackwelder P, Lopez JV. Pyrosequencing of bacterial symbionts within *Axinella corrugata* sponges: diversity and seasonal variability. *PLoS One*. 7:6, June 2012.
14. Sellitto M, Bai G, Serena G, Fricke WF, Sturgeon C, Gajer P, White JR, Koenig SK, Sakamoto J, Boothe D, Gicquelais R, Kryszak D, Puppa E, Catassi C, Ravel J, Fasano A. Proof of concept of microbiome-metabolome analysis and delayed gluten exposure on celiac disease autoimmunity in genetically at-risk infants. *PLoS One*. 7:3, March 2012.
15. Donia MS, Fricke WF, Partensky F, Cox J, Elshahawi SI, White JR, Phillipy AM, Schatz MC, Piel J, Haygood MG, Ravel J, Schmidt EW. Complex microbiome underlying secondary and primary metabolism in the tunicate-*Prochloron* symbiosis. *Proc Natl Acad Sci USA*. doi:10.1073/pnas.1111712108, November 2011.
16. Angiuoli SV, White JR, Matalaka M, White O, Fricke WF. Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. *PLoS One*. 6:10, October 2011.
17. Angiuoli SV, Matalaka M, Gussman A, Galens K, Vangala M, Riley D, Arze C, White JR, White O, Fricke WF. CloVR: A virtual machine for automated and portable sequence analysis from the desktop using cloud computing. *BMC Bioinformatics*. 12:356, September 2011.
18. Telias A, White JR, Pahl DM, Ottesen AR, Walsh CS. Bacterial community diversity and variation in spray water sources and the tomato phyllosphere. *BMC Microbiology*. 11:81, April 2011.
19. Biddle J, White JR, Teske A, House C. Metagenomics of the subsurface Brazos-Trinity Basin (IODP site 1320): comparison with other sediment and pyrosequenced metagenomes. *ISME J*. doi:10.1038/ismej.2010.199, January 2011.
20. Poroyko V, White JR, Wang M, Donovan S, Alverdy J, Liu DC, Morowitz MJ. Gut microbial gene expression in mother-fed and formula-fed piglets. *PLoS One*. 5:8, August 2010.
21. White JR, Navlakha S, Nagarajan N, Ghodsi M, Kingsford C, Pop M. Alignment and clustering of phylogenetic markers – implications for microbial diversity studies. *BMC Bioinformatics*. 11:152, March 2010.
22. White JR, Levy T, Bishop W, Beaty J. Real-time decision fusion for multimodal neural prosthetic devices. *PLoS One*. 5:3, March 2010.
23. Ottesen AR, White JR, Skaltsas D, Newell M, Walsh C. Impact of organic and conventional management on the phyllosphere microbial ecology of an apple crop. *Journal of Food Protection*. 72:11, November 2009.
24. Tenore F, Aggarwal V, White JR, Schieber MH, Thakor NV. Computational complexity versus accuracy in classification of cortical neural signals. *Proceedings of the 4th International IEEE EMBS Conference on Neural Engineering*. 1:750-53, May 2009.
25. Navlakha S, White JR, Nagarajan N, Pop M, Kingsford C. Finding biologically accurate clusterings in hierarchical decompositions using variation of information. *Proceedings of RECOMB 2009, Lectures Notes in Computer Science*. 5541, May 2009.
26. White JR, Nagarajan N, Pop M. Statistical methods for detecting differentially abundant features in clinical metagenomic samples. *PLoS Computational Biology*. 5:4, April 2009.

27. White JR. Protein folding using homotopy methods. [Online] Supplementary case study for Scientific Computing with Case Studies by O'leary DP. December 2008.
28. White JR, Escobar-Paramo P, Mongodin E, Nelson K, DiRuggiero. Extensive genome rearrangements and multiple horizontal gene transfers in a population of *Pyrococcus* isolates from Vulcano Island, Italy. *J. Applied and Environmental Microbiology*. 74:20, October 2008.
29. Roberts M, Zimin A, Hayes W, Hunt BR, Ustun C, White JR, Havlak P, Yorke JA. Improving Phrap-based assembly of the rat using reliable overlaps. *PLoS One*. 3:3, March 2008.
30. White JR, Roberts M, Yorke JA, Pop M. Figaro: a novel statistical method for vector sequence removal. *Bioinformatics*. 24:4, January 2008.

## White Papers, Technical Reports & Book Chapters

1. Fricke WF, White JR. Microbial genomics in foodborne pathogens. In: *Molecular Typing Methods for Tracking Foodborne Microorganisms*. Hauppauge, NY: Nova Science Publishers, 2012.
2. White JR, Arze C, Matalaka M, The CloVR Team, Angiuoli S, Fricke WF. CloVR-16S: Phylogenetic microbial community composition analysis based on 16S ribosomal RNA amplicon sequencing – standard operating procedure, version 1.1. *Nature Precedings*. doi:10.1038/npre.2011.6287.1, August 2011.
3. White JR, Arze C, Matalaka M, The CloVR Team, Angiuoli S, Fricke WF. CloVR-Metagenomics: Functional and taxonomic microbial community characterization from metagenomic whole-genome shotgun (WGS) sequences – standard operating procedure, version 1.0. *Nature Precedings*. doi:10.1038/npre.2011.5886.1, April 2011.
4. Galens K, White JR, Arze C, Matalaka M, Gwinn Giglio M, The CloVR Team, Angiuoli S, Fricke WF. CloVR-Microbe: Assembly, gene finding and functional annotation of raw sequence data from single microbial genome projects – standard operating procedure, version 1.0. *Nature Precedings*. doi:10.1038/npre.2011.5887.1, April 2011.
5. White JR, Matalaka M, Fricke WF, Angiuoli S. Cunningham: a BLAST Runtime Estimator. *Nature Precedings*. doi:10.1038/npre.2011.5593.1, January 2011.