

**CURRICULUM VITAE**  
**DANIEL P. VELTRI**

**CONTACT INFORMATION:**

Work Address: NIH/NIAID Bioinformatics and Computational Biosciences Branch  
5601 Fishers Lane, 4A54  
Rockville, MD 20892  
E-mail: [dan.veltri@gmail.com](mailto:dan.veltri@gmail.com)  
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**EDUCATION:**

Ph.D. Bioinformatics and Computational Biology (2015)  
George Mason University, Manassas, VA 20110  
  
M.S. Bioinformatics and Computational Biology (2013)  
George Mason University, Manassas, VA 20110  
  
B.A. Environmental, Populismic and Organismic Biology, Computer Science Minor (2006)  
University of Colorado at Boulder, Boulder, CO 80309

**CURRENT POSITION:**

2017 – Present Computational Genomics Specialist (NIH Contractor), Medical Science & Computing, LLC  
NIH/NIAID, Bioinformatics and Computational Biosciences Branch, Rockville, MD 20892

**PAST RESEARCH POSITIONS:**

2015 – 2017 Visiting Postdoctoral Research Fellow, J.A. Crouch Ornamental Pathology Lab  
U.S. Department of Agriculture, Agricultural Research Service, Beltsville, MD 20705  
Fellowship Funding: Oak Ridge Institute for Science and Education, Oak Ridge, TN 37830  
  
2014 – 2015 Lab Technician (Bioinformatics), J.A. Crouch Ornamental Pathology Lab  
Rutgers University, Department of Plant Biology and Pathology, New Brunswick, NJ 08901  
  
2014 Biological Science Student Trainee (Pathways Program), J.A. Crouch Ornamental Pathology Lab  
U.S. Department of Agriculture, Agricultural Research Service, Beltsville, MD 20705  
  
2009 – 2015 Graduate Research Assistant, A. Shehu Computational Biology Lab  
George Mason University, Computer Science Department, Fairfax, VA 22030  
  
2010 – 2014 Graduate Research Assistant, N. Kabbani and A. Shehu Labs  
George Mason University, Krasnow Institute, Fairfax, VA 22030  
  
2004 – 2006 Undergraduate Research Assistant, C. Kearns and D. Oliveras Pollinator Lab  
University of Colorado at Boulder, Baker Residential Academic Program, Boulder, CO 80309

**TEACHING POSITIONS:**

2014 Writing in Statistics and the Sciences (Graduate Course)  
George Mason University, Fairfax, VA 22030  
  
2012 – 2014 BRIDGE Scholar (International Bioinformatics and Statistics Graduate Student Mentor)  
George Mason University, Fairfax, VA 22030

- 2010 – 2012 National Science Foundation GK-12 Teaching Fellow (Elementary Math and Science)  
Fairfax County Public Schools, Annandale, VA 22003
- 2006 – 2008 Assistant Language Teacher, Japan Exchange and Teaching (JET) Program (Grades 1-12)  
Aomori City Board of Education, Aomori City, Aomori Prefecture, Japan

#### FELLOWSHIPS AND AWARDS:

- 2015 – 2017 Oak Ridge Institute for Science and Education, Postdoctoral Fellowship (\$65,000/yr)  
2015 AAAS Program for Excellence in Sciences, two year AAAS membership and subscription to Science  
2014 IEEE International Conference on Bioinformatics and Biomedicine, Best Student Paper Award (\$800)  
2014 IEEE International Conference on Bioinformatics and Biomedicine, Travel Award (\$800)  
2013 IEEE International Conference on Comp. Advances in Bio. and Medical Sciences, Travel Award (\$700)  
2012 – 2014 BRIDGE Scholarship, George Mason University (\$3,500/yr)  
2010 – 2012 National Science Foundation and George Mason University, GK-12 Fellowship (\$45,000/yr)

#### BIOINFORMATICS SKILLS:

Programming/Scripting: C++, CSS, HTML, jQuery, MySQL, Python, R, and Ruby.  
Algorithms/Software: ALLPATHS-LG, Augustus, Bioconductor, BLAST, Bowtie, BRAKER, BWA, CLC Genomics Workbench, diagnostic marker discovery, dimensionality reduction (PCA, Isomap, LLE, t-SNE), DOCK, FASTA, feature selection, genome assembly and annotation (Sanger, 454, Illumina and PacBio), GGPLOT2, HISAT2, HMMs, machine learning recognition, Maker, MrBayes, multiple sequence alignment, NAMD, neural networks (Keras+Tensorflow), pattern finding, protein structure prediction, read mapping, SPAdes, TopHat2, UNIX/Linux, Velvet, and VMD.

#### THESES:

- Ph.D. “A Computational and Statistical Framework for Screening Novel Antimicrobial Peptides”  
Committee: A. Shehu (adviser), J. Solka (co-adviser), I. Vaisman and B. Matthews
- M.S. “Physicochemical Feature Selection for Cathelicidin Antimicrobial Peptides”  
Committee: A. Shehu (adviser), B. Bishop and I. Vaisman

#### PEER-REVIEWED JOURNAL PUBLICATIONS:

- 2018 **D. Veltri**, U. Kamath and A. Shehu. *Deep Learning Improves Antimicrobial Peptide Recognition*. **Bioinformatics** 34(16):2740-2747. (DOI:10.1093/bioinformatics/bty179)
- N. Zhang, G. Cai, D.C. Price, H. Qiu, P. Gladioux, Y. Lee, C. Khang, J. Zhu, J.A. Crouch, **D. Veltri**, J.H. Wisecaver, M. LeBrun, J. Luo, B. Hillman and D. Bhattacharya. *Genome wide analysis of the transition to pathogenic lifestyles in Magnaporthales fungi*. **Scientific Reports** 8 Article: 5862. (DOI:10.1038/s41598-018-24301-6)
- Y. Rivera, C. Salgado-Salazar, **D. Veltri**, M. Malapi-Wight and J.A. Crouch. *Genome analysis of the ubiquitous boxwood pathogen Pseudonectria foliicola*. **PeerJ** 6:e5401. (DOI:10.7717/peerj.5401)
- B. Dorjbal, J.R. Stinson, C.A. Ma, M.A. Weinreich, B. Miraghazadeh, J.M. Hartberger, S. Frey-Jakobs, S. Weidinger, L. Moebus, A. Franke, A.A. Schäffer, A. Bulashevskaya, S. Fuchs, S. Ehl, S. Limaye, P.D. Arkwright, T.A. Briggs, C. Langley, C. Bethune, A.F. Whyte, Hana Alachkar, S. Nejentsev, T. DiMaggio, C.G. Nelson, K.D. Stone, M. Nason, E.H. Brittain, A.J. Oler, **D.P. Veltri**, T.R. Leahy, N. Conlon, M.C. Poli, A. Borzutzky, J.I. Cohen, J. Davis, M.P. Lambert, N. Romberg, K.E. Sullivan, K. Paris, A.F. Freeman, L. Lucas, S. Chandrasakan, S. Savic, S. Hambleton, S.Y. Patel, M.B. Jordan, A. Theos, J. Lebensburger, T.P. Atkinson, T.R. Torgerson, I.K. Chinn, J.D. Milner, B. Grimbacher, M.C. Cook, and A.L. Snow. *Hypomorphic CARD11 mutations associated with diverse immunologic phenotypes with or without atopic disease*. **Journal of Allergy and Clinical Immunology**. (In Press; DOI: 10.1016/j.jaci.2018.08.013)

- 2017 **D. Veltri**, U. Kamath and A. Shehu. *Improving recognition of antimicrobial peptides and their target selectivity through machine learning and genetic programming*. **Transactions on Computational Biology and Bioinformatics** 14(2):300-313. (DOI:10.1109/TCBB.2015.2462364)
- 2016 **D. Veltri**, M. Malapi-Wight and J.A. Crouch. *SimpleSynteny: a web-based tool for visualization of microsynteny across multiple species*. **Nucleic Acids Research** 44(W1):W41-W45. (DOI:10.1093/nar/gkw330) [Cover story of issue]
- M. Malapi-Wight, J.E. Demers, **D. Veltri**, R.E. Marra and J.A. Crouch. *LAMP detection assays for boxwood blight pathogens: a comparative genomics approach*. **Scientific Reports** 6 Article: 26140. (DOI:10.1038/srep26140)
- 2015 M. Malapi-Wight, C. Salgado-Salazar, J.E. Demers, **D. Veltri** and J.A. Crouch. *Draft genome sequence of *Dactylonectria macrodidyma*, a plant pathogenic fungus in the Nectriaceae*. **ASM Genome Announcements** 3(2):e00278-15. (DOI:10.1124/jpet.113.203976)
- C. Salgado-Salazar, Y. Rivera, **D. Veltri** and J.A. Crouch. *Polymorphic SSR markers for *Plasmopara obducens* (Peronosporaceae), the newly emergent downy mildew pathogen of *impatiens* (Balsaminaceae)*. **Applications in Plant Sciences** 3(11):1500073. (DOI:10.3732/apps.1500073)
- B.D. Wingfield, P.K. Ades, F.A. Al-Naemi, L.A. Beirn, W. Bihon, J.A. Crouch, Z. Wilhelm de Beer, L. De Vos, T.A. Duong, C.J. Fields, G. Fourie, A.M. Kanzi, M. Malapi-Wight, S.J. Pethybridge, O. Radwan, G. Rendon, B. Slippers, Q.C. Santana, E.T. Steenkamp, P.W.J. Taylor, N. Vaghefi, N.A. van der Merwe, **D. Veltri** and M.J. Wingfield. *Draft genome sequences of *Chrysosporthe austroafricana*, *Diplodia scrobiculata*, *Fusarium nygamai*, *Leptographium lundbergii*, *Limonomyces culmigenus*, *Stagonosporopsis tanacetii* and *Thielaviopsis punctulata**. **IMA Fungus** 6(1):231-246. (DOI:10.5598/imafungus.2015.06.01.15)
- 2013 N. Kabbani, J.C. Nordman, B. Corgiat, **D. Veltri**, A. Shehu and D.J. Adams. *Are nicotinic receptors coupled to G proteins?* **BioEssays** 35(12):1025-1034. (DOI:10.1002/bies.20130008)
- A. Ashoor, J.C. Nordman, **D. Veltri**, K.H.S. Yang, L. Al Kury, Y. Shuba, M. Mahgoub, F.C. Howarth, C. Lupica, A. Shehu, N. Kabbani and M. Oz. *Menthol inhibits 5-HT<sub>3</sub> receptor-mediated currents*. **Journal of Pharmacology and Experimental Therapeutics** 347(2):398-402. (DOI:10.1124/jpet.113.203976)
- A. Ashoor, J.C. Nordman, **D. Veltri**, K.H.S. Yang, L. Al Kury, Y. Shuba, M. Mahgoub, F.C. Howarth, C. Lupica, A. Shehu, N. Kabbani and M. Oz. *Menthol binding and inhibition of alpha7-nicotinic acetylcholine receptors*. **PLoS ONE** 8(7):e67674. (DOI:10.1371/journal.pone.0067674)

#### PEER-REVIEWED CONFERENCE PUBLICATIONS:

- 2018 M. Dua, **D. Veltri**, B. Bishop and A. Shehu. *Guiding Exploration of Antimicrobial Peptide Space with a Deep Neural Network*. Artificial Intelligence Techniques for BioMedicine and HealthCare Workshop (AIBH2018). Madrid, Spain. [Accepted]
- 2014 **D. Veltri**, U. Kamath and A. Shehu. *A novel method to improve recognition of antimicrobial peptides through distal sequence-based features*. IEEE International Conference on Bioinformatics and Biomedicine (BIBM2014). Belfast, UK. (DOI:10.1109/BIBM.2014.6999187) [Awarded best student paper. Acceptance Rate: 20%]
- I. Hashmi, **D. Veltri**, N. Kabbani and A. Shehu. *Knowledge-based search and multi-objective filters: proposed structural models of GPCR dimerization*. 5<sup>th</sup> ACM Conference on Bioinformatics, Comp. Biology and Biomedical Informatics (BCB2014). Newport Beach, CA. (DOI:10.1145/2649387.2649391) [Acceptance Rate: 25%]
- 2013 **D. Veltri** and A. Shehu. *Physicochemical determinants of antimicrobial activity*. 5th International Conference on Bioinformatics and Computational Biology (BICoB2013). Honolulu, HI. (DOI:10.13140/RG.2.1.4695.6403; Proceedings ISBN:978-1-62276-971-1) [Acceptance Rate: 20%]
- E.G. Randou, **D. Veltri** and A. Shehu. *Systematic analysis of global features and model building for recognition of antimicrobial peptides*. IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS2013). New Orleans, LA. (DOI:10.1109/ICCABS.2013.6629215) [Acceptance Rate: 42%]

E.G. Randou, **D. Veltri** and A. Shehu. *Binary response models for recognition of antimicrobial peptides*. ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (BCB2013). Washington, DC. (DOI:10.1145/2506583.2506597) [Acceptance Rate: 19%]

#### ABSTRACTS AND POSTERS:

2018 **D. Veltri**, Z. Li, S. Xirasagar, A.J. Oler, Z. Cheng, K. Huang, J. Barnett, L. Zhang, O. Juarez-Espinosa, Y. Fan, M. Similuk, M. Walkiewicz, C. Hong, J. Johnson, and J.D. Milner. *Balancing Confidentiality and Sharing of Genomic and Phenotypic Data in a Clinical Research System*. 9<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (BCB2018). Washington, DC. [Poster]

S. Xirasagar, A.J. Oler, Z. Li, X. Cheng, K. Huang, **D. Veltri**, M. Similuk, Y. Zhang, C. Hong, M. Walkiewicz, J. Johnson, J. Barnett, L. Zhang, Y. Fan, O. Juarez-Espinosa, M. Lenardo, and J.D. Milner. *The NIAID clinical genomics data repository, Genomic Research Integration System (GRIS): Streamlined data capture, standardization, integration, and analysis to enable identification of immune-related genetic variants for clinical reporting and genomics research*. American Society of Human Genetics (ASHG2018). San Diego, CA. [Poster]

2017 A.J. Oler, S. Xirasagar, Z. Li, Z. Cheng, K. Huang, **D. Veltri**, D. Kaminsky, M. Similuk, Y. Zhang, J. Johnson, C. Hong, J.D. Milner. *Genomic Research Integration System (GRIS): From recording to reporting, a comprehensive solution for clinical genomics research*. 2017 NIH Research Festival. Bethesda, MD. [Poster]

2016 **D. Veltri**, D. Zhang, D. Luster, M. McMahon and J.A. Crouch. *Predicting robust candidates for a boxwood blight immunoassay: an automated computational workflow with broad applications for phytopathology*. 2016 APS Annual Meeting. Tampa, FL. [Poster]

**D. Veltri**, M. Malapi-Wight and J.A. Crouch. *Performing genomic comparison with tools from the SimpleSynteny server*. 2016 APS Potomac Division Meeting. Richmond, VA. [Poster]

2015 **D. Veltri**. *A computational and statistical framework for screening novel antimicrobial peptides*. George Mason University School of Systems Biology Student Research Day, Manassas, VA. [Poster]

**D. Veltri**, M. Malapi-Wight and J.A. Crouch. *SimpleSynteny: An accessible tool for genome comparison*. 28<sup>th</sup> Fungal Genetics Conference. Pacific Grove, CA. [Extended Abstract & Poster]

M. Malapi-Wight, **D. Veltri**, Y. Rivera and J.A. Crouch. *Rearrangements of the MAT1 gene cluster architecture in the genus Calonectria*. 28th Fungal Genetics Conference. Pacific Grove, CA. [Extended Abstract & Poster]

S. Bhattacharya, **D. Veltri**, A. Patel and D. Cox. *Intra-miR-ExploreR, a novel bioinformatics platform for integrated discovery of miRNA:mRNA gene regulatory networks*. 11th International Symposium on Bioinformatics Research and Applications (ISBRA). Norfolk, VA. [Extended Abstract & Poster]

**D. Veltri**, M. Malapi-Wight and J.A. Crouch. *SimpleSynteny: A web-based tool for genome comparison*. Phytobiomes 2015: Designing a New Paradigm for Crop Improvement, Washington, DC. [Poster]

2014 M. Malapi-Wight, E. Ismaiel, N. Saied, Y. Rivera, **D. Veltri**, B. Gehesquiere, K. Heungens and J.A. Crouch. *Comparative genomics of the boxwood blight system: insights into the global diversity of the mating-type locus*. APS-CPS Joint Meeting. Minneapolis, MN. [Poster]

2012 **D. Veltri** and A. Shehu. *Physicochemical features for recognition of antimicrobial peptides*. 2012 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW). Philadelphia, PA. [Extended Abstract & Poster]

#### INVITED PRESENTATIONS:

2018 “Introduction to Deep Learning” Data Science Training Seminar  
National Institute of Environmental Health Sciences, NIH, Durham, NC, USA

- 2016 “Finding Needles in Biological Haystacks Using Machine Learning and Statistics”  
Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, USA
- 2014 “A Novel Method to Improve Recognition of Antimicrobial Peptides through Distal Sequence-Based Features”  
IEEE International Conference on Bioinformatics and Biomedicine, Belfast, UK
- 2013 “Binary Response Models for Recognition of Antimicrobial Peptides”  
ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, Washington, DC, USA
- “Systematic Analysis of Global Features and Model Building for Recognition of Antimicrobial Peptides”  
IEEE International Conference on Computational Advances in Bio. and Medical Sciences, New Orleans, LA, USA
- “Physicochemical Determinants of Antimicrobial Activity”  
5th International Conference on Bioinformatics and Computational Biology, Honolulu, HI, USA
- 2012 “Planning an International Trip (India) for Graduate Students”  
National Science Foundation GK-12 Education Conference, Washington, DC, USA
- “Computational Analysis and Design of Antimicrobial Peptides”  
University of Delhi, Miranda House, New Delhi, India
- “Hands-On Learning in Elementary Science and Education in the USA”  
University of Delhi, Miranda House, New Delhi, India

#### **DEPARTMENTAL PRESENTATIONS:**

- 2018 “Introduction to Deep Learning with Keras”  
National Institute of Allergy and Infectious Diseases, NIH, Bethesda, MD, USA
- 2015 “A Computational and Statistical Framework for Screening Novel Antimicrobial Peptides”  
Ph.D. Dissertation Defense, George Mason University, Fairfax, VA, USA
- 2013 “Physicochemical Feature Selection for Cathelicidin Antimicrobial Peptides”  
School of Systems Biology Student Research Day, George Mason University, Fairfax, VA, USA  
**[Awarded Best Student Presentation]**
- 2009 “Staying Ahead of Evolution: Engineering Novel Antimicrobial Peptides”  
Interdisciplinary Seed Grant Meetings, George Mason University, Fairfax, VA, USA
- 2005 “Research in the Kearns and Oliveras Pollinator Lab”  
Baker Undergraduate Research Symposium, University of Colorado, Boulder, CO, USA

#### **MEETINGS ATTENDED:**

- 2018 Washington DC R Conference, Washington, DC, USA  
ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, Washington, DC, USA
- 2016 American Phytopathological Society, Annual Meeting, Tampa, FL, USA  
American Phytopathological Society, Potomac Division Meeting, Richmond, VA, USA
- 2015 Phytobiomes 2015, Washington, DC, USA  
28th Fungal Genetics Conference, Pacific Grove, CA, USA  
American Phytopathological Society (APS) Potomac Division Meeting, Rehoboth, DE, USA
- 2014 IEEE International Conference on Bioinformatics and Biomedicine, Belfast, UK
- 2013 ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics, Washington, DC, USA  
IEEE International Conference on Computational Advances in Bio. and Medical Sciences, New Orleans, LA, USA  
5th International Conference on Bioinformatics and Computational Biology, Honolulu, HI, USA
- 2012 IEEE International Conference on Bioinformatics and Biomedicine, Philadelphia, PA, USA
- 2004 Guild of Rocky Mountain Population Biologists (GRMPBs) Meeting, Nederland, CO, USA

**TRAINING WORKSHOPS ATTENDED:**

2017 XSEDE HPC Big Data Workshop by Pittsburgh Supercomputing Center  
2013 NCBI Discovery Workshops at the National Library of Medicine at the U.S. National Institute of Health  
2011 Workshop on Comparative Genomics: Special Session at the Smithsonian Institution

**PROFESSIONAL AND SERVICE ACTIVITIES:**

Reviewer: *Bioinformatics, Frontiers in Pharmacology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal of Cellular Biochemistry, Scientific Reports*  
Conference: ACM-BCB 2017 PC Member  
Departmental: Baker Director Search Committee, University of Colorado at Boulder (2005 – 2006)  
Judge, USDA-ARS Beltsville Poster Day (2017)  
Community: Volunteer stream monitor with Virginia Save Our Streams (2000 – Present)  
Friends of Agricultural Research - Beltsville (FAR-B) Elementary School Science Volunteer (2016)

**PROFESSIONAL ORGANIZATIONS:**

American Association for the Advancement of Science (AAAS)  
Institute of Electrical and Electronics Engineers (IEEE)

**OTHER INFORMATION:**

U.S. Citizen  
Languages Spoken: English (native proficiency), Japanese (limited working proficiency)