

Austin G. Meyer

Curriculum Vitae

Education/Post-graduate Training

- 2017–2021 **Residency in Internal Medicine and Pediatrics**, *Ohio State University*, Columbus, OH.
- 2012–2017 **Doctor of Medicine**, *Texas Tech University HSC*, Lubbock, TX.
- 2010–2014 **Doctor of Philosophy, Biochemistry**, *University of Texas at Austin*, Austin, TX.
Track: Computational Biology and Bioinformatics
Mentor: Claus O. Wilke, PhD
- 2015–2017 **Master of Public Health**, *University of North Texas HSC*, Fort Worth, TX.
- 2008–2010 **Master of Science, Biotechnology**, *Texas Tech University HSC*, Lubbock, TX.
Track: Biomedical Research
Mentor: R. Bryan Sutton, PhD
- 2003–2008 **Bachelor of Science, Physics**, *Texas Tech University*, Lubbock, TX.
- 2003–2008 **Bachelor of Arts, Philosophy**, *Texas Tech University*, Lubbock, TX.
- 2012–2014 **Graduate Coursework in Philosophy**, *Texas Tech University*, Lubbock, TX.

Major Projects

- **Doctoral Dissertation:** '*The Role of Structure in Protein Evolution*'
I used metrics calculated from protein structure and energetics to predict the rate and course of viral evolution. Much of the work was funded by a grant extension I co-wrote to the Defense Threat Reduction Agency (DTRA). The work included research on Influenza virus and Machupo virus. [Text Available Here](#)

Academic and Research Positions

- 10/2016–
12/2016 **Epidemiology Elective**, *Centers for Disease Control and Prevention*, Atlanta, GA.
Conducted research through the Influenza Division with the Applied Research and Modeling Team
- 07/2015–
Present **Visiting Researcher**, *University of Texas at Austin*, Austin, TX.
Conducted research through the Center for Computational Biology and Bioinformatics
- 01/2015–
06/2015 **Postdoctoral Fellow**, *University of Texas at Austin*, Austin, TX.
Conducted research through the Center for Computational Biology and Bioinformatics
Studied Influenza and HIV evolution
- 06/2010–
10/2014 **Graduate Research Assistant and Teaching Assistant**, *University of Texas at Austin*, Austin, TX.
Studied protein structural constraints on viral evolution using computational and statistical techniques
Taught courses in biology and bioinformatics
Guided undergraduates and junior graduate students
- 06/2009–
05/2010 **Graduate Research Assistant**, *Texas Tech University Health Sciences Center*, Lubbock, TX.
Conducted experimental protein structure research
Cloned and purified many C2 domain protein constructs
Crystallized C2 domains, collected x-ray diffraction data and solved their structure

- 08/2008– **Teaching Assistant**, *Texas Tech University*, Lubbock, TX.
- 10/2009 Taught 2, 3-hour lab sessions per week covering the topics in the Introduction to Electricity and Magnetism course

Grants, Honors, and Awards

- 2013 **BeWise Immunize Grant**, *Texas Medical Association*, Texas Medical Association Foundation.
- 2010–2011 **Recruitment Fellowship**, *University of Texas at Austin*, Institute for Cell and Molecular Biology.
- 2009 **Research Fellowship**, *Texas Tech University Health Sciences Center*, Center for Cardiovascular Disease and Stroke.
- 2008 **CH Foundation Scholarship**, *Texas Tech University Health Sciences Center*, Department of Cell Biology and Biochemistry.

Professional Membership, Service and Leadership

- Reviewer for:** Systematic Biology, PLOS Pathogens, PLOS Computational Biology, Physical Review X, Molecular Biology and Evolution, BMC Evolutionary Biology, Scientific Reports, Journal of Medical Virology, Computational Biology and Chemistry, Artificial Life.
- Membership:** American Academy of Pediatrics, American College of Physicians, Texas Medical Association, American Medical Association, Society for Molecular Biology and Evolution, American Physical Society, American Chemical Society, Biophysical Society, Mensa

Medical School

- 2012–2017 **Clinical Volunteer**, *Lubbock Free Clinic*, Texas Tech University Health Sciences Center.
- 2014–2017 **Leadership Mentor**, *Lubbock Free Clinic*, Texas Tech University Health Sciences Center.
- 2013–2016 **Council Member**, *Council on Legislation*, Texas Medical Association.
- 2015–2016 **Data Analyst**, *LCME Independent Student Analysis Committee*, Texas Tech University Health Sciences Center.
- 2015–2016 **Delegate Leader**, *Medical Student Section*, Texas Medical Association.
- 2015–2016 **Committee Member**, *Committee on Scientific Issues*, American Medical Association Medical Student Section.
- 2015–2016 **Committee Member**, *Committee on Socioeconomics and Legislative Affairs*, Lubbock, Crosby, and Garza County Medical Society.
- 2015–2016 **Committee Member**, *Speaker's Advisory Committee*, Texas Medical Association.
- 2015–2016 **Committee Member**, *Admission Interview Committee*, Texas Tech University Health Sciences Center.
- 2013, 2015 **Lobbying at First Tuesday at the Capitol**, *Texas Medical Association*.
- 2014 **Contributing Writer**, *in-Training.org*.
- 2011–2014 **Testing Coordinator**, *Lonestar Mensa*, American Mensa.
- 2012–2014 **Mentor to Premedical Students**, *Bernard A. Harris Premedical Society*, Texas Tech University.
- 2013–2014 **Leadership Team Member**, *Lubbock Free Clinic*, Texas Tech University Health Sciences Center.
- 2013, 2014 **BeWise Immunize Event Organizer**, *Lubbock Free Clinic and Texas Medical Association Foundation*, Texas Tech University Health Sciences Center.
- 2013–2014 **Committee Member**, *Committee on Bioethics and Humanities*, American Medical Association Medical Student Section.
- 2013–2014 **TMA/AMA Chapter Delegate**, *School of Medicine*, Texas Tech University Health Sciences Center.
- 2013 **Anatomy Tutor**, *School of Medicine*, Texas Tech University Health Sciences Center.

- 2012–2013 **Committee Member**, *Early Clinical Experience Redesign Committee*, Texas Tech University Health Sciences Center.

Teaching Experience

- 2017 **Lecturer**, *Texas Tech University Health Sciences Center*, School of Medicine.
Topic: Tropical Hemorrhagic Fever Viruses. [Alphavirus/Arenavirus/Bunyavirus Slides](#); [Filovirus Slides](#); [Flavivirus Slides](#)
- 2017 **Lecturer**, *Texas Tech University Health Sciences Center*, School of Medicine.
Topic: Biostatistics and Epidemiology. [Slides](#)
- 2016 **Lecturer**, *Texas Tech University Health Sciences Center*, School of Medicine.
Topic: Biostatistics and Epidemiology, Review for USMLE Step 1. [Slides](#)
- 2015 **Graduate Research Mentor**, *University of Texas at Austin*, Department of Integrative Biology.
- 2011–2015 **Undergraduate Research Mentor**, *University of Texas at Austin*, Department of Integrative Biology.
- 2014 **Teaching Assistant**, *University of Texas at Austin*, Department of Integrative Biology.
Course: Gross and Microscopic Anatomy
- 2012 **Teaching Assistant**, *University of Texas at Austin*, Freshman Research Initiative.
Course: Computational Evolution
- 2008 **Teaching Assistant**, *Texas Tech University*, Department of Physics.
Course: Introduction to Electricity and Magnetism

Professional Presentations

- 2015 **Guest Lecturer**, *University of Texas at Austin*, Department of Integrative Biology.
Topic: PDB files, protein structures, and protein dynamics
- 2014 **Guest Lecturer**, *University of Texas at Austin*, Center for Computational Biology and Bioinformatics, AC3G Seminar Series.
Topic: Simulating the evolution of protein-protein interactions
- 2012 **Guest Speaker**, *University of Texas at Austin*, Department of Integrative Biology, Population Biology Seminar Series.
Topic: Viral Binding at the Molecular Level

Examples of Developed Code

- 2017 **Female versus Male Physician Quality Scores**, An online app written in R showing the male and female physician quality score distributions from parameters in *JAMA Intern Med.* 2017;177(2):206-213, [App Link](#), [Code Link](#).
- 2017 **Statistical versus Biological Significance**, An online app written in R designed to show that there is a difference between statistical and biological significance, [App Link](#), [Code Link](#).
- 2016 **Clinical Biomarkers in Diagnosis of Pneumococcal Pneumonia**, An online app written in R showing the posttest probability of pneumococcal etiology based on clinical biomarker value and pretest conditions. Explanation of analysis and data citations found at [biorxiv](#), [App Link](#), [Code Link](#).
- 2016 **Predictive Value of Clinical Tests**, An online app written in R designed to provide students with an intuitive understanding of clinical test statistics, [App Link](#), [Code Link](#).
- 2012–2015 **Protein Evolution Toolbox**, An assortment of tools written in python, C++ and R by myself and other members of the Wilke lab for working with protein structures and sequences, [Code Link](#).
- 2011 **bpopsim**, An asexual population genetic simulator program and visualization code written in C++ and R, [Code Link](#).

Publication Summary

- [Google Scholar Profile Link](#)
- Total scientific papers: 21
- Papers with 10+ citations: 11
- First author papers: 7
- Total citations: 370
- H-index: 11
- Opinion papers: 3
- Conference Posters: 13

Publications

Peer Reviewed Articles

- [1] R. Rajmohan, R. C. Anderson, D. Fang, **A. G. Meyer**, P. Laengvejkal, P. Julayanont, G. Hannabas, K. Linton, J. Culberson, H. M. R. Khan, J. DeToledo, P. H. Reddy, and M. O'Boyle. White matter deterioration may foreshadow impairment of emotional valence determination in early-stage dementia of the alzheimer type. *Frontiers in Aging Neuroscience*, 9:37, 2017.
- [2] C. D. McWhite, **A. G. Meyer**, and C. O. Wilke. Serial passaging causes extensive positive selection in seasonal influenza a hemagglutinin. *Virus Evolution*, 2, 2016.
- [3] B. R. Jack, **A. G. Meyer**, J. Echave, and C. O. Wilke. Functional sites induce long-range evolutionary constraints in enzymes. *PLOS Biol.*, 14:e1002452, 2016.
- [4] **A. G. Meyer** and C. O. Wilke. The utility of protein structure as a predictor of site-wise dN/dS varies widely among HIV-1 proteins. *J. R. Soc. Interface*, 12:20150579, 2015.
- [5] **A. G. Meyer** and C. O. Wilke. Geometric constraints dominate the antigenic evolution of influenza H3N2 hemagglutinin. *PLOS Pathog.*, 11:e1004940, 2015.
- [6] **A. G. Meyer**, S. J. Spielman, T. Bedford, and C. O. Wilke. Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. *Virus Evolution*, 1:vev006, 2015.
- [7] S. A. Kerr, E. L. Jackson, O. I. Lungu, **A. G. Meyer**, A Demogines, A. D. Ellington, G. Georgiou, C. O. Wilke, and S. L. Sawyer. Computational and functional analysis of the GP1-TfR1 interface reveals host range trade-offs in new-world arenaviruses. *J. Virol.*, 89:11643–11653, 2015.
- [8] A. H. Kachroo, J. M. Laurent, C. M. Yellman, **A. G. Meyer**, C. O. Wilke, and E. M. Marcotte. Systematic humanization of yeast genes reveals conserved functions and genetic modularity. *Science*, 348:921–925, 2015. [Altmetric 99th Percentile. According to Altmetric, among top 1% of papers ever published in Science. Press coverage by NPR, NBC News, Discovery News, and many others.](#)
- [9] **A. G. Meyer**, S. L. Sawyer, A. D. Ellington, and C. O. Wike. Analyzing Machupo virus-receptor binding by molecular dynamics simulations. *PeerJ*, 2:e266, 2014.
- [10] V. Sridhara, **A. G. Meyer**, J. E. Barrick, P. Ravikumar, D. Segre, and C. O. Wilke. Predicting growth conditions from internal metabolic fluxes in an *In-Silico* model of E. coli. *PLOS ONE*, 9:e114608, 2014.
- [11] A. Shahmoradi, D. K. Sydykova, S. J. Spielman, E. L. Jackson, E. T. Dawson, **A. G. Meyer**, and C. O. Wilke. Predicting evolutionary site variability from structure in viral proteins: buriedness, packing, flexibility, and design. *J. Mol. Evol.*, 79:130–142, 2014.
- [12] K. Fuson, A. Rice, R Mahling, A. Snow, P. Shanbhogue K. Nayak, **A. G. Meyer**, G. Redpath, A. Hinderliter, S. T. Cooper, and R. B. Sutton. Alternate splicing of dysferlin C2A confers Ca2+-dependent and Ca2+-independent binding for membrane repair. *Structure*, 22:104–115, 2014.

- [13] J. E. Barrick, G. Colburn, D. E. Deatherage, C. C. Traverse, M. D. Strand, J. J. Borges, D. D. Knoester, A. Reba, and **A. G. Meyer**. Identifying structural variation in haploid microbial genomes from short-read re-sequencing data using breseq. *BMC Genomics*, 15:1039, 2014.
- [14] M. Z. Tien, **A. G. Meyer**, D. K. Sydykova, S. J. Spielman, and Claus O. Wilke. Maximum allowed solvent accessibilities of residues in proteins. *PLOS ONE*, 8:e80635, 2013.
- [15] M. Tien, D. K. Sydykova, **A. G. Meyer**, and C. O. Wilke. A simple Python library to generate model peptides. *PeerJ*, 1:e80, 2013.
- [16] **A. G. Meyer** and C. O. Wilke. Integrating sequence variation and protein structure to identify sites under selection. *Mol. Biol. Evol.*, 30:36–44, 2013. **Fast Tracked**.
- [17] **A. G. Meyer**, E. T. Dawson, and C. O. Wilke. Cross-species comparison of site-specific evolutionary-rate variation in influenza hemagglutinin. *Phil. Trans. R. Soc. B*, 368:20120334, 2013.
- [18] M. P. Scherrer, **A. G. Meyer**, and C. O. Wilke. Modeling coding-sequence evolution within the context of residue solvent accessibility. *BMC Evol. Biol.*, 12:179, 2012.
- [19] A. Reba, **A. G. Meyer**, and J. E. Barrick. Computational tests of a thermal cycling strategy to isolate more complex functional nucleic acid motifs from random sequence pools by in vitro selection. *A. Life*, 13:473—480, 2012. **Awarded Best Synthetic Biology Paper**.
- [20] Y. G. Celebi, R. L. Lichti, H. N. Bani-Salameh, **A. G. Meyer**, B. R. Carroll, J. E. Vernon, P. J. C. King, and S. F. J. Cox. Muonium transitions in 4H silicon carbide. *Physica B*, 404:845–848, 2009.
- [21] H. N. Bani-Salameh, **A. G. Meyer**, B. R. Carroll, R. L. Lichti, K. H. Chow, P. J. C. King, and S. F. J. Cox. Charge-state transitions of muonium in 6H silicon carbide. *Physica B*, 401-402:631–634, 2007.

Opinion Articles

- [1] **A. G. Meyer**. Analysis of infection biomarkers within a bayesian framework reveals their role in pneumococcal pneumonia diagnosis in hiv patients. *available on bioRxiv*, 2017.
- [2] S. J. Spielman*, **A. G. Meyer***, and C. O. Wilke. Increased evolutionary rate in the 2014 West African ebola outbreak is due to transient polymorphism and not positive selection. *bioRxiv*, 2014. *authors contributed equally.
- [3] R. E. Solnick* and **A. G. Meyer***. Law should allow physicians to use their judgment. *Texas Medicine*, 110:11–12, 2014. *authors contributed equally.

Posters, Abstracts, and Policy Proposals

Posters

- [1] **A. G. Meyer**, B. R. Jack, J. Echave, and C. O. Wilke. Functional sites induce long-range evolutionary constraints in enzymes. *Student Research Week*, Texas Tech University Health Sciences Center, Lubbock, TX, 2016.
- [2] **A. G. Meyer** and C. O. Wilke. Geometric constraints dominate the antigenic evolution of influenza H3N2 hemagglutinin. *Student Research Week*, Texas Tech University Health Sciences Center, Lubbock, TX, 2015.
- [3] S. J. Spielman, **A. G. Meyer**, and C. O. Wilke. Apparent increased evolutionary rate in the 2014 west african ebola outbreak signals transient polymorphism and not positive selection. *Ebola Modeling Workshop*, Georgia Institute of Technology, Atlanta, GA, 2015. **Invited**.
- [4] F. S. Thomas, **A. G. Meyer**, S. A. Hattenbach, L. K. Tollack, D. T. Vu, M. Hong, K. Bennett, and F. Prabhu. Population characteristics and medical treatment of blood pressure at the free clinic. *Student Research Week*, Texas Tech University Health Sciences Center, Lubbock, TX, 2014.

- [5] F. S. Thomas, **A. G. Meyer**, S. A. Hattenbach, L. K. Tollack, D. T. Vu, M. Hong, K. Bennett, and F. Prabhu. Effectiveness of diabetes interventions in an urgent care setting. *Society for Student Run Free Clinics Annual Meeting*, Nashville, TN, 2014.
- [6] **A. G. Meyer** and C. O. Wilke. Analyzing machupo virus-receptor binding by molecular dynamics simulation. *Biophysical Society Annual Meeting*, San Francisco, CA, 2014.
- [7] **A. G. Meyer** and C. O. Wilke. Analyzing machupo virus-receptor binding by molecular dynamics simulation. *Student Research Week*, Texas Tech University Health Sciences Center, Lubbock, TX, 2014. **Awarded Best Poster Presentation.**
- [8] **A. G. Meyer**, F. S. Thomas, S. A. Hattenbach, L. K. Tollack, D. T. Vu, M. Hong, K. Bennett, and F. Prabhu. Effectiveness of blood pressure interventions at an urgent care, free clinic for the uninsured. *Society for Student Run Free Clinics Annual Meeting*, Nashville, TN, 2014.
- [9] **A. G. Meyer** and C. O. Wilke. Cross-species comparison of site-specific evolutionary-rate variation in influenza hemagglutinin. *Student Research Week*, Texas Tech University Health Sciences Center, Lubbock, TX, 2013.
- [10] **A. G. Meyer** and C. O. Wilke. Combining protein structure and sequence variation to identify functionally important sites. *Society for Molecular Biology and Evolution Annual Meeting*, Dublin, Ireland, 2012.
- [11] K. L. Fuson, **A. G. Meyer**, K. Knutson, J. W. Gauer, J. Murphy, A. F. Oberhauser, A. Hinderliter, and R. B. Sutton. A link between structure and cooperativity in the C2A domain of Synaptotagmin 1. *Biophysical Society Annual Meeting*, San Francisco, CA, 2012.
- [12] **A. G. Meyer**, N. Quissenberry, K. Fuson, and R. B. Sutton. Functional relevance of mutations and truncations in Dysferlin and Synaptotagmin 1. *Graduate School and Biomedical Sciences Annual Retreat*, Texas Tech University Health Sciences Center, Lubbock, TX, 2010.
- [13] **A. G. Meyer**, N. Quissenberry, K. Fuson, and R. B. Sutton. Cardiomyopathy caused by structural instability in Dysferlin C2 domains: Implications for LGMD2B and CABG. *Center for Cardiovascular Disease and Stroke Symposium*, Texas Tech University Health Sciences Center, Lubbock, TX, 2009.

Policy Proposals

- [1] TMA Ethics Positions on Advance Directives to Agree With AMA Positions. *TexMed Annual Conference*, Texas Medical Association, Austin, TX, 2015.
- [2] Scope of Advance Directives. *TexMed Annual Conference*, Texas Medical Association, Austin, TX, 2015.
- [3] Durability of Advance Directives. *TexMed Annual Conference*, Texas Medical Association, Fort Worth, TX, 2014.
- [4] Advance Directives During Pregnancy. *AMA Annual Conference*, American Medical Association, Chicago, IL, 2014.