

Austin G. Meyer

512 971 0123
✉ austin.g.meyer@gmail.com
🌐 www.meyerlab.org

Education

- 2012–2017 **MD (expected)**, *Texas Tech University Health Sciences Center*, Lubbock, TX.
- 2010–2014 **PhD Biochemistry**, *University of Texas at Austin*, Austin, TX.
 - Track: Computational Biology and Bioinformatics
 - Mentor: Claus O. Wilke, PhD
- 2015–2017 **MPH (expected)**, *University of North Texas Health Science Center*, Fort Worth, TX.
- 2008–2010 **MS Biotechnology**, *Texas Tech University Health Sciences Center*, Lubbock, TX.
 - Track: Biomedical Research
 - Mentor: R. Bryan Sutton, PhD
- 2003–2008 **BS Physics**, *Texas Tech University*, Lubbock, TX.
- 2003–2008 **BA 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– **Epidemiology Internship**, *Centers for Disease Control and Prevention*, Atlanta, GA.
 - 11/2016 Will be conducting research through the Influenza Division with the Applied Research and Modeling Team
- 07/2015– **Visiting Researcher**, *University of Texas at Austin*, Austin, TX.
 - Present Conduct research through the Center for Computational Biology and Bioinformatics
- 01/2015– **Postdoctoral Fellow**, *University of Texas at Austin*, Austin, TX.
 - 06/2015 Conducted research through the Center for Computational Biology and Bioinformatics
 - Studied Influenza and HIV evolution
- 06/2010– **Graduate Research Assistant and Teaching Assistant**, *University of Texas at Austin*, Austin, TX.
 - 10/2014 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– **Graduate Research Assistant**, *Texas Tech University Health Sciences Center*, Lubbock, TX.
 - 05/2010 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

- 09/2007– **Undergraduate Research Assistant**, *Texas Tech University*, Lubbock, TX.
- 05/2008 Performed computational statistical analysis of data to understand hydrogen defects in various semiconductor materials

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:** Systematic Biology, PLOS Pathogens, PLOS Computational Biology, Physical Review X, Molecular Biology and Evolution, Scientific Reports, Journal of Medical Virology, Artificial Life.
- **Membership:** Texas Medical Association, American Medical Association, American College of Physicians, Society for Molecular Biology and Evolution, American Physical Society, American Chemical Society, Biophysical Society, Mensa
- 2012–Present **Clinical Volunteer**, *Lubbock Free Clinic*, Texas Tech University Health Sciences Center.
- 2014–Present **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

- 2016 **Lecturer**, *Texas Tech University Health Sciences Center*, School of Medicine.
Topic: Biostatistics and Epidemiology, Review for USMLE Step 1. [Slides Available Here](#).
- 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

Developed Code

- 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 peer reviewed papers: 21
- Papers with 10+ citations: 10
- First author papers: 7
- Total citations: 240+
- H-index: 10
- Opinion papers: 2
- Conference Posters: 13

Publications

Manuscripts In Review

- [1] **A. G. Meyer**. Analysis of infection biomarkers within a bayesian framework reveals their role in pneumococcal pneumonia diagnosis in hiv patients. *preprint available on bioRxiv*, (Under Review). [Altmetric 74th Percentile](#).

Peer Reviewed Articles

- [1] C. D. McWhite, **A. G. Meyer**, and C. O. Wilke. Serial passaging causes extensive positive selection in seasonal influenza a hemagglutinin. *preprint available on bioRxiv*, (In Press). [Altmetric 95th Percentile](#).
- [2] 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. [Altmetric 98th Percentile](#).
- [3] **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. [Altmetric 84th Percentile](#).
- [4] **A. G. Meyer** and C. O. Wilke. Geometric constraints dominate the antigenic evolution of influenza H3N2 hemagglutinin. *PLOS Pathog.*, 11:e1004940, 2015. [Altmetric 95th Percentile](#).
- [5] **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. [Altmetric 91th Percentile](#).
- [6] 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. [Altmetric 79th Percentile](#).
- [7] 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 350 papers ever published in *Science*. Press coverage by NPR, NBC News, Discovery News, and many others.
- [8] **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. [Altmetric 78th Percentile](#).
- [9] 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. [Altmetric 79th Percentile](#).
- [10] 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.
- [11] 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. [Altmetric 78th Percentile](#).
- [12] 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. [Altmetric 94th Percentile](#).
- [13] 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.
- [14] M. Tien, D. K. Sydykova, **A. G. Meyer**, and C. O. Wilke. A simple Python library to generate model peptides. *PeerJ*, 1:e80, 2013.
- [15] **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**.
- [16] **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.
- [17] 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.

- [18] 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.**
- [19] 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.
- [20] 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] 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. [Altmetric 98th Percentile.](#)
- [2] 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.