Austin G. Meyer

Curriculum Vitae

Education/Post-graduate Training

2017–2021 **Residency, Internal Medicine and Pediatrics**, *Ohio State University Wexner Medical Center and Nationwide Children's Hospital*, Columbus, OH.
Advanced Competency: Global Health
Experience: St. Damien Children's Hospital, Port-au-Prince, HT

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

2019–2022 **Master of Science, Analytics *(In Progress)***, *Georgia Institute of Technology*, Atlanta, GA.
Track: Analytical Tools

2015–2017 **Master of Public Health**, *University of North Texas HSC*, Fort Worth, TX.
Practicum: CDC, Influenza Division
Supervisor: Carrie Reed, DSc

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.
Minor: Mathematics

2003–2008 **Bachelor of Arts, Philosophy**, *Texas Tech University*, Lubbock, TX.
Minor: Mathematics

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 Elective**, *Centers for Disease Control and Prevention*, Atlanta, GA.
12/2016 Conducted research through the Influenza Division with the Applied Research and Modeling Team

07/2015– **Visiting Researcher**, *University of Texas at Austin*, Austin, TX.
06/2017 Conducted 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–
10/2014 **Graduate Research Assistant**, *University of Texas at Austin*, Austin, TX.
Studied protein structural constraints on viral evolution using computational and statistical techniques
Guided undergraduates and junior graduate students

06/2009–
05/2010 **Graduate Research Assistant**, *Texas Tech University HSC*, 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

Teaching Experience

2017 **Lecturer**, *Texas Tech University HSC*, School of Medicine.
Topic: Tropical Hemorrhagic Fever Viruses – 3 lectures. Alphavirus/Arenavirus/Bunyavirus Slides; Filovirus Slides; Flavivirus Slides.

2017 **Lecturer**, *Texas Tech University HSC*, School of Medicine.
Topic: Biostatistics and Epidemiology. Slides.

2016 **Lecturer**, *Texas Tech University HSC*, School of Medicine.
Topic: Biostatistics and Epidemiology, Review for USMLE Step 1. Slides.

2014 **Teaching Assistant**, *University of Texas at Austin*, Department of Integrative Biology.
Course: Gross and Microscopic Anatomy
Taught 2, 3-hour lab sections per week

2012 **Teaching Assistant**, *University of Texas at Austin*, Freshman Research Initiative.
Course: Computational Evolution
Used Avida-ED as an evolutionary model
Taught data analysis using the Python programming language

2008 **Teaching Assistant**, *Texas Tech University*, Lubbock, TX.
Course: Introuction to Electricity and Magnetism
Taught 2, 3-hour lab sections per week

Membership, Service, Leadership, and Learning Opportunities

o **Reviewer for:** Systematic Biology, Physical Review X, Molecular Biology and Evolution, PLOS Pathogens, PLOS Computational Biology, Journal of Theoretical Biology, BMC Evolutionary Biology, Scientific Reports, Gene, Journal of Medical Virology, Computational Biology and Chemistry, Artificial Life.

o **Membership:** American Academy of Pediatrics, American College of Physicians, American Medical Association, Mensa

o **Certifications and Licenses:** Ohio Medical License (License# 35.133841), Certified in Public Health (NBPHE# 13439), HIV Medicine Specialist (AAHIVS)

Residency

o 2017–Present **Clinical Volunteer**, *Columbus Free Clinic*, Ohio State University Medical Center.

o 2017–2019 **Resident Member**, *Evidence-based Practice Policy Group*, Ohio State University Medical Center.

o 2019 **Q&A Panelist**, *Health Careers Exploration Seminar*, Ohio State University.

o 2018 **Pediatric Clinician**, *St. Damien Children's Hospital*, St. Luke Foundation.
Location: Port-au-Prince, Haiti

o 2018 **Q&A Panelist**, *Med/Peds Interest Group*, Ohio State University School of Medicine.

o 2017 **Q&A Panelist**, *Med/Peds Interest Group*, Ohio State University School of Medicine.

Medical School

o 2012–2017 **Clinical Volunteer**, *Lubbock Free Clinic*, Texas Tech University HSC.

o 2013–2016 **Council Member**, *Council on Legislation*, Texas Medical Association.

- ○ 2015–2016 **Data Analyst**, *LCME Independent Student Analysis Committee*, Texas Tech University HSC.
- ○ 2015–2016 **Delegate Leader**, *Medical Student Section*, Texas Medical Association.
- ○ 2015–2016 **Committee Member**, *Speaker's Advisory Committee*, Texas Medical Association.
- ○ 2015–2016 **Committee Member**, *Admission Interview Committee*, Texas Tech University HSC.
- ○ 2013–2014 **Leadership Team Member**, *Lubbock Free Clinic*, Texas Tech University HSC.
- ○ 2013, 2014 **BeWise Immunize Event Organizer**, *Lubbock Free Clinic and Texas Medical Association Foundation*, Texas Tech University HSC.

Graduate School

- ○ 2011–2014 **Testing Coordinator**, *Lonestar Mensa*, American Mensa.

Grants, Honors, and Awards

- ○ 2019 **International Travel Award**, *Nationwide Children's Hospital*.
- ○ 2013 **BeWise Immunize Grant**, *Texas Medical Association*, Texas Medical Association Foundation.
- ○ 2009 **Research Fellowship**, *Texas Tech University HSC*, Center for Cardiovascular Disease and Stroke.
- ○ 2008 **CH Foundation Scholarship**, *Texas Tech University HSC*, Department of Cell Biology and Biochemistry.

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

- ○ 2020 **Ohio COVID-19 Dashboard**, An online app written in R for visualizing data from the Ohio Department of Health allowing normalization per county population and demographic mapping, App Link, Code Link.
- ○ 2020 **COVID-19 US State Tracker Dashboard**, An online app written in R for visualizing data from the COVID Tracking Project allowin doubling time fits and map visualization, App Link, Code Link.
- ○ 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, 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, 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, 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, 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.

Mentoring

○ 2013-2014 **Jeff Du**, Undergraduate research assistant, CPRIT summer research fellowship.
Current position: Medical Student, University of Texas Health Science Center at San Antonio

○ 2012-2014 **Eric Dawson**, Undergraduate research assistant, Completed one first author paper. Went on to work with the Texas Advanced Computing Center. Received undergraduate fellowships. Completed PhD at NIH/Cambridge.
Current position: Bioinformatics scientist, NVIDIA

○ 2011-2012 **Matthew Tien**, Undergraduate research assistant, Completed two first author papers. Completed honors pathway and went on to complete PhD at University of Chicago.
Current position: Postdoctoral fellow, MIT

Publication Summary

○ Google Scholar Profile Link
○ Total peer reviewed papers: 22
○ Papers with 10+ citations: 14
○ First author papers: 6
○ Total citations: >1000
○ H-index: 13
○ Opinion papers: 3
○ Posters: 16

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] 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. Lower activation in frontal cortex and posterior cingulate cortex observed during sex determination test in early-stage dementia of the alzheimer type. *Frontiers in Aging Neuroscience*, 9:156, 2017.

[3] 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.

[4] 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.

[5] **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.

[6] **A. G. Meyer** and C. O. Wilke. Geometric constraints dominate the antigenic evolution of influenza H3N2 hemagglutinin. *PLOS Pathog.*, 11:e1004940, 2015.

[7] **A. G. Meyer**, S. J. Spielman, T. Bedford, and C. O. Wilke. Time dependence of evolutionary metrics during the 2009 pandemic Influenzavirus outbreak. *Virus Evolution*, 1:vev006, 2015.

[8] 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.

[9] 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.

[10] **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.

[11] 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.

[12] 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.

[13] 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.

[14] 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.

[15] 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.

[16] M. Tien, D. K. Sydykova, **A. G. Meyer**, and C. O. Wilke. A simple Python library to generate model peptides. *PeerJ*, 1:e80, 2013.

[17] **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**.

[18] **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.

[19] 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.

[20] 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**.

[21] 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.

[22] 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** and L. W. Pomeroy. The root of mumps virus re-emergence. *Internal Medicine Research Day*, The Ohio State University Wexner Medical Center, Columbus, OH, 2019.

[2] B. N. Rosales and **A. G. Meyer**. Improving the diagnostic utility of clinical biomarkers. *Internal Medicine Research Day*, The Ohio State University Wexner Medical Center, Columbus, OH, 2019.

[3] B. N. Rosales and **A. G. Meyer**. Improving the diagnostic utility of clinical biomarkers. *CHEST Annual Meeting*, 2019. **Discussed on The Curbsiders podcast**.

[4] **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.

[5] **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.

[6] 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**.

[7] 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.

[8] 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.

[9] **A. G. Meyer** and C. O. Wilke. Analyzing machupo virus-receptor binding by molecular dynamics simulation. *Biophysical Society Annual Meeting*, San Francisco, CA, 2014.

[10] **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**.

[11] **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.

[12] **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.

[13] **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.

[14] 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.

[15] **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.

[16] **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.