R. Burke Squires, M.S., is a Computational Genomics Specialist with Medical Sciences and Computing at the National Institute of Allergy and Infectious Diseases' (NIAID) Bioinformatics and Computational Biosciences Branch (BCBB), National Institutes of Health (NIH), where he manages bioinformatics training for NIAID/NIH scientists and oversees commercial bioinformatics software procurement for NIAID. Mr. Squires collaborates with NIAID intramural researchers on projects focused on such pathogens as Ebola, malaria, human papillomavirus, and norovirus. He further supports ongoing BCBB projects such as Nephele, an AWS cloud microbiome analysis portal, the Database of Antimicrobial Activity and Structure of Peptides (DBAASP), and PAVE, a HVP bioinformatics portal.

In addition to his work at NIAID, Mr. Squires teaches data science courses for the National Institute of Environmental Health Sciences, graduate-level programming courses for the Foundation for Advanced Education in the Sciences, and reproducible science courses for the NIH. Courses he teaches include: automated flow cytometry analysis, data munging, data visualization, data versioning and archiving, data science pipelines, exploratory data analysis, and introduction to programming.

Prior to joining the BCBB, NIAID, Mr. Squires worked in the laboratory of Dr. Richard Scheuermann at the University of Texas Southwestern Medical Center on two NIAID-sponsored Bioinformatics Resource Centers – the Influenza Research Database (www.fludb.org) and the Virus Pathogen Bioinformatics Resource Center (http://www.viprbrc.org), where he served as the initial bioinformatics analyst and systems architect. He also contributed influenza virus lifecycles pathways to the Reactome Knowledgebase and co-developed a draft influenza virus extension to the Infectious Disease Ontology. Mr. Squires previously led a bioinformatics group at a genetic vaccine development start-up company in Dallas, Texas, which eventually merged with Macrogenics.

Mr. Squires is a Ph.D. Candidate at the University of Texas at Arlington (UTA), where his doctoral research involves adapting deep learning techniques to design novel algorithms for the elucidation of influenza virus evolution. He received his M.S. in Computer Science (Bioinformatics major) from UTA; his thesis was entitled "*An Influenza Virus Molecular Infection Model and Discrete-Event, Stochastic Simulation*". He received his B.S. in Biochemistry from the University of Dallas, with a concentration in Computer Science.