

C. Titus Brown

EDUCATION	<p>Reed College, Portland, OR; Mathematics; B.A., 1997</p> <p>California Institute of Technology, Davidson Lab (graduate student); Developmental Biology; PhD., 2007</p> <p>California Institute of Technology, Bronner-Fraser Lab (postdoc); Developmental Biology and Bioinformatics; 2007-2008</p>
APPOINTMENTS	<p>Assistant Professor, Microbiology & Molecular Genetics / Computer Science and Engineering Michigan State University, 2008-2014.</p> <p>Associate Professor, Population Health and Reproduction, School of Veterinary Medicine University of California Davis, Jan 2015-July 2021.</p> <p>Professor, Population Health and Reproduction, School of Veterinary Medicine University of California Davis, July 2021-present.</p> <p>Faculty Directory of Community Initiatives, UC Davis DataLab. University of California Davis, November 2020-present.</p>
HONOURS AND AWARDS	<p>Burroughs-Wellcome Fund Computational Biology Fellowship (1999-2004). Withrow Award for Teaching Excellence in Computer Science (2008-2009). Woods Hole Marine Biological Laboratory Summer Fellow (2013). Michigan State University / College of Natural Science Teacher-Scholar Award (2013). Moore Foundation Data Driven Discovery Investigator (2014-2019).</p>
PUBLICATIONS	<p>Full publication list: http://scholar.google.com/citations?user=O4rYanMAAAAJ Blog: http://ivory.idyll.org/blog/ Twitter: http://twitter.com/ctitusbrown ImpactStory: https://profiles.impactstory.org/u/0000-0001-6001-2677</p>
SOFTWARE DEVELOPMENT AND MAINTENANCE	<p>Active open source developer at http://github.com/ctb/ and http://github.com/dib-lab/.</p> <p>Active projects include:</p> <ul style="list-style-type: none">- sourmash, large-scale sequence search by content;- spacegraphcats, metagenome assembly graph query;- genome-grist, workflow for shotgun metagenome decomposition;- charcoal, large-scale genome decontamination analysis;
PROFESSIONAL ACTIVITIES	<ul style="list-style-type: none">- Co-lead, NIH Data Commons Pilot Phase Consortium, 2017-2019.- Lead, Engagement and Training, NIH Common Fund Data Ecosystem, 2019-present.- Member, Advisory Board member for the West Big Data Hub.- Member, Scientific Advisory Board for CZI HCA.- Member, Executive Advisory Board for the Maine NIH INBRE grant.- Software Carpentry Scientific Advisory Board member (2008-2012).- Accredited Carpentries Instructor.- Course director, 2010-2019, Next-Generation Sequence Analysis for Biologists.- Course faculty, 2006-2008, Embryology Course, Woods Hole Marine Biological Laboratory.- Course faculty, 2015-2019, Strategies and Techniques for Analyzing Microbial - Population Structure (STAMPS), Woods Hole Marine Biological Laboratory.- Reviewer for NSF, NIH, Moore Foundation, and Sloan Foundation.- Several now-unmaintained open source bioinformatics tools, including Cartwheel server for comparative sequence analysis, khmer k-mer software.- Moderator, python-ideas mailing list, 2019-present.