

# Michael J. Landis

<b>EDUCATION</b>	<b>Integrative Biology, PhD</b> <b>Computational Biology</b> , Designated Emphasis University of California, Berkeley Expect to graduate Spring 2015  <b>Computer Science, BS</b> California State University of Long Beach Graduated Winter 2004
<b>RESEARCH EXPERIENCE</b>	<b>Graduate Student Researcher, 07/2009 – present</b> Huelsenbeck Lab, <i>UC Berkeley, CA</i>  <b>Research Assistant, 02/2009 – 06/2010</b> Dean Lab, <i>Children's Hospital of Oakland, CA</i>
<b>PUBLICATIONS</b> (* – first co-author )	<b>Landis, M. J.</b> , Matzke, N. J., Moore, B. R., and Huelsenbeck, J. P. <i>Advanced Access</i> . Bayesian Analysis of Biogeography when the Number of Areas is Large. <i>Syst. Biol.</i>  <b>Landis, M. J.*</b> , Schraiber, J. G.*, and Liang, M. 2013. Phylogenetic Analysis Using Lévy Processes: Finding Jumps in the Evolution of Continuous Traits. <i>Syst Biol.</i> 62(2):193-204.  <b>Landis, M. J.</b> and Bedford, T. Phylowood: Interactive Web-based Animations of Biogeographic and Phylogeographic Histories. <i>Submitted: July 2013.</i>
<b>FELLOWSHIPS &amp; AWARDS</b>	NESCent Graduate Fellowship, Fall 2013 Google Summer of Code (NESCent-sponsored), Summer 2012
<b>MENTORSHIP</b>	Jaya Narasimhan (CompSci undergraduate), Fall 2012 – present.
<b>TEACHING EXPERIENCE</b>	<b>Graduate Student Instructor</b> IB164: Human Genetics and Genomics, Fall 2011, <i>UC Berkeley, CA</i> Topics: <i>Human genome variation and population genetics.</i>  IB200A: Principles of Phylogenetics, Spring 2012, <i>UC Berkeley, CA</i> Topics: <i>Theory and methods for phylogenetic inference.</i>
<b>PROFESSIONAL EXPERIENCE</b>	<b>Systems Engineer, 07/2005 - 09/2008</b> Varsity Technologies, <i>San Francisco, CA</i>
<b>SKILLS</b>	C++, Python, R, Javascript, RevBayes.
<b>SERVICE</b>	<b>Graduate Student Association, 09/2012 – 06/2013</b> Co-chair, Integrative Biology, <i>UC Berkeley, CA</i>
<b>OUTREACH</b>	<b>826 Valencia, 06/2009 – 01/2011</b> K-12 Tutor, <i>San Francisco, CA</i>