

Karen A. Cranston

Department of Biology
Duke University
Durham, NC, USA
karen.cranston@gmail.com

<https://twitter.com/kcranston>
<http://kcranston.github.io>
<http://github.com/kcranston>

I am an evolutionary computational biologist who is passionate about how computational tools and skills facilitate the adoption and practice of more efficient, reproducible science. I am the lead PI of Open Tree of Life (<http://opentreeoflife.org>), which synthesizes an online, constantly updating tree of life based on community curation of published evolutionary trees.

Skill summary

Technical: extensive experience with python (web applications, libraries, scripting); knowledge of database (SQL) design, API design / implementation, UI design, Ansible deployment; previous experience with C / C++, Perl

Outreach / education: teaching interactive workshops, developing course material, coordinating training programs, and evidence-based instructor training; focus in on teaching technical and analytical skills to researchers; organization of hackathons for building tools and communities

Research: phylogenetic methods, including gene tree inference, visualization, supertrees; statistical genetics, particularly Bayesian Markov Chain Monte Carlo

Education

PhD (2007) Statistical Genetics. Department of Medical Genetics, University of Alberta, Edmonton, AB, Canada.

B.Sc., Honours, First Class (1996), Genetics. University of Manitoba, Winnipeg, MB, Canada

Employment

Research Scientist

2015-present, Department of Biology, Duke University, Durham, NC

Lead PI of Open Tree of Life (<http://opentreeoflife.org>) project that summarizes published phylogenetic trees into a synthetic tree of life; designing and writing software for storing, accessing and analyzing phylogeny data; leading hackathons and workshops; managing overall project, including software development.

Karen A. Cranston

Training Coordinator and Bioinformatics Project Manager

2010-2015, National Evolutionary Synthesis Center (NESCent), Durham, NC.

Management of informatics support for a broad range of evolutionary science projects; coordination of training programs in informatics and analytical skills for scientists; community building in open-source biodiversity and evolutionary informatics through hackathons and Google Summer of Code.

Postdoctoral Research Associate

2009-2010, Biodiversity Synthesis Center, The Field Museum, Chicago, IL

Interactive visualization of taxonomies and large phylogenies with Encyclopedia of Life and iPlant Collaborative; summarizing large-scale gene tree incongruence across genomes

Postdoctoral Research Associate

2007-2009, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ

PhyLoTA browser, summarizing phylogenetic signal in GenBank; phylogenomic analyses of wild and domesticated rice species

Laboratory technician

1997-2002, Cangene Corporation, Winnipeg, MB.

Maintenance of cell cultures; design and implementation of protein chemistry assays; analytical method validation.

Technical writer 1996-1997, Integrated Engineering Software, Winnipeg, Canada, 1996-1997

Technical documentation and online help systems for engineering simulation software.

Publications

I have 16 peer-reviewed scientific papers, and 7 commentaries / preprints (noted with *).

Phylogenetic methods

Hinchliff, C. E., et al., (2015). Synthesis of phylogeny and taxonomy into a comprehensive tree of life. *Proceedings of the National Academy of Sciences*, 112(41), 12764-12769. <http://dx.doi.org/10.1073/pnas.1423041112>. *In the Altmetrics Top 100 for 2015 and in top 5% overall; 53 news reports; 832 Tweets, 14 blogs; https://www.altmetric.com/details/4529894*

Evans, M. E., et al., (2011). Extreme environments select for reproductive assurance: evidence from evening primroses (*Oenothera*). *New Phytologist*, 191(2), 555-563. <http://dx.doi.org/10.1111/j.1469-8137.2011.03697.x>

Ammiraju, J. S., et al., (2010). Spatiotemporal patterns of genome evolution in allotetraploid species of the genus *Oryza*. *The Plant Journal*, 63(3), 430-442. <http://dx.doi.org/10.1111/j.1365-313X.2010.04251.x>

Cranston, K. A. (2010) Quantifying gene tree incongruence across varying phylogenetic depths. In L. Lacey Knowles, Laura S. Kubatko (Eds.) *Estimating Species Trees: Practical and Theoretical Aspects*, Wiley-Blackwell.

Cranston, K. A., et al., (2010). Phylogenomic analysis of BAC-end sequence libraries in *Oryza* (Poaceae). *Systematic botany*, 35(3), 512-523. <http://dx.doi.org/10.1600/036364410792495872>

Cranston, K. A., et al., (2009). Species trees from highly incongruent gene trees in rice. *Systematic Biology* 58(5), 489-500. <http://dx.doi.org/10.1093/sysbio/syp054>

Cranston, K. A., & Rannala, B. (2007). Summarizing a posterior distribution of trees using agreement subtrees. *Systematic Biology* 56(4), pp. 578-590. <http://dx.doi.org/10.1080/10635150701485091>

Cranston, K., & Rannala, B. (2005). Closing the gap between rocks and clocks. *Heredity*, 94(5), 461-462. <http://dx.doi.org/10.1038/sj.hdy.6800644>

Software and databases

McTavish, E. J., et al., (2015). Phylesystem: a git-based data store for community curated phylogenetic estimates. *Bioinformatics*, btv276. <http://dx.doi.org/10.1093/bioinformatics/btv276>

Ksepka, D.T., et al., (2015) The Fossil Calibration Database, A New Resource for Divergence Dating. *Systematic Biology*. <http://dx.doi.org/10.1093/sysbio/syv025>

Stoltzfus, A., et al., (2013). Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC bioinformatics*, 14(1), 158. <http://dx.doi.org/10.1186/1471-2105-14-158>

Sanderson, M. J., et al., (2008). The PhyLoTA Browser: processing GenBank for molecular phylogenetics research. *Systematic Biology* 57(3), pp. 335-346. <http://dx.doi.org/10.1080/10635150802158688>

Open science, Collaboration, and Education

* Wilson, G., et al., (2016). Good Enough Practices in Scientific Computing. arXiv preprint <http://arxiv.org/abs/1609.00037>

Katz, D.S. et al., (2016). Report on the Second Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE2). *Journal of Open Research Software*. 4(1), p.e7. <http://doi.org/10.5334/jors.85>

Teal, T. K., et al., (2015) Data Carpentry: Workshops to Increase Data Literacy for Researchers. *International Journal of Digital Curation*. 10(1):135-143. <http://dx.doi.org/10.2218/ijdc.v10i1.351>

Cranston, K. A., et al., (2014) Best Practices for Data Sharing in Phylogenetic Research. *PLOS Currents Tree of Life*. Jun 19. Edition 1. <http://dx.doi.org/10.1371/currents.tol.bf01eff4a6b60ca4825c69293dc59645>

* Katz, D. S., et al., (2014). Second Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE2): Submission, Peer-Review and Sorting Process, and Results. arXiv preprint <http://arxiv.org/abs/1411.3464>.

* Vision, T., & Cranston, K. A. (2014) Open data for evolutionary synthesis: an introduction to the NESCent collection. Nature Scientific Data. <http://dx.doi.org/10.1038/sdata.2014.30>

* Cranston, K. A., et al., (2014): Simple rules for sharing phylogenetic data. figshare. <http://dx.doi.org/10.6084/m9.figshare.997763>

Rodrigo, A., et al., (2013). Science incubators: synthesis centers and their role in the research ecosystem. PloS biology, 11(1), e1001468. <http://dx.doi.org/10.1371/journal.pbio.1001468>

* Rees, J. A., et al., (2013): Response to GBIF request for consultation on data licenses. figshare. <http://dx.doi.org/10.6084/m9.figshare.799766>

* Cranston, K. A., et al., (2013): A grassroots approach to software sustainability. figshare. <http://dx.doi.org/10.6084/m9.figshare.790739>

Goff, S. A., et al., (2011). The iPlant collaborative: cyberinfrastructure for plant biology. *Frontiers in plant science*, 2. <http://dx.doi.org/10.3389/fpls.2011.0003>

Education and outreach

- NESCent Academy: coordinated series of hands-on summer workshops in Evolutionary Biology and Informatics, 2010-2014.
- Software / Data Carpentry: certified instructor since 2013; working towards Instructor Training certification in 2017; co-lead development of reproducible science curriculum
- Phylogenetics workshops: taught phylogenetic methods and software in workshops at Wuhan Institute of Virology, Fudan University, Kenyan Medical Research Centre, The Field Museum, and Bodega Bay Marine Laboratory
- Hackathons: co-organized four hackathons on evolutionary informatics through NESCent and Open Tree of Life; see https://informatics.nescent.org/wiki/Main_Page

Professional activities

- Board of Directors: Open Bioinformatics Foundation (<https://open-bio.org/>), 2015-present
- Data Carpentry founding board member (<http://datacarpentry.org>), 2014-present
- Organization administrator for NESCent Google Summer of Code participation, 2011-2013
- Program committee / panelist, Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE), <http://wssspe.researchcomputing.org.uk>, 2013, 2014, 2016
- Society of Systematic Biology council, 2012-2014
- Systematic Biology Editorial Board, 2011-present
- Leadership team, Informatics for Evolutionary Biology (iEvoBio, <http://ievobio.org>) conference, 2013-2016
- Phyloinformatics Research Foundation board member, 2010-present
- Team lead, iPlant Tree Of Life working group on Tree Visualization, 2009-2012

Karen A. Cranston

- Invited participant: iPlant Collaborative (<http://iplantcollaborative.org>) Grand Challenge Workshop on Assembling the Tree of Life to Enable the Plant Sciences, November 2009, Biosphere 2, Oracle, AZ
- Journal referee for: Systematic Biology, Trends Ecology and Evolution, PeerJ, Nucleic Acids Research, Journal of Open Research Software, PLOS Computational Biology, Molecular Biology and Evolution. See [Publons reviewer profile](#) for recent activity.
- National Science Foundation panelist, 2011 - 2014