

Karen A. Cranston

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Education

- 2002-2007 **PhD**, Department of Medical Genetics, University of Alberta, Edmonton, AB, Canada. Thesis title: “Inferring, testing and summarizing a posterior distribution of phylogenies”. Supervisor: Dr. Bruce Rannala.
- 1992-1996 **B.Sc. (Honours, First Class)**, Genetics. University of Manitoba, Winnipeg, MB, Canada

Employment

- 2015- **Research Scientist**, Department of Biology, Duke University, Durham, NC
- 2010-2015 **Training Coordinator and Bioinformatics Project Manager**, National Evolutionary Synthesis Center (NESCent), Durham, NC
- 2009-2010 **Postdoctoral Research Associate**, Biodiversity Synthesis Center / Encyclopedia of Life at the Field Museum of Natural History, Chicago, IL
- 2007-2009 **Postdoctoral Research Associate**, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ
- 1997-2002 **Laboratory technician** in cell culture, protein chemistry and analytical method validation, Cango Corporation, Winnipeg, MB
- 1996-1997 **Technical writer**, Integrated Engineering Software, Winnipeg, Canada, 1996-1997. Technical documentation and online help systems for engineering software.

Peer-reviewed publications

McTavish, E. J., Hinchliff, C. E., Allman, J. F., Brown, J. W., Cranston, K. A., Holder, M. T., ... & Smith, S. A. (2015). Phylesystem: a git-based data store for community curated phylogenetic estimates. *Bioinformatics*, btv276. <http://dx.doi.org/10.1093/bioinformatics/btv276>
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>

Ksepka, D.T., Parham, J.F., Allman, J.F., Benton, M.J., Carrano, M.T., Cranston, K.A., ... & Warnock, R.C.M. (2015) The Fossil Calibration Database, A New Resource for Divergence Dating. *Systematic Biology*. <http://dx.doi.org/10.1093/sysbio/syv025>

Teal, T. K., Cranston, K. A., Lapp, H., White, E., Wilson, G., Ram, K., Pawlik, A. (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., Harmon, L. J., O'Leary, M. A., Lisle, C. (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>

Stoltzfus, A., Lapp, H., Matasci, N., Deus, H., Sidlauskas, B., Zmasek, C. M., ... & Jordan, G. (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>

Rodrigo, A., Alberts, S., Cranston, K., Kingsolver, J., Lapp, H., McClain, C., ... & Wiegmann, B. (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>

Goff, S. A., Vaughn, M., McKay, S., Lyons, E., Stapleton, A. E., Gessler, D., ... & Kleibenstein, D. J. (2011). The iPlant collaborative: cyberinfrastructure for plant biology. *Frontiers in plant science*, 2. <http://dx.doi.org/10.3389/fpls.2011.0003>

Evans, M. E., Hearn, D. J., Theiss, K. E., Cranston, K., Holsinger, K. E., & Donoghue, M. J. (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., Fan, C., Yu, Y., Song, X., Cranston, K. A., Pontaroli, A. C., ... & Wing, R. A. (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.1365-3113X.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., Hurwitz, B., Sanderson, M. J., Ware, D., Wing, R. A., & Stein, L. (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., Hurwitz, B., Ware, D., Stein, L., & Wing, R. A. (2009). Species trees from highly incongruent gene trees in rice. *Systematic Biology* 58(5), 489-500. <http://dx.doi.org/10.1093/sysbio/syp054>

Sanderson, M. J., Boss, D., Chen, D., Cranston, K. A., & Wehe, A. (2008). The PhyLoTA Browser: processing GenBank for molecular phylogenetics research. *Systematic Biology* 57(3), pp. 335-346. <http://dx.doi.org/10.1080/10635150802158688>

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>

Commentaries, preprints, other non-peer reviewed

(published preprints not shown)

Wilson, G., Bryan, J., Cranston, K., Kitzes, J., Nederbragt, L., & Teal, T. K. (2016). Good Enough Practices in Scientific Computing. arXiv preprint [arXiv:1609.00037](https://arxiv.org/abs/1609.00037).

Katz, D.S., Choi, S.T., Wilkins-Diehr, N., Hong, N.C., Venters, C.C., ... & Littauer, R. Report on the Second Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE2). arXiv preprint [arXiv:1507.01715](https://arxiv.org/abs/1507.01715)

Katz, D. S., Allen, G., Hong, N. C., Cranston, K., Parashar, M., Proctor, D., ... & Wilkins-Diehr, N. (2014). Second Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE2): Submission, Peer-Review and Sorting Process, and Results. arXiv preprint [arXiv:1411.3464](https://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*. [doi:10.1038/sdata.2014.30](https://doi.org/10.1038/sdata.2014.30)

Cranston, K. A., Blackburn, D., Brown, J. W., Dececchi, A., Gardner, N., Greshake, B., ... & Wolfe, J. (2014): Simple rules for sharing phylogenetic data. figshare. [doi:10.6084/m9.figshare.997763](https://doi.org/10.6084/m9.figshare.997763)

Rees, J. A., Cranston, K. A., Lapp, H., & Vision, T. (2013): Response to GBIF request for consultation on data licenses. figshare. [doi:10.6084/m9.figshare.799766](https://doi.org/10.6084/m9.figshare.799766)

Cranston, K. A., Vision, T., O'Meara, B., & Lapp, H. (2013): A grassroots approach to software sustainability. figshare. [doi:10.6084/m9.figshare.790739](https://doi.org/10.6084/m9.figshare.790739)

Invited talks

- *Synthesizing phylogeny and taxonomy into a comprehensive tree of life*, Biodiversity Informatics (TDWG) (2014)

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- *Data and services for the tree of life*, Commonwealth Scientific and Industrial Research Organisation (CSIRO) (2014)
- *Technical and social challenges in synthesizing the tree of life*, Agriculture Canada (2014)
- *Enabling science with the tree of life*, Carleton University (2014)
- *Technical and social challenges in synthesizing the tree of life*, <http://phyloseminar.org> (2014)
- *Open Tree of Life: Synthesizing phylogenetic data into a tree of all life*, University of North Carolina Charlotte (2013)
- *Phylogenetics, phylogenomics and phyloinformatics: Finding evolutionary signals in large data sets*, University of Toronto (2010)
- *Automating phylogenetic tree inference from public sequence databases*, University of Missouri, 2009
- *Automating phylogenetic tree inference from public sequence databases*, Botany meetings, 2009
- *Species trees and gene trees from high-throughput sequence data in rice*, University of Michigan, 2009
- *A species tree from 2000 gene trees in rice (Oryza)*, Evolution, 2008
- *The PhyLoTA browser: Processing GenBank for molecular phylogenetic research*, George Washington University, 2008
- *Species trees from gene trees in rice: When 2.5 million characters are not enough...*, University of California Davis, 2008

Grants and Awards

- NSF Special Creativity Award: Collaborative Research: Automated and community-driven synthesis of the tree of life. NSF AVAToL (2014) \$1.4 million (\$1.1 million to Duke, PI Cranston, 2015-2017)
- NSF AVAToL: Collaborative Research: Automated and community-driven synthesis of the tree of life. \$5.76 million (\$927,000 to Duke, PI Cranston, 2012-2015)
- The iPlant Collaborative; a cyberinfrastructure-centered community for a new plant biology - subcontract to Field Museum of Natural History, (\$62000, PI Cranston, 2009-2010) and to Duke University (\$14500, PI Vision, 2011-2011)
- Dissertation Fellowship, University of Alberta (2006)
- Province of Alberta Graduate Student Fellowship (2006)
- Mary Louise Imrie Graduate Student Award, University of Alberta (2006)

- 75th Anniversary Graduate Student Award, Faculty of Medicine and Dentistry, University of Alberta (2004)
- Medical Sciences Graduate Research Assistantship, Faculty of Medicine and Dentistry, University of Alberta (2006 & 2004)

Professional activities

- Board of Directors: Open Bioinformatics Foundation (<https://open-bio.org/>), 2015-present
- Co-organizer: Reproducible science hackathon (<https://github.com/Reproducible-Science-Curriculum/Reproducible-Science-Hackathon-Dec-08-2014>), 2014
- Data Carpentry founding board member (<http://datacarpentry.org>), 2014-present
- Organization administrator for NESCent Google Summer of Code participation, 2011-2013
- Program committee, Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE), <http://wssspe.researchcomputing.org.uk>, 2014 and 2016
- Panelist, First Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE), <http://wssspe.researchcomputing.org.uk>, 2013
- 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-present
- Leadership team, Hackathons, Interoperability and Phylogenetics (HIP) NESCent working group, 2011-present
- Phyloinformatics Research Foundation board member, 2010-present
- Team lead, iPlant Tree Of Life working group on Tree Visualization, 2009-2012
- Co-organizer: Phyloinformatics VoCamp for development of an ontology for evolutionary biology, November 2009, Montpellier, France
- Invited participant: National Evolutionary Synthesis Center (NESCent) Hackathon on Evolutionary Database Interoperability, March 2009, Durham, NC, USA
- 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

Teaching

- Coordinator: NESCent Academy (<http://academy.nescent.org>): a series of hands-on summer workshops in Evolutionary Biology and Informatics, 2010-2014.
- Certified Instructor: Software and Data Carpentry (<http://software-carpentry.org> & <http://datacarpentry.org>), 2013-present
- Instructor: Computational biology workshops, Wuhan Institute of Virology and Fudan University, China, 2013
- Instructor: Phylogenetics workshops, Kenya Medical Research Institute, 2012
- Instructor: Phylogenetics workshop, Research Experience for Undergraduates (REU) Program, Field Museum of Natural History, 2010
- Instructor: Workshop in applied phylogenetics, Bodega Bay Marine Laboratory, 2006