

## Karen A. Cranston

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Biological Informatics Centre of Excellence  
Agriculture and Agri-food Canada  
Ottawa, ON  
karen.cranston@gmail.com

<https://twitter.com/kcranston>  
<http://kcranston.github.io>  
<http://github.com/kcranston>  
<http://orcid.org/0000-0002-4798-9499>

I am an evolutionary computational biologist who is passionate about building computational tools and teaching skills to facilitate the adoption and practice of more efficient, reproducible science. As both project manager at a research facility and lead PI of Open Tree of Life (<http://opentreeoflife.org>), I have been both developer and manager of complex, multi-faceted software projects in evolutionary informatics. I am deeply involved as a teacher and leader in efforts to teach computation skills to scientists through The Carpentries (<https://carpentries.org>).

## 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; teaching technical and analytical skills to researchers; organization of hackathons for building tools and communities

*Management:* project and financial management of scientific research grants, supervising technical staff across multiple projects, agile software development, board member overseeing open source / open science organizations

*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

### Technical Advisor, Bioinformatics

2017-present, Agriculture and Agri-food Canada, Ottawa, ON

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Project manager and technical advisor in biological informatics group, leading development of software for biological specimen collection digitization and management.

### **Research Scientist**

2015-2017, 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.

### **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 19 peer-reviewed scientific papers, and 6 commentaries / preprints (noted with \*). Only papers from 2013-2018 shown below. Full list at <http://kcranston.github.io/research/>.

## Phylogenetic methods

McTavish, E. J., Drew, B. T., Redelings, B., & Cranston, K. A. (2017). How and Why to Build a Unified Tree of Life. *BioEssays*, 39(11). <https://doi.org/10.1002/bies.201700114>

Rees, J., & Cranston, K. (2017). Automated assembly of a reference taxonomy for phylogenetic data synthesis. *Biodiversity Data Journal*, 5, e12581. <https://doi.org/10.3897/BDJ.5.e12581>

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>.

## 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>

## Open science, Collaboration, and Education

Stoltzfus, A., Rosenberg, M., Lapp, H., Budd, A., Cranston, K., Pontelli, E., ... & Vos, R. A. (2017). Community and Code: Nine Lessons from Nine NESCent Hackathons. *F1000Research*, 6. <http://dx.doi.org/10.12688/f1000research.11429.1>

Wilson, G., et al., (2017). Good Enough Practices in Scientific Computing. *PLoS Comput Biol* 13(6): e1005510 <https://doi.org/10.1371/journal.pcbi.1005510>

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>

## **Education and outreach**

- NESCent Academy: coordinated series of hands-on summer workshops in Evolutionary Biology and Informatics, 2010-2014.
- Software / Data Carpentry: Executive Council Chair since 2018; instructor certification in 2013; 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](https://informatics.nescent.org/wiki/Main_Page)

## **Professional activities**

- Chair, Executive Council: The Carpentires (<https://carpentries.org>), 2018-present
- Board of Directors: Open Bioinformatics Foundation (<https://open-bio.org/>), 2015-present
- Data Carpentry founding board member (<http://datacarpentry.org>), 2014-2017
- Co-organizer: Reproducible science hackathon (<https://github.com/Reproducible-Science-Curriculum/Reproducible-Science-Hackathon-Dec-08-2014>), 2014
- 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, 2013-2016
- Leadership team, Hackathons, Interoperability and Phylogenetics (HIP) NESCent working group, 2011-2015
- Board of Directors: Phyloinformatics Research Foundation, 2010-2015

- 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