

REBECCA B. DIKOW *curriculum vitae*

Research Data Scientist
Data Science Lab
Office of the CIO
Smithsonian Institution
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Current Position and Short Biography

Smithsonian Institution, April 2016–present. Research Data Scientist, Data Science Lab, Office of the Chief Information Officer.

Rebecca Dikow is a Research Data Scientist and leads the Smithsonian Institution Data Science Lab, part of the Office of the Chief Information Officer. Since its start in 2016, members of the the Data Science Lab have been conducting biodiversity research using genomics, informatics, and machine learning tools. More recently, Data Science Lab members have begun working with researchers studying digitized collections and archives data outside the biodiversity sphere and strive to collaborate with scholars all across the Smithsonian. The Data Science Lab also provides support for researchers using the High-Performance Computing Cluster and training in data science and bioinformatics tools. Rebecca is also an affiliated faculty member in the George Mason University School of Systems Biology and the Smithsonian-Mason School of Conservation.

Other Affiliations

George Mason University, Spring 2018–present. Affiliated Faculty, School of Systems Biology.

George Mason University, Fall 2019–present. Affiliated Faculty, Smithsonian-Mason School of Conservation

Education

Ph.D. Evolutionary Biology, The University of Chicago, August 2012.

Dissertation: *Genome-level homology and phylogenetic systematics: case studies using Vibrionaceae and Shewanellaceae (Bacteria: Gammaproteobacteria)*

M.S. Evolutionary Biology, The University of Chicago, December 2009.

B.S. *cum laude* Biology (Ecology and Evolutionary Biology), Cornell University, May 2003.

Other Training

Smithsonian Institution, September 2012–April 2016. Biodiversity Genomics Postdoctoral Fellow. Co-advised by Dr. Robert Fleischer (Center for Conservation and Evolutionary Genetics, National Zoological Park) and Dr. Kristofer Helgen (Division of Mammals, National Museum of Natural History).

Past Research Employment

The University of Chicago, Committee on Evolutionary Biology, 2008–2012. Graduate student and administrator for communal and rental computers and equipment.

American Museum of Natural History, 2005–2007. Molecular Systematics Lab Supervisor for Dr. Ward Wheeler.

American Museum of Natural History, 2003–2005. Scientific Assistant for Dr. Mark Siddall.

Cornell University, 2000–2003. Student Research Assistant for Dr. Nelson Hairston Jr.

Preprints

Borowiec, M. L., **Dikow, R. B.**, Frandsen, P. B., McKeeken, A., Valentini, G., White, A. E. 2021. Deep learning as a tool for ecology and evolution. *EcoEvoRxiv* doi:10.32942/osf.io/nt3as.

Publications

Olsen, L. K., Heckenhauer, J., Sproul, J. S., **Dikow, R. B.**, Gonzalez, V. L., Kweskin, M. P., Taylor, A. M., Wilson, S. B., Stewart, R. J., Zhou, X., Holzenthal, R., Pauls, S. U., Frandsen, P. B. 2021. Genome Assemblies and Annotations of *Agrypnia vestita* Walker, and *Hesperophylax magnus* Banks Reveal Substantial Repetitive Element Expansion in Tube Case-making Caddisflies (Insecta: Trichoptera). *bioRxiv* doi: 10.1093/gbe/evab013.

Roa-Varón, A., **Dikow, R. B.**, Carnevale, G., Tornabene, L., Baldwin, C. C., Li, C., Hilton, E. J. 2020. Confronting Sources of Systematic Error to Resolve Historically Contentious Relationships: A Case Study Using Gadiform Fishes (Teleostei, Paracanthopterygii, Gadiformes), *Systematic Biology*, syaa095, doi: 10.1093/sysbio/syaa095.

Tsuchiya, M. T. N., **Dikow, R. B.**, Koepfli, K.-P., Frandsen, P. B., Rockwood, L. L., Maldonado, J. E. 2020. Whole Genome Sequencing of Procyonids Reveals Distinct Demographic Histories in Kinkajou (*Potos flavus*) and Northern Raccoon (*Procyon lotor*), *Genome Biology and Evolution*, evaa255, doi: 10.1093/gbe/evaa255.

Feng, S., Stiller, J., Deng, Y. *et al.* 2020. Dense sampling of bird diversity increases power of comparative genomics. *Nature* 587, 252–257. doi: 10.1038/s41586-020-2873-9.

Legeai F., Santos B. F., Robin S., Bretaudeau A., **Dikow R. B.**, Lemaitre C., Jouan V., Ravallec M., Drezen J.-M., Tagu D., Baudat F., Gyapay G., Zhou X., Liu S., Webb B. A., Brady S. G., Volkoff A.-N. 2020. Genomic architecture of endogenous ichnoviruses reveals distinct evolutionary pathways leading to virus domestication in parasitic wasps. *BMC Biology* doi: 10.1186/s12915-020-00822-3.

Tsuchiya, M. T. N., **Dikow, R. B.**, Cassin-Sackett, L. 2020. First genome sequence of the Gunnison's prairie dog (*Cynomys gunnisoni*), a keystone species and player in the transmission of sylvatic plague. *Genome Biology and Evolution* 12: 5 618-625. doi: 10.1093/gbe/evaa069.

White, A. E., **Dikow, R. B.**, Baugh, M., Jenkins, A., Frandsen, P. B. 2020. Generating segmentation masks of herbarium specimens and a data set for training segmentation models using deep learning. *Applications in Plant Sciences*, invited article for the Special Issue: Machine Learning in Plant Biology. doi: 10.1002/aps3.11352.

Edelman, N. B., Frandsen, P. B., Miyagi, M., Clavijo, B. J., Davey, J., **Dikow, R. B.**, Accinelli, G. G., Van Belleghem, S., Patterson, N. J., Neafsey, D. E., Challis, R. J., Kumar, S., Moreira, G., Salazar, C., Chouteau, M., Counterman, B., Papa, R., Blaxter, M., Reed, R. D., Dasmahapatra, K., Kronforst, M., Joron, M., Jiggins, C. D., McMillan, W. O., Di-Palma, F., Blumberg, A. J., Wakeley, J., Jaffe, D., Mallet, J. 2019. Genomic architecture and introgression shape a butterfly radiation. *Science* 366 (6465), 594-599.

Jones, K. E., Fér, T., Schmickl, R., **Dikow, R. B.**, Funk, V. A., Herrando-Morraira, S., Johnston, P. R., Siniscalchi, C. M., Susanna, A., Sloávk, M., Thapa, R., Watson, L., Mandel, J. R., 2019. An empirical assessment of a single family-wide target capture locus set at multiple evolutionary timescales within the largest family of flowering plants. *Applications in Plant Sciences* 7 (10):Article e11295.

Mandel, J. R., **Dikow, R. B.**, Siniscalchi, C. M., Thapa, R., Watson, L. E., Funk, V. A. 2019. A fully resolved backbone phylogeny reveals numerous dispersals and explosive diversifications throughout the history of Asteraceae. *Proceedings of the National Academy of Sciences* 116 (28) 14083-14088; doi: 10.1073/pnas.19038711116.

Ohdera, A. H., Ames, C. L., **Dikow, R. B.**, Kayal, E., Chiodin, M., Busby, B., La, S., Pirro, S., Collins, A. G., Medina, M., Ryan, J. F. 2019. Box, stalked and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: *Alatina alata* (Cubozoa), *Calvadosia cruzmelitensis* (Staurozoa), and *Cassiopea xamachana* (Scyphozoa). *GigaScience* 8(7). doi: 10.1093/gigascience/giz069.

Ren, Z., von Dohlen, C. D., Harris, A. J., **Dikow, R. B.**, Su, X., Wen, J. in press at *PLoS One*. Congruent phylogenetic relationships of Melaphidina aphids (Aphididae: Eriosomatinae: Fordini) according to nuclear and mitochondrial DNA data with taxonomic implications on generic limits.

Cortes Rodrigues, N., Campana, M., Berry, L., Faegre, S., Derrickson, S., Ha, R., **Dikow, R. B.**, Rutz, C., Fleischer, R. 2019. Population genomics and structure of the critically endangered Mariana crow (*Corvus kubaryi*). *Genes* 10(3) doi 10.3390/genes10030187.

Hawkins, M. T. R., Culligan, R. C., **Dikow, R. B.**, Frasier, C.L., Lei, R., Louis Jr., E. E. 2018. Demographic history of the critically endangered greater bamboo lemur (*Prolemur simus*), evidence of population bottlenecks. *BMC Genomics*. doi: 10.1186/s12864-018-4841-4.

Schuettpelz, E., Frandsen, P. B., **Dikow, R. B.**, Brown, A., Orli, S., Peters, M., Metallo, A., Funk, V. A., Dorr, L. J. 2017. Applications of deep convolutional neural networks to digitized natural history collections. *Biodiversity Data Journal*. doi: 10.3897/BDJ.5.e21139

Mandel, J. R., Barker, M. S., Bayer, R. J., **Dikow, R. B.**, Gao, T-G. Katy E. Jones, K. E., Keeley, S., Kilian, N., Ma, H, Siniscalchi, C. M., Susanna, A, Thapa, R., Watson, L., Funk, V. A. 2017. The Compositae Tree of Life in the age of phylogenomics. *Journal of Systematics and Evolution*. doi:10.1111/jse.12265

Ren, Z. Harris, A. J., **Dikow, R. B.**, Ma, E., Zhong, Y., Wen, J. 2017. Another look at the phylogenetic relationships and intercontinental biogeography of eastern Asian & North American *Rhus* gall aphids (Hemiptera: Aphididae: Eriosomatinae): Evidence from mitogenome sequences via genome skimming. *Molecular Phylogenetics and Evolution*.

Wen, J., Harris, A. J., Ickert-Bond, S. M., **Dikow, R. B.**, Wurdack, K, Zimmer, E. A. 2017. Developing integrative systematics in the informatics and genomic era, and calling for a global Biodiversity Cyberbank. *Journal of Systematics and Evolution*.

Dikow, R. B., Frandsen, P. B., Turcatel, M., Dikow, T. 2017. Genomic and transcriptomic resources for assassin flies including the complete genome sequence of *Proctacanthus coquilletti* (Insecta: Diptera: Asilidae) and 16 representative transcriptomes. *PeerJ*. doi:10.7717/peerj.2951

Nygaard, S., Hu, H., Li, C., Schiott, M., Chen, Z., Yang, Z., Xie, Q., Ma, C., Deng, Y., **Dikow, R. B.**, Rabeling, C., Nash, D. R., Wcislo, W. T., Brady, S. G., Schultz, T. R., Zhang, G., Boomsma, J. J. 2016. Reciprocal genomic evolution in the ant-fungus agricultural symbiosis. *Nature Communications*. doi:10.1038/ncomms12233

Wen, J., Egan, A. N., **Dikow, R. B.**, Zimmer, E. A. 2015. Utility of transcriptome sequencing for phylogenetic inference and character evolution Hörandl, E., Appelhans, M.S. (eds.), *Next-Generation Sequencing in Plant Systematics* 51 Chapter 2, <http://dx.doi.org/10.14630/000003>

Mandel, J. R., **Dikow, R. B.**, Funk, V. A. 2015. Using phylogenomics to resolve mega-families: an example from Compositae. *Journal of Systematics and Evolution*. doi:10.1111/jse.12167

Callicrate, T., **Dikow, R. B.**, Thomas, J., Mullikin, J., Jarvis, E., Fleischer, R. C., and NISC Comparative Sequencing Program. 2014. Genomic resources for the endangered Hawaiian honeycreepers. *BMC Genomics* 15: 1098. doi: 10.1186/1471-2164-15-1098.

Mandel, J. R., **Dikow, R. B.**, Masalia, R., Staton, S. E., Rieseberg, L. H., Kozik, A., Michelmore, R. W., Funk, V. A., Burke, J. M. 2014. A target enrichment method for gathering phylogenetic information from hundreds of loci across the Compositae. *Applications in Plant Sciences* 2:1300085. doi:10.3732/apps.1300085.

Dikow, R. B. and Smith, W. L. 2013. Genome-level homology and phylogeny of Vibrionaceae (Gammaproteobacteria: Vibrionales) with three new complete genome sequences. *BMC Microbiology*. doi:10.1186/1471-2180-13-80

Dikow, R. B. and Smith, W. L. 2013. Complete genome sequences provide a case study for the evaluation of gene-tree thinking. *Cladistics*. doi: 10.1111/cla.12020

Dikow, R. B. 2011. Genome-level homology and phylogeny of *Shewanella* (Gammaproteobacteria: Alteromonadales: Shewanellaceae). *BMC Genomics* 12:237. doi:10.1186/1471-2164-12-237

Dikow, R. B. 2011. Systematic relationships within the Vibrionaceae (Bacteria: Gammaproteobacteria): steps toward a phylogenetic taxonomy. *Cladistics* 27: 9–28. doi: 10.1111/j.1096-0031.2010.00312.x

*Please note name change as of 2009 from R. B. Budinoff to R. B. Dikow.

Murienne, J., Pellens, R. **Budinoff, R. B.**, Wheeler, W. C. and Grandcolas, P. 2008. Phylogenetic analysis of the endemic New Caledonian cockroach *Lauraesilpha*. Testing competing hypotheses of diversification. *Cladistics* 24: 802–812. doi: 10.1111/j.1096-0031.2008.00204.x

Perkins, S. L., **Budinoff, R. B.** and Siddall, M. E. 2005. New gammaproteobacteria associated with bloodfeeding leeches and a broad phylogenetic analysis of leech endosymbionts. *Applied Environmental Microbiology* 71: 5219–5224. doi: 10.1128/AEM.71.9.5219-5224.2005

Siddall M. E. and **Budinoff, R. B.** 2005. DNA-barcoding evidence for widespread introductions of a leech from the South American *Helobdella triserialis* complex. *Conservation Genetics* 6: 467–472. doi: 10.1007/s10592-005-4986-y

Siddall, M. E., **Budinoff, R. B.** and Borda, E. 2005. Phylogenetic evaluation of systematics and biogeography of the leech family Glossiphoniidae. *Invertebrate Systematics* 19: 105–112. doi: 10.1071/IS04034

Budinoff, R. B., Siddall, A. M. and Siddall, M. E. 2004. Twelve variable microsatellite loci for the North American medicinal leech, *Macrobodella decora*. *Molecular Ecology Notes* 4: 491–493. doi: 10.1111/j.1471-8286.2004.00723.x

Other Products

Dikow, R. B., Gupta, S., Taylor, M. H. 2016. Accelerating Plant and Animal Genomics for Biodiversity with the Latest Intel Technologies. Intel Corporation white paper.

Smithsonian Workshops GitHub site

Honors and Awards

- Participant in the Palmer Leadership Development Program, Smithsonian Institution, 2021–2022.
- Biodiversity Genomics Initiative Postdoctoral Fellowship, Smithsonian Institution, 2012–2016.
- Women in Science Fellowship: the Field Museum Women’s Board, 2011–2012 stipend.
- Teaching Award Honorable Mention: The University of Chicago, Biological Sciences Division, 2010–2011 academic year.
- Emerging Pathogen Project: the Field Museum and the University of Chicago, Institute for Genomics and Systems Biology, 2009–2011 stipend.
- Nancy Mollin Michael Scholarship, 2008 stipend.
- NSF GRF Honorable Mention, 2007, 2008.
- NSF REU Fellowship: American Museum of Natural History, 2002.
- Presidential Research Scholar: Cornell University, 1999–2003.
- Girl Scout Gold Award

Grants awarded

- American Women’s History Initiative Representation Matters Grant: *Building tools for large-scale document, image, and metadata processing to uncover the hidden work of women*. PI. 2021 (58,000 USD).
- NMNH ADS Grant: *Functional genomics, symbiosis and the drivers of diversification in parasitoid wasps (Hymenoptera, Ichneumonidae)*. co-PI. 2019 (42,455 USD).
- SI Women’s Committee Grant: *Improving the Representation of Women in Smithsonian Collections*. PI. 2019 (30,000 USD).
- SI Women’s Committee Grant: *Growing the Data Science Lab at the Smithsonian*. PI. 2018 (32,500 USD).
- SI Global Genome Initiative Grant: *Enhancing Genomic and Proteomic Resources for the Study of Silk Evolution in Moths and Caddisflies*. (co-PI; PI: T. Cleland). 2018 (29,030 USD).
- SI Scholarly Studies Grant: *Deepening our understanding of digitized herbarium samples using machine learning*. PI. 2018 (70,000 USD).
- NMNH ADS Grant: *Evolution of Male Secondary Sexual Organs in Eumaeine Butterflies*. (co-PI; PI R. Robbins). 2018 (139,300 USD).
- SI Global Genome Initiative Grant: *Exploratory phylogenomics and differential expression of genes involved in foliar chemical defense in the hyperdiverse tropical tree genus Psychotria*. (co-PI; PI: B. Sedio). 2016 (30,000 USD).
- SI Global Genome Initiative Grant: *Building A Reference Genome For Centrapalus pauciflorus, An African Oilseed Crop (Compositae)*. PI. 2016 (16,250 USD).
- SI Global Genome Initiative Grant: *The Atlantic awning clam genome: Solemya velum* (co-PI, PI: V. González). 2016 (16,250 USD).

SI Global Genome Initiative Grant: *The Caddisfly Genome: Psychomyia flavida* (co-PI, PI: P. Frandsen). 2016 (16,250 USD).

SI Global Genome Initiative Grant: *The Harvestman Genome: Phalangium opilio* (co-PI, PI: V. González). 2016 (16,250 USD).

SMBE Young Investigator Travel Award for travel to SMBE 2015 (2,000 USD).

SI Biodiversity Genomics/Global Genome Initiative Grant. *Reconstructing character evolution in Compositae (Asteraceae) using next-generation target enrichment data*. PI: V. Funk, co-PIs: R. B. Dikow, J. R. Mandel: 2015 (28,000 USD).

SI Biodiversity Genomics/Global Genome Initiative Grant. *Asiloid flies in the Nama Karoo and comparative phylogenomics*. PI: T. Dikow, co-PI: R. B. Dikow: 2015 (23,000 USD).

Nanopore MinION Access Programme: Two MinION devices awarded to sequence bacterial genomes: 2014.

Smithsonian Institution Grand Challenges Level 2: *Development of Smithsonian Biodiversity Genomics Bioinformatic Analysis Pipelines* (co-PI; PI: Thornton Staples): 2013 (75,000 USD).

The University of Chicago: Committee on Evolutionary Biology Pritzker Lab research grant for computational and laboratory resources: 2009, 2011 (11,000 total USD).

American Museum of Natural History: Lerner-Gray Fund for Marine Research: 2010 (1,588 USD).

The University of Chicago: Biological Sciences Division Travel Award: 2010 (500 USD).

The Willi Hennig Society: Marie Stopes Travel Grant: 2008, 2010, 2012 (1,500 total USD).

The Willi Hennig Society: Scholarship for Cladistics Workshop at The Ohio State University: July 2009 (600 USD).

The University of Chicago: Committee on Evolutionary Biology Hinds Fund: 2008 (1,040 USD).

Mentorship

Postdoctoral Fellows

Dr. Jennifer Spillane (June 2021–present).

Dr. Jenna Ekwealor (January 2021–present).

Dr. Carlos Arias (October 2020–present).

Dr. William Mattingly (October 2020–present).

Dr. Alexander White (September, 2018–present).

Dr. Mirian Tsuchiya (February, 2018–November 2020).

Predoctoral Fellows

Alexander Robillard (May, 2019–present).

Graduate Committees

Alexander Robillard, University of Maryland (PhD in progress)

Matthew Valko, George Mason University (PhD in progress)

Alexis Garretson, George Mason University (MS 2020)

Summer Interns and Fellows

Luis Figueroa (California State University Channel Islands; June, 2021–August, 2021, primarily supervised by William Mattingly).

Christelle Inema (University of Chicago; June, 2021–August, 2021).

Dalila Lara (UCSB; June, 2021–August, 2021, primarily supervised by Jenna Ekwealor).

Isabella Schrader (Marshall University; June, 2021–August, 2021).

Madeline Bursell (BYU; May, 2019–July, 2019; June 2021–present).

Seth Wilson (BYU; June, 2019–August, 2019).

Tiana Curry (UCSB; July, 2019–September, 2019).

Alejandro Sanchez (UC Davis; June, 2019–August, 2019).

Sarah Agarrat (UMD; July, 2019–August, 2019).

Chandra Earl (UF; June, 2018–July, 2018).

Katherine Jensen (UNCC; June, 2018–July, 2018).

John Ferry (Duke University; June, 2018–August, 2018).

George Mason University Digital Humanities Internship Students

Megan Glenn (2019–2020)

Grace May (2019–2020)

Teaching

Lead instructor for *Conservation Genomics*, a 10-day Smithsonian-Mason School for Conservation 3-credit graduate course, October 2018, 2019.

Certified Software and Data Carpentry Instructor.

Design and teach workshops in introductory HPC, Unix, Genome Assembly, Targeted Enrichment, RNAseq with V. González, M. Kweskin, M. Trizna (2015–present). Materials available here: [Smithsonian Workshops GitHub site](#).

Teaching Assistant, The University of Chicago: *Environmental Ecology* Winter 2012, Biological Sciences Division. Instructor: Dr. Trevor Price.

Teaching Assistant, The University of Chicago: *Biological Diversity* Fall 2010, Biological Sciences Division. Instructor: Dr. Michael LaBarbera.

Northwestern University: Science and Engineering Research and Teaching Synthesis (SERTS) Program, February 2010.

American Museum of Natural History: Trained one high school student, three NSF REU undergraduates and numerous graduate and post-doctoral visitors in molecular techniques, 2003–2007.

Current Synergistic activities

Coordinate Artificial Intelligence and Machine Learning Reading Group, Smithsonian Institution, 2021–present.

Member of National Museum of Natural History Genomics and Informatics Task-Forces, 2020–present.

Program committee chair for NMNH “Frontiers in Phylogenetics” symposium and Phylopizza (2015–present).

Smithsonian Biodiversity Genomics Fellowship Committee Chair (2017–present).

Participate in weekly “Bioinformatics Office Hours,” providing genomic data analysis advice and scripting support to Smithsonian researchers (2015–present).

Presentations

invited ***Dikow, R. B.** Genome-scale phylogenetics: breakthroughs and continued challenges. II Virtual Meeting of Systematics, Biogeography, and Evolution, online, June 2021.

invited keynote ***Dikow, R. B.** Data-intensive approaches to digitized museum collections. 8th International Euro-Mediterranean Conference (EuroMed 2020), online, November 2020.

***Dikow, R. B.** and *Tsuchiya, M. T. N. Uncovering the Scientific Impact of Women at the Smithsonian. American Women of Science: Recovering History, Defining the Future, online, October 2020.

invited ***Dikow, R. B.** Data-intensive approaches to digitized museum collections. On Scalable Image Informatics (LIMPID) and Applications of Machine Learning to Materials Discovery (IDEAS2) Conference, University of California Santa Barbara, February 2020.

invited ***Dikow, R. B.** Data-intensive approaches to digitized museum collections. University of Chicago Evolutionary Morphology Seminar Series, January 2020.

invited *Kapsalis, E., ***Dikow, R. B.**, *Harmon, E., *Doyle, K. Data intensive approaches to examining American Women’s History. Working Women: The Smithsonian Institution as a Case Study. First annual American Women’s History Symposium, Smithsonian Institution, December 2019.

invited White, A. E., **Dikow, R. B.**, Baugh, M., Jenkins, A., and *Frandsen, P. B. Generating Masks for Image Segmentation in Digitized Herbarium Specimens. Part of the Machine learning: an emerging toolkit for biodiversity science using museum collections symposium. Biodiversity Next. Leiden, Netherlands, October 2019.

invited White, A. E., Trizna, M., Frandsen, P. B., Dorr, L. J., ***Dikow, R.B.**, and Schuettpelz, E. Evaluating geographic patterns of morphological disparity in ferns and lycophytes using deep neural networks. Part of the Machine learning: an emerging toolkit for biodiversity science using museum collections symposium. Biodiversity Next. Leiden, Netherlands, October 2019.

invited *White, A. E., Trizna, M., Frandsen, P. B., Dorr, L. J., **Dikow, R.B.**, and Schuettpelz, E. Evaluating geographic patterns of morphological disparity in ferns and lycophytes using deep neural networks. Part of the Machine Learning in Plant Biology symposium. Botany. Tuscon, August 2019.

invited ***Dikow, R. B.** Data-intensive approaches to digitized museum collections. Machine Vision for Cultural Heritage and Natural Science Collections Meeting. Yale University, April 2019.

invited ***Dikow, R. B.** Data Science at SI. AI at SI: Exploring Artificial Intelligence with Museum Collections Workshop, Washington, DC, November, 2018.

poster Earl, C., White, A. E., Trizna, M. G., Frandsen, P. B., Kawahara, A. Y., Brady, S. G., *Dikow, R. B. Using machine learning to distinguish between and discover patterns of biodiversity in insects. Biological Data Science, Cold Spring Harbor Laboratory, November 2018.

poster White, A. E., *Dikow, R. B., Trizna, M. G., Orli, S., Schuettpelz, E., Frandsen, P. B., Dorr, L. J. Applications of deep convolutional neural networks to digitized herbarium specimens. Biological Data Science, Cold Spring Harbor Laboratory, November 2018.

poster *Tsuchiya, M. T. N. & **Dikow, R. B.** Designing the Smithsonian Genome Hub, a cloud based collaborative tool for biodiversity scientists. Biological Data Science, Cold Spring Harbor Laboratory, November, 2018.

poster González, V. L., ***Dikow, R. B.**, Frandsen, P. B., Kveskin, M., Johnson, G., Gostel, M. R., Muruvanda, T., Allard, M., Keeley, S., Funk, V. A., Mandel, J. R. The genome of an undomesticated African oilseed crop, *Centrapalus pauciflorus* (Compositae). Biological Data Science, Cold Spring Harbor Laboratory, November, 2018.

invited *González, V. L., **Dikow, R. B.**, Frandsen, P. B., Kveskin, M., Johnson, G., Gostel, M. R., Muruvanda, T., Allard, M., Keeley, S., Funk, V. A., Mandel, J. R. Building a reference genome for *Centrapalus pauciflorus* (Compositae), an African oilseed crop. PAG XXVI, San Diego, CA, January, 2018.

invited *Frandsen, P. B. & ***Dikow, R. B.** Digging Deep: applications of deep learning to digitized museum collections. U. S. Library of Congress, January, 2018.

***Dikow, R. B.**, Pagenkopp-Lohan, K. M., Frandsen, P. B. A Whole-Genome Phylogenetic Hypothesis Across The Three Domains Of Life. Genome Informatics, Cold Spring Harbor Laboratory, November, 2017.

***Dikow, R. B.**, Frandsen, P. B., Cruley, D., Davis, D., Gupta, S., Speirs, S., Stern, B. A., Taylor, M., Burba, D. Improving genome annotation strategies for biodiverse species using cloud technologies. Biogenomics 2017, Washington, DC, February, 2017.

poster *González, V. L., ***Dikow, R. B.**, Frandsen, P. B., Kveskin, M., Johnson, G., Gostel, M. R., Muruvanda, T., Allard, M., Keeley, S., Funk, V. A., Mandel, J. R. Building a reference genome for *Centrapalus pauciflorus* (Compositae), an African oilseed crop. Biogenomics 2017, Washington, DC, February, 2017.

poster *Frandsen, P. B., **Dikow, R. B.**, Turcatel, M., Dikow, T. Comparative genomics of Asilidae, Mydidae, and Tabanidae (Diptera): adding to our evolutionary understanding of the center of the fly radiation. Biogenomics 2017, Washington, DC, February, 2017.

*Lim, H. C., Coyle, B., Frandsen, P. B., **Dikow, R. B.**, Johnson, W. E., Braun, M. J. Conservation genomics of the highly endangered Red Siskin. Biogenomics 2017, Washington, DC, February, 2017.

*Hawkins, M. T. R., Culligan, R. C., **Dikow, R. B.**, Frasier, C.L., Lei, R., Louis Jr., E. E. Demographic history of the critically endangered greater bamboo lemur (*Prolemur simus*), evidence of population bottlenecks. Biogenomics 2017, Washington, DC, February, 2017.

poster *Tsuchiya, M. T. N., **Dikow, R. B.**, Koepfli, K. P., Frandsen, P. B., Rockwood, L. L., Kays, R. W., Helgen, K. M., Maldonado, J. E. Comparative genomics of procyonids: testing alternative *de novo* assembly methods and their impact on genome annotation. Biogenomics 2017, Washington, DC, February, 2017.

poster *Frandsen, P. B., **Dikow, R. B.**. Building a biological data science infrastructure at the Smithsonian Institution. Biological Data Science Cold Spring Harbor Laboratory, October, 2016.

poster ***Dikow, R. B.**, Pagenkopp-Lohan, K. M., Frandsen, P. B. A Whole-Genome Phylogenetic Hypothesis Across The Three Domains Of Life. Biological Data Science Cold Spring Harbor Laboratory, October, 2016.

workshop Mandel, J. R., **Dikow, R. B.**, Funk, V. A. Using phylogenomics to resolve mega-families: An example from Compositae. Botanical Society of America 2014, Savannah, GA, July, 2016.

***Dikow, R. B.**. A Whole-Genome Phylogenetic Hypothesis Across The Three Domains Of Life. Society for Molecular Biology and Evolution, Vienna, Austria, July 2015.

***Dikow, R. B.**. A Whole-Genome Phylogenetic Hypothesis Across The Three Domains Of Life. Hennig XXXIV, New York, June 2015.

invited ***Dikow, R. B.**. Comparative genomics: a study across the three domains of life and progress toward bioinformatics workflows for SI researchers. Smithsonian Environmental Research Center. Edgewater, MD, December 2014.

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workshop Mandel, J. R., ***Dikow, R. B.**, Funk, V. A. A target enrichment method for gathering phylogenetic information from hundreds of loci: an example from the Compositae, a.k.a. Asteraceae. Botanical Society of America 2014, Boise, ID, July 2014.

invited ***Dikow, R. B.** Investigating Tasmanian devil disease declines using museum specimens and ancient DNA. Animal Disease Exchange, Smithsonian Conservation Biology Institute, Washington, DC, May 2014.

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***Dikow, R. B.** Genome-scale analyses, gene trees, and gene homology. Hennig XXXI. Riverside, CA, June 2012.

***Dikow, R. B.** Character optimization across genomes and the distribution of phylogenetic signal. CEB & E&E student retreat. The University of Chicago, Chicago, IL, April 2011.

***Dikow, R. B.** Reconstructing genome histories with phylogenetic trees: examples from the Gammaproteobacteria. Hennig XXIX, Genomics Symposium. Honolulu, HI, May 2010.

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Siddall, M. E. & ***Budinoff, R. B.** Bacterial endosymbionts of the mycetomal organs of glossiphoniid leeches; Phylogeny and coevolution. 2004 International Meeting on Evolution, Development and Neurobiology of the Leech. Lille, France, September 2004.

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