

Bibliography & References Cited

1. Croll, D. & McDonald, B. A. The genetic basis of local adaptation for pathogenic fungi in agricultural ecosystems. *Molecular Ecology* **26**, 2027–2040 (Oct. 2016).
2. Grünwald, N. J., McDonald, B. A. & Milgroom, M. G. Population Genomics of Fungal and Oomycete Pathogens. *Annual Review of Phytopathology* **54**, 323–346 (Aug. 2016).
3. Stukenbrock, E. H. Evolution, selection and isolation: a genomic view of speciation in fungal plant pathogens. *New Phytologist* **199**, 895–907 (June 2013).
4. Whitaker, K. *Publishing a reproducible paper* 2017. doi:10.6084/m9.figshare.4720996.v1.
5. Patil, P., Peng, R. D. & Leek, J. A statistical definition for reproducibility and replicability. *bioRxiv*, 066803 (2016).
6. Kamvar, Z. N., Tabima, J. F. & Grünwald, N. J. Poppr: an R package for genetic analysis of populations with clonal, partially clonal, and/or sexual reproduction. *PeerJ* **2**, e281 (Mar. 2014).
7. Boettiger, C. An introduction to Docker for reproducible research. *ACM SIGOPS Operating Systems Review* **49**, 71–79 (Jan. 2015).
8. Nosek, B. A. *Center for Open Science: Strategic Plan* Mar. 2017. <osf.io/ymu94>.
9. Buckheit, J. B. & Donoho, D. L. in *Wavelets and Statistics* 55–81 (Springer, 1995). doi:10.1007/978-1-4612-2544-7_5. <http://dx.doi.org/10.1007/978-1-4612-2544-7_5>.
10. Peng, R. D. Reproducible Research in Computational Science. *Science* **334**, 1226–1227 (Dec. 2011).
11. Baker, M. 1,500 scientists lift the lid on reproducibility. *Nature* **533**, 452–454. ISSN: 0028-0836, 1476-4687 (May 25, 2016).
12. Announcement: Towards greater reproducibility for life-sciences research in Nature. *Nature* **546**, 8–8 (May 2017).
13. Barone, L., Williams, J. & Micklos, D. Unmet Needs for Analyzing Biological Big Data: A Survey of 704 NSF Principal Investigators. *bioRxiv*, 108555 (Feb. 15, 2017).
14. Wilson, G. *et al.* Good Enough Practices in Scientific Computing. Version 2. arXiv: <http://arxiv.org/abs/1609.00037v2> [cs.SE]. <<http://arxiv.org/abs/1609.00037v2>> (Oct. 14, 2016).
15. McKiernan, E. C. *et al.* How open science helps researchers succeed. *eLife* **5**. doi:10.7554/elife.16800. <<http://dx.doi.org/10.7554/eLife.16800>> (July 2016).
16. Lowndes, J. S. S. *et al.* Our path to better science in less time using open data science tools. *Nature Ecology & Evolution* **1**, 0160 (May 2017).
17. Schmidt, B. *et al.* Stepping up Open Science Training for European Research. *Publications* **4**, 16 (June 2016).
18. Bolton, M. D., Thomma, B. P. H. J. & Nelson, B. D. *Sclerotinia sclerotiorum* (Lib.) de Bary: biology and molecular traits of a cosmopolitan pathogen. *Molecular Plant Pathology* **7**, 1–16 (Jan. 2006).

19. US Canola Association. *National Sclerotinia Initiative* <http://www.uscanola.com/site/epage/102383_956.htm> (2017).
20. Attanayake, R. N. *et al.* Inferring outcrossing in the homothallic fungus *Sclerotinia sclerotiorum* using linkage disequilibrium decay. *Heredity* **113**, 353–363 (Apr. 2014).
21. Huang, H., Kozub, G., *et al.* Temperature requirements for carpogenic germination of sclerotia of *Sclerotinia sclerotiorum* isolates of different geographic origin. *Botanical Bulletin of Academia Sinica* **32**, 279–286 (1991).
22. Carbone, I. & Kohn, L. M. A microbial population-species interface: nested cladistic and coalescent inference with multilocus data. *Molecular Ecology* **10**, 947–964 (Apr. 2001).
23. Lehner, M. S. & Mizubuti, E. S. G. Are *Sclerotinia sclerotiorum* populations from the tropics more variable than those from subtropical and temperate zones? *Tropical Plant Pathology* **42**, 61–69 (Jan. 2017).
24. Lehner, M. S., de Paula Júnior, T. J., Del Ponte, E. M., Mizubuti, E. S. & Pethybridge, S. J. Independently founded populations of *Sclerotinia sclerotiorum* from a tropical and a temperate region have similar genetic structure. *PloS one* **12**, e0173915 (2017).
25. Attanayake, R. N., Carter, P. A., Jiang, D., del Río-Mendoza, L. & Chen, W. *Sclerotinia sclerotiorum* Populations Infecting Canola from China and the United States Are Genetically and Phenotypically Distinct. *Phytopathology* **103**, 750–761 (July 2013).
26. Kidwell, M. C. *et al.* Badges to Acknowledge Open Practices: A Simple, Low-Cost, Effective Method for Increasing Transparency. *PLOS Biology* **14** (ed Macleod, M. R.) e1002456 (May 2016).
27. *Crop Production 2016 Summary* Accessed: 2017-05-28. Jan. 2017. <<http://usda.mannlib.cornell.edu/usda/current/CropProdSu/CropProdSu-01-12-2017.pdf>>.
28. *Crop Values 2016 Summary* Accessed: 2017-05-28. Jan. 2017. <http://usda.mannlib.cornell.edu/usda/current/CropValuSu/CropValuSu-02-24-2017_revision.pdf>.
29. del Río, L. E. *et al.* Impact of *Sclerotinia* Stem Rot on Yield of Canola. *Plant Disease* **91**, 191–194 (Feb. 2007).
30. Markell, S. *et al.* *Sclerotinia* of Canola. *North Dakota State University Extension*. Publication PP-1410. <<http://library.ndsu.edu/tools/dspace/load/?file=/repository/bitstream/handle/10365/5291/pp1410.pdf>> (2009).
31. Shea, K., Thrall, P. H. & Burdon, J. J. An integrated approach to management in epidemiology and pest control. *Ecology Letters* **3**, 150–158 (Mar. 2000).
32. Billiard, S., López-villavicencio, M., Hood, M. E. & Giraud, T. Sex, outcrossing and mating types: unsolved questions in fungi and beyond. *Journal of Evolutionary Biology* **25**, 1020–1038 (Apr. 2012).
33. Sirjusingh, C. & Kohn, L. M. Characterization of microsatellites in the fungal plant pathogen, *Sclerotinia sclerotiorum*. *Molecular Ecology Notes* **1**, 267–269 (Dec. 2001).
34. Arnaud-Hanod, S., Duarte, C. M., Alberto, F. & Serrão, E. A. Standardizing methods to address clonality in population studies. *Molecular Ecology* **16**, 5115–5139 (2007).

35. Broman, K. *Tools for Reproducible Research* <<http://kbroman.org/Tools4RR/>> (2016).
36. Sparks, A. *et al.* Ecology and Epidemiology in R: Disease Progress over Time. *The Plant Health Instructor*. doi:10.1094/phi-a-2008-0129-02. <<https://doi.org/10.1094/phi-a-2008-0129-02>> (2008).
37. R Core Team. *R: A Language and Environment for Statistical Computing* R Foundation for Statistical Computing (Vienna, Austria, 2017). <<https://www.R-project.org/>>.
38. Nielsen, L. H. *Sharing your data and software on Zenodo* May 2017. doi:10.5281/zenodo.802100. <<https://doi.org/10.5281/zenodo.802100>>.
39. Zhou, F., Zhang, X.-L., Li, J.-L. & Zhu, F.-X. Dimethachlon Resistance in *Sclerotinia sclerotiorum* in China. *Plant Disease* **98**, 1221–1226 (Sept. 2014).
40. Aldrich-Wolfe, L., Travers, S. & Nelson, B. D. Genetic Variation of *Sclerotinia sclerotiorum* from Multiple Crops in the North Central United States. *PLOS ONE* **10** (ed Wang, Z.) e0139188 (Sept. 2015).
41. Phillips, D. V., Carbone, I., Gold, S. E. & Kohn, L. M. Phylogeography and Genotype-Symptom Associations in Early and Late Season Infections of Canola by *Sclerotinia sclerotiorum*. *Phytopathology* **92**, 785–793 (July 2002).
42. Derbyshire, M. *et al.* The Complete Genome Sequence of the Phytopathogenic Fungus *Sclerotinia sclerotiorum* Reveals Insights into the Genome Architecture of Broad Host Range Pathogens. *Genome Biology and Evolution* **9**, 593–618 (Mar. 2017).
43. Langmead, B. & Salzberg, S. L. Fast gapped-read alignment with Bowtie 2. *Nature Methods* **9**, 357–359 (Mar. 2012).
44. Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078–2079 (June 2009).
45. McKenna, A. *et al.* The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Research* **20**, 1297–1303 (July 2010).
46. Staats, M. & van Kan, J. A. L. Genome Update of *Botrytis cinerea* Strains B05.10 and T4. *Eukaryotic Cell* **11**, 1413–1414 (Oct. 2012).
47. Kendall, M. & Colijn, C. Mapping Phylogenetic Trees to Reveal Distinct Patterns of Evolution. *Molecular Biology and Evolution* **33**, 2735–2743 (June 2016).
48. Jombart, T., Kendall, M., Almagro-Garcia, J. & Colijn, C. treespace : Statistical exploration of landscapes of phylogenetic trees. *Molecular Ecology Resources*. doi:10.1111/1755-0998.12676. <<https://doi.org/10.1111/1755-0998.12676>> (May 2017).
49. Wegmann, D., Leuenberger, C., Neuenschwander, S. & Excoffier, L. ABCtoolbox: a versatile toolkit for approximate Bayesian computations. *BMC bioinformatics* **11**, 116 (2010).
50. Kelleher, J., Etheridge, A. M. & McVean, G. Efficient Coalescent Simulation and Genealogical Analysis for Large Sample Sizes. *PLoS Comput Biol* **12**, 1–22 (May 2016).
51. Freeman, S. *et al.* Active learning increases student performance in science, engineering, and mathematics. *Proceedings of the National Academy of Sciences* **111**, 8410–8415 (May 2014).