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COMPUTATIONAL EXPERIENCE

I am an experienced devops engineer of several packages for population genetics, epidemiology, and static web publishing in the R programming language listed below. My goal in software development is to ensure that my applications are **open**, and **accessible** to researchers regardless of computational skills. Above all, I aim to make sure that my software is robust, consistent, and correct through careful design and test-driven development practices.

Developer Practices

Version Control (git), Continuous Integration (GitHub Actions), Unit Testing, Memory Profiling

Cloud/HPC Frameworks

AWS, Sun Grid Engine, SLURM workload manager, Docker, Open Science Framework

Languages

Expert R

Competent BASH, PYTHON, XPATH, XSLT, JAVASCRIPT, C, MAKE, L^AT_EX, PERL

Can Patch C++

Learning RUST, SUPERCOLLIDER

AUTHORED SOFTWARE

Selected R Packages

Maintainer [sandpaper](#) *User interface for The Carpentries Workbench, a portable toolchain to write, build, and deploy accessible lessons in tech using Markdown*

Maintainer [tinkr](#) *Translate Markdown to XML and back again*

Maintainer [poppr](#) *Analysis of populations with mixed reproductive modes*

Maintainer [aweek](#) *Easy conversion of dates to weeks that begin on any day of the week.*

EMPLOYMENT

2020–Present **Lesson Infrastructure Developer**, *The Carpentries*, remote.

I redesigned and transitioned the underlying build process for more than 50 open source and active lessons, which serve more than 10,000 learners annually for [The Carpentries](#) volunteer community. This culminated in the creation and deployment of [The Carpentries Workbench](#), a portable lesson infrastructure, which separated the content of lessons from the build and styling components that has significantly improved the quality of life for the more than 100 Lesson Developers and Maintainer volunteers in The Carpentries.

Products

- [The Carpentries Workbench](#) — A suite of R packages and GitHub Actions to build, maintain, validate, and deploy accessible lessons for data and coding skills.
- [tinkr](#) — An R package in collaboration with [rOpenSci](#) that transforms Markdown to XML and back again. This package is used for validation of markdown elements without regular expressions and is the engine behind the experimental [babeldown](#) package, which provides automated human language translation of Markdown documents using the DeepL API.
- [Carpentries GitHub Actions](#) — Tools for securely provisioning and deploying Carpentries Lessons with arbitrary code on GitHub.
- [Lesson Transition Tool](#) — Automated and flexible transition between Carpentries-style lesson (built with Jekyll) to The Carpentries Workbench. This rearranged folder structure, updated Markdown syntax, and removed unneeded tooling and generated output to reduce the size of the repository and allow the git history to reflect authorship.

Timeline

- **R&D (2020)** — **Research** of the fragmented landscape of build strategies for lessons and, iterating on feedback from the community, **designed** an initial prototype for the lesson infrastructure with deployment strategies.
- **Alpha Testing (2021)** — **Successful alpha test** of prototype, **directed** initial design of website frontend, automated safe and reproducible rendering of literate programming in lessons, and **implemented** first iteration of workflow to automate transition of lessons to new infrastructure.
- **Beta Testing (2022)** — **Released** The Workbench to the community, achieved full feature parity with the former infrastructure, gathered and **iterated on feedback** from early adopters, **coordinated** and initiated **beta testing** phase with official lesson Maintainers and Instructors, and **strategically planned** to seamlessly transition more than 50 official lessons by Spring 2023.
- **Rollout and Capacity Building (2023)** — Finalized beta testing phase, **coordinated the seamless and secure rollout** of The Workbench to all lessons in April–May 2023. **Increased capacity** within The Core Team by **training** three colleagues in R package development and creating [comprehensive developer documentation](#) about The Workbench design and testing practices.
- **Supervisor:** R. Davey

- 2018–2020 **Research Software Engineer**, *Jombart Lab*, ICL, London, UK.
I develop tools and resources for outbreak analytics in all aspects from data validation, analysis, visualization, and reporting.
- Collaborated with MSF (Doctors Without Borders) in the R4EPis project to produce standardized and automated situation report templates for field epidemiologists
 - Created and contributed to packages for outbreak response
 - Taught workshops introducing R to field epidemiologists
 - **Lab Head: Dr. Thibaut Jombart**
- 2017–2018 **Postdoctoral Research**, *Everhart Lab*, UNL, Lincoln, NE.
My projects involve understanding the population genetics and genomics of *Sclerotinia sclerotiorum*, the causal agent of white mold on dry bean.
- Assessed genetic diversity of populations of *S. sclerotiorum* across the United States within white mold screening nurseries and producer fields.
 - Created a pipeline for assembly and filtering of 55 fungicide-exposed isolates of *S. sclerotiorum*.
 - Taught and created a workshop introducing students in the agricultural sciences to data analysis in R.
 - **Lab Head: Dr. Sydney E. Everhart**
- 2012–2016 **Thesis Research**, *Grünwald Lab*, OSU, Corvallis, OR.
I focused on developing software tools for analyzing the population genetics of clonal organisms and demonstrating their applications in a reproducible manner.
- Authored R package for genetic analysis of organisms with mixed reproduction (sexual/clonal) (<https://github.com/grunwaldlab/poppr>)
 - Designed simulation analyses for populations of partially clonal diploid organisms
 - Isolated, maintained, and extracted DNA of *Phytophthora syringae* for the purposes of Genotyping By Sequencing.
 - Analyzed the outbreak of the Sudden Oak Death pathogen, *Phytophthora ramorum* in Curry County, OR.
 - **Research Advisor: Dr. Niklaus J. Grünwald**
- Aug–Dec 2011 **Rotation**, *Jaiswal Lab*, OSU, Corvallis, OR.
Engaged in various research projects combining bioinformatic-based text mining of databases, wet lab, and greenhouse work. **Research Advisor: Dr. Pankaj Jaiswal**
- 2006–2007 **Undergraduate Research Assistant**, *Biology Discipline*, TSU, Kirksville, MO.
As part of a team of undergraduate students, contributed to the annotation of over 2,000 maize genes determined by microarray hybridization analysis to be differentially regulated in the *Zea mays* shoot apical meristem.
- Became proficient in performing and interpreting BLAST and InterProScan searches on sequences, identifying and assessing pertinent primary literature, and using a variety of databases to determine the putative function of maize genes.
 - Collaborated with other researchers on the same project.
 - **Research Mentors: Drs. Brent Buckner and Diane Janick-Buckner**

EDUCATION

- 2018–2020 **Research Software Engineer**, *Imperial College (ICL)*, London, UK.
Department of Infectious Disease Epidemiology

- 2017–2018 **Postdoctoral Scholar**, *University of Nebraska-Lincoln (UNL)*, Lincoln, NE.
Department of Plant Pathology
- 2011–2016 **Ph.D. Plant Pathology**, *Oregon State University (OSU)*, Corvallis, OR.
Defended: 6 December 2016
- 2007 **B.S. Biology**, *Truman State University (TSU)*, Kirksville, MO.
Minor: Chemistry

TEACHING

- 2018–2019 **Introduction to R for Field Epidemiologists**, *Workshop*, RECON.
This series of RECON workshops used classic epidemiological case studies to guide field epidemiologists (who had previously worked in STATA) through a workflow in R, emphasizing good data practices and reproducibility.
- *November 19–20, 2018* at the 2018 ESCAIDE conference in Mater Dei, Malta (60 participants)
 - *October 8–11, 2018* with EPIET Alumni Network in Sofia, Bulgaria (18 participants)
- October 2017 **Reproducible data science for population genetics**, *Workshop*.
The goal of this workshop was to introduce professionals in the biological sciences to the practices of reproducible population genetic data analysis using R. Organized by *PRStatistics*. Course Website: <https://goo.gl/amBbph>
Presented from *2017-10-23* to *2017-10-27* at Margam Discovery Centre, Wales
- Summer 2017 **Introduction to R**, *Workshop*.
I wrote and instructed a three-hour workshop with Dr. Sydney E. Everhart. The goal of the workshop was to give a basic introduction to the R language that included reading data, writing data, and producing figures. <https://everhartlab.github.io/IntroR/>
- *June 14, 2017* North-Central American Phytopathological Society (NCAPS) 2017 Annual Meeting
 - *May 24, 2017* University of Nebraska-Lincoln
- Summer 2016 **Reproducible Research in R**, *Workshop*.
I wrote and instructed a three-hour workshop with Zachary S. L. Foster and Dr. Niklaus Grünwald. The goal of the workshop was to present plant pathologists with the basic tools necessary for performing reproducible science within the R environment. <http://grunwaldlab.github.io/Reproducible-science-in-R/> Presented on *August 1, 2016* at American Phytopathology Society (APS) 2016 National Conference
- Spring 2016 **Graduate Teaching Assistant**, *Botany Dept.*, OSU, Corvallis, OR.
Taught introductory Botany for non-majors focused on emphasizing the role of plants in the environment, agriculture, and society. Two labs of ~30 students.
- Developed lectures, prepared materials, and wrote quizzes for labs each week
 - Proctored all tests and quizzes
 - Graded assignments and provided students with timely feedback
 - Held office hours once a week

2014–2015 **Population Genetics in R, Workshop.**

I wrote and instructed a 4 hour workshop with Drs. Niklaus Grünwald and Sydney Everhart. This workshop introduces tools and concepts that allow researchers to easily perform population genetic analyses in the R statistical environment. <http://grunwaldlab.cgrb.oregonstate.edu/popgen>

- *August 1, 2015* American Phytopathology Society (APS) 2015 National Conference
- *August 9, 2014* American Phytopathology Society (APS) 2014 National Conference
- *May 17, 2014* Oregon State University

Winter 2012 **Graduate Teaching Assistant, Biology Dept., OSU, Corvallis, OR.**

Lead laboratories of ~48 students in organismal diversity, organ systems, plant and animal physiology, genetics, evolution and ecology.

- Developed introductory presentations for quizzes and labs
- Proctored all tests and quizzes
- Graded assignments and provided students with timely feedback
- Held office hours once a week

2009–2011 **English Instructor, Herald NIE, Joong-Dong, Daegu, South Korea.**

Taught basic to intermediate English to Korean students ranging from elementary to middle school with an emphasis on task-based learning techniques.

- Took charge of 18 different classes per week
- Monitored language acquisition of each student via monthly evaluations based on interviews and speaking tests
- Wrote tests, assigned and graded homework pertinent to the level of the students. Initiated and mediated interesting topics for discussion courses

2008–2009 **English Instructor, GnB English, Sangin-2-Dong, Daegu, South Korea.**

Taught basic to intermediate English to Korean students ranging from elementary to middle school in tandem with one of the nine Korean English teachers at the academy.

- Assisted with at least 30 different classes per week
- Monitored language acquisition of students throughout the year
- Gained the ability to be prepared for sudden changes in curriculum and classroom size.

Fall 2006/07 **Undergraduate Teaching Assistant, Biology Discipline, TSU, Kirksville, MO.**

Appointed as teaching assistant for undergraduate cell biology course.

- Helped prepare instructional labs for students of Dr. Diane Janick-Buckner's Cell Biology class
- Responded to student lab questions and referred to professor questions outside of my expertise/knowledge base

COLLABORATIONS

I have taken a leading role in the following inter-organizational collaborations

2018–2020 **The R4EPis Project**, with *RECON* and *MSF*.

This collaboration between MSF (Doctors Without Borders) and the RECON (R Epidemics Consortium) aims to provide a set of situation report templates in RMarkdown with standardized data cleaning and summary statistics for reports on four common outbreak scenarios and three surveys.

- In a constant, iterative process with field epidemiologists, we discussed expectations of input data and appropriate summaries, developed tools or found solutions as appropriate. These were tested on simulated and real-world data by the end users (field epidemiologists).
- Developed system for reviewing templates developed by the technical team and worked with the technical leads to review the templates in a fair and equitable manner
- Wrote tests for numerical and structural accuracy.
- Lead remote collaborative sessions with epidemiologists testing templates on their own data, updating templates and code to avoid common pitfalls.
- Trained contributors in package development and github flow to standardize collaboration
- Website: <https://r4epis.netlify.com>

2018–Present **R Epidemics Consortium**.

This consortium brings together field epidemiologists, software developers, educators, and modellers to help nurture and develop the ecosystem of resources in R for epidemiological analysis and modelling. My role as secretary and software development coordinator is to ensure that R packages and educational resources developed in the consortium are accessible and follow best practices.

- Roles: Secretary and Software Development Coordinator (2018–2020)
- Maintainer of: <https://reconlearn.org>, *aweeek*, and *incidence*
- Expanded [guidelines for package development and github etiquette](#)
- Coordinated and ran several workshops for introduction to R

I was invited to the following collaborative hackathons:

- 2016 **Hackout3**, *Hackathon*, Berkeley Institute of Data Science, June 20–24.
Hackout 3 brought together field epidemiologists, decision makers, modelers and computer scientists to create free, open-source resources for the real-time monitoring of disease outbreaks.
- Tools for detecting near duplicates in line list data designed for data managers on the ground.
 - Tools for data cleaning, and disease modeling.
 - Creation of the R Epidemics Consortium: <http://www.repidemicsconsortium.org/>
- 2014 **Population Genetics in R**, *Hackathon*, NESCent, March 16–20.
The event aimed to help foster an interoperating ecosystem of scalable tools and resources for population genetics data analysis in the popular R platform.
- Website for community contributed tutorials on population genetic analysis in R <http://popgen.nescent.org>
 - New tools for analyzing multiple gene phylogenies in R <http://cran.r-project.org/package=apex>
 - New contributions to the core data structure of the *adegenet* package
 - Special issue of Molecular Ecology: **Population Genomics in R**

SPOKEN LANGUAGES

English **Native**

Korean **Intermediate**

Can manage basic conversation, writing, and reading

OUTREACH, SERVICE, AND EXTRACURRICULAR ACTIVITIES

- 2012–2016 **Radio Host**, *Inspiration Dissemination*, KBVR FM, OSU, Corvallis.
Co-created, produced, and hosted a weekly radio show interviewing graduate students in STEM fields about their research and experiences in graduate school.
- Provided opportunity for graduate students to present their research in a unique form of outreach.
 - Actively worked with graduate students to improve their science communication skills.
 - Assisted undergraduate media students in gaining real world audio post-production experience.
 - Wrote weekly blog post about the week's show at <http://blogs.oregonstate.edu/inspiration>
- 2012–2016 **Active Contributor**, *Bioinformatics Users Group*, OSU.
Contributed presentations and discussions relevant to use of bioinformatics tools such as workflows in the R statistical environment.
- 2012–2014 **Treasurer**, *Graduate Student Association*, Department of Botany and Plant Pathology, OSU.
Balanced the budget, served on bi-annual travel awards committee, helped organize and coordinate group social functions.
- Summer 2005 **Summer Station Manager**, KTRM FM, TSU, Kirksville, MO.
I was the primary authority on personnel decisions, after input from team members. I organized the weekly schedule of DJs, determined the salaries of station directors and balanced a budget.
- 2004–2007 **Radio Announcer**, KTRM FM, TSU, Kirksville, MO.
I ensured successful operation of the transmitter, covered extra scheduled shifts to ensure KTRM stayed on air, and selected appropriate play-lists for listeners.

AWARDS

- 2016 Botany and Plant Pathology Grad. Student Assoc. Travel Award – \$200
- 2016 APS Foundation Student Travel Award – \$500
- 2015 APS Pacific Division Travel Award – \$500
- 2015 OSU Graduate School Travel Award – \$500
- 2015 NESCent Travel award for Population Genetics in R Hackathon – \$650
- 2014 OSU Botany and Plant Pathology Anita Summers Travel Award – \$1000
- 2014 Most Innovative [Radio] Program – Intercollegiate Broadcasting System
- 2013 Seattle Institute For Statistical Genetics Travel Award – \$450
- 2006 Truman State University Summer Research Stipend – \$3000
- 2003 Truman State University Presidential Leadership Scholarship – \$2000

PEER REVIEW SERVICE

I have reviewed for the following journals, including articles describing original research and software applications:

The Journal of Open Source Software, Molecular Plant-Microbe Interactions, Molecular Ecology, Methods in Ecology and Evolution, Phytopathology, Ecology and Evolution, Tropical Plant Pathology, Journal of Aquaculture Research, rOpenSci

PEER REVIEWED PUBLICATIONS

1. Thompson, RN, Stockwin, JE, van Gaalen, RD, Polonsky, JA, **Kamvar, ZN**, Demarsh, PA, Dahlqwert, E, Li, S, Miguel, E, Jombart, T, Lessler, J, Cauchemez, S, Cori, A (2019). Improved inference of time-varying reproduction numbers during infectious disease outbreaks. *Epidemics*, 100356. doi: [10.1016/j.epidem.2019.100356](https://doi.org/10.1016/j.epidem.2019.100356)
2. Polonsky JA, Baidjoe A, **Kamvar ZN**, Cori A, Durski K, Edmunds WJ, Eggo RM, Funk S, Kaiser L, Keating P, Polain de Waroux O, Marks M, Moraga P, Morgan O, Nouvellet P, Ratnayake R, Roberts CH, Whitworth J, Jombart T. (2019) Outbreak analytics: A developing data science for informing the response to emerging pathogens. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 374(1776), 20180276. doi: [10.1098/rstb.2018.0276](https://doi.org/10.1098/rstb.2018.0276)
3. **Kamvar ZN**, Cai J, Pulliam JRC, Schumacher J, Jombart T. Epidemic curves made easy using the R package *incidence* [version 1; peer review: 1 approved, 2 approved with reservations]. F1000Research 2019, 8:139. (doi: [10.12688/f1000research.18002.1](https://doi.org/10.12688/f1000research.18002.1))

software: <https://github.com/reconhub/incidence>
doi: [10.5281/zenodo.1404718](https://doi.org/10.5281/zenodo.1404718)
4. Miorini TJJ, **Kamvar ZN**, Higgins R, Raetano CG, Steadman JR, Everhart SE. (2019) Variation in pathogen aggression and cultivar performance against *Sclerotinia sclerotiorum* in soybean and dry bean from Brazil and the U.S. *Tropical Plant Pathology* 44:73–81 doi: [10.1007/s40858-018-00273-w](https://doi.org/10.1007/s40858-018-00273-w)

data/analysis: <https://github.com/everhartlab/SscPhenoProj>
doi: [10.17605/OSF.IO/2X7FC](https://doi.org/10.17605/OSF.IO/2X7FC)
5. Pannullo A, **Kamvar ZN**, Miorini TJJ, Steadman JR, Everhart SE. (2019) Genetic variation and structure of *Sclerotinia sclerotiorum* populations from soybean in Brazil. *Tropical Plant Pathology*

44:53–64 doi: [10.1007/s40858-018-0266-5](https://doi.org/10.1007/s40858-018-0266-5)

data/analysis: <https://github.com/everhartlab/brazil-sclerotinia-2017>
doi: [10.17605/OSF.IO/E4UPH](https://doi.org/10.17605/OSF.IO/E4UPH)

6. **Kamvar ZN**, Everhart SE. (2019) Something in the agar does not compute: on the discriminatory power of mycelial compatibility in *Sclerotinia sclerotiorum*. *Tropical Plant Pathology* **44**:32–40 doi: [10.1007/s40858-018-0263-8](https://doi.org/10.1007/s40858-018-0263-8)
[Download the un-formatted PDF](#)
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simulations: <https://github.com/everhartlab/sclerotinia-review-2017>
doi: [10.17605/OSF.IO/B8VD3](https://doi.org/10.17605/OSF.IO/B8VD3)

7. **Kamvar ZN**, Amaradasa BS, Jhala R, McCoy S, Steadman JR, Everhart SE. (2017) Population structure and phenotypic variation of *Sclerotinia sclerotiorum* from dry bean (*Phaseolus vulgaris*) in the United States. *PeerJ* **5**:e4152 doi: [10.7717/peerj.4152](https://doi.org/10.7717/peerj.4152)
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data/analysis: <https://github.com/everhartlab/sclerotinia-366>
doi: [10.17605/OSF.IO/EJB5Y](https://doi.org/10.17605/OSF.IO/EJB5Y)

8. Grünwald NJ, Everhart SE, Knaus BJ, **Kamvar ZN**. (2017) Best practices for population genetic analyses. *Phytopathology* **107**:9 doi: [10.1094/PHYTO-12-16-0425-RVW](https://doi.org/10.1094/PHYTO-12-16-0425-RVW)
 9. Tabima JF, Everhart SE, Larsen MM, Weisberg AJ, **Kamvar ZN**, Tancos MA, Smart CD, Chang JH, Grünwald NJ. (2016) Microbe-ID: an open source toolbox for microbial genotyping and species identification. *PeerJ* **4**: e2279 doi: [10.7717/peerj.2279](https://doi.org/10.7717/peerj.2279)
 10. Jombart T, Archer F, Schliep K, **Kamvar ZN**, Harris R, Paradis E, Goudet J, Lapp H (2016). apex: phylogenetics with multiple genes. *Molecular Ecology Resources*. **17**:1 19-26 doi: [10.1111/1755-0998.12567](https://doi.org/10.1111/1755-0998.12567)
 11. **Kamvar ZN**, López-Urbe MM, Coughlan S, Grünwald NJ, Lapp H, Manel S (2016). Developing educational resources for population genetics in R: an open and collaborative approach. *Molecular Ecology Resources*. **17**:1 120-128 doi: [10.1111/1755-0998.12558](https://doi.org/10.1111/1755-0998.12558)
 12. Grünwald NJ, Larsen MM, **Kamvar ZN**, Reeser PW, Kanaskie A, Laine J, Wiese R (2015) First report of the EU1 clonal lineage of *Phytophthora ramorum* on tanoak in an OR forest. *Plant Disease*. **100**:5, 1024-1024. doi: [10.1094/PDIS-10-15-1169-PDN](https://doi.org/10.1094/PDIS-10-15-1169-PDN)
 13. **Kamvar ZN**, Brooks JC and Grünwald NJ (2015) Novel R tools for analysis of genome-wide population genetic data with emphasis on clonality. *Front. Genet.* **6**: 208. doi: [10.3389/fgene.2015.00208](https://doi.org/10.3389/fgene.2015.00208)
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data/analysis: <https://github.com/grunwaldlab/supplementary-poppr-2.0>
doi: [10.5281/zenodo.17424](https://doi.org/10.5281/zenodo.17424)

14. **Kamvar ZN**, Larsen MM, Kanaskie AM, Hansen EM, and Grünwald NJ. (2015) Spatial and temporal analysis of populations of the sudden oak death pathogen in Oregon forests. *Phytopathology*. **105**:7 982-989. doi: [10.1094/PHYTO-12-14-0350-FI](https://doi.org/10.1094/PHYTO-12-14-0350-FI).
-

data/analysis: https://github.com/zkamvar/Sudden_Oak_Death_in_Oregon_Forests
doi: [10.5281/zenodo.13007](https://doi.org/10.5281/zenodo.13007)

15. Weiland JE, Garrido PA, **Kamvar ZN**, Marek SM, Grünwald NJ, and Garzón CD. (2015) Population structure of *Pythium irregulare*, *P. sylvaticum*, and *P. ultimum* in forest nursery soils of Oregon and Washington. *Phytopathology*. **105**:5 684-694. doi: [10.1094/PHYTO-05-14-0147-R](https://doi.org/10.1094/PHYTO-05-14-0147-R)
16. **Kamvar ZN**, Tabima JF, Grünwald NJ. (2014) *Poppr*: an R package for genetic analysis of populations with clonal, partially clonal, and/or sexual reproduction. *PeerJ* **2**: e281. doi: [10.7717/peerj.281](https://doi.org/10.7717/peerj.281)
17. Buckner B, Beck J, Browning, K, Hoxha E, Grantham L, **Kamvar ZN**, Lough A, Nikolova O, and Schnable PS, Scanlon MJ, and Janick-Buckner D. (2007) Involving undergraduates in the annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database. *Genetics* **176**: 741-747. doi: [10.1534/genetics.106.066472](https://doi.org/10.1534/genetics.106.066472)

CONTRIBUTED PRESENTATIONS

1. **Zhian N. Kamvar**. (2022) Building Accessible Lessons with R and Friends. *rstudio::conf(2022)*, Washington DC, USA
slides: <https://bit.ly/BALWRAF>
recording: [Building Accessible Lessons with R and Friends](#)
2. **Zhian N. Kamvar**, François Michonneau. (2021) Using R as a Community Workbench for The Carpentries Lesson Infrastructure. *UseR!* 2021, Online
slides: <https://zkamvar.github.io/user2021>
recording: https://youtu.be/vd8XZSuY_Rs
3. Amrish Baidjoe, Elburg van Boetzelaar, Raphael Brechard, Antonio Isidro Carrión Martín, Kate Doyle, Christopher Ian Jarvis, Thibaut Jombart, **Zhian Kamvar**, Patrick Keating, Anna Kuhne, Annick Lenglet, Pete Masters, Dirk Schumacher, Rosamund Southgate, Carolyn Tauro, Alex Spina, Maria Verdecchia, Larissa Vernier. (2019) Advancing data analytics for field epidemiologists using R: the R4epis innovation project. *UseR!* 2019, Toulouse, FR
slides: <https://bit.ly/2YNAZLx>
4. **Kamvar ZN**, Amaradasa BS, Jhala R, McCoy S, Steadman JR, Everhart SE. (2018) Population structure and phenotypic variation of *Sclerotinia sclerotiorum* from dry bean in the USA. National Sclerotinia Initiative Conference, Bloomington, MN.
doi: [10.6084/m9.figshare.5791713](https://doi.org/10.6084/m9.figshare.5791713)
5. **Kamvar ZN**, Everhart SE, Grünwald NJ. (2017) I Think We're A Clone Now: Factors Influencing Inference of Clonality In Diploid Populations. American Phytopathological Society National Conference, San Antonio, TX.
6. **Kamvar ZN**. (2017) Development and Application of Tools for Genetic Analysis of Clonal Populations. Department of Plant Pathology Seminar Series, University of Nebraska-Lincoln, Lincoln, NE.
7. **Kamvar ZN**. (2017) **Ph. D. Defense Seminar**: Development and Application of Tools for Genetic Analysis of Clonal Populations. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR.

8. **Kamvar ZN**, Brooks J, Grünwald NJ. (2016) Tools for analysis of clonal population genetic data in R. American Phytopathological Society National Conference, Tampa, FL.
url: <https://github.com/grunwaldlab/poppr-poster-aps-2016>
9. **Kamvar ZN**, Larsen MM, Kanaskie AM, Hansen EM, Grünwald NJ. (2015) Evidence for at least two introductions of the sudden oak death pathogen into Oregon forests. American Phytopathological Society National Conference, Pasadena, CA.
url: <https://github.com/zkamvar/Presentation-APS2015>
10. **Kamvar ZN**, Tabima JF, Grünwald NJ. (2014) Application of the R package poppr for analysis of population genetic data. American Phytopathological Society National Conference, Minneapolis, MN.
11. **Kamvar ZN** (2013) **Ph.D. Proposal Seminar:** Determination of pattern and process in the evolution of the plant pathogen *Phytophthora syringae*. Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR.
12. **Kamvar ZN** (2013) *Poppr*: An R package for genetic analysis of populations with mixed (clonal/sexual) reproduction. Biology Graduate Student Symposium, Hatfield Marine Science Center, Newport OR.
13. **Kamvar ZN**, Tabima JF, Grünwald NJ (2013) *Poppr*: An R package for genetic analysis of populations with mixed (clonal/sexual) reproduction. Fungal Genetics Conference, Asilomar, CA.
14. **Kamvar ZN**, Grünwald NJ (2012) *Poppr*: An R package for population genetic analysis. OSU Fall CGRB Conference, Oregon State University, Corvallis, OR.
15. Browning K, Fritz A, Hoxha E, and **Kamvar ZN** (2007) Annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database, Maize Genetics Conference, St. Charles, IL.
16. Browning K, Fritz A, Hoxha E, and **Kamvar ZN** (2007) Annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database, Truman Student Research Conference, Truman State University, Kirksville, MO.