

Zhian N. Kamvar, PhD

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I am a **highly-motivated software engineer** of several published packages for population genetics/genomics, epidemiology, and reproducible publishing in the R programming language. As a **domain expert in computational biology**, software engineer, and a science communicator, I have both the specialist and generalist skillsets needed for **efficient communication** and collaboration between team members with **diverse technical backgrounds**. My goal in software development is to ensure that my applications are **robust** and **accessible** to researchers regardless of computational skills. Above all, I aim to ensure my software is usable, efficient, consistent, and correct through best practices in software development and reproducibility.

TECHNICAL SKILLS

Project Management Highly experienced (**10 years**) in **collaborative development** with Git and GitHub; managing projects, teams, and code review

10 years experience in developing well-tested and **cross-disciplinary scientific software**

Employs **problem-forward** approach to addressing researcher needs through iterative feedback and testing

Developed an easy-to-use **open source lesson infrastructure** over three years

Coordinated communications to hundreds stakeholders in separate sub-communities about the impacts of the new infrastructure

Seamless roll out to **>50 source repositories** maintained by **>100 volunteers** for lessons that serve **>10,000 learners annually**

Languages: **Expert R developer** of several widely used R packages (**10 years**)

Experienced in creating unique **Python 3** modules for population genomic simulation analysis pipeline (**3 years**)

Experienced in parsing structured text content in **XPath** and **Lua** (**3 years**)

Developed GitHub Actions to work with the GitHub (REST and GraphQL) API using BASH, R, and **node JS** (**3 years**)

Experience building **reproducible analysis with CI and Docker** (Kamvar, 2017)

Maintained **reproducible pipelines in Make and BASH** (**2 years**) for both continuous integration and HPC frameworks

Implemented **recursive and bit-level operations in C** to vastly improve speed of R code in the poppr package

Communication: **Coached >100 graduate researchers** to communicate their research to broad audiences in the award-winning radio program, Inspiration Dissemination (<https://blogs.oregonstate.edu/inspiration>)

Developed and delivered material for **9 workshops in 3 disciplines** that reached **>300 people**

Published **19 peer-reviewed publications** including **7 first-author publications**

SELECTED PROJECTS (ON GITHUB)

Workflows: [carpentries/lesson-transition](#) *automated workflow to transform Carpentries-style lessons to new infrastructure*

R packages: [carpentries/sandpaper](#) *user interface to reproducibly build and deploy data science lessons*
[ropensci/tinkr](#) *transform markdown to XML and back again*
[grunwaldlab/poppr](#) *analysis of populations with mixed reproductive modes*

Analyses: [zkamvar/clonal-inference-simulations](#) *simulation-based analysis in Python, R, and BASH*
[everhartlab/sclerotinia-366](#) *fully automated and reproducible analysis in Docker*

COLLABORATIONS

- 2021–Present **Maintainer**, *the tinkr R package*, rOpenSci.
Collaboration with Maëlle Salmon (original author) of rOpenSci to create a lightweight R package to parse and transform Markdown documents to XML. This has been used in **validation** of markdown elements and facilitating **automated human language translation**.
- 2018–2019 **Lead Developer**, *R4Epi Project*, Médecins Sans Frontières (Doctors Without Borders).
Collaborated with **diverse team of developers and field epidemiologists** to create a well-tested series of templates for automated outbreak and survey data analysis.

EMPLOYMENT

- 2020–Present **Lesson Infrastructure Developer**, *The Carpentries*.
Lead development and deployment of a modular infrastructure for building reproducible lessons to bring data science skills to researchers worldwide.
- 2018–2020 **Research Software Engineer**, *Imperial College London*.
Developed well-tested R packages for field epidemiology and modelling
(4 peer-reviewed publications, 1 first-author)
- 2017–2018 **Postdoctoral Researcher**, *University of Nebraska-Lincoln*.
Population genetics of the white mold pathogen *Sclerotinia sclerotiorum*
(4 peer-reviewed publications, 2 first-author)
- 2012–2016 **Graduate Research Assistant**, *Oregon State University*, (Dissertation Research).
Development and application of tools for genetic analysis of clonal populations
(9 peer-reviewed publications, 4 first-author)

QUALIFICATIONS

- 2016 **Ph.D. Botany and Plant Pathology (3.65 GPA)**, *Oregon State University (OSU)*, Corvallis, OR, USA.
Dissertation: Development and Application of Tools for Analysis of Clonal Populations
- 2007 **B.S. Biology**, *Truman State University (TSU)*, Kirksville, MO, USA.

SELECTED PEER-REVIEWED PUBLICATIONS

- **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)
data/analysis: <https://github.com/everhartlab/sclerotinia-366>
doi: [10.17605/OSF.IO/EJB5Y](https://doi.org/10.17605/OSF.IO/EJB5Y)
- **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)

PERSONAL REFERENCES

Robert Davey (supervisor)

Director of Technology
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Kari L. Jordan (colleague, former supervisor)

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