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** to build **reproducible data science lessons**

Coordinated communications to hundereds 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**, *R4Epis 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

2020–2023 **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 Softare 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 *Scleortinia 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
data/analysis: https://github.com/everhartlab/sclerotinia-366
doi: 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

Personal References

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