

Zhian N. Kamvar, PhD

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I am a **highly-motivated software engineer** of several published packages for both population genetics/genomics and epidemiology 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.

TECHNICAL SKILLS

- Curriculum: **5 years experience** in collaborative **open source** lesson development targeted towards **interdisciplinary and diverse audiences**
- Developed lessons for **9 workshops** that reached **>300 people** in international conferences
- Collaboratively developed **5 tutorial websites** in **RMarkdown and blogdown** to host **discoverable lessons for non-technical audiences**
- Trained in **evidence-based** undergraduate STEM teaching (CIRTL)
- Technology: Highly experienced (**8 years**) in **collaborative development with Git and GitHub**; managing teams and code review
- Expert R developer** of several widely used R packages (poppr, aweek, incidence) (**8 years**)
- Maintained **reproducible research compendium in Docker** (**2 years**) under continuous integration (Kamvar *et al.* 2017)
- Experienced in creating unique **Python 3** modules for simulation analysis pipeline (**3 years**)
- Highly experienced with continuous integration (**Travis (6 years), Appveyor, and CircleCI**) for **automated testing** on multiple platforms
- Communication: Highly experienced in **quickly troubleshooting** and resolving **>200 forum questions in community forums** for the poppr and adegenet packages (~1 day turnaround)
- Co-founder and host (5 years)** of award-winning **science communication radio program**, Inspiration Dissemination (<http://blogs.oregonstate.edu/inspiration/>)
- Published **19 peer-reviewed publications** including **7 first-author publications**

LEADERSHIP

- 2018–2019 **Lead Developer, R4Epi Project**, Médecins Sans Frontières (Doctors Without Borders).
Remote collaboration with diverse team of developers and field epidemiologists to create a well-tested series of **templates and tutorials for automated outbreak and survey data analysis**.
- 2018–Present **Coordinator of Software Development**, R Epidemics Consortium (RECON).
Worked with software developers, mathematical modellers, and field epidemiologists to **design quality standards for software development, validation testing, and analysis of epidemiological data**.

SELECTED WORKSHOPS/PRIMERS

- 2014–2015 https://grunwaldlab.github.io/Population_Genetics_in_R.
3-hour workshop on R for population genetic analysis using the *poppr* package.
- 2016–Present <https://popgen.nescent.org>.
Peer-reviewed community-submitted tutorials for population genetic analysis in R
- 2017 <https://everhartlab.github.io/IntroR>.
Introduction to R for plant pathologists including data import, reshaping, and graphics
- 2018–Present <https://reconlearn.org/post/stegen>.
Introduction to R for epidemiologists including data cleaning, graphics, and descriptive analysis

SELECTED PROJECTS (ON GITHUB)

- R package: [grunwaldlab/poppr](#) (maintainer) *analysis of populations with mixed reproductive modes*
- Analysis: [everhartlab/sclerotinia-366](#) *fully automated and reproducible analysis in Docker*

EMPLOYMENT

- 2018–Present **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**, *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**, 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)
- **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)

PERSONAL REFERENCES

Richard G. FitzJohn (colleague)

Research Software Engineer
Department of Infectious Disease Epidemiology
Imperial College London
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Sydney E. Everhart (former postdoc advisor)

Assistant Professor
Department of Plant Pathology
University of Nebraska-Lincoln
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Annick Lenglet (current collaborator)

Epidemiology Adviser
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Thibaut Jombart (line manager)

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