

# Zhian N. Kamvar, PhD

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I am a **highly-motivated software engineer** of several published packages for 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. 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 efficient, consistent, and correct through **test-driven development** practices.

## TECHNICAL SKILLS

- Languages: **Expert R developer** of several widely used R packages (poppr, aweek, incidence) (**8 years**)  
Experienced in creating unique **Python 3** modules for population genomic simulation analysis pipeline (**3 years**)  
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
- Testing: Practitioner of **Test Driven Development**, all packages extensively tested (unit, verification, validation, and regression tests)
- Issue Tracking: Highly experienced (**8 years**) in **collaborative development** with Git and GitHub; managing teams and code review
- Continuous Integration: Highly experienced with **Travis (6 years)**, **Appveyor**, and **CircleCI** for **automated testing** on multiple platforms
- Bioinformatics: Experience with both **Sun Grid Engine (4 years)** and **SLURM (1 year)** **HPC frameworks**  
Developed a Makefile and BASH based **variant discovery pipeline** for paired-end Illumina sequencing data
- Communication: Highly experienced in **quickly troubleshooting** and resolving **>200 forum questions** in user forums for the poppr and adegenet packages (~1 day turnaround)  
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)

- R packages: [grunwaldlab/poppr](#) (maintainer) *analysis of populations with mixed reproductive modes*  
[thibautjombart/adegenet](#) (maintainer) *multivariate analysis of population genetics*  
[reconhub/incidence](#) (maintainer) *aggregation and visualization of disease incidence*  
[reconhub/aweeek](#) (maintainer) *easy conversion between date and week formats*
- Analyses: [zkamvar/clonal-inference-simulations](#) *simulation-based analysis in **Python**, **R**, and **BASH***  
[zkamvar/read-processing](#) *variant discovery from 55 *Sclerotinia sclerotiorum* genomes in **Make***  
[everhartlab/sclerotinia-366](#) *fully automated and reproducible analysis in **Docker***

## TEAMWORK

- 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.
- 2018–2020 **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**.

## 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**, 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

### **Richard G. FitzJohn (colleague)**

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### **Sydney E. Everhart (former postdoc advisor)**

Assistant Professor  
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### **Annick Lenglet (current collaborator)**

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### **Thibaut Jombart (line manager)**

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