Zhian N. Kamvar, PhD

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I am a **highly-motivated software engineer** of several published packages for epidemiology, population genetics/genomics and reproducible reports 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 developement** practices.

TECHNICAL SKILLS

Project Management:	**Lead Developer and Designer** of The Carpentries Workbench, a modular platform for writing and deploying reproducible lessons (**3 years**)
	Coordinated rollout to more than **50 lessons** actively maintained by **over 100 volunteer** maintainers
	Researched, designed, and extensively tested modular infrastructure with key stakeholders over 2 years
	Trained colleagues in skills of R Package development and design philosophy of The Carpentries Workbench
Languages:	**Expert R developer** of several widely used R packages (sandpaper, poppr, aweek, apyramid) (**10 years**)
	Experienced in creating unique **Python** 3 modules for population genomic simulation analysis pipeline (**3 years**)
	Maintained **reproducible pipelines in Make and BASH** (**4 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 (**10 years**) in **collaborative development** with Git and GitHub; managing teams and code review
Continuous Integration:	Highly experienced with **GitHub Actions** workflows and automation
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 expereinced 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:	**The Carpentries Workbench (designer)**	*trio of package for writing and deploying reproducible lessons*
	ropensci/tinkr (maintainer)	*convert Markdown to XML and back again*
	grunwaldlab/poppr (maintainer)	*analysis of populations with mixed reproductive modes*
	thibautjombart/adegenet (maintainer)	*multivariate analysis of population genetics*
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

2020–Present   **Lead Developer and Designer**, *The Carpentries Workbench*, The Carpentries.
Worked with **an international community** to build a robust, flexible, and easy to use lesson infrastructure that allowed them to create and maintain subject-specific lessons on the topics ranging from bioinformatics to library data management to image analyses.

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 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**, *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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