

The Carpentries (c/o Community Initiatives)
1000 Broadway, Suite #480
Oakland, CA 94607, USA

To the recruitment team,

I saw the position for [Lesson Infrastructure Technology Developer](#) via the ROpenSci slack channel and I realized that this position is exactly what I've been looking for. I am a research software engineer at Imperial College London developing R packages, automated workflows, and short-course trainings for field epidemiologists in outbreak scenarios. My background in science communication, **8 years experience developing R packages and tutorials for diverse audiences**, discipline in collaborative software engineering practices (test driven development, GitHub flow, and continuous integration), and eagerness to learn and apply new skillsets makes me an ideal candidate for this position. As an academic looking to transition into technical work in the non-profit sector, I'm excited for this opportunity to apply my skills in open-source software development, evidence-based teaching, and communication to the challenge of strengthening the Carpentries' infrastructure.

My skill set lies in the intersection between software development, reproducible research, open science, and communication. **I have been collaboratively developing open source software on GitHub since 2013.** My most successful software project is the R package *poppr*, which has been **featured in >500 peer-reviewed scientific publications**. I strongly believe this project was successful because I took a 'customer-service' approach. With human-centered design, clear documentation, tutorials, workshops, and diligent forum moderation, this approach **significantly reduced the barrier for population genetic analysis in R.**

My work in lesson and workshop management gives me much of the experience needed to be effective for this role. **Over the past 5 years, I have collaboratively designed 4 introductory workshops** in R programming and reproducible research to **non-technical audiences** with backgrounds in plant pathology, population genetics, and epidemiology. The majority of the workshop participants reported an increase of confidence with their ability to use R for their work.

I am also **keenly aware of the infrastructural challenges of curation, hosting, and discoverability of lessons** from my experience co-maintaining <https://popgen.nescent.org>¹. This website hosts peer-reviewed vignettes of population genetic analyses in R that are automatically built and deployed through continuous integration. Our main goal was to ensure that the **technical barriers for contributors were minimized or eliminated.**

For the last year, **my most rewarding leadership experience** has been as one of the technical leads on the R4EPIS² project—a collaboration between the R Epidemics Consortium (RECON) and Médecins Sans Frontières (MSF)—**I have first-hand experience in working remotely with developers and users** (many of whom were non-technical) to design templates and educational materials to get field epidemiologists using R. We used an iterative human-centered design process to ensure that the templates were built in a way that epidemiologists were comfortable using.

The experience I have gained in the last 5 years have given me the insights and technical knowledge needed for this position. I've been very impressed by the work the carpentries have been doing to make software and data management in research more friendly and accessible and I am excited for this opportunity to become a member of the team. As requested in the instructions, the country in which I pay taxes is the United States of America. I would like to thank the recruitment team for considering my application.

Sincerely,

Zhian N. Kamvar, Ph. D.
Attached: Résumé, references

¹Kamvar, Z.N., LópezUribe, M.M., Coughlan, S., Grünwald, N.J., Lapp, H. and Manel, S. (2017), Developing educational resources for population genetics in R: an open and collaborative approach. *Molecular Ecology Resources*, 17: 120-128. doi:[10.1111/1755-0998.12558](https://doi.org/10.1111/1755-0998.12558)

²<https://R4EPIS.netlify.com>

Zhian N. Kamvar, PhD

Dept. of Infectious Disease Epidemiology
Imperial College London W2 1NY, UK
H +44 7444 840264
B zkamvar@gmail.com
<https://zkamvar.netlify.com>
Twitter: [@zhiankamvar](https://twitter.com/zhiankamvar)

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 user 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](https://github.com/grunwaldlab/poppr) (maintainer) *analysis of populations with mixed reproductive modes*
- Analysis: [everhartlab/sclerotinia-366](https://github.com/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
r.fitzjohn@imperial.ac.uk

Sydney E. Everhart (former postdoc advisor)

Assistant Professor
Department of Plant Pathology
University of Nebraska-Lincoln
everhart@unl.edu

Annick Lenglet (current collaborator)

Epidemiology Adviser
Médecins Sans Frontières (Doctors Without Borders)
Amsterdam, Netherlands
Annick.Lenglet@amsterdam.msf.org

Thibaut Jombart (line manager)

Assistant Professor
Department of Infectious Disease Epidemiology
Imperial College London
thibautjombart@gmail.com