

Dr. Zhian N. Kamvar
Dept. of Infectious Disease Epidemiology
Imperial College London, W2 1NY, UK
December 6, 2019

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>