

Dr. Zhian N. Kamvar
Dept. of Infectious Disease Epidemiology
Imperial College London, W2 1NY, UK
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Computational Biology Program

3181 S.W. Sam Jackson Park Road
Portland, OR 97239

To the recruitment team,

I am applying for the position of Computational Biologist. I am a USAmerican 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 bioinformatic data analysis, **8 years experience developing R packages** for diverse audiences, discipline in **team-oriented and 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. Having worked as both as a scientist and software engineer, I am excited for the opportunity to join the OHSU Computational Biology team to support research that will improve human health.

I have all of the desired qualifications for this position. Not only do I have experience in building **bioinformatic pipelines for high-dimensional genomic data**¹, but I have been developing in R and C since 2012 and currently maintain 5 packages on CRAN. All of these packages are tested under continuous integration and one (poppr²) is featured in >500 scientific publications. **I have a solid foundation in creating automated data-processing pipelines** and all of my published papers have the code and data needed to reproduce the results. My most recent first-author analytical work³ is fully reproducible in a Docker container hosted on DockerHub.

For the last year, as one of the technical leads on the R4EPis project⁴—a collaboration between the R Epidemics Consortium (RECON) and Médecins Sans Frontières (MSF)—**I have first-hand experience in working closely with developers and users** (many of whom were not proficient in R) to design code and tests against pathologies unique to epidemiological data. We used validation tests, continuous integration, and code review on GitHub to ensure the quality of contributed code.

This position will be immensely beneficial to my growth as both a bioinformatician and reserach software engineer by giving me the challenges of working on problems that can have a positive impact human health. My background in quantitative science, robust software development, and experience as both a developer and user makes me well-suited to join the OHSU team as a computational biologist. Thank you for your time and consideration, I look forward to hearing from you.

Sincerely,

Zhian N. Kamvar, Ph. D.

Attached: Resumé, references

¹Automated Illumina assembly pipeline: <https://github.com/zkamvar/read-processing>

²R package 'poppr': <https://grunwaldlab.github.io/poppr>

³**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)

⁴<https://r4epis.netlify.com>