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Dr. Zhian N. Kamvar
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Genentech Pharmaceuticals
Data Science and Statistical Computing Group South San Francisco, CA

To Michael and the recruitment team,

I was recommended to apply to the Bioinformatics Software Engineer III position[1] by a colleage of mine, Pawe Pitkowski. He mentioned that the position aligned well with my skill set and, after reading the job description, I must agree. 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 bionformatic data analysis, **8 years experience developing R packages** for diverse audiences, discipline in collaborative software engineering practices (object orientation, test driven development, GitHub flow, and continuous integration), and eagerness to learn and apply new skillsets makes me an ideal candidate for this position. I am excited for this opportunity to join the Genentech team to bring creative solutions to the challenging problems of drug discovery and other bioinformatics challenges to improve human health.

I have all of the desired qualifications for this position. Not only do I have experience in building bioinformatic pipelines, but I have been developing in R and C since 2012 and currently maintain 8 packages on CRAN. All of these packages are tested under continuous integration and one (poppr) is featured in >500 scientific publications. **I have a solid foundation in automated pipelines** and all of my published papers have the code and data needed to reproduce the results. My most recent first-author analytical work, Kamvar *et al.* 2017, is fully reproducible in a Docker container hosted on DockerHub.

The idea of working as a software engineer in bioinformatics is quite appealing to me because this sits at the intersection of two topics I've been passionate about for the past six years: reproducible research and robust software applications. I am keenly aware of the value of sustainable software engineering practices to support improvement of new and legacy codebases. One concrete example is from 2015 when a major version update to a dependency for poppr caused much of its functionality to fail, my test suite allowed me to safely refactor to adapt to the update. **I am passionate about interdisciplinary collaborations**. For the last year, as one of the technical leads on the R4EPIs project—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 define verification 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.

As my carreer focus has shifted from investigative research to scientific software engineering, this position will be immensely beneficial to my trajectory as a research software engineer. My background in quantitative science, robust software development, and experience as both a developer and user makes me well-suited to join the Genentech team as a bioinformatics software engineer. Thank you for your time and consideration, I look forward to hearing from you.

Sincerely,

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

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[1]https://www.gene.com/careers/detail/201908-124116/Bioinformatics-Software-Engineer-III