A crisis of reproducibility has been hitting science headlines in recent years, often laden with finger-pointing at poor statistical practices. Yet, as more disciplines come to rely on custom software for scientific data analysis, the role of poor software engineering practices has become more noticeable. We will discuss how tools and practices from software engineering can help to improve the reproducibility of scientific computing, with a specific look at emerging best practices in computational biology and bioinformatics. In addition to sharing some experiences about life in interdisciplinary research, I will highlight some of my work in applying Bayesian machine learning models to analyze single-cell RNA-sequencing data.

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