

Statement on Sharing / Code and Data Dissemination / Collaboration

We commit to making all scripts, code, and software available via github under the permissive MIT license consistent with the standard operating procedures of the Goff Lab. Each software package and analysis will have an independent, open-source repository for coordinating development with collaborators. Proposed work in benchmark data annotation, model identification and characterization, and analysis will also be conducted on a publicly available github repository as they are generated. Additional communication/coordination will be through Slack, Github Issues, and Pull Requests as required. The proposal has been developed in the open in conjunction with the proposed collaborative network and is currently publicly shared at <https://github.com/gofflab/czi-rfa-2017/>. Additional collaboration in the development of this joint proposal was conducted on Slack. We acknowledge that the final proposal will be made public and submitted to a specific Github repository / wiki established by CZI. All primary and benchmark data will be deposited with the HCA data coordination platform, as well as freely accessible online, and archived on the NCBI short read archive along with all available metadata. Learned basis vectors, workflows, and analyses will be publicly available on a custom web site, archived in conjunction with published manuscripts, and posted to Biorxiv. Stable software builds will be released in the ProjectoR package through the Bioconductor project. Any experimental protocols developed will be deposited with Protocols.io. Preprints derived from this work will be made available through BioRxiv at the time of submission for publication and any published works will cite the CZI grant number for this proposed project as requested.