

Dear CCGP Investigators,

The CCGP bioinformatics team at UCSC has **revised their metadata intake instructions** for non Mini-Core submitted sequencing data. This covers any samples that you sequenced yourselves as part of the CCGP. Previously, we used NCBI forms for metadata submission, but we are moving to a more concise and streamlined process. We expect this will reduce the time it takes to fill out the metadata form when you submit data and greatly reduce the number of errors the data wrangling team needs to handle. Please refer to the <u>updated webpage</u> for instructions on how to submit data.

New WGS metadata intake instructions

As a reminder, you must submit your sequencing data to the bioinformatics team as soon as you receive your data from the UC sequencing core. These links expire quickly, so it is essential that you submit the data as soon as you receive it.

As always, don't hesitate to reach out to the bioinformatics team members <u>Erik</u> <u>Enbody</u> and <u>Mara Baylis</u> if you have any questions.

Reminder of WGS data plan:

We would like to remind you to please share any existing whole genome resequencing data with the CCGP Bioinformatics team as soon as possible.

The WGS short read data will be uploaded to NCBI Short Read Archive (SRA) with current embargo until 2025. It will remain private until either the PI chooses to release the data, or shortly before the planned submission of the first synthetic CCGP publication, whichever comes first.

Once processed, the Bioinformatics team will run the data through their pipeline for alignment, filtration and variant calling. If you are curious, <u>click here</u> to see a visual representation of their pipeline. Your team will then receive VCF files and various quality metrics and visualizations.

As always, we appreciate your participation and collaboration and please don't hesitate to reach out if you have questions or concerns.

-The CCGP Team

California Conservation Genomics Project

www.ccgproject.org



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