Scripps Research

Center for Computational Biology and Bioinformatics (CCBB)
2024

Pricing

Organization	CCBB Hourly Rate
Scripps Internal	$125.00
External non-profit	$250.00
External for-profit	$312.50

CCBB services: Genomics

- Exome, Whole Genome sequencing data analyses, SNPs, indels, CNVs

Whole Genome sequencing

Requirements:

1) Each sample in your project should have recommended read depth.
2) Number of sample submitted are less than 20
3) Sample metadata (sample descriptions) shared with CCBB prior to sequencing
4) Tumor / normal pairs (if any)
5) Reference genomes considered as standard: human, mouse, rat

Standard analysis (CCBB effort level - 2 to 4 hours; 3-5 business days)
Alignment to standard reference genome (human/mouse/rat)

Additional analysis (consult CCBB for effort level and timeline for completion)
Help with visualization of alignments
Custom analysis based on alignment data (.bam) files

SNPs/indels/CNVs (CCBB effort level - 5 hours; 3-5 business days)

Standard analysis
nf-core/sarek workflow to detect variants on whole genome or targeted sequencing data: Data processing uses GATK4 best practices for alignment to reference genome using BWA, Mark Duplicates,Base (Quality Score) Recalibration steps. Variant Calling (germline/somatic variants specific software), Annotation and QC plots/tables provided.

Additional analysis (consult CCBB for effort level and timeline for completion)

Email to ccbb.at.scripps.edu to set up a consultation meeting for additional service(s)

Additional services: Consult CCBB to get a quote/estimation of effort in hours. CCBB service hourly charges apply.

- Software development, custom pipeline implementation
- Re-analysis of older dataset
- Analysis for public dataset
- Specific figures/tables for publications; writing methods section or contribution for scientific papers/grant proposals
- Functional Analysis using Advaita/GSEA/SetRank
- Letter of Support for grants
- GEO/SRA submissions