

UC San Diego Center for Computational Biology & Bioinformatics

Scope of Work 2021 ChIP-Seq/ATAC-Seq Analysis

UCSD Internal rate: \$180/hour

Non-profit rate: \$261/hour

For-profit rate: \$362/hour

Costs below shown for UCSD internal rate

Primary Analysis

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: Bowtie or STAR)
3. Quality control of aligned data (method: RSeQC)
4. Peak calling (method: HOMER/MACS)

Cost:

ChIPseq: \$90/sample for ≤ 20 samples ; \$45/sample for any additional samples above 20 (bulk rate)

ATACseq: \$360/sample

Secondary Analysis

1. Assessment of experimental design and analysis design
2. Differential peak calling (method: Homer, DESeq2, limma, DiffBind)
3. Functional enrichment analysis & pathway analysis

Cost: \$3,600-\$7,200 depending on complexity of design

Data Overlay

1. Assessment of second data set and methods for data overlay (~\$180-\$900)
2. Correlate results and other dataset (~\$1,800-\$4,500)
3. Overlay results and other dataset on significantly dysregulated pathways (~\$900-\$1,800)

Deliverables:

1. Consultation meeting to discuss experimental design, biological questions and analysis
2. Results files from all analyses outlined
3. Open source code from all analyses
4. Summary powerpoint presentation of all results
5. Post-analysis meeting to discuss results