HPC Core: Bioinformatics Analysis Rate 2025 Fall

Category	Analysis Type	Pricing Basis	Internal Rate (USD)	NextLab Rate (USD)	External Profit Rate (USD)	Description	Pipeline Outline
Bioinformatics Consulting	Custom project	Per hour	$55	$83	$165	Bioinformatics guidance, support, and solution	Experimental design, literature review, determination of best practices, methods recommendations, results interpretation
AI/ML Consulting	Custom project	Per hour	$55	$83	$165	Artificial Intelligence (Machine learning and deep learning) guidance, support, and solution	Experimental design, literature review, determination of best practices, methods recommendations, results interpretation
Data Analysis Consulting	Custom project	Per hour	$55	$83	$165	Data analysis guidance, support, and solution	Experimental design, literature review, determination of best practices, methods recommendations, results interpretation
Genomics	Whole Genome Sequencing (WGS)	Per sample	$250	$375	$750	Comprehensive detection of genetic variants across the entire genome, including single-nucleotide changes and larger structural alterations.	FASTQ QC → adapter trimming → BWA-MEM alignment & duplicate marking → post-alignment QC → GATK variant calling → basic CNV/SV screening → VEP/ANNOVAR annotation → QC report & consult
	Whole Exome Sequencing (WES)	Per sample	$230	$345	$690	Identification and annotation of coding-region variants	FASTQ QC → trimming → alignment (BWA-MEM) → post-alignment QC → GATK variant calling (exome

						in your sample's exome.	targets) → annotation → summary report & consult
	Targeted Gene Sequencing	Per sample	$250	$375	$750	Focused analysis of specified gene panels to detect known or novel mutations in selected genes.	FASTQ QC → trimming → alignment to panel regions → variant calling on target genes → annotation → QC/variant summary
	Copy Number Variation (CNV) Analysis	Per sample	$200	$300	$600	Detection of genomic regions with gains or losses (copy number changes) from your sequencing data.	Alignment (or use provided BAM) → CNVkit/ExomeDepth CNV calling → manual review → gene annotation → QC metrics & report
	Structural Variant (SV) Analysis	Per sample	$210	$315	$630	Identification of larger genomic rearrangements such as deletions, duplications, inversions, and translocations.	Alignment (or use provided BAM) → Manta/LUMPY SV calling → filter high-confidence SVs → annotate breakpoints → QC report
	Genome-Wide Association Study (GWAS)	Per hour	$55	$83	$166	Statistical association analysis linking genetic variants to traits or diseases in large cohorts.	Genotype QC (PLINK) → PCA for stratification → optional imputation (Minimac/Beagle) → association testing → multiple testing corrections → Manhattan/QQ plots
	Whole Genome Assembly	Per sample	$250	$375	$750	Bioinformatics guidance, support, and solution with literature Review, Methods Survey, & Tool Recommendation	Generation of a high-quality draft genome sequence, including annotation of genes and genomic features.
Epigenomics & Accessibility	Methylation & Epigenomics Analysis	Per sample	$250	$375	$750	Analysis of DNA methylation or histone	WGBS alignment (Bismark) or array processing → DMR analysis (BSseq/DSS) → peak

						modification patterns to study gene regulation and epigenetic changes.	calling for ChIP-Seq → DMR/peak annotation → QC reports & interpretation
	Chromatin Accessibility (ATAC-Seq)	Per sample	$250	$375	$750	Mapping open chromatin regions to identify regulatory elements and transcription factor binding sites.	FASTQ QC → trimming → alignment (Bowtie2/STAR) → Tn5 cut-site & peak calling (MACS2) → differential accessibility (DiffBind) → QC metrics → report
Transcriptomics	Bulk RNA-Seq Analysis	Per sample	$250	$375	$750	Quantitative profiling of gene expression across whole samples to identify differentially expressed genes.	FASTQ QC → trimming → alignment (STAR/Hisat2) → gene quantification (featureCounts/RSEM) → differential expression (DESeq2/edgeR) → QC plots → summary report
	Single-Cell RNA-Seq (scRNA-Seq) Analysis	Per sample	$260	$390	$780	High-resolution, cell-by-cell gene expression profiling to identify distinct cell populations and their marker genes.	FASTQ QC → Cell Ranger/STARsolo quantification → filtering & QC → normalization (SCTransform) → PCA+UMAP → clustering & annotation → differential expression → QC report
	De Novo Transcriptome Assembly & Annotation	Per sample	$200	$300	$600	Construction of a reference transcriptome for organisms without a reference genome, including functional annotation of transcripts.	Read QC → de novo assembly (Trinity/Velvet) → transcript clustering (CD-HIT) → functional annotation (Trinotate) → assembly quality (TransRate) → summary report
	Spatial Transcriptomics Analysis	Per sample	$280	$420	$840	Mapping gene expression patterns to	bustools) → image registration (Giotto/STUtility) → spot QC

						their spatial locations within tissue sections to reveal tissue architecture and microenvironments.	→ normalization & clustering (Seurat/Scanpy) → spatial gene detection → deconvolution → visualization → pathway enrichment → report & consult
	MicroRNA (miRNA-Seq) Analysis	Per sample	$220	$330	$660	Profiling of small non-coding RNAs (microRNAs) to study their expression and regulatory roles.	Adapter trimming → alignment (miRDeep2/STAR) → miRNA quantification → differential analysis (DESeq2) → QC metrics → summary report
	Long Non-Coding RNA (lncRNA-Seq) Analysis	Per sample	$230	$345	$690	Measurement of long non-coding RNA expression levels to study their potential functions in biology.	FASTQ QC → alignment to transcriptome (STAR) → quantification (featureCounts/RSEM) → differential analysis (DESeq2) → QC report
	Alternative Splicing Analysis	Per hour	$55	$110	$220	Identification and quantification of different splice isoforms to understand transcript diversity.	STAR 2-pass alignment → isoform assembly (StringTie/Cufflinks) → junction quantification (rMATS/LeafCutter) → differential splicing → sashimi plots → report
Metabolomics & Lipidomics	Untargeted Metabolomics Analysis	Per sample	$250	$375	$750	Comprehensive profiling of small-molecule metabolites to discover differences between sample groups.	Feature detection (XCMS/MZmine) → peak alignment & annotation (HMDB) → statistical analysis (MetaboAnalyst) → pathway enrichment → QC → summary report
	Targeted Metabolomics Analysis	Per sample	$250	$375	$750	Quantitative measurement of predefined metabolites using targeted assays.	Targeted feature extraction → calibration curve integration → quantification → QC (internal standards) → statistical summary → pathway annotation
	Lipidomics Analysis	Per sample	$250	$375	$750	Identification and	Lipid feature detection → annotation (LIPID MAPS) →

						quantification of lipid species to study lipid metabolism and related pathways.	differential abundance → QC (calibration) → pathway & network analysis → summary report
Metagenomics & Microbiome	Shotgun Metagenomics Analysis	Per sample	$280	$420	$840	Genome-scale profiling of microbial community composition and function in complex samples.	FASTQ QC → host read removal (KneadData) → taxonomic profiling (Kraken2/MetaPhlAn3) → optional assembly → functional profiling (HUMAnN3) → diversity metrics → summary report
	16S rRNA Sequencing Analysis	Per sample	$280	$420	$840	Targeted sequencing of bacterial 16S rRNA genes to analyze microbial community structure and diversity.	Demultiplex & QC (QIIME2/DADA2) → ASV/OTU calling → taxonomic assignment (SILVA/Greengenes) → alpha/beta diversity → differential abundance → summary report
	Metatranscriptomics Analysis	Per sample	$250	$375	$750	Profiling of active microbial gene expression to understand functional activities in environmental or host-associated samples.	rRNA depletion QC → FASTQ QC → alignment (Salmon) → functional annotation (eggNOG-mapper) → differential expression → pathway enrichment (KEGG) → summary report
Proteomics & PTM	Mass Spectrometry Proteomics Analysis	Per hour	$55	$83	$166	Global analysis of protein abundance and differential expression using mass spectrometry data.	Raw file to mzML → database search (MaxQuant/Proteome Discoverer) → FDR filtering & quantification → differential protein analysis → pathway enrichment → summary report
	Post-Translational Modification (PTM) Analysis	Per hour	$55	$83	$166	Identification and quantification of protein modifications such as	Variable modification search → site localization scoring (PTMProphet) → quantification → functional annotation → summary report

						phosphorylation to study signaling pathways.	
	Protein-Protein Interaction (PPI) Analysis	Per hour	$55	$83	$166	Mapping and analysis of protein interaction networks to identify key partners and functional modules.	Integrate PPI databases (STRING/BioGRID) → network construction & analysis (Cytoscape) → module detection → pathway identification → report
Structural Bioinformatics	Homology Modeling	Per protein	$55	$83	$166	Building 3D models of proteins based on known structures to predict structure-function relationships.	Template search & alignment (BLAST/HHblits) → model building (MODELLER/SWISS-MODEL) → refinement & energy minimization → validation (Ramachandran/QMEAN) → report
	Molecular Docking	Per protein	$55	$83	$166	Predicting how small molecules bind to target proteins for virtual screening or lead optimization.	Receptor prep → ligand library prep → docking runs (AutoDock Vina/Glide) → rescoring (MM-GBSA) → visualization of top hits → summary report
	Molecular Dynamics (MD) Simulation	Per protein	$55	$66	$73	Simulating atomic motions of biomolecules to study dynamics and stability over time.	System setup (solvation/ion placement) → parameterization → equilibration & production (GROMACS/NAMD) → trajectory analysis → report
	QM/MM Simulations	Per protein	$55	$83	$166	High-accuracy quantum/classical simulations to investigate enzyme mechanisms or reaction energetics.	Partition QM/MM → QM setup (basis set) → QM/MM run (Gaussian/ORCA with GROMACS) → energy profile analysis → report
Functional Genomics	CRISPR Screening Analysis	Per sample	$110	$165	$330	Identifying genes essential for a	FASTQ QC → mapping to sgRNA library (MAGeCK) → hit calling & statistics → off-

						phenotype via pooled CRISPR knockout or activation screens.	target checks → pathway enrichment → summary report
	RNAi Screening Analysis	Per sample	$110	$165	$330	Screening gene knockdowns via RNA interference to discover gene functions or drug targets.	FASTQ QC → mapping to shRNA library → dropout score calculation → hit calling → summary report
	Gene Expression Perturbation Analysis	Per sample	$110	$165	$330	Assessing gene expression changes after treatments or perturbations to understand biological responses.	Differential expression (DESeq2) → pathway enrichment (clusterProfiler) → optional regulatory network inference → summary report
	Gene Regulatory Network (GRN) Analysis	Per hour	$250	$375	$750	Constructing and analyzing gene networks to uncover regulatory relationships between genes.	Data normalization (voom/SCTransform) → network inference (ARACNe/WGCNA/GENIE3) → module detection → validation → report
Clinical Trial & Statistics	Survival Analysis	Per hour	$55	$83	$166	Analyzing time-to-event data to estimate survival probabilities and risk factors.	Data cleaning/censoring → Kaplan–Meier curves → Cox proportional hazards modeling → assumption checks → report
	Bayesian Statistical Analysis	Per hour	$55	$83	$166	Performing statistical inference with Bayesian methods to quantify uncertainty in model parameters.	Model specification (priors/likelihood) → MCMC sampling (Stan/JAGS) → convergence diagnostics → posterior predictive checks → report
	RCT Analysis (Randomized Controlled Trials)	Per hour	$55	$83	$166	Statistical analysis of clinical trial data to compare treatment	Data cleaning/randomization checks → ITT vs PP modeling → mixed-effects models for longitudinal outcomes → multiplicity adjustments → report

						effects and account for study design complexities.	
	Adaptive Clinical Trial Analysis	Per hour	$55	$83	$166	Planning and analyzing adaptive trial designs that allow modifications based on interim results.	Interim analysis design & simulations → type I error control & sample size recalculation → interim execution → operating characteristics simulation → report

Charge Per Sample with Biological Replicates & Time Points

- Biological Replicates: Each independent sample (e.g., different individuals, cell lines) counts as one sample for analysis pricing.
- Time Points: If analyzing the same sample across multiple time points, each time point is considered as a separate dataset.

Example Calculation:

- Experiment: 3 replicates × 3 time points = 9 data files
- RNA-Seq Analysis (Bulk RNA-Seq: $250/sample) → 9 × $250 = $2250 total
- Single-Cell RNA-Seq Analysis ($300/sample) → 9 × $260 = $2340 total

Notes:

- All rates assume the client provides raw reads from sequencing platforms, raw FASTQ files, or aligned BAMs (and TIFFs for spatial). Wet-lab (extraction, library prep, sequencing, imaging) completed separately.
- Compute costs are absorbed in these rates. External nonprofit rates are 20% added to internal rates, and an extra 10% added for external profit rates.
- The pipeline description of the column is a potential list of tools and open-source packages. It does not contain any pricing based on any proprietary software, and pipeline modification is determined as per request.