

Bioinformatics and Computational Multi-Omics Support Model

Our goal is to make bioinformatics support easy to access while also creating a sustainable model. Our aim is to remain flexible and easy to work with. A clearly defined analysis using established methods is best handled through a straightforward fee-for-service model. A project that requires substantial exploration, integration, methodological development, or continued scientific input is better approached as a scientific collaboration with appropriate grant-supported effort. We encourage investigators to contact us early, including at the idea, pilot, or grant-planning stage.

1. Initial Consultation

The initial consultation is provided at no charge. We will review the biological question, study design, available or planned data, metadata, data quality, expected deliverables, and computational requirements. After this discussion, we will recommend whether the project is best handled as a defined analytical service or as a scientific collaboration.

2. Defined Analysis / Fee-for-Service

Fee-for-service is most appropriate when the scientific question and deliverables are clearly defined, data and metadata are reasonably complete, data quality is acceptable, established workflows can address the question, and minimal troubleshooting or custom method development is expected. Examples include standard bulk RNA-seq, single-cell RNA-seq, ATAC-seq, ChIP-seq, variant analysis, pathway/enrichment analysis, and re-analysis of existing datasets. We will provide an estimate of expected effort and deliverables.

Proposed Internal Rates

- Faculty / Scientific Director: \$150/hour
- Senior Bioinformatics or Computational Scientist: \$110/hour
- Bioinformatics Analyst: \$85/hour

Whenever practical, we will provide a project-level estimate rather than open-ended hourly billing.

3. Scientific Collaboration

A collaborative model is more appropriate when computational work becomes an integral part of the scientific project. This includes substantial data-quality problems or data rescue, exploratory analysis, multi-omics or multi-dataset integration, large cohort or consortium-scale data, machine learning, custom algorithms, repeated rounds of analysis and experimental refinement, or substantial involvement in biological interpretation, figures, manuscripts, and future study design. For these projects, percent effort on the grant is generally preferable to repeated hourly billing. The appropriate effort should reflect the scope and duration of the computational and scientific contribution.

4. Pilot and Exploratory Projects

We want investigators to be able to explore new ideas before committing substantial resources. Small pilot projects may receive limited exploratory support based on project scope, scientific value, available resources, and team capacity. This may include initial QC, feasibility assessment, preliminary analysis, testing a computational approach, or generation of preliminary figures for pilot applications. If a pilot develops into a larger project, we can transition it to either fee-for-service or a longer-term collaborative model.

5. Grant Development

We encourage investigators to involve the bioinformatics team during grant development, particularly for NIH, DoD, foundation, and other major applications. Support may include study and sequencing design, computational analysis plans, multi-omics strategies, preliminary analysis, methods development, computational-resource planning, budget preparation, and letters of support.

For funded projects requiring ongoing bioinformatics involvement, appropriate percent effort should be included in the grant. Pilot and smaller grants can be handled more flexibly, with support scaled to the available budget and scientific goals.

6. Data Processing, Computing, and Storage

Standard fee-for-service estimates include routine data processing required to complete the agreed analysis and temporary working storage during active analysis. This generally includes routine data transfer and organization, preprocessing and QC, computational processing on available institutional resources, and temporary storage of raw, intermediate, and processed files while the project is active.

Projects requiring unusually large computing resources, extensive cloud computing, specialized commercial software, or very large datasets may require a separate estimate.

7. Extended Storage and Additional Computational Resources

Long-term storage is separate from routine analytical support. If investigators need data retained beyond the normal project period, we can work with them to identify an appropriate institutional, cloud, or project-supported storage option.

Additional costs may apply for long-term storage of large genomic datasets, cloud computing, specialized GPU/HPC use, commercial software licenses, dedicated computational environments, or direct team access to additional computational resources. These needs will be discussed before substantial costs are incurred.