BCG Full Service Pipelines

Qualified members of the Bioinformatics Consulting Group (BCG) can perform standardized analyses for a minimal fee. Each pipeline is a “best practices” implementation of commonly cited, open-source tools and techniques appropriate to the data provided and questions asked. These pipelines may be similar to the self-service pipelines maintained by the BioITeam, but by having one of our Consultants run the pipeline you can be assured that:

- Data quality will be interpreted by experienced bioinformaticians
- Any errors in the pipeline will be addressed by experts
- Parameters will be adjusted appropriately (and with your input if necessary)
- Additional training and/or interpretation can be provided in the context of your project (at additional cost)
- Pipelines may be customized or extended as required for a particular project (at additional cost)

All costs are based on currently approved Service Center rates and the actual amount of labor required for the project. Projects are billed when complete or monthly, whichever comes first. A minimum of four hours of time is assumed for each pipeline. Larger datasets, more complicated experimental designs, or additional interpretation and/or training time can be easily accommodated.

Full service pipelines available

**DNA-Seq Variant Calling Pipeline**: Identification and annotation of SNPs and/or somatic mutations compared to reference genome. 10 hour minimum ($730 internal, $930 external) per project.

**RNA-Seq Analysis Pipeline**: This pipeline uses an annotated genome to identify differential expressed genes/transcripts. 10 hour minimum ($730 internal, $930 external) per project.

**RNA-Seq Downstream Analysis**: Machine learning methods (including clustering, dimensionality reduction, classification and regression modeling, resampling techniques, etc.), ANOVA modeling, and empirical Bayes analysis. 12 hour minimum ($876 internal, $1116 external) per project. This includes 1 hour of training, if needed.

**ChIP-Seq Peak Calling Pipeline**: This pipeline identifies regions of significant protein binding (“peaks”) based on an annotated genome. 10 hour minimum ($730 internal, $930 external) per project.

**Transcriptome Assembly**: Assembly of RNA-seq short reads into a transcriptome. 12 hour minimum ($876 internal, $1116 external) per project.

Rates

Internal customers (payment from a UT Austin account): $73/hour

External customers (anyone paying from a non-UT Austin account): $93/hour

Where to go from here

Email the Consultants at bcg@utgsaf.org with a brief description of your project and analysis needs.