UC San Diego Center for Computational Biology & Bioinformatics

Scope of Work
2020
DNA-seq Analysis

UCSD Internal rate: $180/hour
Non-profit rate: $261/hour
For-profit rate: $362/hour

*For whole genome sequencing, compute and storage cost is passed directly to the investigator. Compute cost averages ~$45/sample for GATK germline variant calling and ~$60/pair of samples for MUTECT somatic variant calling.
**HIPAA-compliant compute is available through iDASH (https://idash.ucsd.edu/cyberinfrastructure) or Amazon Web Services (https://aws.amazon.com/compliance/hipaa-compliance/) for an additional compute cost (~$135/sample for GATK on AWS).

Primary Analysis

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: BWA)
3. Quality control of aligned data (method: RSeQC)
4. Variant calling (method: GATK or MUTECT)
5. Variant annotation (method: ANNOVAR and myVariant.info)

Cost: Whole exome primary analysis $180/sample; Whole genome primary analysis $360/sample (inclusive of compute cost for < 20 samples. >20 samples compute passed directly to customer and bulk rate of 40-80 hours plus compute for <200 samples)

Secondary Analysis

1. Variant prioritization (method: custom variant filtering and prioritization) (0.5 hours/sample)
2. Functional enrichment analysis, pathway analysis and data overlay of variants on significantly dysregulated pathways (method: Hypergeometric test in ToppGene) (0.5 hours/sample)

Cost: Hourly

Other options

1. Assessment of second data set and methods for data overlay (~2-5 hours)
2. Correlate variants with other data types (~10-25 hours)
3. Overlay DNA-seq results on significantly dysregulated pathways (~5-10 hours)
4. Differential network analysis (~25-40 hours)
5. Structural variants (hourly)
6. Copy number variants (hourly)
7. Custom algorithms and pipelines (hourly)

Cost: Hourly

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. Post-analysis meetings to discuss results