

Task Menu

The Task Menu lists all the tasks that can be performed on a specific node. It can be invoked from either a **Data** or **Task node** and appears on the right hand side of the *Analyses* tab. It is *context-sensitive*, meaning that it will only present tasks that the user can perform on the selected node. For example, selecting an *Aligned reads* data node will not present aligners as options.

Clicking a **Data node** presents a variety of tasks:

- Data summary report
- QA/QC
 - Pre-alignment QA/QC
 - ERCC Assessment
 - Post-alignment QA/QC
 - Coverage Report
 - Validate Variants
 - Feature distribution
 - Single-cell QA/QC
 - Cell barcode QA/QC
- Pre-alignment tools
 - Trim bases
 - Trim adapters
 - Filter reads
 - Trim tags
- Post-alignment tools
 - Filter alignments
 - Convert alignments to unaligned reads
 - Combine alignments
 - Deduplicate UMIs
 - Downscale alignments
- Annotation/Metadata
 - Annotate cells
 - Annotation report
 - Publish cell attributes to project
 - Attribute report
 - Annotate Visium image
- Pre-analysis tools
 - Generate group cell counts
 - Pool cells
 - Split matrix
 - Hashtag demultiplexing
 - Merge matrices
 - Descriptive statistics
 - Spot clean
- Aligners
- Quantification
 - Quantify to annotation model (Partek E/M)
 - Quantify to transcriptome (Cufflinks)
 - Quantify to reference (Partek E/M)
 - Quantify regions
 - HTSeq
 - Count feature barcodes
 - Salmon
- Filtering
 - Filter features
 - Filter groups (samples or cells)
 - Filter barcodes
 - Split by attribute
 - Downsample Cells
- Normalization and scaling
 - Impute low expression
 - Impute missing values
 - Normalization
 - Normalize to baseline
 - Normalize to housekeeping genes
 - Scrub deconvolution
 - SCTransform
 - TF-IDF normalization
- Batch removal
 - General linear model
 - Harmony
 - Seurat3 integration
- Differential Analysis
 - GSA
 - ANOVA
 - Kruskal-Wallis
 - Detect alt-splicing (ANOVA)
 - DESeq2(R) vs DESeq2
 - Hurdle model

- Compute biomarkers
- Transcript Expression Analysis - Cuffdiff
- Troubleshooting
- Survival Analysis with Cox regression and Kaplan-Meier analysis - Partek Flow
- Exploratory Analysis
 - Graph-based Clustering
 - K-means Clustering
 - Compare Clusters
 - PCA
 - t-SNE
 - UMAP
 - Hierarchical Clustering
 - AUCCell
 - Find multimodal neighbors
 - SVD
 - CellPhoneDB
- Trajectory Analysis
 - Trajectory Analysis (Monocle 2)
 - Trajectory Analysis (Monocle 3)
- Variant Callers
 - SAMtools
 - FreeBayes
 - LoFreq
- Variant Analysis
 - Fusion Gene Detection
 - Annotate Variants
 - Annotate Variants (SnpEff)
 - Annotate Variants (VEP)
 - Filter Variants
 - Summarize Cohort Mutations
 - Combine Variants
- Copy Number Analysis (CNVkit)
- Peak Callers (MACS2)
- Peak analysis
 - Annotate Peaks
 - Promoter sum matrix
- Motif Detection
- Metagenomics
 - Kraken
 - Alpha & beta diversity
 - Choose taxonomic level
- 10x Genomics
 - Cell Ranger - Gene Expression
 - Cell Ranger - ATAC
 - Space Ranger
 - STARsolo
- V(D)J Analysis
- Biological Interpretation
 - Gene Set Enrichment
 - GSEA
- Correlation
 - Correlation analysis
 - Sample Correlation
 - Similarity matrix
- Export
- Classification
- Task actions
- Feature linkage analysis

Clicking a **Task node** gives you the option to view the *Task results* or perform *Task actions* such as rerunning the task (Figure 1).

Queue

Projects

John Smith

Home > Gene Analysis

Analyses

Data

Log

Project settings

List generator

Quantification

Normalize counts

Quantification Report

Normalized counts

Gene analysis

Feature list

Filtered gene analysis

Feature list

Task menu

Normalize counts

Task results

Task report

Task details

Task actions

Rerun task

Rerun with downstream tasks

Add task description

Delete task

Project disk space

Make a pipeline | Import a pipeline

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Figure 1. Task menu invoked from a Task node

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating: ☆☆☆☆☆ Results: ★★★★★ 51 rates