

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

×

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