

# 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

Make a pipeline | Import a pipeline

Project disk space

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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: 50 rates