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
    - Scran 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

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        - 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
        - AUCell
        - 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).

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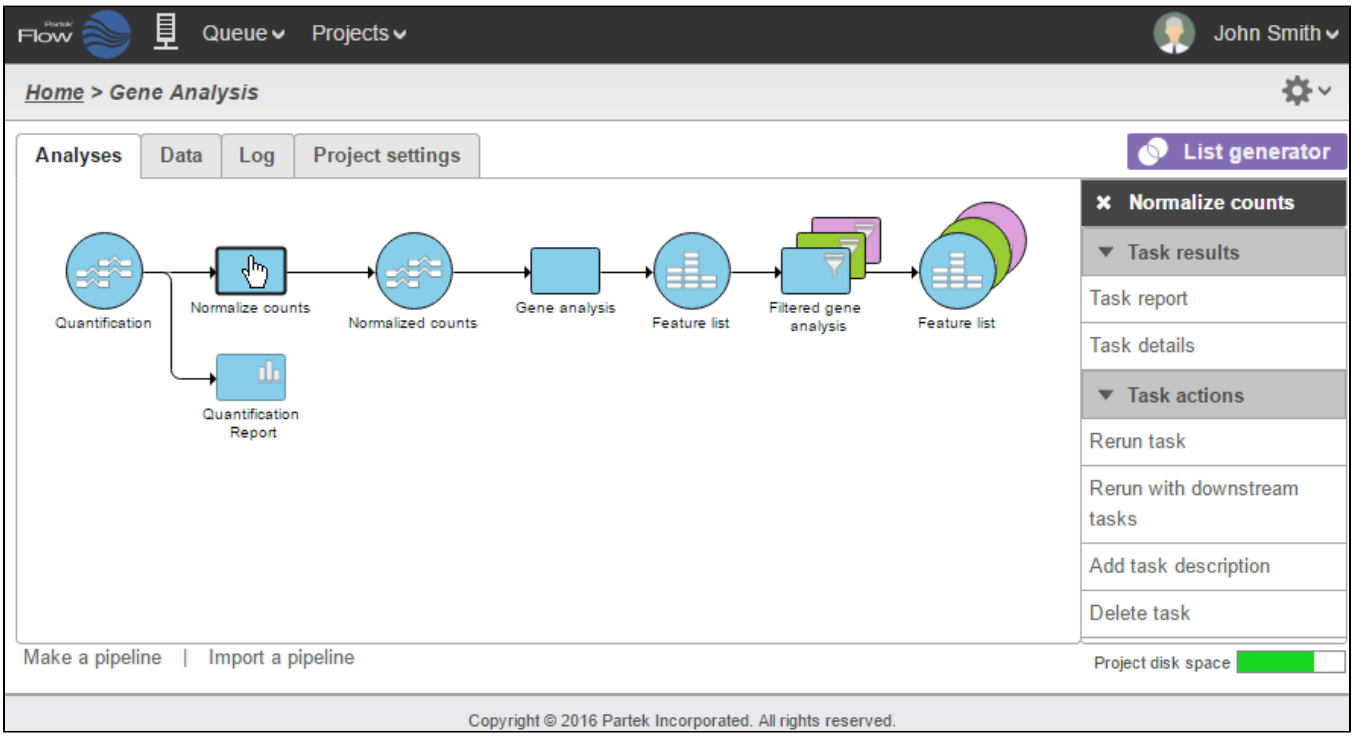

Figure 1. Task menu invoked from a Task node

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: 49 rates

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