STARsolo

What is STARsolo?

STARsolo is a versatile tool developed for single-cell RNA sequencing analysis. It inputs the raw FASTQ reads files, and performs mapping, demultiplexing and quantification for single cell RNA-seq data. It follows CellRanger logic for cell barcode whitelisting and UMI deduplication, and produces nearly identical gene counts in the same format. STARsolo is also running much faster than the CellRanger[1].

Run STARsolo in Partek Flow

Partek Flow wraps STARsolo v2.7.11a and focuses on assays from 10X Genomics.

To run the **STARsolo** task for scATAC-Seq data, select the **Unaligned reads** data node, then select **STARsolo** in the **10x Genomics** section (Figure 1).
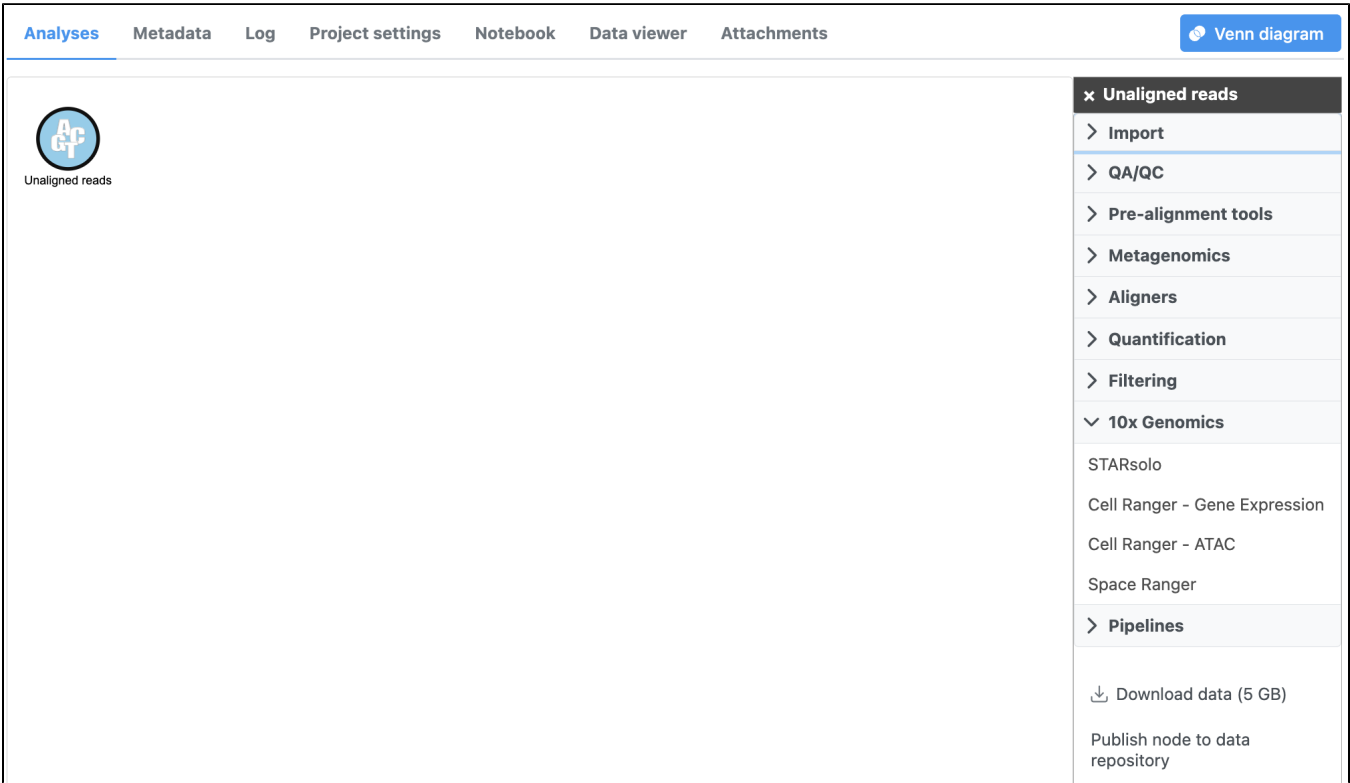

Figure 5. Selecting the STARsolo task for converting fastqs to Single cell counts.

Once the task has been picked, a first time user will be asked to create a index file (Figure 2). Clicking the big blue button of **Create star2.7.8a index** would pop up a new window where lists the requirements that users need to fill in (right panel, Figure 2).

Figure 6. Create star2.7.8a index for STARsolo task in Flow.

Once the right options have been chosen, simply press the **Create** button to finish. The index of ' hg38 - Ensembl 99' has been created as an example here (Figure 3).

Figure 7. Setup interface for STARsolo task in Flow.

The main task menu will be refreshed as above (Figure 3) for **STARsolo** task if the index has been added. Users can go ahead select the **Assay type** before they click the **Finish** button to run the task. The **STARsolo** for this version only handles gene expression data no matter where it's sourced from.

A new data node named **Single cell counts** will be displayed in Flow if the task has been completed successfully (Figure 4). Downstream analysis such as QA/QC, normalization, dimension reduction, clustering, differential analysis, etc will start from the data node.
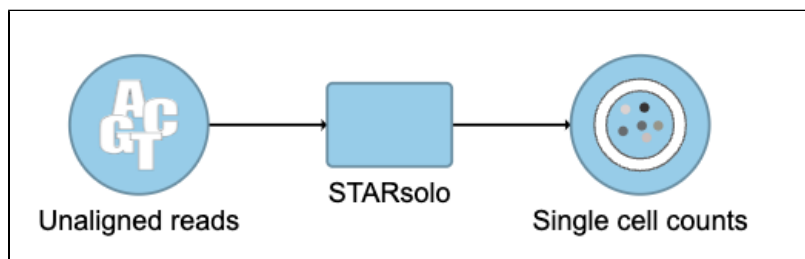
Figure 8. The finished STARsolo task in Flow.

References

1. **doi:** https://doi.org/10.1101/2021.05.05.442755

Additional Assistance

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