Quantifying to an annotation model

RNA-Seq uses the number of sequencing reads per gene or transcript to quantify gene expression. Once reads are aligned to a reference genome, we need to assign each read to a known transcript or gene to give a read-count per transcript or gene.

- Click the **Aligned reads** data node
- Click **Quantification** in the task menu

We will use *Partek E/M* to quantify reads to an annotation model in this tutorial. For more information about the other quantification options, please see the Quantification user guide.

- Click **Quantify to an annotation model (Partek E/M)** (Figure 1)

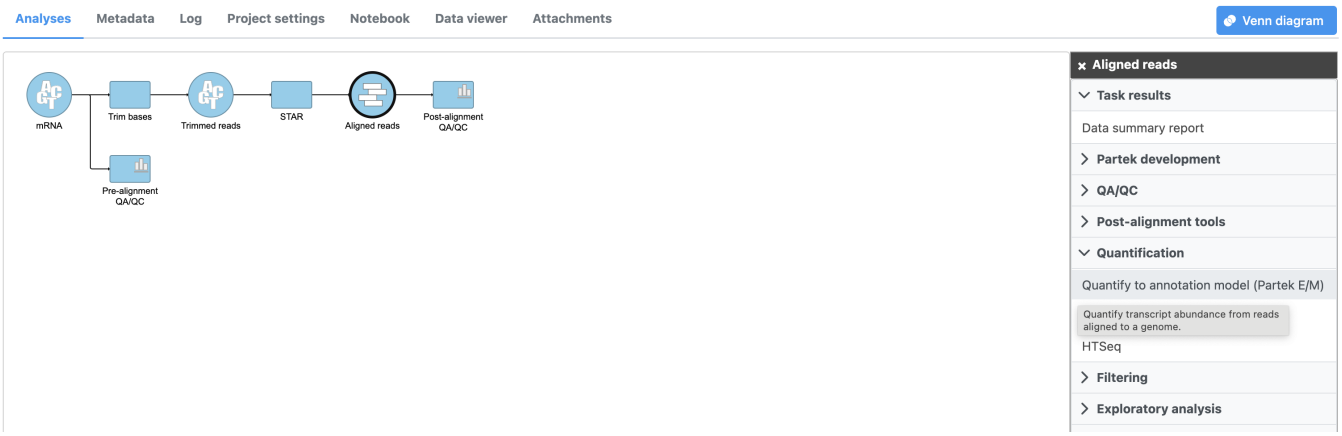

Figure 4. Invoking Quantify to an annotation model (Partek E/M)

We will use the default options for quantification. To learn more about the different options, please see the Quantify to annotation model (Partek E/M) user guide or mouse over the next to each option.

- Choose the latest **RefSeq Transcripts 95** annotation from the *Gene/feature annotation* drop-down menu (you may need to download it first, via Library File Management)
- Click **Finish** (Figure 2)

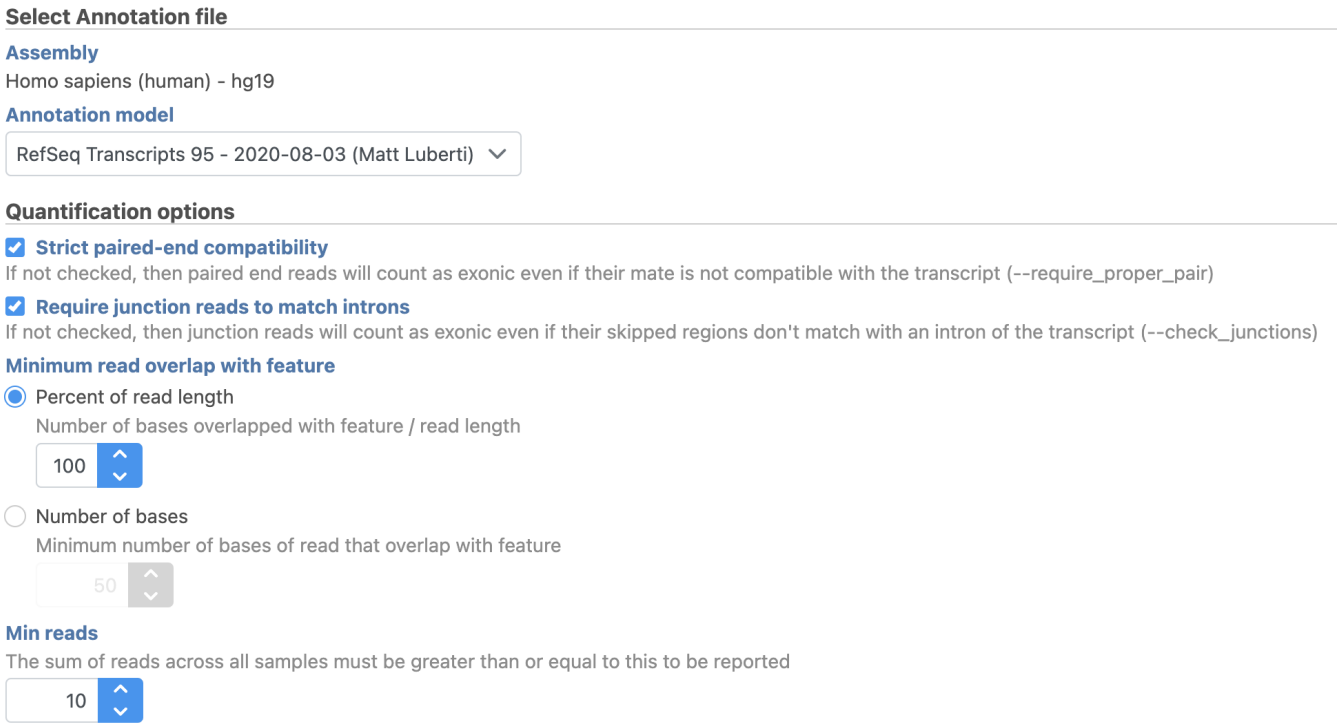

Figure 5. Configuring Quantify to annotation model (Partek E/M)

The *Quantify to annotation model* task node outputs two data nodes, *Gene counts* and *Transcript counts* (Figure 3).

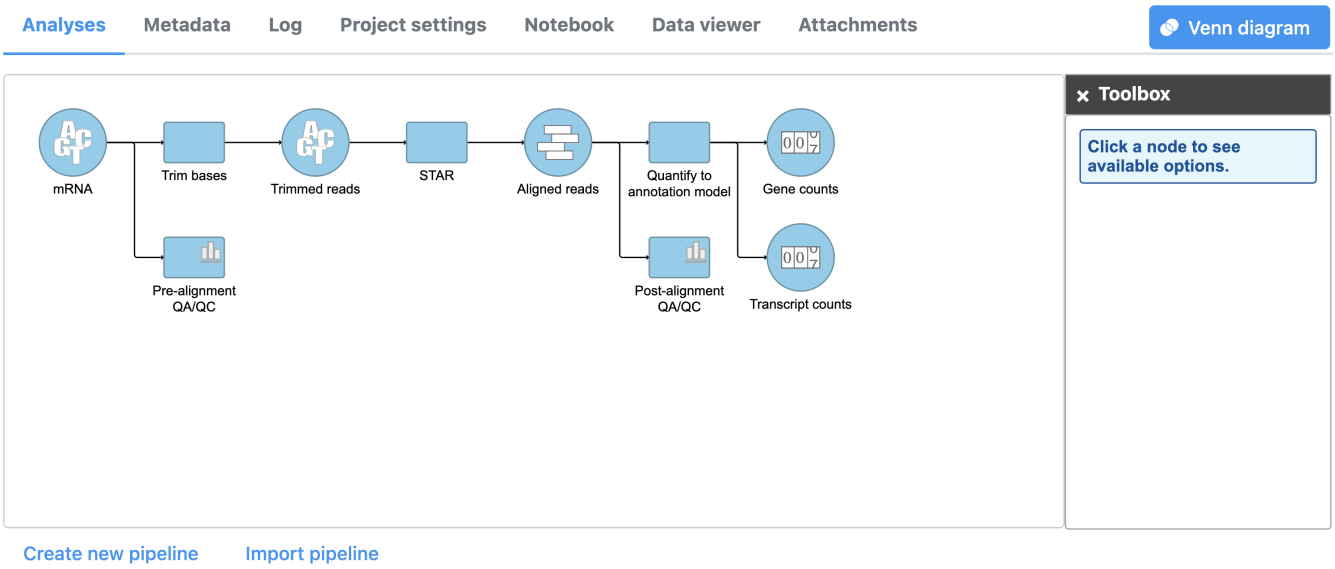

Figure 6. Gene counts and Transcript counts data nodes

To view the results of quantification, we can select either data node output.

- Double-click the **Gene counts** data node to view the task report

The task report details the number of reads within exons, introns, and intergenic regions. For detailed information about the quantification results, see the Quantify to annotation model (Partek E/M) user guide.

« Running post-alignment QA/QC Filtering features »

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