

# 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)

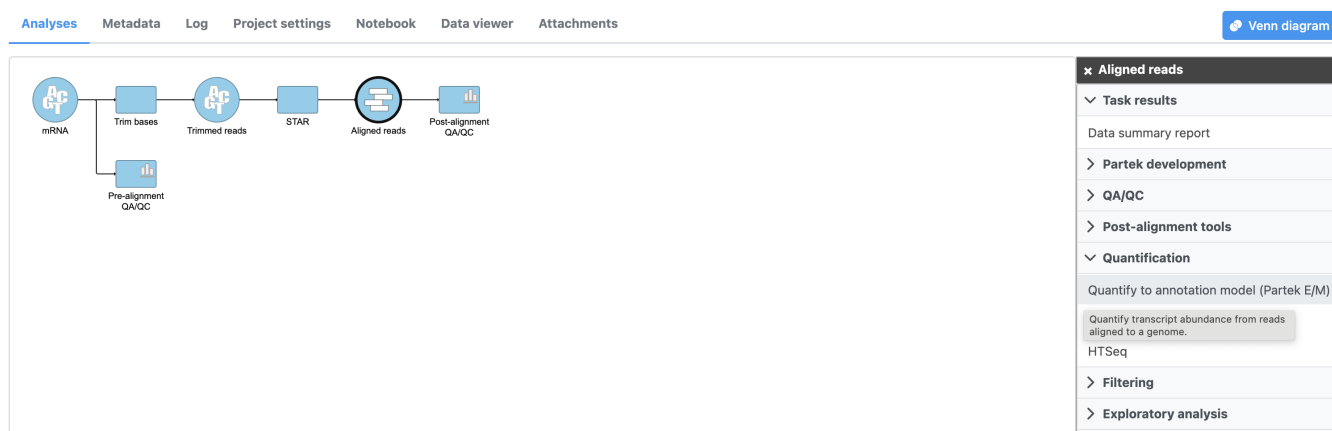



Figure 4. Invoking Quantify to an annotation model (Partek E/M)

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)

### Select Annotation file

#### Assembly

Homo sapiens (human) - hg19

#### Annotation model

RefSeq Transcripts 95 - 2020-08-03 (Matt Luberti) ▼

### Quantification options

#### ☒ Strict paired-end compatibility

If not checked, then paired end reads will count as exonic even if their mate is not compatible with the transcript (--require\_proper\_pair)

#### ☒ Require junction reads to match introns

If not checked, then junction reads will count as exonic even if their skipped regions don't match with an intron of the transcript (--check\_junctions)

#### Minimum read overlap with feature

##### ☒ Percent of read length

Number of bases overlapped with feature / read length

100 ▼

##### ☐ Number of bases

Minimum number of bases of read that overlap with feature

50 ▼

#### Min reads

The sum of reads across all samples must be greater than or equal to this to be reported

10 ▼

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).

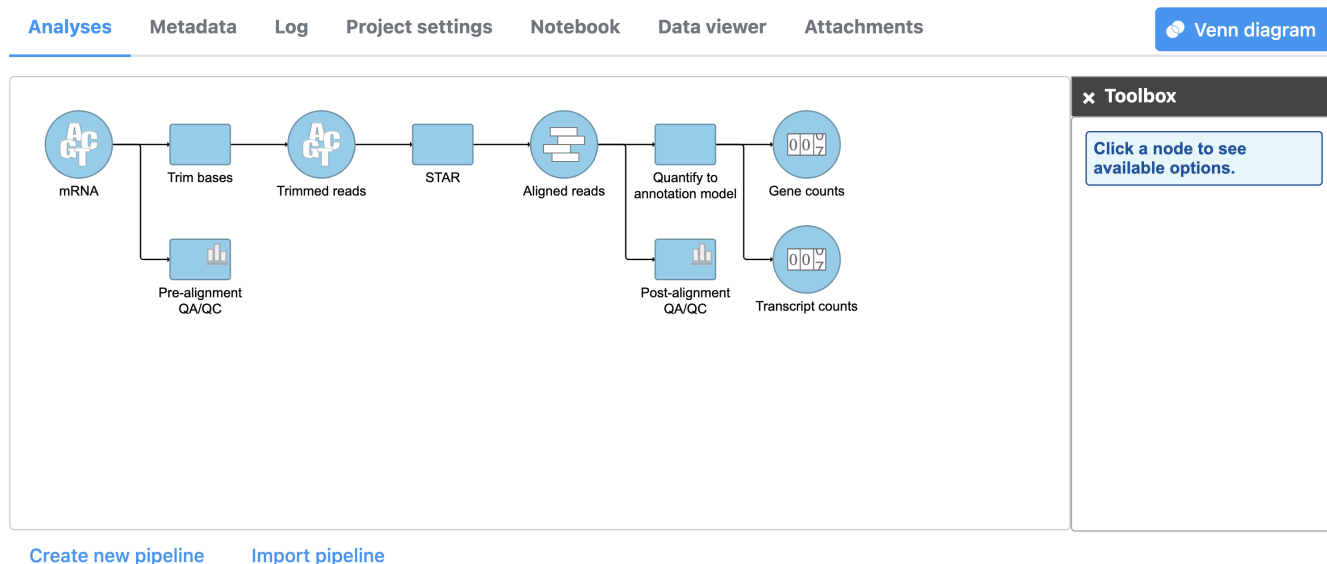


Figure 6. Gene counts and Transcript counts data nodes

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 »](#)

## Additional Assistance

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



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