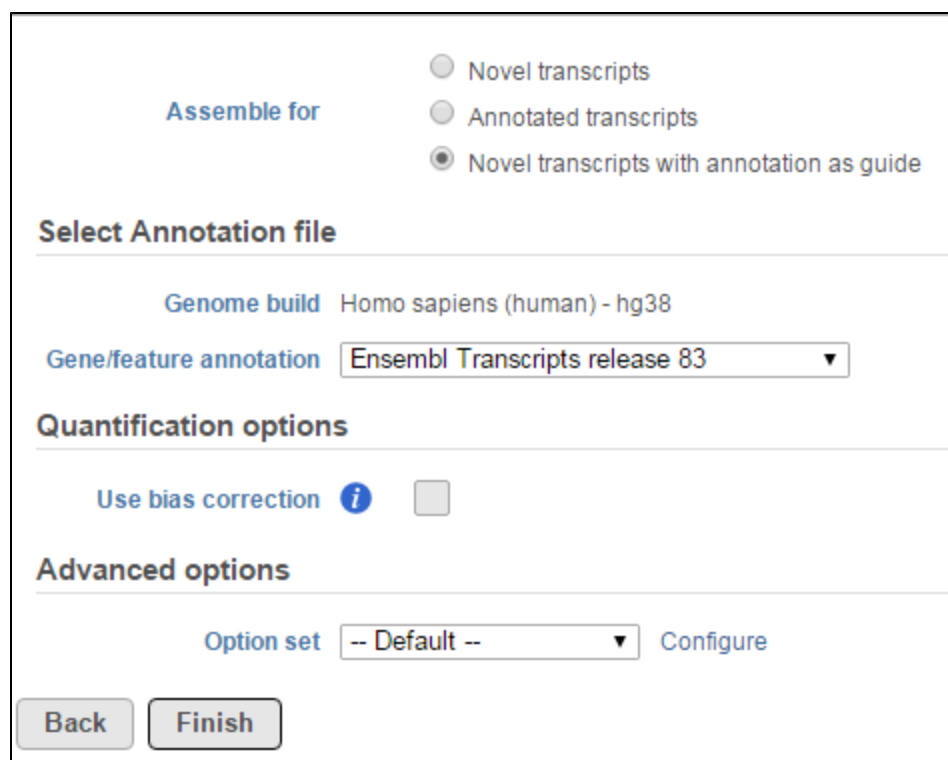


Quantify to transcriptome (Cufflinks)

Cufflinks assembles transcripts and estimates transcript abundances on aligned reads. Implementation details are explained in Trapnell et al. [1]

The Cufflinks task has three options that can be configured (Figure 1):



The image shows a configuration dialog box for Cufflinks. It has a title bar and a main content area. The content is organized into sections: 'Assemble for' with three radio button options, 'Select Annotation file' with a 'Genome build' dropdown and a 'Gene/feature annotation' dropdown, 'Quantification options' with a 'Use bias correction' checkbox, and 'Advanced options' with an 'Option set' dropdown and a 'Configure' button. At the bottom are 'Back' and 'Finish' buttons.

Assemble for

- ☐ Novel transcripts
- ☐ Annotated transcripts
- ☒ Novel transcripts with annotation as guide

Select Annotation file

Genome build: Homo sapiens (human) - hg38

Gene/feature annotation: Ensembl Transcripts release 83

Quantification options

Use bias correction ☐

Advanced options

Option set: -- Default --

Configure

Back Finish

Figure 1. Cufflinks configuration dialog

- **Novel transcript:** this option does not require any annotation reference, it will do de novo assembly to reconstruct transcripts and estimate their abundance
- **Annotation transcript:** this option requires an annotation model to quantify the aligned reads to known transcripts based on the annotation file.
- **Novel transcript with annotation as guide:** this option requires an annotation file to quantify the aligned reads to known transcripts as well as assemble aligned reads to novel transcripts. The results include all transcripts in the annotation file plus any novel transcripts that are assembled.

When the Use bias correction check box is selected, it will use the genome sequence information to look for overrepresented sequences and improve the accuracy of transcript abundance estimates.

References

1. Trapnell C, Williams B, Pertea G, et al. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotech. 2010; 28:511-515.

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:  43 rates