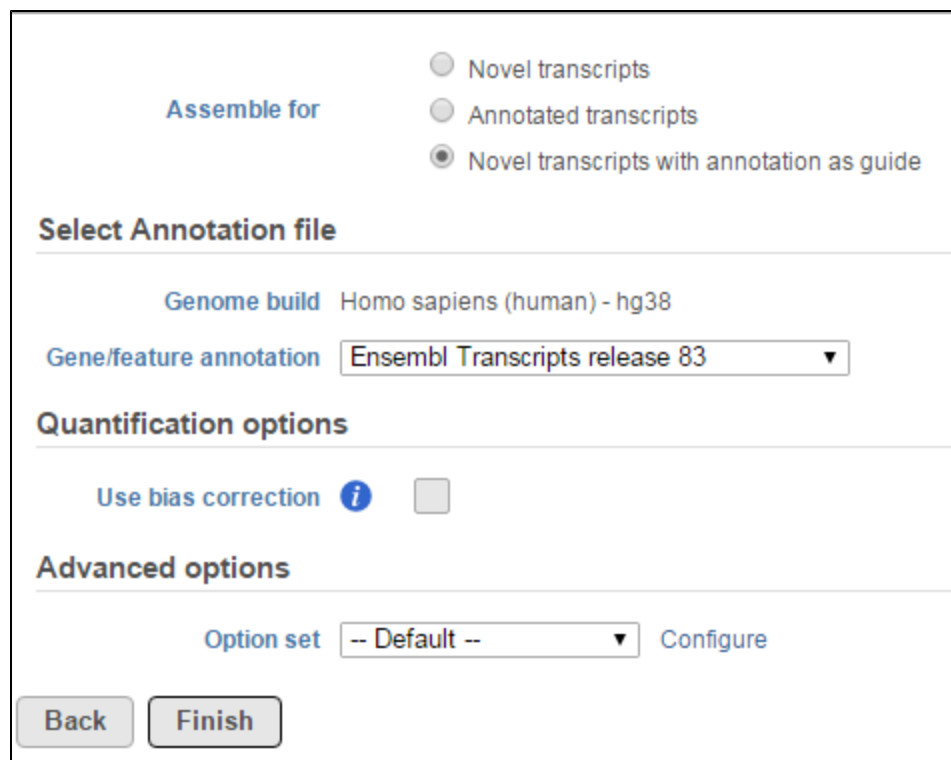


# Quantify to transcriptome (Cufflinks)

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 light blue header with the text 'Assemble for'. Below this are three radio button options: 'Novel transcripts', 'Annotated transcripts', and 'Novel transcripts with annotation as guide'. The third option is selected. Below the radio buttons is a section titled 'Select Annotation file'. It contains a 'Genome build' dropdown menu set to 'Homo sapiens (human) - hg38' and a 'Gene/feature annotation' dropdown menu set to 'Ensembl Transcripts release 83'. Below this is a section titled 'Quantification options' with a 'Use bias correction' checkbox and an information icon. The checkbox is currently unchecked. Below this is a section titled 'Advanced options' with an 'Option set' dropdown menu set to '-- Default --' and a 'Configure' button. At the bottom of the dialog are two buttons: 'Back' and '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