

Option Set Management

Partek Flow allows you to configure advanced settings for various tasks including adapter trimming (Cutadapt), alignment (various aligners), quantification (Cufflinks), differential gene expression analysis (GSA, ANOVA and Cuffdiff), variant detection (Partek, samtools and Freebayes) and variant annotation (SNPEff). User-defined option sets can be saved and applied to other projects.

This user guide will cover the following topics:

- [Saving a Custom Option Set](#)
- [Option Set Management Page](#)
- [Adding an Option Set from the Command Line](#)

Saving a Custom Option Set

A Bowtie alignment task will be used as an example, but the steps are the same for any task that allows configuration of advanced settings. Click **Configure** in the *Advanced options* section on the *Task setup* page (Figure 1).

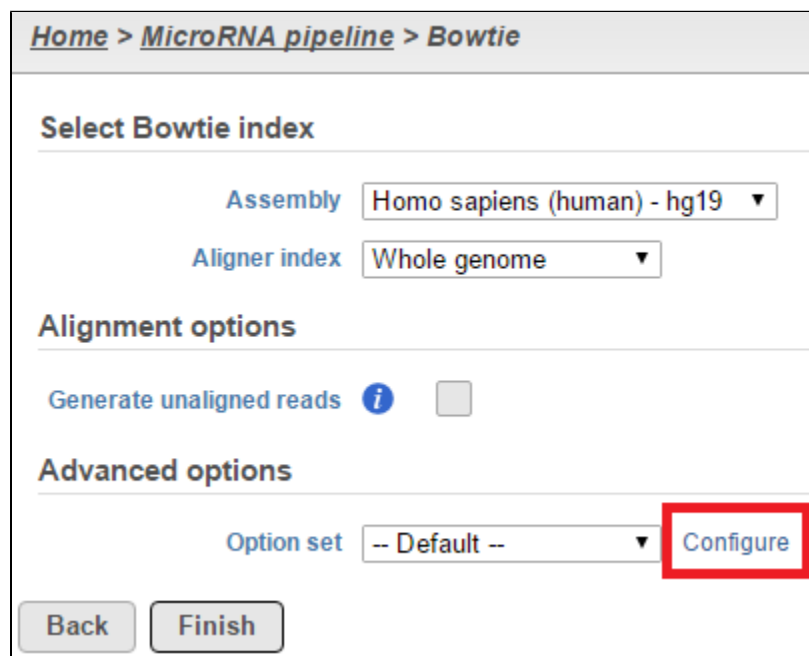


Figure 9. Access to advanced options page through the Configure link. The example shown is on a Task setup page of a Bowtie alignment

In the task-specific *Advanced options* dialog, hover the cursor over the **tool tip** (i) icon to get more information on each setting. Make the desired changes to the settings and click **Save as new** (Figure 2). Note that clicking **Apply** will implement the custom option set for the current task, but the option set will not be saved for use in other projects.

Advanced options

▼ Alignment options

Alignment mode ⓘ Use quality limit ▼

Seed mismatch limit ⓘ 2

Seed length ⓘ 10

Quality limit ⓘ

Enable rounding ⓘ

Try hard ⓘ ☐

Max backtracks ⓘ 125

Strand alignment ⓘ both strands ▼

Quality encoding ⓘ auto-detect ▼

▼ Reporting options

Alignments reported per read ⓘ 1

Max hits ⓘ ☐ 40

Report best hits ⓘ ☐

Apply

Save as new

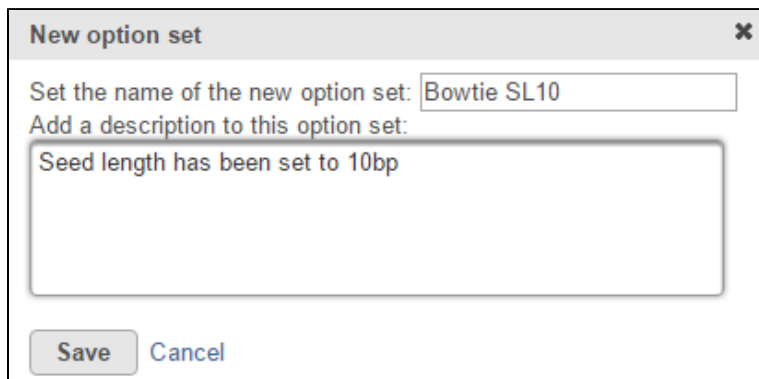
Cancel

The number of bases in the seed. The seed is the first N bases from the 3' end of the read (usually high quality). Bowtie allows a limited number of mismatches in the seed when searching for alignments. A higher seed length will cause the alignment to take less time, but lowers sensitivity (-l)

Figure 10. Advanced options for Bowtie alignment task. The tool tip describes the setting in a pop-out balloon. In this example, the seed length has been ch

Name the new custom option set, add a description (optional) and click **Save** in the *New option set* dialog (Figure 3).

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New option set [X]

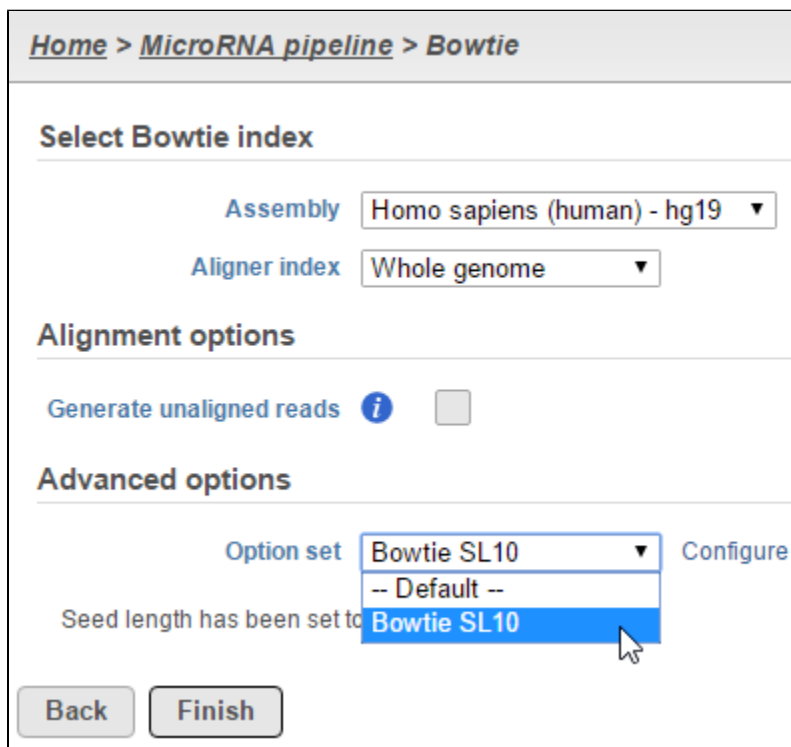
Set the name of the new option set:

Add a description to this option set:

Seed length has been set to 10bp

Figure 11. Name and describe the new custom option set

The saved option set will appear in the drop-down list in the *Advanced options* section on the *Task setup* page (Figure 4). All saved option sets are available to all of the users of the same Partek Flow instance.



[Home](#) > [MicroRNA pipeline](#) > [Bowtie](#)

Select Bowtie index

Assembly

Aligner index

Alignment options

Generate unaligned reads ☐

Advanced options

Option set



-- Default --
 Bowtie SL10

Seed length has been set to

Figure 12. To apply a saved option set, choose it from the drop-down list in the *Advanced options* section of the *Task setup* page

Option Set Management Page

To access the *Option set management* page, click the avatar in the top right corner, choose **Settings** and click **Option set management** on the left (Figure 5). This page can be accessed by administrative and non administrative Partek Flow users.

Choose a task from the selector and all associated option sets will be shown in a table (Figure 5). Click the **Preview** () icon in the *Actions* column to display the option set (Figure 6). Click the **red cross** () icon in the *Actions* column to delete an option set. Note that only the Partek Flow user who created an option set and administrative Partek Flow users are able to delete an option set.

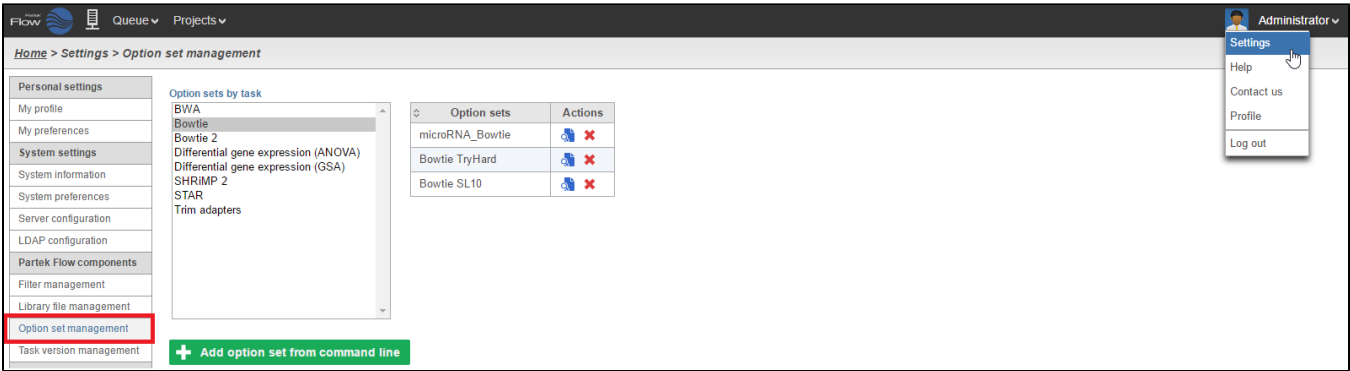


Figure 13. Option set management page displaying three Bowtie task option sets

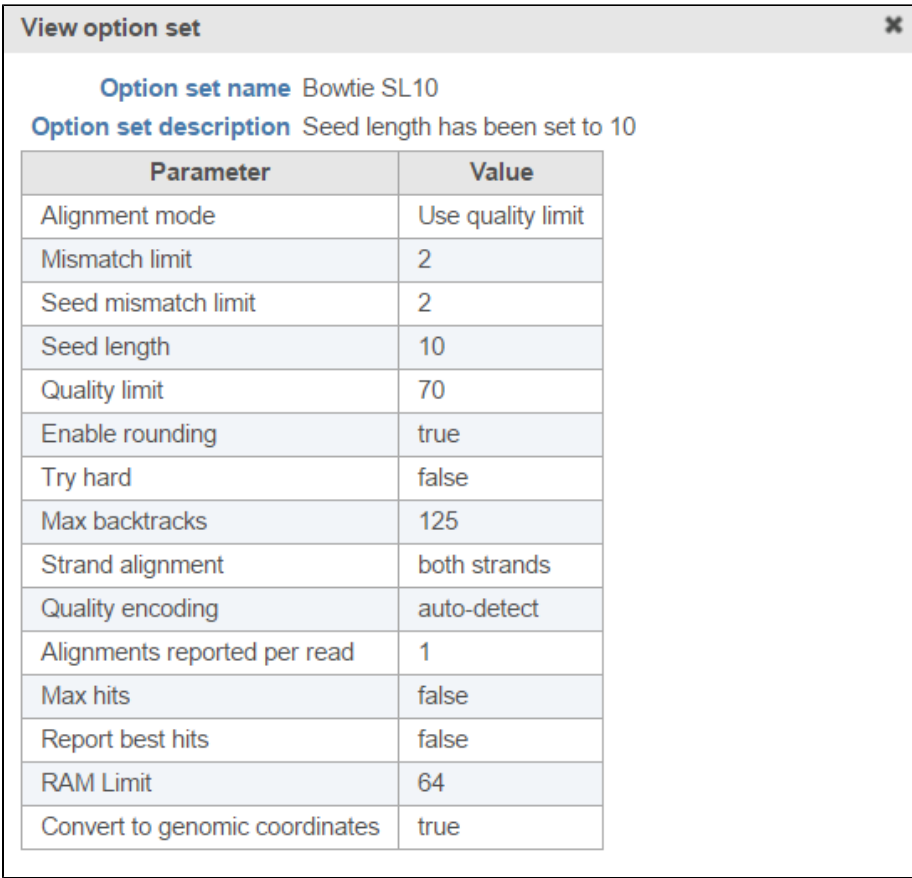


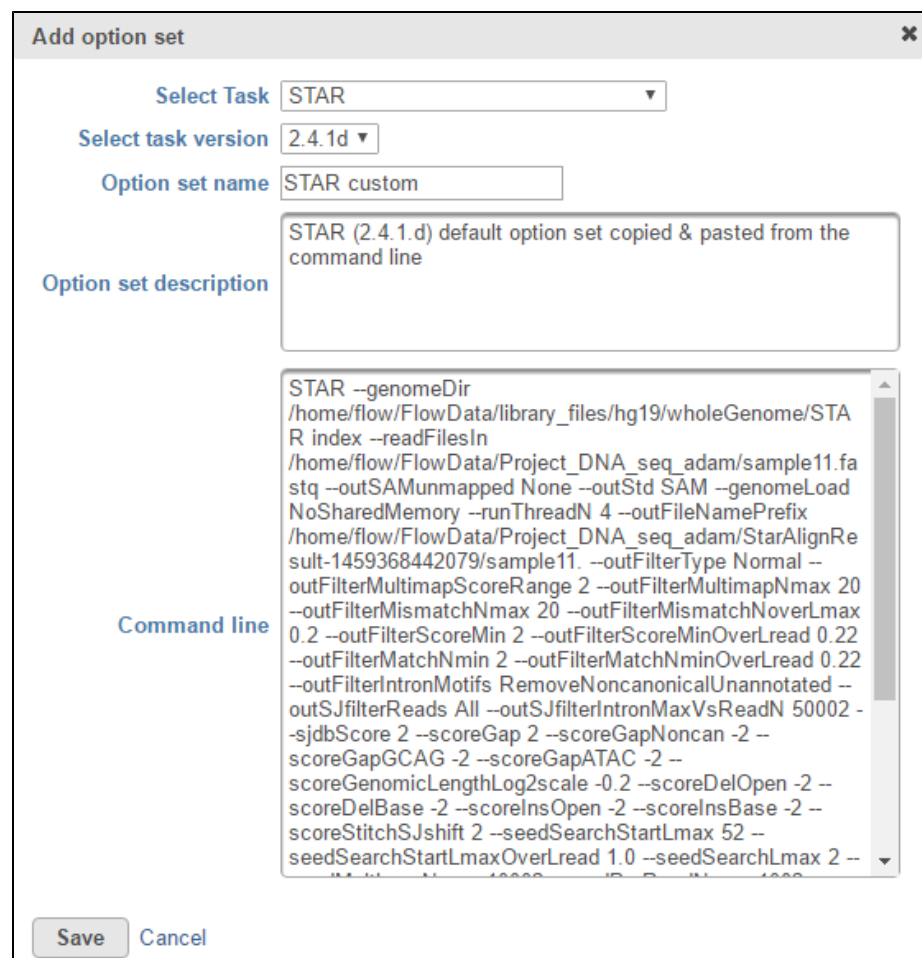
Figure 14. Preview an option set in a table

Adding an Option Set from the Command Line

This is a Partek Flow licensed feature separate from the base license.

User-defined command lines can be copied and pasted to create a custom option set. This is particularly useful if, for example, you have previously run an alignment with custom options on the command line and wish to use the same set of options for an alignment in Partek Flow.

On the *Option set management* page, click the green **Add option set from command line** button (Figure 5). In the *Add option set* dialog (Figure 7), choose a task from the *Select task* drop-down list and the version number (if applicable). Name the option set by typing into the *Name option set* box. Add a description of the option set by typing into the *Option set description* box (optional). Paste the command line from the clipboard into the command line box and click **Save**.



The dialog box is titled "Add option set" and contains the following fields:

- Select Task:** A dropdown menu with "STAR" selected.
- Select task version:** A dropdown menu with "2.4.1d" selected.
- Option set name:** A text input field containing "STAR custom".
- Option set description:** A text area containing "STAR (2.4.1.d) default option set copied & pasted from the command line".
- Command line:** A large text area containing a long command line for STAR, including paths and various parameters like --genomeDir, --readFilesIn, --outSAMunmapped, etc.

At the bottom of the dialog are two buttons: "Save" and "Cancel".

Figure 15. Add option set dialog

The command line will be parsed, validated and converted into a Partek Flow option set. The *Command line parsing report* will summarize the *Command*, *Recognized parameters* and *Ignored parameters* (Figure 8). Partek Flow will ignore parameters with a syntax error or parameters already dealt with by other components of the software (e.g. input/output file paths, performance optimization). Click **OK** to close the report. The option set will now appear on the *Option set management* page (Figure 5) and can be applied to projects (Figure 4).

Command line parsing report		
Command	Recognized parameters	Ignored parameters
STAR	--outFilterType, --outFilterMultimapScoreRange, -- outFilterMultimapNmax, --outFilterMismatchNmax, -- outFilterMismatchNoverLmax, --outFilterScoreMin, -- outFilterScoreMinOverLread, --outFilterMatchNmin, -- outFilterMatchNminOverLread, --outFilterIntronMotifs, -- outSJfilterReads, --outSJfilterIntronMaxVsReadN, --sjdbScore, -- scoreGap, --scoreGapNoncan, --scoreGapGCAG, --scoreGapATAC, -- scoreGenomicLengthLog2scale, --scoreDelOpen, --scoreDelBase, -- scoreInsOpen, --scoreInsBase, --scoreStitchSJshift, -- seedSearchStartLmax, --seedSearchStartLmaxOverLread, -- seedSearchLmax, --seedMultimapNmax, --seedPerReadNmax, -- seedPerWindowNmax, --seedNoneLociperWindow, --alignIntronMin, -- alignIntronMax, --alignSJoverhangMin, --alignSJDBoverhangMin, -- alignWindowsPerReadNmax, --alignTranscriptsPerWindowNmax, -- alignTranscriptsPerReadNmax, --winAnchorMultimapNmax, -- winBinNbits, --winAnchorDistNbins, --winFlankNbins, -- outSAMstrandField, --outSAMattributes	--genomeDir, index, -- readFilesIn, -- outSAMunmapped, -- outStd, -- genomeLoad, -- runThreadN, -- outFileNamePrefix

Figure 16. Command line parsing report

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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