SeqTrimNext
Statistics of pre-processing

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1 Output Files

SeqTrimNext provides several files, the most interesting ones are in the following directories:

- output_files
  - `output.less`, containing an extensive information about the trimming of each sequence. It can be visualised on terminal using the command `less -R`.
  - `used_params.txt`, containing the complete set of parameters used for execution of SeqTrimNext with your data
  - `rejected.txt`, containing a list of rejected sequences together with the reason for their removal.
  - `initial_stats.json`, containing statistics for raw sequences.
  - `stats.json`, containing the statistics of the cleaning process.
  - There is a collection of `folders` that gather sequences with the same MID; each folder contains a `sequences` file (in FastQ format) with useful reads. There may also exists a file with reads containing low complexity regions. If you want to reconstruct a SFF with the useful segment of each pre-processed read, use `sff_info` file in combination with the original SFF file for the `sfffile` tool.
- graphs
  - `size_stats.png`, a graph with the distribution of read lengths in raw data (see Fig. **??**).
  - `qualities.png`, a graph to inspect read qualities in raw data (see Fig. **??**).
  - `PluginExtractInserts_insert_size.png`, a graph with the distribution of read lengths after SeqTrimNext pre-processing (see Fig. 1).
  - There are other graphs (mostly bar plots) that illustrate the quality of pre-processed reads. All are in PNG format.
- latex
  - It is provided as a compressed file `latex.zip` containing all ".tex" files required to compile this document. Graphs are taken from the `graph` folder

2 Relevant parameters

In this section, the relevant parameters used in your experiment are shown. Full information about the parameters can be obtained from file `used_params.txt`

2.1 General

Plugins applied to every sequence, separated by commas. Order is important

1. PluginIndeterminations
2. PluginFindPolyAt
3. PluginAbAdapters
4. PluginUserContaminants
5. PluginContaminants
6. PluginVectors
7. PluginLowQuality
8. PluginLowComplexity
9. PluginExtractInserts

Remove duplicated (clonal) sequences (using CD-HIT 454)

`remove_clonality: false`

Minimum insert size for every trimmed sequence

`min_insert_size_trimmed: 30`

Minimum insert size for each end of paired-end reads; true paired-ends have both single-ends longer than this value

`min_insert_size_paired: 40`

Seqtrim version

`seqtrim_version: 2.0.67`

`min_sequence_size_raw:`

2.2 Quality

Minimum quality value for every nucleotide

`min_quality: 20`

`window_width:`

2.3 Contaminants

Blast E-value used as cut-off when searching for contaminations

`blast_evalue_contaminants: 1.0e-10`

Minimum required identity (%) for a reliable contamination

`blast_percent_contaminants: 85`

Minimum hit size (nt) for considering a true contamination

`min_contam_seq_presence: 40`

Genus of input data: contaminations belonging to this genus will be ignored

`genus:`

Is a contamination considered a source of sequence rejection? (setting to false will only trim contaminated sequences instead of rejecting the complete read)

`contaminants_reject: true`

Path for contaminants database

`contaminants.fasta`

`cont_ribosome.fasta`

3 Pre-processing statistics

Next figure is equivalent to Figure **??** but using output reads (useful sequences). The mode is expected to decrease but the shape of the plot should be similar.

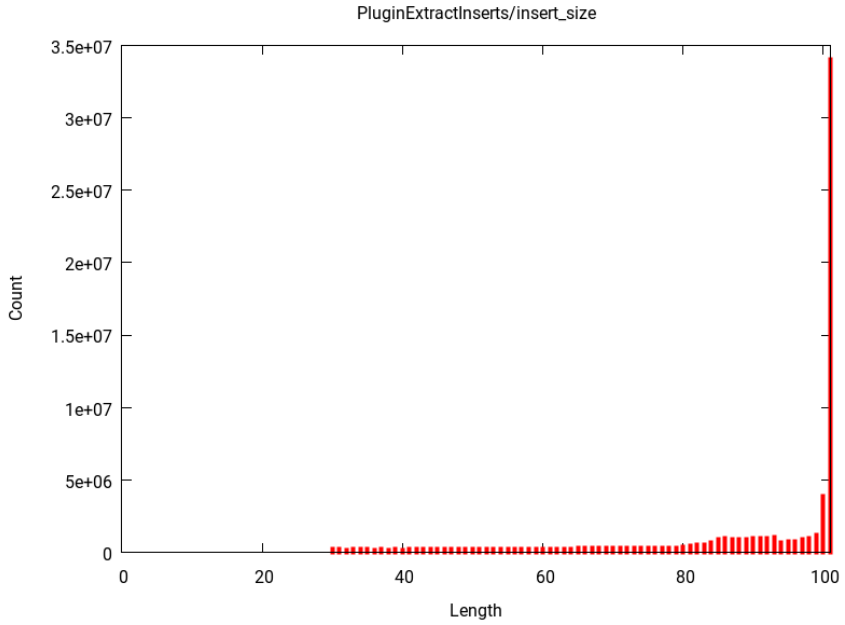

Figure 1: Size distribution of the output sequences. Short sequences (< `min_insert_size_trimmed`) were removed. [PluginExtractInserts_insert_size.png]

Summary statistics of the SeqTrimNext analysis. Be careful and read all warnings that are indicating concerns about your data. In the files `initial_stats.json` and `stats.json` can be found a full statistics of your data and SeqTrimNext pre-processing

Input reads:	total	73858654
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	3179529
	Rejected	8071945
	Low complexity reads	57496
	Mode (bp)	91
	Mean (bp)	90.6
	Output paired reads	62549684
	Total output reads	65729213
Linkers:		

Table 1: List of the most frequent Vectors found among your reads

Vectors	sequences
Cloning vector pAAV-MCS, complete sequence.	330417
Cloning vector pKOHPRT complete sequence.	313215
Enterobacteria phage lambda	114220
Cloning vector pVLH/hsp	37757
Cloning vector pWormgate2, complete sequence.	31987

Table 2: List of the most frequent Adapters found among your reads

Adapters	sequences
TruSeq_Universal_Adapter	457850
ABI_Solid3_Adapter_A	210168
Illumina_Multiplexing_Read2_Sequencing_Primer	182617
ABI_Solid3_GAPDH_Reverse_Primer	170016
Illumina_Single_End_Adapter_1	150398

Table 3: List of the most frequent Contaminants found among your reads

Contaminants	sequences
Podospora anserina S mat+ unordered scaffolds, whole genome shotgun sequence	59592
rRNA_long_subunit_Metazoa_Dasypus	40908
rRNA_small_subunit_Metazoa_Myotis	38118
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	37665
Aspergillus niger CBS 513.88 clone An15	30285

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	1071612592	Inf %	OK
Low Complexity	58484524	Inf %	OK
Poly T	25030090	Inf %	OK
Poly A	26048578	Inf %	OK
Contaminants	33737465	Inf %	OK
Adapters	80090938	Inf %	OK
Vectors	41507287	Inf %	OK
Indeterminations	144742	Inf %	OK
Inserts	5959992410	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	73858654
Output sequences	3179529
Rejected sequences	8071945
Output paired sequences	62549684
Total output sequences	65729213
Low complexity sequences	57496

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	8071945	10.929 %	OK
Short inserts	5440529	7.366 %	OK
Empty Inserts	2238729	3.031 %	rdW3
Contaminants	370224	0.501 %	OK
No Valid Inserts	15760	0.021 %	OK
Low Complexity	4757	0.006 %	OK
Indeterminations	1862	0.003 %	OK
Unexpected Vector	84	0.000 %	OK
Total rejected	8071945	10.929 %	OK

rdW3 Warning!, a 3.031 % of your sequences are empty (without an insert)

References

[1] Falgueras et al. SeqTrim: a high-throughput pipeline for preprocessing any type of sequence reads. *BMC Bioinformatics* 11:38 (2010)

[2] Weizhong Li & Adam Godzik. Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. *Bioinformatics* (2006) 22:1658-9

Thanks you for use SeqTrimNext! Send us any comment to scbi support