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.

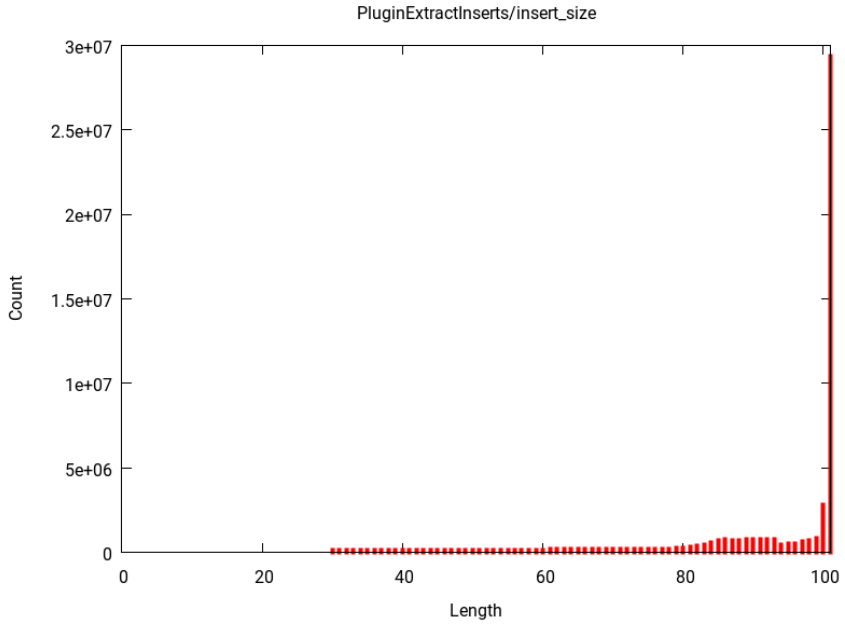

Figure 1: Size distribution of the output sequences. Short sequences (< `min_insert_size_trimmed`) were removed. [PluginExtractInserts_insert_size.png]

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	56172854
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	1787231
	Rejected	4546808
	Low complexity reads	39079
	Mode (bp)	91
	Mean (bp)	92.3
	Output paired reads	49799736
	Total output reads	51586967
Linkers:		

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

Vectors	sequences
Cloning vector pAAV-MCS, complete sequence.	287932
Cloning vector pKOHPRT complete sequence.	284529
Enterobacteria phage lambda	92140
Cloning vector pVLH/hsp	33077
Retroviral expression vector pSFF DNA	28368

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

Adapters	sequences
TruSeq_Universal_Adapter	839830
Illumina_Multiplexing_Read2_Sequencing_Primer	351686
ABI_Solid3_Adapter_A	155000
Illumina_Single_End_Sequencing_Primer	144907
Illumina_Multiplexing_Read1_Sequencing_Primer	134267

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

Contaminants	sequences
rRNA_small_subunit_Metazoa_Myotis	42111
rRNA_long_subunit_Metazoa_Dasypus	40481
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	38139
Podospora anserina S mat+ unordered scaffolds, whole genome shotgun sequence	34377
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	27854

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	598377622	Inf %	OK
Low Complexity	47497976	Inf %	OK
Poly T	19767476	Inf %	OK
Poly A	20599571	Inf %	OK
Contaminants	28355546	Inf %	OK
Adapters	73801722	Inf %	OK
Vectors	33662488	Inf %	OK
Indeterminations	172264	Inf %	OK
Inserts	4767259148	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	56172854
Output sequences	1787231
Rejected sequences	4546808
Output paired sequences	49799736
Total output sequences	51586967
Low complexity sequences	39079

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	4546808	8.094 %	OK
Short inserts	3032354	5.398 %	OK
Empty Inserts	1190367	2.119 %	rdW3
Contaminants	306280	0.545 %	OK
No Valid Inserts	10901	0.019 %	OK
Low Complexity	5149	0.009 %	OK
Indeterminations	1679	0.003 %	OK
Unexpected Vector	78	0.000 %	OK
Total rejected	4546808	8.094 %	OK

rdW3 Warning!, a 2.119 % 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