

SeqTrimNext

Statistics of pre-processing

Plataforma Andaluza de Bioinformática
Universidad de Málaga

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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 exist 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.

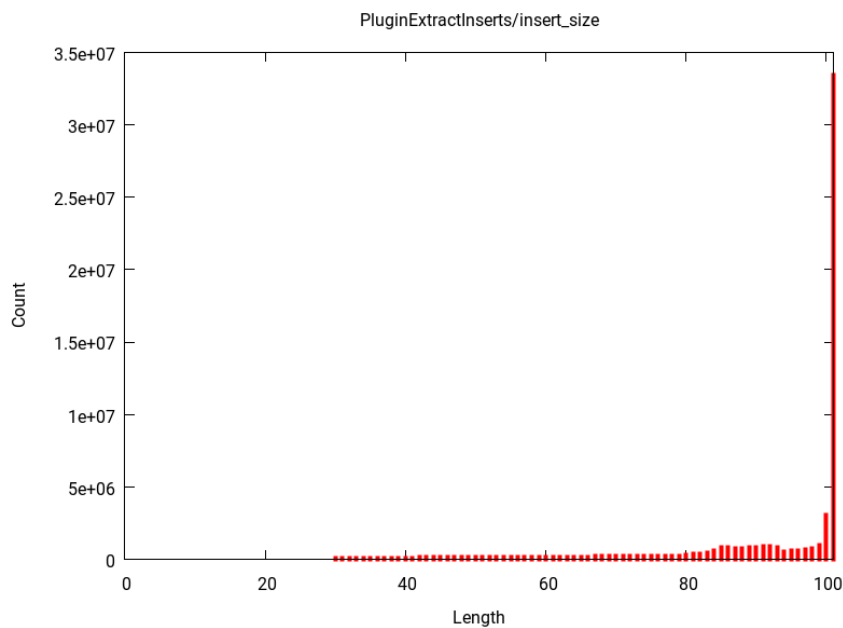


Figure 1: Size distribution of the output sequences. Short sequences ($< \text{min_insert_size_trimmed}$) were removed. [PluginExtractInserts_insert_size.png]

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	62386434
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	1797382
	Rejected	4590501
	Low complexity reads	37749
	Mode (bp)	91
	Mean (bp)	92.7
	Output paired reads	55960802
	Total output reads	57758184
Linkers:		

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

Vectors	sequences
Cloning vector pAAV-MCS, complete sequence.	342451
Cloning vector pKOHPRT complete sequence.	323654
Enterobacteria phage lambda	100414
Cloning vector pVLH/hsp	34638
Cloning vector pWormgate2, complete sequence.	29506

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

Adapters	sequences
TruSeq Universal Adapter	568959
Illumina Multiplexing Read2 Sequencing Primer	227202
ABI Solid3 Adapter A	176333
ABI Solid3 GAPDH Reverse Primer	137776
Illumina Single End Sequencing Primer	128783

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

Contaminants	sequences
rRNA_small_subunit_Metazoa_Myotis	44854
Podospira anserina S mat+ unordered scaffolds, whole genome shotgun sequence	40673
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	36196
rRNA_long_subunit_Metazoa_Dasytus	33482
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	27147

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	625681092	Inf %	OK
Low Complexity	50527835	Inf %	OK
Poly T	21366805	Inf %	OK
Poly A	22501124	Inf %	OK
Contaminants	29413359	Inf %	OK
Adapters	70798412	Inf %	OK
Vectors	38881621	Inf %	OK
Indeterminations	203873	Inf %	OK
Inserts	5355682921	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	62386434
Output sequences	1797382
Rejected sequences	4590501
Output paired sequences	55960802
Total output sequences	57758184
Low complexity sequences	37749

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	4590501	7.358 %	OK
Short inserts	3054186	4.896 %	OK
Empty Inserts	1199280	1.922 %	rdW3
Contaminants	318842	0.511 %	OK
No Valid Inserts	11908	0.019 %	OK
Low Complexity	5479	0.009 %	OK
Indeterminations	746	0.001 %	OK
Unexpected Vector	60	0.000 %	OK
Total rejected	4590501	7.358 %	OK

rdW3 Warning!, a 1.922 % 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