

SeqTrimNext

Statistics of pre-processing

Plataforma Andaluza de Bioinformática
Universidad de Málaga

April 22, 2020

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.

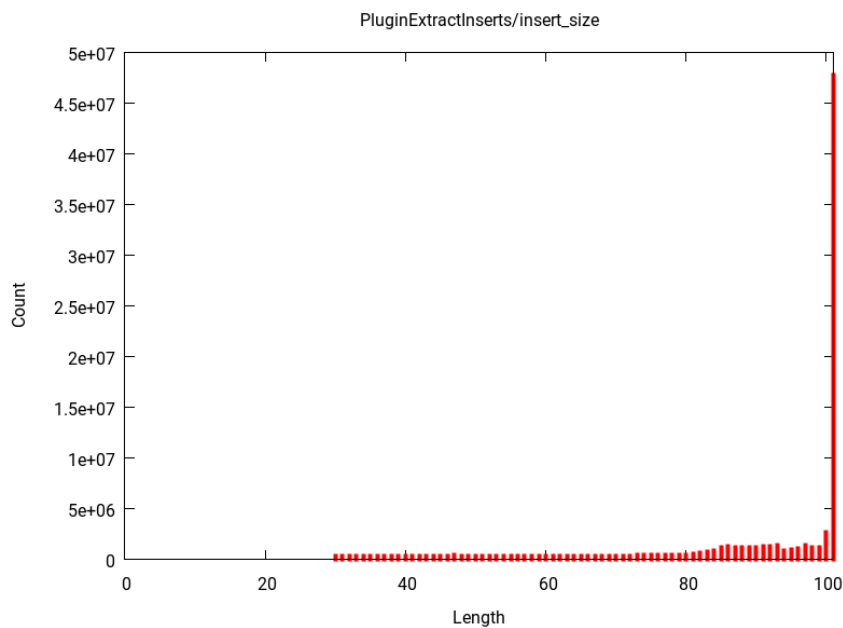


Figure 1: Size distribution of the output sequences. Short sequences ($< \text{min_insert_size_trimmed}$) were removed. [PluginExtractInserts_insert_size.png]

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	104898166
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	6885397
	Rejected	16103444
	Low complexity reads	111235
	Mode (bp)	91
	Mean (bp)	89.4
	Output paired reads	81798090
	Total output reads	88683487
Linkers:		

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

Vectors	sequences
Cloning vector pKOHPR7 complete sequence.	567715
Cloning vector pAAV-MCS, complete sequence.	562833
Enterobacteria phage lambda	154689
Cloning vector pVLH/hsp	60763
Cloning vector pWormgate2, complete sequence.	56212

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

Adapters	sequences
ABI_Solid3_Adapter_A	286049
Illumina_Single_End_Adapter_1	220752
ABI_Solid3_GAPDH_Reverse_Primer	212760
ABI_Solid3_Adapter_B	190560
TruSeq_Universal_Adapter	190281

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

Contaminants	sequences
rRNA_long_subunit_Metazoa_Dasytus	66519
Podospora anserina S mat+ unordered scaffolds, whole genome shotgun sequence	55602
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	53985
rRNA_small_subunit_Metazoa_Myotis	43393
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	37308

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	1975336417	Inf %	OK
Low Complexity	76565328	Inf %	OK
Poly T	42193396	Inf %	OK
Poly A	45143934	Inf %	OK
Contaminants	44013156	Inf %	OK
Adapters	90729087	Inf %	OK
Vectors	63381401	Inf %	OK
Indeterminations	3970903	Inf %	OK
Inserts	7939905367	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	104898166
Output sequences	6885397
Rejected sequences	16103444
Output paired sequences	81798090
Total output sequences	88683487
Low complexity sequences	111235

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	16103444	15.352 %	OK
Short inserts	10444269	9.957 %	rdW2
Empty Inserts	5124271	4.885 %	rdW3
Contaminants	482701	0.460 %	OK
No Valid Inserts	22221	0.021 %	OK
Indeterminations	21740	0.021 %	OK
Low Complexity	8112	0.008 %	OK
Unexpected Vector	130	0.000 %	OK
Total rejected	16103444	15.352 %	OK

rdW2 Warning!, a 9.957 % of your sequences are too short

rdW3 Warning!, a 4.885 % 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