

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 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.

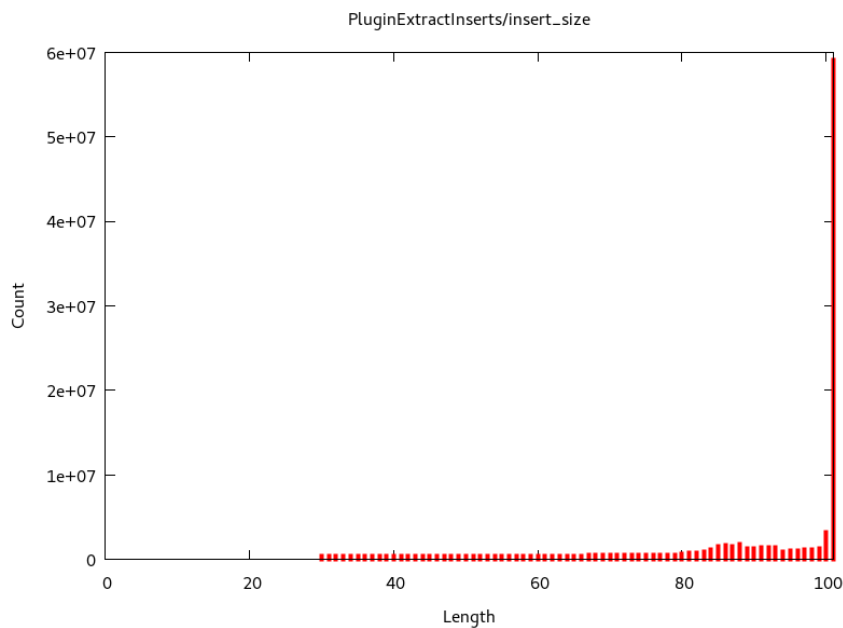


Figure 1: Size distribution of the output sequences. Short sequences ($< \text{min_insert_size_trimmed}$) were removed. [PluginExtractInserts_insert_size.png]

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	127713520
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	6165462
	Rejected	20749297
	Low complexity reads	100093
	Mode (bp)	91
	Mean (bp)	89.7
	Output paired reads	100698668
	Total output reads	106864130
Linkers:		

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

Vectors	sequences
Cloning vector pKOHPR7 complete sequence.	751613
Cloning vector pAAV-MCS, complete sequence.	742042
Enterobacteria phage lambda	185629
Simian virus 40	62814
Artificial DNA for pTnMax5 mini-transposon	61436

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

Adapters	sequences
ABISolid3_Adapter_A	380357
TruSeq_Universal_Adapter	300887
ABISolid3_GAPDH_Reverse_Primer	287710
ABISolid3_EF1_alpha_Sense_Primer	268873
Illumina_Single_End_Adapter_1	245052

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

Contaminants	sequences
rRNA_long_subunit_Metazoa_Dasytus	163644
rRNA_small_subunit_Metazoa_Myotis	152106
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	149301
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	103745
Aspergillus niger CBS 513.88 clone An03	90100

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	2456598216	Inf %	OK
Low Complexity	87154718	Inf %	OK
Poly T	43403709	Inf %	OK
Poly A	48305710	Inf %	OK
Contaminants	102411889	Inf %	OK
Adapters	113465014	Inf %	OK
Vectors	77293382	Inf %	OK
Indeterminations	78011	Inf %	OK
Inserts	9596630406	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	127713520
Output sequences	6165462
Rejected sequences	20749297
Output paired sequences	100698668
Total output sequences	106864130
Low complexity sequences	100093

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	20749297	16.247 %	OK
Short inserts	12187852	9.543 %	rdW2
Empty Inserts	7438006	5.824 %	rdW3
Contaminants	1093974	0.857 %	rdW4
No Valid Inserts	20536	0.016 %	OK
Low Complexity	8168	0.006 %	OK
Indeterminations	606	0.000 %	OK
Unexpected Vector	155	0.000 %	OK
Total rejected	20749297	16.247 %	OK

rdW2 Warning!, a 9.543 % of your sequences are too short

rdW3 Warning!, a 5.824 % of your sequences are empty (without an insert)

rdW4 Warning!, a 0.857 % of your sequences are from a contaminant organism or from organelles

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