

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.

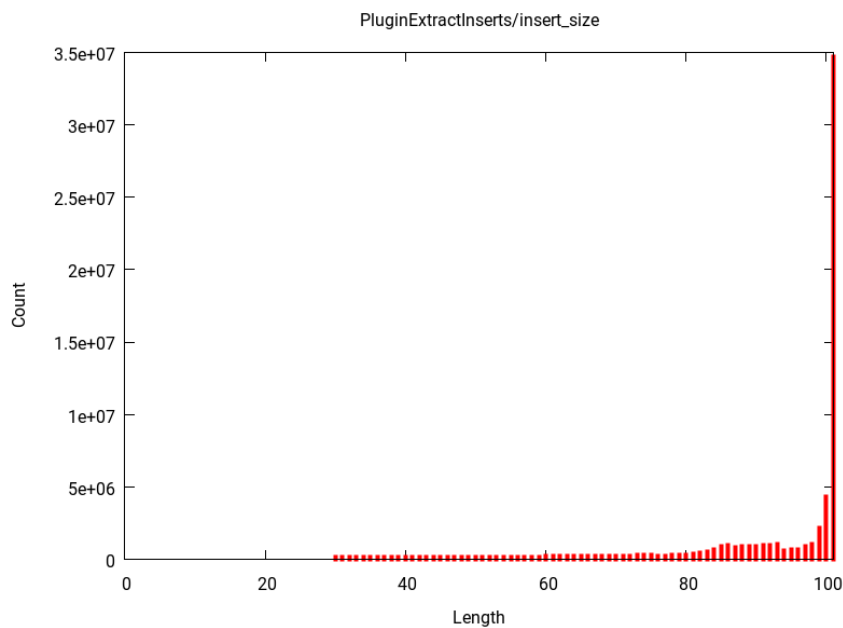


Figure 1: Size distribution of the output sequences. Short sequences ($< \text{min_insert_size_trimmed}$) were removed. [PluginExtractInserts_insert_size.png]

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	70218210
	Smallest read (bp)	101
	Largest read (bp)	101
	Mode (bp)	0
	Mean (bp)	0.0
Output results:	total	1975608
	Rejected	5500255
	Low complexity reads	41749
	Mode (bp)	91
	Mean (bp)	92.5
	Output paired reads	62700598
	Total output reads	64676206
Linkers:		

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

Vectors	sequences
Cloning vector pAAV-MCS, complete sequence.	374510
Cloning vector pKOHPRT complete sequence.	351724
Enterobacteria phage lambda	109945
Cloning vector pVLH/hsp	35260
Cloning vector pWormgate2, complete sequence.	30172

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

Adapters	sequences
TruSeq Universal Adapter	920561
Illumina Multiplexing Read2 Sequencing Primer	405094
ABI Solid3 Adapter A	200468
Illumina Single End Sequencing Primer	176757
Illumina Multiplexing Read1 Sequencing Primer	156113

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

Contaminants	sequences
rRNA_small_subunit_Metazoa_Myotis	56988
Saccharomyces cerevisiae S288c chromosome XII, complete sequence	52223
rRNA_long_subunit_Metazoa_Dasytus	50493
Podospira anserina S mat+ unordered scaffolds, whole genome shotgun sequence	49955
Schizosaccharomyces pombe 972h- chromosome III, complete sequence	38028

Table 4: Summary of nucleotides removed in every plugin.

Plugin	Nucleotides	Percent	Warnings
Low Quality	726163616	Inf %	OK
Low Complexity	55681446	Inf %	OK
Poly T	21783623	Inf %	OK
Poly A	23679359	Inf %	OK
Contaminants	41161385	Inf %	OK
Adapters	93354762	Inf %	OK
Vectors	43932047	Inf %	OK
Indeterminations	219096	Inf %	OK
Inserts	5986004716	Inf %	iW1

iW1 Warning!, only Inf % of nucleotides are useful

4 Rejected reads

Input sequences	70218210
Output sequences	1975608
Rejected sequences	5500255
Output paired sequences	62700598
Total output sequences	64676206
Low complexity sequences	41749

Table 5: Summary of reads removed in every plugin.

Case	Number of sequences	Percent	Warnings
	5500255	7.833 %	OK
Short inserts	3554945	5.063 %	OK
Empty Inserts	1483302	2.112 %	rdW3
Contaminants	444466	0.633 %	OK
No Valid Inserts	10615	0.015 %	OK
Low Complexity	4219	0.006 %	OK
Indeterminations	2607	0.004 %	OK
Unexpected Vector	101	0.000 %	OK
Total rejected	5500255	7.833 %	OK

rdW3 Warning!, a 2.112 % 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