

Fastq quality data.

Your Name here

April 15, 2025

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1 Project characteristics

| |
|-------------------------|
| Project characteristics |
| Contact |
| Phone |
| Institute |
| Mail |
| Start date |

2 Global summaries

Input data: Summarized data on FASTQ files.

```
[fastqq] File ( 1/2) 'E:/biocbuild/bbs-3.21-bioc/tmpdir/Rtmpiuiesc/Rinst21e00343f381a
[fastqq] File ( 2/2) 'E:/biocbuild/bbs-3.21-bioc/tmpdir/Rtmpiuiesc/Rinst21e00343f381a
```

Printout of Fastqq object:

```
> fqq

Class      :      Fastqq
nFiles     :      2
maxSeqLen  :     101
k (Kmer len):      4

nReads     :     200
nr  N   nuc :      2
Min seq len :     101
Max seq len :     101
```

2.1 Project names and read numbers

```
> dfr<-data.frame(file=basename(fileName(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)
```

| | file | sample | reads |
|---|--------------------|--------|-------|
| 1 | g4_l101_n100.fq.gz | g4 | 100 |
| 2 | g5_l101_n100.fq.gz | g5 | 100 |

3 Nucleotide patterns

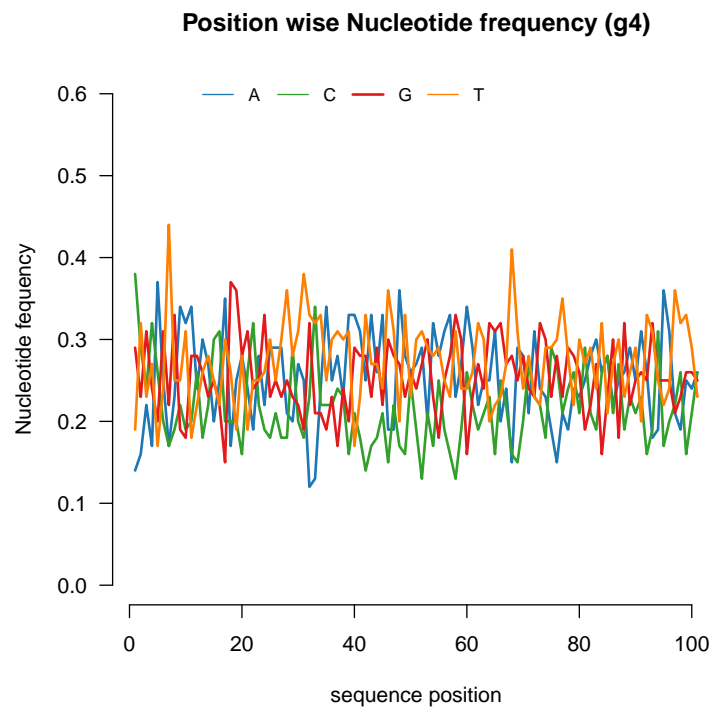
3.1 N nucleotides



3.2 GC content



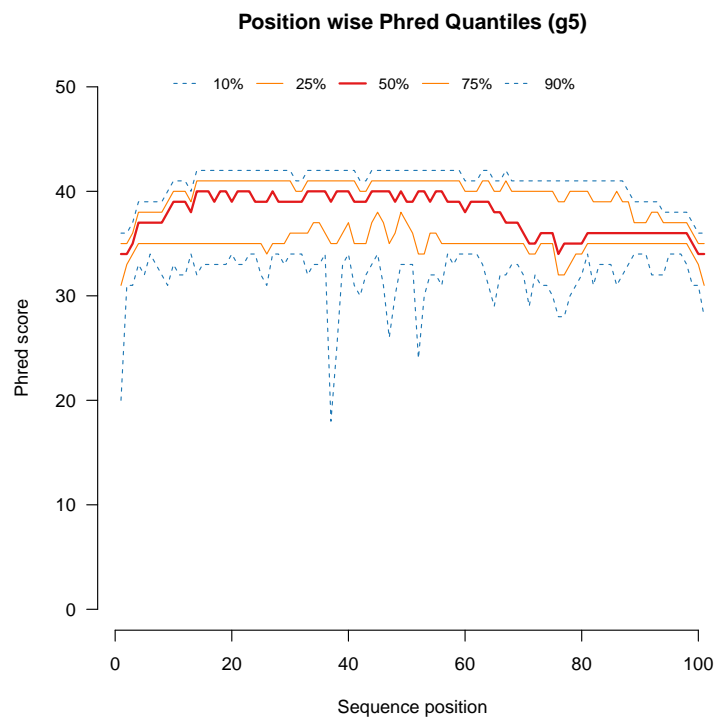
3.3 Nucleotide frequencies





4 Phred qualities





5 Hierarchical clustering

| | |
|------|---|
| 1_g4 | 1 |
| 2_g5 | 2 |

