

Fastq quality data.

Your Name here

October 24, 2023

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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) '/private/tmp/Rtmps1wTtW/Rinst7c0868c8d92/seqTools/extdata/g4_11
```

```
[fastqq] File ( 2/2) '/private/tmp/Rtmps1wTtW/Rinst7c0868c8d92/seqTools/extdata/g5_11
```

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(fileNames(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

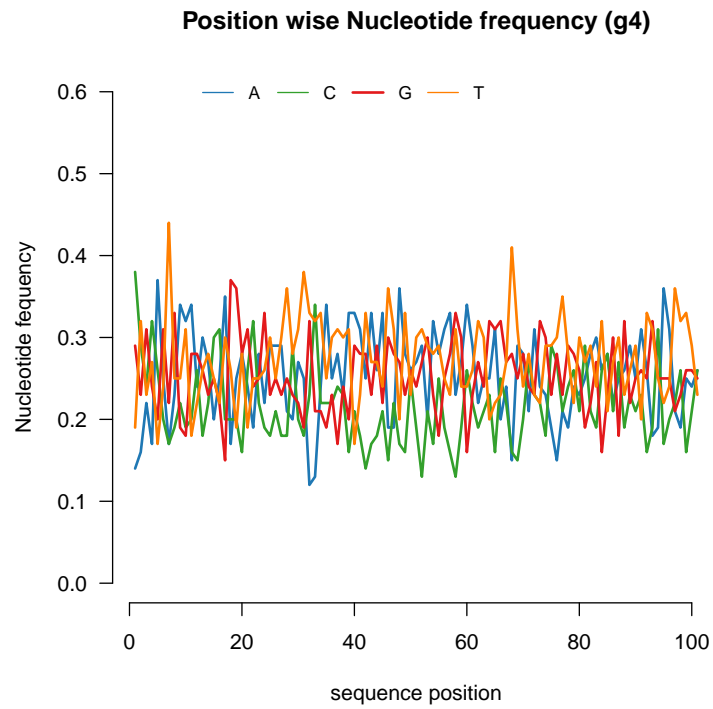
3.1 N nucleotides



3.2 GC content



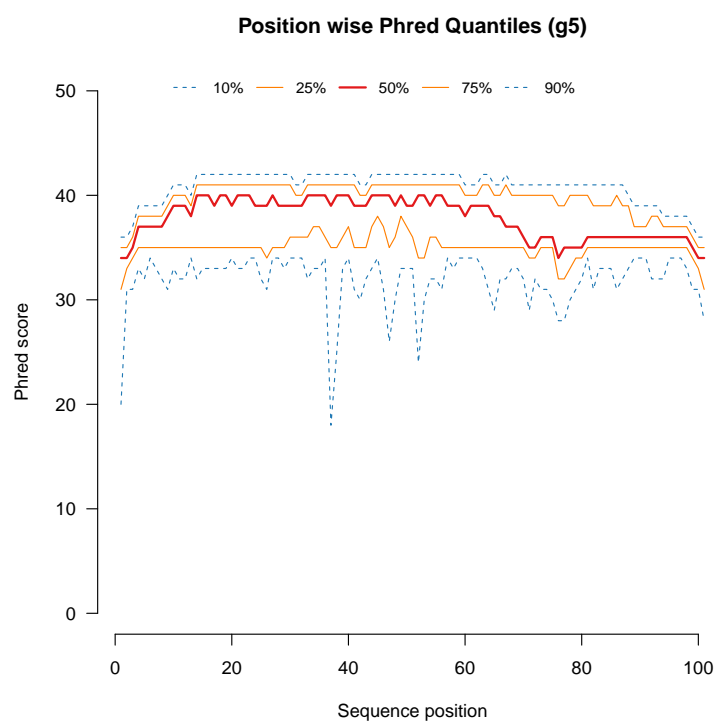
3.3 Nucleotide frequencies





4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2

