

Previous file has been stored in an object called f. We will draw a sample piece from a sequence of many reads. FastqSampler() draws a subsample from a fastq file. Yield() is used to extract the sample from the FastqSampler.

```
> # load ShortRead
> library(ShortRead)
Loading required package: BiocGenerics
Loading required package: parallel
```

Attaching package: 'BiocGenerics'
The following objects are masked from 'package:parallel':

clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
clusterExport, clusterMap, parApply, parCapply, parLapply,
parLapplyLB, parRapply, parSapply, parSapplyLB

The following objects are masked from 'package:stats':

IQR, mad, sd, var, xtabs

The following objects are masked from 'package:base':

Filter, Find, Map, Position, Reduce, anyDuplicated, append,
as.data.frame, cbind, colMeans, colSums, colnames, do.call,
duplicated, eval, evalq, get, grep, grepl, intersect, is.unsorted,
lapply, lengths, mapply, match, mget, order, paste, pmax, pmax.int,
pmin, pmin.int, rank, rbind, rowMeans, rowSums, rownames, sapply,
setdiff, sort, table, tapply, union, unique, unsplit, which,
which.max, which.min

Loading required package: BiocParallel
Loading required package: Biostrings
Loading required package: S4Vectors
Loading required package: stats4

Attaching package: 'S4Vectors'
The following object is masked from 'package:base':

expand.grid

Loading required package: IRanges
Loading required package: XVector

Attaching package: 'Biostrings'
The following object is masked from 'package:base':

strsplit

Loading required package: Rsamtools
Loading required package: GenomInfoDb
Loading required package: GenomicRanges
Loading required package: GenomicAlignments
Loading required package: SummarizedExperiment
Loading required package: Biobase
Welcome to Bioconductor

Vignettes contain introductory material; view with
'browseVignettes()'. To cite Bioconductor, see
'citation("Biobase")', and for packages 'citation("pkgname")'.
Loading required package: DelayedArray
Loading required package: matrixStats

Attaching package: 'matrixStats'
The following objects are masked from 'package:Biobase':

anyMissing, rowMedians

Attaching package: 'DelayedArray'
The following objects are masked from 'package:matrixStats':

colMaxs, colMins, colRanges, rowMaxs, rowMins, rowRanges
The following object is masked from 'package:Biostrings':

type

The following object is masked from 'package:base':

apply

```
>  
> # set a seed for sampling  
> set.seed(1234)  
>  
> # Use FastqSampler with f and select 100 reads  
> fs <- FastqSampler(con = f, n = 100)  
>  
> # new sample yield  
> my_sample <- yield(fs)  
>  
> # print my_sample  
> my_sample  
class: ShortReadQ  
length: 100 reads; width: 50 cycles
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