Aligned reads to the genome

Methylation % per base

Sample merge

Descriptive statistics
getMethylationStats()
getCoverageStats()

Filtering by coverage
filterByCoverage()

Window/region based methylation scores
regionCounts()
tileMethylCounts()

Correlation
getCorrelation()

Clustering and PCA
clusterSamples()
PCASamples()

Differential methylation
calculateDiffMeth()

Annotation
annotate.WithFeature() and similar functions

Visualization
bedgraph()
diffMethPerChr()

Coercion to bioconductor and R objects
as() getData()

Further analysis by user

Input option 1
read.bismark()

Input option 2
read()