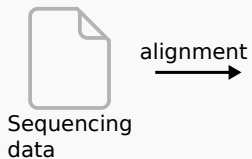
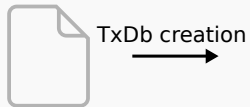


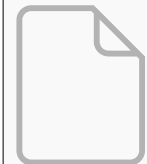
Prerequisites



Annotation data
(GTF, GFF, etc)



ASpli



BAM files



TxDb

1 Read genomic
alignments

loadBAM()

List of GAlignments

3 Count aligned
reads to features

readCounts()

4 Search for novel
splicing events

AsDiscover()

ASpliCounts

5 Differential
usage estimation

DUreport()
junctionDUreport()
DUreportBinSplice()

ASpliAS

ASpliDU

2 Extract features

binGenome()

ASpliFeatures