

# INPUTS



Annotation

experimental  
design



alignments

# ASpli

## 1 Extract features

**binGenome()**

ASpliFeatures

## 2 Count aligned reads to features

**gbCounts()**

ASpliCounts

**jCounts()**

ASpliAS

## 3 Differential usage estimation

**gbDUreport()**

ASpliDU

**jDUreport()**

ASplijDU

## 4 Bin and junction signals integration

**splicingReport()**

ASpliSplicingReport

## 5 Region-based summarization

**integrateSignals()**

ASpliIntegratedSignals

## 6 Integrative reports

**exportIntegratedSignals()**

**exportSplicingReports()**

# OUTPUTS

featuresg()  
featuresb()  
featuresj()  
binMetadata()

countsg()  
rdsj()  
countj()  
e1icounts()  
ie2counts()

**writeCounts()**  
**writeRds()**

irPIR()  
altPSI()  
esPSI()  
allBins()  
junctionsPJU()  
junctionsPIR()  
**writeAS()**

localec()  
localej()  
anchorj()  
anchorc()  
jir()  
jes()  
jalt()  
**writejDU()**

binbased()  
localebased()  
anchorbased()  
**writeSplicingReport( )**

signals()  
filters()

DT interactive  
HTML docs

