

ASpli: An integrative R package for analysing alternative splicing using RNA-seq

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1 Introduction

Genome-wide analysis of alternative splicing has been a very active field of research since the early days of NGS (Next generation sequencing) technologies. Since then, evergrowing data availability and the development of increasingly sophisticated analysis methods have uncovered the complexity of the general splicing repertoire.

In this vignette we describe how to use ASpli, an integrative and user-friendly R package that facilitates the analysis of changes in both annotated and novel AS events.

2 Quick start

Here is an example for a pairwise comparison between 2 conditions (Control vs Treatment, 3 replicates each) using default parameters.

Extract features from genome, define *targets* data.frame with phenotype data, and *mBAMs* data.frame with phenotype data for merged BAMs:

```
> genome <- loadDb("txdb.sqlite")
> features <- binGenome(genome)
> targets <- data.frame(bam = c("CT_1.BAM", "CT_2.BAM", "CT_3.BAM",
                                "TR_1.BAM", "TR_2.BAM", "TR_3.BAM"),
                        genotype = c("CT", "CT", "CT", "TR", "TR", "TR"),
                        stringsAsFactors = FALSE)
> mBAMs <- data.frame(bam=c("CT.BAM", "TR.BAM"), condition=c("CT", "TR"))
```

Read counting against annotated features:

```
> counts <- gbCounts(features = features,
                      targets = targets,
                      minReadLength = 125L,
                      maxISize = 50000)
```

Junction-based *de-novo* counting:

```
> asd <- jCounts(counts = counts,
                  features = features,
                  minReadLength = 125L)
```

Differential signal estimation:

```
> gb <- gbDUREport(counts, contrast = c(-1, 1))
> jdur <- jDUREport(asd, contrast = c(-1, 1))
```

Report and signal integration:

```
> sr      <- splicingReport(gb, jdur, counts)
> is      <- integrateSignals(sr,asd)
```

Export results:

```
> exportSplicingReports( sr, output.dir="results")
> exportIntegratedSignals(is,sr=sr,
                          output.dir = "results",
                          counts=counts,features=features,asd=asd,
                          mergedBams = mBAMs)
```

3 Getting started

3.1 Installation

ASpli is available at Bioconductor site and can be installed following these steps: `biocLite()`:

```
> if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
> BiocManager::install("ASpli")
> library(ASpli)
```

3.2 Required input data

ASpli requires the following data in order to execute the analysis pipeline:

- BAM and BAI files for each analyzed sample.
- A genome annotation file in the TxDb format, as produced by the `GenomicFeatures` package. The `GenomicFeatures` package provides functions to create TxDb objects based on data downloaded from UCSC Genome Bioinformatics, BioMart or gff/gtf files. See "Creating New TxDb Objects or Packages" in the `GenomicFeatures` vignette for more details. In this example, a TxDb is built from a gtf file:

```
> library(GenomicFeatures)
> TxDb <- makeTxDbFromGFF(
  file="genes.gtf",
  format="gtf")
```

The building of a TxDb object might be time consuming, depending on the size of your genome. If a TxDb has been already created, we strongly recommend saving it as a `sqlite` file and reloading it any time the analysis is run.

```
> saveDb(TxDb,file="gene.sqlite")
```

Please, make sure all files use the same coordinate system.

- Optionally: replicate merged BAM files for each contrasted condition are needed to estimate uniform coverage statistics and to generate graphical reports through the `exportIntegratedSignals` function.

4 Using ASpli

The workflow intended to be used with ASpli is divided in four main steps (Figure 1).

1. Extract features from genome TxDb: `binGenome()`
2. Counting: `gbCounts()`, `jCounts()`
3. Differential signals: `gbDUreport()`, `jDUreport()`
4. Reports: `splicingReport()`, `integrateSignals()`

The main objects classes used to store data and perform operations are:

- `ASpliFeatures`: Contains genomic coordinates
- `ASpliCounts`: Contains number of reads overlapping each genomic feature
- `ASpliAS`: Contains counts of aligned junctions
- `ASpliDU`: Contains results of Differential expression and usage
- `ASpliJDU`: Contains results of Differential Junctions usage
- `ASpliSplicingReport`: Contains differential usage information using different evidences
- `ASpliIntegratedSignals`: Contains signals present in the region

At each step it is possible to export intermediate results. See Section 6: [Appendix: Detailed Outputs](#) for more details.

Figure 1: ASpli core Functionalities

4.1 binGenome: Binning the genome

The `binGenome` method is a one-stop function to:

- split genes into subgenomic features called bins
- extract junction, gene and bin coordinates
- infer bin splicing events from annotation

`binGenome`'s output is an object of class `ASpliFeatures`. Methods `featuresg`, `featuresb`, `featuresj` can be used to access genes, bins and junctions coordinates as `GRanges` (`GRanges` objects defined in the `GenomicRanges` package.)

```
> annFile      <- aspliExampleGTF()
> aTxDb        <- makeTxDbFromGFF(annFile)
> features     <- binGenome( aTxDb )
> geneCoord    <- featuresg( features )
```

```
> binCoord      <- featuresb( features )
> junctionCoord <- featuresj( features )
```

In the case gene symbols were available, they could be appended as follow:

```
> symbols      <- data.frame( row.names = genes( aTxDb ),
                             symbol = paste( 'This is symbol of gene:',
                                             genes( aTxDb ) ) )
> features     <- binGenome( aTxDb, geneSymbols = symbols )
```

4.1.1 Bin definition

Exon and intron coordinates are extracted from the annotation, but only those from multi-exonic genes are saved for further evaluation. When more than one isoform exists, some exons and introns will overlap. In the same spirit of [1], exons and introns are then subdivided into non-overlapping sub-genic features dubbed **bins**, defined by the boundaries of different exons across transcript variants. These so defined **bins** are maximal sub-genic features entirely included or entirely excluded from any mature transcript (see Fig 2).

For an hypothetical gene named GeneAAA subgenic features are labelled as follow:

- **GeneAAA:E001**: defines first exonic bin
- **GeneAAA:I001**: defines first intronic bin
- **GeneAAA:lo001**: defines first **Intron original**
- **GeneAAA:J001**: defines first annotated junction of GeneAAA
- **chr.start.end**: defines an experimental junction

Bins and junctions are consecutively named from 5' to 3' of reference sequence, irrespective of their gene's strand. This implies that lower numbers are always closer to the 5' of forward strand. Alternative splicing bins are named as exons.

Exonic and intronic bins are further classified into *exclusively exonic bins*, *exclusively intronic bins*, or *alternative splicing bins* (AS) (See Figure 2).

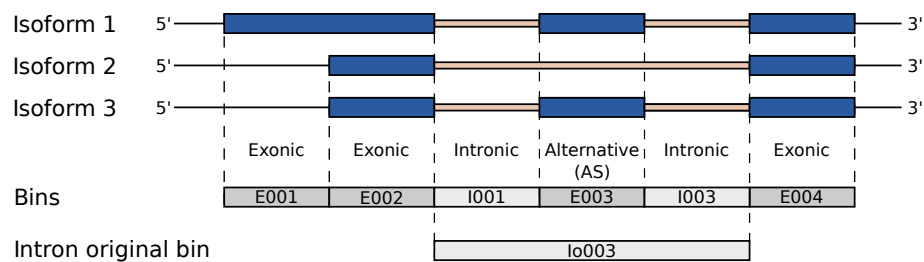


Figure 2: Schema of resulting bins from a gene with three hypothetical transcripts
Those bins that are exonic and intronic in different isoforms are named **AS bins**.

Bins that overlap with the beginning or end of any transcript are labelled as **external**. Please note that an external bin of a transcript may overlap to a non external bin of another transcript, in these cases the bin is still labelled as **external**. In addition to these non overlapping bins, full introns are extracted from annotation and labelled as **lo**)

4.1.2 Splicing event assignment

Each AS bin is further classified considering a three-bin *local splicing model*. Splicing-event categories are assigned to a given bin based on the intronic/exonic character of the analyzed bin and its first neighbors (Figure 3).

For genes presenting two isoforms, this model is able to unambiguously assign a well defined splicing event category to the analyzed bin: exon skipping (ES), intron retention (IR), alternative five prime splicing site (Alt5'SS), or alternative three prime splicing site (Alt3'SS) (see first row of Figure 3).

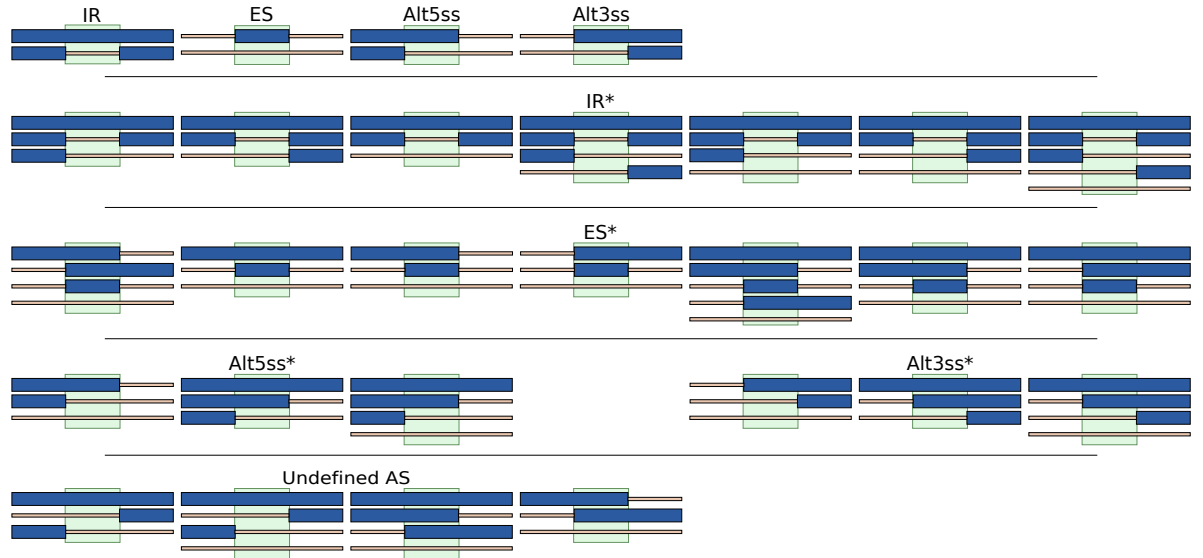


Figure 3: Summary of assignment of splicing events to bins from minimum gene model

The bin being evaluated has a green background highlight. The blue boxes represents exons, while the little light orange boxes represent introns. Gene models shown are plus sense strand.

When more than two isoforms are present, we still found it useful to use the three-bin local model to segment follow up analysis. For these cases (see rows 2-4 of Figure 3) ASpli identify splicing events that involve: intronic subgenic regions surrounded by exons in at least one isoform (bin labelled as IR*), exonic subgenic regions surrounded by two introns in at least one isoform (bin labelled as ES*), exonic regions surrounded by intronic and exonic neighbor bins (bin labelled as Alt5'SS* or Alt3'SS*).

When it is not possible to get a clear splicing-type assignment (last row of Figure 3), bins are labeled as *undefined AS* (UAS).

4.2 Read counting

4.2.1 Targets data.frame definition

BAM file names and experimental factors should be provided as a dataframe that has as many rows as samples. The first column should be named *bam* and should contain the path to a BAM file. Next columns should be used to specify the different experimental factors for each sample.

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For instance, for a two-factor design (e.g. *genotype* and *time*) the *targets* data.frame could have been defined like this:

```
> BAMFiles <- c("path_to_bams/CT_time1_rep1.BAM", "path_to_bams/CT_time1_rep2.BAM",
               "path_to_bams/CT_time2_rep1.BAM", "path_to_bams/CT_time2_rep2.BAM",
               "path_to_bams/TR_time1_rep1.BAM", "path_to_bams/TR_time1_rep2.BAM",
               "path_to_bams/TR_time2_rep1.BAM", "path_to_bams/TR_time2_rep2.BAM")
> (targets <- data.frame( bam = BAMFiles,
                        genotype = c( 'CT', 'CT', 'CT', 'CT',
                                      'TR', 'TR', 'TR', 'TR' ),
                        time      = c( 't1', 't1', 't2', 't2',
                                      't1', 't1', 't2', 't2' ),
                        stringsAsFactors = FALSE ))
```

	bam	genotype	time
1	path_to_bams/CT_time1_rep1.BAM	CT	t1
2	path_to_bams/CT_time1_rep2.BAM	CT	t1
3	path_to_bams/CT_time2_rep1.BAM	CT	t2
4	path_to_bams/CT_time2_rep2.BAM	CT	t2
5	path_to_bams/TR_time1_rep1.BAM	TR	t1
6	path_to_bams/TR_time1_rep2.BAM	TR	t1
7	path_to_bams/TR_time2_rep1.BAM	TR	t2
8	path_to_bams/TR_time2_rep2.BAM	TR	t2

The *targets* data frame contains experimental factor values for each sample. **ASpli** generates simple code-name for each experimental condition concatenating the corresponding factor levels. They can be check using the `getConditions()` function.

```
> getConditions( targets )
```

The order of the conditions given by `getConditions` is the same that in contrast argument of `DUreport.norm` function.

Important 1 The keyword *condition* is internally used by **ASpli** to store experimental condition code-names and SHOULD NOT be used as an experimental factor name in the definition of the *targets* data.frame.

Important 2 Row-names can be defined for the *targets* data.frame to univoqually identify each sample through the analysis. However this is not mandatory. **ASpli** automatically use condition code-names to generate unique sample ids whenever default rownames (i.e. consecutive numbers) were detected in *targets* data.frame.

4.2.2 gbCounts: Summarize read overlaps against all feature levels

The method `gbCounts()` allows to count the number of reads that overlaps each defined feature (i.e. genes, bins, junctions and intron/exon flanking regions). For genes and bins, read density values are also computed as the ratio between the number of reads and the length of a given feature.

```
> counts <- gbCounts(features,
                    targets,
                    minReadLength,
```

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```
maxISize,  
minAnchor=10)
```

- **features**: An object of class `ASpliFeatures`. It is a list of `GRanges` at gene, bin and junction level
- **targets**: A dataframe containing sample, BAM and experimental factors as defined in Section 4.2.1 : [Targets data.frame definition](#).
- **minReadLength**: Reads shorter than *minReadLength* will not be considered to compute E1I and IE2 read coverage (see below).
- **maxISize**: Maximum intron expected size. Junctions longer than `maxISize` will be discarded.
- **minAnchor**: Minimum percentage of *minReadLength* that should be aligned to an exon-intron boundary (see 4.2.2 : [Additional considerations](#)).

The result of `gbCounts()` method is an object of class `ASpliCounts`. Count and read density dataframes can be extracted using accessors methods. An extensive summary of the information stored in these tables is included in 6 : [Appendix: Detailed Outputs](#).

Access data:

```
> GeneCounts <- countsg(counts)  
> GeneRd <- rdsg(counts)  
> BinCounts <- countsb(counts)  
> BinRd <- rdsb(counts)  
> JunctionCounts <- countsj(counts)
```

Export tables to text files:

```
> writeCounts(counts=counts, output.dir = "example")  
> writeRds(counts=counts, output.dir = "example")
```

Additional considerations

- Every intron is considered as a potential retained intron. To analyze putative intron retention events, `ASpli` considers the corresponding upstream and downstream exons (E1 and E2, always in the forward sense). Then, following [2], new artificial ranges that overlap the two retention regions E1I (connecting exon E1 and intron I) and IE2 (connecting intron I and exon E2) are defined:
 - E1I: $[I_s - \text{readLength} (1 - \text{minAnchor}/100), I_s + \text{readLength} (1 - \text{minAnchor}/100)]$
 - IE2: $[I_e - \text{readLength} (1 - \text{minAnchor}/100), I_e + \text{readLength} (1 - \text{minAnchor}/100)]$

where I_s and I_e are the intron start and end coordinates respectively. `minAnchor` is 10% of read length by default (parameter `minAnchor`)

Please check before start the read length of your sequenced library Only those reads which minimum overlap *minReadLength* and without gap in this interval are considered. As a consequence, only reads aligned **within** those two exons/introns are counted.

To access this data:

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```
> eliCounts <- countseli(counts)
> ie2Counts <- countsie2(counts)
```

- For a given gene, the read count number is computed as the number of reads overlapping any exon included in the corresponding annotated gene model. If a single read overlaps more than one exon, it is counted only once. Note that **one read can overlap two different genes, in this case it is counted for both of them**.
- Effective length: is the sum of the length of exonic bins and alternative bins (i.e. all bins except intronic bins).
- Junctions are extracted from BAM files. They are defined as those reads that aligned against disjoint region of the reference genome(N operator of CIGAR notation for aligned reads [3]), and are essential for alternative splicing event quantification and discovery. Junction alignment confidence is extremely important and it should be controlled at the alignment step.

4.2.3 jCounts: Summarize junctions inclusion indices PSI, PIR and PJU

PSI (percent of inclusion) and PIR (percent of intron retention) metrics (see below) are calculated for each bin and experimental condition. The selection of which metric is used is based on the type of splicing event associated with each bin (see 4.1.2 : [Splicing event assignment](#)). In addition, annotation-free inclusion indices (PIR_j and PJU, see below) are estimated using experimentally detected junctions.

```
> asd <- jCounts(counts,
                 features,
                 minReadLength,
                 threshold,
                 minAnchor)
```

Novel arguments for this function call are:

- counts: An object of class `ASpliCounts`
- threshold: Minimum number of reads supporting junctions (Default=5)

Results: An object of class `ASpliAS..` An extensive summary of the information stored in this object is included in 6 : [Appendix: Detailed Outputs](#).

Accessors:

```
> irPIR <- irPIR( asd )
> altPSI <- altPSI( asd )
> esPSI <- esPSI( asd )
> allBins <- joint( asd )
> junctionsPJU <- junctionsPIR( asd )
> junctionsPIR <- junctionsPIR( asd )
```

Export tables to text files:

```
> writeAS(as=asd, output.dir="example")
```

Junction supporting evidence of alternative bin usage ASpli makes use of junction data as supporting evidence of alternative usage of bins. For a general differential splicing event affecting a given bin, it is always possible to define *exclusion* and *inclusion* junctions. The first class of junctions (noted as J_3) pass over the bin of interest, whereas the second ones (note as J_1 and/or J_2) quantify and support the inclusion of start and/or end bin boundaries in the mature transcript. Figure 4 illustrates this point for the different types of splicing events that could affect a given bin. ASpli considers for this analysis junctions that are completely included within a unique gene and have more than a minimum number of reads supporting them (by default this number is five).

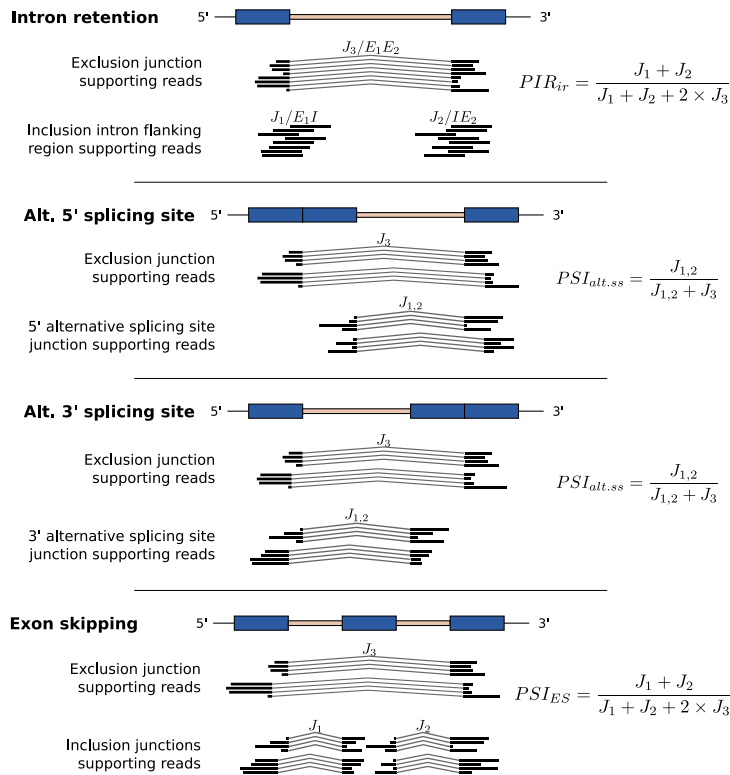


Figure 4: PSI and PIR metrics estimation and their relationship with junctions

PSI (percent spliced in) [?] and PIR (percent of intron retention) metrics are two well known statistics that can be used to quantify the relative weight of inclusion evidence for different kind of splicing events. For each bin, ASpli quantifies the inclusion strength in every experimental condition using the appropriate inclusion index (see Fig 4).

Annotation-free inclusion indices ASpli relies on the direct analysis of experimentally observed splicing junctions in order to study novel (i.e. non-annotated) splicing patterns.

For every experimental junction, ASpli characterizes local splicing patterns considering two hypothetical scenarios. For one hand, assuming that every detected junction might be associated to a possible intron that could be potentially retained, a PIR_{junc} value is computed (upper panel of Figure 5).

On the other hand, every junction also defines potential 5' and 3' splicing sites. It can be the case that one (in an alternative 5' or 3' scenario), or both ends (in case of exon skipping) were shared by other junctions. In this context, it is informative to characterize the relative abundance of the analyzed junction (dubbed J_3) with respect to the locally *competing* ones. ASpli estimates *percentage junction-usage* indices, PJU_{J_1} and PJU_{J_2} , in order to evaluate and quantify this quantities (see bottom panel of figure 5). In order to illustrate this point, we show in figure 6 an hypothetical splicing scenario for a given junction of interest, J_3 . It can be appreciated that PJU_{J_1} quantifies the participation of this junction in the context of a splicing pattern involving the two orange competing junctions, whereas PJU_{J_2} reports on the usage of J_3 in connection with the green competing junction.

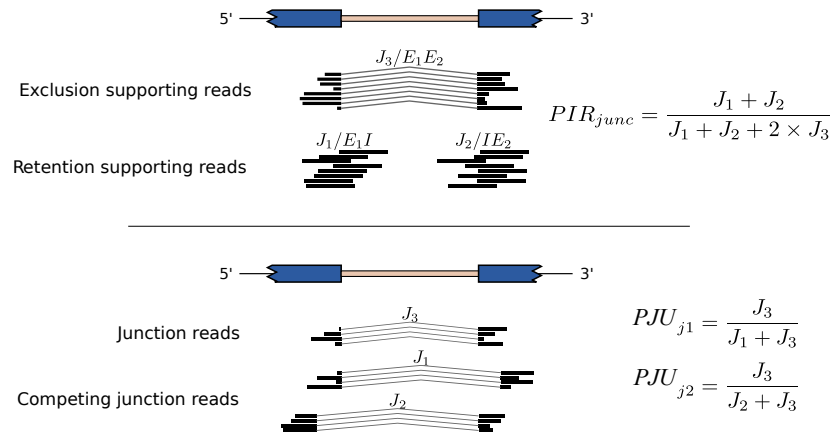


Figure 5: PIR and PJU metrics for junctions

Additional considerations:

- Only those junctions with a minimum number of counts (default=5) in **all** samples of at least 1 condition are used for PIR/PSI analysis.
- For each bin, a PIR or a PSI metric is calculated, depending on the splicing event category assigned to that bin (see section 4.1.2 : [Splicing event assignment](#)). If no splice event was assigned (*this bin is not alternative*), an exon will be considered to be involved in a putative exon skipping splicing event, and an intron will be considered to be involved in a putative intron retention splicing event.

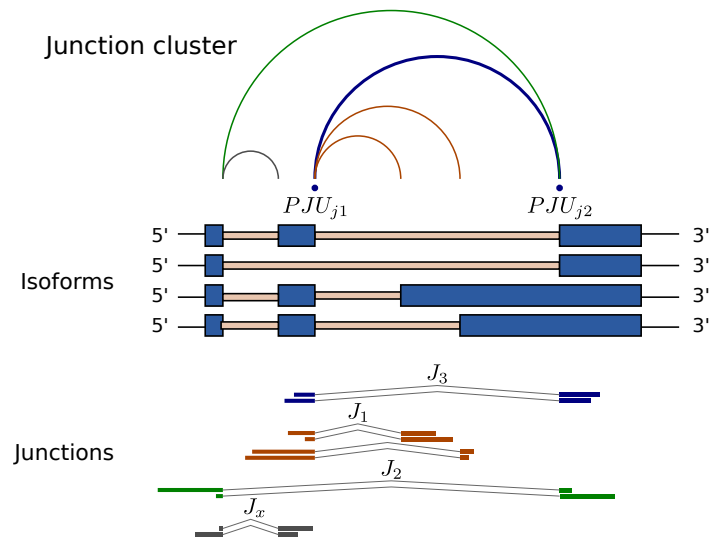


Figure 6: Percentage of junction usage

4.3 Differential signals

ASpli leverages on the statistical framework developed by Smyth and collaborators, implemented in the edgeR R-package [?, ?], to assess for statistically significant changes in gene-expression, bin coverage and junction splicing signals. Under this approach, count data is modeled using a negative binomial model, and an empirical Bayes procedure is considered to moderate the degree of overdispersion across units.

In order to study splicing patterns, gene expression changes should be deconvolved from overall count data. On a very general setting, what we are looking for is to test whether a given unit of a certain group of elements displays differential changes respect to the collective or average behavior. ASpli uses this general idea to assess for statistically significant changes in splicing patterns probed with different genomic features:

- bin-coverage signal: ASpli assesses for differential usage of bins comparing bin's log-fold-changes with the overall log-fold-change of the corresponding gene.
- junction anchorage signal: For every experimentally detected junction, ASpli analyzes differential intron retention changes by considering log-fold-changes of a given experimental junction relative to changes in coverage of left and right junction flanking regions.
- junction locale signal: In the same spirit than MAJIQ and LeafCutter, ASpli defines junction-clusters as sets of junctions that share at least one end with another junction of the same cluster (see Figure 6). In order to characterize changes for a given junction along experimental conditions, ASpli weighs log-fold-change of the junction of interest relative to the mean log-fold-change of junctions belonging to the same cluster.

ASpli makes use of the functionality implemented in the diffSpliceDGE function of the edgeR package to perform all of this comparisons within a unified statistical framework. Given a set of elements (i.e. bins or junctions) of a certain group (i.e. genes, anchorage group or junction-cluster), a negative binomial generalized log-linear model is fit at the element level, considering an offset term that accounts for library normalization and collective changes. Differential usage is assessed testing coefficients of the GLM. At the single element-level,

the relative log-fold-change is reported along with the associated p-value and FDR adjusted q-values. In addition a group-level test is considered to check for differences in the usage of any element of the group between experimental conditions (see *diffSpliceDGE* documentation included in edgeR package for details [?]).

4.3.1 gbDureport: Bin-based coverage differential signals of AS

To run this analysis:

```
> gb <- gbDureport( counts,
  minGenReads = 10,
  minBinReads = 5,
  minRds = 0.05,
  contrast = NULL,
  ignoreExternal = TRUE,
  ignoreIo = TRUE,
  ignoreI = FALSE,
  filterWithContrasted = TRUE,
  verbose = TRUE,
  formula = NULL,
  coef = NULL)
```

Summary of arguments:

- minGenReads (Default=10): Genes with at least an average of minGenReads reads for **any** condition are included into the differential expression test. Bins from genes with at least an average of minGenReads reads for **all** conditions are included into the differential bin usage test.
- minBinReads (Default=5): Bins with at least an average of minGenReads reads for any condition are included into the differential bin usage test.
- minRds (Default=0.05) = genes with at least an average of read density for any condition are included into the differential expression test. Bins belonging to genes with at least an average of minRds read density for **all** conditions are included into the differential bin usage test. Bins with at least an average of minRds read density for **any** condition are included into the differential bin usage test.
- ignoreExternal (Default = TRUE): Ignore first or last transcript bins
- ignoreIo (Default = FALSE) : Ignore intronic bins, test is performed only for exons.
- ignoreI (Default = TRUE): Ignore original introns.
- contrast: Numeric vector of length equal to the number of experimental conditions (as defined by `targets`). The values of this vector are the coefficients of each condition (in the order given by `getConditions()`) to set up the contrast of interest. If contrast = NULL (and also formula=NULL), a pairwise comparison between the second and the first conditions will be considered for calculations (i.e. contrast= c(-1,1,0,...0))

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- `filterWithContrasted`: logical value. If TRUE (default) bins, genes and junctions will be filtered by read counts and read densities using data from the conditions that will be used in the sought comparison (i.e. those which coefficients in contrast argument are different from zero). If FALSE, all conditions will be considered at filtering time. *It is strongly recommended do not change this value*
- `verbose`: shows details of calculations (Default=TRUE)
- `formula`: A formula can be used to specify a specific term to be tested. If `coef` is specified, then that coefficient will be tested. If not, it defaults to the last term in the formula.
- `coef`: for formula only. The coefficient to be tested. If NULL the test defaults to the last term in the formula

The result of `gbDUreport()` method is an object of class `ASpliDU`. Gene expression and bin differential usage information can be extracted using accesors methods. An extensive summary of the information stored in this object is included in 6 : [Appendix: Detailed Ouputs](#).

Accesors:

```
> geneX <- genesDE( gb )
> binDU <- binsDU( gb )
```

Export tab delimited tables:

```
> writeDU(gb, output.dir = "example")
```

Additional considerations

- Bins and junctions from expressed genes are considered if they have enough supporting reads (Default=5) in at least one condition.
- *External bins* are excluded by default in the analysis. However, an *external* bin for one isoform can overlap to a *non external* bin from other isoform that can participate in alternative splicing regulation, `ASpli` allows to optionally include them.
- *lo (original intron)* bins, excluded by default.

Note that the inclusion of those bins affects the estimation of corrected p-values (fdr). The information provided by *lo* bins are highly correlated with their sub bins and increase largely the number of events to be analyzed. The fdr correction become more strict and there is a violation on the fdr correction assumption that all individual tests are independent from each other. If an *lo* bin shows a significant change, there is a very high chance that at least one of their sub bins also shows a significant change.

4.3.2 `jDUreport`: Junction-centered analysis of AS

Based on abundance information of experimentally detected junctions, `jDUreport` considers J_1 , J_2 and J_3 junction sets, as defined in 5 : [PIR and PJU metrics for junctions](#), to analyze annotation-free *junction-anchorage* and *junction-locale* alternative splicing signals (see 4.3 : [Differential signals](#)). In addition, for every annotated bin, this functions tests junction supporting evidence of bin usage (see 4 : [PSI and PIR metrics estimation and their relationship with junctions](#)).

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To run this analysis:

```
> jdu <- jDUreport(asd,
  minAvgCounts          = 5,
  contrast              = NULL,
  filterWithContrasted  = TRUE,
  runUniformityTest     = FALSE,
  mergedBAMs            = NULL,
  maxPValForUniformityCheck = 0.2,
  strongFilter          = TRUE,
  maxConditionsForDispersionEstimate = 24,
  formula               = NULL,
  coef                  = NULL,
  maxFDRForParticipation = 0.05,
  useSubset             = FALSE)
```

Summary of arguments:

- asd: An object of class `ASpliAS` with results of PSI and PIR using experimental junction
- minAvgCounts (Default=5): Minimum average counts for filtering.
- runUniformityTest (Defaults = FALSE): Run uniformity test on **Intron Retention** in order to detect non-uniform read coverage along the intron. This test compares the standard deviation of the inner intron region (11 bases from both ends) to the mean of both intron ends. Numbers closer to 0 mean more uniform coverage. This is an experimental feature, requires the existence of one merged BAM per experimental condition and takes some time to run.
- mergedBAMs: Path to merged BAMs for each testing condition. *If no merged BAMs exist (for example, paired samples without replicates), use the same BAMs as targets.*
- maxPValForUniformityCheck: To speed up uniformity test only check junctions with $pval < maxPValForUniformityCheck$ (Default=0.2)
- strongFilter: If strongFilter is TRUE, then we discard junction clusters with at least one junction that doesn't pass the filter.
- maxConditionsForDispersionEstimate: In order to reduce resource usage, estimate dispersion for statistics tests with a reduced number of conditions.
- maxFDRForParticipation: In order to calculate junctionPSI participation, only use significant junctions (*ie junctions with $FDR < maxFDRForParticipation$*). (Default=0.05)
- useSubset: Experimental. *It is strongly recommended to leave the default, FALSE.*

Results are stored in an `ASpliJDU` object. Note that this analysis considers junctions that are completely included within a unique gene and have enough supporting reads (MinAvgCounts, Default = 5)

Accessors:

```
> localej( jdu )
> localec( jdu )
> anchorj( jdu )
> anchorc( jdu )
> jir( jdu )
```

```
> jes( jdu )
> jalt( jdu )
```

`localc` and `localj` together with `anchorc` and `anchorj` data.frames provide information regarding statistically significant changes observed in connection with junction usage inside *locale* and *anchorage*-junction clusters respectively. `jir`, `jes` and `jalt` accessors provide information regarding junction support of bin usage.

Export tab delimited table:

```
> writeJDU(jdu,output.dir = "test")
```

4.4 Integrative reports

4.4.1 `splicingReport`: bin and junction signals integration

This function combines differential splicing information from different sources. Bin and junction usage information is integrated in three steps. First, *bin* and annotated junction information (`jir`, `jes`, `jalt`) are consolidated. Then, bins that overlap with *locale*-J3 junctions (junctions that cover the entire locale region) are identified and the corresponding signals are combined. Finally, the same procedure is performed for bins and *anchorage*-J3 junctions.

To run this analysis

```
> sr      <- splicingReport(gb,
                           jdur,
                           counts)
```

Results are stored in an `ASpliSplicingReport` object.

Accessors:

```
> binbased( sr )
> localebased( sr )
> anchorbased( sr )
```

`binbased(sr)` data.frame combines information from bins and annotated junctions. For each case, either ΔPSI or ΔPIR statistics is reported based on the *bin* splicing type. `localebased(sr)` is a data.frame with information from bins and *locale* junctions. Statistics for each junction are located in columns prefixed with "junction" and statistics for the corresponding cluster are prefixed with the "cluster" keyword. Changes in *participation* coefficients are also reported. If *locale* clusters matched a *bin*, the corresponding bin statistics are also included. The data structure of `anchorbased(sr)` data.frame is similar to the `localebased(sd)` one. All data.frames also include junction count records for debugging purposes.

Export tab delimited table (see 4.4.3 : `exportSplicingReport`: [Export splicing reports in HTML pages](#) for interactive html reports):

```
> writeSplicingReport( sr, output.dir = "test")
```


4.4.2 `integrateSignals()`: Region specific summarization of differential usage signals.

This function integrates different usage signals reported in overlapping genomic regions:

- **bin** signal: a bin is called differentially-used by ASpli if it displays statistically significant coverage changes ($\text{fdr} < 0.05$, by default) and, additionally, one of the two supplementary conditions hold: either the bin fold-change level is greater than a given threshold (3 fold changes, by default) or changes in inclusion levels of bin-supporting junctions (ΔPIR or ΔPSI according to the bin class surpasses a predefined threshold (0.2 by default)).
- **anchorage** signal: statistically significant changes are found at the cluster level ($\text{cluster.fdr} < 0.05$ by default) for the considered $\{J_1, J_2, J_3\}$ junction set (see upper panel of Fig 5) and, at the same time, $|\Delta\text{PIR}_{J_3}|$ is larger than a given threshold (0.3 by default).
- **locale** signal: statistically significant changes are found at the cluster level ($\text{cluster.fdr} < 0.01$ by default) for the analysed junction cluster $\{J_1, \dots, J_S, \dots, J_n\}$ (see 6) and, at the same time, there is at least one junction J_S within the cluster presenting statistically significant changes at the single unit level ($\text{junction.fdr} < 0.05$, by default) with $|\Delta\text{Participation}_{J_S}|$ larger than a given threshold (0.3 by default). In the case that statistically significant changes were detected at the unit-level for more than one junction of a given cluster, the one displaying the largest participation change was considered and reported as the cluster's representative junction.

```
> is      <- integrateSignals(sr, asd,
                             bin.FC = 3, bin.fdr = 0.05, bin.inclusion = 0.2,
                             nonunif = 1, usenonunif = FALSE,
                             bjs.inclusion = 10, bjs.fdr = 0.01,
                             a.inclusion  = 0.3, a.fdr = 0.01,
                             l.inclusion  = 0.3, l.fdr = 0.01,
                             otherSources = NULL, overlapType = "any")
```

Arguments:

- **sr**: An object of class `ASpliSplicingReport`
- **asd**: An object of class `ASpliDU`
- **bin.FC**: fold change threshold for bin signals. By default only bin signals with $\text{bin.fc} > \log_2(3)$ are retained.
- **bin.fdr**: Maximum FDR for bin signals.
- **bin.inclusion**: Minimum level of change for junction support inclusion signals (either ΔPIR or ΔPSI) associated to bins who already passed **bin.FC** and **bin.fdr** filters.
- **nonunif**: Maximum value of non-uniformity for intronic bins ($\text{nonunif} \ll 1$ means homogeneous coverage)
- **usenonunif**: Whether to use non uniformity as filter.
- **bjs.inclusion**: Minimum level of change for junction support inclusion signals (either ΔPIR or ΔPSI).
- **bjs.fdr**: Maximum FDR for annotated junctions.

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- `a.inclusion`: Minimum level of inclusion change for *anchorage* junctions.
- `a.fdr`: Maximum FDR for *anchorage* junctions.
- `l.inclusion`: Minimum level of *participation* change for *locale* junctions..
- `l.fdr`: Maximum FDR for *locale* junctions.
- `otherSources`: If user wants to compare ASpli results with results from other methods, *otherSources* must be a `GenomicRange` object with all the regions found with the other methods. It will be integrated with a new column next to signals information.
- `overlapType`: Matching criterium for region overlaps. Defaults to "any" and can be any of the following: "any", "start", "end", "within", "equal".

Results are stored in an `ASpliIntegratedSignals` object.

Accessors:

```
> signals( is )
> filters( is )
```

`filters(is)` stores the parameter values used to filter the different usage signals to be integrated (e.g. minimum fold-changes, statistical thresholds, minimal inclusion values, etc).

`signals(is)` contains region-based information of splicing signals. Table 1 shows the first 5 columns of this data.frame. Columns `b`, `bjs`, `ja` and `jl` stand for bin, bin-junction-support, junction-anchorage and junction-locale signals. Non-zero entries indicate the presence of the corresponding signal for the considered genomic range. An asterisk indicates overlap but not an exact match between the genomic ranges where the examined signals were observed.

region	b	bjs	ja	jl
Chr1:45560-45645	1	1	0	0	
Chr1:387673-388267	1	1	1	1	...
Chr1:406793-406902	1	1	0	*	

Table 1: First five columns of `signals(is)` data.frame

In this example a bin-signal (*b*) was found in region *Chr1:406793-406902*. A matching bin-junction supporting signal was also reported (*bjs*), so both discoveries were merged. Finally, a significant *locale* cluster overlapped the region, but genomic ranges did not match, so an * was used for that signal.

4.4.3 `exportSplicingReport`: Export splicing reports in HTML pages.

This function makes use of the `DT` R-package [4], a wrapper of the JavaScript library 'DataTables' to export *splicing report* results into interactive html pages.

```
> exportSplicingReports( sr,
  output.dir="sr",
  openInBrowser = F,
  maxBinFDR = 0.2,
  maxJunctionFDR = 0.2 )
```

Arguments:

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- `sr`: An object of class `ASpliSplicingReport`
- `output.dir`: HTML reports output directory
- `openInBrowser`: logical. Whether results are automatically displayed just after exporting.
- `maxBinFDR` (Default = 0.2) Only export info for bins with $FDR < \text{maxBinFDR}$
- `maxJunctionFDR` (Default = 0.2): Only export info for junctions with $FDR < \text{maxJunctionFDR}$

The result is an HTML page, where you can easily browse the tables stored in an *ASpliSplicingReport* object.

4.4.4 `exportIntegratedSignals()`: Export integrated signals into HTML pages.

This function makes use of the *DT* R-package [4], a wrapper of the JavaScript library 'DataTables', to export region-based integrated signal results into interactive html pages.

```
> exportIntegratedSignals( is, output.dir="is",
                           sr, counts, features, asd,
                           mergedBams,
                           jCompletelyIncluded = FALSE, zoomRegion = 1.5,
                           useLog = FALSE, tcex = 1, ntop = NULL, openInBrowser = F,
                           makeGraphs = T, bforce=FALSE
                           )
```

Arguments:

- `is`: An object of class `ASpliIntegratedSignals`
- `sr`: An object of class `ASpliSplicingReport`
- `counts`: An object of class `ASpliCount`
- `features`: An object of class `ASpliFeatures`
- `asd`: An object of class `ASpliAS`
- `output.dir`: HTML reports output directory
- `mergedBams` Dataframe with two columns, `bams` and `conditions`. Bams are paths to merged bam files for each condition. These will be used to produce coverage plots if `makeGraph=TRUE`.
- `jCompletelyIncludedIf TRUE` only plot junctions completely included inside the plot region. Otherwise plot any overlapping junctions, not necessarily contained in the region of interest
- `useLogPlot` counts log
- `tcexText` size
- `ntopOnly` show *n* top signals
- `openInBrowser` Open reports in browser when done
- `makeGraphsGenerate` graphs in reports
- `bforceForce` plot generation even if plot already exists on disk

The result is an HTML page, where you can easily browse the tables stored in an ASplilntegratedSignals object.

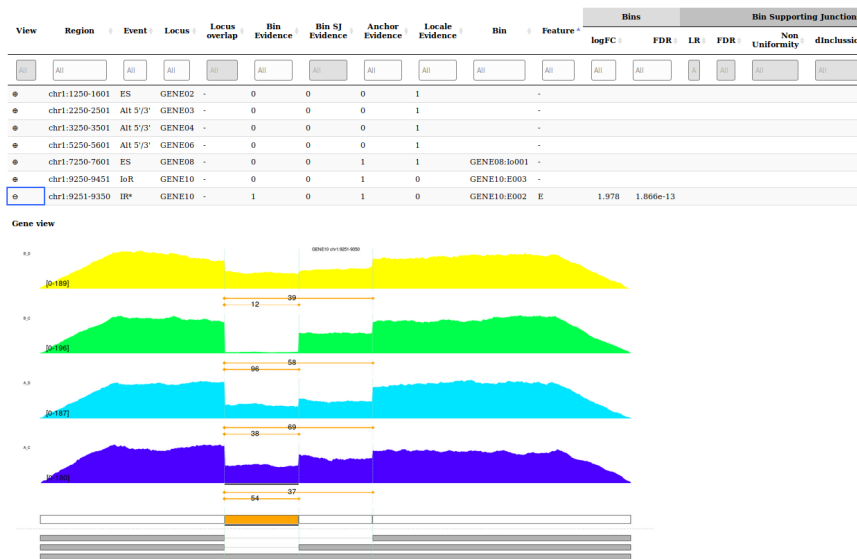


Figure 7: Example of integrate signal DataTable report

5 Case studies

ASpli provides a small synthetic data set to test the whole pipeline. It consists of

- a genome with ten genes with multiple isoforms
- a set of twelve **BAM** files from an experiment with a two×two factorial design
- four merged **BAM** files (merged replicates, one per condition)
- a **GTF** file with the corresponding annotation.

5.1 2x2 experimental design

The two factors in this example are called **f1** and **f2**. **f1** can have value **A** or **B** and **f2** can have value **C** or **D**, defining four conditions: **A.C**, **A.D**, **B.C** and **B.D**. Table 2 summarizes the experimental design.

sample	f1	f2	replicate	condition
1	A	C	0	A.C
2	A	C	1	A.C
3	A	C	2	A.C
4	A	D	0	A.D
5	A	D	1	A.D
6	A	D	2	A.D
7	B	C	0	B.C
8	B	C	1	B.C
9	B	C	2	B.C
10	B	D	0	B.D
11	B	D	1	B.D
12	B	D	2	B.D

Table 2: Experimental design of the example data set

The first step of the workflow is to build the TxDb object and extract their features.

```
> library( ASpli )
> library( GenomicFeatures )
```

Load a small *gtf*. In this case `gtfFileName` contains the full path to the example *gtf* file in your system.

```
> gtfFileName <- aspliExampleGTF()
```

Then, create a TxDb object using `makeTxDbFromGFF`

```
> genomeTxDb <- makeTxDbFromGFF( gtfFileName )
```

Extract the genomic features (`binGenome` should produce a brief summary of the parsed genome).

```
> features <- binGenome( genomeTxDb )
> # * Number of extracted Genes = 10
> # * Number of extracted Exon Bins = 38
> # * Number of extracted intron bins = 34
> # * Number of extracted transcripts = 25
> # * Number of extracted junctions = 23
> # * Number of AS bins (not include external) = 17
> # * Number of AS bins (include external) = 17
> # * Classified as:
> #       ES bins = 1          (6%)
> #       IR bins = 3          (18%)
> #       Alt5'ss bins = 2      (12%)
> #       Alt3'ss bins = 2      (12%)
> #       Multiple AS bins = 9   (53%)
> #       classified as:
> #               ES bins = 1          (11%)
> #               IR bins = 4          (44%)
> #               Alt5'ss bins = 2      (22%)
> #               Alt3'ss bins = 1      (11%)
>
```

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Then load the alignment and define your targets. `aspliExampleBAMList()` provides the full path to the BAMs files.

```
> BAMFiles <- aspliExampleBamList()
```

Define the *targets* data.frame:

```
> targets <- data.frame(
  row.names = paste0('Sample', c(1:12)),
  bam = BAMFiles,
  f1 = c('A', 'A', 'A', 'A', 'A', 'A',
        'B', 'B', 'B', 'B', 'B', 'B'),
  f2 = c('C', 'C', 'C', 'D', 'D', 'D',
        'C', 'C', 'C', 'D', 'D', 'D'),
  stringsAsFactors = FALSE)
```

Experimental conditions are inferred from the experimental factors appearing in the *target* data.frame:

```
> getConditions(targets)
> #[1] "A_C" "A_D" "B_C" "B_D"
```

We define a data.frame with path information for merged bams ¹.

```
> mBAMs <- data.frame(bam = sub("_[02]", "", targets$bam[c(1,4,7,10)]),
  condition= c("A_C", "A_D", "B_C", "B_D"))
```

Next step is to overlap reads and features:

```
> counts<- gbCounts(features = features,
  targets = targets,
  minReadLength = 100,
  maxISize = 5000,
  minAnchor = 10)
```

And also quantify junctions:

```
> asd <- jCounts(counts = counts,
  features = features,
  minReadLength = 100,
  threshold = 5,
  minAnchor = 10)
```

At this point we can start asking different questions regarding differential gene expression and splicing patterns. `ASpli` allows to do this by defining *contrasts* or by using the *formula* approach. This feature allows the user to choose the framework that better (i.e. more easily) serve to test the sought effect.

¹BAM files obtained combining replicates of the same experimental conditions (estimated using 'samtools merge ...'). These files are needed to estimate non-uniformity coverage and to produce graphical output reports

5.1.1 The contrast approach

Table 3 shows different examples of contrasts that can be used to test for different hypothesis:

Test	contrast
AS between f2 :C and D conditions, for f1 =A samples	c(-1, 1, 0, 0)
AS between f2 :C and D conditions, for f1 =B samples	c(0, 0,-1, 1)
Interaction effect (i.e. differences between the above-mentioned contrasts)	c(1,-1,-1, 1)

Table 3: Test and contrasts

To continue our mini-tutorial we will focus on the last contrast of Table 3. We will test whether the differential patterns observed between D and C levels of **f2** are different for A and B **f1** levels. The interaction contrast corresponds to:

$$I = (B.D - B.C) - (A.D - A.C) \quad 1$$

As Table 3 shows, the coefficients of the terms in this expression can be represented in the *contrast* vector $[1, -1, -1, 1]$, where we have taken the order given by `getConditions` function in consideration.

We estimate gene differential expression and annotation-based differential splicing patterns for the contrast of interest as follow:

```
> gb <- gbDUreport(counts, contrast = c( 1, -1, -1, 1 ) )
```

`genesDE()` and `binsDU()` accessors report the statistical significance results. We can see that in this example no evidence of a statistically significant interaction term was found at gene expression level. However, 9 out of 14 bins displayed statistically significant interaction effect ($\text{fdr} < 0.01$)

```
> genesDE(gb)
      symbol locus_overlap gene_coordinates start end length effective_length
GENE01 GENE01          -      chr1:1-700    1  700    700             700
GENE02 GENE02          -    chr1:1001-1800 1001 1800    800             550
GENE03 GENE03          -    chr1:2001-2800 2001 2800    800             650
GENE04 GENE04          -    chr1:3001-3800 3001 3800    800             650
GENE05 GENE05          -    chr1:4001-4800 4001 4800    800             650
GENE06 GENE06          -    chr1:5001-5800 5001 5800    800             650
GENE07 GENE07          -    chr1:6001-6800 6001 6800    800             650
GENE08 GENE08          -    chr1:7001-7800 7001 7800    800             800
GENE09 GENE09          -    chr1:8001-8800 8001 8800    800             800
GENE10 GENE10          -    chr1:9001-9800 9001 9800    800             800
      logFC      pvalue    gen.fdr
GENE01 0.007549285 0.9350761 0.9403511
GENE02 0.007639230 0.9366388 0.9403511
GENE03 0.007534440 0.9352261 0.9403511
GENE04 0.007530088 0.9352369 0.9403511
GENE05 0.007589196 0.9347152 0.9403511
GENE06 0.007546634 0.9351211 0.9403511
GENE07 0.007493651 0.9376253 0.9403511
GENE08 0.007477439 0.9356954 0.9403511
GENE09 0.007390949 0.9403511 0.9403511
GENE10 0.007543393 0.9350793 0.9403511

> binsDU(gb)
```

	feature	event	locus	locus_overlap	symbol	gene_coordinates
GENE10:E002	E	IR*	GENE10	-	GENE10	chr1:9001-9800
GENE05:E002	E	Alt5ss	GENE05	-	GENE05	chr1:4001-4800
GENE09:E002	E	IR	GENE09	-	GENE09	chr1:8001-8800
GENE09:E004	E	IR	GENE09	-	GENE09	chr1:8001-8800
GENE05:E003	E	Alt3ss	GENE05	-	GENE05	chr1:4001-4800
GENE10:E003	E	Alt3ss*	GENE10	-	GENE10	chr1:9001-9800
GENE06:E003	E	Alt5ss*	GENE06	-	GENE06	chr1:5001-5800
GENE07:E002	E	IR*	GENE07	-	GENE07	chr1:6001-6800
GENE08:E004	E	IR*	GENE08	-	GENE08	chr1:7001-7800
GENE07:E003	E	ES*	GENE07	-	GENE07	chr1:6001-6800
GENE06:E002	E	Alt5ss*	GENE06	-	GENE06	chr1:5001-5800
GENE08:E002	E	IR*	GENE08	-	GENE08	chr1:7001-7800
GENE09:E003	E	-	GENE09	-	GENE09	chr1:8001-8800
GENE08:E003	E Undefined AS		GENE08	-	GENE08	chr1:7001-7800
	start	end	length	logFC	pvalue	bin.fdr
GENE10:E002	9251	9350	100	1.977667415	1.332765e-14	1.865870e-13
GENE05:E002	4251	4350	100	1.150225212	7.618908e-12	5.333235e-11
GENE09:E002	8251	8350	100	-0.781175999	1.292015e-08	6.029401e-08
GENE09:E004	8451	8600	150	0.548669223	3.893320e-06	1.362662e-05
GENE05:E003	4501	4600	100	-0.490747655	6.879261e-05	1.926193e-04
GENE10:E003	9351	9450	100	-0.523224419	2.154957e-04	5.028232e-04
GENE06:E003	5351	5450	100	0.573447595	2.806660e-04	5.613319e-04
GENE07:E002	6251	6350	100	0.645565633	4.119553e-04	7.209217e-04
GENE08:E004	7451	7600	150	-0.472724302	4.848299e-03	7.541798e-03
GENE07:E003	6351	6450	100	-0.283057484	1.775386e-02	2.485540e-02
GENE06:E002	5251	5350	100	-0.274220353	2.018694e-02	2.569247e-02
GENE08:E002	7251	7350	100	0.285668703	1.222908e-01	1.426726e-01
GENE09:E003	8351	8450	100	0.030260327	7.833095e-01	8.435641e-01
GENE08:E003	7351	7450	100	-0.004371574	9.653519e-01	9.653519e-01

The analysis of annotation-free junction-based AS events can be done with ²:



²Note that as we required to compute non-uniform intron coverage, we should specify merged-BAMs information

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```
> jdur <- jDureport(asd,
  contrast = c( 1, -1, -1, 1 ) ,
  runUniformityTest = TRUE,
  mergedBams = mBAMs)
```

Results for junction-based events matching bin ranges can be accessed through `jir(jdur)`, `jes(jdur)` and `jalt(jdur)` accessors (see 4.3.2 : `jDureport`: [Junction-centered analysis of AS](#)).

Here we show the output corresponding to results of the *locale*-junction cluster analysis. Information regarding *locale* cluster-level tests can be retrieved using:

```
> localec(jdur)
```

	size	cluster.LR	pvalue	FDR	range	participation
1	3	133.453135	1.049591e-29	7.347136e-29	chr1.1250.1601	0.7774086
5	3	112.928798	3.004851e-25	1.051698e-24	chr1.7250.7601	0.5937500
4	3	62.858923	2.240569e-14	5.227995e-14	chr1.6250.6601	0.5371622
3	3	42.405725	6.190330e-10	1.083308e-09	chr1.5250.5601	0.5760369
2	2	23.474442	1.265842e-06	1.772179e-06	chr1.2250.2501	0.9064327
6	2	13.975357	1.852225e-04	2.160929e-04	chr1.3250.3501	0.7954545
7	2	2.330294	1.268779e-01	1.268779e-01	chr1.9250.9451	NA

```
  dParticipation
1      0.5958106
5      0.5075431
4      0.1718485
3      0.3489837
2      0.7642527
6      0.5562201
7      NA
```

Rows are ordered by FDR values. Row names correspond to cluster-ids. The *participation* and *dParticipation* values for the cluster junction displaying the most significant change are shown in the last two columns of the table. Note that NA's are reported for cluster-7 as no statistically significant changes were found for any junction of that cluster.

```
> localej(jdur)[,1:8]
```

	cluster	log.mean	logFC	pvalue	FDR	annotated
chr1.7250.7601	5	4.386581	2.5698302	1.085528e-17	1.953951e-16	Yes
chr1.1250.1601	1	5.648657	-1.4212860	1.714979e-16	1.543481e-15	Yes
chr1.6250.6601	4	4.741467	1.5433340	5.512323e-11	3.307394e-10	Yes
chr1.1250.1301	1	5.206200	1.3095445	1.734985e-09	7.807431e-09	Yes
chr1.1400.1601	1	5.018664	1.2177648	6.210246e-08	2.235689e-07	Yes
chr1.5350.5601	3	4.486500	-1.4944137	8.745607e-08	2.623682e-07	Yes
chr1.7250.7351	5	4.369234	-1.3260083	5.328221e-07	1.370114e-06	Yes
chr1.2250.2501	2	5.048033	-1.0919992	5.965726e-05	1.342288e-04	Yes
chr1.7450.7601	5	4.745954	-0.9015632	1.449218e-04	2.898436e-04	Yes
chr1.6250.6351	4	4.815917	-0.8278715	2.635205e-04	4.743370e-04	Yes
chr1.5450.5601	3	4.890771	0.7430116	8.320551e-04	1.361545e-03	Yes
chr1.3250.3401	6	5.251088	-0.6763645	9.538747e-04	1.430812e-03	Yes
chr1.2350.2501	2	5.003752	-0.6424916	6.665585e-03	9.229271e-03	Yes
chr1.6450.6601	4	5.572384	-0.4350641	1.043428e-02	1.341550e-02	Yes
chr1.3250.3501	6	4.902878	0.4333971	8.022524e-02	9.627029e-02	Yes
chr1.5250.5601	3	4.321928	-0.5156791	1.066013e-01	1.199265e-01	Yes
chr1.9250.9351	7	4.058894	-0.4440972	1.991296e-01	2.108431e-01	Yes
chr1.9250.9451	7	4.080373	0.2484127	4.090542e-01	4.090542e-01	Yes
participation dParticipation						
chr1.7250.7601		0.5937500	0.5075431			
chr1.1250.1601		0.7774086	0.5958106			
chr1.6250.6601		0.4760148	0.3442580			
chr1.1250.1301		0.4624697	0.3495129			
chr1.1400.1601		0.3559322	0.2462977			
chr1.5350.5601		0.5410628	0.4501537			
chr1.7250.7351		0.4716981	0.2963427			
chr1.2250.2501		0.8578199	0.7642527			
chr1.7450.7601		0.5804598	0.4108169			
chr1.6250.6351		0.3310811	0.1724095			
chr1.5450.5601		0.5760369	0.3489837			
chr1.3250.3401		0.7954545	0.5562201			
chr1.2350.2501		0.9064327	0.7642527			
chr1.6450.6601		0.5371622	0.1718485			
chr1.3250.3501		0.7607656	0.5562201			
chr1.5250.5601		0.5318182	0.4626938			
chr1.9250.9351		0.6233766	0.3880825			
chr1.9250.9451		0.7647059	0.3880825			

We integrate all our data:

```
> sr      <- splicingReport(gb, jdur, counts = counts)
> is      <- integrateSignals(sr,asd)
```

And finally we export integrate signals into an interactive html page

```
> exportIntegratedSignals( is, output.dir="aspliExample",
                           sr, counts, features, asd, mBAMs)
>
```

5.1.2 The formula approach

In ASpli it is also possible to use *formulas* to test different hypothesis. In our example we will consider the following formula to model our data:

```
> form <- formula(~f1+f2+f1:f2)
```

This formula correspond to the following model matrix:

```
> model.matrix(form,targets)

      (Intercept) f1B f2D f1B:f2D
Sample1          1  0  0         0
Sample2          1  0  0         0
Sample3          1  0  0         0
Sample4          1  0  1         0
Sample5          1  0  1         0
Sample6          1  0  1         0
Sample7          1  1  0         0
Sample8          1  1  0         0
Sample9          1  1  0         0
Sample10         1  1  1         1
Sample11         1  1  1         1
Sample12         1  1  1         1
attr(,"assign")
[1] 0 1 2 3
attr(,"contrasts")
attr(,"contrasts")$f1
[1] "contr.treatment"

attr(,"contrasts")$f2
[1] "contr.treatment"
```

Table 4 summarizes three statistical comparisons that could be implemented considering the second, third and fourth coefficient of the model:

Test contrast coefficient heightB.C-A.C $c(-1, 0, 1, 0)$ 2A.D-A.C $c(-1, 1, 0, 0)$ 3(B.D-B.C)-(A.D-A.C) $c(1, -1, -1, 1)$ 4

Table 4: Experimental design of the example data set

In this way, to test for an interaction effect with the *formula* framework, we should run:

```
> gb <- gbDureport(counts, formula = form, coef = 4)
> jdur <- jDureport(asd, formula = form, coef = 4,
  runUniformityTest = TRUE,
  mergedBams = mBAMs)
```

5.2 Paired experimental design

The *formula* approach can easily handle paired designs. We will consider a subset of the originally included samples to simulate a paired experiment (see Table 5). In this case **f1** could denote experimental units and **f2** levels, treatment/control conditions.

sample	f1	f2	replicate	condition
1	A	C	0	A.C
4	A	D	0	A.D
7	B	C	0	B.C
10	B	D	0	B.D

Table 5: Experimental design for a minimalistic paired design

```
> targets <- targets[c(1,4,7,10),]
> formula <- formula(~f1+f2)
> gb <- gbDureport(counts, formula = form)
> jdur <- jDureport(asd, formula = form)
> sr <- splicingReport(gb, jdur, counts = counts)
> is <- integrateSignals(sr,asd)
```

6 Appendix: Detailed Ouputs

Here is the content of all the info present in ASpli objects. Some of them are common in several tables. ASpliCounts:

- Gene counts (`countsg`) and gene read densities (`rdsg`) dataframes contain the following information (see table 6 for an example):

row.names Gene name as reported in annotation data.

symbol An optional name for the gene, that must be provided at the moment of feature extraction (see section 4.1.1 : [Bin definition](#)).

locus_overlap overlapping *loci*.

gene_coordinates format `chromosome:start-end`.

start, end,length

effective_length gene length using only annotated exons.

sample data gene read counts/densities (one column per sample).

- Bin counts (`countsb`) and bin read densities (`rdsb`) dataframes contain the following information:

row.names : see 4.1 : `binGenome`: [Binning the genome](#) .

feature Options are: **E** for exonic bins, **I** for intronic bins and **lo** for introns before splitting. See 4.1 : `binGenome`: [Binning the genome](#)

event Splicing event assigned to the bin (see section 4.1.1:[Splicing event assignment](#))

sample data bin read counts/densities (one column per sample)

- Junction counts (`countsj`) dataframe contains the following information:

row.names: Junction name in format `chromosome.start.end` (see 4.1 : `binGenome`: [Binning the genome](#)).

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junction: If junction coincides with a junction inferred from the annotation, the name is shown as is given in section 4.1:binGenome: [Binning the genome](#) , otherwise it is noHit.

gene: Locus that contains the junction.

strand: gene's strand

multipleHit: **yes** if junction spans multiple genes.

bin_spanned: Bin's names spanned by the junction.

j_within_bin: If junction falls within a single bin, the name of that bin is shown.

sample data: Junction counts (one column per sample).

- E1l (**e1lcounts**) and IE2 (**ie2counts**) flanking region count dataframes contain the following information:

row.names: Junction name in format `chromosome.start.end` (see 4.1 : binGenome: [Binning the genome](#)).

junction: If junction coincides with a junction inferred from the annotation, the name is shown as is given in section 4.1.1:Bin definition, otherwise contains noHit.

gene: Name of the locus that contains the junction.

strand: Strand sense of the gene.

multipleHit: **yes** if junction spans multiple genes.

sample data: Junction counts (one column per sample).

Row names	symbol	locus_overlap	gene_coordinates	start	end	length	effective_length	Sample 1	Sample 2	...
GENE01	GENE01	-	chr1:1-700	1	700	700	700	324	314	n
GENE02	GENE02	-	chr1:1001-1800	1001	1800	800	550	327	333	n
GENE03	GENE03	-	chr1:2001-2800	2001	2800	800	650	342	321	n
GENE04	GENE04	-	chr1:3001-3800	3001	3800	800	650	313	337	n
...

Table 6: [Gene counts table example](#)

ASpliAS:

- irPIR
 - event: Type of event assigned by ASpli when binning.
 - J1: Semicolon separated list of all the junctions with an end matching the start of the intron. J2: Semicolon separated list of all the junctions with an end matching the end of the intron. J3: Semicolon separated list of all the junctions overlapping the intron. All the columns from J1 to J2 represent the J1 counts in the different samples for each bin. The counts are the sum of all the J1 junctions. All the columns from J2 to J3 represent the J2 counts in the different samples for each bin. The counts are the sum of all the J2 junctions. All the columns from J3 to

the first condition represent the J3 counts in the different samples for each bin. The counts are the sum of all the J3 junctions. The last columns are the PIR metrics calculated for each condition. The PIR metric is calculated as: $PIR = (J1 + J2)/(J1 + J2 + 2*J3)$ Where the junctions are the sum by condition.

- altPSI
 - event: Type of event assigned by ASpli when binning.
 - J1(J2): Semicolon separated list of all the junctions with an end matching the end of alt5'SS(alt3'SS).
 - J3: Semicolon separated list of all the junctions with an end matching the start of alt5'SS or the start of alt3'SS. All the columns from J1 to J2 represent the J1 counts in the different samples for each bin. The counts are the sum of all the J1 junctions. All the columns from J2 to J3 represent the J2 counts in the different samples for each bin. The counts are the sum of all the J2 junctions. All the columns from J3 to the first condition represent the J3 counts in the different samples for each bin. The counts are the sum of all the J3 junctions.
 - The last columns are the PSI metrics calculated for each condition. The PSI metric is calculated as: $PSI = (J12)/(J12 + J3)$. Where J12 is J1 if it's an alt 5' event or J2 if it's an alt 3' event and the junctions are the sum by condition.
- esPSI
 - event: Type of event assigned by ASpli when binning
 - J1: Semicolon separated list of all the junctions with an end on the alternative exon.
 - J2: Semicolon separated list of all the junctions with an end on the alternative exon.
 - J3: Semicolon separated list of all the junctions overlapping the alternative exon. All the columns from J1 to J2 represent the J1 counts in the different samples for each bin. The counts are the sum of all the J1 junctions. All the columns from J2 to J3 represent the J2 counts in the different samples for each bin. The counts are the sum of all the J2 junctions. All the columns from J3 to the first condition represent the J3 counts in the different samples for each bin. The counts are the sum of all the J3 junctions.
 - The PSI metric is calculated as: $PSI = (J1 + J2)/(J1 + J2 + 2*J3)$ Where the junctions are the sum by condition.
- junctionsPIR
 - PIR metric for each experimental junction using e1i and ie2 counts. Exclusion junction is the junction itself. This output helps to discover new introns as well as new retention events.
 - hitIntron: If the junction matches a bin, the bin is shown here.
 - hitIntronEvent: If the junction matches a bin, the type of event assigned by ASpli to this bin. All the columns from hitIntronEvent up to the first repetition of the samples names in the columns, represent the J1 counts in the different samples for each region. From there to the next time the names of the columns repeat themselves, the J2 counts and from there to the first condition, the J3 counts.

- The last columns are the PIR metrics calculated for each condition. The PIR metric is calculated as: $PIR = (J1 + J2)/(J1 + J2 + 2*J3)$ Where the junctions are the sum by condition.
- junctionsPJJU
 - Given a junction, it is possible to analyze if it shares start, end or both with another junction. If so, it is because there is alternative splicing.
 - Junction: name of the junction.
 - Gene: gene it belongs to.
 - Strand: gene strand.
 - multipleHit: if other gene overlaps the gene the junction belongs to.
 - symbol: gene symbol.
 - gene_coordinates: gene coordinates.
 - bin_spanned: semicolon separated list of all the bins spanned by this junction.
 - j_within_bin: other junctions in the bins.
 - StartHit: all the junctions sharing the start with this junction and $PJJU_{j1} = J3/(J1 + J3)$ for each condition.
 - EndHit: all the junctions sharing the end with this junction and $PJJU_{j2} = J3/(J2 + J3)$ for each condition.
 - All the columns between j_within_bin and StartHit are the counts for J3 in the different samples for each region. From there to EndHit, the J1 counts and $PJJU_{j1} = J3/(J1 + J3)$ for each condition. Then after EndHit, the J2 counts and $PJJU_{j2} = J3/(J2 + J3)$.
 - Rownames are J3 range.
 - StartHit is J1 range and EndHit is J2 range.
- ASpliJDU
 - if it is novel (known CHEQUEAR)
 - which bins it spans
 - if the junction is completely included in an annotated bin, which would indicate that the AS event is a possible *exintron* [5].
 - locale: data.frame with information about statistically significant changes in junction usage inside *locale*-junction clusters.
 - size: number of junctions belonging to the cluster.
 - cluster.LR: likelihood ratio of cluster differential usage.
 - pvalue: pvalue of cluster differential usage.
 - FDR: fdr of cluster differential usage.
 - range: cluster location.
 - participation: participation of the significant junction ($FDR < \text{maxFDRForParticipation}$) presenting maximal participation value inside the cluster

- dParticipation: delta participation of the significant junction ($FDR < \max FDR_{ForParticipation}$) presenting maximal participation value inside the cluster
- localej
 - cluster: name of the cluster the junction belongs to
 - log.mean: log of mean counts accross all conditions for this junction
 - logFC: log fold change of junction accross conditions
 - pvalue: pvalue of junction
 - FDR: FDR of junction
 - annotated: is junction annotated or new
 - participation: the maximal participation value observed across contrasted conditions
 - dParticipation: delta participation of the maximal participation value observed across contrasted conditions
 - From dParticipation to the end, junction counts for all samples
- anchorc
 - cluster.LR: likelihood ratio of cluster differential usage.
 - pvalue: pvalue of cluster differential usage.
 - FDR: fdr of cluster differential usage.
- anchorj
 - log.mean: log of mean counts accross all conditions for this junction
 - logFC: log fold change of junction accross conditions
 - LR: likelihood ratio of junction differential usage.
 - pvalue: pvalue of junction
 - FDR: FDR of junction
 - J1.pvalue: pvalue of J1 junction
 - J2.pvalue: pvalue of J2 junction
 - NonUniformity: if non uniformity test was performed, numbers closer to zero mean uniformity and closer to one mean non uniformity
 - dPIR: junction delta PIR
 - annotated: is junction annotated or new
 - From annotated to the end, junction counts for all samples
- jir
 - J3: J3 junction/s
 - logFC: log fold change of junction accross conditions
 - log.mean: log of mean counts accross all conditions for this junction
 - pvalue: pvalue of junction

- FDR: FDR of junction
- LR: likelihood ratio of junction differential usage.
- NonUniformity: if non uniformity test was performed, numbers closer to zero mean uniformity and closer to one mean non uniformity
- dPIR: junction delta PIR
- multiplicity: do multiple junctions cross the region
- From multiplicity to the end, junction counts for all samples
- jes
 - event: type of event
 - J3: J3 junction/s
 - logFC: log fold change of junction accross conditions
 - log.mean: log of mean counts accross all conditions for this junction
 - pvalue: pvalue of junction
 - FDR: FDR of junction
 - LR: likelihood ratio of junction differential usage.
 - dPSI: junction delta PSI
 - multiplicity: do multiple junctions cross the region
 - From multiplicity to the end, junction counts for all samples
- jalt
 - event: type of event
 - J3: J3 junction/s
 - logFC: log fold change of junction accross conditions
 - log.mean: log of mean counts accross all conditions for this junction
 - pvalue: pvalue of junction
 - FDR: FDR of junction
 - LR: likelihood ratio of junction differential usage.
 - dPSI: junction delta PSI
 - multiplicity: do multiple junctions cross the region
 - From multiplicity to the end, junction counts for all samples

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