

Using refGenome package

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1 refGenome package

The `refGenome` package provides functionality for managing of genome annotation data, especially for Ensembl and UCSC data.

2 Object types inside refGenome package

The central classes inside this package are `refGenome` derived (S4) classes. The class contains two slots: `env` (`environment`) and `basedir` (`character`). All annotation data is kept in `data.frames` inside the `env` slot. Saving and loading `refGenome` derived objects works on the complete content of the environment. This mechanism also avoids generation of copies and allows addition of new data inside of member functions. The `basedir` slot keeps a path on a hard-disc which is intended as location where data files and object versions can be kept.

The package contains three derived class lineages `refGenome`, `refExons` and `refJunctions`. For each lineage there are classes for Ensembl and UCSC defined, e.g. `ensemblGenome` and `ucscGenome`. The exon classes focus on annotated exon positions and the junction classes focus on adjacent exons.

2.1 Creation of empty refGenome objects

Empty objects of `refGenome` derived classes can be created with `ensemblGenome()` or `ucscGenome()`. After creation of an empty object the first step usually is to set the `basedir` address:

```
> library(refGenome)
> beg <- ensemblGenome()
> basedir(beg) <- system.file("extdata", package="refGenome")
```

The "basedir" folder is intended to contain all data which is associated with the current annotation set, e.g. downloaded gtf files, saved object data, saved SQLite versions of the data and potentially sequence information. In order to fill an empty object, annotation data has to be imported from external files.

2.2 Importing annotation data

The basic importing mechanism for `refGenome` objects is to import a "gtf" file. Therefore, the "gtf" files have to be downloaded. The download source and mechanism is explained for `ensemblGenome` and `ucscGenome` separately. There are specialized mechanisms in order to provide additional information either from within the gtf file (ensembl) or via other external files (ucsc).

2.3 Saving and loading data

The data content of `refGenome` objects can be saved and re-loaded in several ways. One way is the `saveGenome` method where the content is written into a compressed ".RData" file. One alternative is to write the content into a SQLite database via `writeDB`.

3 Ensembl Genomes

The `ensemblGenome` class is specialized for managing annotation data for ensemble Genomes.

3.1 Download and import data

For `ensemblGenome` objects, gtf files can be downloaded from Ensemble servers. Therefore, go to

```
http://www.ensembl.org/info/data/ftp/index.html
```

and choose a file from the "Gene sets" column. They are labeled "GTF". For example Version 62 of human genomic annotation can be downloaded from

```
ftp://ftp.ensembl.org/pub/release-80/gtf/homo_sapiens/Homo_sapiens.GRCh38.80.gtf.gz
```

A copy of the obtained file should then be placed in the the "basedir" directory. With the appropriate setting of `basedir`, annotation data can be imported with:

```
> ens_gtf <- "hs.ensembl.62.small.gtf"
> read.gtf(beg, ens_gtf)
```

```
[read.gtf.refGenome] Reading file 'hs.ensembl.62.small.gtf'.
```

```
[GTF]          135 lines processed.
[read.gtf.refGenome] Extracting genes table.
[read.gtf.refGenome] Finished.
```

```
> beg
```

```
Object of class 'ensemblGenome' with 135 rows and 15 columns.
```

```
  id      seqid      source      feature  start    end
1  1  GL000213.1  protein_coding      exon 138767 139339
```

```

2 2 GL000213.1 protein_coding      CDS 138767 139287
3 3 GL000213.1 protein_coding start_codon 139285 139287
4 4 GL000213.1 protein_coding      exon 134276 134390
5 5 GL000213.1 protein_coding      CDS 134276 134390
6 6 GL000213.1 protein_coding      exon 133943 134116
  score strand frame      protein_id transcript_name
1      .      -      .      <NA>    BX072566.1-201
2      .      -      0 ENSP00000329990 BX072566.1-201
3      .      -      0      <NA>    BX072566.1-201
4      .      -      .      <NA>    BX072566.1-201
5      .      -      1 ENSP00000329990 BX072566.1-201
6      .      -      .      <NA>    BX072566.1-201
  gene_id      transcript_id      gene_name      exon_number
1 ENSG00000237375 ENST00000327822 BX072566.1      1
2 ENSG00000237375 ENST00000327822 BX072566.1      1
3 ENSG00000237375 ENST00000327822 BX072566.1      1
4 ENSG00000237375 ENST00000327822 BX072566.1      2
5 ENSG00000237375 ENST00000327822 BX072566.1      2
6 ENSG00000237375 ENST00000327822 BX072566.1      3

```

The top lines of the contained table are shown when the object is printed.

4 UCSC Genomes

Downloading of annotation data for UCSC genomes is a bit more complicated than for Ensemble Genomes because additional data must be downloaded in separate files. The Homepage for UCSC browser can be found under:

<http://genome.ucsc.edu/>

In order to import UCSC annotation data into `refGenome` objects files containing the data have to be downloaded from the UCSC Table Browser which can be found under:

<http://genome.ucsc.edu/cgi-bin/hgTables>

or by following the "Table Browser" link in the left panel on the homepage. On the Table Browser:

- Select genome, assembly and track (UCSC genes)
- Choose table (knownGene)
- Choose output format (GTF -gene transfer format for knownGene table)
- Insert a name for the output file
- Download the file (get output)

The basic table to be imported is "knownGene". The knownGene table has to be downloaded in GTF format (otherwise the read.gtf function will complain about "wrong number of columns").

In order to extend the available information additionally the tables "kgXref", "knownToEnsembl" and "knownIsoforms" can be downloaded and imported. These tables come in plain "csv" format. Select "all fields from selected table" as output format.

Do not use "add custom tracks" or modify the tables elsewhere tracks because the importing functions will check for appropriate number of columns.

After downloading, all tables should be placed into a separate folder which we from now on call "basedir".ucscGenome objects keep a basedir as standard location for all writing and reading procedures.

```
> uc <- ucscGenome()
> basedir(uc) <- "/my/ucsc/basedir"
> read.gtf(uc, "ucsc_knownGene.gtf")
> addXref(uc, "kgXref.csv")
> addEnsembl(uc, "knownToEnsembl.csv")
> addIsoforms(uc, "ucsc_knownisoforms.csv")
```

4.1 Load stored data

Once, annotation data is imported and stored, ucscGenome objects can be restored with the loadGenome function which is shown below on example data:

```
> ucfile <- system.file("extdata", "hs.ucsc.small.RData", package="refGenome")
> uc <- loadGenome(ucfile)
> ensfile <- system.file("extdata", "hs.ensembl.62.small.RData", package="refGenome")
> ens <- loadGenome(ensfile)
```

5 Extracting data subsets

There are specialized functions for extracting data for multiple purposes.

5.1 Extracting data for sets of seqid's

For preparation of seqid based extraction, the contained seqid's can be tabled:

```
> tableSeqids(ens)
      1 GL000213.1
111      24
```

Extraction of subsets based on seqid can be done with extractSeqids. The sequence id's for extraction are specified as regular expression:

```
> en1 <- extractSeqids(ens, "^1$")
> en1
```

Object of class 'ensemblGenome' with 111 rows and 15 columns.

```

  id seqid start  end feature score strand frame
25  1     1 11869 12227  exon      .      +      .
34  2     1 11872 12227  exon      .      +      .
41  3     1 11874 12227  exon      .      +      .
28  4     1 12010 12057  exon      .      +      .
29  5     1 12179 12227  exon      .      +      .
35  6     1 12190 12227  CDS       .      +      0

      gene_id  transcript_id  source
25  ENSG00000223972  ENST00000456328  pseudogene
34  ENSG00000249291  ENST00000515242  protein_coding
41  ENSG00000253101  ENST00000518655  protein_coding
28  ENSG00000223972  ENST00000450305  pseudogene
29  ENSG00000223972  ENST00000450305  pseudogene
35  ENSG00000249291  ENST00000515242  protein_coding

      gene_name  transcript_name  exon_number
25  DDX11L1     DDX11L1-002     1
34  AL627309.2  AL627309.2-201  1
41  DDX11L11    DDX11L11-201   1
28  DDX11L1     DDX11L1-001    1
29  DDX11L1     DDX11L1-001    2
35  AL627309.2  AL627309.2-201  1

      transcript_biotype
25  processed_transcript
34  nonsense_mediated_decay
41  nonsense_mediated_decay
28  transcribed_unprocessed_pseudogene
29  transcribed_unprocessed_pseudogene
35  nonsense_mediated_decay

```

It looks cumbersome for single chromosomes but allows extraction of complex patterns.

5.2 Extracting primary assembly data

Usually the interesting part of the annotation data is the the primary assembly (where alternative haplotypes are excluded). Therefore functions which return the proper terms are supplied:

```

> ensPrimAssembly()

[1] "^[0-9]{1,2}$|^ [XY] |MT$"

> ucPrimAssembly()

[1] "^chr[0-9XYM]{1,2}$"

```

Extraction of primary assembly `seqid`'s `i` is done by:

```

> enpa<-extractSeqids(ens,ensPrimAssembly())
> tableSeqids(enpa)

```

```

1
111

> ucpa<-extractSeqids(uc,ucPrimAssembly())
> tableSeqids(ucpa)

chr1
6

```

5.3 Extract features

Subsets defined by features can also be tabled and extracted:

```

> tableFeatures(enpa)

      CDS      exon start_codon stop_codon
      8      98          3         2

> enpf<-extractFeature(enpa,"exon")
> enpf

Object of class 'ensemblGenome' with 98 rows and 15 columns.
  id seqid start  end feature score strand frame
25  1     1 11869 12227  exon     .      +     .
34  2     1 11872 12227  exon     .      +     .
41  3     1 11874 12227  exon     .      +     .
28  4     1 12010 12057  exon     .      +     .
29  5     1 12179 12227  exon     .      +     .
42  8     1 12595 12721  exon     .      +     .
      gene_id  transcript_id      source
25  ENSG00000223972  ENST00000456328  pseudogene
34  ENSG00000249291  ENST00000515242  protein_coding
41  ENSG00000253101  ENST00000518655  protein_coding
28  ENSG00000223972  ENST00000450305  pseudogene
29  ENSG00000223972  ENST00000450305  pseudogene
42  ENSG00000253101  ENST00000518655  protein_coding
      gene_name transcript_name exon_number
25  DDX11L1      DDX11L1-002      1
34  AL627309.2  AL627309.2-201    1
41  DDX11L11     DDX11L11-201     1
28  DDX11L1      DDX11L1-001      1
29  DDX11L1      DDX11L1-001      2
42  DDX11L11     DDX11L11-201     2
      transcript_biotype
25  processed_transcript
34  nonsense_mediated_decay
41  nonsense_mediated_decay
28  transcribed_unprocessed_pseudogene
29  transcribed_unprocessed_pseudogene
42  nonsense_mediated_decay

```

5.4 Extract data for single genes and transcripts

There are some functions which extract objects that contain data for single genes (or transcripts). These functions provide a closer insight into specific regions.

Objects which contain data for vectors of gene-names can be extracted with

```
> dxs <- extractByGeneName(enpa, "DDX11L1")
> dxu <- extractByGeneName(ucpa, "DDX11L1")
```

When gene-names did not match in the gtf-table of the object, a message including all names of not matching gene-names will be printed. When no gene-name matches, a message will be printed and the function returns NULL, which can be tested for later on.

Additionally subsets can also be extracted based on gene-id

```
> dxs <- extractByGeneId(enpa, "ENSG00000223972")
> dxu <- extractByGeneId(ucpa, "ENSG00000223972")
```

```
[1] "ENSG00000223972"
```

From these extracts we can view the contained transcripts with the `tableTranscript.id` function:

```
> tableTranscript.id(enpa)

ENST00000408384 ENST00000417324 ENST00000423562
                1                8                10
ENST00000430492 ENST00000438504 ENST00000450305
                9                12                6
ENST00000456328 ENST00000461467 ENST00000469289
                3                2                2
ENST00000473358 ENST00000488147 ENST00000515242
                3                11               7
ENST00000518655 ENST00000537342 ENST00000538476
                8                7                13
ENST00000541675
                9
```

```
> tableTranscript.id(ucpa)
```

```
uc001aaa.3 uc010nxr.1
            3         3
```

Data for interesting transcripts can be extracted by `extractTranscript`:

```
> extractTranscript(ens, "ENST00000456328")
```

Object of class 'ensemblGenome' with 3 rows and 15 columns.

	transcript_id	id	seqid	start	end	feature	score	strand
1	ENST00000456328	1	1	11869	12227	exon	.	+
2	ENST00000456328	9	1	12613	12721	exon	.	+
3	ENST00000456328	14	1	13221	14409	exon	.	+

```

frame      gene_id      source gene_name
1      . ENSG00000223972 pseudogene  DDX11L1
2      . ENSG00000223972 pseudogene  DDX11L1
3      . ENSG00000223972 pseudogene  DDX11L1
transcript_name exon_number transcript_biotype
1      DDX11L1-002          1 processed_transcript
2      DDX11L1-002          2 processed_transcript
3      DDX11L1-002          3 processed_transcript

```

```
> extractTranscript(uc, "uc010nxr.1")
```

Object of class 'ucscGenome' with 3 rows and 14 columns.

```

transcript_id id seqid start end feature score strand
1 uc010nxr.1 4 chr1 11874 12227 exon 0 +
2 uc010nxr.1 5 chr1 12646 12697 exon 0 +
3 uc010nxr.1 6 chr1 13221 14409 exon 0 +
frame      gene_id      source gene_name      ensembl
1      . uc010nxr.1 hg19_knownGene  DDX11L1 ENST00000456328
2      . uc010nxr.1 hg19_knownGene  DDX11L1 ENST00000456328
3      . uc010nxr.1 hg19_knownGene  DDX11L1 ENST00000456328
clusterId
1      1
2      1
3      1

```

6 Accumulate data for whole genes

The function `getGenePositions` accumulates position data for whole genes. Genes are grouped by `gene_name`. For both, *ensemblGenome* and *ucscGenome* the `gene_name` column is not present after the standard `gtf-import`. For *ucscGenome*, `addXref` must be used. Respective warnings are thrown.

```
> gpe <- getGenePositions(ens)
> gpe
```

```

id      gene_id      gene_name      seqid start end
2 2 ENSG00000223972 DDX11L1          1 11869 14409
7 7 ENSG00000249291 AL627309.2      1 11872 14412
8 8 ENSG00000253101 DDX11L1          1 11874 14409
3 3 ENSG00000227232 WASH7P           1 14363 29806
6 6 ENSG00000243485 MIR1302-10       1 29554 31109
1 1 ENSG00000221311 MIR1302-10       1 30366 30503
5 5 ENSG00000237613 FAM138A           1 34554 36081
4 4 ENSG00000237375 BX072566.1 GL000213.1 108007 139339
strand start_codon stop_codon
2      +          NA          NA
7      +      12190          NA
8      +      13548      13817
3      -          NA          NA
6      +          NA          NA

```

```

1      +          NA          NA
5      -          35736        35140
4      -          139287       108028

> gpu <- getGenePositions(uc)
> gpu

  id   gene_id gene_name seqid start  end strand
1  1 uc001aaa.3  DDX11L1  chr1 11874 14409      +
  start_codon stop_codon
1           NA          NA

```

There is a slight difference between both results: The last column is `gene_id` for `ensemblGenome` and `clusterID` for `ucscGenome`. This is due to different information which is available for each.

7 Exon and splice-junction based views (only for Ensembl genomes)

7.1 Extract exon based table

Exon based view on annotation data can be obtained with `ensemblExons` which returns an object of class `ensemblExons`. Basically `ensemblExons` calls `extractFeature` for feature type "exon". Information about presence of cds start or end and start-codon or stop-codon is added.

```

[refExons.refGenome] Extracting tables.
[refExons.refGenome] Adding 'CDS'.
[refExons.refGenome] Adding 'start_codon'.
[refExons.refGenome] Adding 'stop_codon'.
[refExons.refGenome] Finished.

```

```

[refExons.refGenome] Extracting tables.
[refExons.refGenome] Adding 'CDS'.
[refExons.refGenome] Adding 'start_codon'.
[refExons.refGenome] Adding 'stop_codon'.
[refExons.refGenome] Finished.

```

```
> enex
```

Object of class 'ensemblExons' with 109 rows and 18 columns.

```

  id seqid start  end score strand frame      gene_id
53  1     1 11869 12227     .      +      . ENSG00000223972
74  2     1 11872 12227     .      +      . ENSG00000249291
77  3     1 11874 12227     .      +      . ENSG00000253101
47  4     1 12010 12057     .      +      . ENSG00000223972
48  5     1 12179 12227     .      +      . ENSG00000223972
78  8     1 12595 12721     .      +      . ENSG00000253101
  transcript_id      source gene_name
53 ENST00000456328  pseudogene  DDX11L1

```

```

74 ENST00000515242 protein_coding AL627309.2
77 ENST00000518655 protein_coding DDX11L11
47 ENST00000450305 pseudogene DDX11L1
48 ENST00000450305 pseudogene DDX11L1
78 ENST00000518655 protein_coding DDX11L11
  transcript_name exon_number
53 DDX11L1-002 1
74 AL627309.2-201 1
77 DDX11L11-201 1
47 DDX11L1-001 1
48 DDX11L1-001 2
78 DDX11L11-201 2
  transcript_biotype cds_start cds_end
53 processed_transcript NA NA
74 nonsense_mediated_decay 318 0
77 nonsense_mediated_decay NA NA
47 transcribed_unprocessed_pseudogene NA NA
48 transcribed_unprocessed_pseudogene NA NA
78 nonsense_mediated_decay NA NA
  start_codon stop_codon
53 NA NA
74 318 NA
77 NA NA
47 NA NA
48 NA NA
78 NA NA

```

7.2 Extract splice-junction based views from `ensemblExons`

From `ensemblExons` information about adjacency of exons (which defines annotated splice-sites) can be obtained by putting exons with equal `transcript_id` and subsequent `exon_number` side by side.

The start and end positions of adjacent exons are renamed to `lstart`, `lend` and `rstart` and `rend`. The "l" prefix refers to the exon with lower start and end coordinates (i.e. left, lower `exon_number`). The "r" prefix refers to the exons with higher start and end coordinates (i.e. right, higher `exon_number`).

Setting `coding=TRUE` will restrict the result to exons for which `source` and `gene_biotype` equal "protein_coding".

```

> jens <- getSpliceTable(ens)
> jens

```

Object of class 'ensemblJunctions' with 92 rows and 13 columns.

```

  id      seqid lstart  lend rstart  rend      gene_id
1  1  GL000213.1 108007 108247 109884 110007  ENSG000000237375
2  2  GL000213.1 109884 110007 118422 118588  ENSG000000237375
3  3  GL000213.1 118422 118588 119629 119673  ENSG000000237375
4  4  GL000213.1 119629 119673 121073 121143  ENSG000000237375
5  5  GL000213.1 121073 121143 126648 126718  ENSG000000237375
6  6  GL000213.1 126648 126718 129228 129365  ENSG000000237375
  gene_name strand  transcript_id lexid rexid

```

```

1 BX072566.1 - ENST00000327822 112 115
2 BX072566.1 - ENST00000327822 115 117
3 BX072566.1 - ENST00000327822 117 119
4 BX072566.1 - ENST00000327822 119 121
5 BX072566.1 - ENST00000327822 121 123
6 BX072566.1 - ENST00000327822 123 125

```

```

transcript_biotype
1 nonsense_mediated_decay
2 nonsense_mediated_decay
3 nonsense_mediated_decay
4 nonsense_mediated_decay
5 nonsense_mediated_decay
6 nonsense_mediated_decay

```

```

> juc <- getSpliceTable(uc)
> juc

```

Object of class 'ucscJunctions' with 4 rows and 12 columns.

```

  id seqid lstart  lend  rstart  rend  gene_id gene_name
1  1  chr1  11874 12227  12613 12721 uc001aaa.3  DDX11L1
2  2  chr1  12613 12721  13221 14409 uc001aaa.3  DDX11L1
3  3  chr1  11874 12227  12646 12697 uc010nxr.1  DDX11L1
4  4  chr1  12646 12697  13221 14409 uc010nxr.1  DDX11L1
  strand transcript_id lexicid rexid
1      +      uc001aaa.3      1      2
2      +      uc001aaa.3      2      3
3      +      uc010nxr.1      4      5
4      +      uc010nxr.1      5      6

```

This generally leads to repeated occurrence of start and end positions when a splice-junction is contained in multiple transcripts. Additionally a handful splice-sites with multiple gene-id's are present.

The `unifyJunc` therefore calculates `nGenes` which represents the multiplicity of each gene-id at each splice-site and then selects a gene-id for which `nGenes` is maximal.

`unifyJuncs` adds a `uid` column to the basic `gtf` table which identifies each `seqid`, left-end, right-start combination uniquely. `unifyJuncs` also adds a new `ujc` table inside the contained environment.

`getUnifiedJuncs` takes the result of `unifyJuncs` and adds `gene_name` and strand information.

```

> ujens <- unifyJuncs(jens)
> ujuc <- unifyJuncs(juc)
> jeg <- getGenePositions(jens)
> jug <- getGenePositions(juc)
> ujens

```

Object of class 'ensemblJunctions' with 51 rows and 12 columns.

```

  id seqid lstart  lend  rstart  rend nSites  gene_id
1  1  1  12010 12057  12179 12227      1 ENSG00000223972
2  2  1  11874 12227  12595 12721      1 ENSG00000253101

```

```

3 3      1 11869 12227 12613 12721      3 ENSG00000223972
4 4      1 12613 12697 12975 13052      1 ENSG00000223972
5 5      1 12613 12721 13221 14409      1 ENSG00000223972
6 6      1 12613 12721 13225 14412      1 ENSG00000249291

```

```

strand fexid cnNmd gene_name
1      +   41     1   DDX11L1
2      +   64     0   DDX11L1
3      +   42     2   DDX11L1
4      +   43     1   DDX11L1
5      +   47     1   DDX11L1
6      +   63     0   AL627309.2

```

```
> jug
```

```

id      gene_id gene_name seqid start  end strand
1 1 uc001aaa.3  DDX11L1 chr1 11874 14409      +
start_codon stop_codon
1      NA      NA

```

The result tables of `unifyJuncs` and `getGenePositions` are stored inside the internal environment of `ensemblJunctions`. From there, the results can easily be reproduced without recalculation. The tables are automatically included in `saveGenome` and `load.ensembl.juncs` mechanisms.

8 Overlapping

The overlap function is used to supply annotation for genomic ranges. The function takes two `data.frame`'s which contain query (`qry`) and reference (`ref`) ranges respectively. Each dataset will be identified by its id.

The routine assumes that query and reference tables are ascending sorted by column 'start'. Otherwise the result will be incorrect (i.e. missing hits). The function assumes that there is no overlap between reference ranges. It will otherwise return only one, possibly arbitrary, hit per query range.

The function returns a `data.frame`. For each query range, there will be one row.

```

> qry<-data.frame(
+           id=1:6,
+           start=c(10,18,61,78,82,110),
+           end=c(15,22,63,87,90,120))
> ref<-data.frame(
+           id=1:5,
+           start=c(20,40,60,80,100),
+           end=c(25,45,65,85,105))
> overlap(qry,ref)

overlap leftDiff rightDiff queryid refid
0      no          0          5          1          0

```

1	l	2	3	2	1
2	n	1	2	3	3
3	b	2	2	4	4
4	r	2	5	5	4
5	no	5	0	6	0

The query and reference record are identified by "queryid" and "refid". The type of overlap is encoded in the "overlap" column. The overlap encodings are explained as follows:

- **no**. The query range does not overlap with any reference ranges.
- **l** The query range overhangs the matching reference range on the left (lower coordinate) side.
- **n** The query range is completely contained within a reference range. There is no overhang.
- **b** The query range overhangs the matching reference range on both sides.
- **r** The query range overhangs the matching reference range on the right (higher coordinate) side.

The added "leftDiff" and "rightDiff" columns contain the distance between the query and reference range boundaries: leftDiff is the difference between the left (lower coordinate) margins and rightDiff is the difference between the right (higher coordinate) margins.

8.1 Overlapping for splice-junctions

The `overlapJuncs` function is specialized for annotation of splice events in BAM alignment data. The function takes two arguments: a `data.frame` providing query data and a `refJunctions` object providing annotation data.

8.1.1 Query data

Query data for `overlapJuncs` are BAM alignment gap-sites. These gap-sites are defined by one or multiple gapped alignments of RNA-seq reads to a reference genome. Due to the splicing process, a variable fraction of the reads align in two or more fractions to the reference genome. Two adjacent alignment fractions define the position of a gap-site.

The position of the alignment fractions are named **lstart** and **lend** for the left (i.e. lower genomic coordinates) alignment interval and **rstart** and **rend** for the right (i.e. higher genomic coordinates) alignment interval.

The two genomic intervals of a gap-site implicitly define a third interval: The gap in between (alignment gap).

The biological meaning of gap-sites is that alignment gaps correspond to introns and the left and right align regions correspond to adjacent exon boundaries.

Due to the fact that gapped alignments do not cover whole exons, the inner boundaries of gap-sites are biological meaningful and the outer boundaries of gap-sites usually are technical artifacts.

Therefore the `overlapJuncs` function searches and rates overlaps by inner gap boundaries (`lend`, `rstart`) whereas the outer boundaries solely define whether

any overlap with annotated splice-sites is present.

The `query data.frame` defines one gap-site in each row. Therefore the table is expected to contain the following columns:

- **id**: Consecutive (unique) integral values.
- **seqid**: Character values for reference sequence identifiers (e.g. 'chr1' or '1').
- **lstart**: Position of first nucleotide of left alignment region
- **lend**: Position of last nucleotide of left alignment region.
- **rstart**: Position of first nucleotide of right alignment region.
- **rend**: Position of last nucleotide of right alignment region.

All genomic positions are 1-based (i.e. first position of sequence has position 1).

```
> # + + + + + + + + + + + + + + + + #
> # A) Example query data
> # + + + + + + + + + + + + + + + + #
> ##           1           2           3           4           5           6           7 ##
> qry <- data.frame(id = 1:7, seqid = "1",
+                   lstart = c(10100L, 11800L, 12220L, 12220L, 12220L, 32000L, 40000L),
+                   lend = c(10100L, 12000L, 12225L, 12227L, 12227L, 32100L, 40100L),
+                   rstart = c(10200L, 12200L, 12057L, 12613L, 12650L, 32200L, 40200L),
+                   rend = c(10300L, 12250L, 12179L, 12620L, 12700L, 32300L, 40300L))
> ##           1           2           3           4           5           6           7 ##
```

8.1.2 Reference data

The reference data for the `overlapJuncs` function is can be obtained from a `refGenome` object with the `getSpliceJuncs` function.

```
> ensfile <- system.file("extdata", "hs.ensembl.62.small.RData",
+                         package="refGenome")
> # Load Ensembl genome
> ens <- loadGenome(ensfile)
> # Calculate junction positions:
> junc <- getSpliceTable(ens)
```

8.1.3 Overlapping results

Junction based annotation of annotation gap-sites is done by the `overlapJuncs` function.

```
> res <- overlapJuncs(qry, junc)
```

The `overlapJuncs` function returns a `data.frame`. As an overlap result is returned for every query record, the output and the query `data.frame` contain the same number of rows.

The first two columns (`qid` and `refid`) provide the query id (the id from the query `data.frame`) and a `refid` (the id for the identified optimal overlap). Records without overlap can be identified with a `refid` value of 0.

The validity of the overlap is defined by the distance of the inner boundaries between the query and the reference site. The distance for the left alignment region is given in `ldiff` and the distance for the right alignment region is given in `rdiff`. The sum of the absolute `ldiff` and `rdiff` values is given by `sod` (sum of distances). The optimal hit is defined as the one with the lowest `sod` value. An exact hit will have `sod=0`.

The result table provides `gene_id`, `transcript_id`, `gene_name` and `strand`.

9 Workflows

9.1 Establish a standard set of `refGenome` objects for Ensembl

The following example assumes, that a downloaded *GTF* file has been downloaded and unzipped into a target location (`endir`):

```
> library(refGenome)
> endir <- "../refGenomes/hsEns76"
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> # Read GTF
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> en76 <- ensemblGenome()
> basedir(en76) <- endir
> read.gtf(en76, "Homo_sapiens.GRCh38.76.gtf")
> saveGenome(en76, "en76.RData")
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> # Extract primary assembly
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> enpa76 <- extractSeqids(en76, ensPrimAssembly())
> saveGenome(enpa76, "enpa76.RData")
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> # Extract Exons
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> enex76 <- refExons(enpa76)
> saveGenome(enex76, "enex76.RData")
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> # Extract Junctions
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> enjc76 <- getSpliceTable(enpa76)
> saveGenome(enjc76, "enjc76.RData")
>
> # + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + #
> # Extract data.frame
```


10.2 transcriptModel object

Objects of class `transcriptModel` contain data on single transcripts like gene-id, gene-name, strand or coordinates.

Transcript objects can be extracted from `geneModel` objects by name and by index which is the usual way to create `transcriptModel` objects.

10.2.1 Extraction by index

```
> tr <- getTranscript(gm, 1)
> tr
```

An object of class 'transcriptModel'.

```
ID           : ENST00000450305
Name          : DDX11L1-001
Gene ID       : ENSG00000223972
Gene Name     : DDX11L1
Start        : 12.010                End           : 13.670
Start codon   : NA                   Stop codon    : NA
5' prime utr : NA                   3' prime utr : NA
Seq Name     : 1
Strand       : +
```

10.2.2 Extraction by ID

```
> tr <- getTranscript(gm, "ENST00000450305")
> tr
```

An object of class 'transcriptModel'.

```
ID           : ENST00000450305
Name          : DDX11L1-001
Gene ID       : ENSG00000223972
Gene Name     : DDX11L1
Start        : 12.010                End           : 13.670
Start codon   : NA                   Stop codon    : NA
5' prime utr : NA                   3' prime utr : NA
Seq Name     : 1
Strand       : +
```

From a `transcriptModel` object, exon and CDS tables can be extracted.

```
> getExonData(tr)
```

	start	end	exon_number	seqid	strand
1	12010	12057	1	1	+
2	12179	12227	2	1	+
3	12613	12697	3	1	+
4	12975	13052	4	1	+
5	13221	13374	5	1	+
6	13453	13670	6	1	+

```
> getCdsData(tr)
```

```

      start   end exon_number seqid strand
1 12010 12057         1      1      +
2 12179 12227         2      1      +
3 12613 12697         3      1      +
4 12975 13052         4      1      +
5 13221 13374         5      1      +
6 13453 13670         6      1      +

```

11 Gene model objects

11.1 Gene model

Gene model objects organize data for single genes. The Gene model objects are created using gene-id's from `refGenome` objects as shown below.

```

> ensfile<-system.file("extdata",
+   "hs_en82_grch38_small.gtf", package="refGenome")
> en82s <- ensemblGenome()
> basedir(en82s) <- dirname(ensfile)
> read.gtf(en82s, "hs_en82_grch38_small.gtf")

[read.gtf.refGenome] Reading file 'hs_en82_grch38_small.gtf'.

[GTF]          64 lines processed.
[read.gtf.refGenome] Extracting genes table.
[read.gtf.refGenome] Found 9 gene records.
[read.gtf.refGenome] Finished.

> gt <- getGeneTable(en82s)

> gm <- geneModel(en82s, "ENSG00000227232")

```

Upon 'interior=FALSE' in `geneModel` function internal gene structure elements (exons, transcripts) are not extracted.

11.2 Transcript model

Transcript model objects contain data for a single transcript. They are intended for use inside `geneModel` objects.

```

> tr <- getTranscript(gm, 1)
> tr

An object of class 'transcriptModel'.
ID           : ENST00000488147
Name         : WASH7P-001
Gene ID      : ENSG00000227232
Gene Name    : WASH7P
Start        : 14.404                End           : 29.570
Start codon  : NA                    Stop codon    : NA
5' prime utr: NA                    3' prime utr: NA
Seq Name     : 1
Strand       : -

```