

IVAS : Identification of genetic Variants affecting Alternative Splicing

Seonggyun Han and Sangsoo Kim

May 3, 2016

Contents

1	Introduction	1
2	The input data set	2
2.1	The genotype data	2
2.2	The expression data	2
2.3	The SNP marker position data	2
2.4	The transcripts model data	2
3	The example dataset : data from Geuvadis RNA sequencing project of 1000 Genome samples	3
4	Loading data	3
5	Running the IVAS package for detecting SQTLs	3
5.1	Separating the TxDb object based on a single chromosome.	3
5.2	Finding alternative exons of a single gene	4
5.3	Finding SNPs which belongs to alternative exons and flanking introns	6
5.4	Finding SQTLs	6
6	Identification of SQTLs in multiple genes	6
7	Visualizing the result	7
8	Session Information	7

1 Introduction

Alternative splicing controls relative expression ratios of mature mRNA isoforms from a single gene. Mapping studies of Splicing Quantitative Trait Loci (SQTL), a genetic variant affecting the alternative splicing, are important steps to understand gene regulations and protein activity [1]. We present an effective and user-friendly computational tool to detect SQTLs using transcript expression data from RNA-seq and genotype data, both measured on the same sample. As RNA sequencing (RNA-seq) provides insight into relatively precise measurements of expression level of transcript isoforms from a gene, it is a useful tool to analyze complicated biological phenomena of RNA transcripts including the alternative splicing [2]. The mapping analysis uses two statistical models : Linear regression model [3] and/or Generalized linear mixed model [5].

2 The input data set

The next subsection introduces the input data. To run this tool, two experimental data sets (an expression data frame from RNA-seq and a genotype data frame) are required. Moreover, we also need a data frame for positions of SNP markers and GTF file for transcript models. As any other genome-wide analyses, it is recommended to use as many samples as possible, usually of population scale, in order to guarantee a statistically significant result.

2.1 The genotype data

The genotype data should be prepared as a simple matrix data. Each column represents an individual and its name should match that of the expression matrix described below (2.2)

	ind1	ind2	ind3	ind4
SNP1	AA	AA	AT	TT
SNP2	CG	CC	GG	CG
SNP3	TT	TT	AT	TT

2.2 The expression data

The expression matrix must comprise expression values of transcripts from RNA-seq. We may obtain them by using alignment tools such as cufflinks. Each column represents an individual and its name should match that of the genotype matrix described above (2.1)

	ind1	ind2	ind3	ind4
transcript1	10.5	15.4	6.7	12.4
transcript2	6.4	7.2	4.5	9.2
transcript3	15.4	14.5	13.2	17.8

2.3 The SNP marker position data

To search SNPs affecting alternative splicing, a data frame comprising genomic location of each SNP is required. It consists of following columns: SNP(SNP marker name), CHR(chromosome number), and locus(SNP position).

SNP	CHR	locus
SNP1	1	4964005
SNP2	1	23513047

2.4 The transcripts model data

We need a reference GTF(General Feature Format) file including information about gene structures such as the positions of exons, introns, and transcripts of genes. The GTF file must be TxDb object from the *GenomicFeatures* package [4].

3 The example dataset : data from Geuvadis RNA sequencing project of 1000 Genome samples

This example uses filtered data from an origin data generated by Geuvadis RNA sequencing project, available at <http://www.geuvadis.org/web/geuvadis/RNAseq-project> [6]. The example expression data includes transcripts of 11 randomly selected genes. The genotype data comprises SNPs in those genes.

4 Loading data

For this analysis, you need to load the *IVAS* package, SNP data, expression data, SNP position data, and TxDb object from GTF.

Loading *IVAS* package :

```
> library(IVAS)
```

Loading expression data :

```
> data(sampleexp)
```

Loading SNP data :

```
> data(samplesnp)
```

Loading SNP position data :

```
> data(samplesnplocus)
```

Loading TxDb object :

```
> sampleDB <- system.file("extdata", "sampleDB", package="IVAS")
```

```
> sample.Txdb <- loadDb(sampleDB)
```

If you want to create the TxDb object from a GTF file, you need to use the `makeTxDbFromGFF` function in the *GenomicFeatures* package.

5 Running the IVAS package for detecting SQTs

5.1 Separating the TxDb object based on a single chromosome.

The `chrseparate` function separates the TxDb object based on a single chromosome for mapping analysis of expression and genotype in a single chromosome.

To use this function :

```
> filtered.txdb <- chrseparate(sample.Txdb,19)
```

```
> filtered.txdb
```

TxDb object:

```
# Db type: TxDb
```

```
# Supporting package: GenomicFeatures
```

```
# Data source: /data/sampleGTF
```

```
# Organism: Homo Sapience
```

```
# miRBase build ID: NA
```

```
# transcript_nrow: 64
```

```
# exon_nrow: 239
```

```
# cds_nrow: 184
# Db created by: GenomicFeatures package from Bioconductor
# Creation time: 2015-03-11 03:54:50 +0900 (Wed, 11 Mar 2015)
# GenomicFeatures version at creation time: 1.19.6
# RSQLite version at creation time: 1.0.0
# DBSCHEMAVERSION: 1.0
```

In this example, We filter the TxDb object with only the chromosome 6.

5.2 Finding alternative exons of a single gene

The `findAlternative` function finds flanking introns of alternative exons from a single gene. To run this function, it requires `trans.exon.range`, `trans.intron.range`, and `txTable`. The `trans.exon.range` is a range of exons based on transcripts using the `exonsBy` function in *GenomicFeatures* package. The `trans.intron.range` is a range of introns based on transcripts using the `intronsBy` function in *GenomicFeatures* package. The `txTable` has information about transcripts (start site, chromosome number, etc).

```
> trans.exon.range <- exonsBy(filtered.txdb,by="tx")
> trans.intron.range <- intronsByTranscript(filtered.txdb)
> txTable <- select(filtered.txdb, keys=names(trans.exon.range),
+                   columns=c("TXID","TXNAME","GENEID","TXSTART","TXEND"),keytype="TXID")
> Altvalue <- findAlternative("ENSG00000170889",txTable,trans.exon.range,
+                             trans.intron.range,19)
> Altvalue
```

`$alterIntron`

GRanges object with 6 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	19	[54704757, 54705027]	+
[2]	19	[54705478, 54710143]	+
[3]	19	[54710331, 54711265]	+
[4]	19	[54704830, 54705027]	+
[5]	19	[54710331, 54710420]	+
[6]	19	[54705478, 54711265]	+

seqinfo: 1 sequence from an unspecified genome; no seqlengths

`$tableBygene`

	TXID	GENEID	TXNAME	TXSTART	TXEND
1	40	ENSG00000170889	ENST00000302907	54704610	54711515
2	41	ENSG00000170889	ENST00000391752	54704740	54711515
3	42	ENSG00000170889	ENST00000402367	54704740	54711515
4	43	ENSG00000170889	ENST00000391751	54704742	54711515
5	44	ENSG00000170889	ENST00000391753	54705001	54711515
6	45	ENSG00000170889	ENST00000441429	54705028	54711498

`$exonRange`

GRangesList object of length 6:

`$40`

GRanges object with 5 ranges and 3 metadata columns:

seqnames	ranges	strand	exon_id	exon_name	exon_rank
----------	--------	--------	---------	-----------	-----------

	<Rle>	<IRanges>	<Rle>		<integer>	<character>	<integer>
[1]	19	[54704610, 54704756]	+		172	<NA>	1
[2]	19	[54705028, 54705149]	+		176	<NA>	2
[3]	19	[54705355, 54705477]	+		177	<NA>	3
[4]	19	[54710144, 54710330]	+		178	<NA>	4
[5]	19	[54711266, 54711515]	+		181	<NA>	5

\$41

GRanges object with 5 ranges and 3 metadata columns:

	seqnames	ranges	strand		exon_id	exon_name	exon_rank
[1]	19	[54704740, 54704829]	+		173	<NA>	1
[2]	19	[54705028, 54705149]	+		176	<NA>	2
[3]	19	[54705355, 54705477]	+		177	<NA>	3
[4]	19	[54710144, 54710330]	+		178	<NA>	4
[5]	19	[54711266, 54711515]	+		181	<NA>	5

\$42

GRanges object with 5 ranges and 3 metadata columns:

	seqnames	ranges	strand		exon_id	exon_name	exon_rank
[1]	19	[54704740, 54704829]	+		173	<NA>	1
[2]	19	[54705028, 54705149]	+		176	<NA>	2
[3]	19	[54705355, 54705477]	+		177	<NA>	3
[4]	19	[54710144, 54710330]	+		178	<NA>	4
[5]	19	[54710421, 54711515]	+		180	<NA>	5

...

<3 more elements>

seqinfo: 1 sequence from an unspecified genome; no seqlengths

\$intronRange

GRangesList object of length 6:

\$40

GRanges object with 4 ranges and 0 metadata columns:

	seqnames	ranges	strand
	<Rle>	<IRanges>	<Rle>
[1]	19	[54704757, 54705027]	+
[2]	19	[54705150, 54705354]	+
[3]	19	[54705478, 54710143]	+
[4]	19	[54710331, 54711265]	+

\$41

GRanges object with 4 ranges and 0 metadata columns:

	seqnames	ranges	strand
[1]	19	[54704830, 54705027]	+
[2]	19	[54705150, 54705354]	+
[3]	19	[54705478, 54710143]	+
[4]	19	[54710331, 54711265]	+

\$42

GRanges object with 4 ranges and 0 metadata columns:

```

      seqnames          ranges strand
[1]      19 [54704830, 54705027]    +
[2]      19 [54705150, 54705354]    +
[3]      19 [54705478, 54710143]    +
[4]      19 [54710331, 54710420]    +

...
<3 more elements>
-----
seqinfo: 1 sequence from an unspecified genome; no seqlengths
In this example, we will search SQTls in the ENSG00000170889.

```

5.3 Finding SNPs which belongs to alternative exons and flanking introns

The `overlapsnp` function searches SNPs in alternative exons and the flanking introns.

```

> ch.snp.locus <- as.matrix(samplesnplocus[samplesnplocus[,2] == 19,])
> ch.snps <- matrix(ch.snp.locus[is.element(ch.snp.locus[,1],rownames(samplesnp)),],
+                 ncol=3,byrow=FALSE)
> ch.snps.range <- GRanges(seqnames=Rle(19),ranges=IRanges(start=as.integer(ch.snps[,3]),
+                 end=as.integer(ch.snps[,3])),metadata=ch.snps[,1])
> overlapsnp <- findOversnp(Altvalue,ch.snps.range)
> overlapsnp

  range          snp
1 "54704757-54705027" "rs3810232"

```

5.4 Finding SQTls

Using the output data from the `Altvalue` function and the `overlapsnp` function, significant SNPs affecting the alternative splicing can be identified by the `sqtlfinder` function.

```

> sqtl.result <- sqtlfinder(Altvalue,overlapsnp,sampleexp,samplesnp,"lm")
> sqtl.result

  SNP          CHR targetExon          intron of SNP          type P.value
1 "rs3810232" "19" "54704610-54704756" "54704757-54705027" "A5SS" "9.60009815744455e-14"
  per.P.value gene          method strand
1 "sig"          "ENSG00000170889" "lm"    "+"

```

In this example, We will run the function with the linear regression model.

6 Identification of SQTls in multiple genes

The functions in the *IVAS* package perform mapping analysis using a single gene. However, the `MsqtlFinder` function in the *IVAS* package enables one to analyze multiple genes using the multi-thread version of `foreach` function. Moreover, it joins the results on the genes from `sqtlfinder` function and calculates the FDR using P-values of the results.

```

> final.result <- MsqtlFinder(sampleexp,samplesnp,samplesnplocus,sample.Txdb,"lm",1)

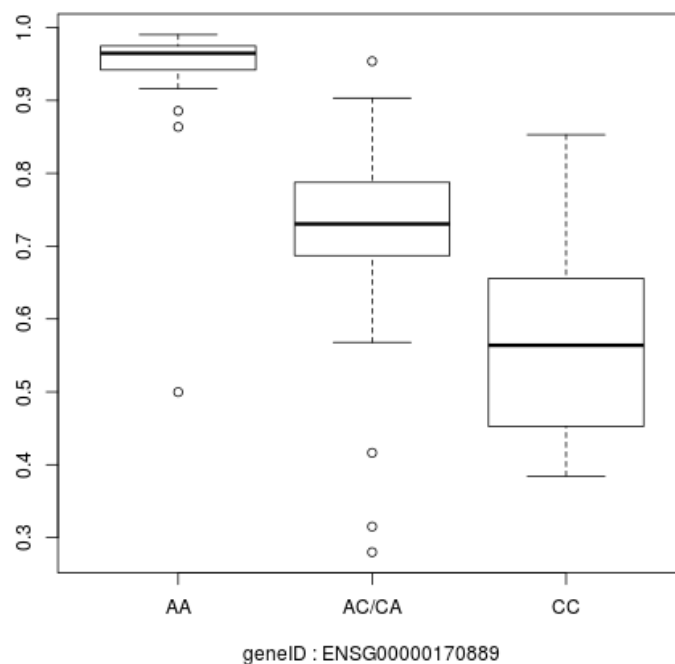
```

MsqtlFinder shows chromosome numbers during mapping analysis. The last argument denotes the number of threads(a single processor in this example)

7 Visualizing the result

To visualize the results into boxplot, the *IVAS* package provides the `saveBplot` function. Using the dataframe from the output of `sqtlfinder` or `MsqtlFinder` function, we can make the boxplot.

```
> saveBplot(sqtl.result, sampleexp, samplesnp, samplesnplocus, filtered.txdb, "./result")
```



The output png files are saved in "result" folder.

8 Session Information

```
R version 3.3.0 (2016-05-03)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 14.04.4 LTS
```

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C               LC_TIME=en_US.UTF-8
[4] LC_COLLATE=C             LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C                  LC_ADDRESS=C
[10] LC_TELEPHONE=C          LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats4    parallel  stats      graphics  grDevices  utils      datasets  methods
[9] base
```

other attached packages:

```
[1] IVAS_1.4.0          GenomicFeatures_1.24.0 AnnotationDbi_1.34.0
[4] Biobase_2.32.0      GenomicRanges_1.24.0  GenomeInfoDb_1.8.0
[7] IRanges_2.6.0       S4Vectors_0.10.0      BiocGenerics_0.18.0
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.4.5          XVector_0.12.0         MASS_7.3-45
[4] splines_3.3.0          zlibbioc_1.18.0        GenomicAlignments_1.8.0
[7] BiocParallel_1.6.0     doParallel_1.0.10      lattice_0.20-33
[10] foreach_1.4.3          minqa_1.2.4            tools_3.3.0
[13] grid_3.3.0             SummarizedExperiment_1.2.0 nlme_3.1-127
[16] DBI_0.4                iterators_1.0.8         lme4_1.1-12
[19] Matrix_1.2-6           nloptr_1.0.4           rtracklayer_1.32.0
[22] codetools_0.2-14      bitops_1.0-6           RCurl_1.95-4.8
[25] biomaRt_2.28.0         RSQLite_1.0.0          Biostrings_2.40.0
[28] Rsamtools_1.24.0      XML_3.98-1.4           BiocStyle_2.0.0
```

References

- [1] Keyan Zhao, Zhi-xiang Lu, Juw Won Park, Qing Zhou, Yi Xing. 2013. GLiMMPS: robust statistical model for regulatory variation of alternative splicing using RNA-seq data. *Genome Biol* 14, R74.
- [2] Joseph K. Pickrell, John C. Marioni, Athma A. Pai, Jacob F. Degner, Barbara E. Engelhardt, Everlyne Nkadori, Jean-Baptiste Veyrieras, Matthew Stephens, Yoav Gilad, Jonathan K. Pritchard. 2010. Understanding mechanisms underlying human gene expression variation with RNA sequencing. *Nature* 464, 768-722.
- [3] N.E. Breslow and D.G. Clayton. 1993. Approximate Inference in Generalized Linear Mixed Models. *Journal of the American Statistical Association* 88 421: 9-25.
- [4] Michael Lawrence, et al. 2013. Software for Computing and Annotating Genomic Ranges. *PLoS Comput Biol.* 9(8): e1003118.
- [5] Chambers, J. M. 1992. Linear models. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth, and Brooks Cole.
- [6] Tuuli Lappalainen, et al. 2013. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature* 501, 506-511.