Introducción a Bioconductor

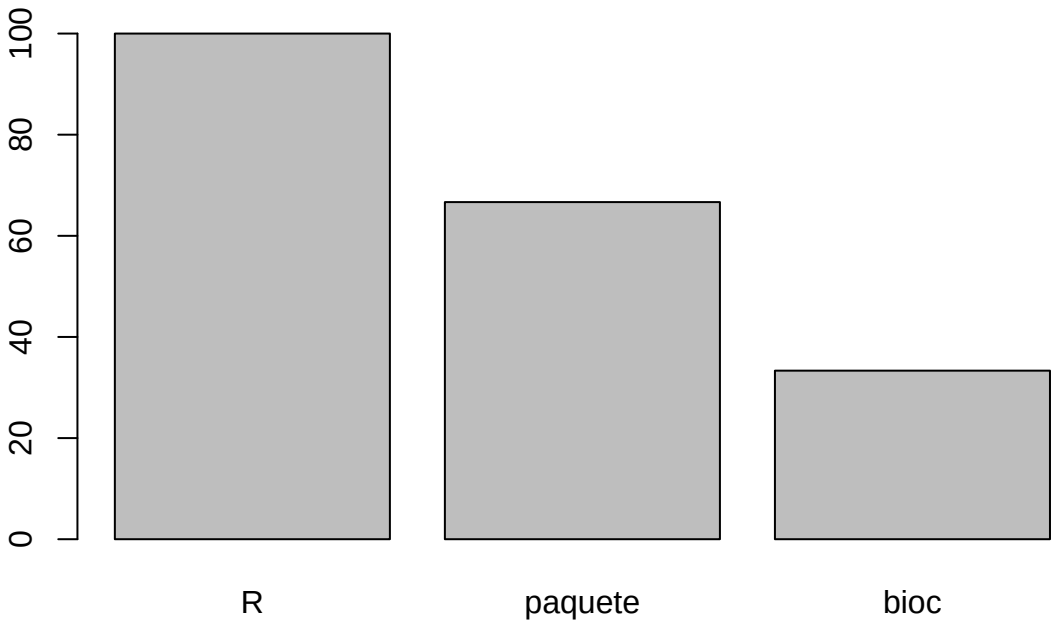
Sesión 1.3

Leonardo Collado-Torres

Octubre 24, 2016

- ¿Quién ha escuchado que es R?
- ¿Quién sabe que es un paquete de R?
- ¿Quién sabe que es Bioconductor?

```
x <- c('R' = 30, 'paquete' = 20, 'bioc' = 10)
x <- x / max(x) * 100
barplot(x)
```



Paquete de R

- Es la forma en que uno puede expander lo que podemos hacer con R
- Agrupa código, documentación de como usar las funciones y ejemplos demostrando lo que uno puede hacer.
- Los mejores paquetes explican como las funciones se relacionan en un documento *vignette* y tienen pruebas para verificar que el código está funcionando correctamente.

- ¿Qué paquetes de R acabamos de usar?

```
?max
?barplot
```

- Exploremos un paquete

```
help(package = 'stats')
```

¿Qué es Bioconductor?

- Es un repositorio de paquetes de R enfocados en resolver problemas biológicos
- También es una organización que revisa los paquetes para que sean de alta calidad y funcionen adecuadamente
- Ayudan a usuarios nuevos y ofrecen cursos
- En un escenario ideal, los usuarios terminan siendo desarrolladores de sus propios paquetes

- http://bioconductor.org/

Home Install Help

About *Bioconductor*

Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data. Bioconductor uses the R statistical programming language, and is open source and open development. It has two releases each year, 1211 software packages, and an active user community. Bioconductor is also available as an AMI (Amazon Machine Image) and a series of Docker images.

News

- Bioconductor 3.3 is available.
- Bioconductor F1000 Research Channel launched.
- Orchestrating high-throughput genomic analysis with *Bioconductor* (abstract) and other recent literature.
- Read our latest newsletter and course material.
- Use the support site to get help installing, learning and using Bioconductor.

Install »

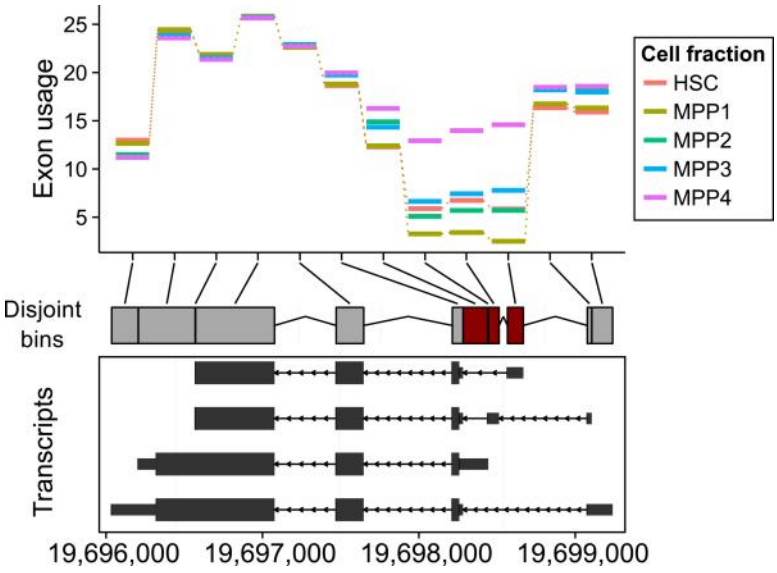
Get started with *Bioconductor*

- Install *Bioconductor*
- Explore packages
- Get support
- Latest newsletter
- Follow us on twitter
- Install R

Use »

Create bioinformatic solutions with *Bioconductor*

- Software, Annotation, and Experiment packages
- Amazon Machine Image
- Latest release annoucement
- Support site



¿Cómo encuentro paquetes?

- Google, PubMed, ...
- BiocViews: paquetes organizados por las tareas que realizan.
- Hay paquetes de código (software), de datos (experiment) y de anotación
- Ejercicio: ¿qué paquetes nos servirían para expresión diferencial de exones?

¡No hagan trampa!

Home » BiocViews

All Packages

Bioconductor version 3.3 (Release)

Autocomplete biocViews search:

- Software (1211)
  - AssayDomain (435)
  - BiologicalQuestion (409)
  - Infrastructure (261)
  - ResearchField (298)
  - StatisticalMethod (366)
  - Technology (762)
  - WorkflowStep (630)
- AnnotationData (917)
- ExperimentData (293)

Packages found under Software:

Show All entries

Package	Maintainer
a4	Tobias Verbeke, Willem Ligtenberg
a4Base	Tobias Verbeke, Willem Ligtenberg
a4Classif	Tobias Verbeke, Willem Ligtenberg
a4Core	Tobias Verbeke, Willem Ligtenberg
a4Preproc	Tobias Verbeke, Willem Ligtenberg

All Packages

Bioconductor version 3.3 (Release)

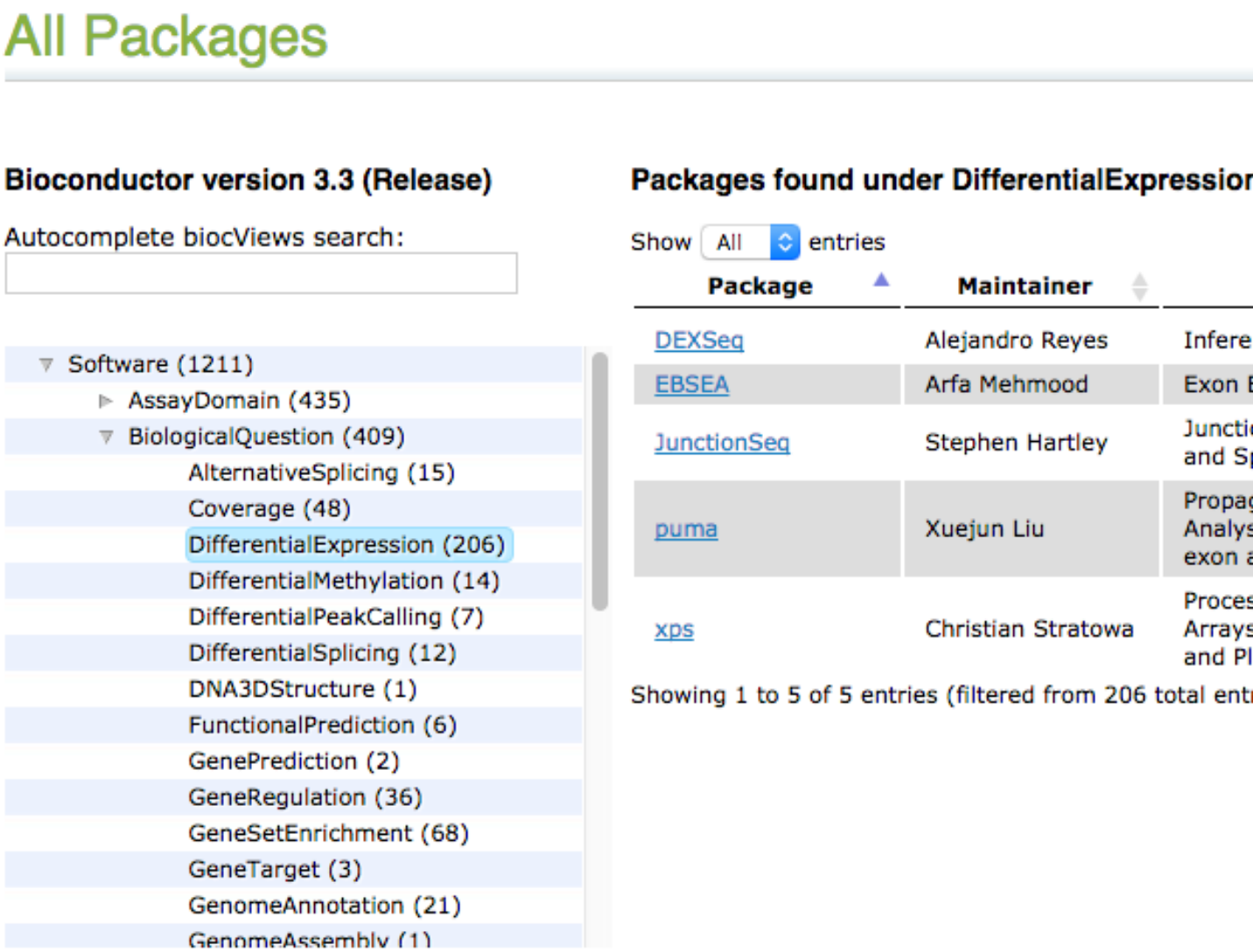
Autocomplete biocViews search:

- Software (1211)
  - AssayDomain (435)
  - BiologicalQuestion (409)
    - AlternativeSplicing (15)
    - Coverage (48)
    - DifferentialExpression (206)
    - DifferentialMethylation (14)
    - DifferentialPeakCalling (7)
    - DifferentialSplicing (12)
    - DNA3DStructure (1)
    - FunctionalPrediction (6)
    - GenePrediction (2)
    - GeneRegulation (36)
    - GeneSetEnrichment (68)
    - GeneTarget (3)
    - GenomeAnnotation (21)
    - GenomeAssembly (1)

Packages found under DifferentialExpressi

Show All entries

Package	Maintainer	
ABSSeq	Wentao Yang	ABS mo
acde	Juan Pablo Acosta	Arti Exp
AffyExpress	Xuejun Arthur Li	Affy
affylmGUI	Yifang Hu, Gordon Smyth, Keith Satterley	GU
AgiMicroRna	Pedro Lopez-Romero	Pro Agi
ALDEx2	Greg Gloor	Ana var
ampliQueso	Michal Okoniewski	Ana
anota	Ola Larsson	ANa
ArrayTools	Arthur Li	ger
AtlasRDF	James Malone	Ger pac
BADER	Andreas Neudecker	Bay Sec



Encontrando paquetes vía *workflows*

- Un *workflow* es un documento que explica como realizar cierto tipo de análisis
- Útil cuando no conocemos las palabras clave
- Involucran más de un paquete y explican como se relacionan
- Son documentos que no cambian muy seguido
- http://bioconductor.org/help/workflows/

Home » Help » Workflows

Bioconductor Workflows

Bioconductor provides software to help analyze diverse high-throughput genomic data. Comm
workflows include:

Basic Workflows

- Sequence Analysis Import fasta, fastq, BAM, gff, bed, wig, and other sequence formats. Tri
transform, align, and manipulate sequences. Perform quality assessment, ChIP-seq, differe
expression, RNA-seq, and other workflows. Access the Sequence Read Archive.
- Oligonucleotide Arrays Import Affymetrix, Illumina, Nimblegen, Agilent, and other platforms
quality assessment, normalization, differential expression, clustering, classification, gene se
enrichment, genetical genomics and other workflows for expression, exon, copy number, SN
methylation and other assays. Access GEO, ArrayExpress, Biomart, UCSC, and other commu
resources.
- Annotation Resources Introduction to using gene, pathway, gene ontology, homology annot
the AnnotationHub. Access GO, KEGG, NCBI, Biomart, UCSC, vendor, and other sources.
- Annotating Genomic Ranges Represent common sequence data types (e.g., from BAM, gff,
wig files) as genomic ranges for simple and advanced range-based queries.
- Annotating Genomic Variants Read and write VCF files. Identify structural location of variant
compute amino acid coding changes for non-synonymous variants. Use SIFT and PolyPhen
packages to predict consequence of amino acid coding changes.
- Changing genomic coordinate systems with rtracklayer::liftOver The liftOver facilities develo
conjunction with the UCSC browser track infrastructure are available for transforming data i
formats. This is illustrated here with an image of the NHGRI GWAS catalog that is, as of Oct
distributed with coordinates defined by NCBI build hg38.

About This Document »

Package name	sequencing
Built with Bioconductor (R)	3.4 (3.3.1)
Last Built	Fri, 07 Oct 2016 06:04:03 -0700
Last Modified	Tue, 13 Sep 2016 01:53:27 -0700 (r120890)
Source Package	sequencing_0.99.120890.tar.gz
Windows Binary	sequencing_0.99.120890.zip
Mac OS X 10.10 (Yosemite)	sequencing_0.99.120890.tgz
R Script	sequencing.R

To install this workflow under Bioconductor 3.3, start R and enter:

```
source("http://bioconductor.org/workflows.R")
workflowInstall("sequencing")
```

Introduction to Bioconductor for Sequence

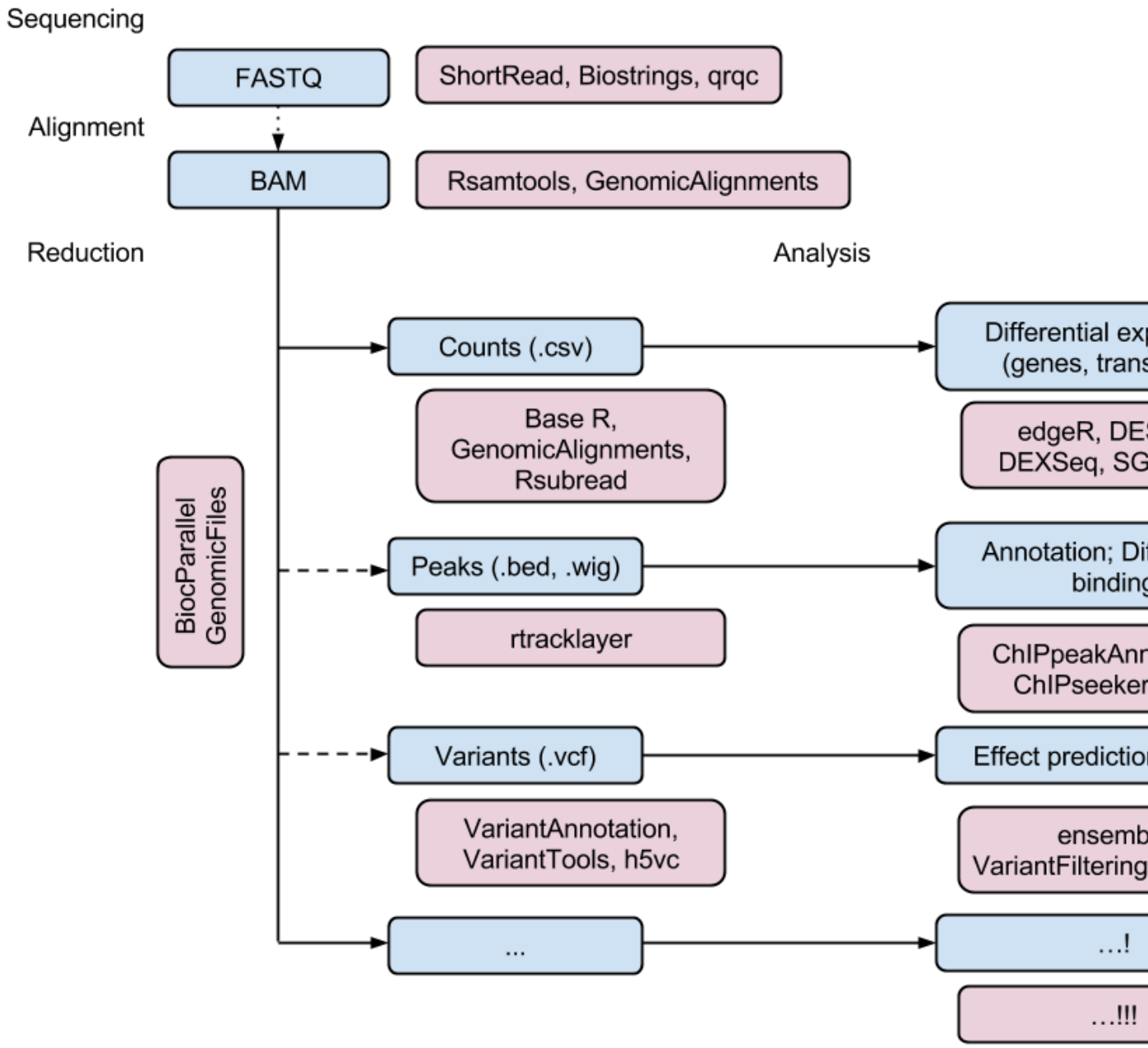
Sonali Arora, Martin Morgan

Contents

Bioconductor enables the analysis and comprehension of high- throughput genomic data. We h
number of packages that allow rigorous statistical analysis of large data while keeping technol
artifacts in mind. Bioconductor helps users place their analytic results into biological context, w
opportunities for visualization. Reproducibility is an important goal in *Bioconductor* analyses. D
types of analysis can be carried out using *Bioconductor*, for example

- Sequencing : RNASeq, ChIPSeq, variants, copy number..
- Microarrays: expression, SNP, ...
- Domain specific analysis : Flow cytometry, Proteomics ..

For these analyses, one typically imports and works with diverse sequence-related file types, i
fasta, fastq, BAM, gtf, bed, and wig files, among others. *Bioconductor* packages support impor
and advanced sequence manipulation operations such as trimming, transformation, and alignm
including quality assessment.



Encontramos un paquete... ¿qué sigue?

- Explorar la *vignette* para ver que podemos hacer con el paquete
- Generalmente incluye un ejemplo completo con código que podemos correr y obtener los mismos resultados
- Muchos tienen artículos asociados que explican a más detalle los métodos usados en el paquete

DEXSeq

platforms all | downloads top 5% | posts 17 / 0.8 / 2 / 2 | in Bioc 5 years
build ok | commits 1.83 | test coverage unknown

Inference of differential exon usage in RNA-Seq

Bioconductor version: Release (3.3)

The package is focused on finding differential exon usage using RNA-seq exon counts between with different experimental designs. It provides functions that allows the user to make the nec statistical tests based on a model that uses the negative binomial distribution to estimate the between biological replicates and generalized linear models for testing. The package also provi functions for the visualization and exploration of the results.

Author: Simon Anders <sanders at fs.tum.de> and Alejandro Reyes <alejandro.reyes at embl.

Maintainer: Alejandro Reyes <alejandro.reyes at embl.de>

Citation (from within R, enter `citation("DEXSeq")`):

Anders S, Reyes A and Huber W (2012). "Detecting differential usage of exons from RNA-seq *Genome Research*, **22**, pp. 4025.

Reyes A, Anders S, Weatheritt R, Gibson T, Steinmetz L and Huber W (2013). "Drift and con differential exon usage across tissues in primate species." *PNAS*, **110**, pp. -5.

Documentation

To view documentation for the version of this package installed in your system, start R and en

```
browseVignettes("DEXSeq")
```

PDF	R Script	Analyzing RNA-seq data for differential exon usage with the "DEXSeq" pa
PDF		Reference Manual
Text		NEWS

Inferring differential exon usage in RNA-Seq da
DEXSeq package

Alejandro Reyes, Simon Anders, Wolfgang Huber

European Molecular Biology Laboratory (EMBL)
Heidelberg, Germany

This vignette describes version 1.18.4 of the *DEXSeq* package.

Last revision of this document: 2016-03-10

Contents

Detalles técnicos

Details

biocViews	DifferentialExpression, RNASeq, Sequencing, Software
Version	1.18.4
In Bioconductor since	BioC 2.9 (R-2.14) (5 years)
License	GPL (>= 3)
Depends	BiocParallel, Biobase, SummarizedExperiment, IRanges(>= 2.5.17), GenomicRanges(>= 1.23.7), DESeq2(>= 1.9.11), AnnotationDbi, RCol S4Vectors
Imports	BiocGenerics, biomaRt, hwriter, methods, stringr, Rsamtools, statmod, geneplotter, genefilter
LinkingTo	
Suggests	GenomicFeatures(>= 1.13.29), pasilla(>= 0.2.22), parathyroidSE, Bioc
SystemRequirements	
Enhances	
URL	
Depends On Me	
Imports Me	
Suggests Me	GenomicRanges, JctSeqData, oneChannelGUI, pasilla, subSeq
Build Report	

Package Archives

Follow Installation instructions to use this package in your R session.

Package Source	DEXSeq_1.18.4.tar.gz
Windows Binary	DEXSeq_1.18.4.zip
Mac OS X 10.9 (Mavericks)	DEXSeq_1.18.4.tgz
Subversion source	(username/password: readonly)
Git source	https://github.com/Bioconductor-mirror/DEXSeq/tree/release-3.3
Package Short Url	http://bioconductor.org/packages/DEXSeq/
Package Downloads Report	Download Stats

Un paquete en CRAN

- https://cran.r-project.org/package=pheatmap

pheatmap: Pretty Heatmaps

Implementation of heatmaps that offers more control over dimensions and appearan

Version:	1.0.8
Depends:	R (≥ 2.0)
Imports:	grid, RColorBrewer, scales, gtable, stats, grDevices, graphics
Published:	2015-12-11
Author:	Raivo Kolde
Maintainer:	Raivo Kolde <rkolde at gmail.com>
License:	GPL-2
NeedsCompilation:	no
Materials:	NEWS
CRAN checks:	pheatmap results

Downloads:

Reference manual:	pheatmap.pdf
Package source:	pheatmap_1.0.8.tar.gz
Windows binaries:	r-devel: pheatmap_1.0.8.zip, r-release: pheatmap_1.0.8.z
OS X Mavericks binaries:	r-release: pheatmap_1.0.8.tgz, r-oldrel: pheatmap_1.0.8.t
Old sources:	pheatmap archive

Reverse dependencies:

Reverse depends:	KOGMWU, LncMod, MM2S
Reverse imports:	FAMILY, NPflow, omics, qiimer, timeSeq
Reverse suggests:	diverse

Instalar paquetes

- CRAN

```
install.packages('pheatmap')
```

- Bioconductor

```
## try http:// if https:// URLs are not supported
source("https://bioconductor.org/biocLite.R")
biocLite("DEXSeq")
```

```
biocLite(c('DESeq2', 'edgeR', 'limma'))
```

- https://www.bioconductor.org/developers/how-to/useDevel/

Usar un paquete

```
library('DESeq2')
```

```
help(package = "DESeq2")
```

DESeq2-package {DESeq2}

DESeq2 package for differential analysis of cou

Description

The main functions for differential analysis are `DESeq` and `results`. See the example analysis steps. Two transformations offered for count data are the "regularized logar `varianceStabilizingTransformation`. For more detailed information on usage, se by typing `vignette("DESeq2")`, or the workflow linked to on the first page of the vi questions should be posted to the Bioconductor support site: http://support.biocondu

Author(s)

Michael Love, Wolfgang Huber, Simon Anders

References

DESeq2 reference:

Michael I Love, Wolfgang Huber, Simon Anders: Moderated estimation of fold cha RNA-seq data with DESeq2. Genome Biology 2014, 15:550. http://dx.doi.org/10.11

DESeq

```
?DESeq
```

```
# see vignette for suggestions on generating
# count tables from RNA-Seq data
cnts <- matrix(rnbinom(n=1000, mu=100, size=1/0.5), ncol=10)
cond <- factor(rep(1:2, each=5))
```

```
## Exploremos los datos
dim(cnts)
```

```
## [1] 100  10
```

```
head(cnts[1:2, 1:5])
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]  322   71   98  117  158
## [2,]   39   99   72   87   34
```

```
cond
```

```
##  [1] 1 1 1 1 1 2 2 2 2 2
## Levels: 1 2
```

Objeto DESeqDataSet

```
# object construction
dds <- DESeqDataSetFromMatrix(cnts, DataFrame(cond), ~ cond)
```

```
## converting counts to integer mode
```

```
class(dds)
```

```
## [1] "DESeqDataSet"
## attr(,"package")
## [1] "DESeq2"
```

```
dds
```

```
## class: DESeqDataSet
## dim: 100 10
## metadata(1): version
## assays(1): counts
## rownames: NULL
## rowData names(0):
## colnames: NULL
## colData names(1): cond
```

Realicemos el análisis

```
# standard analysis
dds <- DESeq(dds)
```

```
## estimating size factors
## estimating dispersions
## gene-wise dispersion estimates
## mean-dispersion relationship
## final dispersion estimates
## fitting model and testing
```

```
dds
```

```
## class: DESeqDataSet
## dim: 100 10
## metadata(1): version
## assays(3): counts mu cooks
## rownames: NULL
```

```
## rowData names(27): baseMean baseVar ... deviance maxCooks
## colnames: NULL
## colData names(2): cond sizeFactor
```

```
res <- results(dds)
res
```

```
## log2 fold change (MAP): cond 2 vs 1
## Wald test p-value: cond 2 vs 1
## DataFrame with 100 rows and 6 columns
##      baseMean log2FoldChange     lfcSE        stat     pvalue      padj
##     <numeric>      <numeric> <numeric>   <numeric>  <numeric> <numeric>
## 1   117.52202     -0.2448061 0.4209514  -0.5815543 0.56086695 0.9138280
## 2    75.73848      0.3990443 0.4487406   0.8892538 0.37386670 0.8255007
## 3    67.00032     -0.3511059 0.4556281  -0.7705976 0.44094546 0.8325772
## 4    90.14277     -0.2984479 0.4410265  -0.6767121 0.49858865 0.8596356
## 5   134.80355     -0.8009444 0.4547022  -1.7614702 0.07815885 0.6513238
## ...       ...            ...       ...         ...        ...       ...
## 96   68.59374    -0.19416658 0.4816400 -0.40313629  0.6868480 0.9781652
## 97  118.02717    -0.05713692 0.4241364 -0.13471356  0.8928384 0.9781652
## 98   74.66650    -0.37327206 0.4769033 -0.78269964  0.4338035 0.8325772
## 99   85.08825    -0.44239910 0.3870804 -1.14291279  0.2530748 0.8255007
## 100  86.50207    -0.01979515 0.4210903 -0.04700927  0.9625058 0.9876606
```

```
example('DESeq', package = 'DESeq2')
```

```
##
## DESeq> # see vignette for suggestions on generating
## DESeq> # count tables from RNA-Seq data
## DESeq> cnts <- matrix(rnbinom(n=1000, mu=100, size=1/0.5), ncol=10)
##
## DESeq> cond <- factor(rep(1:2, each=5))
##
## DESeq> # object construction
## DESeq> dds <- DESeqDataSetFromMatrix(cnts, DataFrame(cond), ~ cond)
## converting counts to integer mode
##
## DESeq> # standard analysis
## DESeq> dds <- DESeq(dds)
## estimating size factors
## estimating dispersions
## gene-wise dispersion estimates
## mean-dispersion relationship
## -- note: fitType='parametric', but the dispersion trend was not well captured by the
```

```
##    function: y = a/x + b, and a local regression fit was automatically substituted.
##    specify fitType='local' or 'mean' to avoid this message next time.

## final dispersion estimates

## fitting model and testing

##
## DESeq> res <- results(dds)
##
## DESeq> # an alternate analysis: likelihood ratio test
## DESeq> ddsLRT <- DESeq(dds, test="LRT", reduced= ~ 1)

## using pre-existing size factors

## estimating dispersions

## found already estimated dispersions, replacing these

## gene-wise dispersion estimates

## mean-dispersion relationship

## -- note: fitType='parametric', but the dispersion trend was not well captured by the
##    function: y = a/x + b, and a local regression fit was automatically substituted.
##    specify fitType='local' or 'mean' to avoid this message next time.

## final dispersion estimates

## fitting model and testing

##
## DESeq> resLRT <- results(ddsLRT)
```

Ejercicio

- Tenemos los identificadores de *UNIPROT* de 6 proteínas humanas de interes. ¿Cuál es el símbolo de los genes para las siguientes proteínas?

P61968

B2RC63

A0A024R9I0

Q13394

Q8NGN1

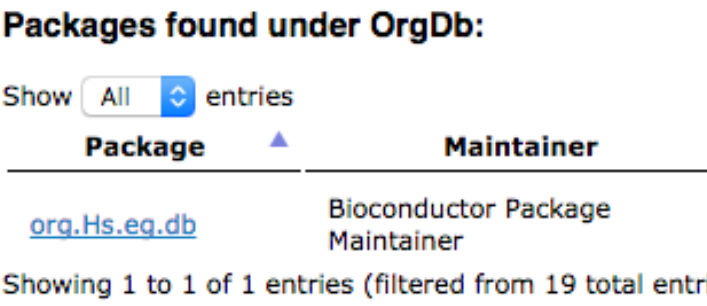
P58417

Pasos a realizar

1. Encontrar que paquete tiene la anotación del genoma humano
2. Encontrar la *vignette* que describe como usar ese paquete
3. Obtener los símbolos de los genes

Solución


Bioconductor version 3.3 (Release)
Autocomplete biocViews search:
Organism (584)
PackageType (642)
BSgenome (83)
cdf (126)
ChipDb (157)
db0 (19)
FRMA (10)
InparanoidDb (8)
MeSHDb (78)
OrganismDb (3)
OrgDb (19)
probe (104)
SNPlocs (3)
TxDb (29)
XtraSNPlocs (3)
SequenceAnnotation (1)
ExperimentData (293)


Packages found under OrgDb:
Show All entries
Package
Maintainer
org.Hs.eg.db
Bioconductor Package Maintainer
Showing 1 to 1 of 1 entries (filtered from 19 total entr

Details

biocViews	AnnotationData, Homo_sapiens, OrgDb, humanLLMappings
Version	3.3.0
License	Artistic-2.0
Depends	R (>= 2.7.0), methods, AnnotationDbi(>= 1.33.10)
Imports	methods, AnnotationDbi
LinkingTo	
Suggests	DBI, annotate, RUnit
SystemRequirements	
Enhances	
URL	

Annotation Database Interface

Bioconductor version: Release (3.3)

Provides user interface and database connection code for annotation data packages using SQLi
storage.

Author: Herve Pages, Marc Carlson, Seth Falcon, Nianhua Li

Maintainer: Bioconductor Package Maintainer <maintainer at bioconductor.org>

Citation (from within R, enter `citation("AnnotationDbi")`):

> Pages H, Carlson M, Falcon S and Li N (2016). *AnnotationDbi: Annotation Database Interface*
> package version 1.34.4.

Documentation

To view documentation for the version of this package installed in your system, start R and en

```
browseVignettes("AnnotationDbi")
```

PDF	R Script	AnnotationDbi: Introduction To Bioconductor Annotation Packages
PDF	R Script	How to use bimaps from the ".db" annotation packages
PDF		Reference Manual
Text		NEWS
Video		Using AnnotationDb objects

```
keytypes(org.Hs.eg.db)
```

```
##  [1] "ACCNUM"       "ALIAS"        "ENSEMBL"      "ENSEMBLPROT"  "
##  [6] "ENTREZID"     "ENZYME"       "EVIDENCE"     "EVIDENCEALL"  "
## [11] "GO"           "GOALL"        "IPI"          "MAP"          "
## [16] "ONTOLOGY"     "ONTOLOGYALL"  "PATH"         "PFAM"         "
## [21] "PROSITE"      "REFSEQ"       "SYMBOL"       "UCSCKG"       "
## [26] "UNIPROT"
```

```
uniKeys <- head(keys(org.Hs.eg.db, keytype="UNIPROT"))
cols <- c("SYMBOL", "PATH")
select(org.Hs.eg.db, keys=uniKeys, columns=cols, keytype="UNIPROT")
```

```
## 'select()' returned 1:many mapping between keys and columns
```

```
##    UNIPROT SYMBOL  PATH
## 1   P04217   A1BG  <NA>
## 2   V9HWD8   A1BG  <NA>
```

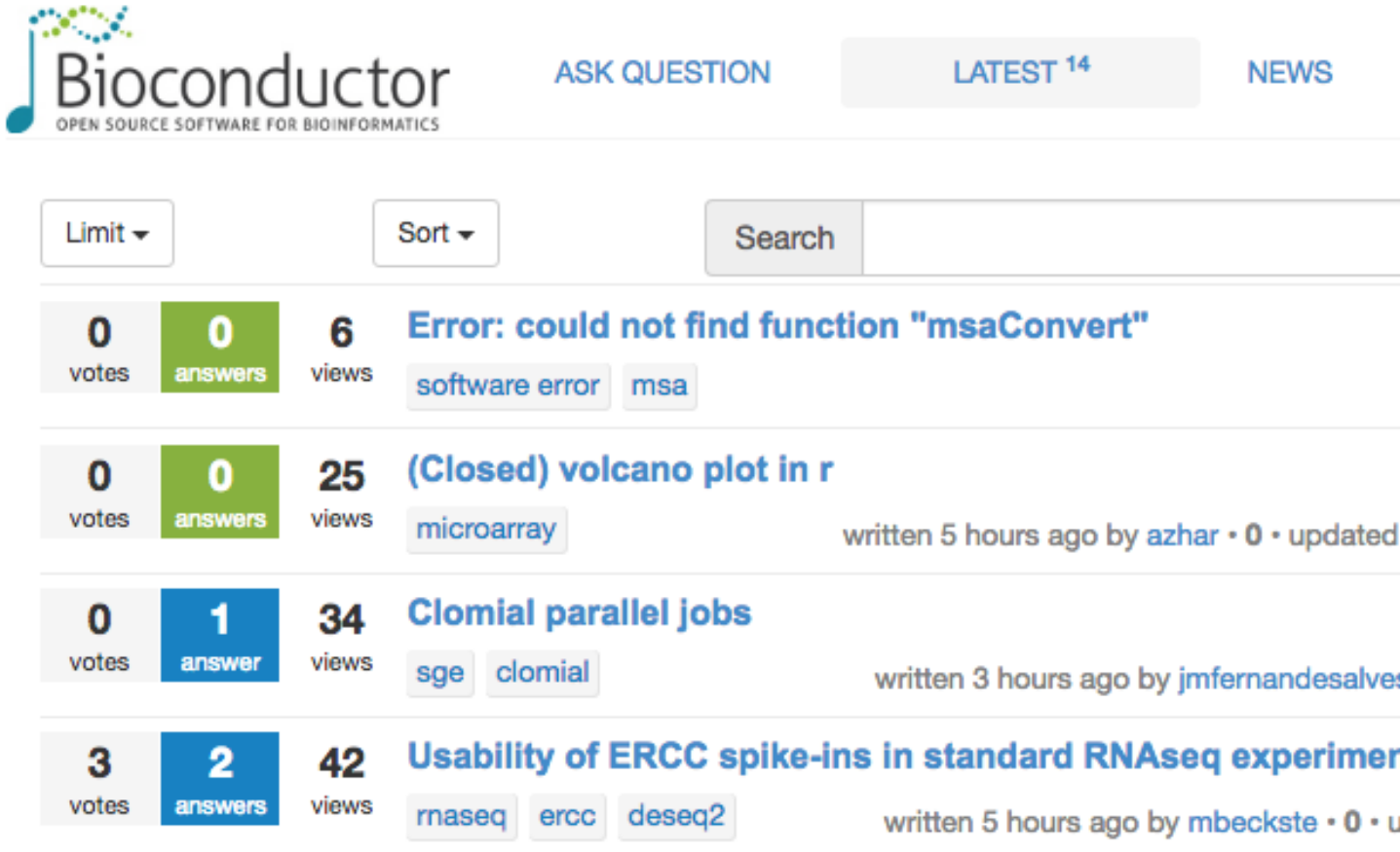
```
library('org.Hs.eg.db')
uniprot <- c('P61968', 'B2RC63', 'A0A024R9I0',
    'Q13394', 'Q8NGN1', 'P58417')
select(org.Hs.eg.db, keys = uniprot,
    columns = 'SYMBOL', keytype = 'UNIPROT')
```

```
## 'select()' returned 1:1 mapping between keys and columns
```

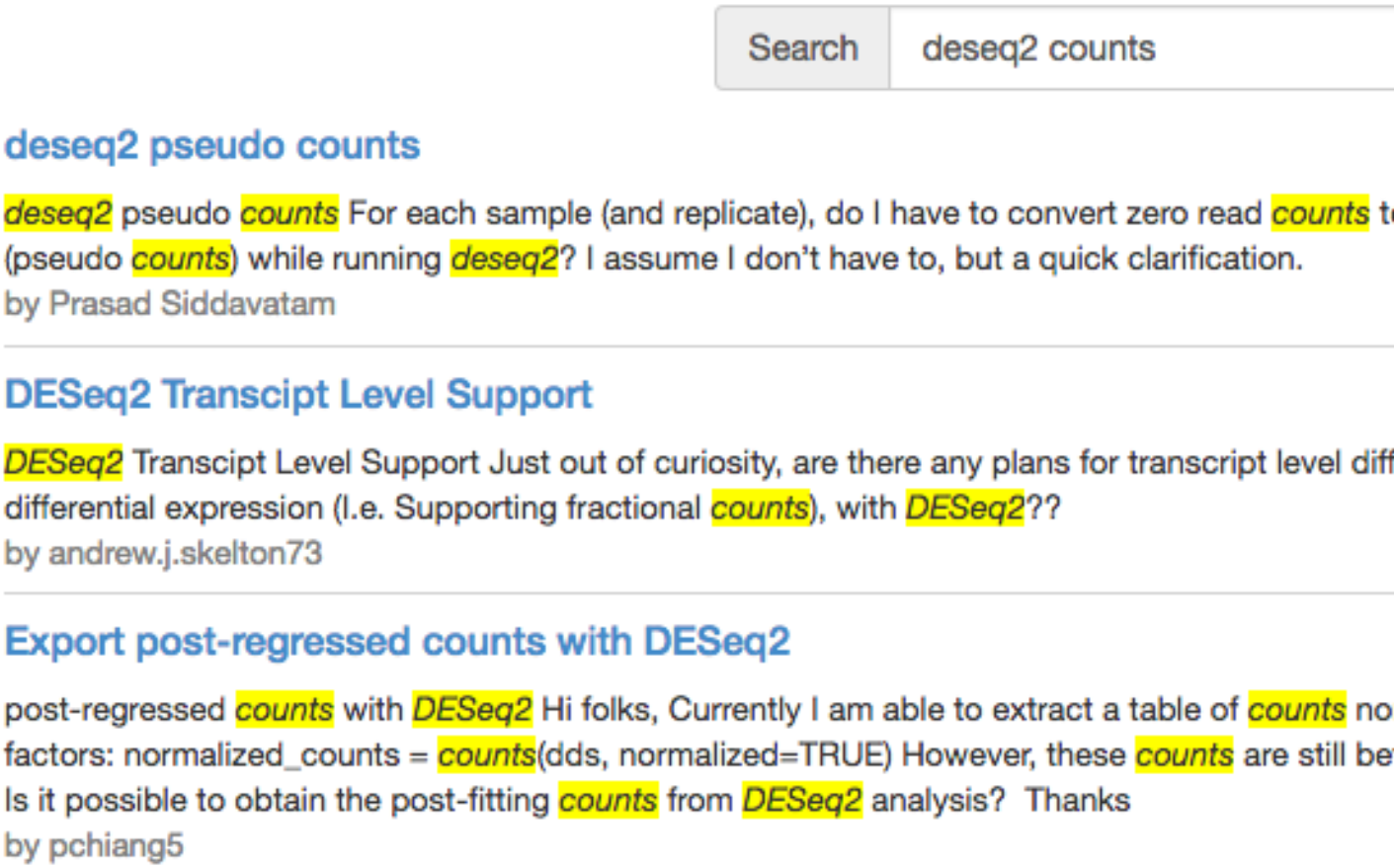
```
##      UNIPROT   SYMBOL
## 1     P61968     LMO4
## 2     B2RC63     GDF2
## 3 A0A024R9I0 ATP6V1C1
## 4     Q13394  MAB21L1
## 5     Q8NGN1    OR6T1
## 6     P58417    NXPH1
```

Buscar ayuda

- https://support.bioconductor.org/



- https://support.bioconductor.org/local/search/page/?q=deseq2+counts



- ¿Qué elementos son importantes para hacer una buena pregunta?

- https://support.bioconductor.org/p/88421/

- https://support.bioconductor.org/p/83911/

Pedir ayuda

- http://www.bioconductor.org/help/support/posting-guide/
- Describir el problema con un ejemplo pequeño que otros puedan reproducir
- Incluir información precisa sobre que paquetes está uno usando y del error
- Etiquetar a los paquetes relacionados para que los autores de ellos sean notificados

Información de R

```
sessionInfo()
```

```
## R version 3.3.1 (2016-06-21)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.11.6 (El Capitan)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] parallel  stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] devtools_1.12.0             org.Hs.eg.db_3.4.0
##  [3] AnnotationDbi_1.35.4        DESeq2_1.13.14
##  [5] SummarizedExperiment_1.3.82 Biobase_2.33.3
```

```
##  [7] GenomicRanges_1.25.94       GenomeInfoDb_1.9.13
##  [9] IRanges_2.7.16              S4Vectors_0.11.18
## [11] BiocGenerics_0.19.2         knitr_1.14
## [13] rmarkdown_1.0               colorout_1.1-2
##
## loaded via a namespace (and not attached):
##  [1] genefilter_1.55.2   locfit_1.5-9.1      splines_3.3.1
##  [4] lattice_0.20-34     colorspace_1.2-6    htmltools_0.3.5
##  [7] yaml_2.1.13         chron_2.3-47        survival_2.39-5
## [10] XML_3.98-1.4        withr_1.0.2         foreign_0.8-67
## [13] DBI_0.5-1           BiocParallel_1.7.8  RColorBrewer_1.1-2
## [16] plyr_1.8.4          stringr_1.1.0       zlibbioc_1.19.0
## [19] munsell_0.4.3       gtable_0.2.0        caTools_1.17.1
## [22] evaluate_0.9        memoise_1.0.0       latticeExtra_0.6-28
## [25] geneplotter_1.51.0  highr_0.6           Rcpp_0.12.7
## [28] acepack_1.3-3.3     xtable_1.8-2        scales_0.4.0
## [31] formatR_1.4         Hmisc_3.17-4        annotate_1.51.1
## [34] XVector_0.13.7      gridExtra_2.2.1     ggplot2_2.1.0
## [37] digest_0.6.10       stringi_1.1.2       grid_3.3.1
## [40] tools_3.3.1         bitops_1.0-6        magrittr_1.5
## [43] RCurl_1.95-4.8      RSQLite_1.0.0       Formula_1.2-1
## [46] cluster_2.0.4       Matrix_1.2-7.1      data.table_1.9.6
## [49] rstudioapi_0.6      rpart_4.1-10        nnet_7.3-12
```

```
library('devtools'); options(width = 120); session_info()
```

```
## Session info -------------------------------------------------------------------------------------
##  setting  value
##  version  R version 3.3.1 (2016-06-21)
##  system   x86_64, darwin13.4.0
##  ui       X11
##  language (EN)
##  collate  en_US.UTF-8
##  tz       America/New_York
##  date     2016-10-18
## Packages -----------------------------------------------------------------------------------------
##  package             * version  date       source
##  acepack               1.3-3.3  2014-11-24 CRAN (R 3.3.0)
##  annotate              1.51.1   2016-09-18 Bioconductor
##  AnnotationDbi       * 1.35.4   2016-07-08 Bioconductor
##  Biobase             * 2.33.3   2016-09-01 Bioconductor
##  BiocGenerics        * 0.19.2   2016-07-08 Bioconductor
##  BiocParallel          1.7.8    2016-08-16 Bioconductor
##  bitops                1.0-6    2013-08-17 CRAN (R 3.3.0)
##  caTools               1.17.1   2014-09-10 CRAN (R 3.3.0)
##  chron                 2.3-47   2015-06-24 CRAN (R 3.3.0)
##  cluster               2.0.4    2016-04-18 CRAN (R 3.3.1)
##  colorout            * 1.1-2    2016-05-05 Github (jalvesaq/colorout@6538970)
##  colorspace            1.2-6    2015-03-11 CRAN (R 3.3.0)
```

```
##  data.table             1.9.6    2015-09-19 CRAN (R 3.3.0)
##  DBI                    0.5-1    2016-09-10 CRAN (R 3.3.0)
##  DESeq2               * 1.13.14  2016-09-08 Bioconductor
##  devtools             * 1.12.0   2016-06-24 CRAN (R 3.3.0)
##  digest                 0.6.10   2016-08-02 CRAN (R 3.3.0)
##  evaluate               0.9      2016-04-29 CRAN (R 3.3.0)
##  foreign                0.8-67   2016-09-13 CRAN (R 3.3.0)
##  formatR                1.4      2016-05-09 CRAN (R 3.3.0)
##  Formula                1.2-1    2015-04-07 CRAN (R 3.3.0)
##  genefilter             1.55.2   2016-05-27 Bioconductor
##  geneplotter            1.51.0   2016-05-05 Bioconductor
##  GenomeInfoDb         * 1.9.13   2016-09-23 Bioconductor
##  GenomicRanges        * 1.25.94  2016-09-11 Bioconductor
##  ggplot2                2.1.0    2016-03-01 CRAN (R 3.3.0)
##  gridExtra              2.2.1    2016-02-29 CRAN (R 3.3.0)
##  gtable                 0.2.0    2016-02-26 CRAN (R 3.3.0)
##  highr                  0.6      2016-05-09 CRAN (R 3.3.0)
##  Hmisc                  3.17-4   2016-05-02 CRAN (R 3.3.0)
##  htmltools              0.3.5    2016-03-21 CRAN (R 3.3.0)
##  IRanges              * 2.7.16   2016-09-29 Bioconductor
##  knitr                * 1.14     2016-08-13 CRAN (R 3.3.0)
##  lattice                0.20-34  2016-09-06 CRAN (R 3.3.0)
##  latticeExtra           0.6-28   2016-02-09 CRAN (R 3.3.0)
##  locfit                 1.5-9.1  2013-04-20 CRAN (R 3.3.0)
##  magrittr               1.5      2014-11-22 CRAN (R 3.3.0)
##  Matrix                 1.2-7.1  2016-09-01 CRAN (R 3.3.0)
##  memoise                1.0.0    2016-01-29 CRAN (R 3.3.0)
##  munsell                0.4.3    2016-02-13 CRAN (R 3.3.0)
##  nnet                   7.3-12   2016-02-02 CRAN (R 3.3.1)
##  org.Hs.eg.db         * 3.4.0    2016-10-06 Bioconductor
##  plyr                   1.8.4    2016-06-08 CRAN (R 3.3.0)
##  RColorBrewer           1.1-2    2014-12-07 CRAN (R 3.3.0)
##  Rcpp                   0.12.7   2016-09-05 CRAN (R 3.3.0)
##  RCurl                  1.95-4.8 2016-03-01 CRAN (R 3.3.0)
##  rmarkdown            * 1.0      2016-07-08 CRAN (R 3.3.0)
##  rpart                  4.1-10   2015-06-29 CRAN (R 3.3.1)
##  RSQLite                1.0.0    2014-10-25 CRAN (R 3.3.0)
##  rstudioapi             0.6      2016-06-27 CRAN (R 3.3.0)
##  S4Vectors            * 0.11.18  2016-10-04 Bioconductor
##  scales                 0.4.0    2016-02-26 CRAN (R 3.3.0)
##  stringi                1.1.2    2016-10-01 CRAN (R 3.3.1)
##  stringr                1.1.0    2016-08-19 CRAN (R 3.3.0)
##  SummarizedExperiment * 1.3.82   2016-09-01 Bioconductor
##  survival               2.39-5   2016-06-26 CRAN (R 3.3.0)
##  withr                  1.0.2    2016-06-20 CRAN (R 3.3.0)
##  XML                    3.98-1.4 2016-03-01 CRAN (R 3.3.0)
##  xtable                 1.8-2    2016-02-05 CRAN (R 3.3.0)
##  XVector                0.13.7   2016-07-24 Bioconductor
##  yaml                   2.1.13   2014-06-12 CRAN (R 3.3.0)
##  zlibbioc               1.19.0   2016-05-05 Bioconductor
```

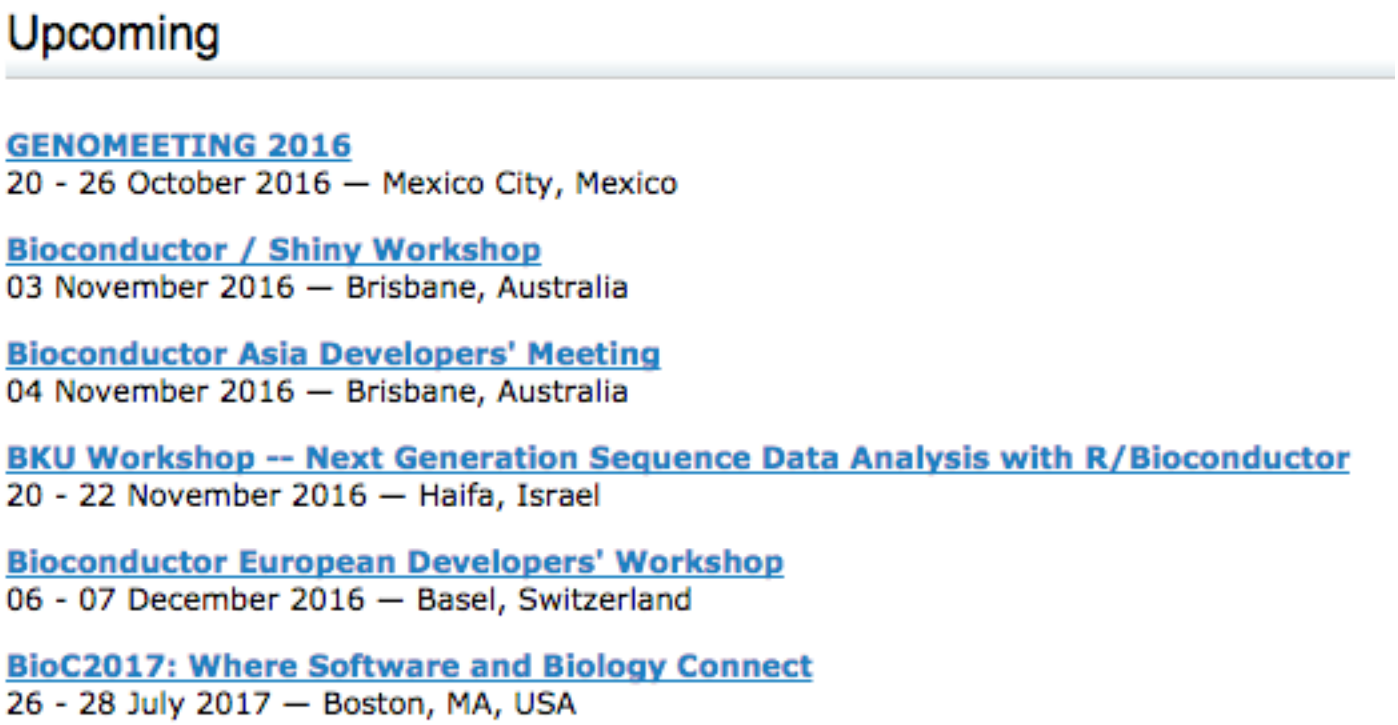
traceback()

```
library('IRanges')
IRanges('a')
traceback()
```

Estar al día

- *NEWS*
- Via twitter: https://twitter.com/bioconductor
- Con las *newsletter* desde la página principal http://bioconductor.org/help/newsletters/2016_January/

- Llendo a cursos http://bioconductor.org/help/events/



- http://bioconductor.org/help/course-materials/

Más información

- http://lcolladotor.github.io/2014/10/16/startBioC#.WAYwcZMrKso
- http://bioconductor.org/about/
- http://bioconductor.org/help/course-materials/2016/CSAMA/lab-1-intro-to-r-bioc/html/L1.2-bioc-intro-morgan.html
- Huber et al., 2015 Nature Methods 12:115-121 https://www.ncbi.nlm.nih.gov/pubmed/25633503