

# Annotating genes, genomes, and variants

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# What is 'Annotation'?

- ▶ Genes – classification schemes (e.g., Entrez, Ensembl), pathway membership, ...
- ▶ Genomes – reference genomes; exons, transcripts, coding sequence; coding consequences
- ▶ System / network biology – pathways, biochemical reactions, ...
- ▶ 'Consortium' resources, TCGA, ENCODE, dbSNP, GTEx, ...

Other definitions (not covered here)

- ▶ SNP (and similar) consequences (*VariantAnnotation*, *VariantFiltering*, *ensemblVEP*)
- ▶ Assign function to novel sequences
- ▶ ...

# Bioconductor Annotation Resources – Packages

## Model organism annotation packages

- ▶ *org.\** – gene names and pathways
- ▶ *TxDb.\** – gene models
- ▶ *BSgenome.\** – whole-genome sequences

## org.\* packages

The 'select' interface:

- ▶ Discovery: keytypes, columns, keys
- ▶ Retrieval: select, mapIds

```
library(org.Hs.eg.db)
keytypes(org.Hs.eg.db)
columns(org.Hs.eg.db)
egid <-
  select(org.Hs.eg.db, "BRCA1", "ENTREZID", "SYMBOL")
```

*org.\** (and other annotation) packages – Under the hood...

SQL (sqlite) data bases

- ▶ `org.Hs.eg_dbconn()` to query using *RSQLite* package
- ▶ `org.Hs.eg_dbfile()` to discover location and query outside *R*.

## TxDb.\* packages

- ▶ Gene models for common model organisms / genome builds / known gene schemes
- ▶ Supports the 'select' interface (keytypes, columns, keys, select)
- ▶ 'Easy' to build custom packages when gene model exist

### Retrieving genomic ranges

- ▶ transcripts, exons, cds,
- ▶ transcriptsBy , exonsBy, cdsBy – group by gene, transcript, etc.

```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
cdsByTx <- cdsBy(txdb, "tx")
```

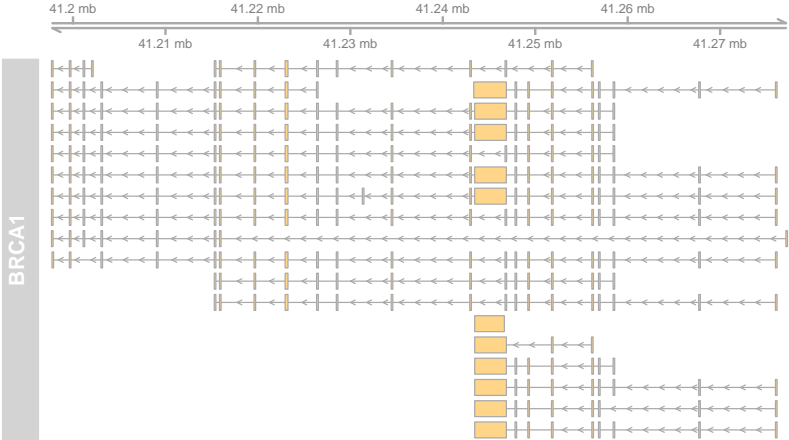
## Example: Visualize BRCA1 Transcripts

```
library(org.Hs.eg.db)
eid <- mapIds(org.Hs.eg.db, "BRCA1", "ENTREZID",
  "SYMBOL")

library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene
txid <- select(txdb, eid, "TXNAME", "GENEID")[["TXNAME"]]
cds <- cdsBy(txdb, by="tx", use.names=TRUE)
brca1cds <- cds[names(cds) %in% txid]

library(Gviz)
tx <- rep(names(brca1cds), elementLengths(brca1cds))
id <- unlist(brca1cds)$cds_id
grt <- GeneRegionTrack(brca1cds, name="BRCA1", id=tx,
  gene="BRCA1", feature=tx, transcript=tx, exon=id)
plotTracks(list(GenomeAxisTrack(), grt))
```

# Example: Visualize BRCA1 Transcripts





## BSgenome.\* Packages: Whole-Genome Sequences

- ▶ 'Masks' when available, e.g., repeat regions
- ▶ Load chromosomes, range-based queries: `getSeq`, `extractTranscriptSeqs`

```
library(BSgenome.Hsapiens.UCSC.hg19)
extractTranscriptSeqs(Hsapiens, brca1cds)

## A DNASTringSet instance of length 20
##      width seq                      names
## [1]  2280 ATGGATTTATCTG...AGCCACTACTGA uc010whl.2
## [2]  5379 ATGAGCCTACAAG...AGCCACTACTGA uc002icp.4
## [3]   522 ATGGATGCTGAGT...AGCCACTACTGA uc010whm.2
## ...    ...    ...
## [18] 3954 ATGCTGAAACTTC...GATTCAAACCTTA uc010cyz.2
## [19] 4017 ATGGATTTATCTG...GATTCAAACCTTA uc010cza.2
## [20] 3207 ATGAATGTAGAAA...GATTCAAACCTTA uc010wht.1
```

## Web-based resources

<i>AnnotationHub</i>	Ensembl, Encode, dbSNP, UCSC data objects, ...
<i>biomaRt</i>	Ensembl and other annotations, <a href="#">url</a>
<i>PSICQUIC</i>	Protein interactions, <a href="#">url</a>
<i>uniprot.ws</i>	Protein annotations, <a href="#">url</a>
<i>KEGGREST</i>	KEGG pathways, <a href="#">url</a>
<i>SRAdb</i>	Sequencing experiments, <a href="#">url</a>
<i>rtracklayer</i>	genome tracks, <a href="#">url</a>
<i>GEOquery</i>	Array and other data, <a href="#">url</a>
<i>ArrayExpress</i>	Array and other data, <a href="#">url</a>

# Web-based resources

Demo

# Summary

## Genes

- ▶ *org.\** packages, `columns()`, `keys()`, `mapIds()`, `select()`.

## Genomes

- ▶ *TxDb.\** packages. `select()`, `exons()`, `exonsBy()` & friends.
- ▶ *BSgenome.\** packages. `FaFile`, `TwoBitFile` files.

## Variants

- ▶ [VariantAnnotation](#), [VariantFiltering](#), [ensemblVEP](#).

## Web-based resources

- ▶ [biomaRt](#), [AnnotationHub](#), and others.

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