

The biomaRt user's guide

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1 Introduction

In recent years a wealth of biological data has become available in public data repositories. Easy access to these valuable data resources and firm integration with data analysis is needed for comprehensive bioinformatics data analysis. The *biomaRt* package, provides an interface to a growing collection of databases implementing the BioMart software suite (<http://www.biomart.org>). The package enables retrieval of large amounts of data

in a uniform way without the need to know the underlying database schemas or write complex SQL queries. Examples of BioMart databases are Ensembl, Uniprot and HapMap. These major databases give biomaRt users direct access to a diverse set of data and enable a wide range of powerful online queries from R.

2 Selecting a BioMart database and dataset

Every analysis with *biomaRt* starts with selecting a BioMart database to use. A first step is to check which BioMart web services are available. The function `listMarts` will display all available BioMart web services

```
> library("biomaRt")
> listMarts()
```

	biomart	version
1	ensembl	ENSEMBL GENES 66 (SANGER UK)
2	snp	ENSEMBL VARIATION 66 (SANGER UK)
3	functional_genomics	ENSEMBL REGULATION 66 (SANGER UK)
4	vega	VEGA 46 (SANGER UK)
5	bacteria_mart_13	ENSEMBL BACTERIA 13 (EBI UK)
6	fungi_mart_13	ENSEMBL FUNGI 13 (EBI UK)
7	fungi_variations_10	ENSEMBL FUNGI VARIATION 13 (EBI UK)
8	metazoa_mart_13	ENSEMBL METAZOA 13 (EBI UK)
9	metazoa_variations_10	ENSEMBL METAZOA VARIATION 13 (EBI UK)
10	plants_mart_13	ENSEMBL PLANTS 13 (EBI UK)
11	plants_variations_10	ENSEMBL PLANTS VARIATION 13 (EBI UK)
12	protists_mart_13	ENSEMBL PROTISTS 13 (EBI UK)
13	protists_variations_10	ENSEMBL PROTISTS VARIATION 13 (EBI UK)
14	msd	MSD (EBI UK)
15	htgt	WTSI MOUSE GENETICS PROJECT (SANGER UK)
16	REACTOME	REACTOME (CSHL US)
17	WS220	WORMBASE 220 (CSHL US)
18	dicty	DICTYBASE (NORTHWESTERN US)
19	biomart	MGI (JACKSON LABORATORY US)
20	g4public	HGNC (EBI UK)
21	pride	PRIDE (EBI UK)
22	prod-intermart_1	INTERPRO (EBI UK)
23	unimart	UNIPROT (EBI UK)
24	biomartDB	PARAMECIUM GENOME (CNRS FRANCE)
25	Eurexpress Biomart	EUREXPRESS (MRC EDINBURGH UK)
26	pepseekerGOLD_mart06	PEPSEEKER GOLD (UNIVERSITY OF MANCHESTER UK)
27	pepseeker2_mart	PEPSEEKER 2 (UNIVERSITY OF MANCHESTER UK)
28	Potato_01	DB POTATO (INTERNATIONAL POTATO CENTER-CIP)
29	Sweetpotato_01	DB SWEETPOTATO (INTERNATIONAL POTATO CENTER-CIP)
30	phytozome_mart	PHYTOZOME (JGI/CIG US)
31	cyanobase_1	CYANOBASE 1 (KAZUSA JAPAN)
32	HapMap_rel27	HAPMAP 27 (NCBI US)
33	CosmicMart	COSMIC (SANGER UK)
34	cildb_all_v2	CILDB INPARANOID AND FILTERED BEST HIT (CNRS FRANCE)
35	cildb_inp_v2	CILDB INPARANOID (CNRS FRANCE)

36	experiments	INTOGEN EXPERIMENTS
37	combinations	INTOGEN COMBINATIONS
38	oncomodules	INTOGEN ONCOMODULES
39	gmap_japonica	RICE-MAP JAPONICA (PEKING UNIVESITY CHINA)
40	europheomeannotations	EUROPHEOME
41	emma_biomart	THE EUROPEAN MOUSE MUTANT ARCHIVE (EMMA)
42	ikmc	IKMC GENES AND PRODUCTS (IKMC)
43	EMAGE gene expression	EMAGE GENE EXPRESSION
44	EMAP anatomy ontology	EMAP ANATOMY ONTOLOGY
45	EMAGE browse repository	EMAGE BROWSE REPOSITORY
46	GermOnline	GERMONLINE
47	Sigenae_Oligo_Annotation_Ensembl_61	SIGENAE OLIGO ANNOTATION (ENSEMBL 61)
48	Sigenae Oligo Annotation (Ensembl 59)	SIGENAE OLIGO ANNOTATION (ENSEMBL 59)
49	Sigenae Oligo Annotation (Ensembl 56)	SIGENAE OLIGO ANNOTATION (ENSEMBL 56)
50	Breast_mart_58	BREAST CANCER CAMPAIGN TISSUE BANK EXPRESSION DATABASE
51	vectorbase_mart_11	VECTORBASE GENES
52	vectorbase_snp_mart_11	VECTORBASE VARIATION
53	expression	VECTORBASE EXPRESSION MART
54	UTRMart	AURA
55	Ensembl56	PANCREATIC EXPRESSION DATABASE (INSTITUTE OF CANCER UK)
56	ENSEMBL_MART_PLANT	GRAMENE 30 ENSEMBL GENES (CSHL/CORNELL US)
57	ENSEMBL_MART_PLANT_SNP	GRAMENE 30 VARIATION (CSHL/CORNELL US)
58	GRAMENE_MARKER_34	GRAMENE 30 MARKERS (CSHL/CORNELL US)
59	GRAMENE_MAP_34	GRAMENE 30 MAPPINGS (CSHL/CORNELL US)
60	QTL_MART	GRAMENE 32 QTL DB (CSHL/CORNELL US)
61	salmosalar_mart	SALMO SALAR UNIGENE MART (CMM CHILE)
62	trucha_mart	ONCORHYNCHUS MYKISS UNIGENE MART (CMM CHILE)

Note: if the function `useMart` runs into proxy problems you should set your proxy first before calling any `biomaRt` functions. You can do this using the `Sys.putenv` command:

```
Sys.putenv("http\_proxy" = "http://my.proxy.org:9999")
```

The `useMart` function can now be used to connect to a specified BioMart database, this must be a valid name given by `listMarts`. In the next example we choose to query the Ensembl BioMart database.

```
> ensembl=useMart("ensembl")
```

BioMart databases can contain several datasets, for Ensembl every species is a different dataset. In a next step we look at which datasets are available in the selected BioMart by using the function `listDatasets`.

```
> listDatasets(ensembl)
```

	dataset	description	version
1	oanatinus_gene_ensembl	Ornithorhynchus anatinus genes (OANA5)	OANA5
2	tguttata_gene_ensembl	Taeniopygia guttata genes (taeGut3.2.4)	taeGut3.2.4
3	cporcellus_gene_ensembl	Cavia porcellus genes (cavPor3)	cavPor3
4	gaculeatus_gene_ensembl	Gasterosteus aculeatus genes (BROADS1)	BROADS1

5	lafricana_gene_ensembl	Loxodonta africana genes (loxAfr3)	loxAfr3
6	mlucifugus_gene_ensembl	Myotis lucifugus genes (myoLuc2)	myoLuc2
7	hsapiens_gene_ensembl	Homo sapiens genes (GRCh37.p6)	GRCh37.p6
8	choffmanni_gene_ensembl	Choloepus hoffmanni genes (choHof1)	choHof1
9	csavignyi_gene_ensembl	Ciona savignyi genes (CSAV2.0)	CSAV2.0
10	fcatus_gene_ensembl	Felis catus genes (CAT)	CAT
11	rnorvegicus_gene_ensembl	Rattus norvegicus genes (RGSC3.4)	RGSC3.4
12	ggallus_gene_ensembl	Gallus gallus genes (WASHUC2)	WASHUC2
13	tbelangeri_gene_ensembl	Tupaia belangeri genes (tupBel1)	tupBel1
14	xtropicalis_gene_ensembl	Xenopus tropicalis genes (JGI4.2)	JGI4.2
15	ecaballus_gene_ensembl	Equus caballus genes (EquCab2)	EquCab2
16	cjacchus_gene_ensembl	Callithrix jacchus genes (calJac3)	calJac3
17	pabelii_gene_ensembl	Pongo abelii genes (PPYG2)	PPYG2
18	drerio_gene_ensembl	Danio rerio genes (Zv9)	Zv9
19	stridecemlineatus_gene_ensembl	Spermophilus tridecemlineatus genes (speTri1)	speTri1
20	tnigroviridis_gene_ensembl	Tetraodon nigroviridis genes (TETRAODON8.0)	TETRAODON8.0
21	ttruncatus_gene_ensembl	Tursiops truncatus genes (turTru1)	turTru1
22	lchalumnae_gene_ensembl	Latimeria chalumnae genes (LatCha1)	LatCha1
23	scerevisiae_gene_ensembl	Saccharomyces cerevisiae genes (EF4)	EF4
24	amelanoleuca_gene_ensembl	Ailuropoda melanoleuca genes (ailMel1)	ailMel1
25	celegans_gene_ensembl	Caenorhabditis elegans genes (WS220)	WS220
26	mmulatta_gene_ensembl	Macaca mulatta genes (MMUL_1.0)	MMUL_1.0
27	p vampyrus_gene_ensembl	Pteropus vampyrus genes (pteVam1)	pteVam1
28	mdomestica_gene_ensembl	Monodelphis domestica genes (monDom5)	monDom5
29	vpacos_gene_ensembl	Vicugna pacos genes (vicPac1)	vicPac1
30	acarolinensis_gene_ensembl	Anolis carolinensis genes (AnoCar2.0)	AnoCar2.0
31	tsyrichta_gene_ensembl	Tarsius syrichta genes (tarSyr1)	tarSyr1
32	ogarnettii_gene_ensembl	Otolemur garnettii genes (OtoGar3)	OtoGar3
33	trubripes_gene_ensembl	Takifugu rubripes genes (FUGU4.0)	FUGU4.0
34	dmelanogaster_gene_ensembl	Drosophila melanogaster genes (BDGP5)	BDGP5
35	pmarinus_gene_ensembl	Petromyzon marinus genes (Pmarinus_7.0)	Pmarinus_7.0
36	eeuropaeus_gene_ensembl	Erinaceus europaeus genes (eriEur1)	eriEur1
37	mmurinus_gene_ensembl	Microcebus murinus genes (micMur1)	micMur1
38	olatipes_gene_ensembl	Oryzias latipes genes (HdrR)	HdrR
39	etelfairi_gene_ensembl	Echinops telfairi genes (TENREC)	TENREC
40	cintestinalis_gene_ensembl	Ciona intestinalis genes (KH)	KH
41	ptroglodytes_gene_ensembl	Pan troglodytes genes (CHIMP2.1.4)	CHIMP2.1.4
42	oprinceps_gene_ensembl	Ochotona princeps genes (OchPri2.0)	OchPri2.0
43	ggorilla_gene_ensembl	Gorilla gorilla genes (gorGor3.1)	gorGor3.1
44	dordii_gene_ensembl	Dipodomys ordii genes (dipOrd1)	dipOrd1
45	nleucogenys_gene_ensembl	Nomascus leucogenys genes (Nleu1.0)	Nleu1.0
46	sscrofa_gene_ensembl	Sus scrofa genes (Sscrofa9)	Sscrofa9
47	mmusculus_gene_ensembl	Mus musculus genes (NCBIM37)	NCBIM37
48	ocuniculus_gene_ensembl	Oryctolagus cuniculus genes (oryCun2.0)	oryCun2.0
49	mgallopavo_gene_ensembl	Meleagris gallopavo genes (UMD2)	UMD2
50	gmorhua_gene_ensembl	Gadus morhua genes (gadMor1)	gadMor1
51	saraneus_gene_ensembl	Sorex araneus genes (sorAra1)	sorAra1
52	dnovemcinctus_gene_ensembl	Dasypus novemcinctus genes (dasNov2)	dasNov2
53	pcapensis_gene_ensembl	Procapia capensis genes (proCap1)	proCap1
54	btaurus_gene_ensembl	Bos taurus genes (UMD3.1)	UMD3.1
55	meugenii_gene_ensembl	Macropus eugenii genes (Meug_1.0)	Meug_1.0
56	sharrisii_gene_ensembl	Sarcophilus harrisii genes (DEVIL7.0)	DEVIL7.0
57	cfamiliaris_gene_ensembl	Canis familiaris genes (CanFam_2.0)	CanFam_2.0

To select a dataset we can update the `Mart` object using the function `useDataset`. In the example below we choose to use the `hsapiens` dataset.

```
ensembl = useDataset("hsapiens_gene_ensembl",mart=ensembl)
```

Or alternatively if the dataset one wants to use is known in advance, we can select a BioMart database and dataset in one step by:

```
> ensembl = useMart("ensembl",dataset="hsapiens_gene_ensembl")
```

3 How to build a biomaRt query

The `getBM` function has three arguments that need to be introduced: filters, attributes and values. *Filters* define a restriction on the query. For example you want to restrict the output to all genes located on the human X chromosome then the filter *chromosome_name* can be used with value 'X'. The `listFilters` function shows you all available filters in the selected dataset.

```
> filters = listFilters(ensembl)
> filters[1:5,]
```

	name	description
1	chromosome_name	Chromosome name
2	start	Gene Start (bp)
3	end	Gene End (bp)
4	band_start	Band Start
5	band_end	Band End

Attributes define the values we are interested in to retrieve. For example we want to retrieve the gene symbols or chromosomal coordinates. The `listAttributes` function displays all available attributes in the selected dataset.

```
> attributes = listAttributes(ensembl)
> attributes[1:5,]
```

	name	description
1	ensembl_gene_id	Ensembl Gene ID
2	ensembl_transcript_id	Ensembl Transcript ID
3	ensembl_peptide_id	Ensembl Protein ID
4	description	Description
5	chromosome_name	Chromosome Name

The `getBM` function is the main query function in `biomaRt`. It has four main arguments:

- `attributes`: is a vector of attributes that one wants to retrieve (= the output of the query).
- `filters`: is a vector of filters that one will use as input to the query.
- `values`: a vector of values for the filters. In case multiple filters are in use, the `values` argument requires a list of values where each position in the list corresponds to the position of the filters in the `filters` argument (see examples below).
- `mart`: is an object of class `Mart`, which is created by the `useMart` function.

Note: for some frequently used queries to Ensembl, wrapper functions are available: `getGene` and `getSequence`. These functions call the `getBM` function with hard coded filter and attribute names.

Now that we selected a BioMart database and dataset, and know about attributes, filters, and the values for filters; we can build a `biomaRt` query. Let's make an easy query for the following problem: We have a list of Affymetrix identifiers from the `u133plus2` platform and we want to retrieve the corresponding EntrezGene identifiers using the Ensembl mappings.

The `u133plus2` platform will be the filter for this query and as values for this filter we use our list of Affymetrix identifiers. As output (attributes) for the query we want to retrieve the EntrezGene and `u133plus2` identifiers so we get a mapping of these two identifiers as a result. The exact names that we will have to use to specify the attributes and filters can be retrieved with the `listAttributes` and `listFilters` function respectively. Let's now run the query:

```
> affyids=c("202763_at","209310_s_at","207500_at")
> getBM(attributes=c('affy_hg_u133_plus_2', 'entrezgene'), filters = 'affy_hg_u133_plus_2', values = affyids, mart =
```

	affy_hg_u133_plus_2	entrezgene
1	209310_s_at	837
2	207500_at	838
3	202763_at	836

4 Examples of biomaRt queries

In the sections below a variety of example queries are described. Every example is written as a task, and we have to come up with a biomaRt solution to the problem.

4.1 Task 1: Annotate a set of Affymetrix identifiers with HUGO symbol and chromosomal locations of corresponding genes

We have a list of Affymetrix hgu133plus2 identifiers and we would like to retrieve the HUGO gene symbols, chromosome names, start and end positions and the bands of the corresponding genes. The `listAttributes` and the `listFilters` functions give us an overview of the available attributes and filters and we look in those lists to find the corresponding attribute and filter names we need. For this query we'll need the following attributes: `hgnc_symbol`, `chromosome_name`, `start_position`, `end_position`, `band` and `affy_hg_u133_plus_2` (as we want these in the output to provide a mapping with our original Affymetrix input identifiers. There is one filter in this query which is the `affy_hg_u133_plus_2` filter as we use a list of Affymetrix identifiers as input. Putting this all together in the `getBM` and performing the query gives:

```
> affyids=c("202763_at", "209310_s_at", "207500_at")
> getBM(attributes=c('affy_hg_u133_plus_2', 'hgnc_symbol', 'chromosome_name', 'start_position', 'end_position', 'band'),
+ filters = 'affy_hg_u133_plus_2', values = affyids, mart = ensembl)
```

	affy_hg_u133_plus_2	hgnc_symbol	chromosome_name	start_position	end_position	band
1	209310_s_at	CASP4	11	104813593	104840163	q22.3
2	207500_at	CASP5	11	104864962	104893895	q22.3
3	202763_at	CASP3	4	185548850	185570663	q35.1

4.2 Task 2: Annotate a set of EntrezGene identifiers with GO annotation

In this task we start out with a list of EntrezGene identifiers and we want to retrieve GO identifiers related to biological processes that are associated with these entrezgene identifiers. Again we look at the output of `listAttributes` and `listFilters` to find the filter and attributes we need. Then we construct the following query:

```
> entrez=c("673", "837")
> goids = getBM(attributes=c('entrezgene', 'go_id'), filters='entrezgene', values=entrez, mart=ensembl)
> head(goids)
```

	entrezgene	go_id
1	673	GO:0000186
2	673	GO:0006468


```

3      673 GO:0006916
4      673 GO:0007264
5      673 GO:0007268

```

4.3 Task 3: Retrieve all HUGO gene symbols of genes that are located on chromosomes 1,2 or Y , and are associated with one the following GO terms: "GO:0051330","GO:0000080","GO:0000114","GO:0000082" (here we'll use more than one filter)

The `getBM` function enables you to use more than one filter. In this case the filter argument should be a vector with the filter names. The values should be a list, where the first element of the list corresponds to the first filter and the second list element to the second filter and so on. The elements of this list are vectors containing the possible values for the corresponding filters.

```

go=c("GO:0051330","GO:0000080","GO:0000114"chrom=c(1,2,"Y")
getBM(attributes= "hgnc_symbol",
      filters=c("go","chromosome_name"),
      values=list(go,chrom), mart=ensembl)

```

```

hgnc_symbol
1      PPP1CB
2      SPDYA
3      ACVR1
4      CUL3
5      RCC1
6      CDC7
7      RHOU

```

4.4 Task 4: Annotate set of identifiers with INTERPRO protein domain identifiers

In this example we want to annotate the following two RefSeq identifiers: NM_005359 and NM_000546 with INTERPRO protein domain identifiers and a description of the protein domains.

```

> refseqids = c("NM_005359","NM_000546")
> ipro = getBM(attributes=c("refseq_dna","interpro","interpro_description"), filters=

```

```

ipro
  refseq_dna interpro      interpro_description
1 NM_000546 IPR002117      p53 tumor antigen
2 NM_000546 IPR010991      p53, tetramerisation
3 NM_000546 IPR011615      p53, DNA-binding
4 NM_000546 IPR013872 p53 transactivation domain (TAD)

```

```

5 NM_000546 IPR000694          Proline-rich region
6 NM_005359 IPR001132      MAD homology 2, Dwarfing-type
7 NM_005359 IPR003619      MAD homology 1, Dwarfing-type
8 NM_005359 IPR013019          MAD homology, MH1

```

4.5 Task 5: Select all Affymetrix identifiers on the hgu133plus2 chip and Ensembl gene identifiers for genes located on chromosome 16 between basepair 1100000 and 1250000.

In this example we will again use multiple filters: chromosome_name, start, and end as we filter on these three conditions. Note that when a chromosome name, a start position and an end position are jointly used as filters, the BioMart webservice interprets this as return everything from the given chromosome between the given start and end positions.

```

> getBM(c('affy_hg_u133_plus_2','ensembl_gene_id'), filters = c('chromosome_name','start','end'),
+ values=list(16,1100000,1250000), mart=ensembl)

```

```

      affy_hg_u133_plus_2  ensembl_gene_id
1      1557146_a_at  ENSG00000261713
2                      ENSG00000261713
3                      ENSG00000261720
4                      ENSG00000181791
5                      ENSG00000260702
6      215502_at  ENSG00000260532
7                      ENSG00000260403
8                      ENSG00000259910
9                      ENSG00000162009
10     214555_at  ENSG00000162009
11                      ENSG00000184471
12     205845_at  ENSG00000196557
13                      ENSG00000196557

```

4.6 Task 6: Retrieve all entrezgene identifiers and HUGO gene symbols of genes which have a "MAP kinase activity" GO term associated with it.

The GO identifier for MAP kinase activity is GO:0004707. In our query we will use go as filter and entrezgene and hgnc_symbol as attributes. Here's the query:

```

> getBM(c('entrezgene','hgnc_symbol'), filters='go', values='GO:0004707', mart=ensembl)

```

```

      entrezgene  hgnc_symbol
1      5601      MAPK9
2     225689      MAPK15
3      5599      MAPK8
4      5594      MAPK1
5      6300      MAPK12

```

4.7 Task 7: Given a set of EntrezGene identifiers, retrieve 100bp upstream promoter sequences

All sequence related queries to Ensembl are available through the `getSequence` wrapper function. `getBM` can also be used directly to retrieve sequences but this can get complicated so using `getSequence` is recommended. Sequences can be retrieved using the `getSequence` function either starting from chromosomal coordinates or identifiers. The chromosome name can be specified using the *chromosome* argument. The *start* and *end* arguments are used to specify *start* and *end* positions on the chromosome. The type of sequence returned can be specified by the *seqType* argument which takes the following values: 'cdna'; 'peptide' for protein sequences; '3utr' for 3' UTR sequences; '5utr' for 5' UTR sequences; 'gene_exon' for exon sequences only; 'transcript_exon' for transcript specific exonic sequences only; 'transcript_exon_intron' gives the full unspliced transcript, that is exons + introns; 'gene_exon_intron' gives the exons + introns of a gene; 'coding' gives the coding sequence only; 'coding_transcript_flank' gives the flanking region of the transcript including the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'coding_gene_flank' gives the flanking region of the gene including the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'transcript_flank' gives the flanking region of the transcript excluding the UTRs, this must be accompanied with a given value for the upstream or downstream attribute; 'gene_flank' gives the flanking region of the gene excluding the UTRs, this must be accompanied with a given value for the upstream or downstream attribute.

In MySQL mode the `getSequence` function is more limited and the sequence that is returned is the 5' to 3'+ strand of the genomic sequence, given a chromosome, as start and an end position.

Task 4 requires us to retrieve 100bp upstream promoter sequences from a set of EntrezGene identifiers. The *type* argument in `getSequence` can be thought of as the filter in this query and uses the same input names given by `listFilters`. In our query we use `entrezgene` for the *type* argument. Next we have to specify which type of sequences we want to retrieve, here we are interested in the sequences of the promoter region, starting right next to the coding start of the gene. Setting the *seqType* to `coding_gene_flank` will give us what we need. The *upstream* argument is used to specify how many bp of upstream sequence we want to retrieve, here we'll retrieve a rather short sequence of 100bp. Putting this all together in `getSequence` gives:

```
> entrez=c("673","7157","837")
> getSequence(id = entrez, type="entrezgene", seqType="coding_gene_flank", upstream=100, mart=ensembl)
```

4.8 Task 8: Retrieve all 5' UTR sequences of all genes that are located on chromosome 3 between the positions 185514033 and 185535839

As described in the previous task `getSequence` can also use chromosomal coordinates to retrieve sequences of all genes that lie in the given region. We also have to specify which type of identifier we want to retrieve together with the sequences, here we choose for `entrezgene` identifiers.

```
> utr5 = getSequence(chromosome=3, start=185514033, end=185535839,
+                    type="entrezgene", seqType="5utr", mart=ensembl)
> utr5
```

V1	V2
.....GAAGCGGTGGC	1981

4.9 Task 9: Retrieve protein sequences for a given list of EntrezGene identifiers

In this task the `type` argument specifies which type of identifiers we are using. To get an overview of other valid identifier types we refer to the `listFilters` function.

```
> protein = getSequence(id=c(100, 5728), type="entrezgene",
+                       seqType="peptide", mart=ensembl)
> protein
```

peptide	entrezgene
MAQTPAFDKPKVEL ...	100
MTAIIKEIVSRNKRR ...	5728

4.10 Task 10: Retrieve known SNPs located on the human chromosome 8 between positions 148350 and 148612

For this example we'll first have to connect to a different BioMart database, namely `snp`.

```
> snpmart = useMart("snp", dataset="hsapiens_snp")
```

The `listAttributes` and `listFilters` functions give us an overview of the available attributes and filters. From these we need: `refsnp_id`, `allele`, `chrom_start` and `chrom_strand` as attributes; and as filters we'll use:

chrom_start, chrom_end and chr_name. Note that when a chromosome name, a start position and an end position are jointly used as filters, the BioMart webservice interprets this as return everything from the given chromosome between the given start and end positions. Putting our selected attributes and filters into getBM gives:

```
> getBM(c('refsnp_id','allele','chrom_start','chrom_strand'), filters = c('chr_name','chrom_start','chrom_end'), val
```

	refsnp_id	allele	chrom_start	chrom_strand
1	rs1134195	G/T	148394	-1
2	rs4046274	C/A	148394	1
3	rs4046275	A/G	148411	1
4	rs13291	C/T	148462	1
5	rs1134192	G/A	148462	-1
6	rs4046276	C/T	148462	1
7	rs12019378	T/G	148471	1
8	rs1134191	C/T	148499	-1
9	rs4046277	G/A	148499	1
10	rs11136408	G/A	148525	1
11	rs1134190	C/T	148533	-1
12	rs4046278	G/A	148533	1
13	rs1134189	G/A	148535	-1
14	rs3965587	C/T	148535	1
15	rs1134187	G/A	148539	-1
16	rs1134186	T/C	148569	1
17	rs4378731	G/A	148601	1

4.11 Task 11: Given the human gene TP53, retrieve the human chromosomal location of this gene and also retrieve the chromosomal location and RefSeq id of it's homolog in mouse.

The getLDS (Get Linked Dataset) function provides functionality to link 2 BioMart datasets which each other and construct a query over the two datasets. In Ensembl, linking two datasets translates to retrieving homology data across species. The usage of getLDS is very similar to getBM. The linked dataset is provided by a separate Mart object and one has to specify filters and attributes for the linked dataset. Filters can either be applied to both datasets or to one of the datasets. Use the listFilters and listAttributes functions on both Mart objects to find the filters and attributes for each dataset (species in Ensembl). The attributes and filters of the linked dataset can be specified with the attributesL and filtersL arguments. Entering all this information into getLDS gives:

```
human = useMart("ensembl", dataset = "hsapiens_gene_ensembl")
mouse = useMart("ensembl", dataset = "mmusculus_gene_ensembl")
getLDS(attributes = c("hgnc_symbol","chromosome_name", "start_position"),
      filters = "hgnc_symbol", values = "TP53",mart = human,
      attributesL = c("refseq_dna","chromosome_name","start_position"), martL = mouse)

V1 V2      V3      V4 V5      V6
1 TP53 17 7512464 NM_011640 11 69396600
```

5 Using archived versions of Ensembl

It is possible to query archived versions of Ensembl through *biomaRt*. There are currently two ways to access archived versions.

5.1 Using the archive=TRUE

First we list the available Ensembl archives by using the `listMarts` function and setting the archive attribute to TRUE. Note that not all archives are available this way and it seems that recently this only gives access to few archives if you don't see the version of the archive you need please look at the 2nd way to access archives.

```
> listMarts(archive=TRUE)
```

	biomart	version
1	ensembl_mart_51	Ensembl 51
2	snp_mart_51	SNP 51
3	vega_mart_51	Vega 32
4	ensembl_mart_50	Ensembl 50
5	snp_mart_50	SNP 50
6	vega_mart_50	Vega 32
7	ensembl_mart_49	ENSEMBL GENES 49 (SANGER)
8	genomic_features_mart_49	Genomic Features
9	snp_mart_49	SNP
10	vega_mart_49	Vega
11	ensembl_mart_48	ENSEMBL GENES 48 (SANGER)
12	genomic_features_mart_48	Genomic Features
13	snp_mart_48	SNP
14	vega_mart_48	Vega
15	ensembl_mart_47	ENSEMBL GENES 47 (SANGER)
16	genomic_features_mart_47	Genomic Features
17	snp_mart_47	SNP
18	vega_mart_47	Vega
19	compara_mart_homology_47	Compara homology
20	compara_mart_multiple_ga_47	Compara multiple alignments
21	compara_mart_pairwise_ga_47	Compara pairwise alignments
22	ensembl_mart_46	ENSEMBL GENES 46 (SANGER)
23	genomic_features_mart_46	Genomic Features
24	snp_mart_46	SNP
25	vega_mart_46	Vega
26	compara_mart_homology_46	Compara homology
27	compara_mart_multiple_ga_46	Compara multiple alignments
28	compara_mart_pairwise_ga_46	Compara pairwise alignments
29	ensembl_mart_45	ENSEMBL GENES 45 (SANGER)
30	snp_mart_45	SNP
31	vega_mart_45	Vega
32	compara_mart_homology_45	Compara homology
33	compara_mart_multiple_ga_45	Compara multiple alignments
34	compara_mart_pairwise_ga_45	Compara pairwise alignments
35	ensembl_mart_44	ENSEMBL GENES 44 (SANGER)
36	snp_mart_44	SNP
37	vega_mart_44	Vega
38	compara_mart_homology_44	Compara homology

```

39 compara_mart_pairwise_ga_44 Compara pairwise alignments
40             ensembl_mart_43  ENSEMBL GENES 43 (SANGER)
41             snp_mart_43      SNP
42             vega_mart_43     Vega
43     compara_mart_homology_43      Compara homology
44 compara_mart_pairwise_ga_43 Compara pairwise alignments

```

Next we select the archive we want to use using the `useMart` function, again setting the archive attribute to `TRUE` and giving the full name of the BioMart e.g. `ensembl_mart_46`.

```
> ensembl = useMart("ensembl_mart_46", dataset="hsapiens_gene_ensembl", archive = TRUE)
```

If you don't know the dataset you want to use could first connect to the BioMart using `useMart` and then use the `listDatasets` function on this object. After you selected the BioMart database and dataset, queries can be performed in the same way as when using the current BioMart versions.

5.2 Accessing archives through specifying the archive host

Use the <http://www.ensembl.org> website and go down the bottom of the page. Click on 'view in Archive' and select the archive you need. Copy the url and use that url as shown below to connect to the specified BioMart database. The example below shows how to query Ensembl 54.

```

> listMarts(host='may2009.archive.ensembl.org')
> ensembl54=useMart(host='may2009.archive.ensembl.org', biomart='ENSEMBL_MART_ENSEMBL')
> ensembl54=useMart(host='may2009.archive.ensembl.org', biomart='ENSEMBL_MART_ENSEMBL', dataset='hsapiens_gene_ensembl')

```

6 Using a BioMart other than Ensembl

To demonstrate the use of the `biomaRt` package with non-Ensembl databases the next query is performed using the Wormbase BioMart (WormMart). We connect to Wormbase, select the gene dataset to use and have a look at the available attributes and filters. Then we use a list of gene names as filter and retrieve associated RNAi identifiers together with a description of the RNAi phenotype.

```

> wormbase=useMart("wormbase_current",dataset="wormbase_gene")
> listFilters(wormbase)
> listAttributes(wormbase)
> getBM(attributes=c("name","rna","rna_phenotype","phenotype_desc"),
+       filters="gene_name", values=c("unc-26","his-33"),
+       mart=wormbase)
>

```

	name	rnai	rnai_phenotype	phenotype_desc
1	his-33	WBRNAi00000104	Emb Nmo	embryonic lethal Nuclear morphology alteration in early embryo
2	his-33	WBRNAi00012233	WT	wild type morphology
3	his-33	WBRNAi00024356	Ste	sterile
4	his-33	WBRNAi00025036	Emb	embryonic lethal
5	his-33	WBRNAi00025128	Emb	embryonic lethal
6	his-33	WBRNAi00025393	Emb	embryonic lethal
7	his-33	WBRNAi00025515	Emb Lva Unc	embryonic lethal larval arrest uncoordinated
8	his-33	WBRNAi00025632	Gro Ste	slow growth sterile
9	his-33	WBRNAi00025686	Gro Ste	slow growth sterile
10	his-33	WBRNAi00025785	Gro Ste	slow growth sterile
11	his-33	WBRNAi00026259	Emb Gro Unc	embryonic lethal slow growth uncoordinated
12	his-33	WBRNAi00026375	Emb	embryonic lethal
13	his-33	WBRNAi00026376	Emb	embryonic lethal
14	his-33	WBRNAi00027053	Emb Unc	embryonic lethal uncoordinated
15	his-33	WBRNAi00030041	WT	wild type morphology
16	his-33	WBRNAi00031078	Emb	embryonic lethal
17	his-33	WBRNAi00032317	Emb	embryonic lethal
18	his-33	WBRNAi00032894	Emb	embryonic lethal
19	his-33	WBRNAi00033648	Emb	embryonic lethal
20	his-33	WBRNAi00035430	Emb	embryonic lethal
21	his-33	WBRNAi00035860	Egl Emb	egg laying defect embryonic lethal
22	his-33	WBRNAi00048335	Emb Sister Chromatid Separation abnormal (Cross-eyed)	embryonic lethal
23	his-33	WBRNAi00049266	Emb Sister Chromatid Separation abnormal (Cross-eyed)	embryonic lethal
24	his-33	WBRNAi00053026	Emb Sister Chromatid Separation abnormal (Cross-eyed)	embryonic lethal
25	unc-26	WBRNAi00021278	WT	wild type morphology
26	unc-26	WBRNAi00026915	WT	wild type morphology
27	unc-26	WBRNAi00026916	WT	wild type morphology
28	unc-26	WBRNAi00027544	Unc	uncoordinated
29	unc-26	WBRNAi00049565	WT	wild type morphology
30	unc-26	WBRNAi00049566	WT	wild type morphology

7 biomaRt helper functions

This section describes a set of biomaRt helper functions that can be used to export FASTA format sequences, retrieve values for certain filters and exploring the available filters and attributes in a more systematic manner.

7.1 exportFASTA

The data.frames obtained by the getSequence function can be exported to FASTA files using the exportFASTA function. One has to specify the data.frame to export and the filename using the file argument.

7.2 Finding out more information on filters

7.2.1 filterType

Boolean filters need a value TRUE or FALSE in biomaRt. Setting the value TRUE will include all information that fulfill the filter requirement. Setting FALSE will exclude the information that fulfills the filter requirement and will return all values that don't fulfill the filter. For most of the filters, their name indicates if the type is a boolean or not and they will usually start with "with". However this is not a rule and to make sure you got the type right you can use the function `filterType` to investigate the type of the filter you want to use.

```
> filterType("with_affy_hg_u133_plus_2",ensembl)

[1] "boolean_list"
```

7.2.2 filterOptions

Some filters have a limited set of values that can be given to them. To know which values these are one can use the `filterOptions` function to retrieve the predetermined values of the respective filter.

```
> filterOptions("biotype",ensembl)

[1] "[3prime_overlapping_ncrna,antisense,IG_C_gene,IG_C_pseudogene,IG_D_gene,IG_J_gene,IG_J_p
```

If there are no predetermined values e.g. for the `entrezgene` filter, then `filterOptions` will return the type of filter it is. And most of the times the filter name or its description will suggest what values one can use for the respective filter (e.g. `entrezgene` filter will work with `entrezgene` identifiers as values)

7.3 Attribute Pages

For large BioMart databases such as Ensembl, the number of attributes displayed by the `listAttributes` function can be very large. In BioMart databases, attributes are put together in pages, such as sequences, features, homologs for Ensembl. An overview of the attributes pages present in the respective BioMart dataset can be obtained with the `attributePages` function.

```
> pages = attributePages(ensembl)
> pages
```

```
[1] "feature_page"      "structure"          "transcript_event" "homologs"           "snp"
```

To show us a smaller list of attributes which belong to a specific page, we can now specify this in the `listAttributes` function as follows:

```
> listAttributes(ensembl, page="feature_page")
```

	name	des
1	ensembl_gene_id	Ensembl
2	ensembl_transcript_id	Ensembl Trans
3	ensembl_peptide_id	Ensembl Pr
4	description	Des
5	chromosome_name	Chromos
6	start_position	Gene St
7	end_position	Gene
8	strand	
9	band	
10	transcript_start	Transcript St
11	transcript_end	Transcript
12	external_gene_id	Associated G
13	external_transcript_id	Associated Transcr
14	external_gene_db	Associated
15	transcript_db_name	Associated Trans
16	transcript_count	Transcri
17	percentage_gc_content	% GC
18	gene_biotype	Gene
19	transcript_biotype	Transcript
20	source	
21	status	Statu
22	transcript_status	Status (tra
23	go_id	GO Term A
24	name_1006	GO T
25	definition_1006	GO Term De
26	go_linkage_type	GO Term Eviden
27	namespace_1003	G
28	goslim_goa_accession	GOSlim GOA Acce
29	goslim_goa_description	GOSlim GOA Des
30	pubmed	P
31	ucsc	
32	pdb	
33	clone_based_ensembl_gene_name	Clone based Ensembl g
34	clone_based_ensembl_transcript_name	Clone based Ensembl transcr
35	clone_based_vega_gene_name	Clone based VEGA g
36	clone_based_vega_transcript_name	Clone based VEGA transcr
37	ccds	
38	embl	EMBL (Gen

39	ens_hs_gene	Ensembl to LRG link
40	ens_hs_transcript	Ensembl to LRG link transcr
41	ens_hs_translation	Ensembl to LRG link transla
42	ox_ens_lrg_transcript__dm_dbprimary_acc_1074	LRG to Ensembl link tr
43	entrezgene	Entre
44	ottt	VEGA transcript ID(s)
45	ottg	VEGA gene ID(s)
46	shares_cds_with_enst	Ensembl transcript (where OTTT shares CDS wi
47	shares_cds_with_ottt	HAVANA transcript (where ENST shares CDS wi
48	shares_cds_and_utr_with_ottt	HAVANA transcript (where ENST identical
49	hgnc_id	HGNC
50	hgnc_symbol	HGN
51	hgnc_transcript_name	HGNC transcr
52	ipi	
53	merops	M
54	mim_morbid_accession	MIM Morbid A
55	mim_morbid_description	MIM Morbid Des
56	mim_gene_accession	MIM Gene A
57	mim_gene_description	MIM Gene Des
58	mirbase_accession	mirBase Acce
59	mirbase_id	mirBa
60	mirbase_gene_name	mirBase g
61	mirbase_transcript_name	mirBase transcr
62	protein_id	Protein (Gen
63	refseq_peptide	RefSeq Pr
64	refseq_peptide_predicted	RefSeq Predicted Pr
65	refseq_genomic	RefSeq Genom
66	rfam	
67	rfam_transcript_name	Rfam transcr
68	unigene	Un
69	uniprot_sptrembl	UniProt/TrEMBL A
70	uniprot_swissprot	UniProt/Swis
71	uniprot_swissprot_accession	UniProt/SwissProt A
72	uniprot_genename	UniProt G
73	wikigene_name	WikiG
74	wikigene_id	Wik
75	wikigene_description	WikiGene Des
76	hpa	Human Protein Atlas Ant
77	dbass3_id	Database of Aberrant 3' Splice Sites (DBA
78	dbass3_name	DBASS3 G
79	dbass5_id	Database of Aberrant 5' Splice Sites (DBA
80	dbass5_name	DBASS5 G
81	refseq_mrna	Ref
82	refseq_mrna_predicted	RefSeq mRNA p
83	refseq_ncrna	RefS

84	refseq_ncrna_predicted	RefSeq ncRNA p
85	efg_agilent_sureprint_g3_ge_8x60k	Agilent SurePrint G3 GE 8x60k
86	efg_agilent_wholegenome_4x44k_v1	Agilent WholeGenome 4x44k
87	efg_agilent_wholegenome_4x44k_v2	Agilent WholeGenome 4x44k
88	affy_hc_g110	Affy HC G110
89	affy_hg_focus	Affy HG FOCUS
90	affy_hg_u133_plus_2	Affy HG U133-PLUS-2
91	affy_hg_u133a_2	Affy HG U133A_2
92	affy_hg_u133a	Affy HG U133A
93	affy_hg_u133b	Affy HG U133B
94	affy_hg_u95av2	Affy HG U95AV2
95	affy_hg_u95b	Affy HG U95B
96	affy_hg_u95c	Affy HG U95C
97	affy_hg_u95d	Affy HG U95D
98	affy_hg_u95e	Affy HG U95E
99	affy_hg_u95a	Affy HG U95A
100	affy_hugene1	Affy HuGene FL
101	affy_huex_1_0_st_v2	Affy HuEx 1_0 st v2
102	affy_hugene_1_0_st_v1	Affy HuGene 1_0 st v1
103	affy_u133_x3p	Affy U133 X3P
104	agilent_cgh_44b	Agilent CGH 44b
105	codelink	Codelink
106	illumina_humanwg_6_v1	Illumina HumanWG 6
107	illumina_humanwg_6_v2	Illumina HumanWG 6
108	illumina_humanwg_6_v3	Illumina HumanWG 6
109	illumina_humanht_12	Illumina Human HT
110	phalanx_onearray	Phalanx OneArr
111	anatomical_system	Anatomical System (eg
112	development_stage	Development Stage (eg
113	cell_type	Cell Type (eg
114	pathology	Pathology (eg
115	atlas_celltype	GNF/Atlas c
116	atlas_diseasestate	GNF/Atlas disea
117	atlas_organismpart	GNF/Atlas organ
118	family_description	Ensembl Family Des
119	family	Ensembl Protein Fami
120	pirsf	PIRSF SuperF
121	superfamily	Superf
122	smart	
123	profile	PR
124	prints	P
125	pfam	
126	tigrfam	TI
127	protein_feature_seg_dm_hit_name_1048	
128	interpro	Int

129	<code>interpro_short_description</code>	Interpro Short Des
130	<code>interpro_description</code>	Interpro Des
131	<code>transmembrane_domain</code>	Transmembran
132	<code>signal_domain</code>	Signa
133	<code>ncoils</code>	

We now get a short list of attributes related to the region where the genes are located.

8 Local BioMart databases

The biomaRt package can be used with a local install of a public BioMart database or a locally developed BioMart database and web service. In order for biomaRt to recognize the database as a BioMart, make sure that the local database you create has a name conform with

```
database_mart_version
```

where database is the name of the database and version is a version number. No more underscores than the ones showed should be present in this name. A possible name is for example

```
ensemblLocal_mart_46
```

.

8.1 Minimum requirements for local database installation

More information on installing a local copy of a BioMart database or develop your own BioMart database and webservice can be found on <http://www.biomart.org> Once the local database is installed you can use biomaRt on this database by:

```
listMarts(host="www.myLocalHost.org", path="/myPathToWebservice/martservice")
mart=useMart("nameOfMyMart",dataset="nameOfMyDataset",host="www.myLocalHost.org", path="/myPathToWebservice/martser
```

For more information on how to install a public BioMart database see: <http://www.biomart.org/install.html> and follow link databases.

9 Session Info

```
> sessionInfo()
```

```
R version 2.15.0 RC (2012-03-22 r58802)
Platform: i386-apple-darwin9.8.0/i386 (32-bit)
```

```
locale:
[1] C
```

```
attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
[1] biomaRt_2.12.0
```

```
loaded via a namespace (and not attached):
[1] Rcurl_1.91-1 XML_3.9-4    tools_2.15.0
```

```
> warnings()
```

```
NULL
```