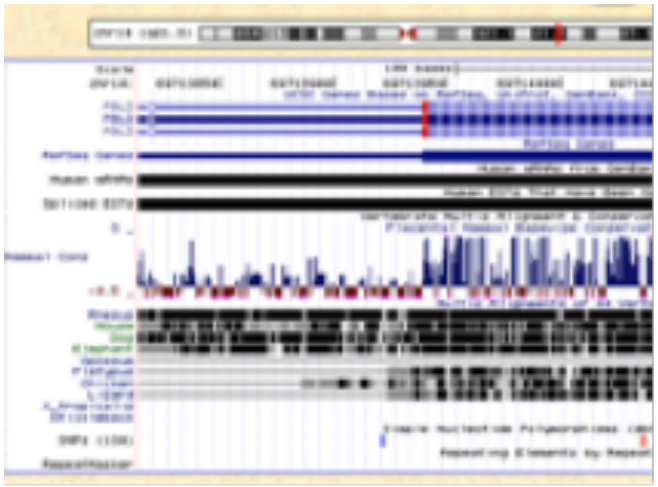
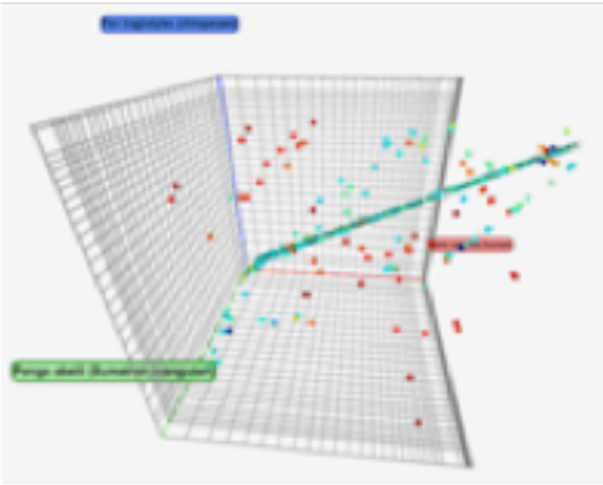
Computational Genomics

Data Retrieval I





Data Retrieval
Retrieving Data From UCSC

Table Browser

Table Browser

Use this tool to retrieve and export data from the Genome Browser annotation track database. You can limit retrieval based on data attributes and intersect or merge with data from another track, or retrieve DNA sequence covered by a track. More...

Select dataset

clade: Mammal **genome:** Human **assembly:** Dec. 2013 (GRCh38/hg38)
group: Genes and Gene Predictions **track:** GENCODE V38
table: knownGene describe table schema

Define region of interest

region: genome position chrX:15,560,138-15,602,945 lookup define regions
identifiers (names/accessions): paste list upload list

Optional: Subset, combine, compare with another track

filter: create
intersection: create

Retrieve and display data

output format: all fields from selected table Send output to Galaxy GREAT
output filename: (leave blank to keep output in browser)
file type returned: plain text gzip compressed

get output summary/statistics

Data Retrieval
Retrieving Data From UCSC

Table Browser

- Retrieving all coding exons corresponding to: ***Homo sapiens* ChrX**

Select dataset

clade: Mammal **genome:** Human **assembly:** Dec. 2013 (GRCh38/hg38)
group: Genes and Gene Predictions **track:** GENCODE V38
table: knownGene describe table schema

Define region of interest

region: genome position chrX:15,560,138-15,602,945 lookup define regions
identifiers (names/accessions): paste list upload list

Optional: Subset, combine, compare with another track

filter: create
intersection: create

Retrieve and display data

output format: all fields from selected table Send output to Galaxy GREAT
output filename: (leave blank to keep output in browser)
file type returned: plain text gzip compressed

get output summary/statistics

Data Retrieval

Retrieving Data From UCSC

Table Browser

- Retrieving all coding exons corresponding to: ***Homo sapiens* ChrX**

```
#chrom	chromStart	chromEnd	name	score	strand	thickStart	thickEnd	reserved	blockCount	blockSizes	chromStarts	name2	cdsStartStat	cdsEndStat	exonFrames	type	geneName	geneName2	geneType	transcriptClass
source	transcriptType	tag	level	tier
chrX	15494565	15600960	ENST00000679162.1	0	-	15500533	15600911	789624	19	284,88,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,235,
0,5932,69458,71687,73160,75729,77058,77635,78801,81100,83523,86655,90909,93187,94778,97147,97663,100279,106160,	uc288ugk.1	none	none	-1,2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,	none	ACE2	none	none	coding	havana_homo_sapiens	nonsense_mediated_decay
RNA_Seq_supported_only,inferred_transcript_model,overlapping_locus	2	all
chrX	15494565	15600960	ENST00000679212.1	0	-	15494839	15600911	789624	18	284,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,235,
0,69458,71687,73160,75729,77058,77635,78801,81100,83523,86655,90909,93187,94778,97147,97663,100279,106160,	uc288uii.1	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,	none	ACE2	none	none	coding	havana_homo_sapiens	protein_coding
RNA_Seq_supported_only,appris_alternative_2,basic,inferred_transcript_model,overlapping_locus	2	basic,all
chrX	15518188	15600960	ENST00000679278.1	0	-	15518927	15600911	789624	18	791,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,235,
0,45835,48064,49537,52106,53435,54012,55178,57477,59900,63032,67286,69564,71155,73524,74040,76656,82537,	uc288ukw.1	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,	none	ACE2	none	none	coding	havana_homo_sapiens	protein_coding
RNA_Seq_supported_only,appris_alternative_2,basic,overlapping_locus	2	basic,all
chrX	15550714	15600960	ENST00000678046.1	0	-	15551072	15600911	789624	18	365,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,235,
0,13309,15538,17011,19580,20909,21486,22652,24951,27374,30506,34760,37038,38629,40998,41514,44130,50011,	uc288spv.1	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,	none	ACE2	none	none	coding	havana_homo_sapiens	protein_coding
RNA_Seq_supported_only,appris_alternative_2,basic,inferred_transcript_model,overlapping_locus	2	basic,all
chrX	15557038	15580438	ENST00000677282.1	0	-	15561904	15580312	789624	11	4975,195,117,101,59,173,123,99,145,227,158,	0,6985,9214,10687,13256,14585,15162,16328,18627,21050,23242,	uc288rms.1	none	none
2,2,2,0,1,2,2,2,1,2,0,	none	ACE2	A0A7D6JAD5	none	coding	havana_homo_sapiens	protein_coding	CAGE_supported_TSS,RNA_Seq_supported_only,basic,inferred_transcript_model,overlapping_locus	2	basic,all
chrX	15557038	15601208	ENST00000680121.1	0	-	15561904	15600911	789624	19	4975,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,289,26,
0,6985,9214,10687,13256,14585,15162,16328,18627,21050,24182,28436,30714,32305,34674,35190,37806,43687,44144,	uc289ajk.1	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,-1,	none	ACE2	Q9BYF1	none	coding	havana_homo_sapiens	protein_coding
CAGE_supported_TSS,CCDS,RNA_Seq_supported_only,appris_principal_2,basic,overlapping_locus	2	basic,all
chrX	15557038	15602155	ENST00000427411.2	0	-	15561904	15600911	789624	19	4975,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,289,200,
0,6985,9214,10687,13256,14585,15162,16328,18627,21050,24182,28436,30714,32305,34674,35190,37806,43687,44917,	uc004cxb.3	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,-1,	none	ACE2	Q9BYF1	none	coding	ensembl_havana_transcript_homo_sapiens	protein_coding
CAGE_supported_TSS,CCDS,RNA_Seq_supported_only,alternative_5_UTR,appris_principal_2,basic,inferred_transcript_model,overlapping_locus	2	basic,all
chrX	15557038	15607236	ENST00000678073.1	0	-	15561904	15600911	789624	19	4975,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,289,100,
0,6985,9214,10687,13256,14585,15162,16328,18627,21050,24182,28436,30714,32305,34674,35190,37806,43687,50098,	uc288sqw.1	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,-1,	none	ACE2	Q9BYF1	none	coding	havana_homo_sapiens	protein_coding
CCDS,RNA_Seq_supported_only,alternative_5_UTR,appris_principal_2,basic,inferred_transcript_model,overlapping_locus	2	canonical,basic,all
chrX	15561032	15600960	ENST00000252519.8	0	-	15561904	15600911	789624	18	981,195,117,101,59,173,123,99,145,227,170,98,106,113,144,94,159,235,
0,2991,5220,6693,9262,10591,11168,12334,14633,17056,20188,24442,26720,28311,30680,31196,33812,39693,	uc004cxa.3	none	none	2,2,2,0,1,2,2,2,1,2,0,1,0,1,1,0,0,0,	none	ACE2	Q9BYF1	none	coding	havana_homo_sapiens	protein_coding
CAGE_supported_TSS,CCDS,Ensembl_canonical,MANE_Select,appris_principal_2,basic,overlapping_locus	2	basic,all
chrX	15561035	15566287	ENST00000471548.5	0	-	15561904	15566287	789624	4	270,498,195,35,	0,480,2988,5217,	uc064yct.1	none	none	-1,2,2,0,	none	ACE2	none	none	coding	havana_homo_sapiens
nonsense_mediated_decay	cds_start_NF,mRNA_start_NF,overlapping_locus	2	all
chrX	15561046	15675608	ENST00000649243.1	0	-	15600989	15659062	789624	20	967,195,117,123,99,145,227,170,98,106,113,144,94,159,289,195,114,86,59,166,
0,2977,5206,11154,12320,14619,17042,20174,24428,26706,28297,30666,31182,33798,39679,78515,83869,97969,103290,114396,	uc286crf.1	none	none	-1,-1,-1,-1,-1,-1,-1,-1,-1,-1,-1,-1,-1,-1,2,2,2,0,-1,-1,	none	RP11-478H11.3-001	A0A3B3IT09	none	coding
havana_homo_sapiens	nonsense_mediated_decay	Ensembl_canonical,appris_principal_1,basic,overlapping_locus,readthrough_transcript	2	canonical,basic,all
chrX	15561879	15566709	ENST00000473851.1	0	-	15561879	15561879	16646144	3	134,195,457,	0,2144,4373,	uc064ycu.1	none	none	-1,-1,-1,	none	ACE2	none	none	nonCoding	havana_homo_sapiens
retained_intron	overlapping_locus	2	all
chrX	15602880	15621484	ENST00000421585.1	0	+	15602880	15602880	25600	2	101,473,	0,18131,	uc064ycw.1	none	none	-1,-1,	none	GS1-594A7.3	none	none	nonCoding	havana_homo_sapiens	lncRNA
Ensembl_canonical,basic	2	canonical,basic,all
```

This is a BED File

Example:

Here's an example of an annotation track, introduced by a **header line**, that is followed by a complete BED definition:

```
track name=pairedReads description="Clone Paired Reads" useScore=1
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

Data Retrieval
Retrieving Data From UCSC

Table Browser

Example:

Here's an example of an annotation track, introduced by a **header line**, that is followed by a complete BED definition:

```
track name=pairedReads description="Clone Paired Reads" useScore=1
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

- The first three required BED fields are:

  chrom - The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).

  chromStart - The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.

  chromEnd - The ending position of the feature in the chromosome or scaffold. The chromEnd base is not included in the display of the feature, however, the number in position format will be represented. For example, the first 100 bases of chromosome 1 are defined as chrom=1, chromStart=0, chromEnd=100, and span the bases numbered 0-99 in our software (not 0-100), but will represent the position notation chr1:1-100. Read more here.

  chromStart and chromEnd can be identical, creating a feature of length 0, commonly used for insertions. For example, use chromStart=0, chromEnd=0 to represent an insertion before the first nucleotide of a chromosome.

Data Retrieval
Retrieving Data From UCSC

Table Browser

Example:

Here's an example of an annotation track, introduced by a **header line**, that is followed by a complete BED definition:

```
track name=pairedReads description="Clone Paired Reads" useScore=1
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

- The 9 additional optional BED fields are:

  name - Defines the name of the BED line. This label is displayed to the left of the BED line in the Genome Browser window when the track is open to full display mode or directly to the left of the item in pack mode.

  score - A score between 0 and 1000. If the track line useScore attribute is set to 1 for this annotation data set, the score value will determine the level of gray in which this feature is displayed (higher numbers = darker gray). This table shows the Genome Browser's translation of BED score values into shades of gray:

shade									
score in range	≤ 166	167-277	278-388	389-499	500-611	612-722	723-833	834-944	≥ 945

Data Retrieval
Retrieving Data From UCSC

Table Browser

Example:

Here's an example of an annotation track, introduced by a **header line**, that is followed by a complete BED definition:

```
track name=pairedReads description="Clone Paired Reads" useScore=1
chr22 1000 5000 cloneA 960 + 1000 5000 0 2 567,488, 0,3512
chr22 2000 6000 cloneB 900 - 2000 6000 0 2 433,399, 0,3601
```

- **strand** - Defines the strand. Either "." (=no strand) or "+" or “-".
- **thickStart** - The starting position at which the feature is drawn thickly (for example, the start codon in gene displays). When there is no thick part, thickStart and thickEnd are usually set to the chromStart position.
- **thickEnd** - The ending position at which the feature is drawn thickly (for example the stop codon in gene displays).
- **itemRgb** - An RGB value of the form R,G,B (e.g. 255,0,0). If the track line itemRgb attribute is set to "On", this RBG value will determine the display color of the data contained in this BED line. NOTE: It is recommended that a simple color scheme (eight colors or less) be used with this attribute to avoid overwhelming the color resources of the Genome Browser and your Internet browser.
- **blockCount** - The number of blocks (exons) in the BED line.
- **blockSizes** - A comma-separated list of the block sizes. The number of items in this list should correspond to blockCount.
- **blockStarts** - A comma-separated list of block starts. All of the blockStart positions should be calculated relative to chromStart. The number of items in this list should correspond to blockCount.

In BED files with block definitions, the first blockStart value must be 0, so that the first block begins at chromStart. Similarly, the final blockStart position plus the final blockSize value must equal chromEnd. Blocks may not overlap.