Training materials

- Ensembl training materials are protected by a CC BY license 
- http://creativecommons.org/licenses/by/4.0/
- If you wish to re-use these materials, please credit Ensembl for their creation
- If you use Ensembl for your work, please cite our papers
- http://www.ensembl.org/info/about/publications.html

Browsing Genes and Genomes with Ensembl

Ben Moore

Ensembl Outreach

EMBL-EBI

Helsinki - 14th June 2016

Structure for this workshop

Introduction to Ensembl

Exploring Ensembl - Genomic regions, Genes and Transcripts

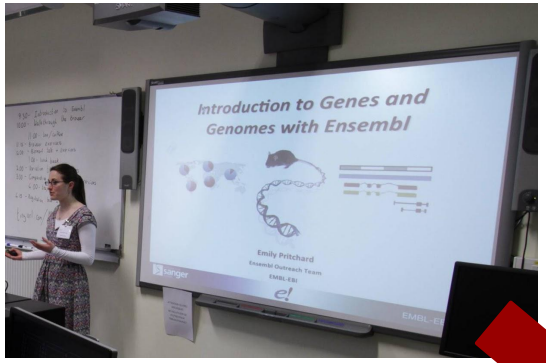
Variation data

The Variant Effect Predictor

- Web-interface
- Perl Script
- REST API

http://www.ebi.ac.uk/~bmoore/workshops/

Structure



Presentation:

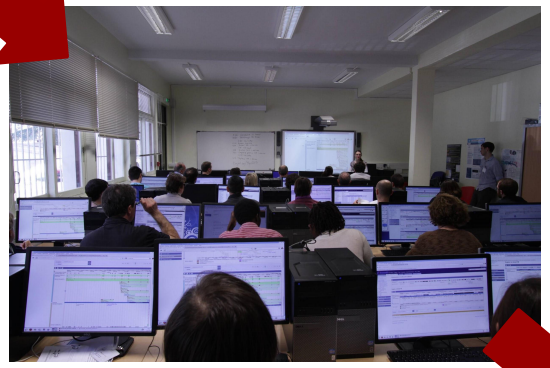
What the data/tool is

How we produce/process the data

Demo:

Getting the data

Using the tool



Follow along if you want to

Exercises:

Trying things out for yourself (alone/pairs?)

Going beyond the demo

Not a test!

Extra Exercises

http://www.ebi.ac.uk/~bmoore/workshops/

http://www.ebi.ac.uk/~bmoore/workshops/

Course materials

www.ebi.ac.uk/~bmoore/workshops

- Presentations
- Coursebook (demos and exercises)
- Plain Text Files for exercises
- Answerbook (exercise answers)

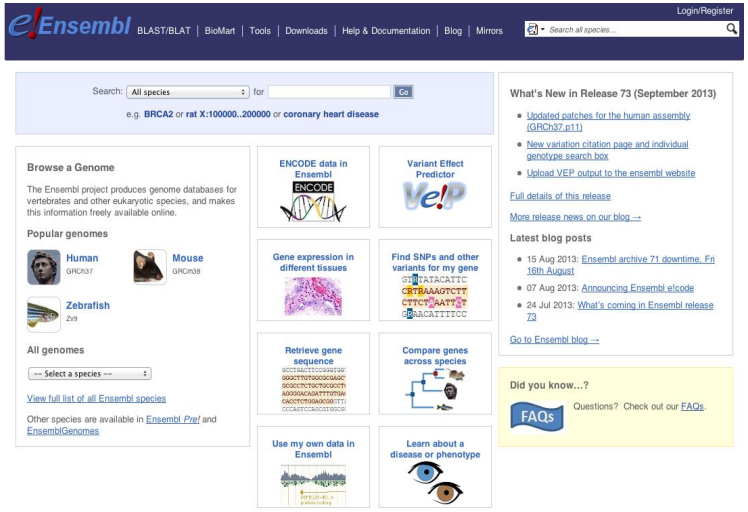
http://www.ebi.ac.uk/~bmoore/workshops/

Objectives

- What is Ensembl?
- What type of data can you get in Ensembl?
- How to navigate the Ensembl browser website.
- Where to go for help and documentation.

http://www.ebi.ac.uk/~bmoore/workshops/

Exploring the Ensembl genome browser



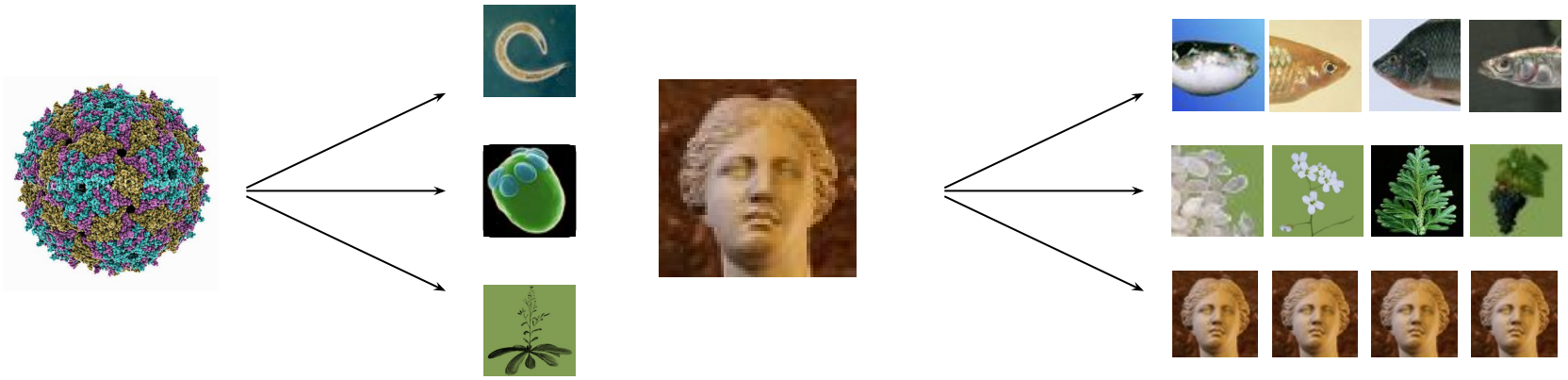
EMBL-EBI

wellcome trust sanger institute

Why do we need genome browsers?

1977: 1st genome to be sequenced (5 kb)

2004: finished human sequence (3 Gb)

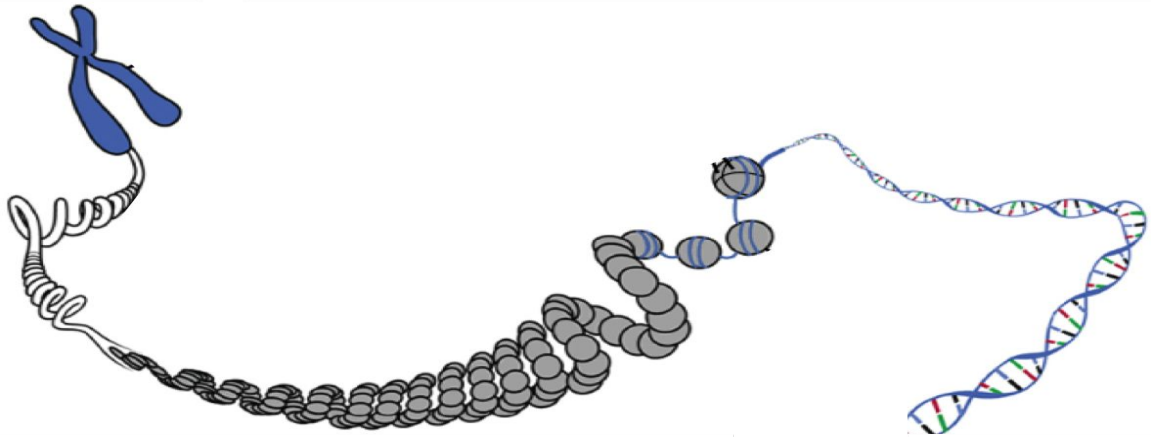


http://www.ebi.ac.uk/~bmoore/workshops/

Why do we need genome browsers?

http://www.ebi.ac.uk/~bmoore/workshops/

Ensembl- unlocking the code

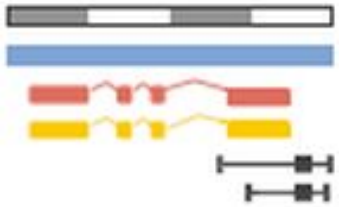


- *Genomic assemblies* - automated gene annotation
- *Variation* - Small and large scale sequence variation with phenotype associations
- *Comparative Genomics* - Whole genome alignments, gene trees
- *Regulation* - Potential promoters and enhancers, DNA methylation

http://www.ebi.ac.uk/~bmoore/workshops/

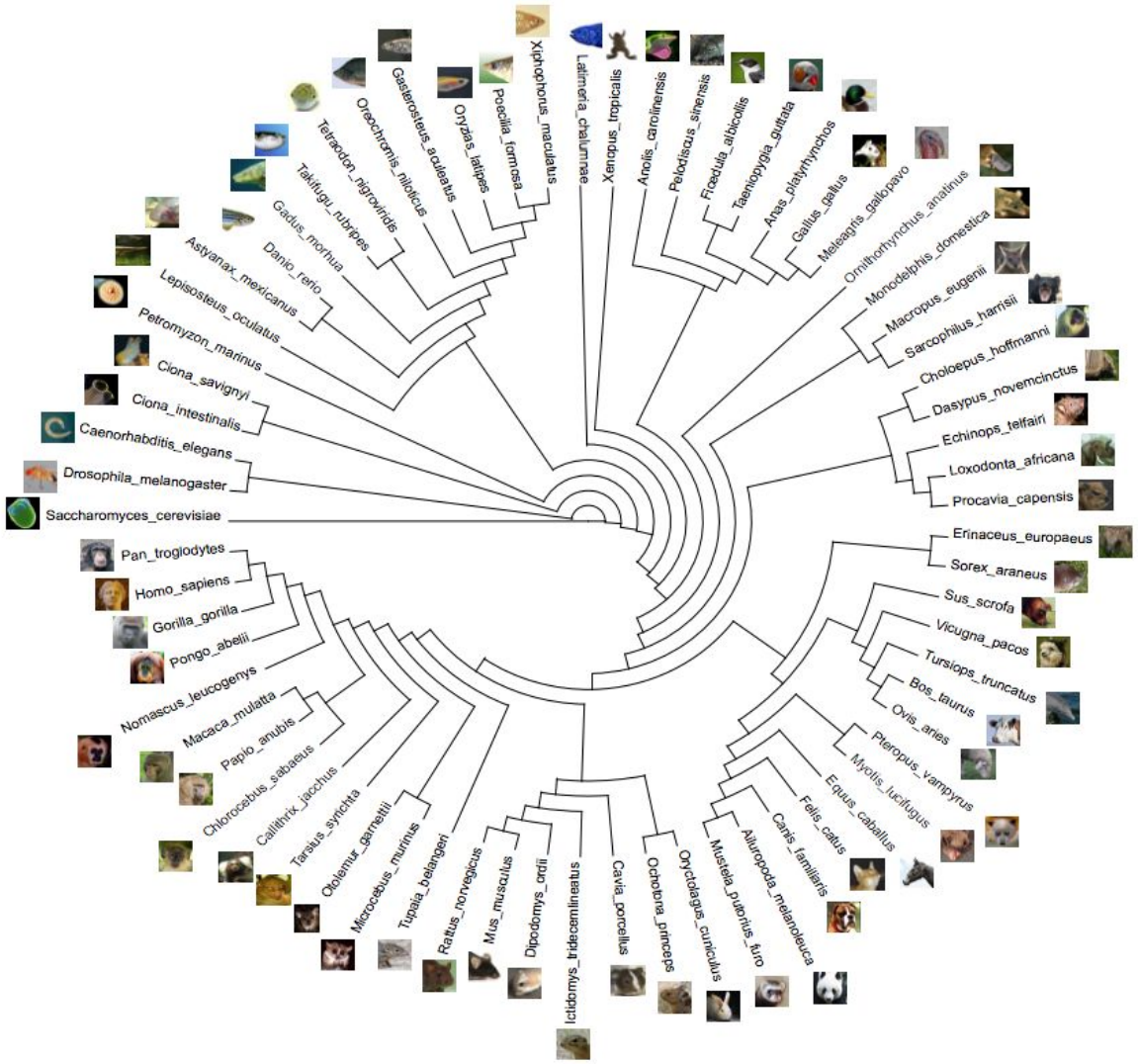
Ensembl Features

- Gene builds for ~70 species
- Gene trees
- Regulatory build
- Variation display and VEP
- Display of user data
- BioMart (data export)
- Programmatic access via the APIs
- Completely Open Source



http://www.ebi.ac.uk/~bmoore/workshops/

Ensembl- access to 70+ genomes



http://www.ebi.ac.uk/~bmoore/workshops/

Ensembl Genomes- expanding Ensembl

www.ensembl.org

- Vertebrates  


- Other representative species

http://www.ebi.ac.uk/~bmoore/workshops/

Ensembl Genomes- expanding Ensembl

www.ensembl.org

www.ensemblgenomes.org

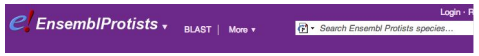
- Vertebrates

- Other representative species

- Bacteria

- Fungi

- Protists



- Metazoa

- Plants

http://www.ebi.ac.uk/~bmoore/workshops/

What is a genome assembly?

Sequence reads

```
                    CGGCCTTTGGGCTCCGCCTTCAGCTCAAGA
  CAGCTGTCCCAGATGAC     ACTTAACTTCCCTCCCAGCTGTCC
GGGCTCCGCCTTCAGCTC                    TCCCAGCTGTCCCAGATGACGCCAT
                   AACTTCCCTCCCAGCT
   CGGCCTTTGGGCTCC                    TCCGCCTTCAGCTCAAGACTTAACTTC
                    CAGATGACGCC
```

Match up overlaps

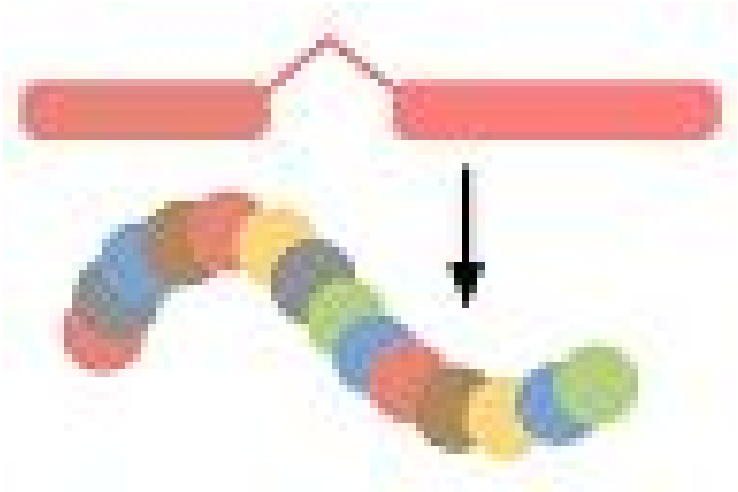
```
CGGCCTTTGGGCTCCGCCTTCAGCTCAAGA   AACTTCCCTCCCAGCT    CAGATGACGCC
           TCCGCCTTCAGCTCAAGACTTAACTTC  TCCCAGCTGTCCCAGATGACGCCAT
       GGGCTCCGCCTTCAGCTC   ACTTAACTTCCCTCCCAGCTGTCC
CGGCCTTTGGGCTCC                          CAGCTGTCCCAGATGAC
```

Genome assembly

```
CGGCCTTTGGGCTCCGCCTTCAGCTCAAGACTTAACTTCCCTCCCAGCTGTCCCAGATGACGCCAT
```

http://www.ebi.ac.uk/~bmoore/workshops/

Genes and Transcripts



EMBL-EBI

wellcome trust sanger institute

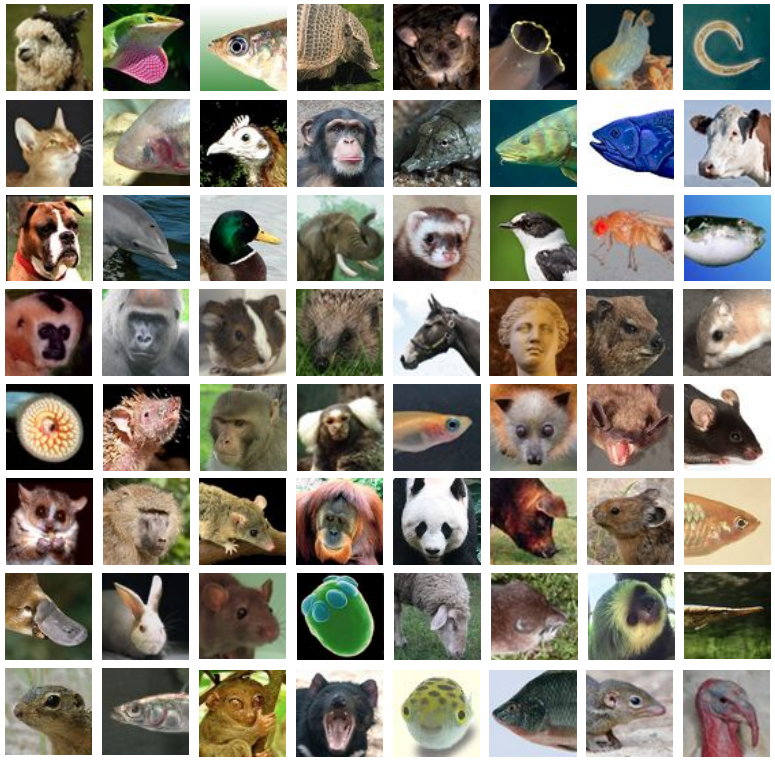
Ensembl and Havana annotation

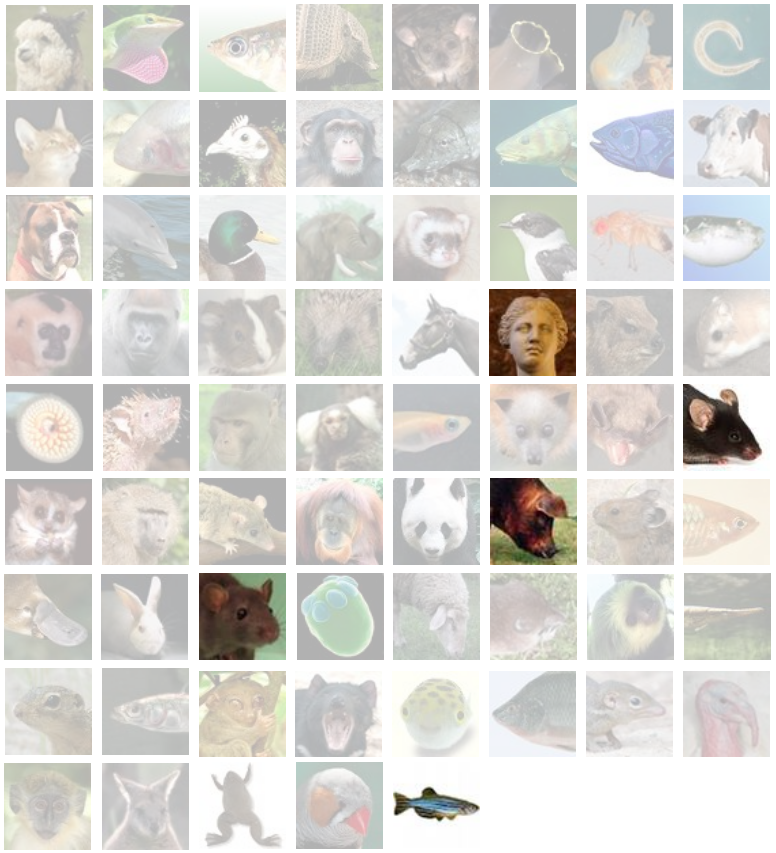
Ensembl

havana

Automatic annotation

Manual annotation

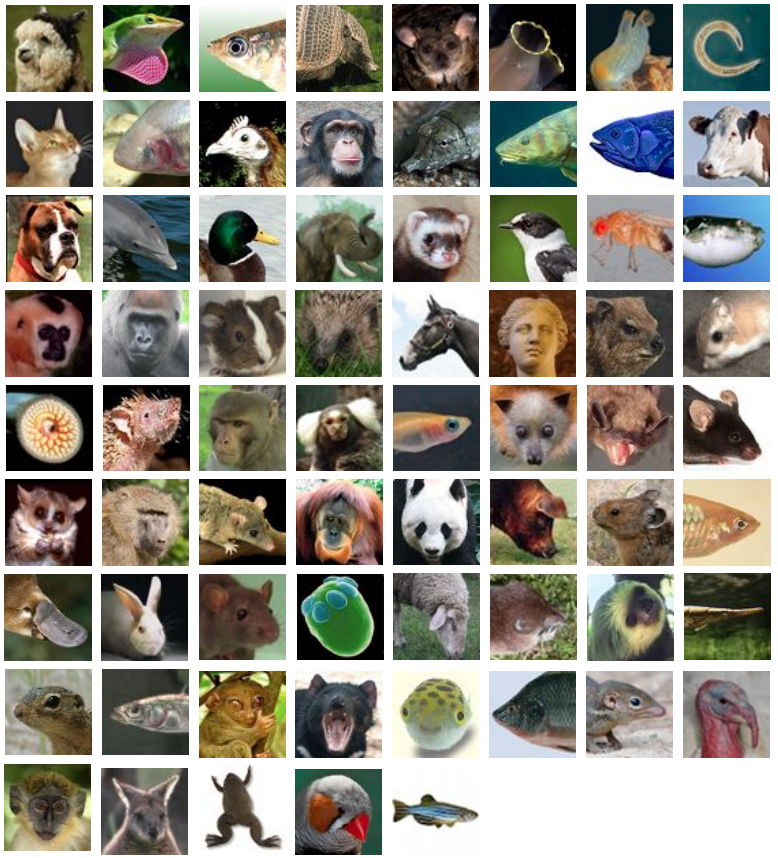




http://www.ebi.ac.uk/~bmsec/workshops/

Automatic gene annotation

- Genome-wide determination using the Ensembl automated pipeline
- Predictions based on experimental (biological) data



http://www.ebi.ac.uk/~bmoore/workshops/

Biological Evidence

- International Nucleotide Sequence databases

ENA European Nucleotide Archive

GenBank

DDBJ DNA Data Bank of Japan

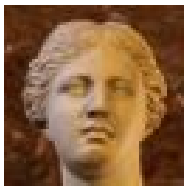
- Protein sequence databases
  - Swiss-Prot: manually curated
  - TrEMBL: unreviewed translations

UniProt

- NCBI RefSeq

RefSeq genomes·transcripts·proteins

  - Manually annotated proteins and mRNAs (NP, NM)



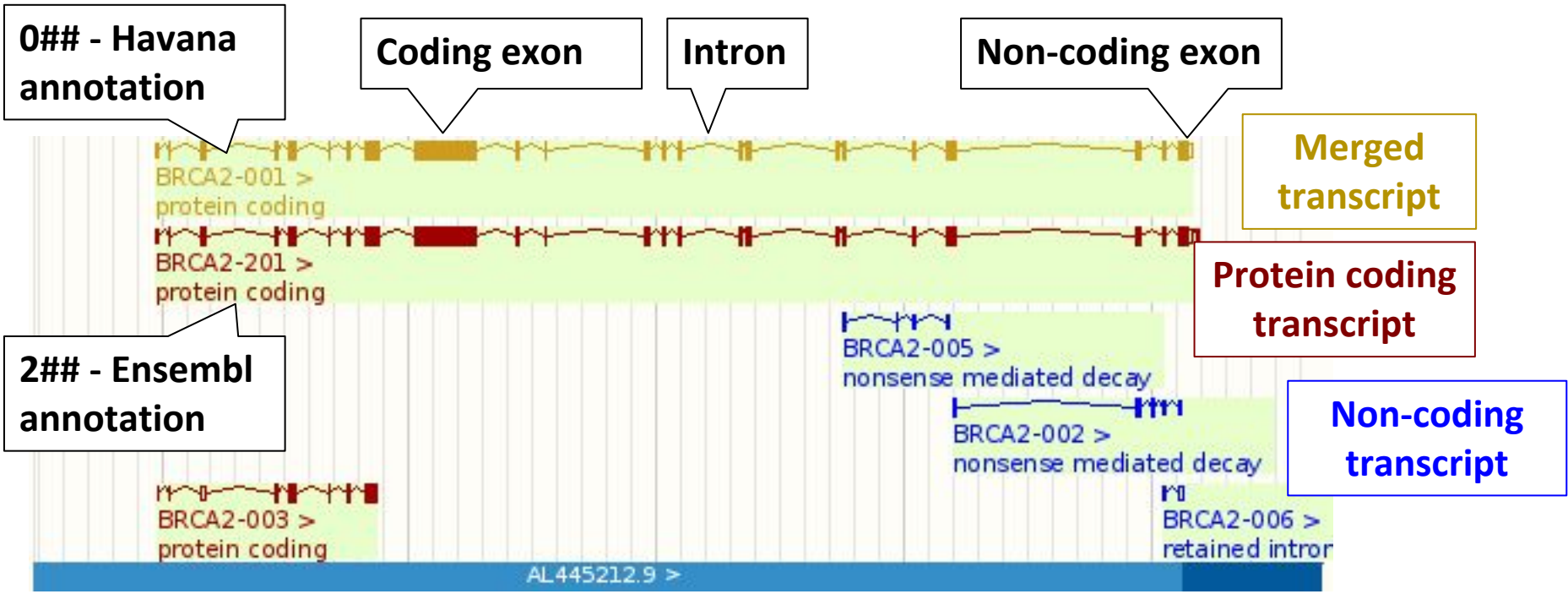
http://www.ebi.ac.uk/~bmoore/workshops/

Other species

- Infer genes from homology to other species
  - predict genes in  by mapping cDNAs/proteins from  to the  genome.
- RNAseq data

http://www.ebi.ac.uk/~bmoore/workshops/

Gene views



http://www.ebi.ac.uk/~bmoore/workshops/

Golden transcripts

- Identical annotation

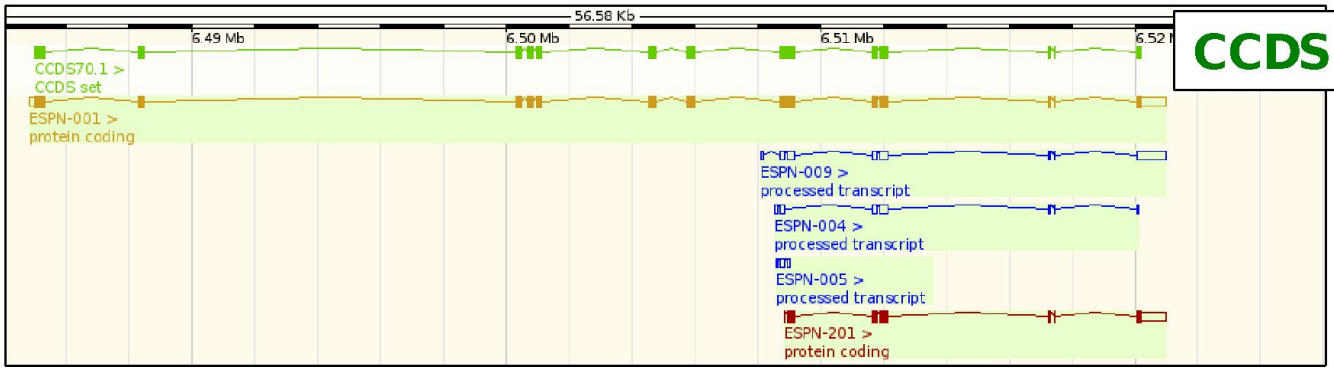
- Higher confidence and quality

http://www.ebi.ac.uk/~bmoore/workshops/

CCDS transcripts

- Consensus coding DNA sequence set
- Agreement between EBI, WTSI, UCSC and NCBI

http://www.ncbi.nlm.nih.gov/CCDS/CcdsBrowse.cgi



http://www.ebi.ac.uk/~bmoore/workshops/

Ensembl stable IDs

- ENSG########## Ensembl Gene ID
- ENST########## Ensembl Transcript ID
- ENSP########## Ensembl Peptide ID
- ENSE########## Ensembl Exon ID
- ENSR########## Ensembl Regulatory region ID

- For non-human species a suffix is added:

  MUS (*Mus musculus*) for mouse ENSMUSG###

  DAR (*Danio rerio*) for zebrafish: ENSDARG###

http://www.ensembl.org/info/genome/stable_ids/index.html

Variation

EMBL-EBI

wellcome trust sanger institute

Variation types

1) Small scale in one or few nucleotides of a gene

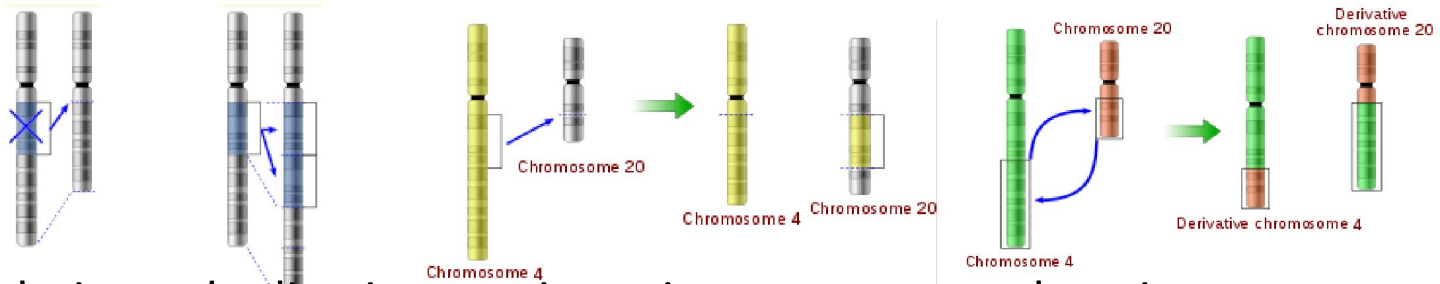
- Small insertions and deletions (DIPs or indels)
- Single nucleotide polymorphism (SNP)

A G A C T T G A C C T G T C T – A A C T G G A

T G A C T T G A C – T G T C T G A A C G G G A

2) Large scale in chromosomal structure (structural variation)

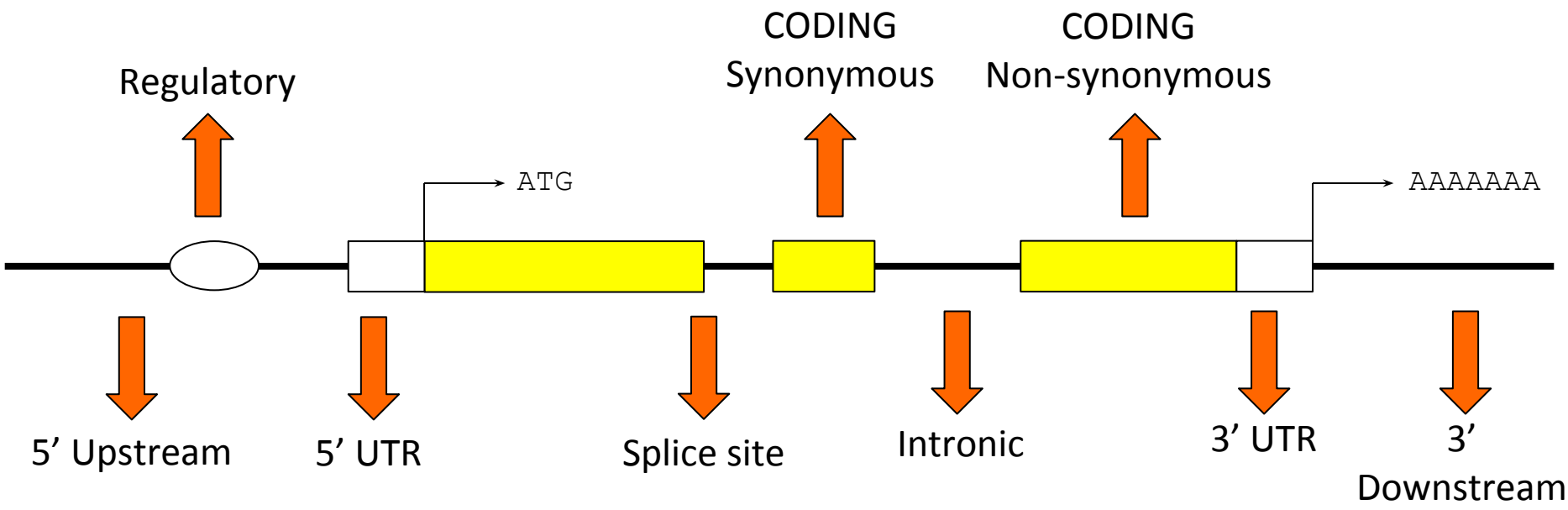
- Copy number variations (CNV)
- Large deletions/duplications, insertions, translocations



deletion duplication insertion translocation

http://www.ebi.ac.uk/~bmoore/workshops/

Variation consequences



http://www.ebi.ac.uk/~bmoore/workshops/

Consequence terms

* SO term	SO description	SO accession	Old Ensembl term
transcript_ablation	A feature ablation whereby the deleted region includes a transcript feature	SO:0001893	Transcript ablation
splice_donor_variant	A splice variant that changes the 2 base region at the 5' end of an intron	SO:0001575	Essential splice site
splice_acceptor_variant	A splice variant that changes the 2 base region at the 3' end of an intron	SO:0001574	
stop_gained	A sequence variant whereby at least one base of a codon is changed, resulting in a premature stop codon, leading to a shortened transcript	SO:0001587	Stop gained
frameshift_variant	A sequence variant which causes a disruption of the translational reading frame, because the number of nucleotides inserted or deleted is not a multiple of three	SO:0001589	Frameshift coding
stop_lost	A sequence variant where at least one base of the terminator codon (stop) is changed, resulting in an elongated transcript	SO:0001578	Stop lost
initiator_codon_variant	A codon variant that changes at least one base of the first codon of a transcript	SO:0001582	Non synonymous coding
inframe_insertion	An inframe non synonymous variant that inserts bases into in the coding sequence	SO:0001821	
inframe_deletion	An inframe non synonymous variant that deletes bases from the coding sequence	SO:0001822	
missense_variant	A sequence variant, that changes one or more bases, resulting in a different amino acid sequence but where the length is preserved	SO:0001583	
transcript_amplification	A feature amplification of a region containing a transcript	SO:0001889	Transcript amplification
splice_region_variant	A sequence variant in which a change has occurred within the region of the splice site, either within 1-3 bases of the exon or 3-8 bases of the intron	SO:0001630	Splice site
incomplete_terminal_codon_variant	A sequence variant where at least one base of the final codon of an incompletely annotated transcript is changed	SO:0001626	Partial codon
synonymous_variant	A sequence variant where there is no resulting change to the encoded amino acid	SO:0001819	Synonymous coding
stop_retained_variant	A sequence variant where at least one base in the terminator codon is changed, but the terminator remains	SO:0001567	
coding_sequence_variant	A sequence variant that changes the coding sequence	SO:0001580	Coding unknown
mature_miRNA_variant	A transcript variant located with the sequence of the mature miRNA	SO:0001620	Within mature miRNA
5_prime_UTR_variant	A UTR variant of the 5' UTR	SO:0001623	5prime UTR
3_prime_UTR_variant	A UTR variant of the 3' UTR	SO:0001624	3prime UTR
intron_variant	A transcript variant occurring within an intron	SO:0001627	Intronic
NMD_transcript_variant	A variant in a transcript that is the target of NMD	SO:0001621	NMD transcript
non_coding_exon_variant	A sequence variant that changes non-coding exon sequence	SO:0001792	Within non coding gene
nc_transcript_variant	A transcript variant of a non coding RNA	SO:0001619	
upstream_gene_variant	A sequence variant located 5' of a gene	SO:0001631	Upstream
downstream_gene_variant	A sequence variant located 3' of a gene	SO:0001632	Downstream
TFBS_ablation	A feature ablation whereby the deleted region includes a transcription factor binding site	SO:0001895	Tfbs ablation
TFBS_amplification	A feature amplification of a region containing a transcription factor binding site	SO:0001892	Tfbs amplification
TF_binding_site_variant	A sequence variant located within a transcription factor binding site	SO:0001782	Regulatory region
regulatory_region_variant	A sequence variant located within a regulatory region	SO:0001566	
regulatory_region_ablation	A feature ablation whereby the deleted region includes a regulatory region	SO:0001894	Regulatory region ablation
regulatory_region_amplification	A feature amplification of a region containing a regulatory region	SO:0001891	Regulatory region amplification
feature_elongation	A sequence variant that causes the extension of a genomic feature, with regard to the reference sequence	SO:0001907	Feature elongation
feature_truncation	A sequence variant that causes the reduction of a genomic feature, with regard to the reference sequence	SO:0001906	Feature truncation
intergenic_variant	A sequence variant located in the intergenic region, between genes	SO:0001628	Intergenic

http://www.ensembl.org/info/docs/variation/predicted_data.html

http://www.ebi.ac.uk/~bmoore/workshops/

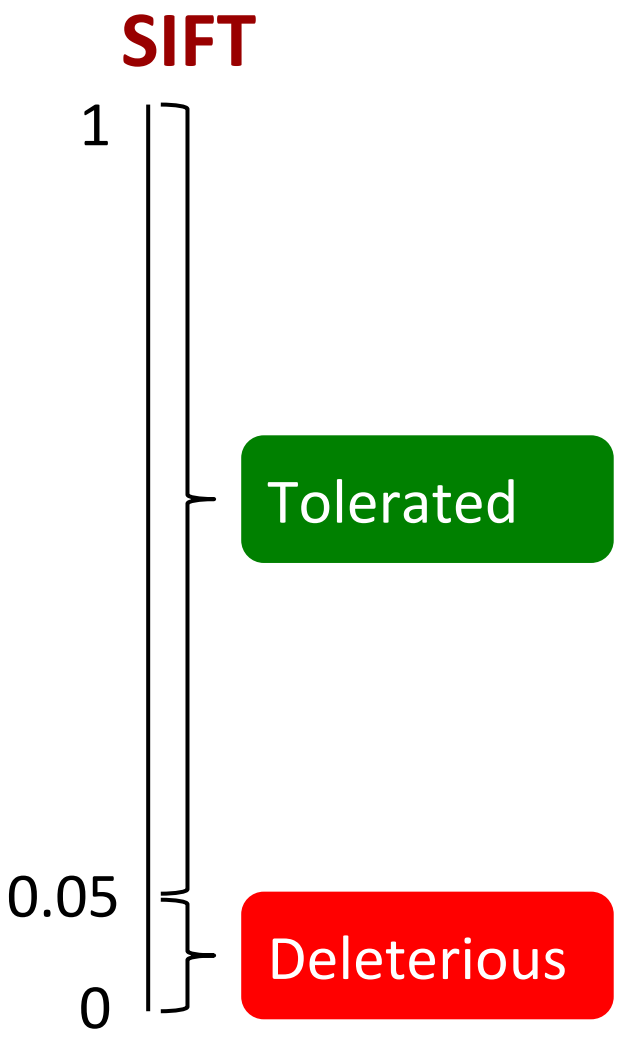
Missense variants- pathogenicity

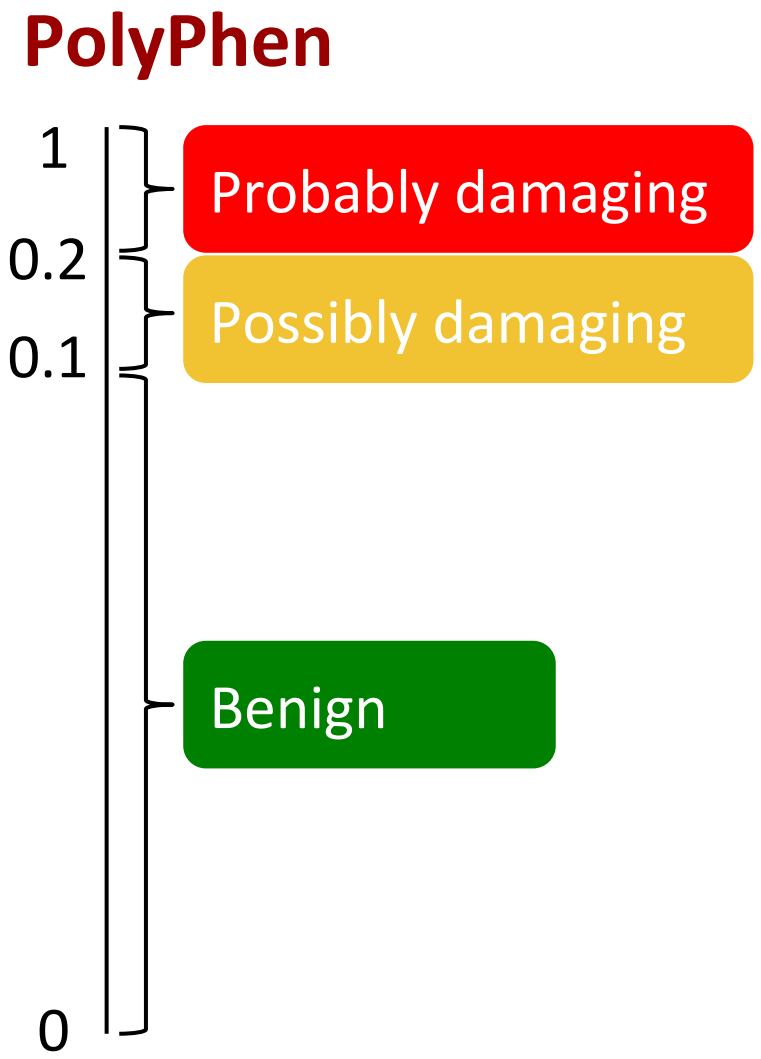
SIFT and PolyPhen score changes in amino acid sequence based on:

- How well conserved the amino acid is
- The chemical change in the amino acid

http://www.ebi.ac.uk/~bmoore/workshops/

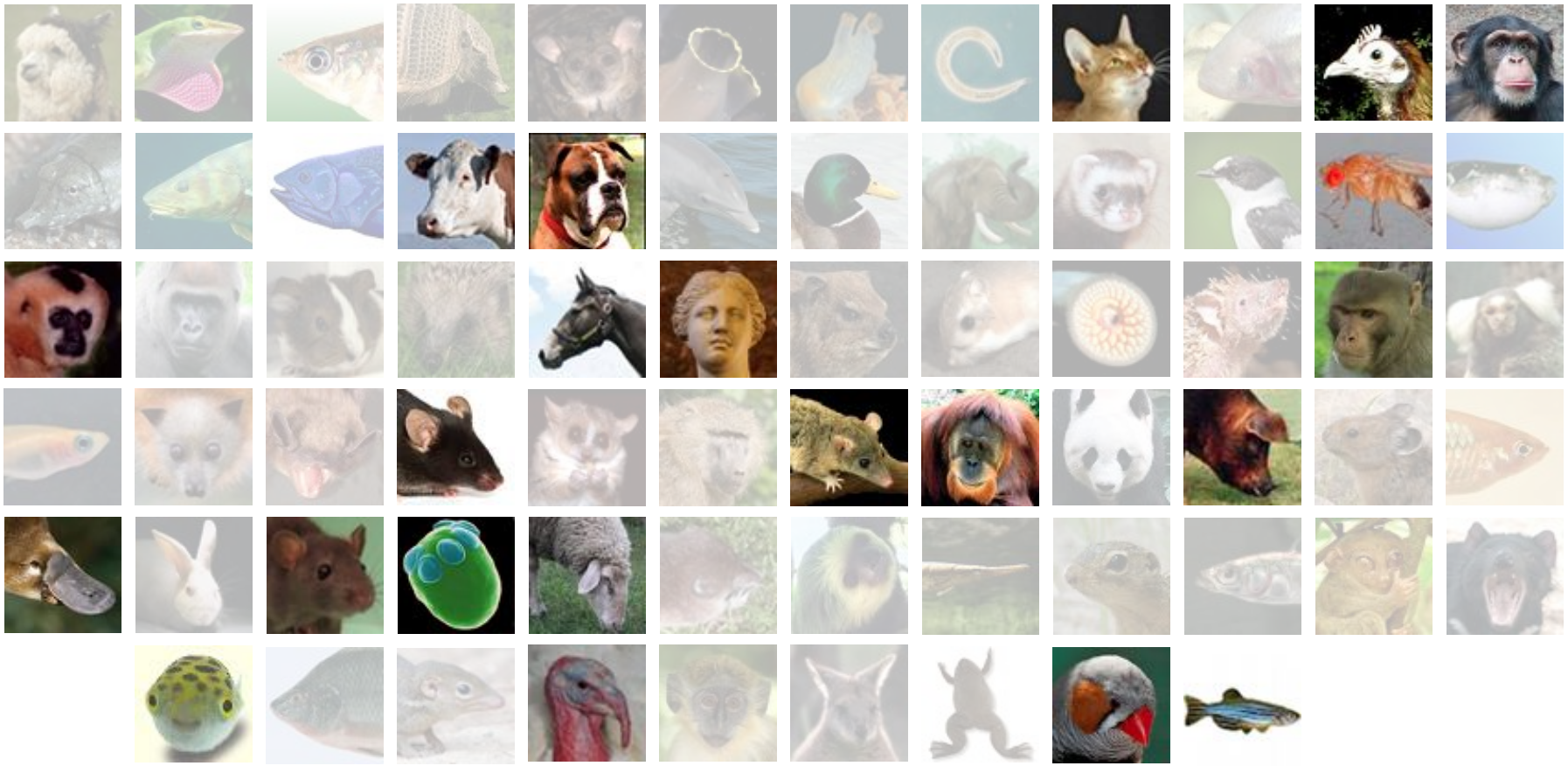
Missense variants- pathogenicity





http://www.ebi.ac.uk/~bmoore/workshops/

Species with variation data

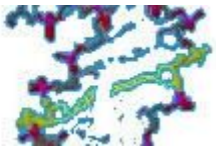


+ Ensembl Plants, Fungi, Protists and Metazoa

http://www.ensembl.org/info/genome/variation/sources_documentation.html

Variation sources

dbSNP
Short Genetic Variations



orphanet

OMIM®

DGVarchive

DECIPHER v5.1
GRCh37

PubMed

HGMD®
The Human Gene Mutation Database
Cardiff

UniProt

European genome-phenome archive

GEFOS

GIANT

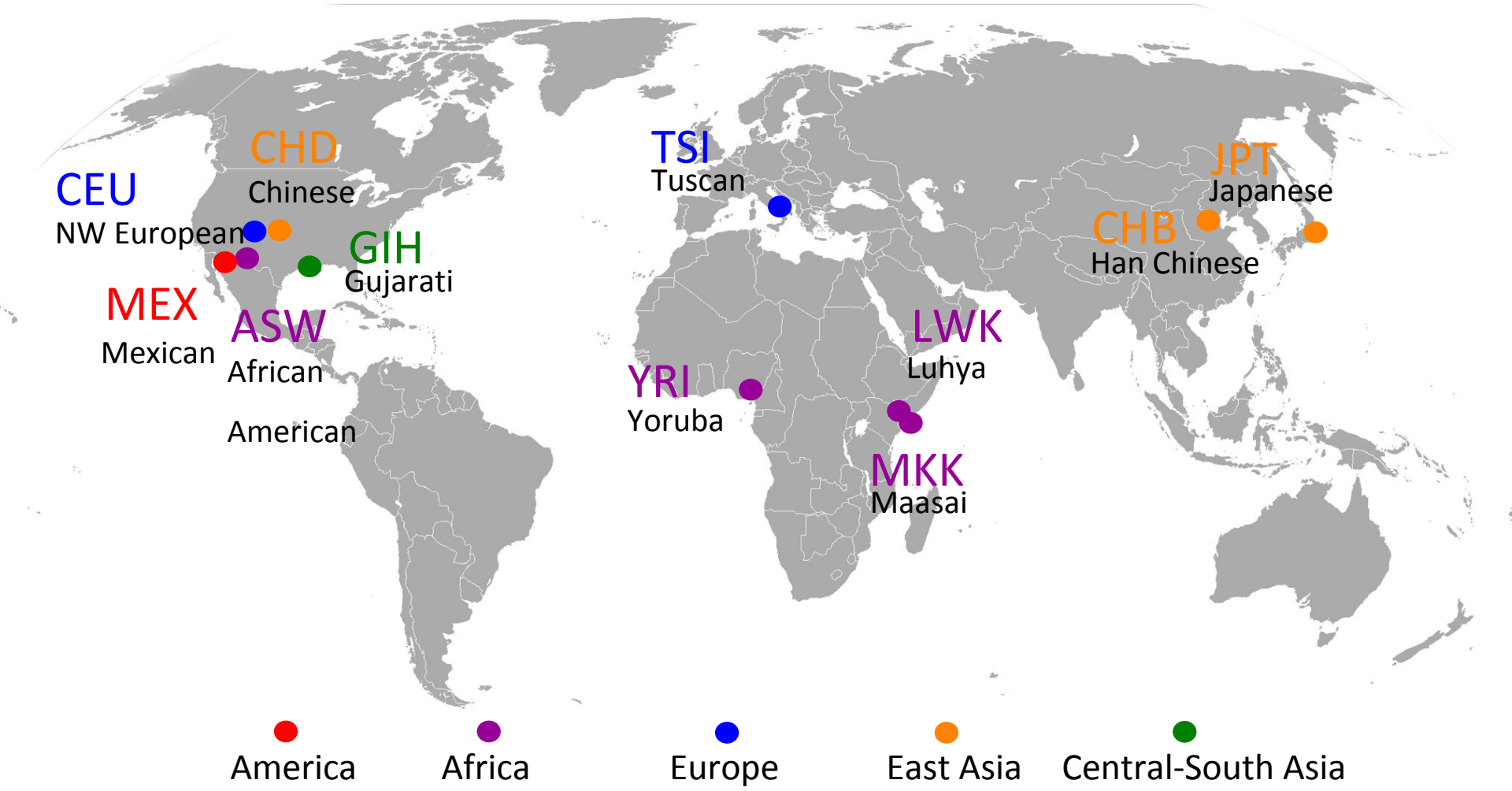
Genetics

http://www.ensembl.org/info/docs/variation/sources_documentation.html

http://www.ebi.ac.uk/~bmoore/workshops/

HapMap project

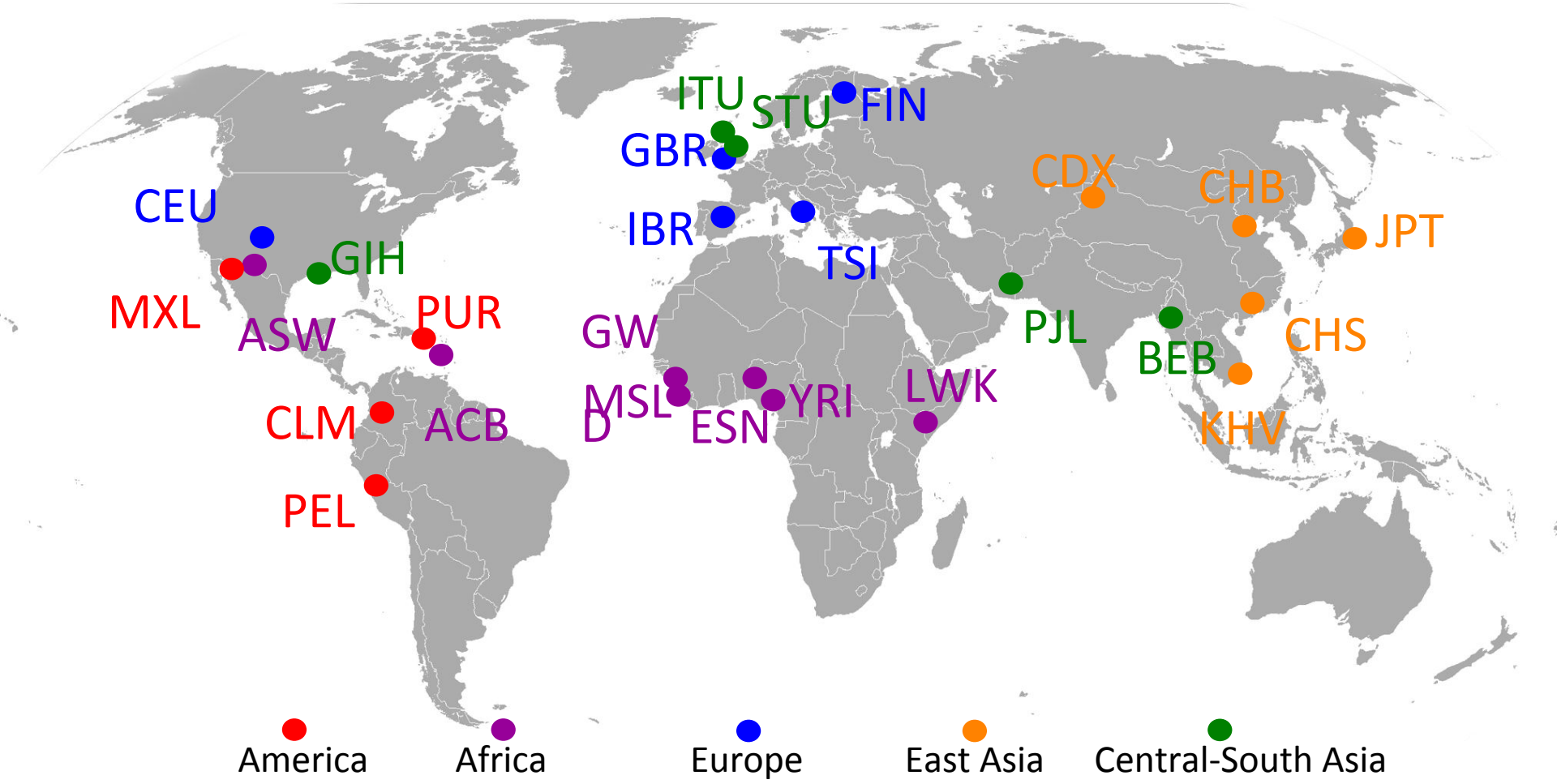
Genotyping 1,301 individuals from 11 populations.



http://www.ebi.ac.uk/~bmoore/workshops/

1000 genomes project

Sequencing 2,500 individuals at 4X coverage



http://www.ebi.ac.uk/~bmoore/workshops/

http://www.ensembl.org/Help/Faq?id=328

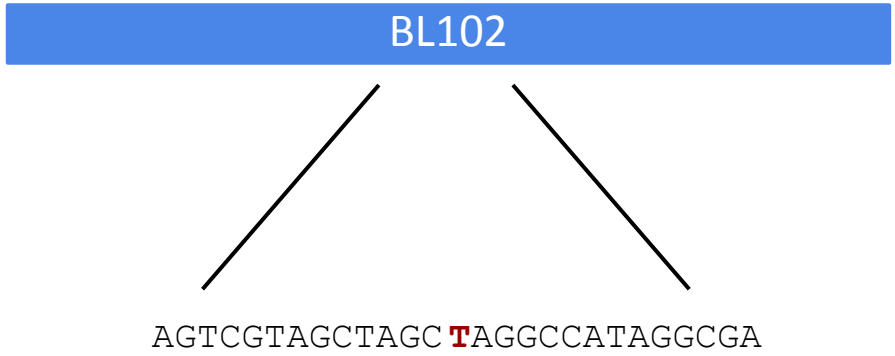
Reference alleles


BL


AL


CM


IM



Frequency T = 0.05, frequency G = 0.95
G is the allele in all primates
T causes disease susceptibility

T is allele in the contig used
- T is the reference allele
- G is the alternate allele
- Alleles are T/G

http://www.ebi.ac.uk/~bmoore/workshops/

Allele strand

AGTCGTAGCTAGC **T/G** AGGCCATAGGCGA

TCGCCTATGGCCT **A/C** GCTAGCTACGACT

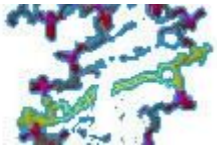
Exon sequence:

TATGGCCT**A/C**GCTAGC

Ensembl

Alleles in database = T/G
Alleles in gene = A/C

dbSNP
Short Genetic Variations



Alleles = A/C -ve strand or
T/G +ve strand

PubMed

Alleles = A/C or T/G
Often lack further info

http://www.ebi.ac.uk/~bmoore/workshops/

Hands on

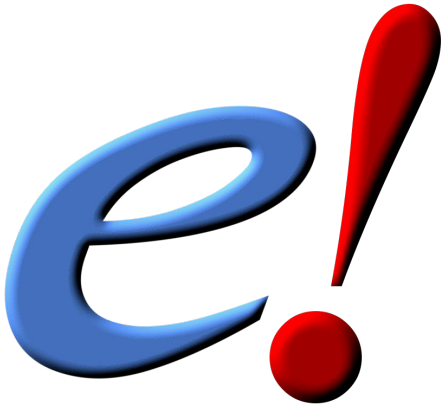
- We're going to look at a gene *MCM6* to find variants in the gene.
- We will look at the region of *MCM6* to find variants in the region.
- We will look at a variant rs4988235 to find more information about it.
- Demo: coursebook page 6-21
- Exercises: coursebook page 21-23
    - Answers: answer book page 3-5

http://www.ebi.ac.uk/~bmoore/workshops/

Data Mining with BioMart

EMBL-EBI

wellcome trust sanger institute



Outline of this session

- What is BioMart?
- The principle: 4 steps
- Demo and Exercises

http://www.ebi.ac.uk/~bmoore/workshops/

What is BioMart?

- A tool is your browser:
  - Export Ensembl data with no programming required
  - Build queries with a few mouse clicks
  - Generates customisable datatables and files

http://www.ebi.ac.uk/~bmoore/workshops/

Why use BioMart?

For things that would be time consuming/ difficult with the Ensembl browser

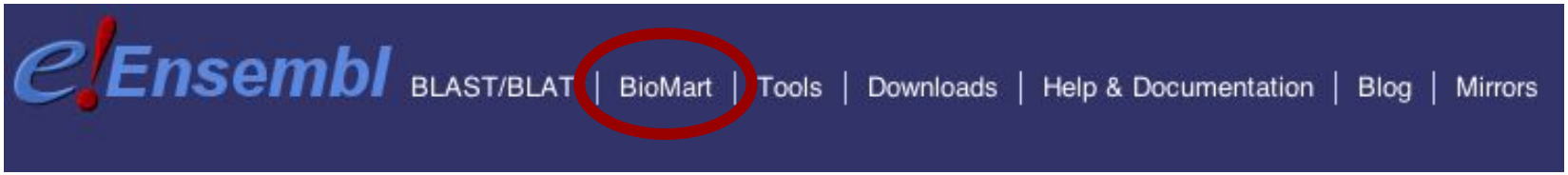
- Query multiple things (gene/ variants) at once:
  - ID conversions
  - Gene locations
  - Download sequences

- Export large amounts of data

http://www.ebi.ac.uk/~bmoore/workshops/

Where to find BioMart

- www.ensembl.org/biomart/martview



- metazoa.ensembl.org/biomart/martview

http://www.ebi.ac.uk/~bmoore/workshops/

Availability

Ensembl

Ensembl Plants

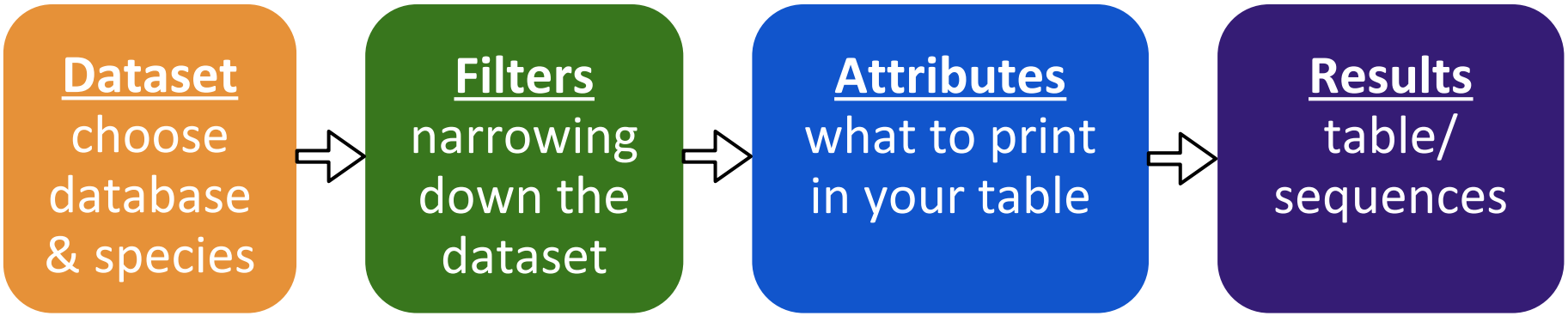
Ensembl Fungi (some exceptions)

Ensembl Metazoa

Ensembl Protists (some exceptions)

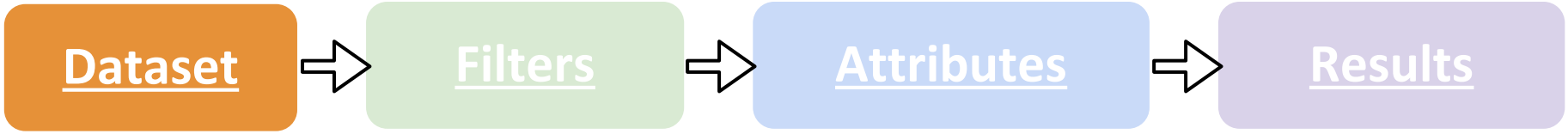
http://www.ebi.ac.uk/~bmoore/workshops/

How do I use BioMart?
The 4 steps



http://www.ebi.ac.uk/~bmoore/workshops/

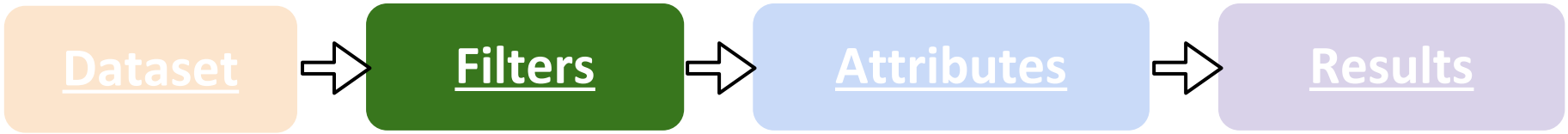
Step 1: Dataset



- Define the database that you want to search with your filters
    - Genes, Variation, Regulation

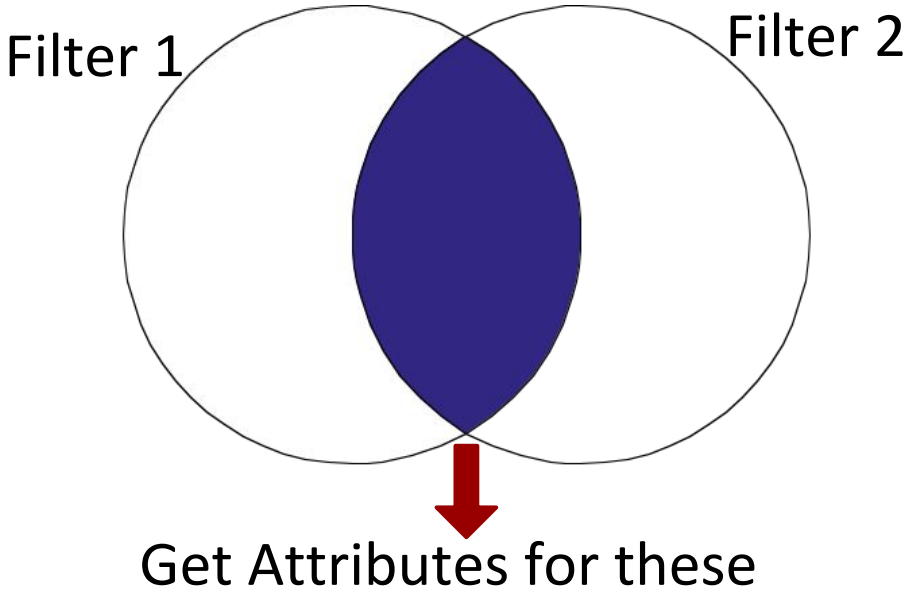
- Define the species

Step 2: Filters



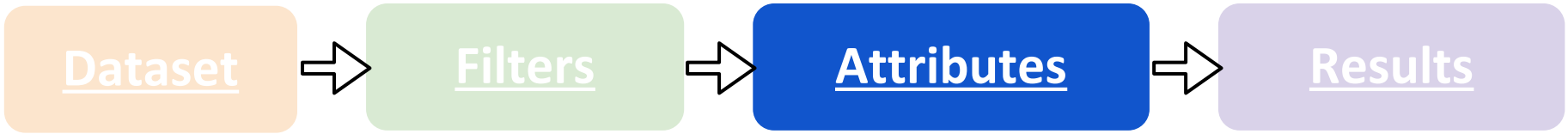
Define a (large) set of genes/variants by combinations of parameters, eg:

- A region
- A list of IDs
- Function (GO term)
- Phenotypes



http://www.ebi.ac.uk/~bmoore/workshops/

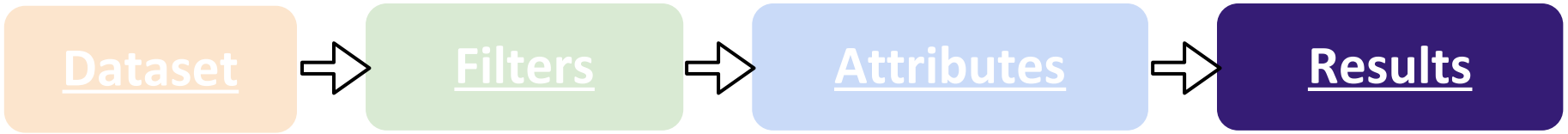
Step 3: Attributes



Define the data you want for that set, e.g:

- IDs
- Features
- Sequences
- Orthologues/Paralogues

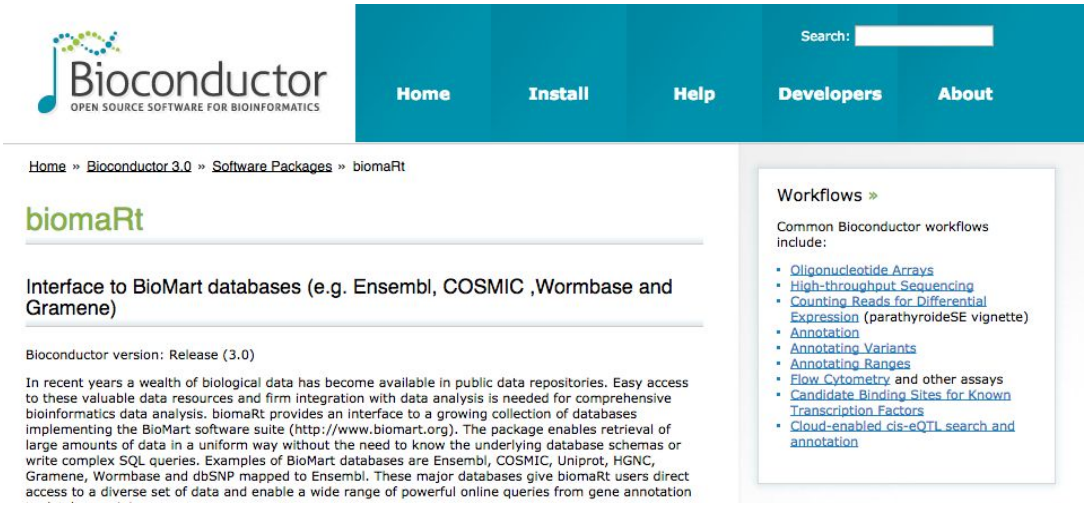
Step 4: Results



View and download the datatable in a number of formats:

- html
- tsv
- csv
- xls
- fasta

biomaRt



- Bioconductor provides tools for the analysis and comprehension of high-throughput genomic data using R statistical programming language.
- Package for Biomart called BiomaRt : http://www.bioconductor.org/packages/release/bioc/html/biomaRt.html
- Easy to install in R :
  - source("http://bioconductor.org/biocLite.R")
  - biocLite("biomaRt")
- Documentation:http://www.bioconductor.org/packages/release/bioc/vignettes/biomaRt/inst/doc/biomaRt.pdf

http://www.ebi.ac.uk/~bmoore/workshops/

Hands on

- We're going to look at a set of six *Homo sapiens* variants *rs333, rs334, rs344, rs1800413, rs74653330* and *rs137854567* and find out:
  - Their location
  - Their alleles
  - Their MAF
  - Their phenotype associations
  - Their flanking sequences

- Demo: coursebook page 24-28

http://www.ebi.ac.uk/~bmoore/workshops/

What is the VEP?

Determine the **effect of variants** (SNPs, insertions, deletions, CNVs or structural variants):

- Variant Co-ordinates
- VCF
- HGVS
- Variant IDs

- Affected gene, transcript and protein sequence
- Pathogenicity
- Frequency data
- Regulatory consequences
- Splicing consequences
- Literature citations

http://www.ebi.ac.uk/~bmoore/workshops/

Species that work with the VEP

http://www.ebi.ac.uk/~bmoore/workshops/

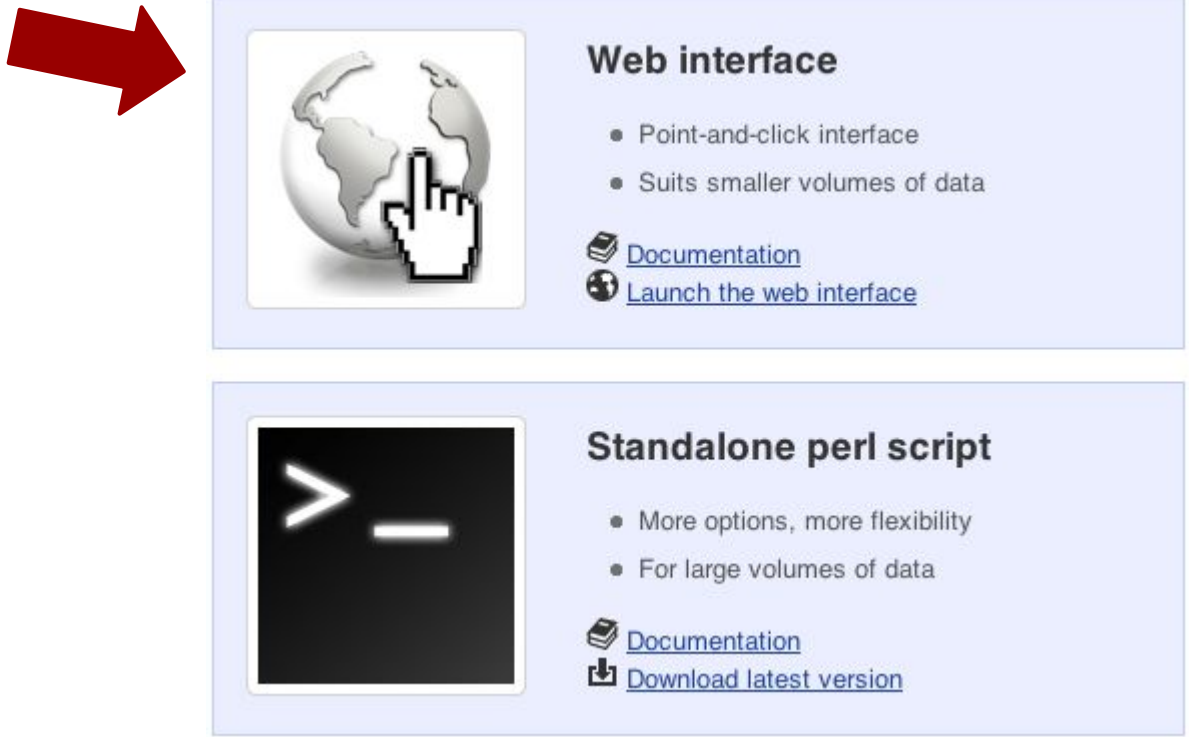
Set up a cache

- Speed up your VEP script with an offline cache.
- Use prebuilt caches for Ensembl species.
- Or make your own from GTF and FASTA files - even for genomes not in Ensembl.

http://www.ensembl.org/info/docs/tools/vep/script/vep_cache.html

Use the VEP

Variant Effect Predictor



http://www.ensembl.org/info/docs/tools/vep/index.html

http://www.ebi.ac.uk/~bmoore/workshops/

VEP plugins

- Plugins add extra functionality to the VEP
- They may extend, filter or manipulate the output of the VEP
- Plugins may make use of external data or code

Hands on

We have identified four variants on human chromosome nine, an A deletion at 128328461, C->A at 128322349, C->G at 128323079 and G->A at 128322917.

We will use the **Ensembl VEP** to determine:

- Whether my variants have already been annotated in Ensembl
- What genes are affected by my variants?
- Do any of my variants affect gene regulation?
  - Demo: coursebook page 29-33

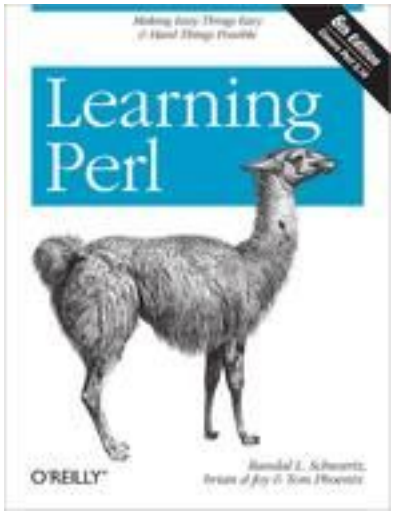
Ensembl data through the Perl API

- Database querying using Perl scripts
- We use object-oriented Perl

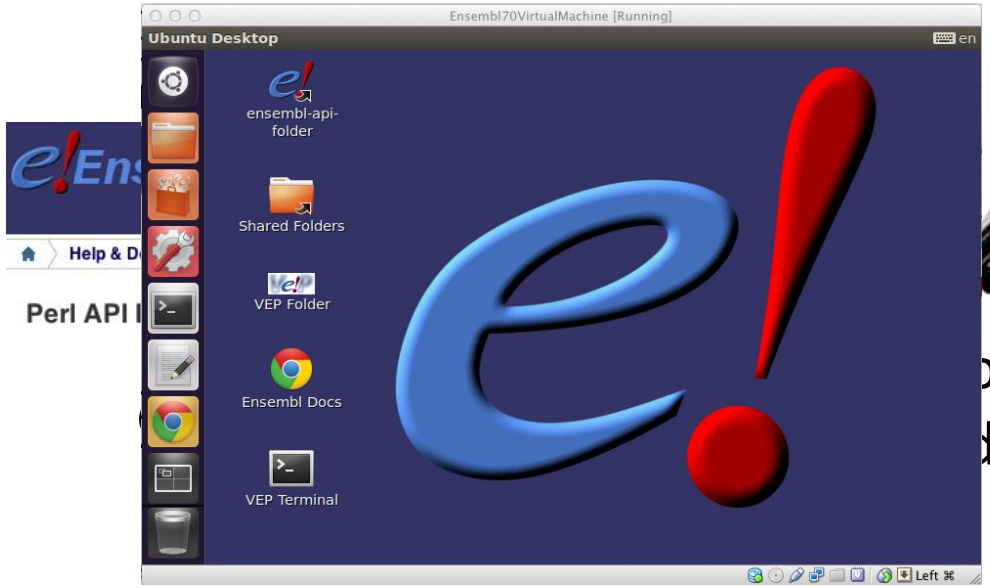

```
my $gene_adaptor = $registry->
    get_adaptor( 'human', 'core', 'gene' );

my $gene = $gene_adaptor->
    fetch_by_display_label( 'brca2' );

print $gene->stable_id, "\n";
```

http://www.ensembl.org/info/data/api.html

Perl API



Learn Perl



oad more
dules)

Get out all possible Ensembl data. Output in any format you like.

```
#!/usr/bin/perl
use strict;
use warnings;
use Bio::EnsEMBL::Registry;

my $registry = "Bio::EnsEMBL::Registry";

$registry->load_registry_from_db(
    -host => 'ensembldb.ensembl.org',
    -user => 'anonymous'
);

my $transcript_adaptor = $registry -> get_adaptor('Mouse', 'Core', 'Transcript');

my @transcripts = @{ $transcript_adaptor->fetch_all };

while (my $transcript = shift @transcripts) {

    my @refseqs = @{ $transcript->get_all_object_xrefs('RefSeq%') };

    if (@refseqs) {
        print $transcript->stable_id;

        while (my $refseq = shift @refseqs) {

            print ", ", $refseq->display_id;

        }

        print "\n";
    }
}
```

Write scripts

Learn Ensembl API

Running the VEP through the Perl API

- I want a script that gets a gene name from the command line and prints its sequence.

- We've already learnt how to use the API and know our way around the documentation
- We need to write a script.

Hands on

We have identified a number of human variants, which are contained in the VCF available at: www.ebi.ac.uk/~bmoore/workshops

We will use the **Standalone Perl script for VEP** to determine:

- What genes are affected by my variants?
- Do any of the variants affect protein structure/function?
  - Demo: coursebook page 34-37

Data access via REST

- We've had a Perl API for a long time …
- … but not everybody works in Perl
- Our RESTful service allows language agnostic access to our data.
- Visit rest.ensembl.org for installation, documentation and examples

What is REST?

- REST allows you to query the database using simple URLs giving output in plain text format

eg `http://rest.ensembl.org/xrefs/symbol/homo_sapiens/BRCA2?content-type=application/json`

gives

`[{"type":"gene","id":"ENSG00000139618"},{"type":"gene","id":"LRG_293"}]`

- This means you can write scripts in any language to construct these URLs and read their output

Hands on

We have identified a single common variant in a cohort of patients with hypertension

Use grch37.rest.ensembl.org for GRCh37

We will use the **REST API** to determine:

- What genes are affected by my variant?
- Does the variant affect protein structure/function?
  - Demo: coursebook page 38-40
  - Exercises: coursebook page 41
    - Answers: answer book page 6-7

Feedback survey

https://www.surveymonkey.co.uk/r/Helsinki2016

Wrap-up

Ensembl is a genome browser which integrates:

- gene annotation
- variation
  - The VEP
- comparative genomics
- regulation

http://www.ebi.ac.uk/bmoore/workshops/

How is all this data organised?

- Ensembl browser sites
  - Main website, *Pre!*, *Archive!*
- BioMart 'DataMining tool'
- Ensembl Database (open source)
  - Perl-API, REST API, MySQL
- FTP download site
  - http://www.ensembl.org/info/data/ftp/index.html

Help and documentation

Course online http://www.ebi.ac.uk/training/online/subjects/11

Tutorials www.ensembl.org/info/website/tutorials

Flash animations

www.youtube.com/user/EnsemblHelpdesk

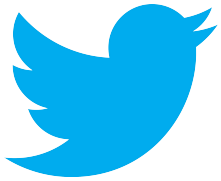
http://u.youku.com/Ensemblhelpdesk

Email us helpdesk@ensembl.org

Ensembl public mailing lists dev@ensembl.org, announce@ensembl.org

Follow us

www.facebook.com/Ensembl.org



@Ensembl

www.ensembl.info

http://www.ebi.ac.uk/bmoore/workshops/

Publications

http://www.ensembl.org/info/about/publications.html

Yates, A. *et al*

Ensembl 2016

Nucleic Acids Research

http://nar.oxfordjournals.org/content/early/2015/12/19/nar.gkv1157.full

McLaren W, Pritchard B, Rios D, Chen Y, Flicek P, Cunningham F

Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor

*BMC Bioinformatics*26(16):2069-70(2010)

http://bioinformatics.oxfordjournals.org/content/26/16/2069

Giulietta M Spudich and Xosé M Fernández-Suárez

Touring Ensembl: A practical guide to genome browsing

BMC Genomics **11**:295 (2010)

www.biomedcentral.com/1471-2164/11/295

Ensembl 2016

http://www.ebi.ac.uk/bmoore/workshops/

Acknowledgements

The Entire Ensembl Team

Andrew Yates[1], Wasiu Akanni[1], M. Ridwan Amode[1], Daniel Barrell[1,2], Konstantinos Billis[1], Denise Carvalho-Silva[1], Carla Cummins[1], Peter Clapham[2], Stephen Fitzgerald[1], Laurent Gil[1], Carlos García Girón[1], Leo Gordon[1], Thibaut Hourlier[1], Sarah E. Hunt[1], Sophie H. Janacek[1], Nathan Johnson[1], Thomas Juettemann[1], Stephen Keenan[1], Ilias Lavidas[1], Fergal J. Martin[1], Thomas Maurel[1], William McLaren[1], Daniel N. Murphy[1], Rishi Nag[1], Michael Nuhn[1], Anne Parker[1], Mateus Patricio[1], Miguel Pignatelli[1], Matthew Rahtz[2], Harpreet Singh Riat[1], Daniel Sheppard[1], Kieron Taylor[1], Anja Thormann[1], Alessandro Vullo[1], Steven P. Wilder[1], Amonida Zadissa[1], Ewan Birney[1], Jennifer Harrow[2], Matthieu Muffato[1], Emily Perry[1], Magali Ruffier[1], Giulietta Spudich[1], Stephen J. Trevanion[1], Fiona Cunningham[1], Bronwen L. Aken[1], Daniel R. Zerbino[1] and Paul Flicek[1,2,*]

[1]European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK and [2]Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge, CB10 1SA, UK

Funding

wellcome trust

National Human Genome Research Institute

CTTV Centre for Therapeutic Target Validation

BLUEPRINT epigenome

EMBL

BBSRC bioscience for the future

BioMedBridges

MedBioinformatics

Co-funded by the European Union

http://www.ebi.ac.uk/bmoore/workshops/

Training materials

- Ensembl training materials are protected by a CC BY license 
- http://creativecommons.org/licenses/by/4.0/
- If you wish to re-use these materials, please credit Ensembl for their creation
- If you use Ensembl for your work, please cite our papers
- http://www.ensembl.org/info/about/publications.html

http://www.ebi.ac.uk/bmoore/workshops/