Centre for
Tropical Livestock
Genetics and Health

Genomic data management

Getinet M. Tarekegn, PhD

ROSLIN SRUC ILRI INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE CGIAR

Who am I?

Centre for Tropical Livestock Genetics and Health

Academic background:

- BSc in Animal Sciences …….Haramaya University
- MSc in Animal Genetics and Breeding ……..Haramaya University
- BSc in Computer Sciences ……Bahir Dar University
- Postgraduate studies in Higher Education……Leeds Met. University, UK
- Visiting researcher in Small Ruminant Genomics …Inner Mongolian Agri.University, China
- PhD in Applied Genetics (Livestock Genomics)…. AAU, 2016
- Post-doc/Visiting researcher in African Goat Genomics … BecA-ILRI, 2016/2017
- Post-doc in Dairy cattle genetics and genomics…….. SLU, Sweden, 2017-2020
- Geneticist and Bioinformatician, Scotland's Rural College (SRUC)… 2022 and onwards

Affiliations:

✓ Geneticist and Bioinformatician, Scotland's Rural College (SRUC),
King's Building, University of Edinburgh, UK

✓ Adjunct Prof of Livestock Genomics and Bioinformatics, Addis Ababa University, Ethiopia

https://scholar.google.com/citations?user=yOA-j4gAAAAJ&hl=en&oi=ao

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Edinburgh Genetic Evaluation Service (EGENES)

Centre for Tropical Livestock Genetics and Health

- EGENES is a leading centre for the development and delivery of genetic improvement tools for the livestock industry.
- The team at EGENES produces national genetic and genomic evaluations for all dairy cattle and sheep and for the UK's biggest beef breeds.
- uses performance and pedigree data recorded by farmers, breeders and other industry players.
- These data are combined, quality controlled and analysed to produce routine genetic evaluations, which are then fed back to industry.

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Centre for Tropical Livestock Genetics and Health

Edinburgh Genetic Evaluation Services

A centre for the development and delivery of genetic improvement tools for our livestock industries.

Focus areas:

- Dairy breeds
- Major Beef breeds
- Five sheep breed
- Carcass evaluation

- 5 Geneticist and 4 programmers

- National evaluations
- Interbull
- Interbeef

- M3GE project

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Outline

- SNP genotypes
- Quality control
- Converting the snps data to different formats
- Plink practicals

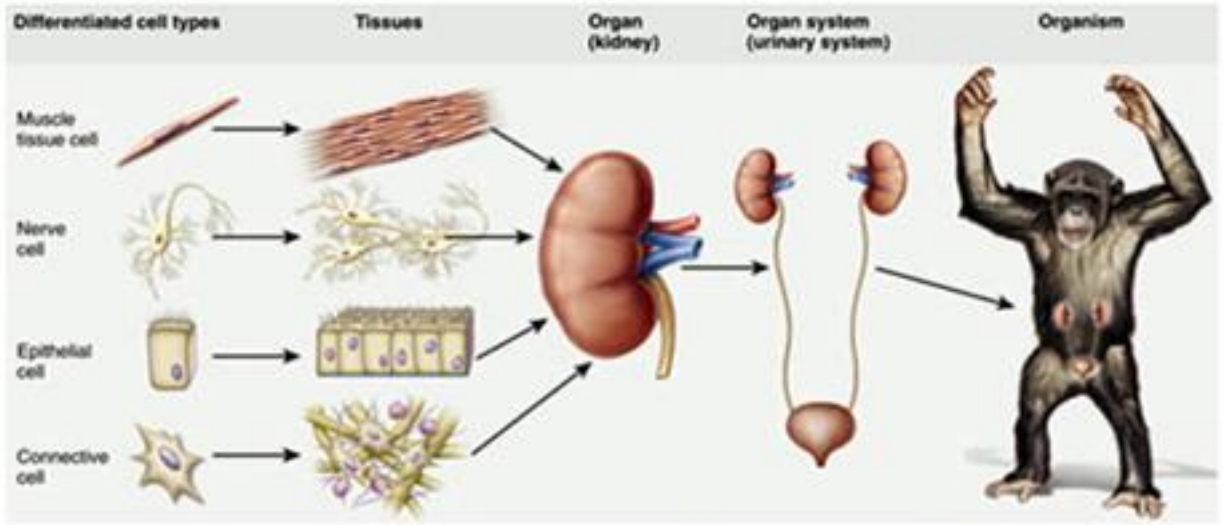
Learning objectives:

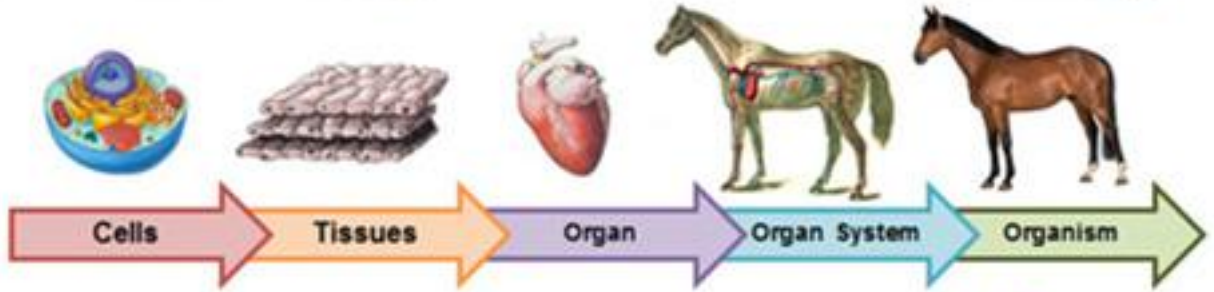
- Understand how to filter genotype data and converting to different formats

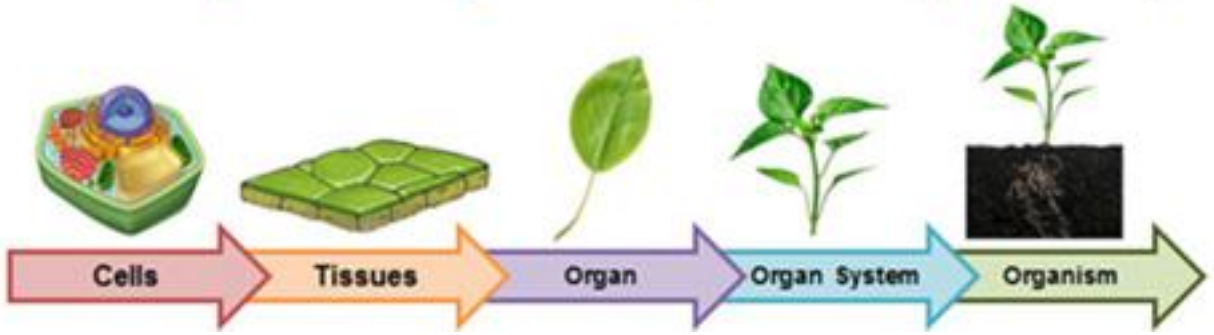
Learning outcome:

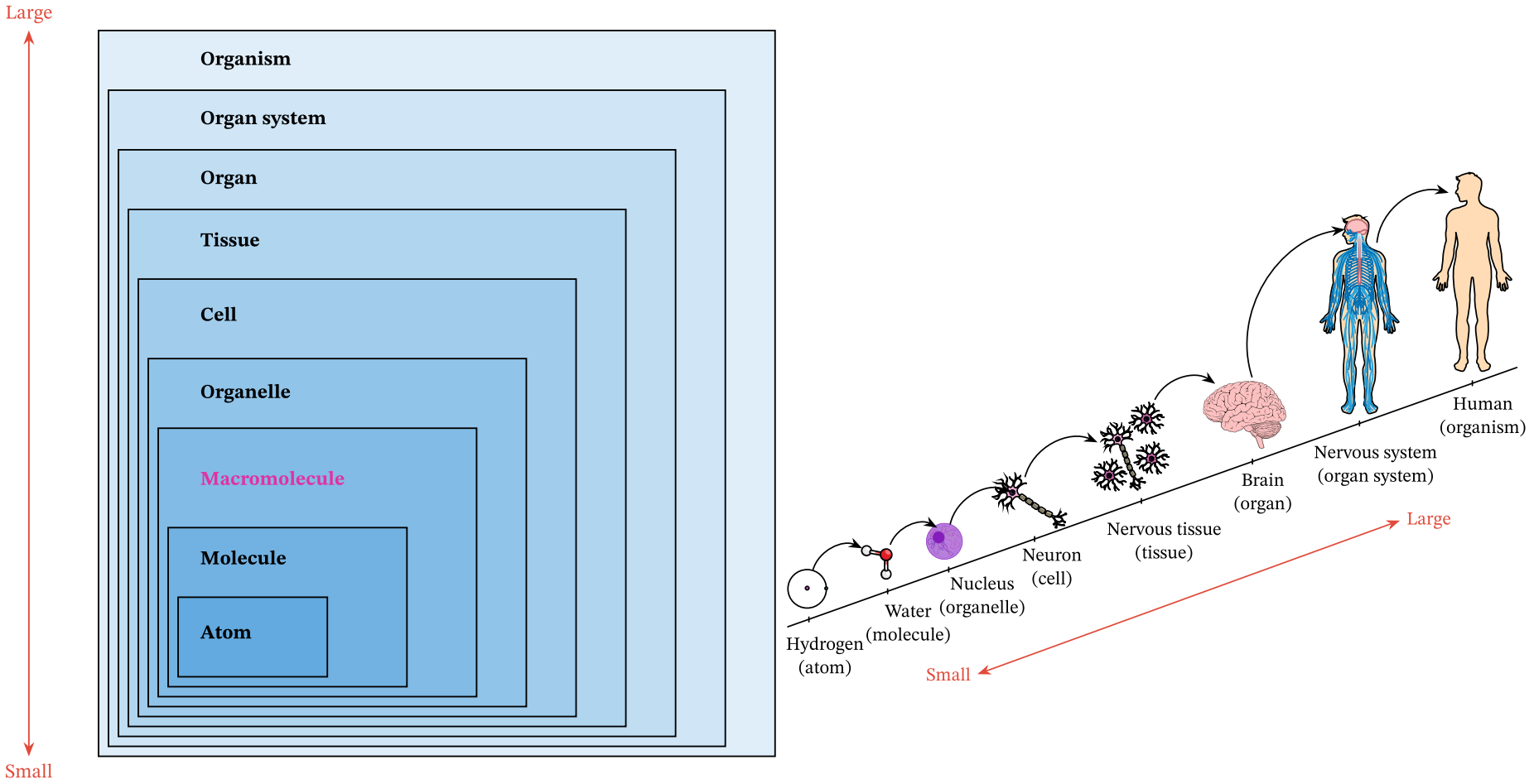
- All trainees are capable of handling genotype data

Biological levels of Organization of living things





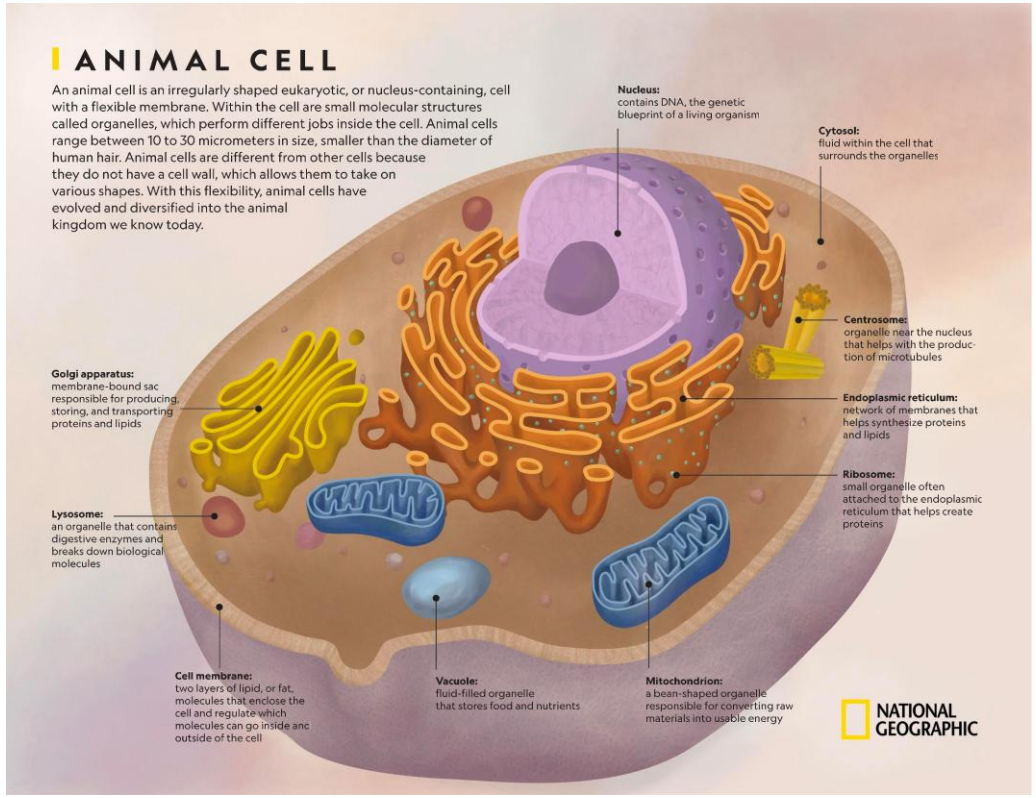


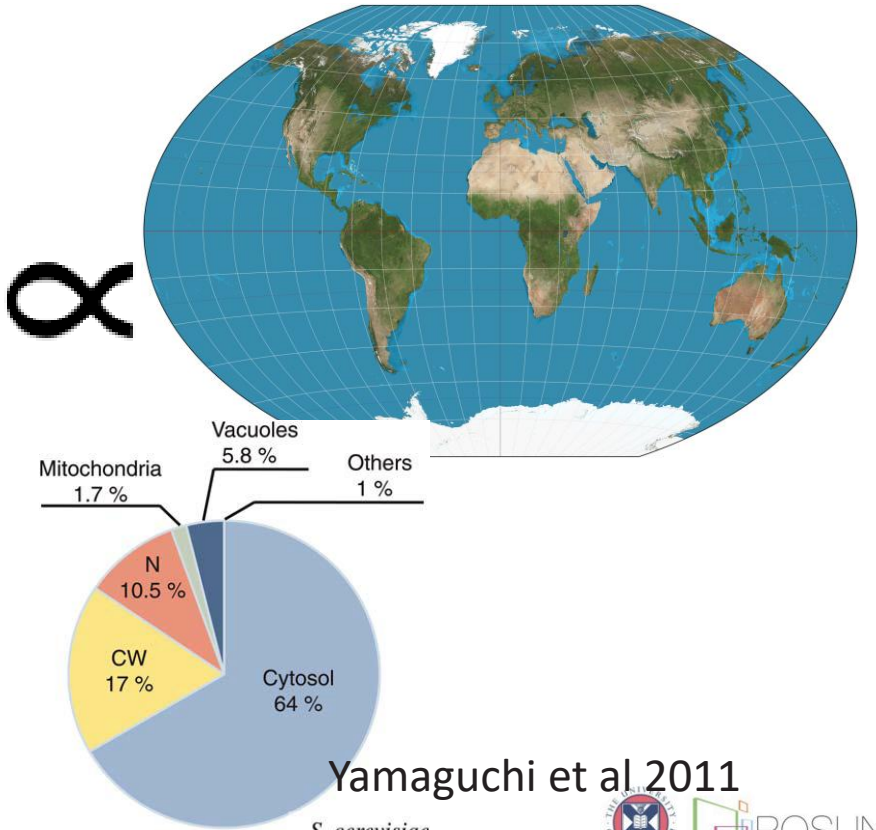


A diagram showing the biological levels of organization from an atom to a multicellular organism https://www.nagwa.com/en/explainers/430187521519/

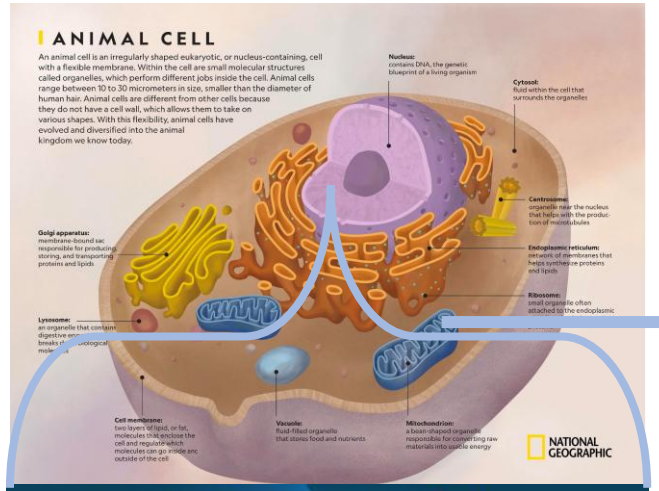
Cell is the smallest unit of life.

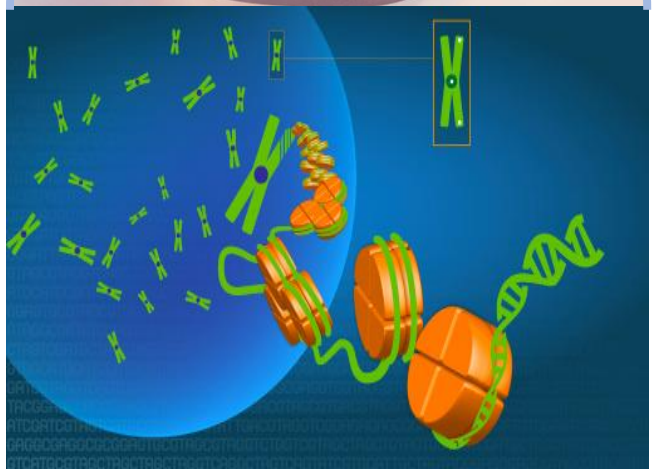
- can divide, multiply, grow and respond to stimuli from the environment; but is it as smallest in size as we expect?

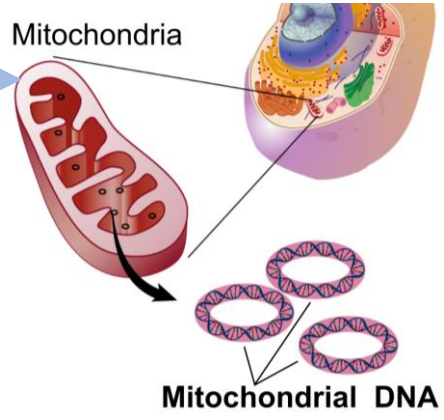


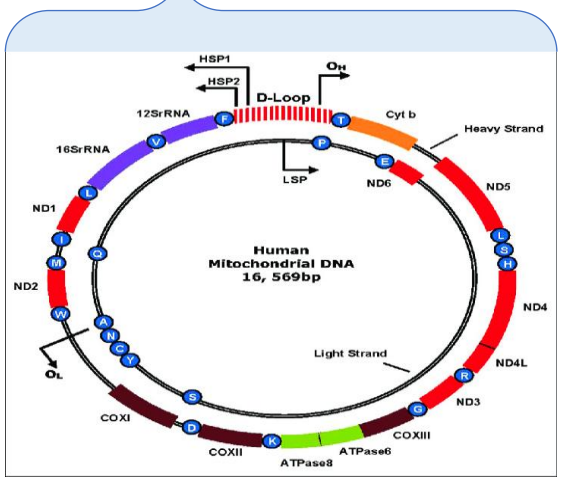


Yamaguchi et al 2011









- 5 cm long (about 2 inches) each chr, and all 46 chrs be about **2 m**

Interesting Facts about DNA

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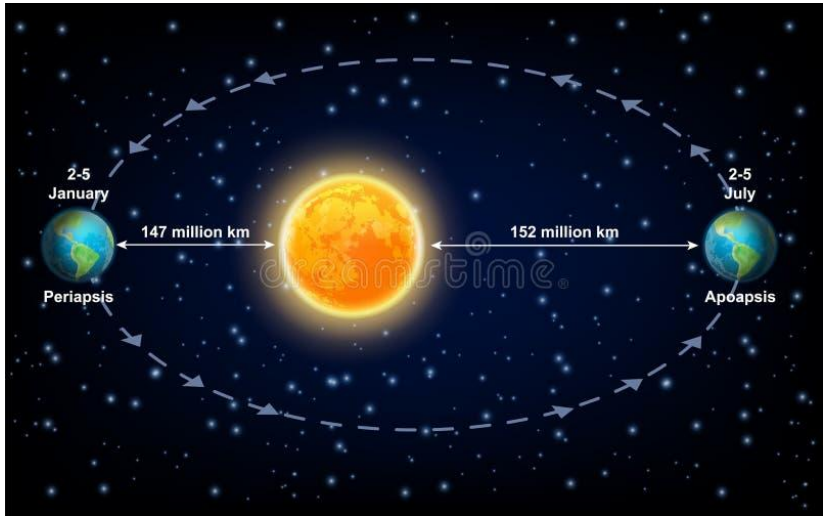
- Your DNA Could Go From Earth to the Sun 600 Times!

  Your DNA is incredibly long - if stretched out, the DNA in your body could reach from the Earth to the Sun and back over 600 times.
- Each human cell contains approximately 6 feet of DNA, which is compacted into a structure called chromatin to fit inside the nucleus.
- If all the DNA in your body was uncoiled, it would stretch 67 billion miles long - equivalent to about 150,000 round trips to the Moon.

https://www.ancestry.com/c/dna-learning-hub/dna-facts#:~:text=1.,stretch%20over%2067%20billion%20miles.

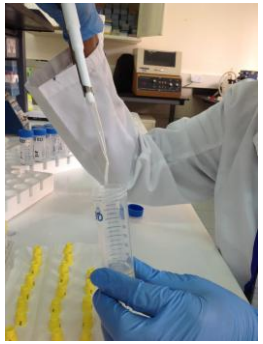


A human cell contains 46 chromosomes:
The human body contains an estimated 37.2 trillion cells, with the number varying by sex and age:

- **Males**: Approximately 36 trillion cells
- **Females**: Approximately 28 trillion cells
- **Children**: Approximately 17 trillion cells
- **Newborns**: Approximately 26 billion cells

… starts at the field

Sampling



Extracting the DNA

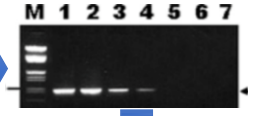
Quality check

WGS

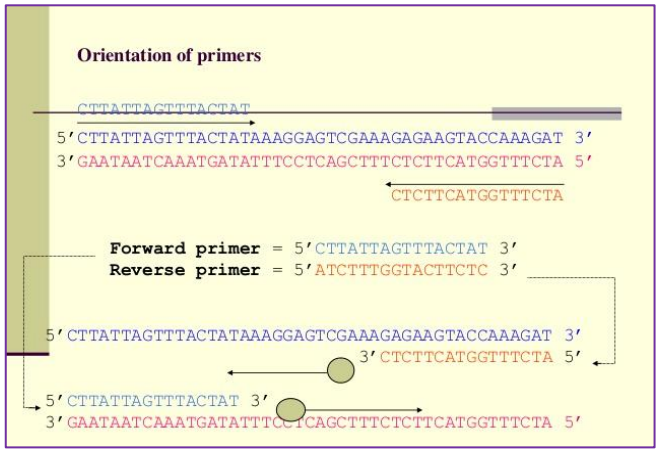
Genotyping

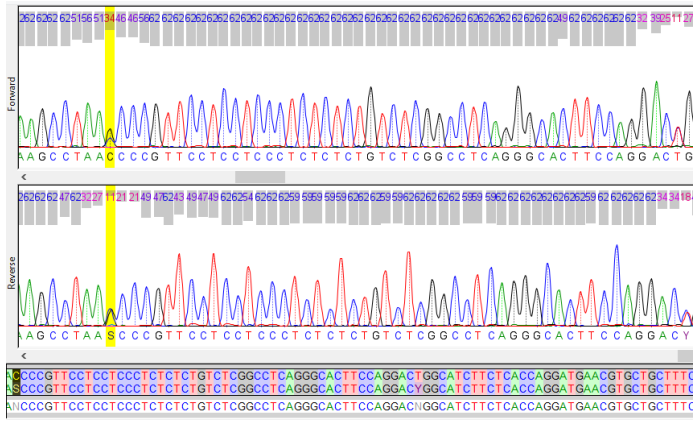
OR

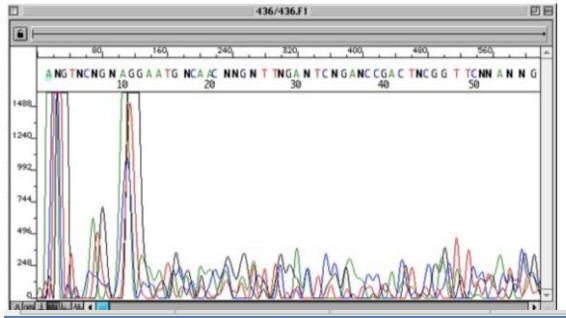
PCR

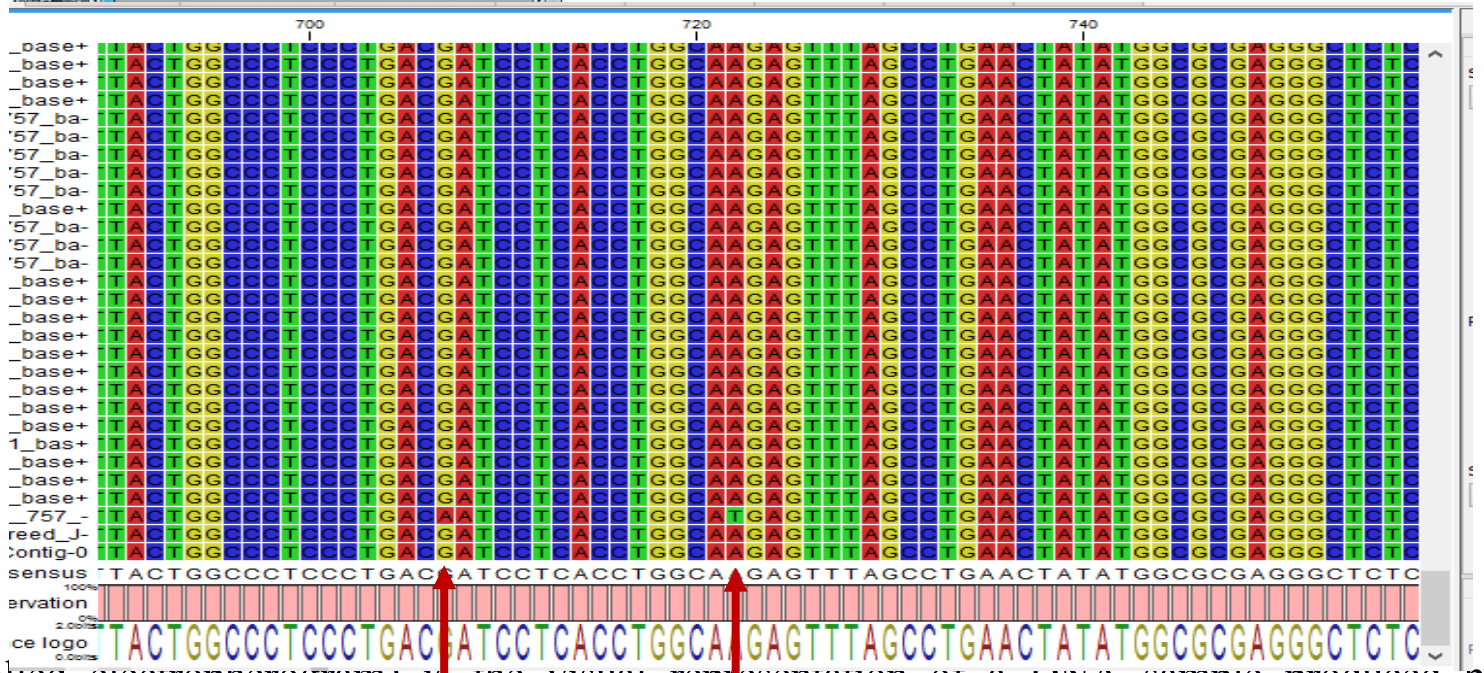


Sanger sequences









- A chromatogram (sometimes also called electropherogram) is the visual representation of a DNA sample produced by a sequencing machine

2 variants

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WGS/NGS data

fastq format

```
@A00291:9:H5N3MDMXX:1:1101:1181:1094 1:N:0:ATGCCTAA
GNTGGCTTTGGGGGTTTTGGAATCGTGATACCAGAGGATGCCTACGAAAGAGTTAAATAC
+
F#FFFF:FFFFF:::FFF::FFFFFFFFFFF:FFFFFFFFFFFF:FFFFFFFFFFFFFFF
```

Each read is represented by four lines. These lines are:

1. A sequence identifier with information about the sequencing run and the cluster.
2. The sequence (the base calls; A, C, T, G and N).
3. A separator, which is simply a plus (+) sign.
4. The base call quality scores.

https://knowledge.illumina.com/software/general/software-general-reference_material-list/000002211

WGS data handling pipeline

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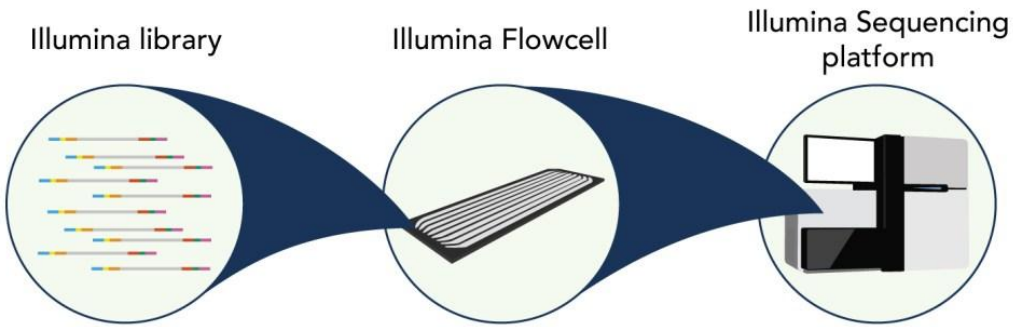
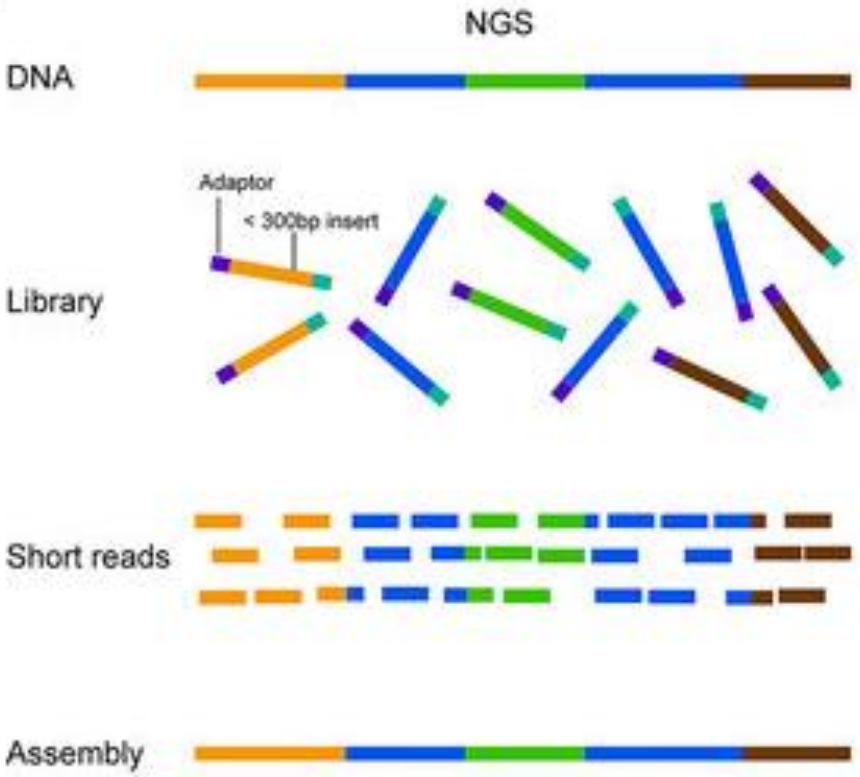
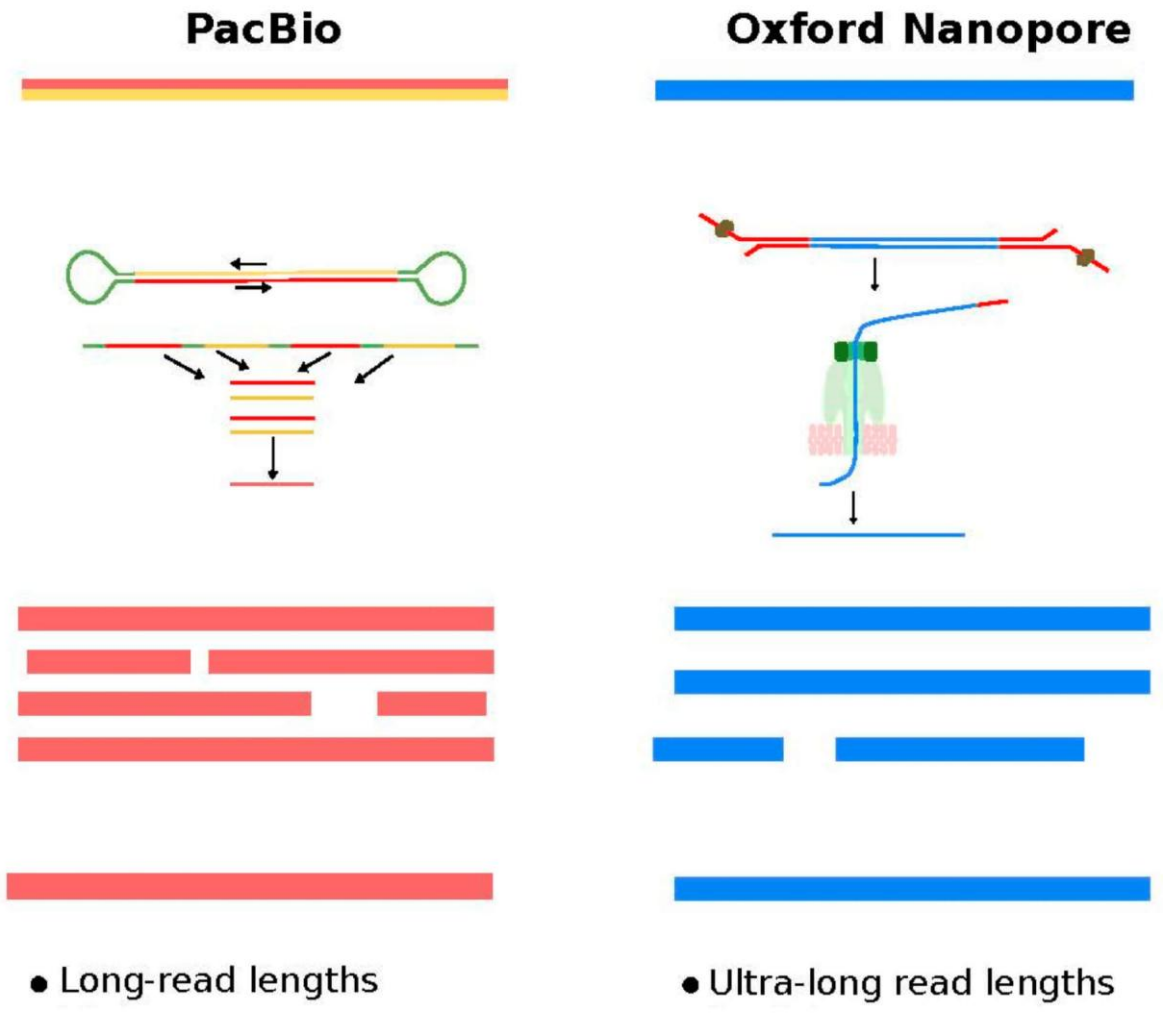




https://www.nature.com/articles/s41597-024-03342-9


PacBio
Oxford Nanopore
• Long-read lengths
• Ultra-long read lengths

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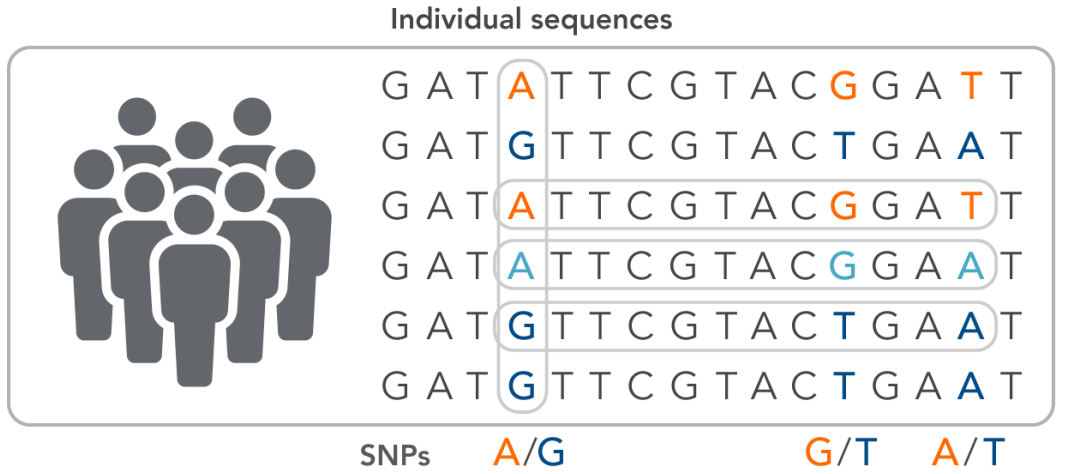
Single-nucleotide polymorphisms (SNP) genotypes

- A single nucleotide polymorphism (SNP) is a variation at a single position in a DNA sequence among individuals.
- SNPs:
  - the most abundant genetic markers
  - have been widely used in **genomic** research
    - disease gene mapping
    - Medical and clinical diagnostics
    - forensic tests
    - genetic diversity
    - GWAS
    - Prediction



https://eu.idtdna.com/pages/education/decoded/article/genotyping-terms-to-know

Are all mutations SNPs?

articles

Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium*

* A partial list of authors appears on the opposite page. Affiliations are listed at the end of the paper.

The human genome holds an extraordinary trove of information about human development, physiology, medicine and evolution. Here we report the results of an international collaboration to produce and make freely available a draft sequence of the human genome. We also present an initial analysis of the data, describing some of the insights that can be gleaned from the sequence.

The rediscovery of Mendel's laws of heredity in the opening weeks of the 20th century[1–3] sparked a scientific quest to understand the nature and content of genetic information that has propelled biology for the last hundred years. The scientific progress made falls naturally into four main phases, corresponding roughly to the four quarters of the century. The first established the cellular basis of heredity: the chromosomes. The second defined the molecular basis of heredity: the DNA double helix. The third unlocked the informational basis of heredity, with the discovery of the biological mechanism by which cells read the information contained in genes and with the invention of the recombinant DNA technologies of cloning and sequencing by which scientists can do the same.

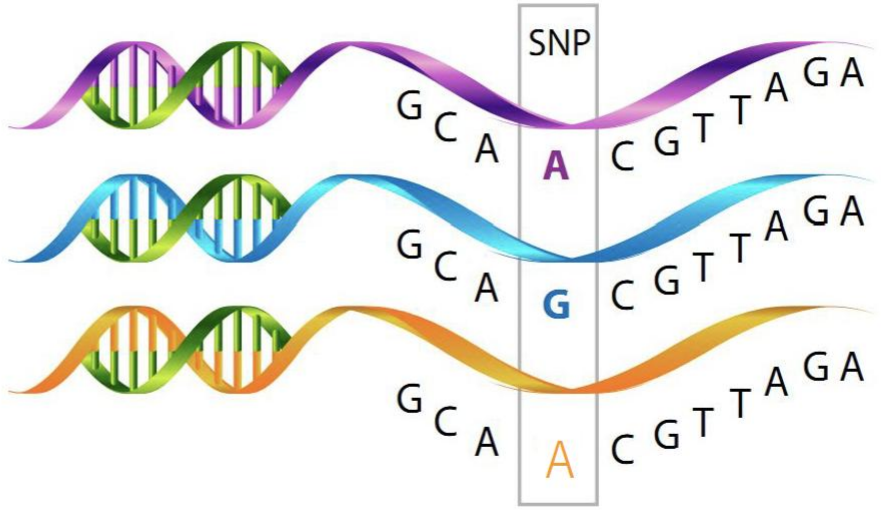
The last quarter of a century has been marked by a relentle to decipher first genes and then entire genomes, spawning t of genomics. The fruits of this work already include the j sequences of 500 viruses and viroids, 205 naturally oc plasmids, 185 organelles, 31 eubacteria, seven archae fungus, two animals and one plant.

Here we report the results of a collaboration involving 20 from the United States, the United Kingdom, Japan, Germany and China to produce a draft sequence of the genome. The draft genome sequence was generated from a p map covering more than 96% of the euchromatic part of the genome and, together with additional sequence in public da it covers about 94% of the human genome. The sequer produced over a relatively short period, with coverage risir about 10% to more than 90% over roughly fifteen mont sequence data have been made available without restricti updated daily throughout the project. The task ahead is to pr finished sequence, by closing all gaps and resolving all ambi Already about one billion bases are in final form and the bringing the vast majority of the sequence to this standard straightforward and should proceed rapidly.

The sequence of the human genome is of interest in respects. It is the largest genome to be extensively sequence being 25 times as large as any previously sequenced genor eight times as large as the sum of all such genomes. It is t vertebrate genome to be extensively sequenced. And, uniqu the genome of our own species.

Much work remains to be done to produce a complete f sequence, but the vast trove of information that has l available through this collaborative effort allows a global per on the human genome. Although the details will change coordinate regulation of the genes in the clusters.

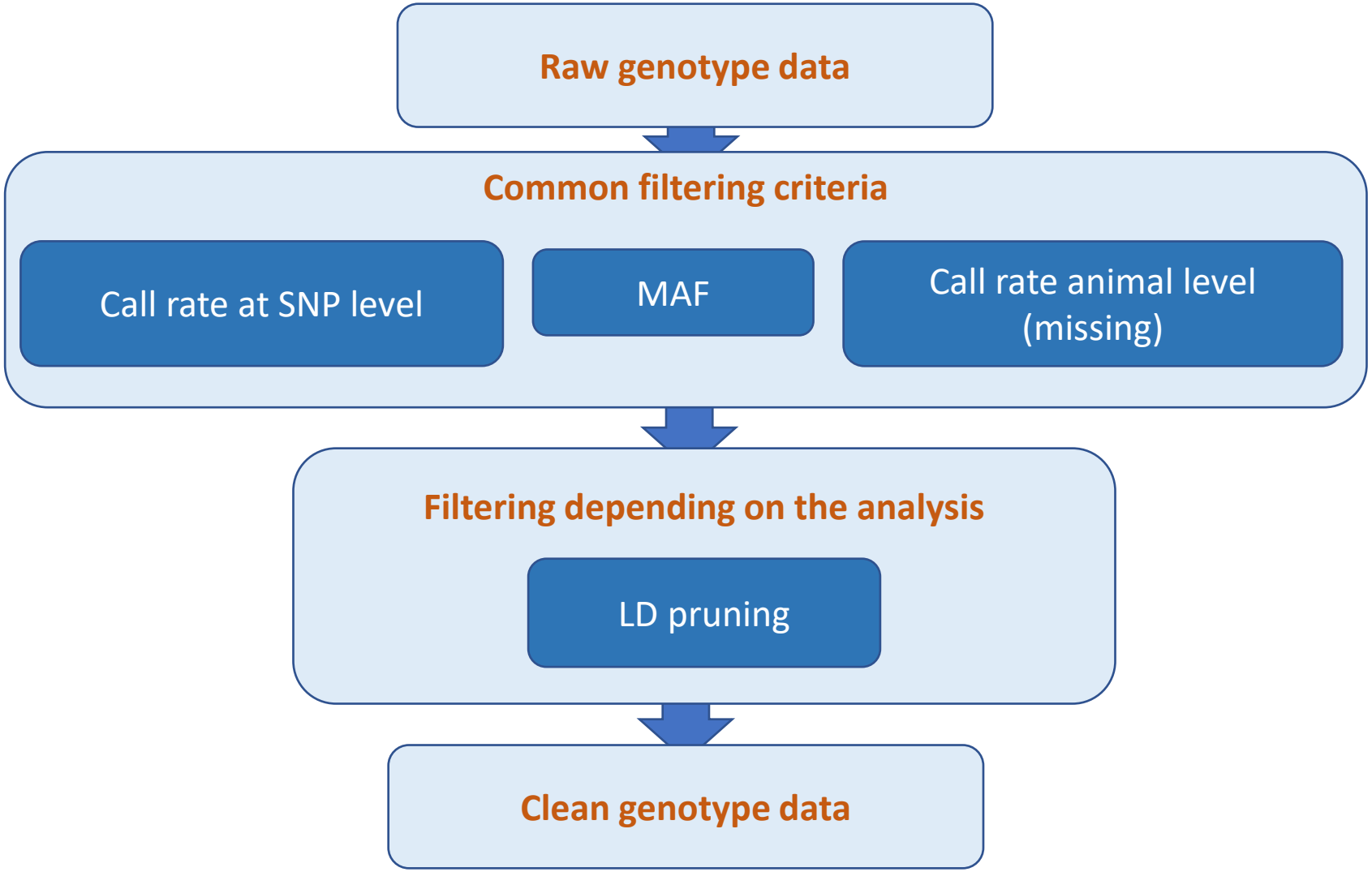
- There appear to be about 30,000–40,000 protein-coding genes in the human genome—only about twice as many as in worm or fly. However, the genes are more complex, with more alternative splicing generating a larger number of protein products.
- The full set of proteins (the 'proteome') encoded by the human genome is more complex than those of invertebrates. This is due in part to the presence of vertebrate-specific protein domains and motifs (an estimated 7% of the total), but more to the fact that vertebrates appear to have arranged pre-existing components into a richer collection of domain architectures.
- Hundreds of human genes appear likely to have resulted from



http://neuroendoimmune.files.wordpress.com/2014/03/snp.png

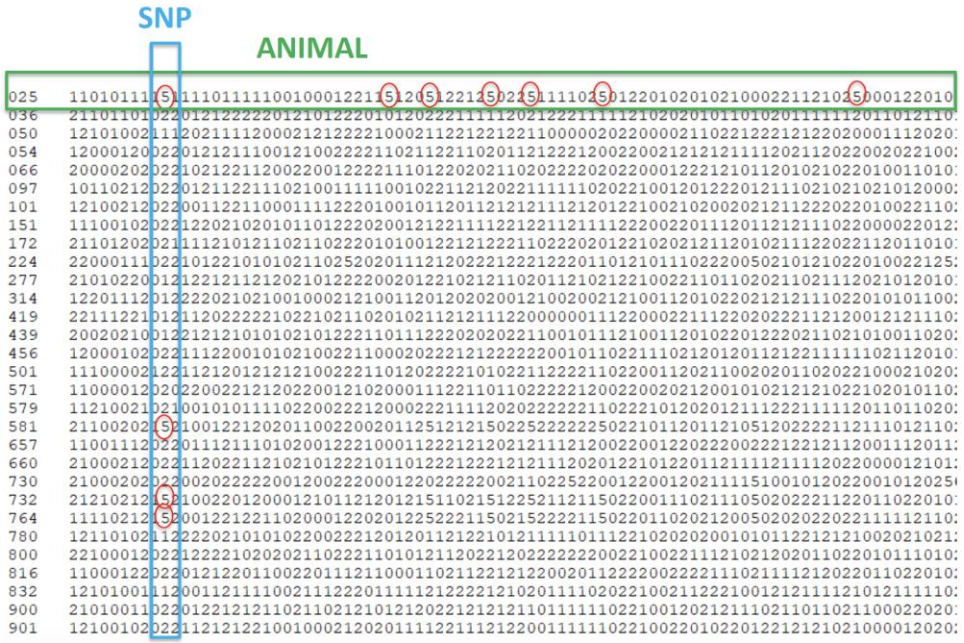
- To say a SNP, the available polymorphism needs to be observed at appreciable frequency (traditionally, at least 1%) in the human population for instance.

Quality control parameters



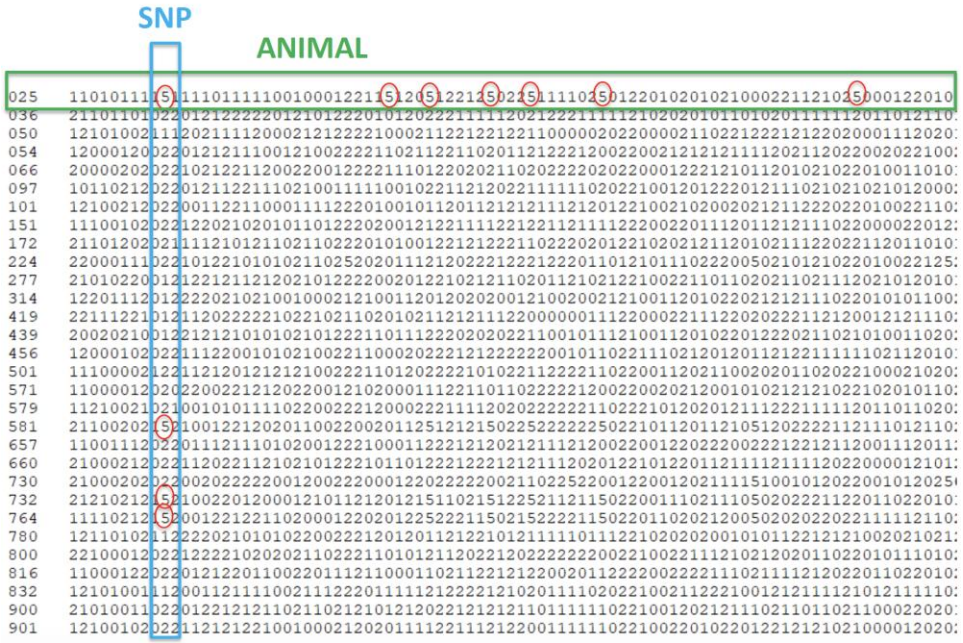
1. **Call rate at SNP level:** the call rate for a given SNP is **the proportion of individuals** in the study for which the corresponding SNP information is not missing.

- E.g. using a call rate of 95%, meaning we retain SNPs for which there is less than 5% missing data.



2. Sample-level filtering (call rate):

- Individuals who have missing genotype data across more than a pre-defined percentage of the typed SNPs need to be excluded.
- This proportion of missingness across SNPs is referred to as the **sample call rate**, and we apply a threshold of 95%.
- That is, individuals who are missing genotype data for more than 5% of the typed SNPs are removed.



3. MAF (SNP-level filtering): A large degree of homogeneity at a given SNP across study participants generally results in inadequate power to infer a statistically significant relationship between the SNP and the trait under study.

- remove SNPs for which the MAF is less than 1%.
  - In some instances, particularly small sample settings, a cut of point 5% is applied.
    - MAF is the lowest of the two allele frequecies
    - $p = freq(A)$
    - $q = 1 - p = freq(B)$
    - $MAF = min(p, q)$
    - A fixed marker ($p = 0$ or $p = 1$) gives no information
    - An almost-fixed marker ($p = 0.0001$ or $p = 0.9999$) gives almost no info

4. LD pruning:

- Linkage disequilibrium (LD) is **the nonrandom association of alleles of different loci (Slatkin, 2008).**
- **LD pruning** is the r**emoving loci based on high levels of pairwise LD**.
- Better results of **population structure** and **Principal Component Analysis (PCA)** are assumed to be obtained if the markers used are not in linkage disequilibrium with each other.
- If any pair of markers within the window are in LD greater than the specified threshold, the first marker in the pair will be pruned.

SNP genotype file format, and how can we manage the data?

Formats of the input file

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Map file

```
0       snp6964-scaffold12561-13292     0       0
0       snp7949-scaffold12878-8765      0       0
0       snp7961-scaffold12886-28972     0       0
0       snp7962-scaffold1289-6273       0       0
0       snp8461-scaffold1305-10877      0       0
0       snp8463-scaffold1305-74425      0       0
0       snp8464-scaffold1305-146599     0       0
0       snp8466-scaffold1306-22563      0       0
0       snp8716-scaffold1310-23370      0       0
0       snp9138-scaffold1331-33874      0       0
0       snp9158-scaffold1333-23917      0       0
0       snp9659-scaffold13458-6636      0       0
0       snp9687-scaffold1348-7500       0       0
1       snp19065-scaffold1917-222828    0       0
1       snp4303-scaffold1134-142270     0       0
1       snp14078-scaffold1560-21647     0       21647
1       snp14079-scaffold1560-51801     0       51801
1       snp14080-scaffold1560-100946    0       100946
1       snp14082-scaffold1560-185575    0       185575
1       snp14083-scaffold1560-228319    0       228319
1       snp14084-scaffold1560-297224    0       297224
1       snp14085-scaffold1560-330454    0       330454
1       snp14086-scaffold1560-378997    0       378997
1       snp14087-scaffold1560-412202    0       412202
1       snp14088-scaffold1560-452762    0       452762
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1       snp14090-scaffold1560-516844    0       516844
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1       snp14092-scaffold1560-614162    0       614162
1       snp14093-scaffold1560-666974    0       666974
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1       snp14099-scaffold1560-920888    0       920888
1       snp14100-scaffold1560-986550    0       986550
1       snp14101-scaffold1560-1032913   0       1032913
1       snp2819-scaffold1082-727669     0       1087568
1       snp2817-scaffold1082-658683     0       1156554
```

ped file

```
AA 1011001 0 0 1 -9 A G C A A G A G G A G A G G G A G G
AB 1011002 0 0 1 -9 A A C A A G G G G G G A G G G A G G
AC 1011003 0 0 1 -9 A A C A A A A G G G G G G A G G G A
AD 1011004 0 0 2 -9 A A C A A A A G G G G A G A G A G G
AA 1011005 0 0 1 -9 A G C C A A A G G G G A G G A A G G
AB 1011006 0 0 2 -9 A G C C A G A G G G G A G G G A G G
AC 1011007 0 0 1 -9 A G C C A A A A G G G G G A G A A A
AD 1011008 0 0 2 -9 A G C A A A A A G G G A G A G A G A
AA 1011009 0 0 2 -9 A A C A A G A G G G G G G G A A G G
AB 1011011 0 0 1 -9 A G A A A A G G G G G A G A G G G A
AC 1011015 0 0 1 -9 A G C A A A A G G A A A G G G A G G
AD 1011016 0 0 1 -9 A G A A A A A G G G A A G A G G G G
AA 1011017 0 0 1 -9 A G A A A A A A A A G A G A G A G G
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AB 1011026 0 0 2 -9 A A C A A G G G G G G A G G G A G A
AC 1011028 0 0 1 -9 A G A A A A A A G G G A G A A A G G
AD 1011029 0 0 2 -9 A A A A A G A G G G G A G A G A G G
AA 1011030 0 0 2 -9 A G C A A G A G G G A A A G A G A G G
AB 1011032 0 0 1 -9 G G A A A G A G G G A A G G G A G G
AC 1011033 0 0 2 -9 G G C A A G A G G G A A G A G A G G
AD 1011035 0 0 1 -9 A G C A A A A G G G G A G A G G G A
AA 1011036 0 0 1 -9 A G C C A G G G G A G A G A G A G A
AB 1011037 0 0 1 -9 A G C C G G G G G G A A G A G A A A
AC 1011038 0 0 1 -9 A G A A A G A G G G G G G A A A G G
AD 1011039 0 0 2 -9 A A A A A G A G G G G A A G G G A G
```
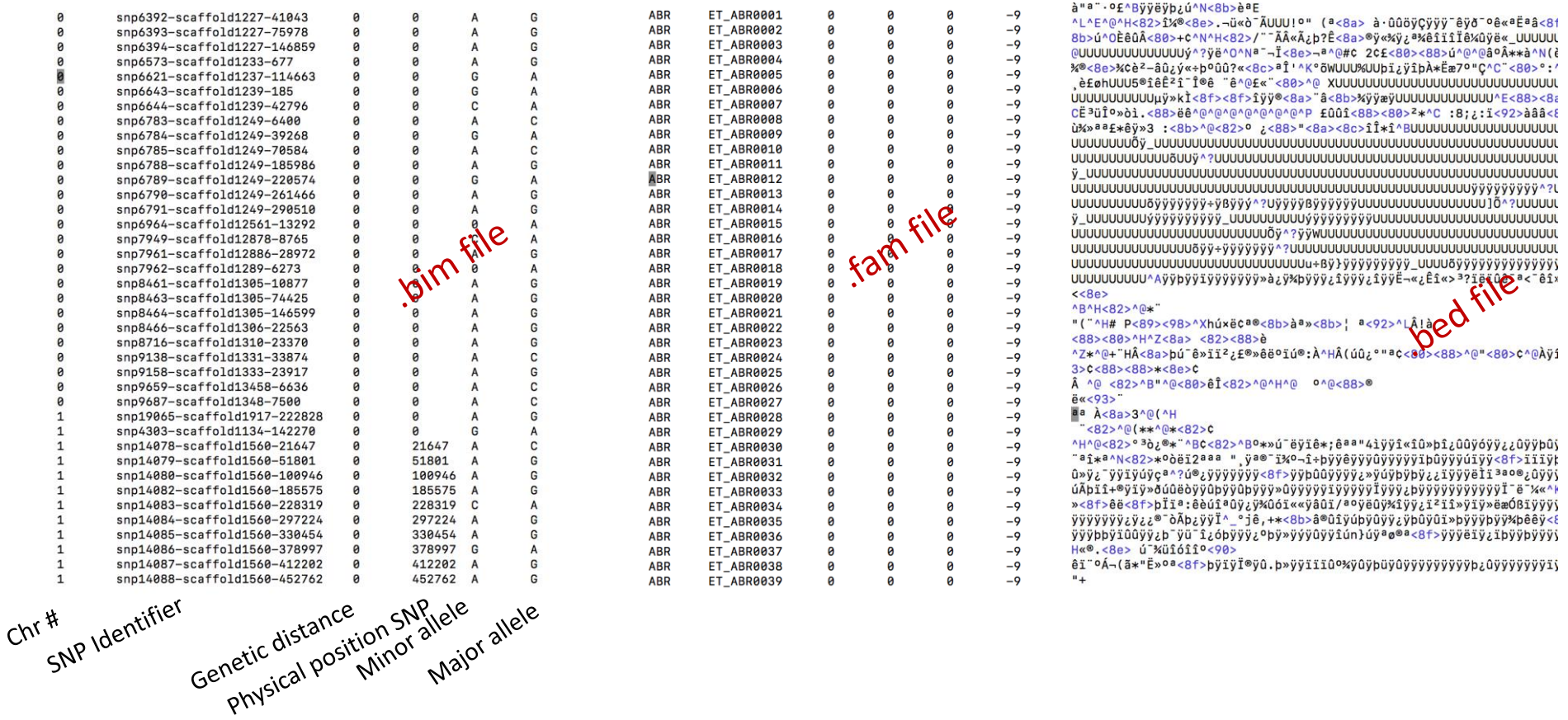

Formats of the input file … Cont'd

.bim, .fam and *.bed* file formats



- Major allele: the most common allele for a given SNP
- Minor allele: the least common (or rarer) allele

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File formats for GBLUP analysis

SNP data file

```
UGA42014    2100212121111121110010011112110200121022001212010110112111102112112101011011010 2
UGA42019    2010112021121120101111120121000110121112100212020211021211212111122202100001101 02
UGA42029    1011102011211110100001121121100101111022001211111210011121201212111201101110210 01
UGA42039    1000201012210220101011120011010201111021110112021111121211211221012111101111211 11
UGA42047    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42051    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42052    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42056    1021011100212100210001111221200111011011001210211200001111110202101210211110121 10
UGA42057    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42061    1000201012210220101011120011010201111021110112021111121211211221012111101111211 11
UGA42085    1010112011210221010100021122011111121122101212011211112211202212022102010011200 12
UGA42088    0011101001201110201012221110110102002021111101112101110112210211101110202221221 10
UGA42094    0112111011111101100002212221210101112121102100112101110022110111210200102111211 01
UGA42095    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42098    1000201012210220101011120011010201111021110112021111121211211221012111101111211 11
UGA42101    0121012010111101200102121210200112112111011110112110000112200112100201201110111 10
UGA42108    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42109    1011102011211110100001121121100101111022001211111210011121201212111201101110210 01
UGA42127    2000202022220220000000020022000200220022000222020220022222022022202222022000000200 02
UGA42136    1000201012210220101011120011010201111021110112021111121211211221012111101111211 11
UGA42137    1021011100212100210001111221200111011011001210211200001111110202101210211110121 10
UGA42138    0121012010111101200102121210200112112111011110112110000112200112100201201110111 10
UGA42139    1000201012210220101011120011010201111021110112021111121211211221012111101111211 11
```

Map file

Index	Name	Chromosome	Position	GenTrain Score	SNP	ILMN Strand	Customer Strand	NormID
1	ARS-BFGL-BAC-10172	14	6371334	0.9176	[A/G]	TOP	TOP	2
2	ARS-BFGL-BAC-1020	14	7928189	0.9413	[T/C]	BOT	TOP	2
3	ARS-BFGL-BAC-10245	14	31819743	0.7646	[T/C]	BOT	BOT	2
4	ARS-BFGL-BAC-10345	14	6133529	0.8906	[A/C]	TOP	TOP	2
5	ARS-BFGL-BAC-10365	14	27005721	0.9206	[A/C]	TOP	BOT	1
6	ARS-BFGL-BAC-10375	14	6616434	0.9258	[A/G]	TOP	TOP	2
7	ARS-BFGL-BAC-10591	14	17544926	0.7439	[A/G]	TOP	TOP	1
8	ARS-BFGL-BAC-10867	14	34639444	0.9085	[G/C]	BOT	BOT	101
9	ARS-BFGL-BAC-10919	14	31267746	0.8255	[A/G]	TOP	TOP	2
10	ARS-BFGL-BAC-10951	10	17911906	0.9056	[T/G]	BOT	BOT	2
11	ARS-BFGL-BAC-10952	10	18882288	0.9184	[A/G]	TOP	TOP	2
12	ARS-BFGL-BAC-10960	10	20609250	0.5678	[A/G]	TOP	TOP	2
13	ARS-BFGL-BAC-10972	10	20792754	0.8432	[G/C]	BOT	BOT	102
14	ARS-BFGL-BAC-10975	10	21225382	0.7991	[A/G]	TOP	TOP	2
15	ARS-BFGL-BAC-10986	10	26527257	0.8941	[A/C]	TOP	BOT	2
16	ARS-BFGL-BAC-10993	10	78512500	0.8649	[A/G]	TOP	BOT	2
17	ARS-BFGL-BAC-11000	10	79252023	0.9433	[T/G]	BOT	BOT	2
18	ARS-BFGL-BAC-11003	10	80410977	0.8842	[T/C]	BOT	BOT	2
19	ARS-BFGL-BAC-11007	10	80783719	0.9110	[T/C]	BOT	BOT	2
20	ARS-BFGL-BAC-11025	10	84516867	0.8711	[T/G]	BOT	BOT	2

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Quality control QC using plink in R

The following script helps to evaluate the QC in plink.

- Download plink from: https://www.cog-genomics.org/plink/
- put plink (only the executable file) at your working directory

Quality Control exercise

```
####conver the data from .ped to .bed format
system("./plink --file Sheep05_724 --make-bed --chr-set 26 --out Sheep05_724")
#missing at SNP level
system("./plink --bfile Sheep05_724 --chr-set 26 --make-bed --geno 0.01 --out Sheep05_afterQC")
#minor allele frequency
system("./plink --bfile Sheep05_724 --chr-set 26 --make-bed --geno 0.10 --maf 0.10 --out Sheep05_afterQC")
#missing at animal level
system("./plink --bfile Sheep05_724 --chr-set 26 --make-bed --geno 0.10 --maf 0.10 --mind 0.05 --out
Sheep05_afterQC
```

ld-pruning

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LD-pruning:

```
system("./plink --bfile Sheep05_afterQC --chr-set 26 --indep-pairwise 50 10 0.5 ")
system("./plink --bfile Sheep05_afterQC --extract plink.prune.in --make-bed --chr-set 26 --out Sheep05_afterQC_pruned")
#To generate the PCA:
system("./plink --bfile Sheep05_afterQC_pruned --chr-set 26 --pca --outSheep05_afterQC_pruned_pca ")
#to generate structure format
system("./plink --bfile Sheep05_afterQC_pruned --recode-structure --chr-set 26 –out Sheep05_afterQC_pruned_structure")
```

Note: For the admixture, you can still use the .bed format

Tips

```
#To generate other population genetics parameters:
#To generate the MAF from bed file:
system("./plink --bfile Sheep05_afterQC --chr-set 26 --freq --out Sheep05_afterQC_maf")
# To generated expected and observed heterozygosity, and hwe:
system("./plink --bfile Sheep05_afterQC --hardy --chr-set 26 --out Sheep05_afterQC_het")
#To generate coefficient of inbreeding:
system("./plink --bfile Sheep05_afterQC --chr-set 26 --het --out Sheep05_afterQC_Fx")
```

Why checking the PCA is important before proceeding to genomic evaluation?

- It helps to know the structure of the target population so that it gives idea whether we need to implement stratification in the model we will be fitting
- It also helps to provide feedback to the farmers about the structure of the animals they own

PCA

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```
install.packages("tidyverse")
library(tidyverse)
# read in result files
eigenValues <- read_delim("PATH/Sheep05_afterQC_pruned_pca.eigenval", delim = " ", col_names = F)
eigenVectors <- read_delim("PATH/Sheep05_afterQC_pruned_pca.eigenvec", delim = " ", col_names = F)
eigenVectors
eigenValues
## Proportion of variation captured by each vector
eigen_percent <- round((eigenValues / (sum(eigenValues))*100), 2)
# PCA plot
ggplot(data = eigenVectors) +
geom_point(mapping = aes(x = X3, y = X4, color = X1, shape = X1), size = 1, show.legend = F ) +
geom_hline(yintercept = 0, linetype="dotted") +
geom_vline(xintercept = 0, linetype="dotted") +
labs(title = "PCA",
x = paste0("Principal component 1 (",eigen_percent[1,1]," %)"),
y = paste0("Principal component 2 (",eigen_percent[2,1]," %)"),
colour = "Breed:", shape = "Breed:") +
theme_minimal()
```

PCA plot generated from the example data (*blackface*)

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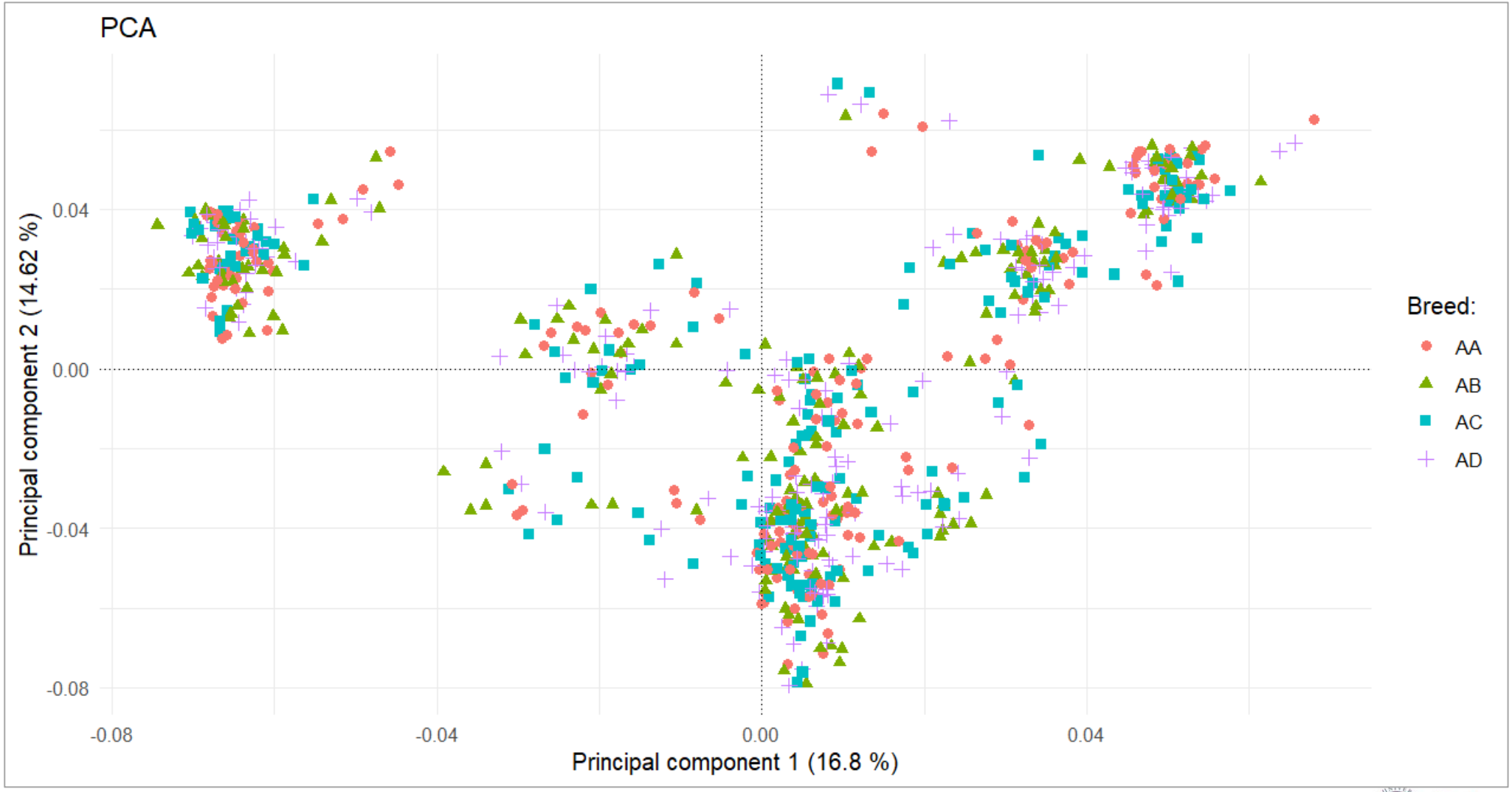

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Admixture package

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Why admixture is preferred?

(*AlexanderandLange.,2012.EnhancementstotheADMIXTUREalgorithmforindividualancestryestimation.Read*)

- *Helps to generate the breed proportion of* **large dataset**
- ADMIXTURE estimates in dividual ancestries by efficiently computing maximum likelihood estimates in a parametric model.
    1. **ADMIXTURE** can be used to estimate the number of underlying populations through **cross-validation.**
    2. Individuals of known ancestry can be exploited in supervised learning to yield more precise ancestry estimates.
    3. By penalizing small admixture coefficients for each individual, one can encourage model parsimony, often yielding more interpretable results for small data sets or data sets with large numbers of ancestral populations.
    4. By exploiting multiple processors, large data sets can be analyzed even more rapidly.

Running admixture

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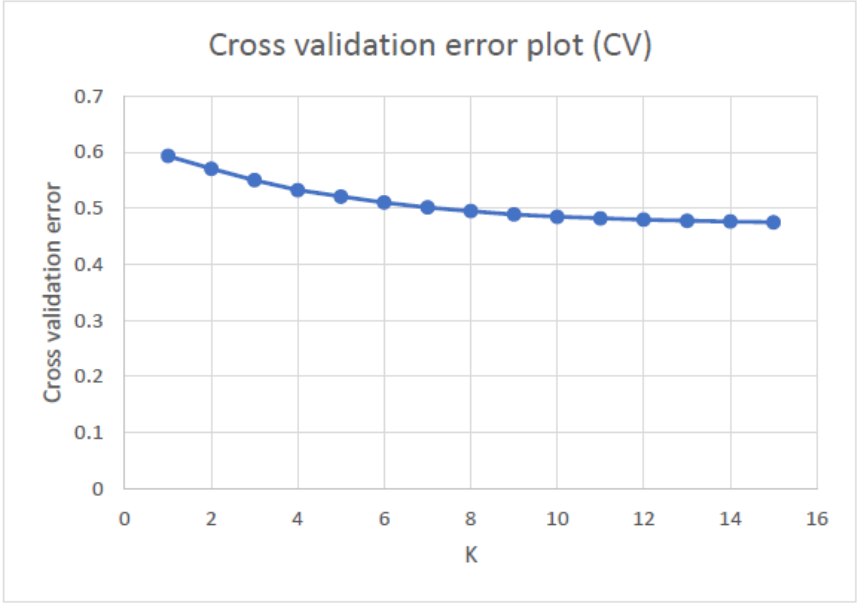
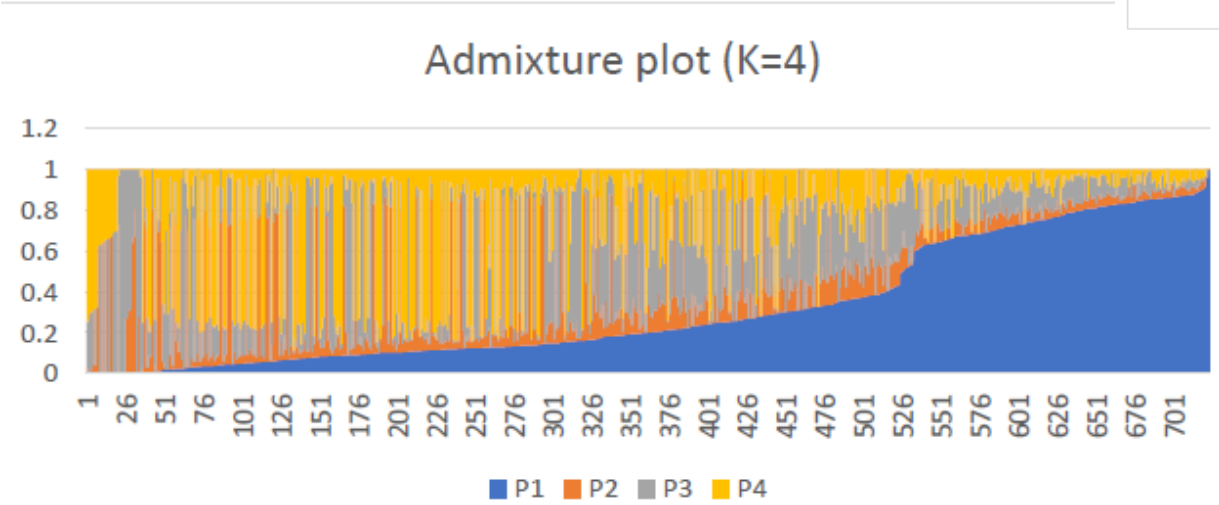
- **Generating the input file:**
- ADMIXTURE requires unlinked (i.e.LD-pruned) SNPs in plink format.
- It is very easy to generate the input file from a VCF containing such SNPs.
- Plink helps to generate the .bed file which can be read by ADMIXTURE
- Thedefaultcross-validation5-foldCV(you can change as the K value you expect to be) and starts as K=2.
- **ADMIXTURE produced 2 files:**. *Q* which contains cluster assignments for each individual and. *P* which contains for each SNP the population allele frequencies.
- The default cross-validation 5-fold CV (you can change as the K-value you expect to be) and starts as K = 2.
- Grep the results to access the CV error log Files as: grep 'CV error' log_*

- **Running population admixture in using admixture package**

```
bed=/PATH/shp724afterQCFinal.bed
mkdir -p / PATH /newFolder
out=/ PATH / newFolder
cd / PATH / newFolder
for k in $(echo {1..15..1});
do echo ${k};
../admixture --cv=10 ${bed} ${k} > ${out}/log_${k}.txt;
done
grep 'CV error' log_*
```





Formatting the genotype data for GWAS

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- # pick chromosomes of interest for GWAS:
- ./plink --file Sheep05_724 --recode --chr 1-26 --out Sheep05_afterQC
- #converting from Allele form to numeric for blupf90 package
- ./plink --bfile Sheep05_afterQC --chr-set 26 --recode A --out shp_blupf90
- # removing first line or header
- cat shp_blupf90.raw | sed 1d > snpblup.txt
- #rmoving column
- awk '{$1=$3=$4=$5=$6="";print $0}' snpblup.txt > snpblup1.txt
- #removing space from column
- awk '{s=$1;gsub($1 FS,x);$1=$1;print s FS $0}' OFS= snpblup1.txt > snpblup2.txt
  - OR use this command: sed -i "s/ //g“ snpblup1.txt
- #adding and removing space between column 1 and 2
- awk '{print ""$1" "$2 }’ snpblup2.txt >snpblupclean3.txt
- #slecting map file
- awk '{print ""$2" "$1" "$4 }' shp724afterQCFinal.map > gwasmapxxx.txt

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CTLGH Funders

Bill & Melinda Gates foundation

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UKRI Biotechnology and Biological Sciences Research Council

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