

test

January 24, 2025

```
[2]: setwd('../data/TP_DATA_PROG/')
```

1 I. Study of a monogenic disease: Clouston's disease

1.1 a: Genetic linkage analysis - lodscore method

1.1.1 a.1. Install the paramlink package and call the library

```
[3]: install.packages('paramlink')  
library(paramlink)
```

Updating HTML index of packages in '.Library'

Making 'packages.html' ...
done

PLEASE NOTE:

Paramlink has been superseded by the `ped suite` packages

(<https://magnusdv.github.io/pedsuite/>).

It is maintained for legacy purposes only, and should not be used in new projects.

1.1.2 a.2. Read and view the data file

```
[ ]: cols<-c('Family_number','Individual_number','Father_number','Mother_number',  
  ↪ 'Sex',  
  ↪ 'Disease_status','marker1_1','marker1_2','marker2_1','marker2_2','marker3_1','marker3_2','m  
  
fam<-read.table('I.a.Paramlink/fam.txt')  
colnames(fam)<-cols  
fam[1:5,1:10]
```

		Family_number <int>	Individual_number <int>	Father_number <int>	Mother_number <int>	Sex <int>
A data.frame: 5 × 10	1	1	1	0	0	1
	2	1	2	0	0	2
	3	1	21	0	0	2
	4	1	5	1	2	1
	5	1	4	1	2	1

Q1: genotype of the first marker of the individual of id 5

```
[ ]: for (row in 1:nrow(fam)){
      if (fam[row,'Individual_number']==5){
        cat(fam[row,]$marker1_1,fam[row,]$marker1_2)
      }
    }
```

9 1

The genotype of the individual 5 is 9/1

1.1.3 a.3. Data transformation for linkage analysis and descriptive statistics

```
[ ]: x=linkdat(fam)
```

Family ID: 1.
47 individuals.
22 affected, 25 non-affected.
10 nuclear subfamilies.
13 markers.

Q2:

```
[7]: ## count the number of families in family number of fam
fam$Family_number
```

1. 1 2. 1 3. 1 4. 1 5. 1 6. 1 7. 1 8. 1 9. 1 10. 1 11. 1 12. 1 13. 1 14. 1 15. 1 16. 1 17. 1 18. 1 19. 1
20. 1 21. 1 22. 1 23. 1 24. 1 25. 1 26. 1 27. 1 28. 1 29. 1 30. 1 31. 1 32. 1 33. 1 34. 1 35. 1 36. 1 37. 1
38. 1 39. 1 40. 1 41. 1 42. 1 43. 1 44. 1 45. 1 46. 1 47. 1

There is 1 family in the dataset

```
[ ]: affected_indiv<-c()
      unaffected_indiv<-c()

      for (i in 1:nrow(fam)){
        if (fam[i,'Disease_status']==1){
          affected_indiv<-c(affected_indiv,fam[i,'Individual_number'])
        } else {
          unaffected_indiv<-c(unaffected_indiv,fam[i,'Individual_number'])
        }
      }
```

```

    }
}

paste0('affected indiv:',length(affected_indiv))
paste0('unaffected indiv:',length(unaffected_indiv))

```

'affected indiv:25'

'unaffected indiv:22'

There is:

- 25 affected
- 22 unaffected

13 markers are analyzed

Q3:

[]: x

	ID	FID	MID	SEX	AFF	V1	V2	V3	V4	V5
1	1	0	0	1	2	-/-	-/-	-/-	-/-	-/-
2	2	0	0	2	1	-/-	-/-	-/-	-/-	-/-
3	21	0	0	2	1	-/-	-/-	-/-	-/-	-/-
4	5	1	2	1	2	9/1	5/10	4/2	2/3	3/2
5	4	1	2	1	1	-/-	-/-	-/-	-/-	-/-
6	3	1	2	1	2	-/-	-/-	-/-	-/-	-/-
7	6	0	0	2	1	-/-	-/-	-/-	-/-	-/-
8	36	0	0	2	1	3/9	6/8	4/4	6/5	1/2
9	26	5	21	1	2	9/2	5/6	4/2	2/3	3/2
10	25	5	21	2	1	1/2	10/6	2/2	3/3	2/2
11	23	5	21	2	2	9/2	5/5	4/4	2/4	3/3
12	30	0	0	1	1	-/-	-/-	-/-	-/-	-/-
13	22	5	21	2	2	9/2	5/5	4/4	2/4	3/3
14	27	0	0	1	1	1/1	2/9	3/4	3/4	3/3
15	24	5	21	2	2	9/2	5/6	4/2	2/3	3/2
16	32	0	0	1	1	2/2	9/3	4/4	2/5	3/4
17	44	26	36	2	2	9/3	5/6	4/4	2/6	3/1
18	43	26	36	2	2	9/9	5/8	4/4	2/5	3/2
19	42	26	36	2	1	-/-	-/-	-/-	-/-	-/-
20	41	26	36	1	2	9/9	5/8	4/4	2/5	3/2
21	40	26	36	2	1	3/2	6/6	4/2	6/3	1/2
22	39	26	36	1	1	3/2	6/6	4/2	6/3	1/2
23	38	26	36	1	2	9/3	5/6	4/4	2/6	3/1
24	37	26	36	2	1	3/2	6/6	4/2	6/3	1/2
25	31	30	23	1	1	2/9	5/9	4/4	4/3	3/3
26	29	27	22	1	1	1/2	9/5	4/4	4/4	3/3
27	28	27	22	2	2	9/1	5/2	4/3	2/3	3/3

28	35	32	24	1	2	9/2	5/3	4/4	2/5	3/4
29	34	32	24	1	2	9/2	5/9	4/4	2/2	3/3
30	33	32	24	2	2	9/2	5/3	4/4	2/5	3/4
31	14	0	0	1	1	1/2	3/10	4/4	4/4	3/3
32	7	3	6	2	2	9/1	5/6	4/6	2/4	3/2
33	8	3	6	1	1	-/-	-/-	-/-	-/-	-/-
34	9	3	6	2	1	1/4	6/6	6/4	4/6	2/2
35	10	3	6	1	1	-/-	-/-	-/-	-/-	-/-
36	11	3	6	1	1	-/-	-/-	-/-	-/-	-/-
37	12	3	6	1	1	1/4	6/6	6/4	4/6	2/2
38	13	3	6	2	2	9/1	5/6	4/6	2/4	3/2
39	18	0	0	1	1	5/1	9/5	2/7	6/6	2/2
40	15	14	7	2	2	9/2	5/10	4/4	2/4	3/3
41	16	14	7	2	1	1/1	6/3	6/4	4/4	2/3
42	17	14	7	1	2	-/-	-/-	-/-	-/-	-/-
43	19	18	15	1	2	9/5	5/9	4/2	2/6	3/2
44	20	18	15	2	2	9/1	5/9	4/2	2/6	3/2
45	47	0	0	1	1	-/-	-/-	-/-	-/-	-/-
46	46	47	13	2	1	1/8	6/8	6/3	4/5	2/2
47	45	47	13	2	2	9/8	5/5	4/4	2/7	3/3

Only first 5 markers are shown. Use option 'markers=' to print specified markers.

They have taken each 2 markers and transformed them into one column of format allele1/allele2
 \Leftrightarrow representing the genotype

Q4

```
[ ]: summary(x)
```

Pedigree:

47 individuals

11 founders, 36 nonfounders; bit size = 61

10 nuclear subfamilies

22 affected by disease, 25 unaffected, 0 with unknown affection status

Marker data:

13 markers in total

13 individuals with no available genotypes: 1, 2, 21, 4, 3, 6, 30, 42, 8, 10, 11, 17, 47

0 % missing alleles (excluding ungenotyped individuals)

Chromosome distribution of markers:

chromosome unknown: 13 markers

Allele number distribution:

3 alleles: 1 marker

```
4 alleles: 4 markers
5 alleles: 2 markers
6 alleles: 2 markers
7 alleles: 4 markers
```

Model parameters:

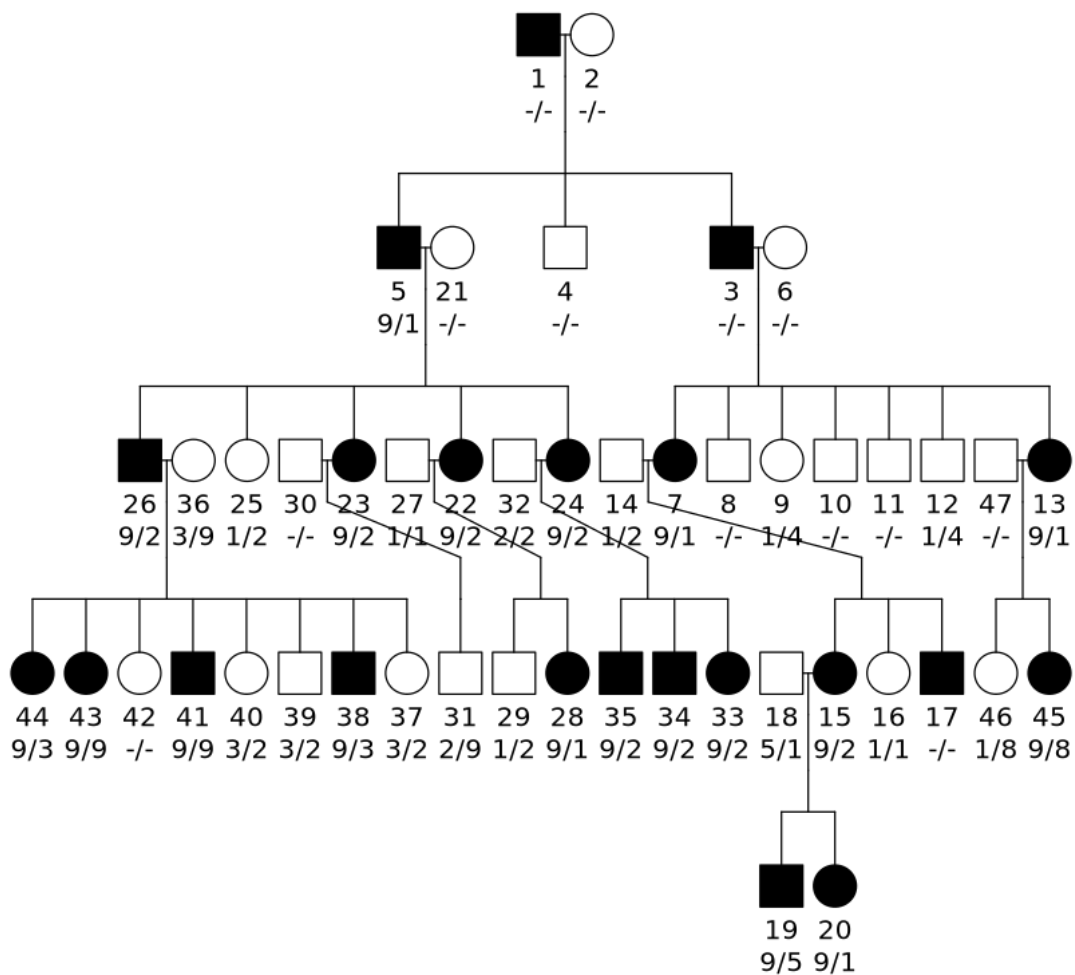
No model parameters set

There is:

- 11 founder individuals
- 13 with unknown genotypes
- 4 markers with 7 alleles

1.1.4 a.4. Family tree drawing for 1st marker

```
[ ]: plot(x, marker=1)
```



Q5: For indiv 15,16 and 17 repsectively:

- 9/2
- 1/1
- missing (-/-)

1.1.5 a.5. Definition of the genetic model to be considered for linkage analyses

Here Dd and DD are the at-risk genotypes, since it's autosomal dominant and d is the deleterious allele (so dominant allele)

[12]: `xdom=setModel(x, model=1, penetrances = c(0.00001,1,1), dfreq=0.00001)`

Here we have $Phenocopy = P(affected/DD) = 0.00001$

1.1.6 a.6. Linkage analyses with lodscore calculation for given theta values

```
[13]: lod_values=lod(xdom, theta=c(0,0.05,0.1,0.15,0.2,0.25,0.3,0.4,0.5))
```

```
[ ]: lod_values
```

	M1	M2	M3	M4	M5	M6
theta=0:	7.673800	7.247411	4.762693	8.171219	6.0050443	4.969872
theta=0.05:	7.035453	6.653626	4.309984	7.511664	5.4606032	4.555357
theta=0.1:	6.365581	6.030791	3.848484	6.819437	4.8898188	4.121439
theta=0.15:	5.661047	5.376151	3.371107	6.091242	4.2903721	3.666446
theta=0.2:	4.918254	4.686580	2.871736	5.323255	3.6599709	3.188760
theta=0.25:	4.133297	3.958642	2.346428	4.511135	2.9968532	2.687328
theta=0.3:	3.302875	3.189035	1.795610	3.650405	2.3012371	2.162844
theta=0.4:	1.528959	1.530367	0.682811	1.782355	0.8643605	1.069246
theta=0.5:	0.000000	0.000000	0.000000	0.000000	0.0000000	0.000000

	M7	M8	M9	M10	M11	M12
theta=0:	5.7141323	5.2550744	4.2537353	3.5643218	0.2874061	1.061945
theta=0.05:	5.1742276	4.7499732	3.8555848	3.2523734	3.5708778	4.285454
theta=0.1:	4.6083512	4.2271963	3.4424404	2.9319108	3.4368453	4.088351
theta=0.15:	4.0141596	3.6832892	3.0136955	2.6029704	3.1568696	3.741883
theta=0.2:	3.3894121	3.1151478	2.5688442	2.2654917	2.8032430	3.318095
theta=0.25:	2.7327781	2.5213329	2.1077616	1.9191995	2.3982856	2.839221
theta=0.3:	2.0462455	1.9051123	1.6317013	1.5634218	1.9533074	2.316724
theta=0.4:	0.6694062	0.6923811	0.6734622	0.8170073	0.9867355	1.184283
theta=0.5:	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0.000000

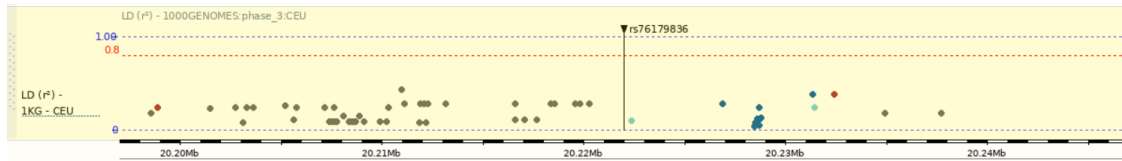
	M13
theta=0:	-32.1732679
theta=0.05:	2.1590621
theta=0.1:	2.3859584
theta=0.15:	2.3427504
theta=0.2:	2.1757203
theta=0.25:	1.9301442
theta=0.3:	1.6262113
theta=0.4:	0.8847441
theta=0.5:	0.0000000

Q6 We can the same pattern for markers M1 to M10: max lod score is obtained for theta=0 and its value in each of these markers is higher than 3 -> reject the null hypothesis -> conclusion is this gene is very close to each of these genetic markers. And if the disease gene is close to them all it means that the first 10 markers are in cluster, they are very close.

For marker 11 and 12 the max lod score is obtained for same theta value = 0.05 and the value is higher than 3 so we can reject the null hypothesis and conclude that the probable location of the disease locus is around 0.05 cM from these markers.

For the marker 13, there is no theta value for which the lod-score is higher than 3, but for theta=0

the lod-score = $-32 < -2$ so the null hypothesis is not rejected, hence we can exclude that the disease gene is close to this marker.



Q7 The recombination rate is between 0 and 0.5 so the confidence interval for the recombination rate will be in this range. Here theta max is 0 because it is for theta = 0 that we have the maximum of the lod score. It means that the lower bound of the confidence interval will be equal to 0 and the intersection is the upper bound. We approximate it.

Confidence interval for Marker 1 is ranging between $[0, 0.07]$

1.1.7 a.7. Linkage analyses with determination of maximum lodscore

```
[27]: lod(xdom, marker=c(5,7,8,12), theta='max')
```

	M5	M7	M8	M12
LOD:	6.005044	5.714132	5.255074	4.28823977
t_max:	0.000000	0.000000	0.000000	0.04508497

Q8 Interpretation of the results:

For markers M_5 , M_7 and M_8 , θ_{max} is 0 which means that the markers is very close to the disease gene.

For marker M_{12} , θ_{max} is 0.045 with a lod score of $0.045 > 3$, which is -

Q9

```
[26]: ## as.matrix(lod_values)
for (i in 1:ncol(lod_values)){
  max_lod=max(lod_values[,i])
  cat('max lod value for marker',i,'is',max_lod,'\n')
}
```

```
max lod value for marker 1 is 7.6738
max lod value for marker 2 is 7.247411
max lod value for marker 3 is 4.762693
max lod value for marker 4 is 8.171219
max lod value for marker 5 is 6.005044
max lod value for marker 6 is 4.969872
max lod value for marker 7 is 5.714132
max lod value for marker 8 is 5.255074
max lod value for marker 9 is 4.253735
max lod value for marker 10 is 3.564322
```



```
max lod value for marker 11 is 3.570878
max lod value for marker 12 is 4.285454
max lod value for marker 13 is 2.385958
```

Q10 Markers 1-10 all have the same pattern of lod scores relative to θ values: The highest lod score is at θ_0 and the lowest at $\theta_{0.5}(= 0)$, with lod scores > 3 , which means that the markers are at very close proximity to the disease gene.

1.1.8 a.8. Linkage analyses by modifying marker allele frequencies

```
[43]: ## -- before when they were equifrequent
as.data.frame(lod_values[, "M5"])
```

	lod_values[, "M5"] <dbl>
0	6.0050443
0.05	5.4606032
0.1	4.8898188
0.15	4.2903721
0.2	3.6599709
0.25	2.9968532
0.3	2.3012371
0.4	0.8643605
0.5	0.0000000

```
[30]: ## -- after modifying allele frequencies
xdom5=modifyMarker(xdom,marker = 5, afreq = c(0.1, 0.1, 0.1, 0.7))
lod(xdom5, marker=5, theta=c(0, 0.05, 0.1, 0.15, 0.2, 0.25, 0.3, 0.4, 0.5))
```

	M5
theta=0:	6.1601384
theta=0.05:	5.6089781
theta=0.1:	5.0311016
theta=0.15:	4.4242603
theta=0.2:	3.7862270
theta=0.25:	3.1152044
theta=0.3:	2.4110015
theta=0.4:	0.9454197
theta=0.5:	0.0000000

Q11 Results have been modified slightly in each, overall the same pattern (decreasing when increasing theta values) with only a small increase of lod values of when we changed the frequencies, and then reaching 0 when $\theta = 0.5$

why? –

1.1.9 a.9. Impact of misspecifying the genetic model

```
[ ]: xrec=setModel(x, model=2, penetrances=c(0.00001,0.00001, 1), dfreq=0.00001)
      lod(xrec)
```

	M1	M2	M3	M4	M5	M6
theta=0:	-11.52737	-20.34523	0.8394887	-20.80169	-11.46918	-16.24291
	M7	M8	M9	M10	M11	M12
theta=0:	-6.483199	-3.089972	1.408298	-14.51178	-16.13149	-8.403986
	M13					
theta=0:	-3.274896					

Q12 Markers $M_1, M_2, M_4, M_5, M_6, M_7, M_8, M_{10}, M_{11}, M_{12}, M_{13}$ have a negative value < -2 for θ_{max} , which means that the markers are far from the disease gene.

Except for M_3 and M_9 which have a positive value however ranging between $-2 < lodscore < 3$ hence nothing can be concluded

In this section we have changed the mode of inheritance from autosomal dominant to autosomal recessive, we can clearly see the differences in the results as in here we haven't concluded any marker that is in close proximity to the disease gene, this is because the mode of inheritance changes the at risk genotypes which in return affect the calculation of the lod score

This is the importance of the disease model's influence, it's crucial to be near the true model.

The lod score is parametric because it's affected by genetic mode of the disease and the allelic frequencies

1.2 b: Familial association analysis - TDT

```
!./fbat.exe
```

```
*****
*
*          * * *          *          *
*  *          * * *          *          *
*  *          * * *          *          *
*  *          * * *          *          *
*  *          * * *          *          *
*  *          * * *          *          *
*  *          * * *          *          *
*
*      Xin Xu  C1999-2009          v2.0.4(beta1)  *
*      Program for Population Genetics          *
*      Harvard School of Public Health          *
*
*****
```

```
>> log resfbat
logging to file "resfbat" is on
>> load fbat.ped
read in: 6 markers from 651 pedigrees (652 nuclear families,2011 persons)
```

Q13 There are:

- 652 nuclear families
- 2011 persons i.e. $\frac{2011}{652} \approx 3$ individuals per family
- 6 markers

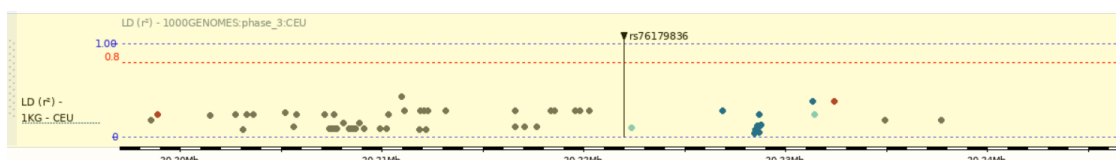
```
>> fbat
```

```
trait affection; offset 0.000; model additive; test bi-allelic; minsize 10; min_freq 0.000; p
```

Marker	Allele	afreq	fam#	S-E(S)	Var(S)	Z	P
SNP2	1	0.636	409	3.500	138.750	0.297	0.766365
SNP2	2	0.364	409	-3.500	138.750	-0.297	0.766365
SNP3	1	0.370	402	2.000	140.500	0.169	0.866009
SNP3	2	0.630	402	-2.000	140.500	-0.169	0.866009
SNP4	1	0.403	425	5.000	148.500	0.410	0.681582
SNP4	2	0.597	425	-5.000	148.500	-0.410	0.681582
SNP5	1	0.626	393	-4.500	136.750	-0.385	0.700377
SNP5	2	0.374	393	4.500	136.750	0.385	0.700377
SNP6	1	0.212	283	-52.000	91.000	-5.451	5.01e-008
SNP6	2	0.788	283	52.000	91.000	5.451	5.01e-008

Q14 An informative family is a family where there exists at least one parent that is heterozygous (make sure)

All SNPs are present in the results, i.e., they have at least 10 informative families (lowest one is 283), hence no, there are no markers for which the number of informative families is insufficient



Q15

Q16 According to the results coming from **fbat**, SNP6 is in association with the disease, it's actually the only one in the table with a p-value less than 0.05, thus there is a significant association. It's either that SNP6 is the disease gene or is in linkage disequilibrium with the disease gene. Allele 2 is the at-risk allele that is more transmitted from a heterozygous parent to a diseasee child, since the $S - E(S) > 0$

From Ensembl plot, r^2 is below threshold for all nearby markers, meaning that none of the markers are in linkage disequilibrium with the SNP of interest (SNP6) **rs76179836**, so we can conclude that it is the causal variant

2 II. Study of a multifactorial disease: rheumatoid arthritis

2.1 a. Genetic linkage analysis—affected sib-pairs method

2.2 b. Genome-wide association analysis

```
[1]: %cd ../data/TP_DATA_PROG/II.a.Plink
```

```
/mnt/g/my_stuff/masters/saclay/courses/M1/NGS/part_2/data/TP_DATA_PROG/II.a.Plink
```

2.2.1 b.1. A few quality control steps

Q19 The QC to consider:

- missing SNP, call rate greater than 95%
- missing individuals, call rate greater than 95%
- minor allele frequency greater than 5%
- Hardy-Weinberg equilibrium p-value greater than 0.001
- homogeneity of the population (PCA)

First we shall start by removing missing data, i.e. individuals (rows) missing more than 5% as well as SNPs (cols) missing more than 5% (call rate for both is greater than 95%)

For individuals:

```
[ ]: %./plink.exe --file hapmap --mind 0.05 --make-bed --out Ind
```

```
PLINK v1.90b5 32-bit (14 Nov 2017)          www.cog-genomics.org/plink/1.9/
(C) 2005-2017 Shaun Purcell, Christopher Chang  GNU General Public License v3
Logging to Ind.log.
```

Options in effect:

```
--file hapmap
--make-bed
--mind 0.05
--out Ind
```

```
8025 MB RAM detected; reserving 2047 MB for main workspace.
Allocated 1535 MB successfully, after larger attempt(s) failed.
.ped scan complete (for binary autoconversion).
Performing single-pass .bed write (50971 variants, 89 people).
--file: Ind-temporary.bed + Ind-temporary.bim + Ind-temporary.fam written.
50971 variants loaded from .bim file.
89 people (89 males, 0 females) loaded from .fam.
89 phenotype values loaded from .fam.
0 people removed due to missing genotype data (--mind).
Using 1 thread (no multithreaded calculations invoked).
Before main variant filters, 89 founders and 0 nonfounders present.
Calculating allele frequencies... done.
Total genotyping rate is 0.994134.
```

50971 variants and 89 people pass filters and QC.
Among remaining phenotypes, 44 are cases and 45 are controls.
--make-bed to Ind.bed + Ind.bim + Ind.fam ... done.

Starting with 89 individuals (44 cases and 45 controls), we have removed 0 individuals with missing data, so we have maintained all individuals during this quality check step.

Next SNP:

```
[4]: %./plink.exe --bfile Ind --geno 0.05 --make-bed --out IndMk
```

```
PLINK v1.90b5 32-bit (14 Nov 2017)          www.cog-genomics.org/plink/1.9/
(C) 2005-2017 Shaun Purcell, Christopher Chang  GNU General Public License v3
Logging to IndMk.log.
```

Options in effect:

```
--bfile Ind
--geno 0.05
--make-bed
--out IndMk
```

```
8025 MB RAM detected; reserving 2047 MB for main workspace.
Allocated 1535 MB successfully, after larger attempt(s) failed.
50971 variants loaded from .bim file.
89 people (89 males, 0 females) loaded from .fam.
89 phenotype values loaded from .fam.
Using 1 thread (no multithreaded calculations invoked).
Before main variant filters, 89 founders and 0 nonfounders present.
Calculating allele frequencies... done.
Total genotyping rate is 0.994134.
1509 variants removed due to missing genotype data (--geno).
49462 variants and 89 people pass filters and QC.
Among remaining phenotypes, 44 are cases and 45 are controls.
--make-bed to IndMk.bed + IndMk.bim + IndMk.fam ... done.
```

Starting from 50971 SNPs, we have removed 1509 SNPs with missing data, so we have maintained 49462 SNPs during this quality check step.

- raw data: 50971 variants
- variants that didnt pass SNP QC call rate > 95: 1509
- variants that passed SNP QC: 49462

Next is filtration based on Minor Allel Frequency (MAF) lower than 5% as SNPs should be common enough to associate a causal variant with a disease (susceptibility genes are frequent)

```
[5]: %./plink.exe --bfile IndMK --maf 0.05 --make-bed --out IndMkMAF
```

```
PLINK v1.90b5 32-bit (14 Nov 2017)          www.cog-genomics.org/plink/1.9/
(C) 2005-2017 Shaun Purcell, Christopher Chang  GNU General Public License v3
Logging to IndMkMAF.log.
```

Options in effect:

```
--bfile IndMK
--maf 0.05
--make-bed
--out IndMkMAF
```

```
8025 MB RAM detected; reserving 2047 MB for main workspace.
Allocated 1535 MB successfully, after larger attempt(s) failed.
49462 variants loaded from .bim file.
89 people (89 males, 0 females) loaded from .fam.
89 phenotype values loaded from .fam.
Using 1 thread (no multithreaded calculations invoked).
Before main variant filters, 89 founders and 0 nonfounders present.
Calculating allele frequencies... done.
Total genotyping rate is 0.996817.
14169 variants removed due to minor allele threshold(s)
(--maf/--max-maf/--mac/--max-mac).
35293 variants and 89 people pass filters and QC.
Among remaining phenotypes, 44 are cases and 45 are controls.
--make-bed to IndMkMAF.bed + IndMkMAF.bim + IndMkMAF.fam ... done.
```

From the previously filtered set of 49462 SNPs, we have removed 14169 SNPs with MAF lower than 5%, so we have maintained 35293 SNPs during this quality check step.

- starting data: 49462 variants
- variants that didnt pass $MAF > 5$: 14169
- variants that passed MAF QC: 35293

Next is Hardy-Weinberg equilibrium (HWE), the hypothesis here is that frequency of alleles is the expected frequency in a population, so conducting a χ^2 test for conformity is testing for the null hypothesis that the observed genotype frequencies are in HWE

$$H_0(HWE) : p^2 + 2pq + q^2 = 1$$

```
[6]: %./plink.exe --bfile IndMKMAF --hwe 0.05 --hardy --make-bed --out IndMkMAFHWE
```

```
PLINK v1.90b5 32-bit (14 Nov 2017)          www.cog-genomics.org/plink/1.9/
(C) 2005-2017 Shaun Purcell, Christopher Chang  GNU General Public License v3
Logging to IndMkMAFHWE.log.
```

Options in effect:

```
--bfile IndMKMAF
--hardy
--hwe 0.05
--make-bed
--out IndMkMAFHWE
```

```
8025 MB RAM detected; reserving 2047 MB for main workspace.
Allocated 1535 MB successfully, after larger attempt(s) failed.
```

```

35293 variants loaded from .bim file.
89 people (89 males, 0 females) loaded from .fam.
89 phenotype values loaded from .fam.
Using 1 thread (no multithreaded calculations invoked).
Before main variant filters, 89 founders and 0 nonfounders present.
Calculating allele frequencies... done.
Total genotyping rate is 0.996644.
--hardy: Writing Hardy-Weinberg report (founders only) to IndMkMAFHWE.hwe ...
done.
--hwe: 945 variants removed due to Hardy-Weinberg exact test.
34348 variants and 89 people pass filters and QC.
Among remaining phenotypes, 44 are cases and 45 are controls.
--make-bed to IndMkMAFHWE.bed + IndMkMAFHWE.bim + IndMkMAFHWE.fam ... done.

```

In here, we start with 35293 SNPs, and we have removed 945 SNPs that did not pass the HWE test, so we have 34348 SNPs that passes this filter.

- starting data: 35293 variants
- variants that didnt pass HWE, with a p-value of 0.05: 945 (removed those with p-value < 0.05, since rejecting HWE null hypothesis)
- variants that passed HWE QC: 34348

Overall this is a summary of the QC steps and stats:

QC step	Starting data	Removed	Passed	Final data
Individuals, call rate > 95	89	0	0	89 indiv
SNPs, call rate > 95	50971	1509	49462	49462 variants
SNPs, MAF > 5	49462	14169	35293	35293 variants
SNPs, HWE p-value > 0.05	35293	945	34348	34348 variants

End filtered data:

- 89 individuals (rows)
- 34348 SNPs (columns)

b.2. Allelic and genotypic association tests

```
[7]: %./plink.exe -bfile IndMkMAFHWE --assoc --ci .095 --out res_allelic
```

```

PLINK v1.90b5 32-bit (14 Nov 2017)                www.cog-genomics.org/plink/1.9/
(C) 2005–2017 Shaun Purcell, Christopher Chang    GNU General Public License v3
Logging to res_allelic.log.
Options in effect:
--assoc
--bfile IndMkMAFHWE
--ci .095
--out res_allelic

```

```

8025 MB RAM detected; reserving 2047 MB for main workspace.
Allocated 1535 MB successfully, after larger attempt(s) failed.
34348 variants loaded from .bim file.
89 people (89 males, 0 females) loaded from .fam.
89 phenotype values loaded from .fam.
Using 1 thread (no multithreaded calculations invoked).
Before main variant filters, 89 founders and 0 nonfounders present.
Calculating allele frequencies... done.
Total genotyping rate is 0.996651.
34348 variants and 89 people pass filters and QC.
Among remaining phenotypes, 44 are cases and 45 are controls.
Writing C/C --assoc report to res_allelic.assoc ... done.

This generates the results in a table form in one file res_allelic.assoc.

```

Q.20 Since we have 34348 variants, we consequently have 34348 statistical tests to conduct (χ^2 tests for association). Thus it is crucial to account for the multiple testing problem, and this is done by adjusting the p-values. The bonferroni technique is a Family-Wise Error Rate (FWER) correction method, it is very conservative and it is calculated by dividing the significance level by the number of tests. Here we take the significance level $\alpha = 0.05$ and divide it by the number of tests 34348 to get the new significance level

$$\alpha_{new} = \frac{0.05}{34348} \approx 1.45 \times 10^{-6}$$

Alternatively, the p-value is adjusted and the corrected value to test for significance becomes 1.45×10^{-6}

So this is to answer the question, that's the p-value considered to reject the null hypothesis for the allelic association test with Bonferroni correction.

In fact, instead of comparing with it manually we can get the corrected p-values from the software and compare directly with the significance level 5%.

In order to perform correction in PLINK, we need to run the latter command with an `--adjust` flag

```
plink --assoc --bfile IndMkMAFHWE --ci .095 --out res_allelic --adjust
```

This will generate a new file `res_allelic.assoc.adjusted` with the adjusted p-values from various MTC methods, and this is a sample of the output:

CHR	SNP	UNADJ	GC	BONF	HOLM	SIDAK_SS	SIDAK_SD	FDR_BH	FDR_BY
2	rs2222162	5.918e-06	3.082e-05	0.2033	0.2033	0.184	0.184	0.05829	0.6424
9	rs10810856	7.723e-06	3.867e-05	0.2653	0.2653	0.233	0.233	0.05829	0.6424
2	rs4675607	8.05e-06	4.007e-05	0.2765	0.2765	0.2416	0.2416	0.05829	0.6424
2	rs4673349	8.485e-06	4.191e-05	0.2915	0.2914	0.2528	0.2528	0.05829	0.6424

We want to see results before and after Bonferroni correction. What we care for is the 3rd column UNADJ (no correction applied) and the 5th column BONF: this corrected p-value can be directly compared to 0.05 to determine significance.

To test, we will use the awk command to compare the column to the significance level

Those with p-value less than 0.05 are considered significant, before correction:

```
$ awk '{if ($3>0.05) print $5}' res_allelic.assoc.adjusted | tail -
n +2 | wc -l
2289
```

(what this command does: it prints the 3rd col which is the unadjusted p-value from the adjusted result file, then filters those that are less than 0.05, removes header then counts them)

after Bonferroni correction:

```
$ awk '{if ($5<=0.05) print $5}' res_allelic.assoc.adjusted | tail -n +2 | wc -l
0
```

(what this command does: it prints the 5th col which is the bonferroni corrected p-value from the adjusted result file, then filters those that are less than 0.05, removes header then counts them)

As we can see, none of the SNPs are significant after Bonferroni correction, which is expected since the corrected p-value is very very low (a very conservative correction method).

On the opposite, before correction, 2289 tests were rejected without applying any correction, i.e. 2289 SNPs were considered significant without accounting for multiple testing.

Reflection: 2289 variants were thought to be causal susceptibility genes for RA, but after correction, none of them were significant. This shows the large number of false positives that can be generated when not accounting for multiple testing. And it shows as well how conservative the Bonferroni correction is.

Q21

```
[12]: %./plink.exe -bfile IndMkMAFHWE --logistic --ci .095 --out res_gen
```

In here the p-value is coming from logistic regression, from Wald test for the coefficients β of the genotypes.

This time we will won't use the `--adjust` flag, and we will use the corrected significance level for Bonferroni to compare with the one p-value obtained in results file `res_gen.assoc`. P-value is in column 12.

Before correction, on significance level 0.05:

```
awk '{if ($12<0.05) print $12}' res_gen.assoc.logistic | tail -
n +2 | wc -l
2032
```

After bonferroni on $\alpha_{bonf} = 1.45 \times 10^{-6}$:

```
awk '{if ($12<1.45e-6) print $12}' res_gen.assoc.logistic | tail -n +2 | wc -l
0
```

Q22 We can notice similar result.

In terms of correction both the allelic and genotypic association tests are similar, the number of significant SNPs is reduced to 0 after Bonferroni correction, which is expected since the corrected p-value is very low.

In terms of unadjusted values, in allelic association test, 2289 SNPs were significant, while in genotypic association test, 2032 SNPs were significant, which is a bit less than the allelic association test and relatively very close.

This difference can be due to the fact:

- We're performing χ^2 test in allelic association test, while we're performing logistic regression in genotypic association test, and both tests are different in terms of the hypothesis they test hence might have different results.
- In genotypic test, we evaluate the association between different genotypes (e.g., AA, AG, GG) and the disease, allowing it to detect specific genotypes that are at risk. In contrast, an allelic test examines the association of individual alleles (e.g., A or G) with the trait and may not detect the same level of association as the genotypic test.

Q23 *It's very important to note that the most important quality step is to test for the homogeneity of SNP data, this is done by PCA and should prove that case and controls are from the same population, and it's not mentioned here*

This is crucial because if the cases and controls are from different populations, the results will be biased and the association tests will be invalid.

To analyze **CHB and JPT together** (chinese and japanese populations) we have to make sure that both populations are in fact homogeneous, which is not carried in our quality control steps. For this purpose, having 2 populations in the same analysis wouldn't be recommended as they are different genetically, they are very likely to be different in terms of their neutral SNPs and this will lead to biased results.