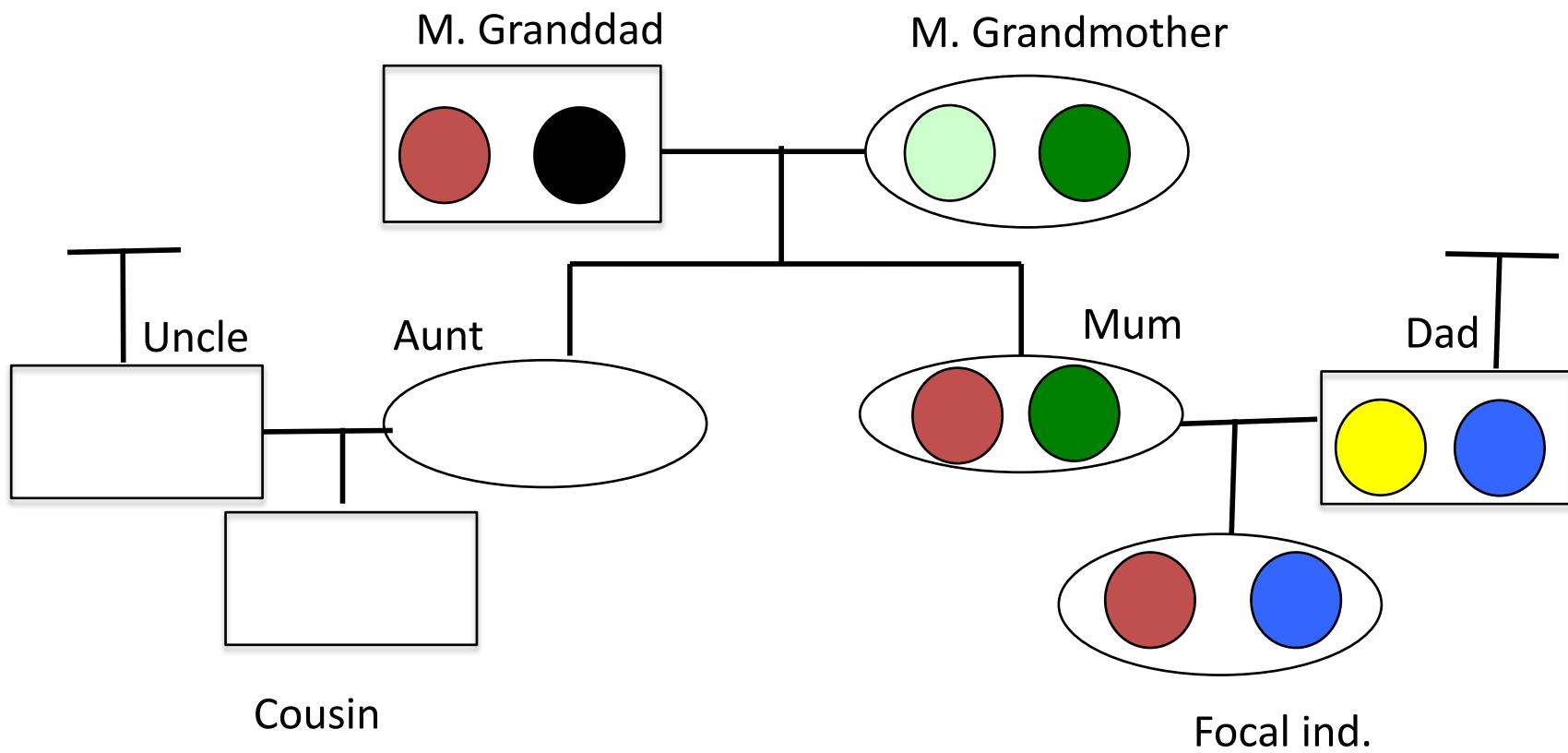
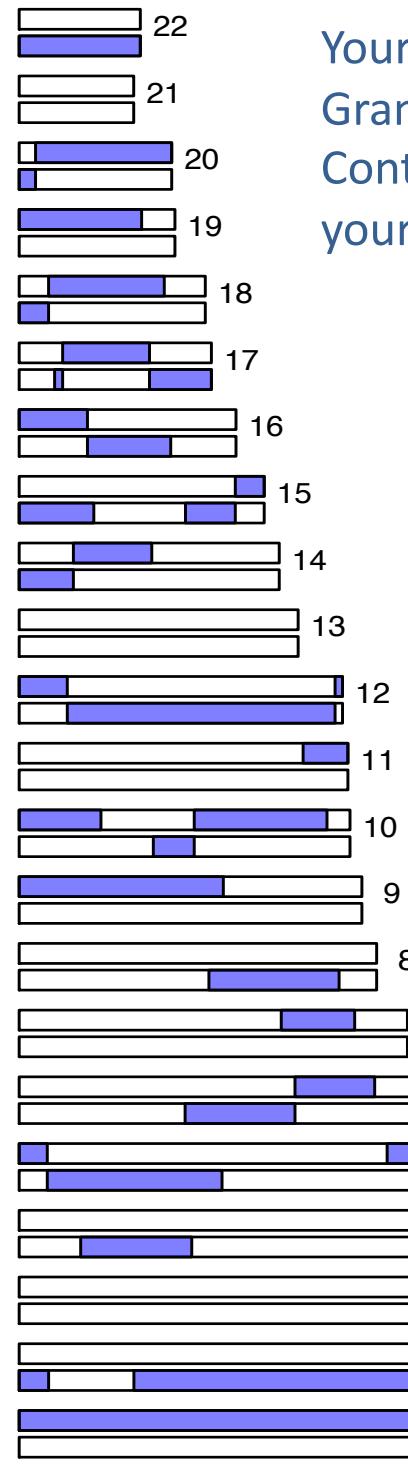


Lecture 3 Eve102

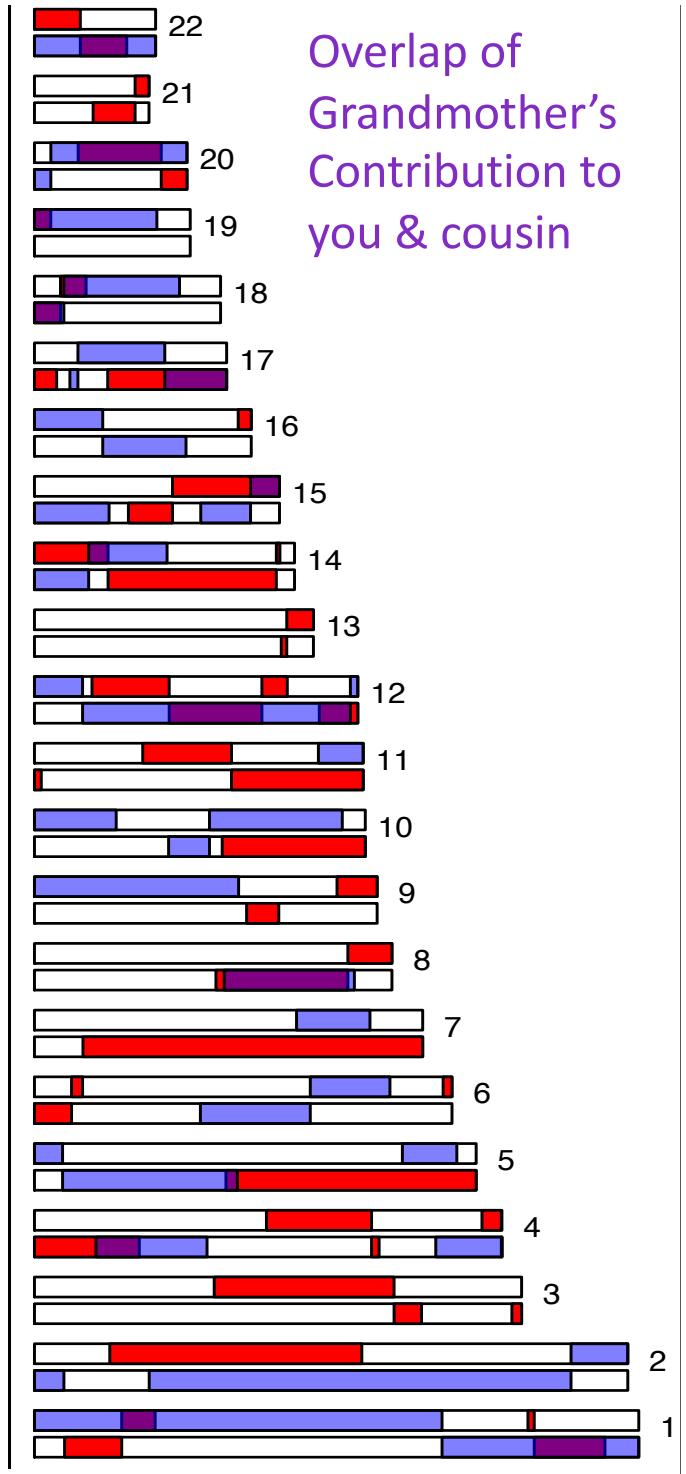




Your maternal
Grandmother's
Contribution to you



Your maternal
Grandmother's
Contribution to
your cousin

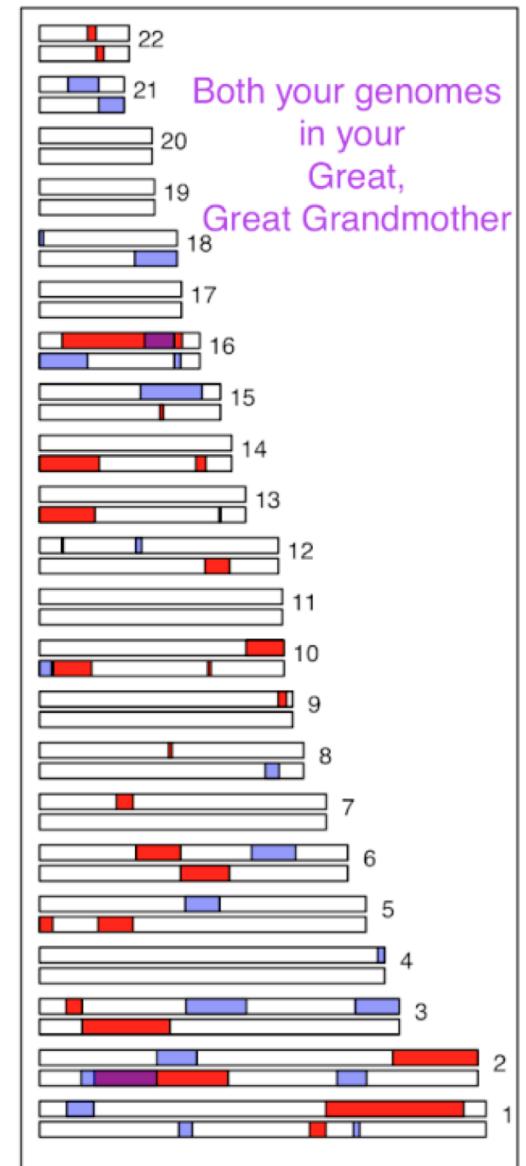
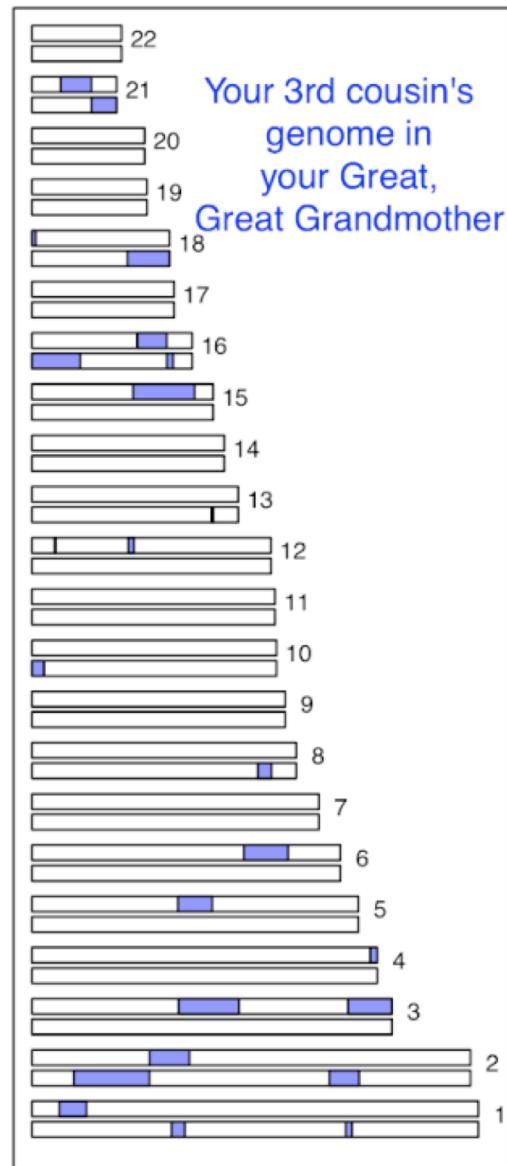
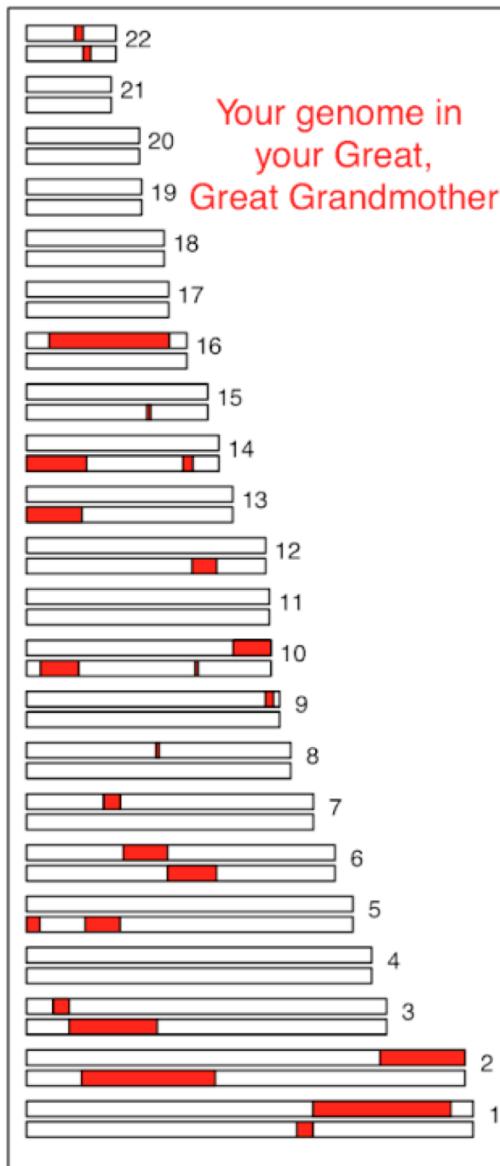


Overlap of
Grandmother's
Contribution to
you & cousin

A person and their 1st cousin
On 23&me

Half identical
1039 cM
38 segments





Me and my 3rd cousin (?)
On 23&me

Half identical
66 cM
3 segments



To find alleged Golden State Killer, investigators first found his great-great-great-grandparents

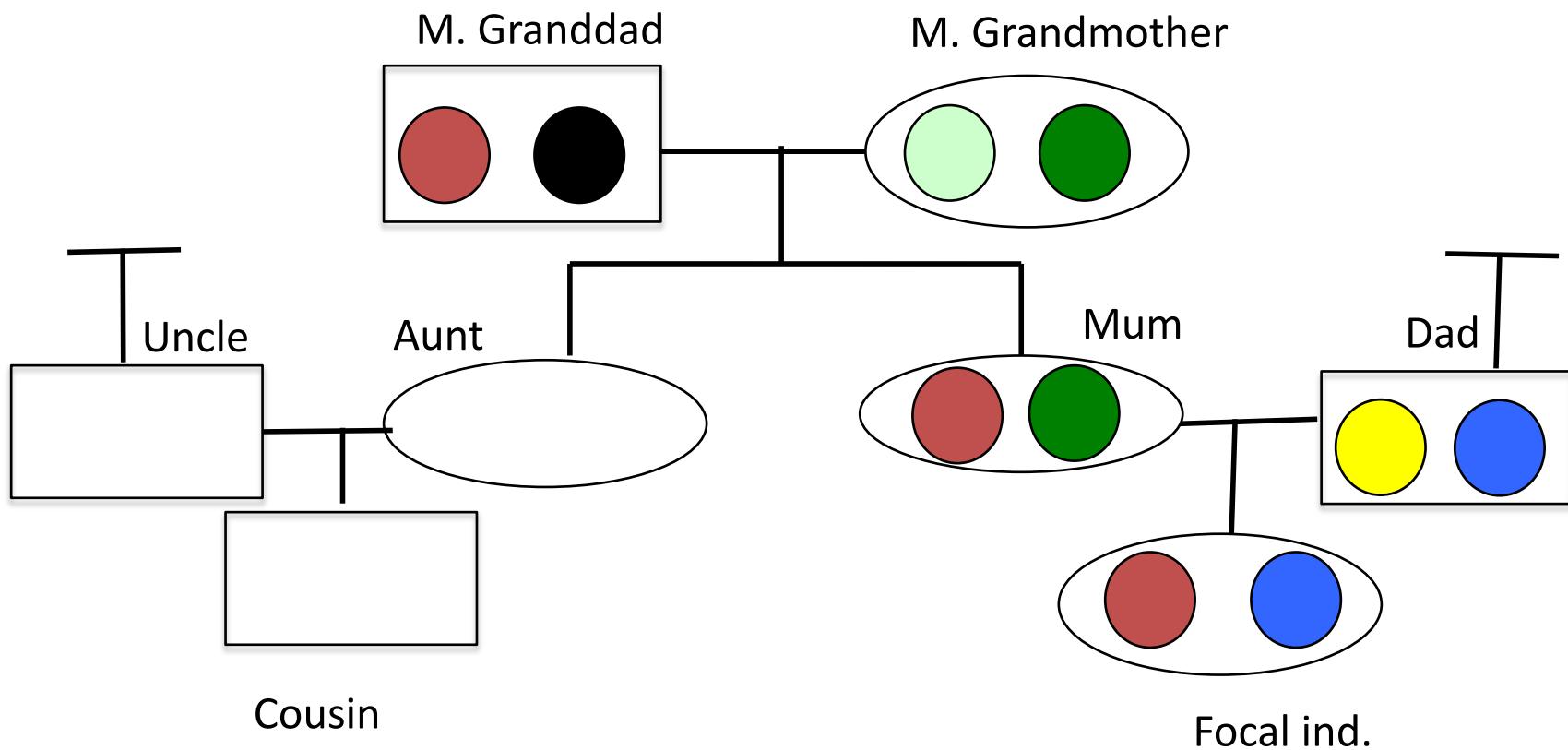
Gedmatch

By Justin Jouvenal April 30  Email the author

To qualify as a 'match' in the genealogical time frame, results must have a largest Autosomal segment that has at least 700 SNPs and be at least 7 cM. It must have BOTH. Results with the largest segment less than 7 cM are highlighted in pink. In general, the results shown below use thresholds LESS than 7cM / 700 SNPs. PLEASE verify any result shown on this list with the one-to-one comparison tool before assuming any match is real. To check the number of SNPs, click on the 'A' on the same line to view the one-to-one comparison detail.

Please DO NOT send emails to anyone on this list without first using the one-to-one utility to verify that it is a legitimate match.
DO NOT create mass mailing lists from these results.

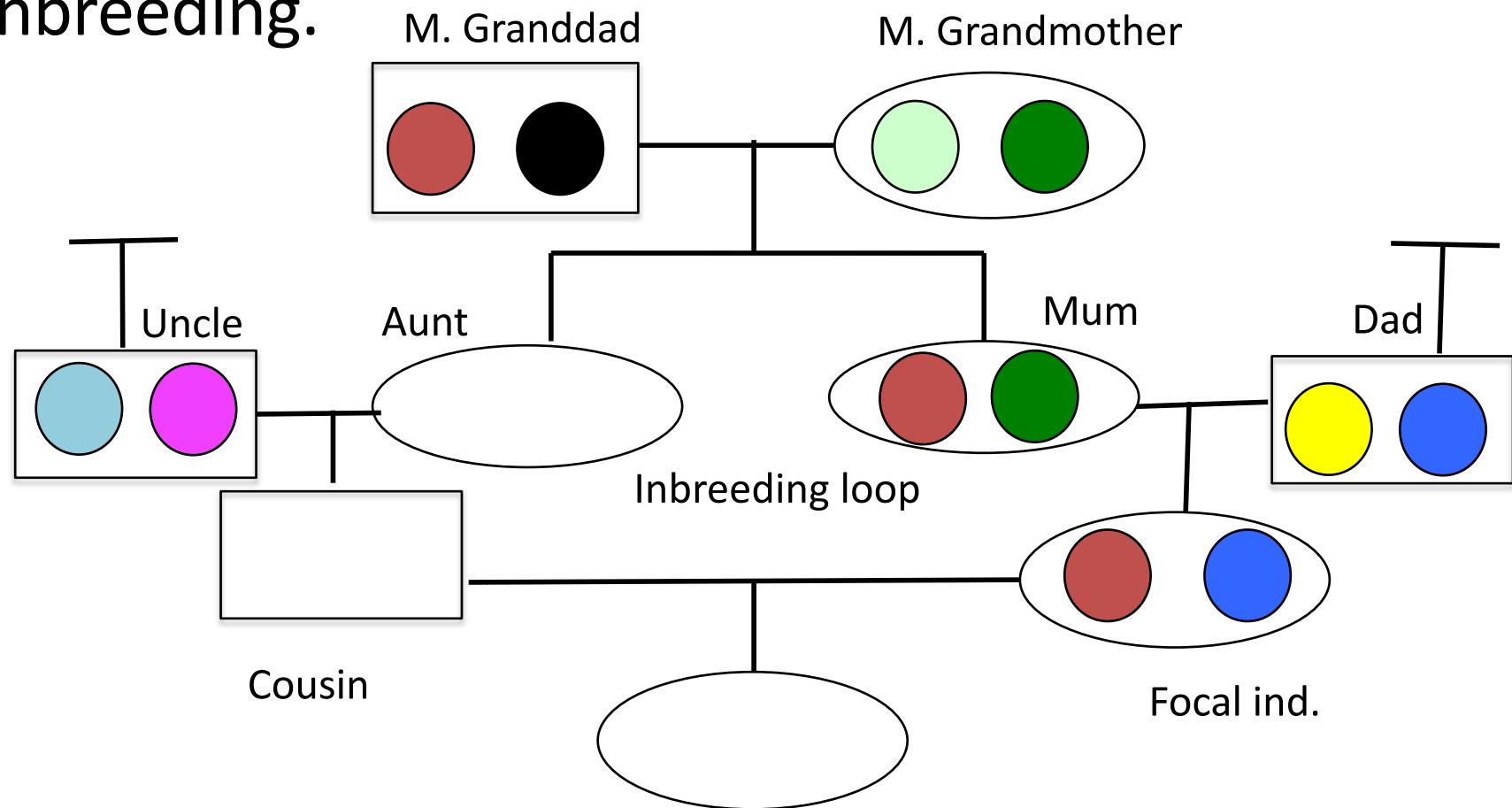
Kit Nbr	Type	List	Select	Sex	GED/WikiTree	Haplogroup		Autosomal			X-DNA			Name (* => alias)	Email	
						Mt	Y	Details	Total cM	largest cM	Gen	Details	Total cM	largest cM	Gen	
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	106.7	49.5	3.5	X	6.2	6.2		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M				A	52.3	25.0	4.1	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	46.5	27.4	4.1	X	6.9	6.9		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M	GED			A	40.1	21.3	4.2	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	31.5	21.2	4.4	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	31.1	20.7	4.4	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M	GED			A	29.7	29.7	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M				A	29.3	29.3	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M				A	28.7	15.8	4.5	X	0	0		
V4	L	<input type="checkbox"/>	<input type="checkbox"/>	M		H3	I1	A	28.7	28.7	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	U				A	28.5	22.6	4.5	X	7.3	7.3		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M	GED			A	28.1	17.7	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	27.9	15.7	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	M	GED			A	27.6	27.6	4.5	X	0	0		
F2	L	<input type="checkbox"/>	<input type="checkbox"/>	F				A	27	16.8	4.5	X	11.5	6.4		



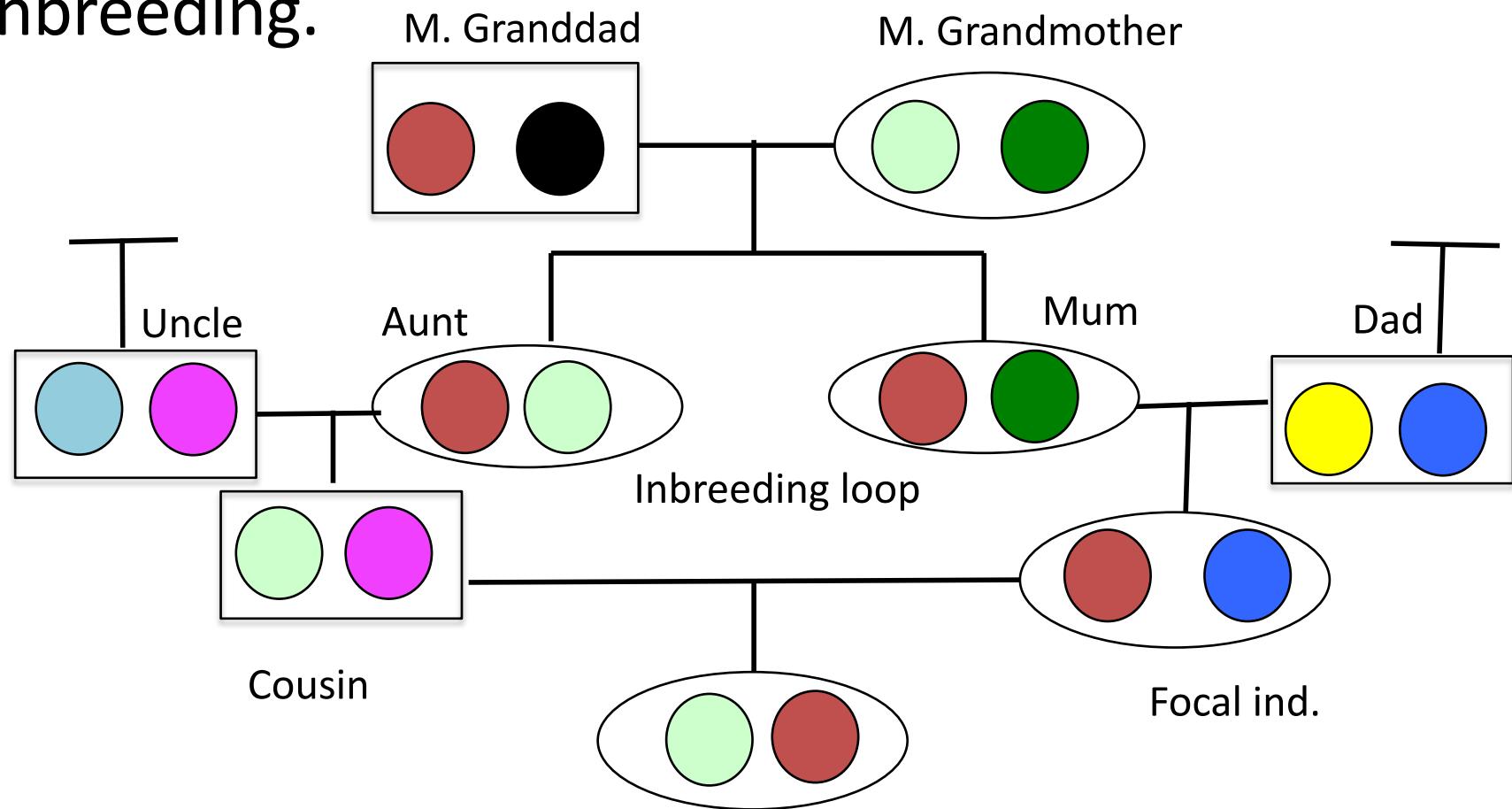
$$f = \text{Coefficient of kinship} = 0 \times r_0 + r_1/4 + r_2/2$$

Notes: Equation 2.3, page 16

Inbreeding.



Inbreeding.

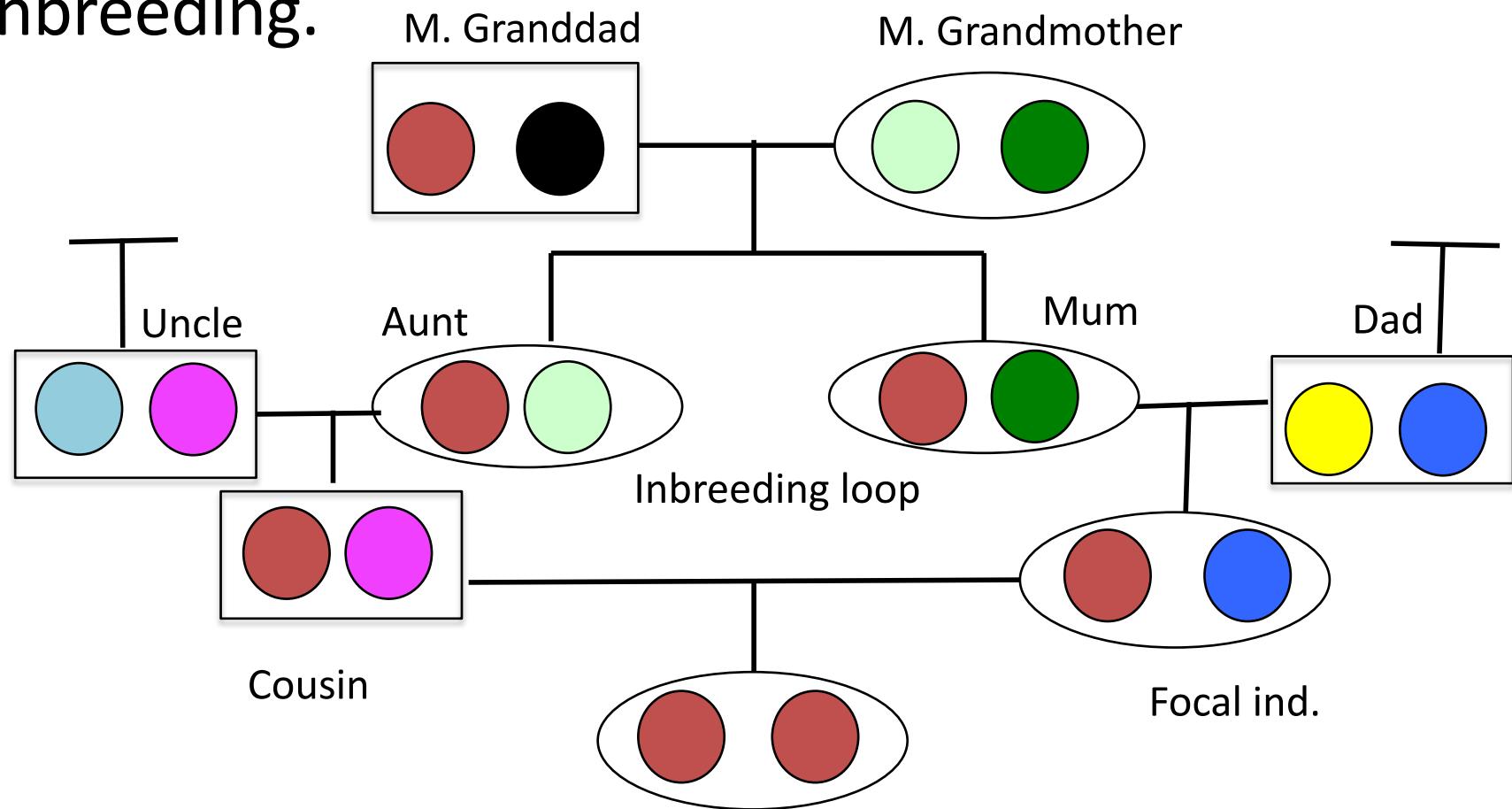


What's the probability that the child of first cousins
Is heterozygote?

If freq is p

Notes: Equation 2.7 page 20

Inbreeding.



What's the probability that the child of first cousins
Is heterozygote?

If freq is p

Notes: Equation 2.7 page 20

Notes: Equation 2.7 and 2.8 page 20

Generalized HW

Inbreeding coefficient $F =$
probability that an individual
inherits two alleles identical by
descent at a locus

AA

$$(1-F)p^2+Fp$$

Aa

$$(1-F)2p(1-p)$$

aa

$$(1-F)(1-p)^2+F(1-p)$$

Inbreeding:

Increases proportion of homozygotes
Decreases proportion of heterozygotes

Note no change in
allele frequency.
Only genotype frequency

Estimating Inbreeding coefficients

Notes: Equations 5&6, pages 9-10.



Figure 1. Blue- and white-flowered plants of *Linanthus parryae* from the Mojave Desert near Pearblossom, California, USA. D. W. Schemske.

Imagine that we knew the population frequency
Of the blue colour allele to be 0.1.

If we observed that only 10%
of the population are heterozygotes (blue/white allele),
what is our estimate of the inbreeding coefficient?

Population structure

- Inbreeding is just one form of assortative mating.
- A common form of assortative mating: population structure or population subdivision, where mating takes place within sub-groups of the whole population.

F statistics as a measure of population structure

- Wright (1943, 1951) defined F_{XY} as:
- the correlation between random gametes, drawn from the same X, relative to Y.
- Measures the reduction in heterozygosity of X relative to that expected in Y.
- Often in hierarchical manner: F_{IS} , F_{ST} , and F_{IT}
- There are a number of different estimators of F statistics.

We summarize the differences in allele frequencies across populations by F statistics



Figure 1. Blue- and white-flowered plants of *Linanthus parryae* from the Mojave Desert near Pearblossom, California, USA. D. W. Schemske.

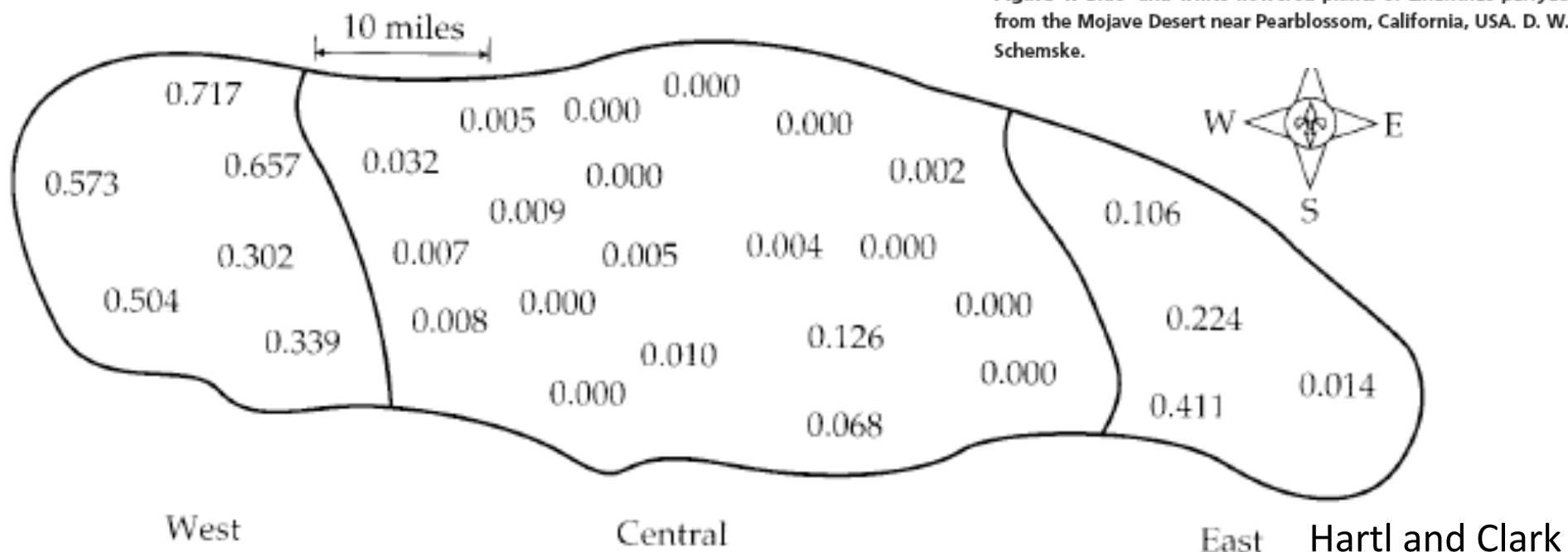
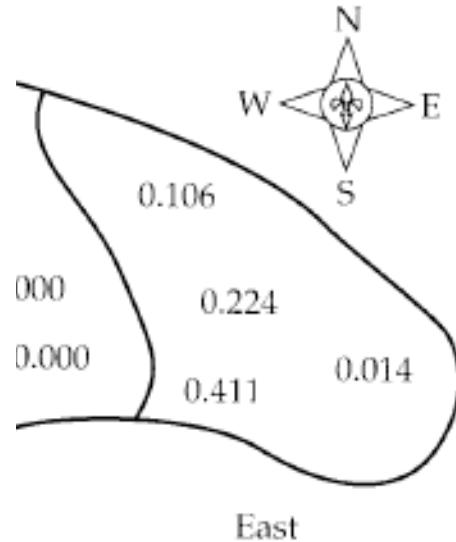


FIGURE 6.13 Estimated frequency of a recessive allele for blue flower color in populations of *Linanthus parryae* in an area of approximately 900 square miles in the Mojave desert. Each allele frequency is based on an examination of approximately 4000 plants over an area of about 30 square miles. (After Wright 1943a.)



Taken from Wright 1943



Figure 1. Blue- and white-flowered plants of *Linanthus parryae* from the Mojave Desert near Pearblossom, California, USA. D. W. Schemske.

	allele freq	Heterozygosity ($H_S = 2p_S q_S$)	$F_{ST} = 1 - H_S / H_T$
	0.106	0.190	0.383
	0.224	0.348	-0.132
	0.411	0.484	-0.577
	0.014	0.028	0.910
Average	0.189	0.262	0.146

$$H_T = 2p_T(1-p_T) = 2 \times 0.189 \times (1-0.189) = 0.307$$

$$\bar{F}_{ST} = 1 - \bar{H}_S / H_T = 0.146$$

Imagine that in the top population we observe that Individual Heterozygosity is actually 0.1
What Is F_{IS} and F_{IT} ?

- F_{ST} = proportion of the variance due to between-population (rather than within-population) differences.
- Low values of F_{ST} indicate that on average differences are found among individuals from the same population rather than in one population but not the other.

If you look at polymorphic sites in a sample of Maasai and Inuits, most differences are found *among individuals from the same population* rather than in one population but not the other.



In other words, the genomes of these two Inuits is only slightly more (~15%) similar to one another than are the genomes of an Inuit and a Maasai.