Relatedness inference using RNA-seq data from *Glossophaga soricina* bats

Franco, Enza

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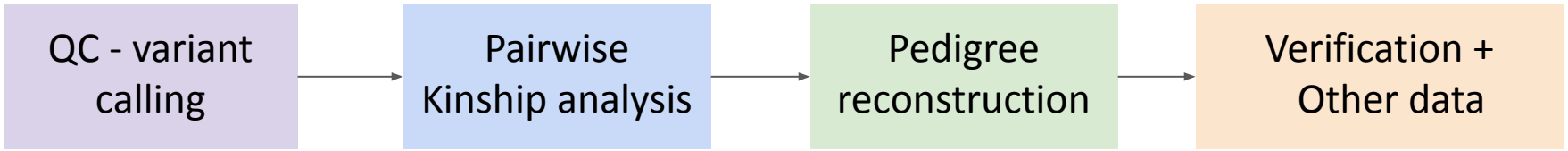
Relatedness inference in bats



- IBD (PRIMUS)
- Kinship coefficient (REAP or King)

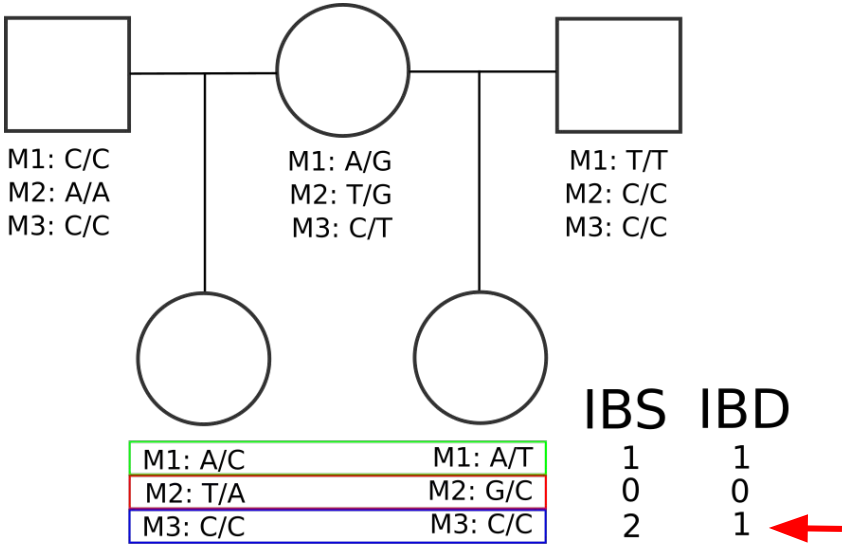
- Pairwise consistency checking PRIMUS
- Sex, Chr X, mtDNA, age

IBS is not kinship: the risk of overestimation

Identical by state (IBS) = proportion of alleles with the same state

Identical by descent (IBD) = proportion of alleles inherited by a common ancestor

Kinship = probability that two alleles sampled at random from two individuals are identical by descent (overall genetic relatedness expected from a pedigree)



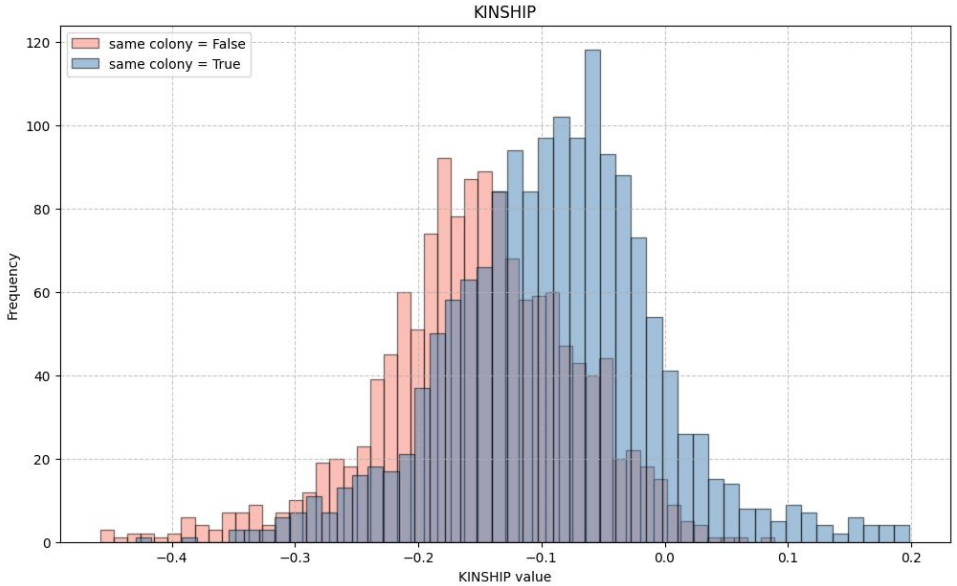
The half-siblings example

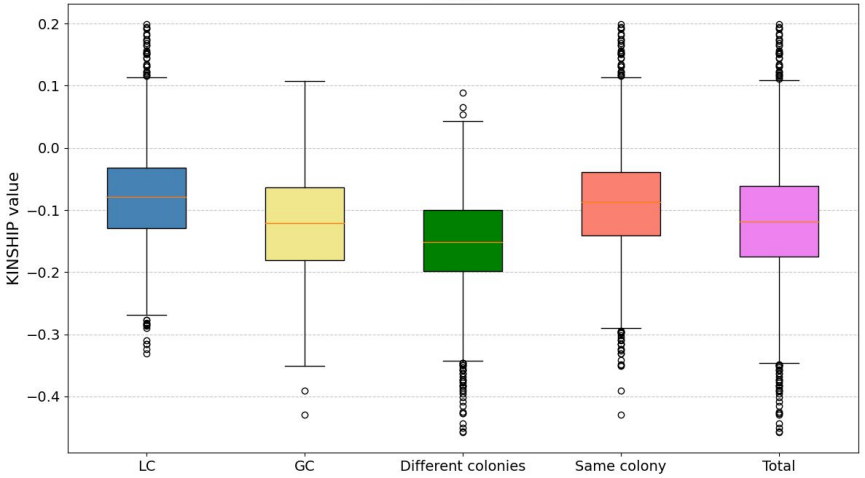
1. IBD implies IBS.
2. IBS do not imply IBD necessarily.
3. Considering IBS as IBD leads to **relatedness overestimation**.

Kinship coefficient analysis: individuals of the same colony are more related

55k high-quality markers (prepared to GN)

105 individuals -> 5460 pairwise analyses



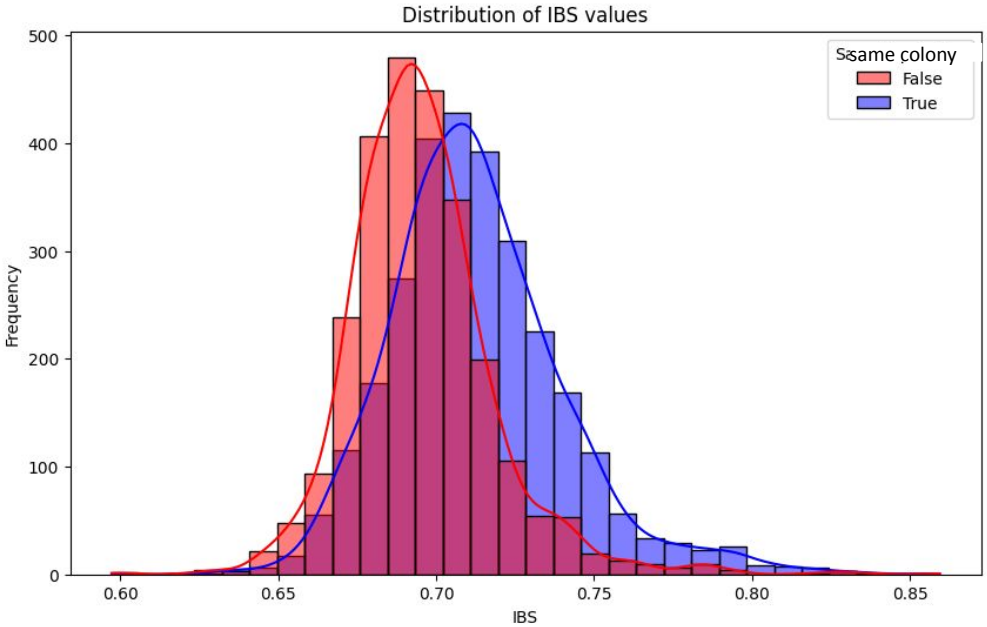


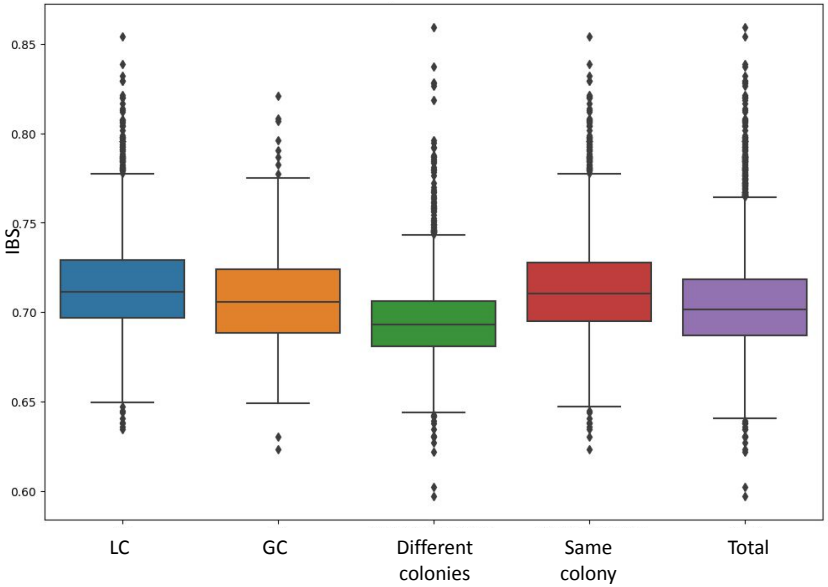
- Kinship ≤ 0 (unrelatedness)
- Kinship coefficient estimated using the method developed by Manichaikul et al. 2010 (https://doi.org/10.1093/bioinformatics/btq559)

IBS: same conclusion of Kinship

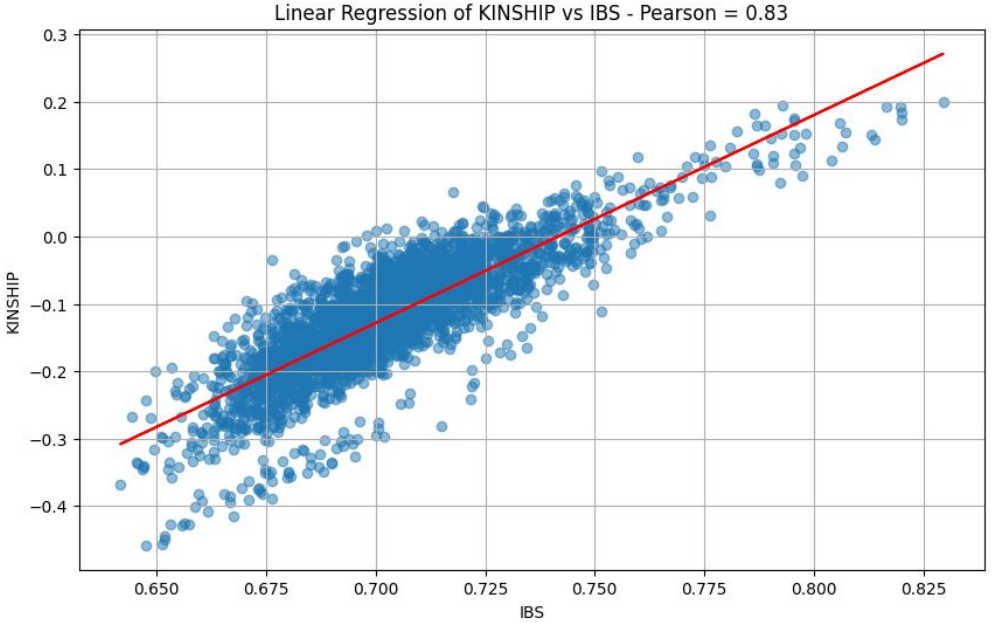
55k high-quality markers (prepared to GN)

105 individuals = 5460 pairwise analyses





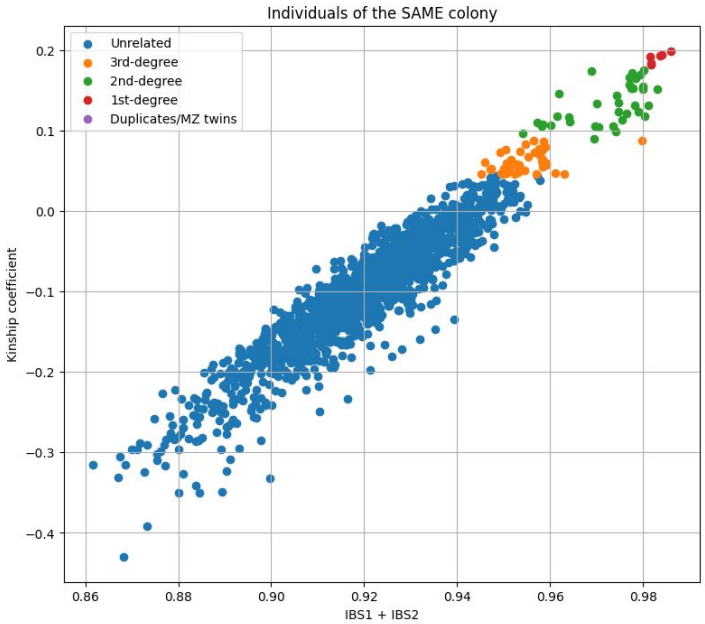
Kinship vs IBS: strongly correlates

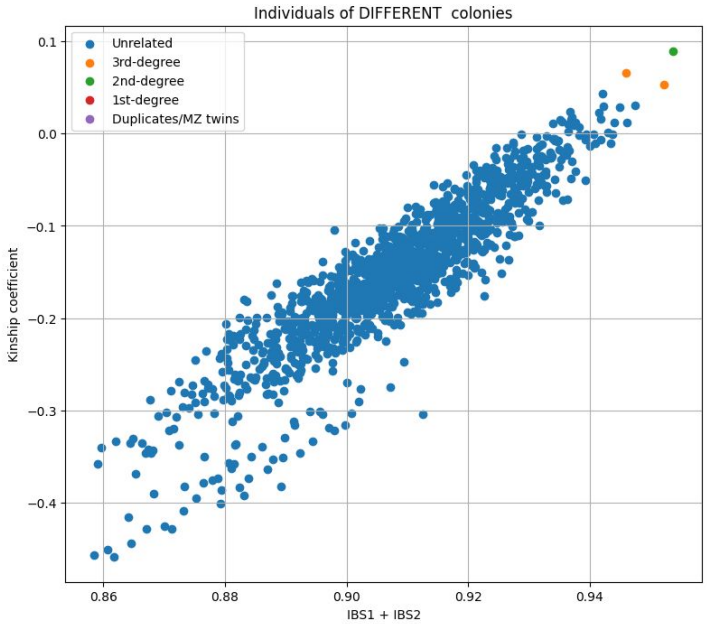


Kinship positively correlates with IBS (R pearson = 0.83)

NOTE: IBS is the proportion of shared alleles. Those markers with two shared alleles (IBS2) will sum 2, and those with one shared allele (IBS1) will sum 1.

Kinskip vs IBS stratified by relatedness





NOTE: Here IBS1 and IBS2 are directly summed (so it differs from just IBS). Here:

1 - (IBS1+IBS2) = IBS0

IBS0 could be interpreted as the proportion of markers where the pair of bats do not share alleles.

Kinship ≤ 0 (unrelatedness)

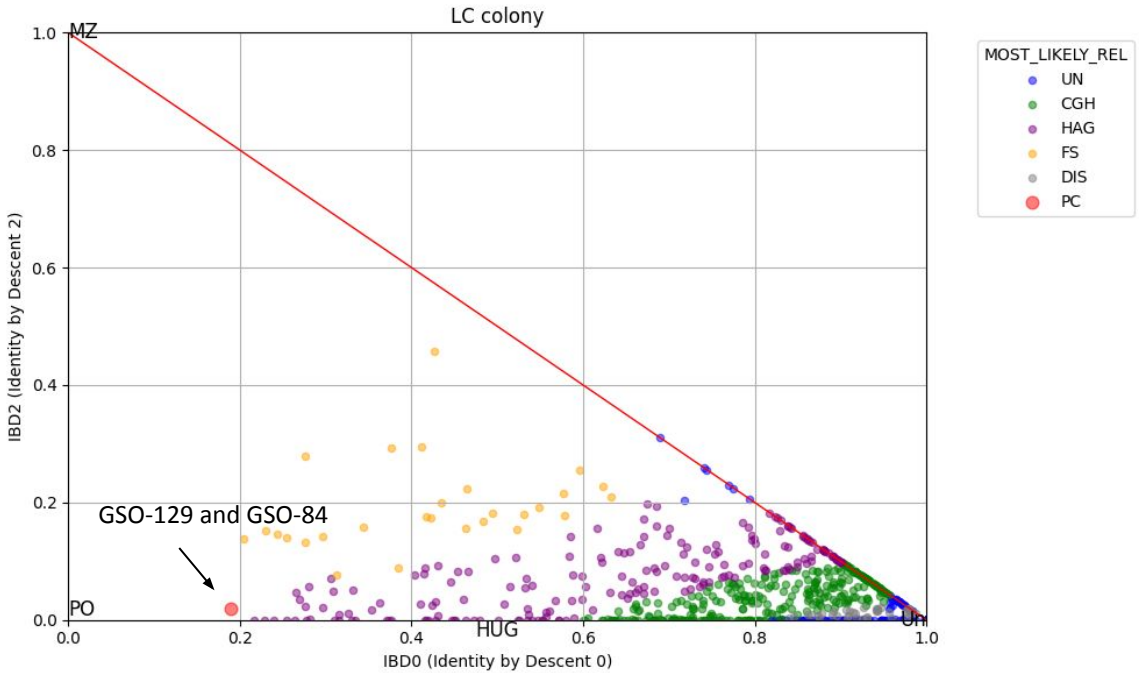
Each point is a pairwise comparison of two bats

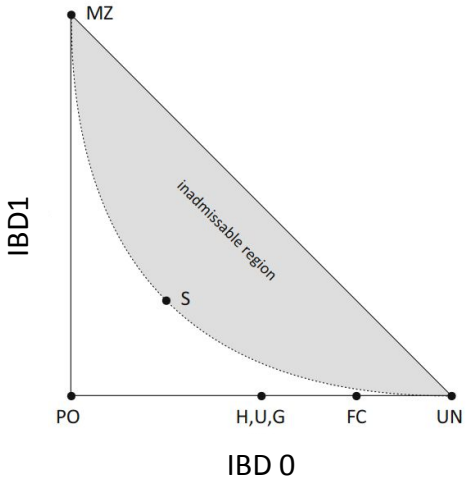
IBS1 + IBS2 is the proportion of markers sharing one or two alleles between compared bats.

Identical by descent analysis

IBD0 + IBD1 + IBD2 = 1

IBD0 = probability of sharing 0 alleles by descent
IBD2 = probability of sharing two alleles by descent





Vigeland, M. D. (2020). Relatedness coefficients in pedigrees with inbred founders. *Journal of mathematical biology*, *81*(1), 185-207.

Note: The problem of inbreeding

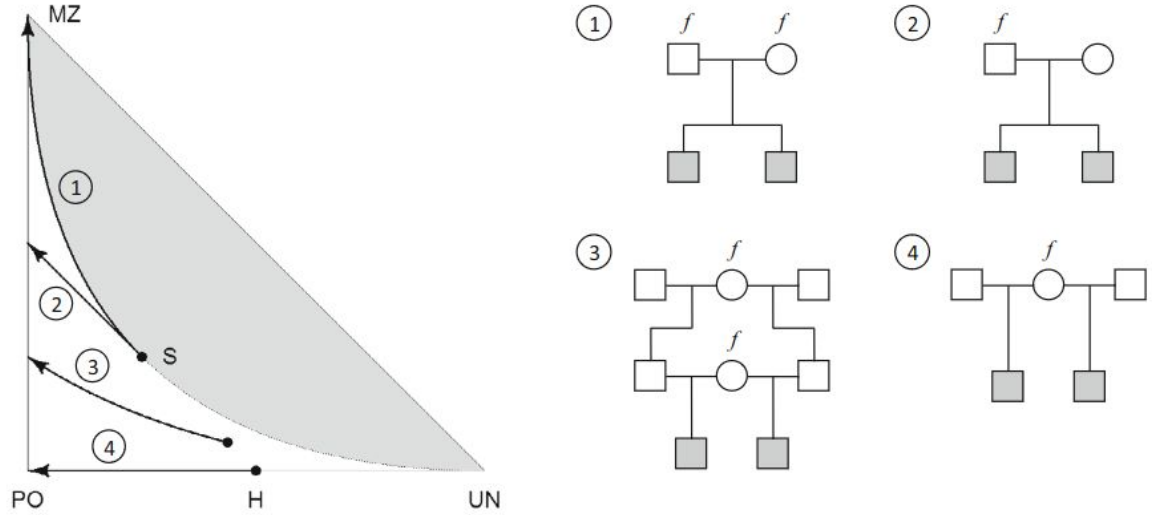
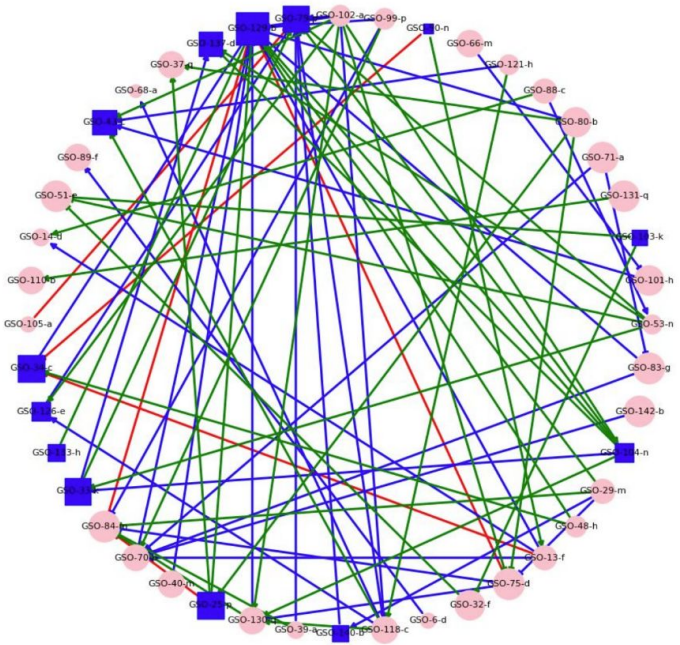


Fig. 4 The effect of founder inbreeding in full sib and a selection of full-and half-sib relationships. Each arrow traces the IBD coefficients as the level of founder inbreeding increases from 0 to 1

Panmixia (random mating) and relatedness in the LC colony



1st, 2nd, and 3rd degree relationships in the LC colony

reconstructed from the kinship analysis

edges (red) -> first degree relationship (e.g., parent, full siblings)

edges (blue) -> second degree relationships (e.g., grandparent, uncle, half siblings)

edges (green) -> third degree relationships (e.g., cousins)

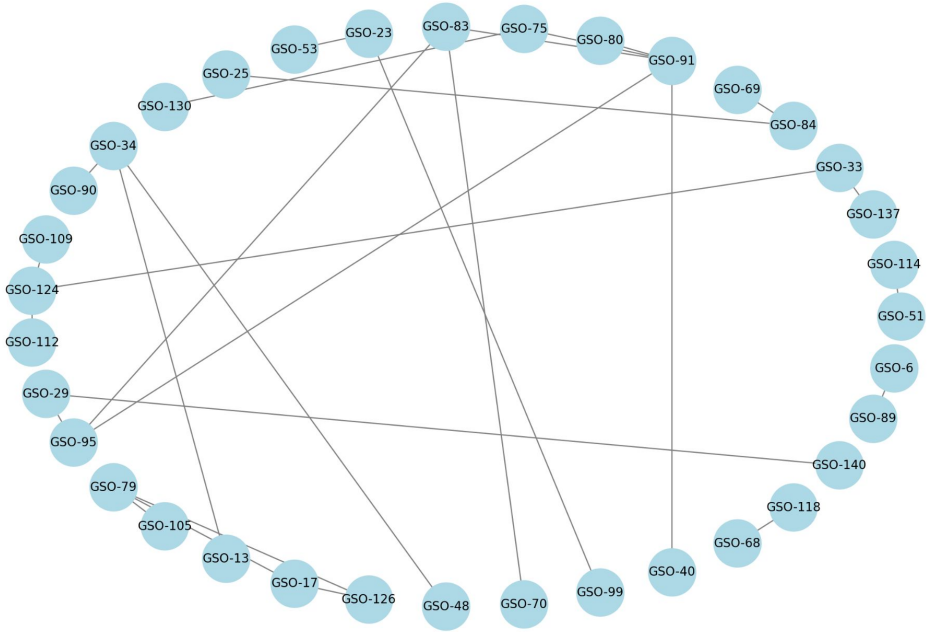
Females -> circles

Males -> squares

Age -> size

Consistency

First degree relationships



Consistent siblings