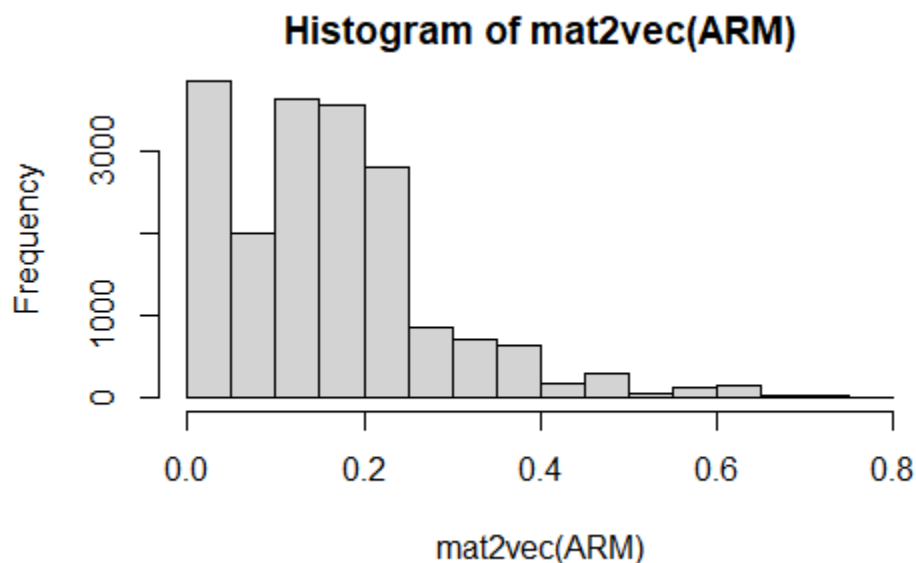
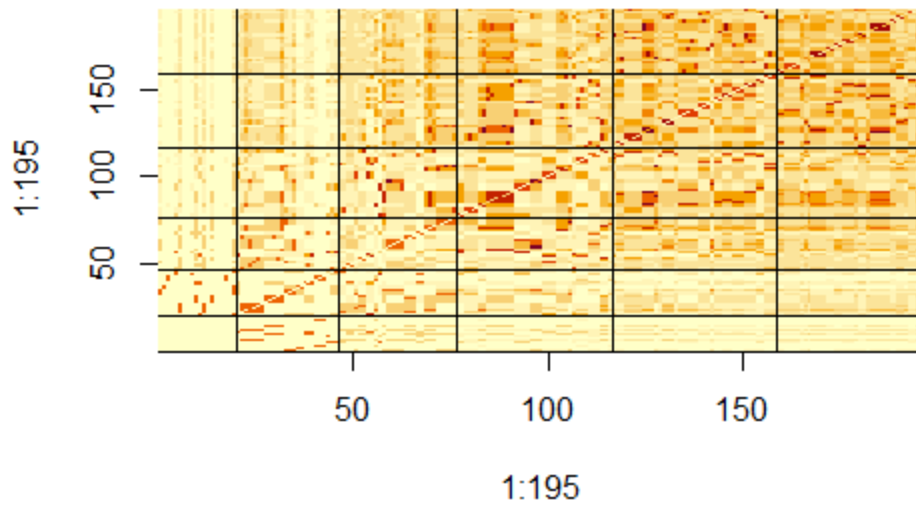


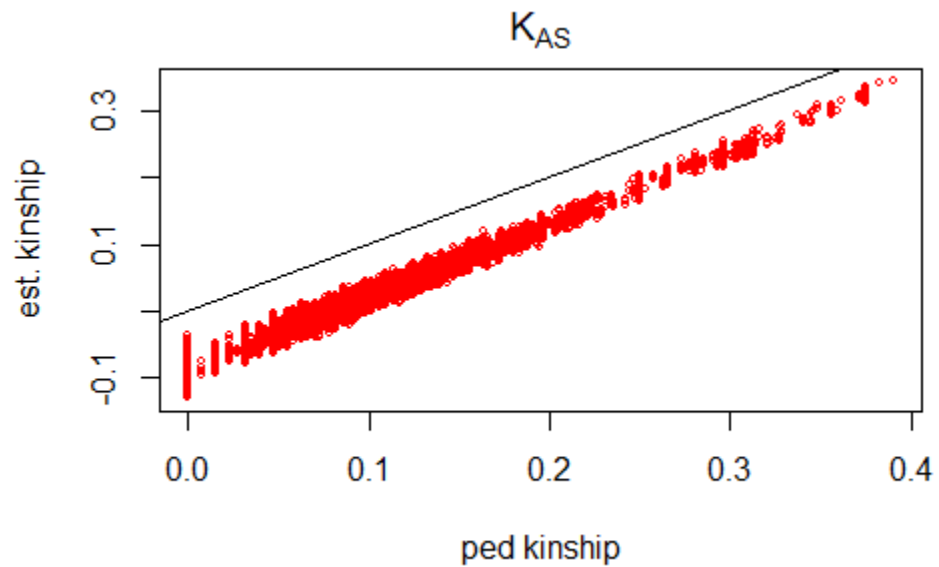
- Load a pedigree from a monogamous population using `read.table`.  
Explore the pedigree:
  - What are the first, second and third column?
    - ind (individual), dam, sire
  - How many founders in this pedigree?
    - 20
  - Find at least two families with sibships of four (just inspect the pedigree)
    - families: 28:32; 59:62
- Calculate the additive relationship matrix of individuals from this pedigree using `JGTeach::pedARM`.
  - What is the pedigree relatedness among the sibship previously identified? 0.5
  - and of these individuals with their parents? 0.5
  - Examine sibship 92:95. What is special about it? The parents are related (matrix values are not 1, 0.5, or 0)
- Plot a histogram of the relatedness using only off diagonal elements. The function `hierfstat::mat2vec` will be useful.



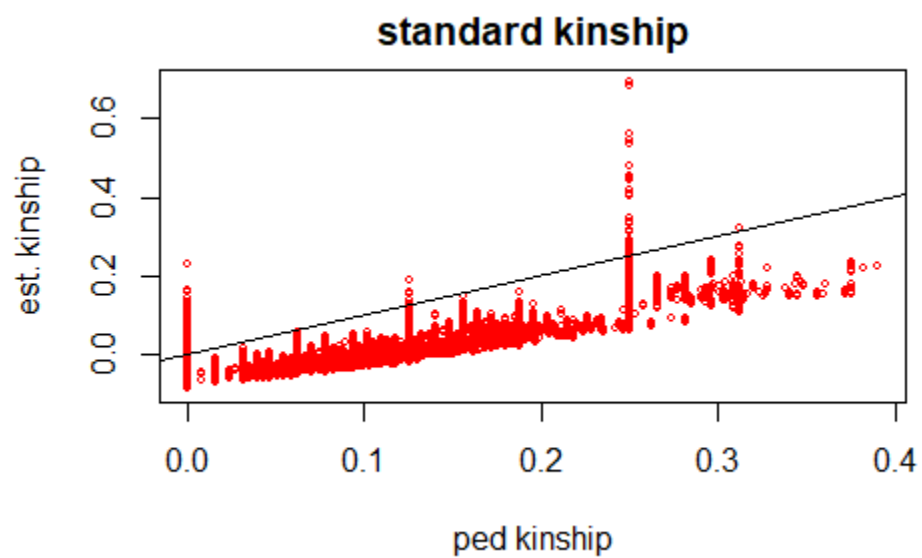
**Comments?** There is not a lot of inbreeding among the individuals  
 Transform the relatedness matrix into a kinship and inbreeding matrix using `hierfstat::GRM2kinship`.  
 Plot a heatmap of resulting matrix using `image` and `interpret`. We see increasing inbreeding



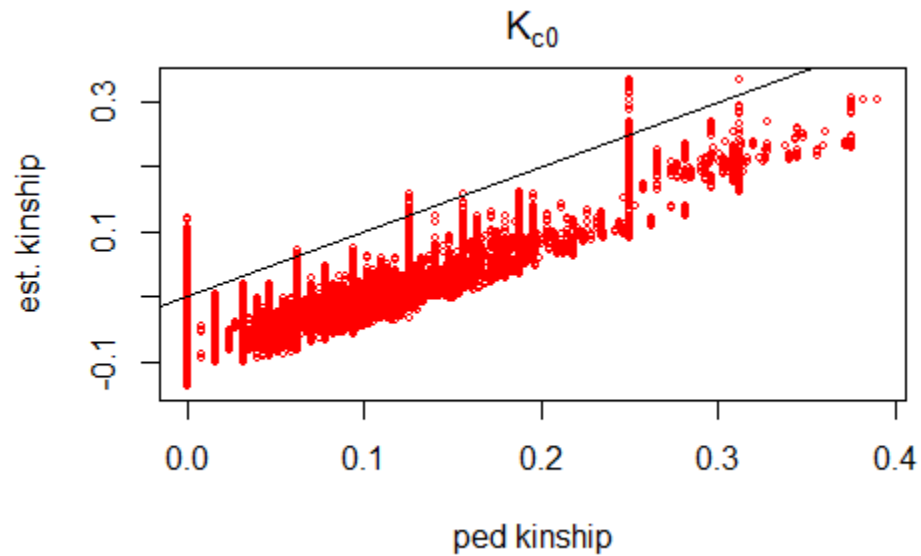
4. We have generated genotypes dosage from these individuals. First download, then load this file using `readRDS`, and compute
  - a. Allele sharing kinship using `hierfstat::beta.dosage`



- b. Standard GRM (average of ratios) as computed in e.g. GCTA using `gaston::GRM`;

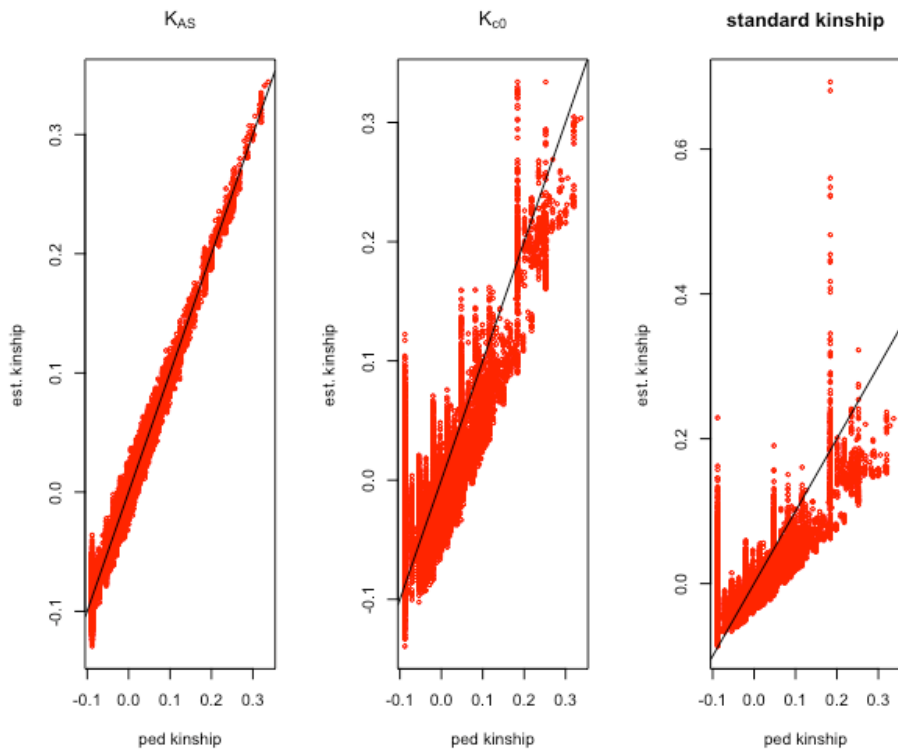


- c. Standard GRM (ratio of averages) using JGTeach::Kc0.



Compare each to the expected values obtained from the pedigree and discuss.

5. Redo these comparisons after having “rescaled” the pedigree kinship such that mean expected kinship is 0.



**Discuss.**

6. We will now compare these three estimators of genomic kinship using the subset of Chromosome 22 we used in previous practical. Start by computing the three estimators:
7. Produce a heat map for each (this may take some time, you might want to save the results to an external file for future inspection, hence the commented call to `png`), after having removed the main diagonal (which contains the self kinships), and arranging samples according to `super_population` first, and then `population`.

**Discuss the resulting heatmaps, in the light of what you know about human population demographic history.**