Practical example

Database of genotype information for a practical example: a file called Testset

Database description:

- input file type: genepop
- genetic markers used for genotyping: microsatellites
- number of genetic markers: 5
- total number of animals: 15
- number of subpopulations: 3

Program needed for the calculation: Genalex

1. Calculate average observed and expected heterozygosity, effective allele number and F_{IS} index across markers and breeds (subpopulations) in dataset. Describe the level of diversity resulting from all analysed parameters.
2. Calculate F – statistic (F_{IS}, F_{IT}, F_{ST}) and describe the level of diversity in the dataset.
3. Which breeds are the most genetically similar/distant in dataset based on the F_{ST} index and Nei's genetic distances? Explain your opinion.
4. What can you say about the state of diversity/genetic differentiation in dataset based on the results of PCA analysis?