Manual for KINGROUP v2.08+
Chapter 2
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Introduction

This chapter describes how to perform analysis reported in the following studies: (Konovalov 2006; Konovalov *et al.* 2005a; Konovalov & Heg 2008a; Konovalov & Heg 2008b; Konovalov *et al.* 2005b)

Population Allele Frequencies

The population allele frequencies could be inferred from the sample as per (Konovalov & Heg 2008a) via Menu | Alleles | Generate … and then by selecting "Konovalov&Heg(2008)" option.

Pairwise Relatedness

The pairwise relatedness estimators could be accessed via Menu | Relatedness | Pairwise.
- The "KINSHIP" option calculates relatedness estimates as per the KINSHIP program
- The "Konovalov&Heg(2008)" option calculates relatedness estimates as per (Konovalov & Heg 2008a)
- The "Maximum Likelihood" option calculates relatedness estimates as per (Konovalov & Heg 2008b)

Large data sets.

The displayed number of pair-wise relatedness values is limited to the maximum of 1000. If the complete set of the pair-wise values is needed, select the "**save to file**" check box in the "**Sort**" pane, see the following screenshot.
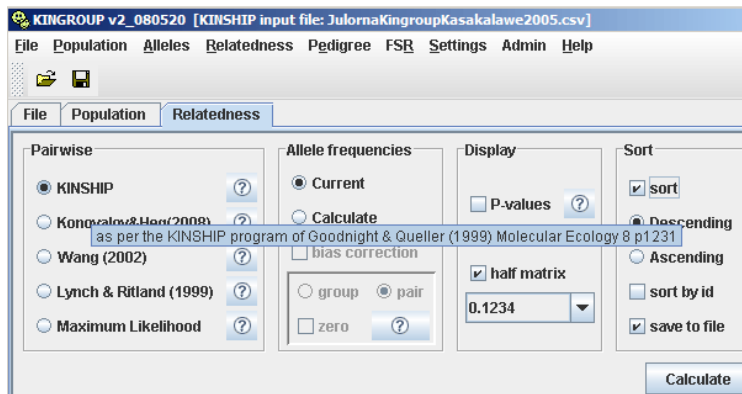
References

Konovalov DA (2006) Accuracy of four heuristics for the full sibship reconstruction problem in the presence of genotype errors. *Series on Advances in Bioinformatics and Computational Biology*, **3**, 7-16.

Konovalov DA, Bajema N, Litow B (2005a) Modified SIMPSON $O(n^3)$ algorithm for the full sibship reconstruction problem. *Bioinformatics*, **21**, 3912-3917.

Konovalov DA, Heg D (2008a) Estimation of Population Allele Frequencies From Small Samples Containing Multiple Generations *Series on Advances in Bioinformatics and Computational Biology* **6**, 321-331.

Konovalov DA, Heg D (2008b) A maximum-likelihood relatedness estimator allowing for negative relatedness values *Molecular Ecology Resources*, **8**, 256-263.

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