GENOTYPE

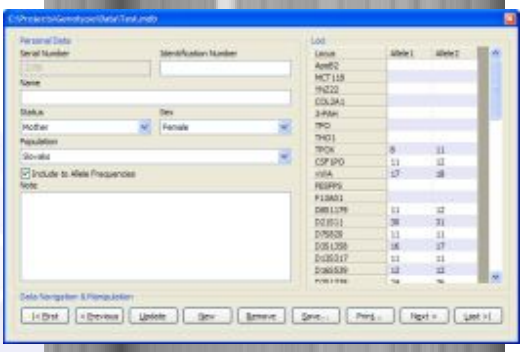
DNA identification software

- ✓ **personal identification** for forensic purposes
- ✓ **paternity and kinship** testing
- ✓ **population-genetic studies** and analyses
- ✓ **teaching** population genetic

GENOTYPE

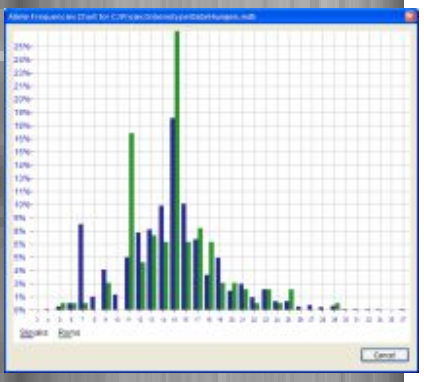
Basic Characteristics

The program Genotype makes it possible to create and evaluate a database comprising data on any number of individuals described by a set of basic characteristics (name, gender, etc.), with determined genotypes at any number of polymorphic genetic loci with co-dominant alleles. It is particularly designed to store and evaluate data on DNA polymorphism (SNPs, RFLPs, VNTRs, STRs), though it can be used also for other genetic polymorphic systems, including polymorphism of the mitochondrial and Y-chromosomal DNA. Within Genotype, separate databases can be established (and evaluated) at a time, with any number of populations in each of them. Genotype comes as a result of the cooperation of scientists from the Department of Molecular Biology at the Faculty of Natural Sciences, Comenius University, Bratislava, and software analysts from the private company Kvant s.r.o.



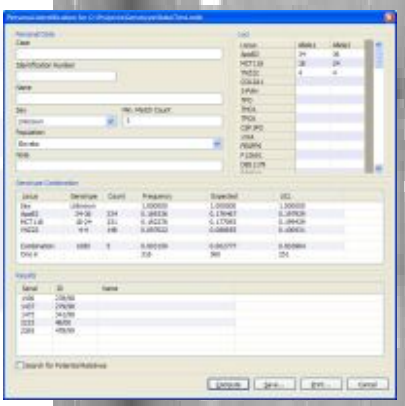
Population - Genetic Parameters

- any number of arbitrarily named populations and any number of examined loci with any number of alleles;
- the allele frequencies, their standard deviations and their 95% upper confidence limit;
- the genotype frequencies empirically observed as well as the genotype frequencies expected under random-mating (calculated from the allele frequencies assuming Hardy-Weinberg equilibrium) and their 95% upper confidence limits;
- the values of heterozygozity H (both empirically observed and expected under Hardy-Weinberg equilibrium), polymorphism information content PIC, and probability of genotypic identity of two individuals drawn at random from the database (PGI);
- the graphical output of both the allele and the genotype frequencies.



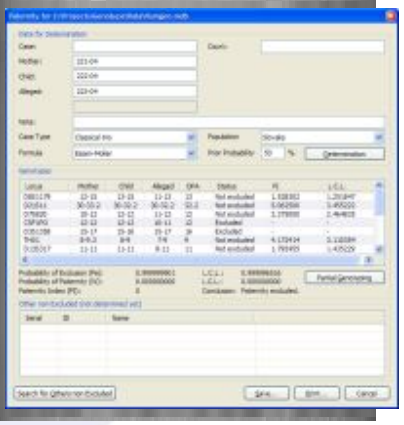
Paternity and Kinship Determination

- the exclusion probability Pe, i.e. the probability that a man, drawn at random from the population, will be excluded as a father of the given child;
- the paternity index PI as well as the probability of paternity W (under selected prior probability) using the Bayes theorem;
- motherless cases;
- fatherless cases;
- searching for other non-excluded individuals in the database;
- partial genotyping (assuming only a selected set of loci);
- silent alleles support.



Personal Identification

- searching for all individuals with a given combination of genotypes (or alleles) at a specified set of loci;
- calculating both the observed and expected frequencies of this combination;
- searching for potential first-degree relatives of the individual with specified combination.



KVANT s.r.o.

Kvant spol. s r.o., FMFI UK, Mlynska dolina
842 48 Bratislava, Slovakia
Tel/Fax.: +421 2 6541 1344/+421 2 6541 1353
www.kvant.com; kvant@kvant.com