SOFTGENETICS®
Software PowerTools for Genetic Analysis

Contact Information:
John Fosnacht
SoftGenetics LLC
The Oakwood Centre
Suite 350
State College PA 16803

FOR IMMEDIATE RELEASE

Kinship Analysis of Monoecious Plant and Invertebrate data added to GeneMarker Software

June 1, 2009, State College PA SoftGenetics LLC announced the addition of a new Kinship and Data Base searching function for Monoecious organisms has been added to its GeneMarker software. The new functionality provides Agricultural, Ecological as well as Entomological researchers with a single tool to perform the analysis of microsatellite data and Kinship analysis eliminating the need for often errant and tiresome data transfer into other Kinship Analysis programs.

GeneMarker's Relationship testing employs the rigorous statistical analysis of identity by descent (IBD) calculations to determine kinship levels . GeneMarker's database search tool identifies samples with the same STR profile and calculates the random match probability (the probability that a randomly selected individual from a population will have an identical STR profile at the DNA markers tested). The same tool also searches the database and identifies files with the highest likelihood ratio for each relationship level to the experimental sample. Genetic Analysis Parameters allow setting tolerances for mistyping or mutation, limiting the number of retrieved samples by LR score or total number of samples, parent/child, sibling and half sibling search results. Allele frequencies for different species and different populations within a species can be easily uploaded and used in the relationship testing applications. The 'Save to Database' function provides easy database updates in GeneMarker; it accepts current project genotype results, previously archived genotype .txt (tab or comma delimited) or .cmf file formats. The 'Kinship Analysis' tool provides a report table with probabilities and likelihood ratios across three generations for sample pairs.

"Database searches", states Teresa Snyder-Leiby, GeneMarker Product Manager, "for exact duplicate and near relative samples are extremely useful in applications such as determining plant and animal population diversity, relatedness of individuals within populations, identification of successful breeding individuals or clonal purity of asexually reproducing populations. Kinship analyses are powerful tools but have many challenges due to remote DNA sampling of animal populations, lack of information on known breeding pairs, and mobility of individuals (animal migration and seed dispersal). Short Tandem Repeats (STR), simple sequence repeats (SSR) or microsatellite analysis has the ability to provide complete individual profiles.

Microsatellites are variable regions in genomic DNA which are amplified with specific primers by Polymerase Chain Reaction (PCR). Many polymorphic plant and animal STR markers that follow Mendelian inheritance have been identified. The likelihood that unrelated individuals will share the same STR profile can range from 1 in a million or more, depending on the number of loci compared between the two samples. Related individuals have more shared loci than those that are unrelated. The higher the number and diversity of loci included in the genotype the greater the significance of the likelihood ratio results. Kinship formulas have been established in the literature to calculate the relatedness between individuals based on shared loci".

The company offers 30-day trials and no cost web-based training on its genetic analysis software packages Interested parties may request the software on the company website: www.softgenetics.com or via email: info@softgenetics.com.

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SoftGenetics, LLC specializes in the development of genetic analysis tools for both research and diagnostic applications. Hallmarks of SoftGenetics software tools are advanced technologies, providing exceptional accuracy, and sensitivity in an easy-to use Windows® user interface.