

AMPGEN

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Technology description

Summary

A parcel of windows-based routines, which is able to import DNA profiles directly from laboratory data to provide the statistical interpretation of a match (with user-prescribed stringency) in missing persons database, and will conduct kinship analysis, with the aid of DNA profiles of relatives. The report generated from this routine charts pedigrees, and provides confidence bounds for frequency estimates, and likelihood ratios. The routines are linked to disclosable summaries of validated DNA forensic population databases, with option of linking additional user-specified databases. The software is designed for a personal computer, so that it can be used in courts and in field offices. Help files, attached with the software, provide technical details of computations, which will also aid in training analysts for using the software.

The current version is able to evaluate the statistical strength of: (i) coincidental match probability in typical DNA forensic investigations, (ii) interpret DNA mixture evidence, (iii) assign missing persons in respective families in mass disaster scenarios, and (iv) conduct parentage and kinship analyses with DNA typing. Linked with worldwide and curated DNA typing databases, this software, with its graphic interphases, is user-friendly, in which the input data can be transported from laboratory analyzers without data re-entry, and hence avoids human transcriptional errors. The high throughput feature of the software will allow users to apply this tool in high volume laboratories conducting: (i) forensic, (ii) parentage, and (iii) pedigree-based studies. In a modular setting, AMPGEN will perform three groups of tasks. Once the program is initiated, the screen displays these three tasks:

Transfer evidence (i.e., computation of coincidental match probability for a single donor DNA profile); Mixture Analysis (i.e., exclusion probability and likelihood ratios for various mixture hypotheses); and Kinship Analysis (i.e., attribution of question profile as a family member of a specified set of relatives; standard or deficient parentage analysis being special case of such a kinship analysis).

Once a user specifies one or more of these tasks, relevant profiles can be imported (avoiding transcriptional error, or data re-entry), and a series of parameters can be selected, based on the standard operating procedures that generated the profile data. The user can click on the specific task to be performed during the session, so that the routine will proceed to gather input parameters and data for the relevant sets of computations.

Institution

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