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PARENTE: Computer Program for Parentage Analysis

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PARENTE is a user-friendly software package that conducts parentage inference using molecular data from diploid codominant markers. Based on the principle of genetic compatibility, PARENTE looks for maternity, paternity, or simultaneously for both potential parents, using multilocus genotypes and birth and death dates of individuals (if available). It also calculates the probability of successfully allocating an individual offspring to its parents. PARENTE is free and can be downloaded from: <http://www2.ujf-grenoble.fr/leca/membres/manel.html>.

Parentage Analysis

Parentage analyses using multilocus genotypes are widely used to assess reproductive success, mating patterns, kinship, and fitness in natural popula-

tions and are gaining widespread use with the development of highly polymorphic molecular markers (Luikart and England 1999; Petrie and Kempnaers 1998; Queller et al. 1993; Sunnucks 2000). These analyses are especially useful when studying breeding systems with multiple mating, e.g., when individuals of one sex have more than one mating partner of the opposite sex. In this case, it is possible to investigate the "genetic mating system" of the species, to evaluate the actual reproductive success of males (Coltman 1999; Pemberton et al. 1992), and to construct pedigrees. Parentage analysis allows one to confirm monogamy in some species (Brotherton et al. 1997; Heller et al. 1993; Ribble 1991) and to demonstrate extrapair copulation in others (Girman et al. 1997; Goosens et al. 1998; Sillero-Zubiri et al. 1996). They are also useful when direct mating observations are difficult (Clapham and Palsboll 1997; McRae and Kovaks 1994).

The general principle of parentage analysis is to assign assumed parents to an individual based on the genetic compatibility between the candidate parents and individuals of the next generation. Many approaches, based on maximum likelihood estimations and/or Bayesian inference, have been developed recently, but they often remain theoretical and difficult for biologists to apply (Bernatchez and Duchesne 2000; Gerber et al. 2000; Neff et al. 2000a, 2000b, 2001). A few computer programs that perform parentage analysis are available (e.g., PROBMAX, Danzmann 1997; CERVUS, Marshall et al. 1998; NEWPAT, Amos, available online at <http://www.zoo.cam.ac.uk/zoostaff/amos/newpat.htm>; PATRI, Nielsen et al. 2001). Although they can take into account typing errors, mutation rates, null alleles (CERVUS), sex-linked loci (NEWPAT), or even an incomplete sampling of the candidate parents (PATRI and CERVUS), they do have some limitations. One major drawback is that most of these programs assign only one parent to an offspring, usually assuming the previous knowledge of the other parent (such situations apply only to species providing parental care). Additionally, compared with paternity analysis programs, parentage analysis software seldom provides the identification of offspring-parental pairs. PROBMAX is the only program able to find pairs of parents, but the previous knowledge of parental mating combination is required, and this is not often available

from field data. It is also possible to find both parents by running CERVUS twice—this can be a difficult and time-consuming process. Another weakness of the programs is that they are restricted to only one generation and do not take into account birth and death dates. As a consequence, they require that some individuals be defined as candidate parents and others as offspring.

The user-friendly application PARENTE (which means "parentage" in French) facilitates parentage analysis and allows consideration of frequent field situations, which is not possible with presently available software. PARENTE can determine paternity, maternity, and also both parents simultaneously (without a priori assumptions) for each offspring, since the mother is not always known from field data. In addition, our software uses the ages of individuals (if available), since it is necessary in parentage analysis to consider only individuals old enough to be potential parents.

Program Description

Principle

PARENTE performs parentage analysis using data from all types of diploid codominant markers (i.e., microsatellites, SNP, allozymes, and so forth). It infers parentage for every individual in the genotype file, or for an individual of interest, considering the dates of birth and death of each one. As a consequence, only individuals old enough to reproduce and still be alive when the young are conceived are considered as potential parents. In this way, several generations from the sampled population can be considered in the same file.

First, from one single genotype file and for each individual, the program builds a list of potential parents (single mothers, single fathers, or pairs) according to birth and death dates. Then, in this list, the program looks for potential mothers and fathers for each individual according to the principle of genetic compatibility: for each locus, the young should inherit one allele from his mother and one from his father. Considering that errors are possible (e.g., mutations, typing errors, null alleles), some "allelic incompatibilities" can be allowed between the offspring and the parents. This error definition makes it possible to accept some loci for which one of the alleles cannot be inherited by any of the parents.

Probability Computation

The probability of successfully allocating an individual offspring to its parents is based not only on its multilocus genotype but also on the error rate and the sampling rate of the population.

First, the program calculates the allelic frequencies for each locus in the sampled population. Next, it computes the probability of the expected genotype of an offspring, given the observed genotypes of the triplet (mother, father, offspring), assuming a uniform weight for all potential parents pairs (see the program documentation for further details). The program assumes that the loci are in Hardy-Weinberg equilibrium, do not show linkage disequilibrium, and exhibit a Wright-Fisher type of reproduction (finite and constant N , random mating with respect to the gene being studied, and nonoverlapping generations).

Input Files

A single input file (text) is required for the data, containing the names and the multilocus genotypes of the individuals. If available, the program uses the following optional individual data: sex, date of birth, date of death, and multilocus genotype. A second file contains several parameters defined before running the software: the minimum age difference between a young and his potential father and mother, the error rate, the maximum number of missing alleles per individual that is acceptable to perform the analysis, an estimate of the proportion of the population sampled, and the maximum number of allelic incompatibilities between genotypes of offspring and parents.

Output File

Four output files are produced: a first file with compatible parent pairs for each individual, two files with single parents (one for potential fathers and one for potential mothers), and a file with the

individuals for which no parent has been found.

Obtaining the Program

PARENTE is free and can be downloaded from: <http://www2.ujf-grenoble.fr/leca/membres/manel.html>. It is available on a PC Windows platform. The distribution of the package includes executable programs, sample test data files, and documentation of the program. The binary file is also available upon request from the authors.

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