PedAgree

version 1.00

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A Program for Detecting Autosomal Marker Mendelian Incompatibilities in Pedigree Data

Language : C, C++
Executables :

- Linux
- Solaris 2.6-9
- MS-Dos

PedAgree detects autosomal marker Mendelian incompatibilities.

1 Command

- Linux and Solaris: `PedAgree [inputfile]  [n]  [> outfile]`
- MS-Dos: `PedAgree inputfile [n] > outfile`
- `inputfile`: A pedigree file with the following format :
  `pedigree ident father mother sex variable1 variable2...`
  PedAgree needs pedigree file only and doesn't need locus file. The pedigree file have a very strict format because PedAgree need to distinguish markers from other variables.
  - `pedigree`, `ident`, `father` and `mother` can be a string (maximum number of characters is 15).
  - `sex` must be `1` for males or `2` for females.
  - Variables can be markers, qualitative or quantitative traits.

  Each field is separed by a tab. Marker information must be considered as a field and each allele must be separed by at least a blank. Marker alleles must be numbered alleles between 0 and 160. Alleles don't need to be recoded. But sometimes, the number of alleles can have a influence on the execution rapidity. If a marker have fewer 160 alleles and the maximum number of alleles is 160, you must recode alleles. The maximum number of variables is 100 and the maximun size of a record is 1060 characters.
- `n`: `n` is the maximum number of parental genotypes by nuclear family. `n` must be largest than 32. `n` value has an influence on the execution rapidity. Default is 256.
- `> outfile`: to have results on a file.
- Without parameter : PedAgree will ask you `inputfile` and `n`, and doesn't perform with `outfile`.

2 Output

2.1 Format errors detection

Format errors are described. The first record give the pattern. There are several kinds of format errors:

- Fields `pedigree`, `ident`, `father`, `mother` and `sex` with a blank.
- If there is not conformity with the first record.
- If the firt character of a field is a blank.
- If an allele is not a integer.
- If a marker has more than two alleles.
- If sex is not `1` or `2`.
- If allele number is greater than 160.

Individuals half typed are checked because such a situation is unusual, but it's not a format error. PedAgree can handle this situation without difficulty.

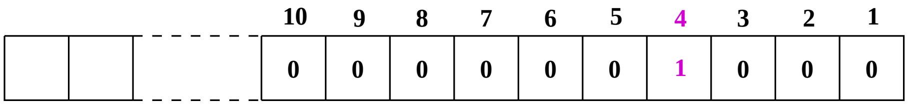
2.2 Incompatibilities detection

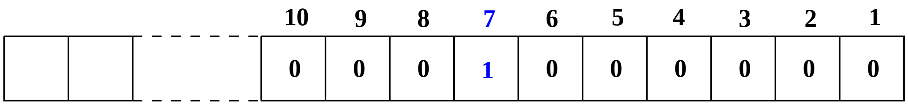
If there are no format errors, following informations are given:

- Number of records
- Number of pedigrees
- Size of the largest pedigree
- Number of variables
- Number of markers
- Number of alleles from each marker
- Inbreeding loop(s)
- Incompatibilities description (cf chapter 4). Pedigree and ident names are kept.
- If it's necessary to increase `n`, the maximum number of parental genotypes by nuclear family.

3 Data encoding

PedAgree uses assembler. A marker with two alleles **4** and **7** is encoding like this:





Algoritm uses logical functions.

4 Incompatibilities detection

The program performs four steps for each pedigree and each marker locus.

4.1 First step: Nuclear familiy incompatibilities

The first step detects mendelian incompatibilities in each nuclear family of a pedigree using the known individual's genotypes. This step checks for inconsistencies between parents and offspring considering both parents simultaneously. Every nuclear family in a pedigree is checked even if an error is detected for another nuclear family in the same pedigree.

4.2 Second step: Incompatibilities between nuclear families

The second step checks nuclear family relationships This step is performed if no error was detected in the first step.

4.3 Third step: Multiple mariages

The third step checks nuclear family relationships for parents who have children with different spouses. This step is performed if no error was detected in the first and the second steps and if there is at least a multiple mariage.

4.4 Fourth step: Inbreeding loops

Inbreeding loops and mariage loops don't need to be break. Mariage loops are treated like multiple mariages. Inbreeding loops are treated. This step is performed if no error was detected in the first, the second and the third sped and if there is at least an inbreeding loop.