PEDIG:
a Fortran Package for Pedigree Analysis
Suited for large populations

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This software, specifically developed for the analysis of large populations, is a set of independent programs written in Fortran, to calculate probabilities of gene origin, relationship and inbreeding coefficient, and to characterize the quality of pedigree information.

V6 updates:
- *ngen.f, prob_orig.f, segreg.f* with a reference population provided by the user
- *contribution.f* provides many more outputs
- *colleau.f*, *lineage.f* programs added

V4-V5 updates:
- Most programs in dynamic allocation
- Binaries provided for linux
- Modification of *ped_util.f* to cope with delimiters, codes of unknown parents and to propose different codifications of individuals in output file

V3 update:
- Addition of *verif_ped.f, contribution.f, anc_comm.f* programs

V2 updates :
- Addition of program *intgend.f*
- Addition of program *grain.f* from R Baumung
- Création of the output file '*list_ancestors*' by *prob_orig.f*, usable as input file by *grain.f*
- Small bugs fixed

Content of the zip file

This downloaded archive includes 7 directories:
- doc: PEDIG User's guides in French and English, as well as some papers derived from it.
- Source: complete and self-sufficient source codes
- Bin: executables for Windows (Dos)
- Bin_linux: executables for Linux
- Ex1, ex2, ex3, ex4: examples gathering the input, parameter, log and output files of the programmes

For Windows or Linux, executables of repertory bin or bin_linux can be directly used. For other operating systems or in case of recompilation need, a fortran compiler is needed. For Windows, the free gfortran compiler is available at https://gcc.gnu.org/wiki/GFortranBinaries

This software is freely available at
https://eng-gabi.jouy.hub.inrae.fr/services-resources/software/pedig

Citation : **Pedig should be cited as :**

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General presentation of the programs

Preparation of a pedigree file for the other programs

Let us assume you have a complete and large pedigree file with original Ids (14 digits maximum, with unknown parents coded in a standardized way, eg, with '0') and you are interested only in the ancestors of some individuals of interest. The program *ped_util* can :
- select the individuals of interest and trace back all their ancestors
- if requested, trace back only on a limited number of generations
- if requested, iteratively discard useless pedigree information (i.e. ancestors without pedigree and with one progeny only in the selected subpopulation)
- recode this pedigree sequentially, according to animal Id order (option 'N'), or parents before progeny (option 'T'), of progeny before parents (option 'R')
- if requested, save some accompanying information as sex or birth year, which is used by several programs.

An example is provided in 'ex3'. The file 'geneal' included all ancestors of individuals in the file 'reference', based on the complete pedigree file 'original_geneal'.

Pedigree checking

The program *verif_ped.f* checks that the pedigree is possible. An impossible pedigree corresponds an individual present in his own pedigree. If the program finds a pedigree error, it performs several searches to propose corrections.

An example is provided in 'ex4'.

Characterization of the pedigree information

The program *ngen.f* computes the average number of known ancestors, the percentage of known ancestors per generation, and the number of equivalent complete generations traced (defined as the sum over all generations of the proportion of known ancestors at each generation). These statistics are provided by sex and birth year, or for a reference population provided by the user. These statistics are computed only for individuals with at least one known parent. The percentage of known ancestors is stored in an output file for each individual or for the reference population. These parameters could be useful, for instance, to rigorously interpret and compare inbreeding coefficients across individuals or years, by restricting the analysis to individuals with the same amount of pedigree information.

The program *anc_comm.f* searches for ancestors common to a given group of individuals or common to the parents of the individuals of this group. For each ancestor common to all parents of these individuals, it generates a reduced pedigree file, limited to the necessary pathways between this ancestor and the individuals analysed. The number of output files is equal to the number of such ancestors. This program is particularly useful to draw a

genealogical tree up to a common ancestor of a group of individuals (eg, affected by a common recessive defect).

The program *intgen.f* computes generation intervals by sex and birth year of the progeny on the four sire-son, sire-daughter, dam-son, and dam-daughter pathways. It uses the birth year information in the pedigree file.

The program *intgend.f* computes generation intervals in days, by sex and birth year of the progeny. It uses the birth date information in the pedigree file, assumed to be on the yyyymmdd format and on position 4 in the file. Only complete and valid dates comprised between January 1st 1950 (19500101) and December 31st 2010 (20101231) are used.

The program *imp_ped.f* prints the parents, grandparents, greatgrandparents… of a list of individuals. The number of generations is given by the user. The user has to give the column number of the animal identification.

The program *lineage.f* trace back the maternal and paternal lineages of each individual. The maternal lineage is the female founder on the maternal pathway. The paternal lineage is the male founder on the paternal pathway.

Inbreeding

Two programs are available to compute inbreeding coefficients of all individuals in a population. The first one, *meuw.f*, uses the method described by Meuwissen and Luo (1992), which is a modification of the method of Quaas (1976). This approach uses the Cholesky factor of the relationship matrix. According to Meuwissen and Luo, each row of this factor is built by tracing the entire pedigree of each individual and the inbreeding coefficient is then obtained from the elements of this row and from the inbreeding coefficients of the ancestors. This method is very fast, at least for pedigrees with less than 15-20 generations and should be preferred for standard analyses. It also provides the inverse of the Mendelian variance to be used in $\mathbf{A}^{-1}$.

A second program, *vanrad.f*, relies upon VanRaden's method (1992), derived from the tabular method. Its principle consists in building the relationship matrix (max size=5000) of each individual and of its ancestors. The inbreeding coefficients of all these animals are then deducted from the diagonal elements of this matrix. This program is about three times slower than *meuw.f* but it offers two interesting options. (a) It makes it possible to compute inbreeding coefficients for a given number of generations considered and, therefore, to distinguish close from far inbreeding. (b) It also makes it possible to assume inbred or related founders and this assumption is very useful when the pedigree information is heterogeneous. Note, however, that these two options are mutually exclusive.

These two programs provide inbreeding coefficients of inbred individuals in an output file.

The programme *grain.f* (Baumung et al, 2015) computes ancestral and partial inbreeding by simulation and « gene dropping ». Different indicators are available :
   (1) classical inbreeding coefficient
   (2) ancestral inbreeding (f_{a_BAL}) according to Ballou's definition (1997) with the following iterative formula: $f_a = [f_{a(s)} + (1- f_{a(s)})f_s + f_{a(d)} + (1- f_{a(d)})f_d]/2$, where f_a and f are ancestral and classical inbreeding. Indices s or d represent values for sire and dam. In the formula, f_a and f are assumed to be independent. If not, f_a is over-estimated.
   (3) ancestral inbreeding (f_{a_KAL}) according to Kalinowski's definition (2000). The classical

coefficient is split into two parts, whether alleles already have met inbreeding in the past (ancestral inbreeding, f_{a_KAL}) or meet it for the first time (new inbreeding, $f_{\_new}$).

(4) ancestral inbreeding (f_{a_BAU}) according to Baumung's definition. The concept relies on the fact that alleles having met inbreeding in the past are more likely to be not deleterious than the other.

(5) Partial inbreeding coefficient, ie the probability that an individual is homozygous for an allele transmitted by a specific ancestor. The sum over all ancestors is the total inbreeding coefficient (Lacy et al. 1996; Lacy 1997).

Probabilities of gene origin

The program *prob_orig.f* computes the probabilities of gene origin for a reference population, ie a group of individuals defined for instance according to their sex and birth period, or a list provided by the user. These probabilities are combined all together to estimate an effective number of founders. The output file provides the non-zero contributions of each ancestor (founder or not) on one hand, and the non zero contributions of each founder on the other hand. The founder contributions sum to one, whereas the ancestors contributions sum to more than one, due to the redundancy.

Optionally, this program iteratively detects the ancestors (not only founders) with the greatest marginal contribution, as defined by Boichard *et al* (1997), and combines these contributions into an effective number of ancestors. This effective number of ancestors is lower than the effective number of founders because it accounts for bottlenecks in the pedigree. It is also less sensitive to missing pedigrees.

This programme provides an output file called '*list_ancestors*' which can be used as an input file by *grain.f*

The program *segreg.f* simulates the segregation of founder alleles in the population, estimates founder gene frequencies by gene counting in the reference population and combines these frequencies to estimate the effective number of remaining genomes in the reference population.

A frequent application of probabilities of gene origins is the computation of the contributions of a limited number of origins to a population, as well as their evolution over time. For instance, one could be interested in the evolution of the contributions of the different original breeds in a crossbred population or in a synthetic line. This can be done by the repeated use of *prob_orig* by defining different reference populations but this is tedious. The program *etr.f* performs this analysis in one run. It relies on the classification of the founders, allocated to a number of origins. The origin of the founders should be provided in the pedigree file. Optionally, when the origin is not known exactly, because the pedigree information is incomplete, default values of genetic composition could be provided according to sex and birth year. If this information is omitted, an individual with unknown parents is assumed to belong to origin number one. Optionally, the output file provides the genetic composition of each individual.

The *contribution.f* program computes the contributions of a list of ancestors to a reference population defined by sex and birth year or according to a list provided by the user.

Relationship Coefficients

Computing the entire (or even a part of the) relationship matrix of a large population is a huge task. A convenient way to do it is to generate a progeny from all possible matings and

to compute the inbreeding coefficient of these progeny. Three programs are provided, either to compute a small relationship matrix or to get an estimate of the average relationship level in a population.

The programs *par3.f* and *parente.f* compute the complete relationship matrix for one or two groups of individuals. The algorithms are very different.

In *parente.f* , the individuals of interest and all their ancestors are listed from the pedigree file, and the corresponding complete matrix is built with the tabular method. Only the part of this matrix corresponding to the individuals of interest is saved. If two groups are defined, the output distinguished the within and between groups relationships matrices. **This method is suited to a limited number of individuals of interest (several dozens or hundreds).**

Alternatively, *par3.f* builds the relationship matrix term by term by generating a progeny for each couple of interest and computes its inbreeding coefficient with Meuwissen's method. In contrast with the previous program, it does not present any strong limitation in terms of memory. Due to its fixed cost (inbreeding coefficients are computed first for all parents in the pedigree file), *par3* is preferable for large applications, whereas *parente* is recommended in small applications. Note however that par3 can be long for large applications: for the example provided in *ex3*, *par3* took about 2 mn to compute about 10 million coefficients).

The program *par2.f*, conceptually very close to *par3.f,* estimates the average relationship between a set of individuals on one hand, and a reference group on the other hand. The list of individuals of interest is provided in a second file, in addition to the pedigree file. The population of reference could be defined either from the pedigree file by selecting a subgroup according to its sex and birth year, or in the third file. A progeny is generated from each mating and its inbreeding coefficient is estimated by Meuwissen's method.

To estimate the average relationship level in a large population, the program *par.f* computes relationship coefficients on repeated random samples, according to predefined strata: random samples of males or females in the whole population born during a given period, random samples of complete herds ; random samples within region (assuming that the herd identification provides the region Id) ; random couples. The method is the following: determination of the candidate reference population; random sampling in this reference population; computation of the relationship matrix with the tabular method ; computation of the corresponding statistics.

Finally, *colleau.f* implements the method described by JJ Colleau (2002) to estimate relationships between groups of individuals. This method is by far the most efficient to compute relationships. The user provides a list of individuals, distributed into n groups. The program computes (a) the average relationship between groups; (b) the average relationship between each individual of group 1 with each of the other groups.

User's Guide

The binaries provide results in English. The software can also provide outputs in French. To switch to English, copy format_en.incl as format.incl, to switch to French copy format_fr.incl as format.incl, and then recompile all programs. If you use gfortran, compilation can be done with *compil.bat*.

Most of these programs can read the same pedigree file, which contains the following information with a space separator. Note that some programs read and use only some of these informations.

- Individual Identification, numbered sequentially from 1 to N. The file is sorted according to this number.
- Sire Id. An unknown sire is coded 0 or with a negative number. In this latter case, the negative number corresponds to a group used in VanRaden's method
- Dam Id. Same rules as for the sire
- Birth year (for instance, 89 or 1989). This information is used for the definition of the reference population (for instance, in the analysis with *prob_orig.f* of the group of females born form 1992 to 1994). **This information is not used to sort individuals** and, therefore, incoherences between parent and progeny are accepted. For *intgend.f,* this value should be a date (yyyymmdd).
- Sex: Males are coded 1, females are coded 2.
- Group of origin: Groups are coded from 1 to ngroup. Group number one is default group. This information is used only by *etr.f*.
- Herd Id, used only by *par.f* to compute within herd or within region relationship coefficients. The region Id is obtained from the first 2 digits of the herd Id, which is on 8 digits. This choice related to the French herd Id may be easily modified in the code by the user.

Some of the programs read only the first three columns.

It is advised to prepare one unique file including these 7 informations in this order, for instance by using *ped_util*. Such a complete file could be used by all programs. However, if one is interested only to inbreeding coefficients (for instance), only the first three informations are necessary.

Although all algorithms used require a preliminary sort of individual in such way that parents appear before progeny, **this constraint is not necessary in the pedigree file**. Indeed, all programs perform this ordering internally, and this step is very fast. In contrast, original Id numbers are not supported and individuals should be sequentially numbered.

Years (in parameters, in the pedigree file etc) could be coded over 4 digits (eg, 1989).

Some other programs require other input files, containing the list of individuals of interest. For each individual, this file provides
- the individual Id, as coded in the pedigree file
- the group Id, ie 1 or 2, the individual belongs to. If one group is defined (coded 1), only one matrix is computed. If two groups are defined, within group and between groups individual relationship coefficients are provided.

Each program uses a simple parameter file, containing the following information

program *ped_util.f*
`Name of the original pedigree file '
'Name of the file of the individual of interest'
'Name of output file'
Maximum number of generations traced
Number of other informations saved (integers)
Elimination of useless information (y/n)
Optional: code of unknown parent (default value: 0 (zero)
Optional: code of delimiter in the input pedigree file (default value: ' ' (blank).
Optional: order of numbering (default value: 'N' = Id order, 'T' = parents before progeny,
      'R' = progeny before parents)

Optional: number of header lines in the original pedigree file
Optional: number of header lines in the file of individuals of interest

The pedigree file includes triplets (individual – sire –dam), coded with 14 digits maximum and separated by at least a blank. The output file includes all individuals of interest and their ancestors (original and recoded Ids).

program *verif_ped.f*
'Name of pedigree file'

program *ngen.f*
(a) with reference population
'Name of pedigree file'
'Name of reference file'
'Name of output file' (no if no output file)
Number of generations traced
Number of generations printed

(b) without reference population
'Name of pedigree file'
no
sex (1/2), first and last birth year of the reference
'Name of output file' (no if no output file)
Number of generations traced
Number of generations printed

program *anc_comm.f*
'Name of pedigree file'
'Name of file with with the analysed individuals'
'Name of output file'

program *intgen.f* and *intgend.f*
'Name of pedigree file'

program *imp_ped.f*
'Name of pedigree file'
'Name of file with with the analysed individuals'
'Name of output file'
Number of generations printed
Column number of animal identification in pedigree file.

program *lineage.f*
'Name of pedigree file'
 'Name of output file'
Column number of animal identification in pedigree file.

program *etr.f*
'Name of pedigree file'
'Name of output file', including the genetic composition of each individual
optionally, for each birth year (one row per year) : birth year, average genetic composition of males (in per thousand), average genetic composition of females. If a year is omitted, the genotype is assumed of origin 1.

Example with three origins
        1975 400 400 200   700 0 300

> **program *meuw.f***
> 'Name of pedigree file'
> 'Name of output file'
>
> **program *vanrad.f***
> 'Name of pedigree file'
> 'Name of output file'
> number of generations considered (0=all)
> if previous line is 0, for each founder group, average within founder group relationship
>   (optional)
>
> **program *grain.f***
> 'Name of pedigree file'
> Number of simulations
> Option (0 to 5), see below
> 'Name of ancestors file to be analysed (*list_ancestors* recommended)'

Options 0 to 5 are the following: 1 for total inbreeding, 2 for total and partial inbreeding, 3 for total and partial Fab, 4 for total and partial Fac, 5 for total and partial Fak, 0 for all outputs.
If the ancestor file is provided by *prob_orig.f*, its name can be *'list_ancestors'.*

> **program *prob_orig.f***
> (a) with reference population
> 'Name of pedigree file'
> 'Name of output file' ('no' if no file)
> 'Name of the file of the reference population'
> number of important ancestors searched
>
> (b) without reference population
> 'Name of pedigree file'
> 'Name of output file' ('no' if no file)
> no
> number of important ancestors searched, sex and first and last birth year of the
>   reference population considered
>
> **program *segreg.f***
> (a) with reference population
> 'Name of pedigree file'
> 'Name of the file of the reference population
> Number of replicates
>
> (b) without reference population
> 'Name of pedigree file'
> no
> Number of replicates, sex and first and last birth year of the reference population
>   considered
>
> **program *parente.f* and *par3.f***
> 'Name of pedigree file'
> 'Name of studied individuals file'

'Name of output file'

The program asks for a file containing the list of animals to be analysed, as well as their group (1 vs 2). Individuals could be in one group (1) or in two groups (1 or 2). The output file includes one raw per non zero term in the matrix. If 'no' is given as name of output file, this file is not created and only within and between groups relationship statistics are produced.

In *parente.f,* a relationship matrix is build for each individual. The maximum size of this matrix can be given as a fourth parameter.

program *par.f*
'Name of pedigree file'
Option, first and last birth year of the reference population, number of samples, sample size. The list of options is given when option –1 is requested.

program *par2.f*
'Name of pedigree file'
'Name of the file of the individuals of interest'
'Name of the file of the group of reference' (no if no file)
If previous name is 'no', size of the sample (0=whole group), sex, first and last birth year of the reference population

External Subroutines

Programs *segreg, par* and *par2* use randomly sampled numbers. Corresponding routines are those of the **RANLIB** package of Brown and Lovato.
Programs *par* and *ped_util* use the sorting routines of **SLATEX** (Jones et al)
These routines are freely provided by their authors for non commercial purpose and are included in **pedig**.

Applications

These programs have been initially developed for the pedigree analysis of the French dairy cattle populations. Different applications are presented in Maignel (1995), Maignel *et al* (1996) and Boichard *et al* (1996, 1997). The programs are fast. Par3 can be longer in case of large number of relationship coefficients computed.

Examples

Examples are provided in subdirectories ex1, ex2, ex3, and ex4. Each directory include a pedigree file), the parameter files, the log files and the output files. 'ex1' is a small example with few individuals. 'ex2' and 'ex3' correspond to real French populations of small and medium size. 'ex3' provides an example of ped_util use.

In these examples, the pedigree file is geneal, input parameters are in p_xxx (where xxx is the program name), logs are in s_xxx, and output files are in res_xxx.

example of use : meuw <p_meuw >s_meuw

Finally, some examples, extracted from Maignel (1995) are presented in annex.

References

Baumung R., Farkas J., Boichard D., Mészáros G., Sölkner J., Curik I. (2015). Grain: a computer program to calculate ancestral and partial inbreeding coefficients using a gene dropping approach. *Journal of Animal Breeding and Genetics*, 132, 100–108

Boichard D., Maignel L., et Verrier E. (1996). Analyse généalogique des races bovines laitières françaises. *INRA Prod. Anim.* 9, 323-335

Boichard D., Maignel L., et Verrier E. (1997). The value of using probabilities of gene origin to measure genetic variability in a population. *Genet. Sel. Evol* 29, 5-23

Colleau J.J. 2002. An indirect approach to the extensive calculation of relationship coefficients. *Genet. Sel. Evol* 34, 409

Maignel L. (1995) Analyse de la variabilité génétique des bovins laitiers français sur la base de l'information généalogique. Masters Thesis, INAPG, Paris, 70p.

Maignel L., Boichard D., Verrier E. (1996). Genetic variability of French dairy breeds estimated from pedigree information. *Interbull meeting, Veldhoven, Pays Bas, 23-24 Juin 1996, Interbull Bull.,* 14, 49-54

Meuwissen T.H.E. et Luo Z. (1992) Computing inbreeding coefficient in large populations. *Genet. Sel. Evol.* 24, 305-313

Quaas R.L. (1976) Computing diagonal elements of a large numerator relationship matrix. *Biometrics* 92, 949-953

VanRaden P.M. (1992) Accounting for inbreeding and crossbreeding in genetic evaluation for large populations. *J. Dairy Sci.* 75, 3136-3144.

Annex

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Program
PED_UTIL

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```
        date and time  Tue Aug  4 15:36:08 2015

         Length of animal Id      :            14
         Code of unknown parents : 0

        Pedigree file :original_geneal
        File of reference animals : reference
        Output file :geneal
        Maximum Nb of generations traced :         100
        Number of parameters to be read and written :          4
        Elimination of useless pedigree   : n
        Code of unknown parents : 0000000000
        Delimitor of input file : ' '
        Animal numbering option : N

        Memory required for allocation (Gb) :                   1

        First records of the pedigree file
               1  AT00002026    0000000000    0000000000       1950     1    3    0
               2  AT00002180    0000000000    0000000000       1950     1    3    0
               3  AT00002503    0000000000    0000000000       1950     1    3    0
               4  AT00002920    0000000000    0000000000       1950     1    3    0
               5  AT00003130    0000000000    0000000000       1950     1    3    0
               6  AT00003170    0000000000    0000000000       1950     1    3    0
               7  AT00003210    0000000000    0000000000       1950     1    3    0
               8  AT00003815    0000000000    0000000000       1950     1    3    0
               9  AT00004420    0000000000    0000000000       1950     1    3    0
              10  AT18121789    0000000000    0000000000       1950     1    3    0
         Nb of individuals in the pedigree file :      108979
         Nb of individuals in the list         :        4412

         Selection of ancestors
         ----------------------
         At iteration   1,        4447  ancestors selected   and  18  generation Nr updated
         At iteration   2,        3459  ancestors selected   and  27  generation Nr updated
         At iteration   3,        2541  ancestors selected   and  22  generation Nr updated
         At iteration   4,        1959  ancestors selected   and  19  generation Nr updated
         At iteration   5,        1394  ancestors selected   and  15  generation Nr updated
         At iteration   6,         850  ancestors selected   and  11  generation Nr updated
         At iteration   7,         369  ancestors selected   and   7  generation Nr updated
         At iteration   8,         130  ancestors selected   and   0  generation Nr updated
         At iteration   9,          40  ancestors selected   and   0  generation Nr updated
         At iteration  10,           9  ancestors selected   and   0  generation Nr updated
         At iteration  11,           0  ancestors selected   and   0  generation Nr updated

          Output format : (3i10,4i10,3(1x,a14),1x,4i3)
         First records of the output file

  1  0  0      1950  2  1  0 000000002B    0000000000    0000000000
  2  0  0      1950  2  1  0 0000000312    0000000000    0000000000
  3  0  0      1950  1  1  0 0000000344    0000000000    0000000000
  4  0  0      1950  1  1  0 0000000602    0000000000    0000000000
  5  0  0      1969  1  1  0 0000000809    0000000000    0000000000

            19610  records written in the file geneal
          END of SELECTION
```

Programme VERIF_PED

(IN FRENCH)

Date et heure de debut : Sun Nov 7 13:58:32 2010

        VERIFICATION DU PEDIGREE

Entrez le nom du fichier de pedigree
Fichier lu :geneal

 Nombre d individus :   2351
 On cherche a ordonner le pedigree par iterations
   en commencant par les fondateurs puis
   en descendant le pedigree
 It / Classés Total / a l It / Restent a classer
 1   86   44   2265
 2   970   884   1381
 3   1814   844   537
 4   1979   165   372
 5   2020   41   331
 6   2020   0   331
 7   2020   0   331

 Ce pedigree est impossible
 Recherche des causes possibles

 Phase 1 : Edition des animaux non classés
        avec descendants (400 premiers)
 Individu   Pere   Mere Descendants
      98   1408   1503   1
     247   1770   1930   2
     883   1146   1159   3
            ....
 Nombre total non classé avec descendants : 98

 Phase 2 : verification simple sur 2 générations
 a) On cherche des individus issus d eux memes
 0 individu(s) issus d eux memes

 b) On cherche des parents issus de leur produit
 0 parent(s) issus de leurs produits

 Phase 3 : Recherches de boucles complexes
 Elimination comme parents
   des individus non classés (un par un)
   et analyse des consequences sur le pedigree

  Ind   Elimine NDesc Iter Corrections
   1   98   1   11   5
   2   247   2   5   331
 Cette correction resout le probleme !

Program NGEN

Computation by sex and birth year of :

- the average number of ancestors by individual
- the percentage of known ancestors per generation
- the number of equivalent complete generations


```
**************************************************
 Birth year :  1991
 Sex              :    2
 With known parents
 # animals :     2182
 Number of equivalent complete generations  :     3.85
 Average number of ancestors per individual :    66.02


 Generations  Proportion

      1       1.0000
      2        .8498
      3        .7263
      4        .5873
      5        .3726
      6        .2024
      7        .0855
      8        .0246
      9        .0050
     10        .0006
     11        .0001
     12        .0000
```

Program MEUW

```
        Inbreeding Statistics
        *********************


Total number of animals               :    106520
Number of inbred animals              :     18500
Average inbreeding (of inbred animals) :     2.487
Maximum inbreeding                     :    31.250


     Class            #
      0        5    15862.
      5       10     2001.
     10       15      513.
     15       20       49.
     20       25        3.
     25       30       71.
     30       35        1.
```

Program
PROB_ORIG

Number of important ancestors to be detected :   50
 Sex of the reference population   :   2
 First and last birth year :   88   91

 # animals read :   106520
 # non parents   :   64674
  Reference population :   9971
  # founders   :   6109
Number of effective founders: 68.8

| | Id | S | AN | Contributions | | | sire | dam | # pg | Eff # of ancestors | |
				raw	marg	cumul				Mini	Maxi
1	1937	0	70	.0960	.0960	.0960	934	7763	1982	11.12	106.91
2	421	0	63	.0898	.0898	.1859	167	5545	3139	11.93	57.47
3	2158	0	76	.0830	.0830	.2689	396	26580	2645	13.35	41.20
4	4516	0	80	.0709	.0709	.3397	1962	84480	1459	13.61	34.16
5	398	0	63	.0687	.0687	.4085	139	5281	1132	17.02	29.42
6	4196	0	77	.0842	.0421	.4506	688	69034	2575	17.95	27.97
7	6666	2	55	.0365	.0365	.4871	225	5516	3	20.33	26.97
8	4727	0	82	.0239	.0239	.5110	5198	72478	592	21.19	26.56
9	396	0	62	.0612	.0197	.5307	239	5247	1568	21.80	26.29

With 50 ancestors,
 Lower bound :   25.18
 Upper bound :   25.34

Program PAR

```
   Relationship statistics
   **********************

date, time of beginning Mar 28 16:01:02 1996

Name of pedigree file
Read file :/prod2/dbo/r12



 Type the following parameters
 1:Option  2:First birth year  3: Last birth year 4:Number of
samples  5:Sample size

   Option -1 : help
   Option  0 : males
   Option  1 : whole female population
   Option  2 : females within herd
   Option  3 : females within region
```

```
OPTION sampling of the whole female population
**************************************************

   50 random samples of size    50

First birth year :  88
Last birth year  :  91
# animals read   :  106520
Pedigree errors :   0
Number of candidates : 9971


 Number of samples             :      50.
 Average sample size           :      50.0
 Number of coefficients        :    61250.
 Mean of coefficients          :      .029
 Standard dev of coefficients  :      .033


                    Frequency of coefficients

  0-  1  :     21184.  35 : **********************************
  1-  2  :     11862.  19 : *******************
  2-  3  :      7736.  13 : *************
  3-  4  :      6504.  11 : ***********
  4-  5  :      3618.   6 : ******
  5-  6  :      1824.   3 : ***
  6-  7  :      2293.   4 : ****
  7-  8  :      1646.   3 : ***
  8-  9  :       867.   1 : *
  9- 10  :       373.   1 : *
 10- 11  :       151.   0 :
 11- 12  :        62.   0 :
 12- 13  :      1424.   2 : **
 13- 14  :       912.   1 : *
 14- 15  :       501.   1 : *
 15- 16  :       168.   0 :
 16- 17  :        91.   0 :
 17- 18  :        16.   0 :
 18- 19  :        11.   0 :
 19- 20  :         5.   0 :
 20- 21  :         1.   0 :
 25- 26  :         1.   0 :

 date and time of end  Thu Mar 28 16:02:33 1996
```

```
OPTION Within herd sampling of females
***********************************************
All herds are considered
First birth year :  88
Last birth year  :  91
# animals read   :  106520
Pedigree errors :  0
Number of herds      : 656
Number of candidates : 9579


 Number of samples             :       656.
 Average sample size           :       14.1
 Number of coefficients        :    117388.
 Mean of coefficients          :       .042
 Standard dev of coefficients  :       .045



                        Frequency of coefficients
  0-  1  :     28412.  24 : ************************
  1-  2  :     18739.  16 : ****************
  2-  3  :     14604.  12 : ************
  3-  4  :     13627.  12 : ************
  4-  5  :      8943.   8 : ********
  5-  6  :      5422.   5 : *****
  6-  7  :      5602.   5 : *****
  7-  8  :      4406.   4 : ****
  8-  9  :      2703.   2 : **
  9- 10  :      1475.   1 : *
 10- 11  :       828.   1 : *
 11- 12  :       354.   0 :
 12- 13  :      3965.   3 : ***
 13- 14  :      2823.   2 : **
 14- 15  :      2010.   2 : **
 15- 16  :      1229.   1 : *
 16- 17  :       723.   1 : *
 17- 18  :       312.   0 :
 18- 19  :       217.   0 :
 19- 20  :       125.   0 :
 20- 21  :        62.   0 :
 21- 22  :        19.   0 :
 22- 23  :        14.   0 :
 23- 24  :         3.   0 :
 24- 25  :         1.   0 :
 25- 26  :       465.   0 :
 26- 27  :       160.   0 :
 27- 28  :        58.   0 :
 28- 29  :        58.   0 :
 29- 30  :        12.   0 :
 30- 31  :         4.   0 :
 31- 32  :        10.   0 :
 32- 33  :         1.   0 :
 37- 38  :         2.   0 :
```