User's Guide to

DmuTrace

A program for extracting the pedigree for a subset of animals from a larger pedigree

Version 2

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Contents

1 Preface

DmuTrace is a program to extract a subset from a large pedigree file. The traced pedigree file can be used as input for DMU.

Initially Trace check the pedigree file for consistency, i.e. it should be possible to trace all individuals back to base populations (phantom parent groups) indicated by negative ID's.

A sort variable in the pedigree file can be used for checking that an individual is born after its parents. If the sort variable is day of birth in the format yyyymmdd, it can be checked that there is at least a specified number of days between between its day of birth and day of birth for its parents. Different minimum days can be specified for sire and dam.

A file with ID's of the individuals to be traced is read. First it is checked that all individuals specified for tracing are included in the total pedigree file. A pedigree file with all the specified individuals specified for tracing and all their ancestors. Additional a pruned pedigree file is build. The pruning can be more or less aggressive. The mildest pruning removes non-informative individuals, which is individuals not specified for tracing and with only one link to individuals specified for tracing is extracted with all the specified animals and all their ancestors. More aggressive pruning can be performed by removing individuals more than a specified number of generations before individuals specified for tracing.

The program can also calculate contributions from each of the base populations to each individual and the degree of heterozygosity between all possible combination's of the base populations.

If the base populations specified in the pedigree file are phantom parent groups (PHG's), and the PHG's have contributions from different breeds, the breed contribution to the PHG's can be specified in a file. Calculation of breed contributions and heterozygosity will then be based on breed contributions to the PHG's.

The trace programs are distributed free of charge, but the Center of Quantitative Genetics and Genomics (QGG), Aarhus University owns the source code of DmuTrace.

Great care has been put into the development in order to insure correct computations. If, however, errors are found they will be attended as quickly as possible. Correct use of the programs are entirely the responsibility of the end user and neither QGG nor the author will in any way be financially responsible for the results of use or misuse of results form the programs.

2 Program parameters

Program parameters are read from standard input using NAMELIST IO.

The format of the file is:

```
&DIRECTIVES
MAX_NIV      =  25
MAX_A        =  10000000
MAX_PHG      =  500
PED_FILE     =  TOTAL_PEDIGREE
PROB_FILE    =  PROB
N_BPOP       =  0
BPROP_FILE   =  BPROP
OPT1         =  1
OPT2         =  1
GPRUNE       =  0
DOB_CHECK    =  No
MIN_ACC_BD   =  1
MAX_ACC_BD   =  2147483647
MIN_D_SBD    =  1
MIN_D_DBD    =  1
/
```

The parameter values above are the default values set by DmuTrace.

The variables in the file read from standard input have the following meaning:

MAX_NIV	Maximum number of generations to look back for base population (PHG's). If the recursive procedure for looking up ancestors exceeds this value without reaching the base population (PHG), the animal is marked as an animal that can not be traced back to base population (PHG). MAX_NIV should be set to a value that is reasonable for the maximum number of generations that is possible for the spices in question and the time frame in the pedigree file
MAX_A	Maximum number of animals that can be in the pedigree. This must be at least the number of animals in the total pedigree
MAX_PHG	Maximum number of PHG's. This value must be at least the number of different PHG's in the total pedigree file
PED_FILE	Name of the total pedigree file
PROB_FILE	Name of the file with ID's of individuals to trace
N_BPOP	Number of base populations (breeds). (Must be specified if breed proportions for base population are taken into account)
BPROP_FILE	Name of file with proportions from base populations in PHG's (is only used if N_BPOP > 0 is specified)
OPT1	= 1 − > Tracing = 2 − > Tracing + calculation of breed proportions and Heterozygosity
OPT2	= 1 − > Using ID's for the total pedigree file = 2 − > Renumber ID's (This can be used to create ID's for use in DMU and MiX99 for pedigree files using ID'S > $2^{31} - 1$. In this case the original ID is included in the output files)

GPRUNE	= 0 − > Standard pruning by removing non-informative ancestors = n − > Pruning to max n generations back from individuals specified for tracing (in the PROB_FILE)
DOB_CHECK	= Y or y − > Check for sort variable as day of birth in the format yyyymmdd = N or n − > Check for sort variable as an integer numbers
MIN_ACC_BD	Smallest value accepted as a legal day of birth
MAX_ACC_BD	Largest value accepted as a legal day of birth. If this is set to 0 (zero) the date of execution is used, which is also the default value if no configuration file is specified
MIN_D_SBD	If number of days between an animals day of birth and the day of birth of its sire is below this value, information is written to a error file
MIN_D_DBD	If number of days between an animals day of birth and the day of birth of its dam is below this value, information is written to a error file

It is only necessary to specify variables when the default value is not sufficient, so if the default values can be used, the following content of the file piped into the program is sufficient:

```
&DIRECTIVES
PED_FILE        =   YOUR_TOTAL_PED
PROB_FILE       =   YOUR_FILE_WITH_ID's
/
```

3 Description of input data sets

3.1 Total pedigree file

The pedigree file (TOTAL_PED), in ASCII format, must have the following information on each line:

Var. No.	Content
1	ID
2	Sire ID
3	Dam ID
4	Birth date for individual ID (sort var.)

The three ID's are read and treated as long integers (64 bit). This means that the largest ID that can be handled is $2^{63} - 1 = 9223372036854775807$. Base populations or PHG's must have negative numbers. The Birth date (sort var.) must be in a format so animals can be accessed in birth date order (yyyymmdd, day number from some fixed date etc.). The value in the birth date column is included in the files with the traced pedigree. Thereby the files can be used directly as pedigree files for the DMU-packaged.

3.2 File with ID's for individuals to trace ("PROB")

The "PROB" file (in ASCII format) must have the following information on each line:

Var. No.	Content
1	ID (correspond to ID in the total pedigree file)

3.3 File with "breed proportions" in base population groups

If N_BPOP> 0 is specified, a file with base populations proportions in each PHG's must supplied, have the following information on each line (in ASCII format):

Var. No.	Content
1	PHG ID
2-N_BPOP+1	Proportions of genes from each of the N_BPOP in this PHG (real)

4 Description of output data sets

The program produces a number of output files. The files will have the name of the ”PROB” file with an extension. The contents of the files will be described in the following:

4.1 Traced pedigree file (”PED”)

A pedigree file with all individuals specified in the PROB file and their ancestors. The extension for this data set is PED.

The format of this file is ASCII and the variables depends on the value specified for OPT2.

Var. no.	OPT2 = 1 Meaning	OPT2 = 2 Meaning
1	Original ID (long integer)	Renumbered ID (integer)
2	Original sire ID (long integer)	Renumbered sire ID (integer)
3	Original dam ID (long integer)	Renumbered dam ID (integer)
4	Birth date (sort var.) (integer)	Birth date (sort var.) (integer)
5	Completeness of the pedigree expressed as known generations (real)	Completeness of the pedigree expressed as known generations (real)
6		Original ID (long integer)

4.2 Pruned pedigree file (”PRUNE”)

A pruned pedigree file with all individuals specified in the PROB file and all their informative ancestors. The extension for this data set is PRUNE. In this file all pruned parents are allocated to the base population (PHG) -999999997.

The format of this file is ASCII and the variables depends on the value specified for OPT2.

Var. no.	OPT2 = 1 Meaning	OPT2 = 2 Meaning
1	Original ID (long integer)	Renumbered ID (integer)
2	Original sire ID (long integer)	Renumbered sire ID (integer)
3	Original dam ID (long integer)	Renumbered dam ID (integer)
4	Birth date (sort var.) (integer)	Birth date (sort var.) (integer)
5		Original ID (long integer)

4.3 Breed composition (”BCONTRIB”) and heterozygosity (”HET”) files

If calculation of base population (PHG) contributions and heterozygosity are requested (OPT1 = 2), two additional files are created. One with proportions from base populations in each animal in the traced pedigree (file name extension BCONTRIB), and one with heterozygosity (file name extension HET).

The format of the file with ”breed compositions” is ASCII and the variables depends on the value of OPT2.

Var. no.	OPT2 = 1	OPT2 = 2
	Meaning	Meaning
1	Original ID (long integer)	Renumbered ID (integer)
2	Renumbered base population ID (integer)	Renumbered base population ID (integer)
3	Contribution from base population (real)	Contribution from base population (real)
4	Original ID (long integer)	

The file with ”breed heterozygosity” is ASCII and the variables depends on the value of OPT2.

Var. no.	OPT2 = 1	OPT2 = 2
	Meaning	Meaning
1	Original ID (long integer)	Renumbered ID (integer)
2	Renumbered ID for base population i (integer)	Renumbered ID for base population i
3 3	Renumbered ID for base) population j (integer)	Renumbered ID for base base population j (integer)
4 4	Heterozygosity between base populations i and j (real)	Heterozygosity between base populations i and j (real)
5		Original ID (long integer)

4.4 Renumbered PHG (”PHG_RENUM”)

If renumbering of ID’s is ordered (Opt1=2) or computation of contributions from base populations/breeds are ordered (Opt2=2), a file with renumbered base populations (phantom parent group) ID’s is created. This file contains the link between the base population ID’s in the total pedigree file and the base population ID’s in the ”BCONTRIB” and ”HET” file. The extension for the file is PHG_RENUM. The format of this file is ASCII and it has 2 variables.

Var. no.	Meaning
1	Original phantom parent (base population) ID (long integer)
2	Renumbered phantom parent ID (-1* assigned base population number (integer)

4.5 Pedigree errors

The total pedigree file (Total_Ped) is checked for consistency. If errors are found, a number of error files are produced. The error conditions, name of the error files and there contents are explained in the listing from the program.

5 Example on running the trace program

In the following a few examples on how to run DmuTrace is given.
All the examples are using the same total pedigree file and the same file with individuals to trace.

The total pedigree file (TOTAL_PEDIGREE) contains 19 individuals:

```
1  −11  −21   20000101
2  −11  −21   20010201
3  −11  −21   20000301
4  −12  −22   20010401
5  −12  −22   20000501
6  −12  −22   20010601
101  1  2   20030101
102  3  4   20030201
103  5  4   20030301
104  5  4   20030401
105  5  6   20030501
201  101  102  20060101
202  103  102  20060201
203  103  104  20060301
204  105  104  20060401
206  105  102  20060501
301  201  202  20080101
302  203  202  20080601
303  203  204  20080301
```

The file with individuals to trace (PROB) contains ID's for 3 individuals:

```
301
302
303
```

5.1 Example 1: Tracing and standard pruning

This example is a simple tracing in order to extract the pedigree for the 3 individuals in the file "PROB".

The instruction file for this example (ex1.DIR) contains:

```
&DIRECTIVES
PED_FILE = TOTAL_PEDIGREE
PROB_FILE = PROB
/
```

The output printed to standard output and the files produced by DmuTrace is on the following pages.

```
DmuTrace ver. 2                                                               21-11-2012 - 21:48:21



  _____________________________________________________________________________
  |                                                                           |
  |      ****    *        * *     * *******  ****     **      ***   *****     |
  |      *   *   * *     ** *     *    *     *   *   *  *    *   *  *         |
  |      *    *  *  *   * * *     *    *     *   *  *    *  *       *         |
  |      *     * *    *   * *     *    *     ****   *    *  *       ***       |
  |      *    *  *        * *     *    *     * *    ******  *       *         |
  |      *   *   *        *  *   *     *     *  *   *    *   *   *  *         |
  |      ****    *        *   ***      *     *   *  *    *    ***   *****     |
  |                                                                           |
  |                           Version:    2                                   |
  |                                                                           |
  |      A program to extract pedigree information for a subset of            |
  |      individuals from a larger pedigree file                              |
  |                                                                           |
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  |      E-mail: per.madsen@agrsci.dk                                         |
  |                                                                           |
  |___________________________________________________________________________|
Name of pedigree file .................. TOTAL_PEDIGREE
Name of file with individuals to trace . PROB

(Trace only)

(Using original ID's)

The sort variable (column no, 4) in the total pedigree file
is assumed to be an integer number with a value
larger then the sort variable of any of its parents

A sort variable value <= 0 is assumed to be unknown
and is not used in checking sort variables


Statistics for the pedigree file
--------------------------------

No. of individuals ............................................          19
No. of individuals inserted ...................................           0
No. of phantom parent groups ..................................           4
No. of individuals that should be traced ......................           3
No. of phantom parent groups with repeated information ........           0
No. of individuals with repeated pedigree information .........           0
No. of individuals with inconsistent pedigree information .....           0
No. of individuals that should be traced not in pedigree file .           0
No. of individuals that can not be traced back to PHG's .......           0
No. of these that should be traced ............................           0


PHANTOM PARENT GROUPS = BASE POPULATIONS(B POP)
-----------------------------------------------

Direct links and contribution expressed as no. of genomes and gene proportions

                                                      All in traced ped.       Marked for traced
                                                    ----------------------  ----------------------
                PHG  B POP        Sire         Dam     Genomes   Gene prop     Genomes   Gene prop
--------------------------------------------------------------------------------------------------
                -11      1           3           0        3.06  0.17013889        0.31  0.10416667
                -12      3           3           0        5.94  0.32986111        1.19  0.39583333
                -21      2           0           3        3.06  0.17013889        0.31  0.10416667
                -22      4           0           3        5.94  0.32986111        1.19  0.39583333
--------------------------------------------------------------------------------------------------
SUM                                                      18.00  1.00000000        3.00  1.00000000
--------------------------------------------------------------------------------------------------
```

```
DmuTrace ver. 2                                                               21-11-2012 - 21:48:21


          Description of output files
          ---------------------------

-------------------------------------------------------------------------------
A pedigree file has been created.
It contains 18 records
File name: PROB.PED

The format is ASCII and it has 5 variables

The variables are:
   1. Original ID            (long integer)
   2. Original sire ID       (long integer)
   3. Original dam ID        (long integer)
   4. Birth date (sort var.) (integer)
   5. Known generations      (real)
-------------------------------------------------------------------------------

A pruned pedigree file has been created.
It contains 13 records
File name: PROB.PRUNE

The format is ASCII and it has 4 variables

The variables are:
   1. Original ID            (long integer)
   2. Original sire ID       (long integer)
   3. Original dam ID        (long integer)
   4. Birth date (sort var.) (integer)
-------------------------------------------------------------------------------

A file with renumbered phantom parent groups ID's has been created.
-1 times the assigned base population number is used as the renumbered PHG ID
It contains 4 records
File name: PROB.PHG_RENUM

The format is ASCII and it has 2 variables
(2 integer).

The variables are:
   1. The original PHG ID (long integer)
   2. Renumbered PHG ID   (integer)
-------------------------------------------------------------------------------

EOJ
```

The complete pedigree for the 3 individuals in the "PROB" file:

```
         1         −11         −21    20000101   0.0000000E+00
         2         −11         −21    20010201   0.0000000E+00
         3         −11         −21    20000301   0.0000000E+00
         4         −12         −22    20010401   0.0000000E+00
         5         −12         −22    20000501   0.0000000E+00
         6         −12         −22    20010601   0.0000000E+00
       101           1           2    20030101     1.000000
       102           3           4    20030201     1.000000
       103           5           4    20030301     1.000000
       104           5           4    20030401     1.000000
       105           5           6    20030501     1.000000
       201         101         102    20060101     2.000000
       202         103         102    20060201     2.000000
       203         103         104    20060301     2.000000
       204         105         104    20060401     2.000000
       301         201         202    20080101     3.000000
       302         203         202    20080601     3.000000
       303         203         204    20080301     3.000000
```

The pruned pedigree for the 3 individuals in the "PROB" file:

```
         4         −12         −22    20010401
         5         −12         −22    20000501
       102  −999999997           4    20030201
       103           5           4    20030301
       104           5           4    20030401
       105           5  −999999997    20030501
       201  −999999997         102    20060101
       202         103         102    20060201
       203         103         104    20060301
       204         105         104    20060401
       301         201         202    20080101
       302         203         202    20080601
       303         203         204    20080301
```

5.2 Example 2: Tracing and aggressive pruning

This example is a simple tracing as in example 1, but with pruning so no individuals in the pruned pedigree is more than one generation back from the 3 individuals in the file "PROB".

The instruction file for this example (ex2.DIR) contains:

```
&DIRECTIVES
PED_FILE = TOTAL_PEDIGREE
PROB_FILE = PROB
GPRUNE   = 1
/
```

The output printed to standard output and the files produced by DmuTrace is on the following pages.

```
DmuTrace ver. 2                                                              22-11-2012 - 12:45:38



   ____________________________________________________________________________
  |                                                                            |
  |      ****    *        * *     * *******  ****     **      ***   *****     |
  |      *   *   * *     ** *     *    *     *   *   *  *    *   *  *         |
  |      *    *  *  *   * * *     *    *     *   *  *    *  *       *         |
  |      *     * *    *   * *     *    *     ****   *    *  *       ***       |
  |      *    *  *        * *     *    *     * *    ******  *       *         |
  |      *   *   *        *  *   *     *     *  *   *    *   *   *  *         |
  |      ****    *        *   ***      *     *   *  *    *    ***   *****     |
  |                                                                            |
  |                          Version:    2                                     |
  |                                                                            |
  |      A program to extract pedigree information for a subset of             |
  |      individuals from a larger pedigree file                               |
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  |      E-mail: per.madsen@agrsci.dk                                          |
  |                                                                            |
  |____________________________________________________________________________|
Name of pedigree file .................. TOTAL_PEDIGREE
Name of file with individuals to trace . PROB

(Trace only)

(Using original ID's)

Pruning to max. generation back from data         1

The sort variable (column no, 4) in the total pedigree file
is assumed to be an integer number with a value
larger then the sort variable of any of its parents

A sort variable value <= 0 is assumed to be unknown
and is not used in checking sort variables


Statistics for the pedigree file
--------------------------------

No. of individuals ...........................................           19
No. of individuals inserted ..................................            0
No. of phantom parent groups .................................            4
No. of individuals that should be traced .....................            3
No. of phantom parent groups with repeated information ........           0
No. of individuals with repeated pedigree information .........           0
No. of individuals with inconsistent pedigree information .....           0
No. of individuals that should be traced not in pedigree file .           0
No. of individuals that can not be traced back to PHG's .......           0
No. of these that should be traced ...........................            0
```

```
DmuTrace ver. 2                                                              22-11-2012 - 12:45:38



PHANTOM PARENT GROUPS = BASE POPULATIONS(B POP)
-----------------------------------------------

Direct links and contribution expressed as no. of genomes and gene proportions

                                                      All in traced ped.       Marked for traced
                                                    ----------------------  ----------------------
                PHG  B POP        Sire         Dam     Genomes   Gene prop     Genomes   Gene prop
--------------------------------------------------------------------------------------------------
                 -11     1           3           0        3.06  0.17013889        0.31  0.10416667
                 -12     3           3           0        5.94  0.32986111        1.19  0.39583333
                 -21     2           0           3        3.06  0.17013889        0.31  0.10416667
                 -22     4           0           3        5.94  0.32986111        1.19  0.39583333
--------------------------------------------------------------------------------------------------
SUM                                                      18.00  1.00000000        3.00  1.00000000
--------------------------------------------------------------------------------------------------


          Description of output files
          ---------------------------

-------------------------------------------------------------------------------
A pedigree file has been created.
It contains 18 records
File name: PROB.PED

The format is ASCII and it has 5 variables

The variables are:
   1. Original ID            (long integer)
   2. Original sire ID       (long integer)
   3. Original dam ID        (long integer)
   4. Birth date (sort var.) (integer)
   5. Known generations      (real)
-------------------------------------------------------------------------------

A pruned pedigree file has been created.
It contains 7 records
File name: PROB.PRUNE

The format is ASCII and it has 4 variables

The variables are:
   1. Original ID            (long integer)
   2. Original sire ID       (long integer)
   3. Original dam ID        (long integer)
   4. Birth date (sort var.) (integer)
-------------------------------------------------------------------------------

A file with renumbered phantom parent groups ID's has been created.
-1 times the assigned base population number is used as the renumbered PHG ID
It contains 4 records
File name: PROB.PHG_RENUM

The format is ASCII and it has 2 variables
(2 integer).

The variables are:
   1. The original PHG ID (long integer)
   2. Renumbered PHG ID   (integer)
-------------------------------------------------------------------------------

EOJ
```

The complete pedigree for the 3 individuals in the "PROB" file:

```
         1      -11      -21   20000101  0.0000000E+00
         2      -11      -21   20010201  0.0000000E+00
         3      -11      -21   20000301  0.0000000E+00
         4      -12      -22   20010401  0.0000000E+00
         5      -12      -22   20000501  0.0000000E+00
         6      -12      -22   20010601  0.0000000E+00
       101        1        2   20030101   1.000000
       102        3        4   20030201   1.000000
       103        5        4   20030301   1.000000
       104        5        4   20030401   1.000000
       105        5        6   20030501   1.000000
       201      101      102   20060101   2.000000
       202      103      102   20060201   2.000000
       203      103      104   20060301   2.000000
       204      105      104   20060401   2.000000
       301      201      202   20080101   3.000000
       302      203      202   20080601   3.000000
       303      203      204   20080301   3.000000
```

The pruned pedigree for the 3 individuals in the "PROB" file:

```
       201 -999999997 -999999997    20060101
       202 -999999997 -999999997    20060201
       203 -999999997 -999999997    20060301
       204 -999999997 -999999997    20060401
       301        201        202    20080101
       302        203        202    20080601
       303        203        204    20080301
```

5.3 Example 3: Tracing and computation of contributions and heterozygosity

This example is a simple tracing as in example 1, but with with computation on gene contributions from each base populations and hetoryzygosity between all possible combination's of base populations.

The instruction file for this example (ex3.DIR) contains:

```
&DIRECTIVES
PED_FILE = TOTAL_PEDIGREE
PROB_FILE = PROB
OPT1 = 2
/
```

The output printed to standard output and the files produced by DmuTrace is on the following pages.

```
DmuTrace ver. 2                                                               22-11-2012 - 12:56:26



  _____________________________________________________________________________
  |                                                                           |
  |      ****    *        * *     * *******  ****     **      ***   *****     |
  |      *   *   * *     ** *     *    *     *   *   *  *    *   *  *         |
  |      *    *  *  *   * * *     *    *     *   *  *    *  *       *         |
  |      *     * *    *   * *     *    *     ****   *    *  *       ***       |
  |      *    *  *        * *     *    *     * *    ******  *       *         |
  |      *   *   *        *  *   *     *     *  *   *    *   *   *  *         |
  |      ****    *        *   ***      *     *   *  *    *    ***   *****     |
  |                                                                           |
  |                           Version:    2                                   |
  |                                                                           |
  |      A program to extract pedigree information for a subset of            |
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  |                                                                           |
  |___________________________________________________________________________|
Name of pedigree file .................. TOTAL_PEDIGREE
Name of file with individuals to trace . PROB

Option 1 specified.......................         2
(Trace + breed proportions + heterozygosity)

(Using original ID's)

The sort variable (column no, 4) in the total pedigree file
is assumed to be an integer number with a value
larger then the sort variable of any of its parents

A sort variable value <= 0 is assumed to be unknown
and is not used in checking sort variables


Statistics for the pedigree file
--------------------------------


No. of individuals ............................................          19
No. of individuals inserted ...................................           0
No. of phantom parent groups ..................................           4
No. of individuals that should be traced ......................           3
No. of phantom parent groups with repeated information ........           0
No. of individuals with repeated pedigree information .........           0
No. of individuals with inconsistent pedigree information .....           0
No. of individuals that should be traced not in pedigree file .           0
No. of individuals that can not be traced back to PHG's .......           0
No. of these that should be traced ............................           0


PHANTOM PARENT GROUPS = BASE POPULATIONS(B POP)
-----------------------------------------------

Direct links and contribution expressed as no. of genomes and gene proportions

                                                      All in traced ped.       Marked for traced
                                                    ----------------------  ----------------------
                PHG  B POP        Sire         Dam     Genomes   Gene prop     Genomes   Gene prop
--------------------------------------------------------------------------------------------------
                 -11     1           3           0        3.06  0.17013889        0.31  0.10416667
                 -12     3           3           0        5.94  0.32986111        1.19  0.39583333
                 -21     2           0           3        3.06  0.17013889        0.31  0.10416667
                 -22     4           0           3        5.94  0.32986111        1.19  0.39583333
--------------------------------------------------------------------------------------------------
SUM                                                      18.00  1.00000000        3.00  1.00000000
--------------------------------------------------------------------------------------------------
```

```
DmuTrace ver. 2                                                               22-11-2012 - 12:56:26


          Simple statistics for the traced pedigree
          -----------------------------------------

    Contribution from base populations to all individuals
    -------------------------------------------------

Base population     N-obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1               18   0.17013890       0.21200803        0.0000000       0.50000000
       2               18   0.17013890       0.21200803        0.0000000       0.50000000
       3               18   0.32986110       0.21200803        0.0000000       0.50000000
       4               18   0.32986110       0.21200803        0.0000000       0.50000000
-----------------------------------------------------------------------------------------


    Contribution from base populations to individuals with contribution > 0
    -------------------------------------------------------------------

Base population     N-obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1                9   0.34027779       0.17430417       0.62500000E-01   0.50000000
       2                9   0.34027779       0.17430417       0.62500000E-01   0.50000000
       3               14   0.42410713       0.12542853       0.12500000       0.50000000
       4               14   0.42410713       0.12542853       0.12500000       0.50000000
-----------------------------------------------------------------------------------------


    Heterozygosity all individuals
    --------------------------

Base populations
----------------
     1     2        N-obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
     1     2           18   0.21354167       0.38351995        0.0000000        1.0000000
     1     3           18   0.39930556E-01   0.74110501E-01    0.0000000       0.25000000
     1     4           18   0.39930556E-01   0.74110501E-01    0.0000000       0.25000000
     2     3           18   0.39930556E-01   0.74110501E-01    0.0000000       0.25000000
     2     4           18   0.39930556E-01   0.74110501E-01    0.0000000       0.25000000
     3     4           18   0.37326390       0.36006922        0.0000000        1.0000000
-----------------------------------------------------------------------------------------


    Heterozygosity for individuals with specific heterozygosity > 0
    -----------------------------------------------------------

Base populations
----------------
     1     2        N-obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
     1     2            6   0.64062500       0.41446030       0.93750000E-01    1.0000000
     1     3            5   0.14375000       0.68465322E-01   0.62500000E-01   0.25000000
     1     4            5   0.14375000       0.68465322E-01   0.62500000E-01   0.25000000
     2     3            5   0.14375000       0.68465322E-01   0.62500000E-01   0.25000000
     2     4            5   0.14375000       0.68465322E-01   0.62500000E-01   0.25000000
     3     4           12   0.55989581       0.29389453       0.93750000E-01    1.0000000
-----------------------------------------------------------------------------------------
```

The complete pedigree for the 3 individuals in the ”PROB” file:

```
     1         −11         −21     20000101    0.0000000E+00
     2         −11         −21     20010201    0.0000000E+00
     3         −11         −21     20000301    0.0000000E+00
     4         −12         −22     20010401    0.0000000E+00
     5         −12         −22     20000501    0.0000000E+00
     6         −12         −22     20010601    0.0000000E+00
   101           1           2     20030101     1.000000
   102           3           4     20030201     1.000000
   103           5           4     20030301     1.000000
   104           5           4     20030401     1.000000
   105           5           6     20030501     1.000000
   201         101         102     20060101     2.000000
   202         103         102     20060201     2.000000
   203         103         104     20060301     2.000000
   204         105         104     20060401     2.000000
   301         201         202     20080101     3.000000
   302         203         202     20080601     3.000000
   303         203         204     20080301     3.000000
```

The pruned pedigree for the 3 individuals in the ”PROB” file:

```
     4         −12          −22     20010401
     5         −12          −22     20000501
   102  −999999997            4     20030201
   103           5            4     20030301
   104           5            4     20030401
   105           5   −999999997     20030501
   201  −999999997          102     20060101
   202         103          102     20060201
   203         103          104     20060301
   204         105          104     20060401
   301         201          202     20080101
   302         203          202     20080601
   303         203          204     20080301
```

The file with contributions from base populations:

```
           1           1  0.500000000000000
           1           2  0.500000000000000
           2           1  0.500000000000000
           2           2  0.500000000000000
           3           1  0.500000000000000
           3           2  0.500000000000000
           4           3  0.500000000000000
           4           4  0.500000000000000
           5           3  0.500000000000000
           5           4  0.500000000000000
           6           3  0.500000000000000
           6           4  0.500000000000000
         101           1  0.500000000000000
         101           2  0.500000000000000
         102           1  0.250000000000000
         102           2  0.250000000000000
         102           3  0.250000000000000
         102           4  0.250000000000000
         103           3  0.500000000000000
         103           4  0.500000000000000
         104           3  0.500000000000000
         104           4  0.500000000000000
         105           3  0.500000000000000
         105           4  0.500000000000000
         201           1  0.375000000000000
         201           2  0.375000000000000
         201           3  0.125000000000000
         201           4  0.125000000000000
         202           1  0.125000000000000
         202           2  0.125000000000000
         202           3  0.375000000000000
         202           4  0.375000000000000
         203           3  0.500000000000000
         203           4  0.500000000000000
         204           3  0.500000000000000
         204           4  0.500000000000000
         301           1  0.250000000000000
         301           2  0.250000000000000
         301           3  0.250000000000000
         301           4  0.250000000000000
         302           1  6.250000000000000E-002
         302           2  6.250000000000000E-002
         302           3  0.437500000000000
         302           4  0.437500000000000
         303           3  0.500000000000000
         303           4  0.500000000000000
```

The file with heterozygosity between base populations:

```
           1           1           2   1.00000000000000
           2           1           2   1.00000000000000
           3           1           2   1.00000000000000
           4           3           4   1.00000000000000
           5           3           4   1.00000000000000
           6           3           4   1.00000000000000
         101           1           2  0.500000000000000
         102           1           3  0.250000000000000
         102           1           4  0.250000000000000
         102           2           3  0.250000000000000
         102           2           4  0.250000000000000
         103           3           4  0.500000000000000
         104           3           4  0.500000000000000
         105           3           4  0.500000000000000
         201           1           2  0.250000000000000
         201           1           3  0.125000000000000
         201           1           4  0.125000000000000
         201           2           3  0.125000000000000
         201           2           4  0.125000000000000
         202           1           3  0.125000000000000
         202           1           4  0.125000000000000
         202           2           3  0.125000000000000
         202           2           4  0.125000000000000
         202           3           4  0.250000000000000
         203           3           4  0.500000000000000
         204           3           4  0.500000000000000
         301           1           2  9.375000000000000E-002
         301           1           3  0.156250000000000
         301           1           4  0.156250000000000
         301           2           3  0.156250000000000
         301           2           4  0.156250000000000
         301           3           4  9.375000000000000E-002
         302           1           3  6.250000000000000E-002
         302           1           4  6.250000000000000E-002
         302           2           3  6.250000000000000E-002
         302           2           4  6.250000000000000E-002
         302           3           4  0.375000000000000
         303           3           4  0.500000000000000
```

5.4 Example 4: Tracing and computation of contributions and heterozygosity

This example is a simple tracing as in example 3 but three of the unknown parents groups (Phantom Parent Groups) are assumed to be pure breed of breed 1, 2 and 3 respectively, while the last group consists of 3-way crosses ($B1 \times B2) \times B3$). This is accomplished by specifying that there are there are 3 base populations (N_BPOP=3) and that the breed composition of the unknown parent groups are in the file specified for BPROP_FILE.

The instruction file for this example (ex4.DIR) contains:

```
&DIRECTIVES
PED_FILE = TOTAL_PEDIGREE
PROB_FILE = PROB
OPT1 = 2
BPROP_FILE = B_PROP
N_BPOP = 3
/
```

The file with breed proportions in the Phantom Parent Groups contains:

```
−11 1 0 0
−21 0 1 0
−12 0 0 1
−22 .25 .25 .5
```

The output printed to standard output and the files produced by DmuTrace is on the following pages.

```
DmuTrace ver. 2                                                              22−11−2012 − 13:09:05



  _____________________________________________________________________________
  |                                                                           |
  |      ****    *        * *     * *******  ****     **      ***   *****     |
  |      *   *   * *     ** *     *    *     *   *   *  *    *   *  *         |
  |      *    *  *  *   * * *     *    *     *   *  *    *  *       *         |
  |      *     * *    *   * *     *    *     ****   *    *  *       ***       |
  |      *    *  *        * *     *    *     * *    ******  *       *         |
  |      *   *   *        *  *   *     *     *  *   *    *   *   *  *         |
  |      ****    *        *   ***      *     *   *  *    *    ***   *****     |
  |                                                                           |
  |                           Version:    2                                   |
  |                                                                           |
  |      A program to extract pedigree information for a subset of            |
  |      individuals from a larger pedigree file                              |
  |                                                                           |
  |      Per Madsen                                                           |
  |      Faculty of Agricultural Science, University of Aarhus                |
  |      Dept. of Genetics and Biotechnology                                  |
  |      Research Centre Foulum                                               |
  |      DK−8830 Tjele, Denmark                                               |
  |      Ph.: (+45) 89 99 12 16        Fax: (+45) 89 99 13 00                 |
  |      E−mail: per.madsen@agrsci.dk                                         |
  |                                                                           |
  |___________________________________________________________________________|
Name of pedigree file .................. TOTAL_PEDIGREE
Name of file with individuals to trace . PROB

Option 1 specified......................          2
(Trace + breed proportions + heterozygosity)

(Using original ID’s)

Name of file with proportions in PHG’s ..B_PROP
No. of base populations ................          3

The sort variable (column no, 4) in the total pedigree file
is assumed to be an integer number with a value
larger then the sort variable of any of its parents

A sort variable value <= 0 is assumed to be unknown
and is not used in checking sort variables


Statistics for the pedigree file
--------------------------------

No. of individuals ............................................          19
No. of individuals inserted ...................................           0
No. of phantom parent groups ..................................           4
No. of individuals that should be traced ......................           3
No. of phantom parent groups with repeated information ........           0
No. of individuals with repeated pedigree information .........           0
No. of individuals with inconsistent pedigree information .....           0
No. of individuals that should be traced not in pedigree file .           0
No. of individuals that can not be traced back to PHG’s .......           0
No. of these that should be traced ............................           0
```

```
DmuTrace ver. 2                                                              22−11−2012 − 13:09:05



PHANTOM PARENT GROUPS
---------------------

Direct links and contribution expressed as no. of genomes and gene proportions

                                                All in traced ped.   Marked for traced
                                            ----------------------  ----------------------
               PHG        As Sire      As Dam  Genomes   Gene prop     Genomes   Gene prop
------------------------------------------------------------------------------------------
                −11          3           0        3.06  0.17013889        0.31  0.10416667
                −12          3           0        5.94  0.32986111        1.19  0.39583333
                −21          0           3        3.06  0.17013889        0.31  0.10416667
                −22          0           3        5.94  0.32986111        1.19  0.39583333
------------------------------------------------------------------------------------------
SUM                                              18.00  1.00000000        3.00  1.00000000
------------------------------------------------------------------------------------------


BASE POPULATIONS
----------------
Contribution expressed as genomes and gene proportions

                                           All                    Traced
                                    ----------------------  ----------------------
       Base population                 Genomes   Gene prop     Genomes   Gene prop
----------------------------------------------------------------------------------
             1                            4.55  0.25260417        0.61  0.20312500
             2                            4.55  0.25260417        0.61  0.20312500
             3                            8.91  0.49479167        1.78  0.59375000
----------------------------------------------------------------------------------
SUM                                      18.00  1.00000000        3.00  1.00000000
----------------------------------------------------------------------------------


          Simple statistics for the traced pedigree
          -----------------------------------------

    Contribution from base populations to all individuals
    -------------------------------------------------

Base population     N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1               18   0.25260416       0.15900603       0.12500000       0.50000000
       2               18   0.25260416       0.15900603       0.12500000       0.50000000
       3               18   0.49479166       0.31801206        0.0000000       0.75000000
-----------------------------------------------------------------------------------------


    Contribution from base populations to individuals with contribution > 0
    -------------------------------------------------------------------

Base population     N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1               18   0.25260416       0.15900603       0.12500000       0.50000000
       2               18   0.25260416       0.15900603       0.12500000       0.50000000
       3               14   0.63616073       0.18814279       0.18750000       0.75000000
-----------------------------------------------------------------------------------------


    Heterozygosity all individuals
    --------------------------

Base populations
----------------
     1     2        N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
     1     2           18   0.24641927       0.36916602        0.0000000        1.0000000
     1     3           18   0.17903645       0.10952467        0.0000000       0.37500000
     2     3           18   0.17903645       0.10952467        0.0000000       0.37500000
-----------------------------------------------------------------------------------------
```

The complete pedigree for the 3 individuals in the "PROB" file:

```
     1      −11      −21    20000101   0.0000000E+00
     2      −11      −21    20010201   0.0000000E+00
     3      −11      −21    20000301   0.0000000E+00
     4      −12      −22    20010401   0.0000000E+00
     5      −12      −22    20000501   0.0000000E+00
     6      −12      −22    20010601   0.0000000E+00
   101        1        2    20030101     1.000000
   102        3        4    20030201     1.000000
   103        5        4    20030301     1.000000
   104        5        4    20030401     1.000000
   105        5        6    20030501     1.000000
   201      101      102    20060101     2.000000
   202      103      102    20060201     2.000000
   203      103      104    20060301     2.000000
   204      105      104    20060401     2.000000
   301      201      202    20080101     3.000000
   302      203      202    20080601     3.000000
   303      203      204    20080301     3.000000
```

The pruned pedigree for the 3 individuals in the "PROB" file:

```
     4        −12        −22   20010401
     5        −12        −22   20000501
   102 −999999997          4   20030201
   103          5          4   20030301
   104          5          4   20030401
   105          5 −999999997   20030501
   201 −999999997        102   20060101
   202        103        102   20060201
   203        103        104   20060301
   204        105        104   20060401
   301        201        202   20080101
   302        203        202   20080601
   303        203        204   20080301
```

The file with contributions from base populations ("BCONTRIB") contains from 1 to N_BPOP lines per individual in the traced pedigree (only lines for contributions > 0 are generated). Base populations/breeds are numbered according to the renumbering information in the "PHG_RENUM" file

```
           1           1  0.500000000000000
           1           2  0.500000000000000
           2           1  0.500000000000000
           2           2  0.500000000000000
           3           1  0.500000000000000
           3           2  0.500000000000000
           4           1  0.125000000000000
           4           2  0.125000000000000
           4           3  0.750000000000000
           5           1  0.125000000000000
           5           2  0.125000000000000
           5           3  0.750000000000000
           6           1  0.125000000000000
           6           2  0.125000000000000
           6           3  0.750000000000000
         101           1  0.500000000000000
         101           2  0.500000000000000
         102           1  0.312500000000000
         102           2  0.312500000000000
         102           3  0.375000000000000
         103           1  0.125000000000000
         103           2  0.125000000000000
         103           3  0.750000000000000
         104           1  0.125000000000000
         104           2  0.125000000000000
         104           3  0.750000000000000
         105           1  0.125000000000000
         105           2  0.125000000000000
         105           3  0.750000000000000
         201           1  0.406250000000000
         201           2  0.406250000000000
         201           3  0.187500000000000
         202           1  0.218750000000000
         202           2  0.218750000000000
         202           3  0.562500000000000
         203           1  0.125000000000000
         203           2  0.125000000000000
         203           3  0.750000000000000
         204           1  0.125000000000000
         204           2  0.125000000000000
         204           3  0.750000000000000
         301           1  0.312500000000000
         301           2  0.312500000000000
         301           3  0.375000000000000
         302           1  0.171875000000000
         302           2  0.171875000000000
         302           3  0.656250000000000
         303           1  0.125000000000000
         303           2  0.125000000000000
         303           3  0.750000000000000
```

The file with heterozogosity (”HET”) contains from 0 to $N\_BPOP \times (N\_BPOP - 1)/2$ lines per individual in the traced pedigree (only lines for heterozygosity > 0 are generated).Base populations/breeds are numbered according to the renumbering information in the ”PHG_RENUM” file.

```
           1           1           2   1.00000000000000
           2           1           2   1.00000000000000
           3           1           2   1.00000000000000
           4           1           3  0.250000000000000
           4           2           3  0.250000000000000
           5           1           3  0.250000000000000
           5           2           3  0.250000000000000
           6           1           3  0.250000000000000
           6           2           3  0.250000000000000
         101           1           2  0.500000000000000
         102           1           2  0.125000000000000
         102           1           3  0.375000000000000
         102           2           3  0.375000000000000
         103           1           2  3.125000000000000E-002
         103           1           3  0.187500000000000
         103           2           3  0.187500000000000
         104           1           2  3.125000000000000E-002
         104           1           3  0.187500000000000
         104           2           3  0.187500000000000
         105           1           2  3.125000000000000E-002
         105           1           3  0.187500000000000
         105           2           3  0.187500000000000
         201           1           2  0.312500000000000
         201           1           3  0.187500000000000
         201           2           3  0.187500000000000
         202           1           2  7.812500000000000E-002
         202           1           3  0.281250000000000
         202           2           3  0.281250000000000
         203           1           2  3.125000000000000E-002
         203           1           3  0.187500000000000
         203           2           3  0.187500000000000
         204           1           2  3.125000000000000E-002
         204           1           3  0.187500000000000
         204           2           3  0.187500000000000
         301           1           2  0.177734375000000
         301           1           3  0.269531250000000
         301           2           3  0.269531250000000
         302           1           2  5.468750000000000E-002
         302           1           3  0.234375000000000
         302           2           3  0.234375000000000
         303           1           2  3.125000000000000E-002
         303           1           3  0.187500000000000
         303           2           3  0.187500000000000
```

5.5 Example 5: Reconding of ID’s, tracing and computation of contributions and heterozygosity

This example is the same as example 3, except that ID’s are recoded. Due to the recoding of ID’s, the ”PED”, ”PRUNE”, ”BCONTRIB” and ”HET” has an extra column containing the original ID.

The instruction file for this example (ex5.DIR) contains:

```
&DIRECTIVES
PED_FILE = TOTAL_PEDIGREE
PROB_FILE = PROB
OPT1 = 2
OPT2 = 2
/
```

The output printed to standard output and the files produced by DmuTrace is on the following pages.

```
DmuTrace ver. 2                                                                26−11−2012 − 15:29:18



  _____________________________________________________________________________
  |                                                                           |
  |      ****    *        * *     * *******  ****     **      ***   *****     |
  |      *   *   * *     ** *     *    *     *   *   *  *    *   *  *         |
  |      *    *  *  *   * * *     *    *     *   *  *    *  *       *         |
  |      *     * *    *   * *     *    *     ****   *    *  *       ***       |
  |      *    *  *        * *     *    *     * *    ******  *       *         |
  |      *   *   *        *  *   *     *     *  *   *    *   *   *  *         |
  |      ****    *        *   ***      *     *   *  *    *    ***   *****     |
  |                                                                           |
  |                           Version:    2                                   |
  |                                                                           |
  |      A program to extract pedigree information for a subset of            |
  |      individuals from a larger pedigree file                              |
  |                                                                           |
  |      Per Madsen                                                           |
  |      Faculty of Agricultural Science, University of Aarhus                |
  |      Dept. of Genetics and Biotechnology                                  |
  |      Research Centre Foulum                                               |
  |      DK−8830 Tjele, Denmark                                               |
  |      Ph.: (+45) 89 99 12 16        Fax: (+45) 89 99 13 00                 |
  |      E−mail: per.madsen@agrsci.dk                                         |
  |                                                                           |
  |___________________________________________________________________________|
Name of pedigree file .................. TOTAL_PEDIGREE
Name of file with individuals to trace . PROB

Option 1 specified.......................         2
(Trace + breed proportions + heterozygosity)

Option 2 specified.......................         2
(Using renumbered ID’s)

The sort variable (column no, 4) in the total pedigree file
is assumed to be an integer number with a value
larger then the sort variable of any of its parents

A sort variable value <= 0 is assumed to be unknown
and is not used in checking sort variables


Statistics for the pedigree file
--------------------------------

No. of individuals ............................................          19
No. of individuals inserted ...................................           0
No. of phantom parent groups ..................................           4
No. of individuals that should be traced ......................           3
No. of phantom parent groups with repeated information ........           0
No. of individuals with repeated pedigree information .........           0
No. of individuals with inconsistent pedigree information .....           0
No. of individuals that should be traced not in pedigree file .           0
No. of individuals that can not be traced back to PHG’s .......           0
No. of these that should be traced ............................           0


PHANTOM PARENT GROUPS = BASE POPULATIONS(B POP)
-----------------------------------------------

Direct links and contribution expressed as no. of genomes and gene proportions

                                                       All in traced ped.       Marked for traced
                                                     ----------------------  ----------------------
                PHG  B POP         Sire         Dam     Genomes   Gene prop     Genomes   Gene prop
---------------------------------------------------------------------------------------------------
                 −11     1            3           0        3.06  0.17013889        0.31  0.10416667
                 −12     3            3           0        5.94  0.32986111        1.19  0.39583333
                 −21     2            0           3        3.06  0.17013889        0.31  0.10416667
                 −22     4            0           3        5.94  0.32986111        1.19  0.39583333
---------------------------------------------------------------------------------------------------
SUM                                                       18.00  1.00000000        3.00  1.00000000
---------------------------------------------------------------------------------------------------
```

```
DmuTrace ver. 2                                                                26−11−2012 − 15:29:18


          Simple statistics for the traced pedigree
          -----------------------------------------

    Contribution from base populations to all individuals
    -------------------------------------------------

Base population     N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1               18   0.17013890       0.21200803        0.0000000       0.50000000
       2               18   0.17013890       0.21200803        0.0000000       0.50000000
       3               18   0.32986110       0.21200803        0.0000000       0.50000000
       4               18   0.32986110       0.21200803        0.0000000       0.50000000
-----------------------------------------------------------------------------------------


    Contribution from base populations to individuals with contribution > 0
    -------------------------------------------------------------------

Base population     N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
       1                9   0.34027779       0.17430417       0.62500000E−01   0.50000000
       2                9   0.34027779       0.17430417       0.62500000E−01   0.50000000
       3               14   0.42410713       0.12542853       0.12500000       0.50000000
       4               14   0.42410713       0.12542853       0.12500000       0.50000000
-----------------------------------------------------------------------------------------


    Heterozygosity all individuals
    --------------------------

Base populations
----------------
     1     2        N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
     1     2           18   0.21354167       0.38351995        0.0000000        1.0000000
     1     3           18   0.39930556E−01   0.74110501E−01    0.0000000       0.25000000
     1     4           18   0.39930556E−01   0.74110501E−01    0.0000000       0.25000000
     2     3           18   0.39930556E−01   0.74110501E−01    0.0000000       0.25000000
     2     4           18   0.39930556E−01   0.74110501E−01    0.0000000       0.25000000
     3     4           18   0.37326390       0.36006922        0.0000000        1.0000000
-----------------------------------------------------------------------------------------


    Heterozygosity for individuals with specific heterozygosity > 0
    -----------------------------------------------------------

Base populations
----------------
     1     2        N−obs      Average          S.D.           Min value        Max value
-----------------------------------------------------------------------------------------
     1     2            6   0.64062500       0.41446030       0.93750000E−01    1.0000000
     1     3            5   0.14375000       0.68465322E−01   0.62500000E−01   0.25000000
     1     4            5   0.14375000       0.68465322E−01   0.62500000E−01   0.25000000
     2     3            5   0.14375000       0.68465322E−01   0.62500000E−01   0.25000000
     2     4            5   0.14375000       0.68465322E−01   0.62500000E−01   0.25000000
     3     4           12   0.55989581       0.29389453       0.93750000E−01    1.0000000
-----------------------------------------------------------------------------------------
```

The complete pedigree for the 3 individuals in the "PROB" file:

```
     1    −1    −2    20000101   0.0000000E+00    1
     2    −1    −2    20010201   0.0000000E+00    2
     3    −1    −2    20000301   0.0000000E+00    3
     4    −3    −4    20010401   0.0000000E+00    4
     5    −3    −4    20000501   0.0000000E+00    5
     6    −3    −4    20010601   0.0000000E+00    6
     7     1     2    20030101     1.000000      101
     8     3     4    20030201     1.000000      102
     9     5     4    20030301     1.000000      103
    10     5     4    20030401     1.000000      104
    11     5     6    20030501     1.000000      105
    12     7     8    20060101     2.000000      201
    13     9     8    20060201     2.000000      202
    14     9    10    20060301     2.000000      203
    15    11    10    20060401     2.000000      204
    17    12    13    20080101     3.000000      301
    18    14    13    20080601     3.000000      302
    19    14    15    20080301     3.000000      303
```

The pruned pedigree for the 3 individuals in the "PROB" file:

```
     4    −3    −4    20010401    4
     5    −3    −4    20000501    5
     8     0     4    20030201  102
     9     5     4    20030301  103
    10     5     4    20030401  104
    11     5     0    20030501  105
    12     0     8    20060101  201
    13     9     8    20060201  202
    14     9    10    20060301  203
    15    11    10    20060401  204
    17    12    13    20080101  301
    18    14    13    20080601  302
    19    14    15    20080301  303
```

The file with contributions from base populations (”BCONTRIB”) contains from 1 to N_BPOP lines per individual in the traced pedigree (only lines for contributions > 0 are generated). Base populations/breeds are numbered according to the renumbering information in the ”PHG_RENUM” file

```
           1           1  0.500000000000000               1
           1           2  0.500000000000000               1
           2           1  0.500000000000000               2
           2           2  0.500000000000000               2
           3           1  0.500000000000000               3
           3           2  0.500000000000000               3
           4           3  0.500000000000000               4
           4           4  0.500000000000000               4
           5           3  0.500000000000000               5
           5           4  0.500000000000000               5
           6           3  0.500000000000000               6
           6           4  0.500000000000000               6
           7           1  0.500000000000000             101
           7           2  0.500000000000000             101
           8           1  0.250000000000000             102
           8           2  0.250000000000000             102
           8           3  0.250000000000000             102
           8           4  0.250000000000000             102
           9           3  0.500000000000000             103
           9           4  0.500000000000000             103
          10           3  0.500000000000000             104
          10           4  0.500000000000000             104
          11           3  0.500000000000000             105
          11           4  0.500000000000000             105
          12           1  0.375000000000000             201
          12           2  0.375000000000000             201
          12           3  0.125000000000000             201
          12           4  0.125000000000000             201
          13           1  0.125000000000000             202
          13           2  0.125000000000000             202
          13           3  0.375000000000000             202
          13           4  0.375000000000000             202
          14           3  0.500000000000000             203
          14           4  0.500000000000000             203
          15           3  0.500000000000000             204
          15           4  0.500000000000000             204
          17           1  0.250000000000000             301
          17           2  0.250000000000000             301
          17           3  0.250000000000000             301
          17           4  0.250000000000000             301
          18           1  6.250000000000000E-002        302
          18           2  6.250000000000000E-002        302
          18           3  0.437500000000000             302
          18           4  0.437500000000000             302
          19           3  0.500000000000000             303
          19           4  0.500000000000000             303
```

The file with heterozogosity ("HET") contains from 0 to $N\_BPOP \times (N\_BPOP - 1)/2$ lines per individual in the traced pedigree (only lines for heterozygosity > 0 are generated).Base populations/breeds are numbered according to the renumbering information in the "PHG_RENUM" file.

```
           1           1           2   1.00000000000000              1
           2           1           2   1.00000000000000              2
           3           1           2   1.00000000000000              3
           4           3           4   1.00000000000000              4
           5           3           4   1.00000000000000              5
           6           3           4   1.00000000000000              6
           7           1           2  0.500000000000000            101
           8           1           3  0.250000000000000            102
           8           1           4  0.250000000000000            102
           8           2           3  0.250000000000000            102
           8           2           4  0.250000000000000            102
           9           3           4  0.500000000000000            103
          10           3           4  0.500000000000000            104
          11           3           4  0.500000000000000            105
          12           1           2  0.250000000000000            201
          12           1           3  0.125000000000000            201
          12           1           4  0.125000000000000            201
          12           2           3  0.125000000000000            201
          12           2           4  0.125000000000000            201
          13           1           3  0.125000000000000            202
          13           1           4  0.125000000000000            202
          13           2           3  0.125000000000000            202
          13           2           4  0.125000000000000            202
          13           3           4  0.250000000000000            202
          14           3           4  0.500000000000000            203
          15           3           4  0.500000000000000            204
          17           1           2  9.375000000000000E-002       301
          17           1           3  0.156250000000000            301
          17           1           4  0.156250000000000            301
          17           2           3  0.156250000000000            301
          17           2           4  0.156250000000000            301
          17           3           4  9.375000000000000E-002       301
          18           1           3  6.250000000000000E-002       302
          18           1           4  6.250000000000000E-002       302
          18           2           3  6.250000000000000E-002       302
          18           2           4  6.250000000000000E-002       302
          18           3           4  0.375000000000000            302
          19           3           4  0.500000000000000            303
```