Short User's Guide for the Programs EWPIG2 (Version 3.0.0) and GFPIG (Version 2.0.0) (C Programs for Calculating Economic Weights in Pigs)

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> *Pigs) Institute of Animal Science, Prague Uhříněves.*

Preface

The present version 3.0.0 of EWPIG2 allows for the calculation of the steady state of the sow population of the considered breed(s) and cross(es), for the calculation of the structure of progeny and for the calculation of variables connected with the growth of both pure-bred and cross-bred progeny and with the nutrition of all animal categories. Furthermore, version 3.0.0 calculates all costs and revenues, the profit in the whole production system and the marginal economic values in the same way as the program EWPIG2 version 2.0.0. EWPIG2 version 3.0.0 can be therefore used as stand along program (in the same way as the program EWPIG2 version 2.0.0) or in combination with the program for gene flow GFPIG. Which of these options will be run depends on the parameter gf in file INPUTPBS#.TXT (where # stand for Breeding systems 1, 2, 3 or 4, see Subsection 3.1.2.1 and Chapter 5). If the value of this parameter is zero, the program GFPIG will not be run and the program EWPIG2 calculate next to the marginal economic values only approximate economic weights of traits for specified Breeding system. The calculated approximate economic weights consider the proportions of genes from the individual breeds or lines in all links of a breeding system which are expressed in one generation of progeny. The timing of expected genetic changes in the individual genotypes in all links of a breeding system is not considered. If the value of the parameter gf is one, the program GFPIG is automatically running after running the program EWPIG2 and the true economic weights for direct and maternal traits or trait components are calculated for the evaluated breed in the appropriate Breeding system. This economic weights consider the proportion of genes from the individual breeds or lines and the timing of expected genetic changes in the individual genotypes. This is achieved using gene flow methods and applying discounting of the numbers of gene expression from evaluated breed. In this case, the program EWPIG2 does not calculate the approximate economic weights of traits, but only the trait marginal economic values. The new version 3.0.0 of the program EWPIG2 and the new version 2.0.0 of the program GFPIG calculate the marginal economic values and the approximate or the true economic weights for up to 35 traits, i.e. five new pig traits were included into these versions, namely the number of sow functional teats and four sperm quality traits (sperm volume, sperm concentration, motility and percentage of abnormal spermatozoa in boar ejaculates).

Both programs EWPIG2 and GFPIG are distributed in one installation package and are free of charge. However, their use should be always cited (see citation notices in manuals for these programs).

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Contents

List of Tables

Abbreviations used in the text

AI	artificial insemination
BS	breeding system
°C	degree(s) centigrade, degree(s) Celsius
CW	carcass weight
d	day(s)
DM	dry matter
kJ	kilo Joules
l	litre
LW	live weight
m^3	cubic metre(s) = 1000 litres
ME	metabolisable energy
MJ	Mega Joules
mo.	month(s)
MU	monetary unit
NBA	Number of piglets born alive
NE	net energy
NW	Number of piglets weaned
TNB	Total number of piglets born
yr	year(s)

Chapter 1

Introduction

The most recent program EWPIG2 (Version 3_0_0) is intended for the calculation of the marginal economic values and approximate economic weights (when using it as a stand alone program) or true economic weights (when using EWPIG2 in combination with GFPIG) of up to 35 economically important traits in pig breeds involved in different Breeding systems (see Chapter 5). Moreover, the program will be useful for some economic analyses in different production systems. The impact of production, management and economic circumstances on the economic efficiency of a given production system (measured as profit) can be studied.

The program GFPIG models gene flow of a specific breed involved in different Breeding systems. It calculates the cumulative number of discounted gene expressions of breeding males or females of this breed in an investment period of a chosen Breeding system and, applying the marginal economic values of traits calculated by the program EWPIG2, allows to calculate economic weights for direct and maternal traits or direct and maternal trait components for the evaluated breed in this Breeding system.

The aim of the present manual is to give the users a short and well-arranged instructions how to run both program EWPIG2 and GFPIG.

First, the instructions for installing and running both programs under LINUX are given (see Chapter 2). The description of all input files needed for the program EWPIG2 is given in Chapter 3.1 and for the program GFPIG in Chapter 3.2 Please read carefully description of these files in the manual, because it includes many important comments to the particular input parameters which could not be included in the definition of these parameters straight in these input files. In Chapter 4, a short description of out-put and result files are given.

Furthermore, the manual contains description of the Breeding systems which can be handled with the programs (see Chapter 5) and description of the integrated pig production system (Chapter 6). Within this Chapter, a short description of the calculation of sow herds and progeny structure, definition of sow and progeny categories and some notices to the calculation of growth, energy requirement, feed and other costs, revenues and profit, economic values and economic weights are given.

At the end of this manual, a list of traits for which marginal economic values and economic weights can be calculated is included. You will find a list of all variables used in the program EWPIG2 in Appendix B of the Manual for EWPIG2 and a list of all variables used in the program GFPIG in Appendix B of the manual for GFPIG. The values of all these variables are printed in output files CHECKP* and CHECKGFP (for explanation of these files see manuals for EWPIG2 and GFPIG).

Chapter 2

Installing and running the programs

In the given versions of the programs, files for running the programs under LINUX and WINDOWS are given.

2.1 Installation under LINUX

Version 3.0.0 of program EWPIG2 and the version 2.0.0. of the program GFPIG comes to you as a compressed tar-file with the name EWPIG3_0_0_0.tgz. Copy this file to a directory of your choice and enter the command

tar xvf EWPIG3_0_0_0.tgz

for uncompressing and unarchiving the file. You will get the file structure as described in Section 2.5.

Only for experts in programming. If you want to do changes in the program (source code) by yourself, then you must use the option -lm for compiling the source code when using the compiler gcc because otherwise the mathematical functions would not work; e.g.

gcc -o ewpig3_0_0 ewpig3_0_0.c -lm (in more recent versions of LINUX) or

gcc -lm -o ewpig3_0_0 ewpig3_0_0.c (in older versions of LINUX)

will compile the source file ewpig3_0_0.c to the executable file ewpig3_0_0,

gcc -o gfpig2_0_0 gfpig2_0_0.c -lm (in more recent versions of LINUX) or

gcc -lm -o gfpig2_0_0 ewpig2_0_0.c (in older versions of LINUX)

will compile the source file gfpig2_0_0.c to the executable file gfpig2_0_0.

2.2 Running the program under LINUX

First you must choice the breeding system for which you want to do the calculation (see the description of Breeding systems in Chapter 5). There are four options:

- Breeding System 1: All files you need are in subdirectory BS1.

- Breeding System 2: All files you need are in subdirectory BS2.

- Breeding System 3: All files you need are in subdirectory BS3.

- Breeding System 4: All files you need are in subdirectory BS4.

You are recommended to create one directory for each calculation where you will copy and edit all files you will need. *Then edit first the input file INPUTPBS#.TXT (see Section 3.1.2.1) and choose if you want to run the program EWPIG2 as a stand alone program and to calculate only marginal economic values or approximate economic weight of traits (in this case, the last parameter in this file for gene flow gf must be set to zero) or if you want to run also the program GFPIG for gene flow and to calculate true economic weights of traits (in this case, the last parameter in this file for gene flow gf must be set to one).*[1] Then edit the parameter files PARAP*.TXT and all data input files INPUTP#*.TXT for the program ewpig3_0_0. If you have set the parameter gf to 1 edit further the parameter file PARAGFP.TXT, input files INPUTGFP#.TXT and INPUTGFP#*.TXT for the program gfpig2_0_0.

> ***NOTICE:***
>
> *To learn working with our programs, we recommend the users running the programs first with default input parameters in all input files which are distributed with the programs and looking at the results. In input files, there are many parameters which will be skipped for specific production circumstances and for specific Breeding system (defined by the users) and which can be therefore ignored when editing input files for your specific pig production system. In the results file for each breed, only those input parameters are printed which were used for the specific calculation.* *But be careful not to delete input parameters which you do not need for your specific circumstances. Changing the structure of the input files will cause brake down of the program.*

Breeding System 1. Be sure that you have copied all files from directory BS1 to your working directory. In command line, type just ./bs1.sh in this directory if $gf = 0$ or type just ./gf1.sh if $gf = 1$, press the ENTER button and the program will do the rest for you.

Breeding System 2. Be sure that you have copied all files from directory BS2 to your working directory. In command line, type just ./bs2.sh in this directory if $gf = 0$ or type just ./gf2.sh if $gf = 1$ press the ENTER button and the program will do the rest for you. If you want to calculate true economic weights of traits for both breeds A and C involved in this Breeding system, you have to rename the results file reGFP from the run for one breed (which is chosen in the file PARAGFP.TXT) before you run the programs for the second breed. The results file reGFP will be overwritten in each run.

Breeding System 3. Be sure that you have copied all files from directory BS3 to your working directory. In command line, type just ./bs3.sh in this directory if $gf = 0$ or type just ./gf3.sh if $gf = 1$, press the ENTER button and the program will do the rest for you. Again, you can calculate the true economic weights of traits for all breeds involved in this breeding system (A, B and C) consecutively (when

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[1] The approximate economic weights take into account the numbers of gene expressions of the selected animals of the given breed only in one production cycle in all links of a breeding system and they do not take into account time intervals these genes are expressed in different links of a breeding system, i.e. numbers of gene expressions are not discounted. The true economic weights calculated by the program GFPIG take into account the numbers of gene expressions of selected animals in more generations of progeny (the number of generations depends on the length of investment period inserted by the program user) and time intervals these genes are expressed in different links of a breeding system (by using the discounting procedure).

choosing the appropriate breed in the file PARAGFP.TXT), but you have to save the results file reGFP for each breed with different names, because this results file will be overwritten in each run.

Breeding System 4. Be sure that you have copied all files from directory BS4 to your working directory. In command line, type just ./bs4.sh in this directory if $gf = 0$ or type just ./gf4.sh if $gf = 1$, press the ENTER button and the program will do the rest for you. Again, you can calculate the true economic weights of traits for all breeds involved in this breeding system (A, B, C and D) consecutively (when choosing the appropriate breed in the file PARAGFP.TXT), but you have to save the results file reGFP for each breed with different names, because this results file will be overwritten in each run.

2.3 Installation under Microsoft Windows

The Windows version of the programs is distributed as zip file. It contains the compiled programs. The programs were compiled under Cygwin (http:// www.cygwin.com) and run only in the presence of the le cygwin1. dll which is part of the Windows distribution. If there are problems (for example you get nan, i.e. not a number for some results) install Cygwin on your Windows computer and compile the programs on the computer on which the calculations should be carried out. Cygwin is freely available (install Cygwin with gcc compiler). When compiling the source code, omit the option -lm: gcc -o ewpig3_0_0 ewpig3_0_0.c . The versions of programs EWPIG2 and GFPIG were tested only for Microsoft Windows 7.

2.4 Running the program under Microsoft Windows

The main principle of running the programs under Microsoft Windows is the same as running the programs under Linux. The user can easily start the programs by just double-click on bs#.sh or gf#.sh (where # stand for Breeding systems 1, 2, 3 or 4, see Subsection 3.1.2.1 and Chapter 5) file only if the Cygwin is installed. The command promt window with standard outputs which are printed will appear. This window will be automatically closed regardless of whether the programs have ended successfully or not. In other way, the user can start program from command line window (click on start icon, type cmd and enter, change directory where programs are located, type bs#.sh or gf#.sh). This approach provides more control over how the programs are running.

2.5 List of files needed for running only EWPIG2 as a stand alone program

Read this Section only in the case you want to calculate only marginal economic values of pig traits, i.e. if you will run only the program EWPIG2 as a stand alone program. Than first you have to insert zero for the parameter gf in the appropriate input file INPUTPBS#.TXT for breeding system # (# being 1, 2, 3 or 4, see Section 3.1.2.1).

2.5.1 Directory BS1

This directory contains all files necessary for running the program EWPIG2 for Breeding System 1 (pure-bred system with breed A).

bs1.sh Batch file which starts the calculation for Breeding System 1:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 1
echo '*****************************************'
cp P00P1.TXT P00P.TXT
./ewpig3_0_0
```

ewpig3_0_0 Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT This file contains text for writing the results for the program EWPIG2. See also Section 3.1.4.

P00P1.TXT This file is the original form of P00P.TXT for Breeding System 1. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2. See Subsection 3.1.1.1 for details.

PARAPA.TXT Parameter file which contains the most important parameters for running the program EWPIG2 (see Section 3.1.1.2).

INPUTPBS1.TXT Data input file for program EWPIG2 for Breeding System 1 (see Subsection 3.1.2.1 on page 30). **It contains only the decision parameter gf, which must be set to 0 when running the program EWPIG2 as a stand alone program.**

INPUTP#A.TXT with # = 01, 02, ...,17, 19 to 22 Data input files for program EWPIG2 (see Section 3.1.2).

2.5.2 Directory BS2

This directory contains all files necessary for running the program EWPIG2 for Breeding System 2 with dam breed A and sire breed C.

bs2.sh Batch file which starts the calculation for Breeding System 2:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 2
echo '*****************************************'
cp P00P2.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
```

```
echo I am running breed C in Breeding System 2
echo '*****************************************'
./ewpig3_0_0
```

ewpig3_0_0   Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT   This file contains text for writing the results for the program EWPIG2. See also Section 3.1.4.

P00P2.TXT   This file is the original form of P00P.TXT for Breeding System 2. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2. See Subsection 3.1.1.1 for details.

PARAPA.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed A (see Section 3.1.1.2).

PARAPC.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed C (see Section 3.1.1.2).

INPUTPBS2.TXT   Data input file for program EWPIG2 for Breeding System 2 (see Subsection 3.1.2.1 on page 30). **The last parameter in this file is the decision parameter gf, which must be set to 0 when running the program EWPIG2 as a stand alone program.**

INPUTP#A.TXT with # = 01, 02, ..., 22   Data input files for program EWPIG2 for breed A (see Section 3.1.2).

INPUTP#C.TXT with # = 01, ..., 17, 19, 20, 22   Data input files for program EWPIG2 for breed C (see Section 3.1.2).

2.5.3   Directory BS3

This directory contains all files necessary for running the program EWPIG2 for Breeding System 3 with dam breeds A and B and sire breed C.

bs3.sh   Batch file which starts the calculation for Breeding System 3:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running cross AB in Breeding System 3
echo '*****************************************'
cp P00P3.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed C in Breeding System 3
```

```
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 3
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed B in Breeding System 3
echo '*****************************************'
./ewpig3_0_0
```

ewpig3_0_0   Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT   This file contains text for writing the results for the program EWPIG2. See also Section 3.1.4.

P00P3.TXT   This file is the original form of P00P.TXT for Breeding System 3. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2. See Subsection 3.1.1.1 for details.

PARAPA.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed A (see Section 3.1.1.2).

PARAPB.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed B (see Section 3.1.1.2).

PARAPC.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed C (see Section 3.1.1.2).

PARAPAB.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for cross AB (see Section 3.1.1.2).

INPUTPBS3.TXT   Data input file for program EWPIG2 for Breeding System 3 (see Subsection 3.1.2.1 on page 30). **The last parameter in this file is the decision parameter gf, which must be set to 0 when running the program EWPIG2 as a stand alone program.**

INPUTP#A.TXT with # = 01, ..., 22   Data input files for program EWPIG2 for breed A (see Section 3.1.2).

INPUTP#B.TXT with # = 01, ..., 17, 19 to 22   Data input files for program EWPIG2 for breed B (see Section 3.1.2).

INPUTP#C.TXT with # = 01, ..., 17, 19, 20, 22 Data input files for program EWPIG2 for breed C (see Section 3.1.2).

INPUTP#AB.TXT with # = 01, 02, ..., 14, 16, 18, 21, 22 Data input files for program EWPIG2 for cross AB (see Section 3.1.2).

2.5.4 Directory BS4

This directory contains all files necessary for running the program EWPIG2 for Breeding System 4 with dam breeds A and B and sire breeds C and D.

bs4.sh Batch file which starts the calculation for Breeding System 4:

```
#!/bin/sh
echo ' '
echo ' '
echo '****************************************'
echo I am running cross AB in Breeding System 4
echo '****************************************'
cp P00P4.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '****************************************'
echo I am running breed C in Breeding System 4
echo '****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '****************************************'
echo I am running breed D in Breeding System 4
echo '****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '****************************************'
echo I am running breed A in Breeding System 4
echo '****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '****************************************'
echo I am running breed B in Breeding System 4
echo '****************************************'
./ewpig3_0_0
```

ewpig3_0_0 Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT This file contains text for writing the results for the program EWPIG2. See also Section 3.1.4.

P00P4.TXT This file is the original form of P00P.TXT for Breeding System 4. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2. See Subsection 3.1.1.1 for details.

PARAPA.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for breed A (see Section 3.1.1.2).

PARAPB.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for breed B (see Section 3.1.1.2).

PARAPC.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for breed C (see Section 3.1.1.2).

PARAPD.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for breed D (see Section 3.1.1.2).

PARAPAB.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for cross AB (see Section 3.1.1.2).

INPUTPBS4.TXT Data input file for program EWPIG2 for Breeding System 4 (see Subsection 3.1.2.1 on page 31). **The last parameter in this file is the decision parameter gf, which must be set to 0 when running the program EWPIG2 as a stand alone program.**

INPUTP#A.TXT with # = 01, ..., 22 Data input files for program EWPIG2 for breed A (see Section 3.1.2).

INPUTP#B.TXT with # = 01, ..., 17, 19 to 22 Data input files for program EWPIG2 for breed B (see Section 3.1.2).

INPUTP#C.TXT with # = 01, ...,20, 22 Data input files for program EWPIG2 for breed C (see Section 3.1.2).

INPUTP#D.TXT with # = 01, ..., 17, 19, 20, 22 Data input files for program EWPIG2 for breed D (see Section 3.1.2).

INPUTP#AB.TXT with # = 01, 02, ..., 14, 16, 18, 21, 22 Data input files for program EWPIG2 for cross AB (see Section 3.1.2).

INPUTP04CD.TXT Data input file for program EWPIG2 for cross CD (see Paragraph 3.1.2.5).

2.6 List of files needed for running EWPIG2 with GFPIG

Read this Section only in the case you want to calculate true economic weights of pig traits, i.e. if you will run both the programs, EWPIG2 and GFPIG. Than first you have to insert 1 for the parameter gf in the appropriate input file IN-PUTPBS#.TXT for breeding system # (# being 1, 2, 3 or 4).

2.6.1 Directory BS1

This directory contains all files necessary for running the program EWPIG2 and GFPIG for Breeding System 1 (pure-bred system with breed A).

gf1.sh Batch file which starts the calculation for Breeding System 1:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 1
echo '*****************************************'
cp P00P1.TXT P00P.TXT
./ewpig3_0_0
echo '*****************************************'
echo I am running gene flow for Breeding System 1
echo '*****************************************'
./gfpig2_0_0
```

ewpig3_0_0 Executable file for program EWPIG2 version 3_0_0.

TEXTP_OUT.TXT This file contains text for writing the results for the program EWPIG2.

P00P1.TXT This file is the original form of P00P.TXT for Breeding System 1. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2.

PARAPA.TXT Parameter file which contains the most important parameters for running the program EWPIG2.

INPUTPBS1.TXT Parameter file which contains the information if program GFPIG should be run after running program EWPIG2. **It contains only the decision parameter gf, which must be set to 1 when running the program GFPIG after the program EWPIG2.**

INPUTP#A.TXT with # = 01, 02, ...,17, 21, 22 Data input files for program EWPIG2.

gfpig2_0_0 Executable file for program GFPIG version 2.0.0.

TEXTGFP_OUT.TXT This file contains text for writing the results for the program GFPIG.

PARAGFP.TXT Parameter file which contains information for calculation of relative economic weights with the program GFPIG.

INPUTGFP01.TXT Data input files for program GFPIG (which is equal to the INPUTP19A.TXT for program EWPIG version 3.0.0.)

INPUTGFP02.TXT Data input file with general input parameters.

INPUTGFP#A.TXT with # = 02 and 03 Data input files for program GFPIG.

INPUTGFP04A.TXT Data input files for program GFPIG (which is equal to the INPUTP20A.TXT for program EWPIG version 3.0.0.)

2.6.2 Directory BS2

This directory contains all files necessary for running the program EWPIG2 and GFPIG for Breeding System 2 with dam breed A and sire breed C.

gf2.sh Batch file which starts the calculation for Breeding System 2:

```
#!/bin/sh
echo ' '
echo ' '
echo '****************************************'
echo I am running breed A in Breeding System 2
echo '****************************************'
cp P00P2.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '****************************************'
echo I am running breed C in Breeding System 2
echo '****************************************'
./ewpig3_0_0
echo '****************************************'
echo I am running gene flow for Breeding System 2
echo '****************************************'
./gfpig2_0_0
```

ewpig3_0_0 Executable file for program EWPIG2 version 2.0.0.

TEXTP_OUT.TXT This file contains text for writing the results for the program EWPIG2.

P00P2.TXT   This file is the original form of P00P.TXT for Breeding System 2. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2.

PARAPA.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed A.

PARAPC.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed C.

INPUTPBS2.TXT   Data input file for program EWPIG2 for Breeding System 2. **The last parameter in this file is the decision parameter gf, which must be set to 1 when running the program GFPIG after the program EWPIG2.**

INPUTP#A.TXT with # = 01, 02, ..., 18, 21, 22   Data input files for program EWPIG2 for breed A.

INPUTP#C.TXT with # = 01, ..., 17, 22   Data input files for program EWPIG2 for breed C.

gfpig2_0_0   Executable file for program GFPIG version 2.0.0.

TEXTGFP_OUT.TXT   This file contains text for writing the results for the program GFPIG.

PARAGFP.TXT   Parameter file which contains information for calculation of relative economic weights with the program GFPIG

INPUTGFP01.TXT   Data input files for program GFPIG (which is equal to the INPUTP19*.TXT from the program EWPIG version 1.1.0).

INPUTGFP02.TXT   Data input file with general input parameters.

INPUTGFP#A.TXT with # = 02 and 03   Data input files for breed A for program GFPIG.

INPUTGFP04A.TXT   Data input files for program GFPIG for breed A (which is equal to the INPUTP20A.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#C.TXT with # = 02 and 03   Data input files for breed C for program GFPIG.

INPUTGFP04C.TXT   Data input files for program GFPIG for breed C (which is equal to the INPUTP20C.TXT from the program EWPIG version 3.0.0.)

2.6.3   Directory BS3

This directory contains all files necessary for running the program EWPIG2 and GFPIG for Breeding System 3 with dam breeds A and B and sire breed C.

gf3.sh   Batch file which starts the calculation for Breeding System 3:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running cross AB in Breeding System 3
echo '*****************************************'
cp P00P3.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed C in Breeding System 3
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 3
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed B in Breeding System 3
echo '*****************************************'
./ewpig3_0_0
echo '******************************************'
echo I am running gene flow for Breeding System 3
echo '******************************************'
./gfpig2_0_0
```

ewpig3_0_0   Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT   This file contains text for writing the results for the program EWPIG2.

P00P3.TXT   This file is the original form of P00P.TXT for Breeding System 3. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2.

PARAPA.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed A.

PARAPB.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed B.

PARAPC.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for breed C.

PARAPAB.TXT Parameter file which contains the most important parameters for running the program EWPIG2 for cross AB.

INPUTPBS3.TXT Data input file for program EWPIG2 for Breeding System 3. **The last parameter in this file is the decision parameter** gf**, which must be set to 1 when running the program GFPIG after the program EWPIG2.**

INPUTP#A.TXT with # = 01, ..., 18, 21, 22 Data input files for program EWPIG2 for breed A.

INPUTP#B.TXT with # = 01, ..., 17, 21, 22 Data input files for program EWPIG2 for breed B.

INPUTP#C.TXT with # = 01, ..., 17, 22 Data input files for program EWPIG2 for breed C.

INPUTP#AB.TXT with # = 01, 02, ..., 14, 16, 18, 21, 22 Data input files for program EWPIG2 for cross AB.

gfpig2_0_0 Executable file for program GFPIG version 2.0.0.

TEXTGFP_OUT.TXT This file contains text for writing the results for the program GFPIG.

PARAGFP.TXT Parameter file which contains information for calculation of relative economic weights with the program GFPIG.

INPUTGFP01.TXT Data input files for program GFPIG. (which is equal to the INPUTP19*.TXT from the program EWPIG version 3.0.0).

INPUTGFP02.TXT Data input file with general input parameters.

INPUTGFP#A.TXT with # = 02 and 03 Data input files for breed A for program GFPIG.

INPUTGFP04A.TXT Data input files for program GFPIG. for breed A (which is equal to the INPUTP20A.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#B.TXT with # = 02 and 03 Data input files for breed B for program GFPIG.

INPUTGFP04B.TXT Data input files for program GFPIG. for breed B (which is equal to the INPUTP20B.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#C.TXT with # = 02 and 03 Data input files for breed C for program GFPIG.

INPUTGFP04C.TXT Data input files for program GFPIG. for breed C (which is equal to the INPUTP20C.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#AB.TXT with # = 02 and 03 Data input files for cross AB for program GFPIG.

2.6.4 Directory BS4

This directory contains all files necessary for running the program EWPIG2 and GFPIG for Breeding System 4 with dam breeds A and B and sire breeds C and D.

gf4.sh Batch file which starts the calculation for Breeding System 4:

```
#!/bin/sh
echo ' '
echo ' '
echo '*****************************************'
echo I am running cross AB in Breeding System 4
echo '*****************************************'
cp P00P4.TXT P00P.TXT
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed C in Breeding System 4
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed D in Breeding System 4
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed A in Breeding System 4
echo '*****************************************'
./ewpig3_0_0
echo ' '
echo ' '
echo '*****************************************'
echo I am running breed B in Breeding System 4
echo '*****************************************'
./ewpig3_0_0
echo '*****************************************'
```

```
        echo I am running gene flow for Breeding System 4
        echo '*********************************************'
        ./gfpig2_0_0
```

ewpig3_0_0   Executable file for program EWPIG2 version 3.0.0.

TEXTP_OUT.TXT   This file contains text for writing the results for the program EWPIG2.

P00P4.TXT   This file is the original form of P00P.TXT for Breeding System 4. It will be copied to P00P.TXT before starting the program. It contains the parameters for the breeding system, the breed and the number of the run of EWPIG2.

PARAPA.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed A.

PARAPB.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed B.

PARAPC.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed C.

PARAPD.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for breed D.

PARAPAB.TXT   Parameter file which contains the most important parameters for running the program EWPIG2 for cross AB.

INPUTPBS4.TXT   Data input file for program EWPIG2 for Breeding System 4. **The last parameter in this file is the decision parameter gf, which must be set to 1 when running the program GFPIG after the program EWPIG2.**

INPUTP#A.TXT with # = 01, ..., 18, 21, 22   Data input files for program EWPIG2 for breed A.

INPUTP#B.TXT with # = 01, ..., 17, 21, 22   Data input files for program EWPIG2 for breed B.

INPUTP#C.TXT with # = 01, ..., 18, 22   Data input files for program EWPIG2 for breed C.

INPUTP#D.TXT with # = 01, ..., 17, 22   Data input files for program EWPIG2 for breed D.

INPUTP#AB.TXT with # = 01, 02, ..., 14, 16, 18, 21, 22   Data input files for program EWPIG2 for cross AB.

INPUTP04CD.TXT   Data input file for program EWPIG2 for cross CD.

gfpig2_0_0   Executable file for program GFPIG version 2.0.0.

TEXTGFP_OUT.TXT   This file contains text for writing the results for the program GFPIG.

PARAGFP.TXT   Parameter file which contains information for calculation of relative economic weights with the program GFPIG.

INPUTGFP01.TXT   Data input file for the program GFPIG (which is equal to the INPUTP19*.TXT from the program EWPIG version 3.0.0).

INPUTGFP02.TXT   Data input file with general input parameters.

INPUTGFP#A.TXT with # = 02 and 03   Data input files for breed A for program GFPIG.

INPUTGFP04A.TXT   Data input file for program GFPIG for breed A (which is equal to the INPUTP20A.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#B.TXT with # = 02 and 03   Data input files for breed B for program GFPIG.

INPUTGFP04B.TXT   Data input file for program GFPIG for breed B (which is equal to the INPUTP20B.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#C.TXT with # = 02 and 03   Data input files for breed C for program GFPIG.

INPUTGFP04C.TXT   Data input file for program GFPIG for breed C (which is equal to the INPUTP20C.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#D.TXT with # = 02 and 03   Data input files for breed D for program GFPIG.

INPUTGFP04D.TXT   Data input file for program GFPIG for breed D (which is equal to the INPUTP20D.TXT from the program EWPIG version 3.0.0.)

INPUTGFP#AB.TXT with # = 02 and 03   Data input files for cross AB for program GFPIG.

2.7   Directory DOC

This directory contains license and manuals.

license   This file contains the license conditions. Read them carefully and do not use the program if you do not agree with the license conditions.

2.8   Directory SRC

ewpig3_0_0.c   Source code of version 3.0.0 of program EWPIG2.

gfpig2_0_0.c   Source code of version 2.0.0 of program GFPIG2.

Chapter 3

Input files for EWPIG2 and GFPIG

IMPORTANT REMARK: When editing the input files, keep attention *not to change quotation marks*. All files are read as sequential files and the program recognizes the beginning and the end of texts on the basis of quotation marks. Adding or deleting a quotation mark will cause the program to break down or to calculate wrong results. Do not delete inputs you do not need for your calculation, just ignore them. The programs do not used values which are not relevant for the given Breeding system, for specific breed or for your specific production circumstances. Deleting inputs can cause the program to break down or to calculate wrong results.

Monetary unit: In all input files, the abbreviation MU is used for monetary unit. All values in the distributed version of the program refer to Euros. You can globally replace the abbreviation MU by the abbreviation of your monetary unit in all data input files and in the input file TEXTP_OUT.TXT using any text editor; the results files will then contain the monetary unit specified by you.

Language of the program: The program will need just the numbers for calculations. The texts are read in and printed out to the result file as they are. Therefore, you can freely change the text in all input files as long as you do not modify the quotation marks. For example, you can translate all texts in the input files to another language what will cause the appropriate part of the result file to be printed in the same language as the input files (may be there are some exceptions where the English text will be remained). The length of the texts can be changed, but each text must start and finish with quotation marks. A great part of the text for the results file is read from the file TEXTP_OUT.TXT. You can translate all the text in this file. But be very careful not to change quotation marks.

3.1 Input files for the program EWPIG2

3.1.1 Parameter files

3.1.1.1 Parameter file P00P.TXT

This file is automatically generated. **Do not edit this file.** It contains three parameters (without text) in the following order:

- Breeding System ($bsyst$). This code is

  - 1 for a pure-breeding system of breed A
  - 2 for two-way crossing with dam breed A and sire breed C
  - 3 for three-way crossing with dam breeds A and B and sire breed C; sires of breed B are crossed with dams of breed A to produce AB sows and sires of breed C are crossed with AB sows to produce slaughter animals
  - 4 for four-way crosses with dam breeds A and B and sire breeds C and D; sires of breed B are crossed with dams of breed A to produce AB sows and sires of breed D are crossed with dams of breed C to produce CD boars which are crossed with AB sows to produce slaughter animals

- Breed or cross for which the calculation is carried out ($breed$). This code is

  - 1 for breed A
  - 2 for breed B
  - 3 for breed C
  - 4 for breed D
  - 5 for cross A x B
  - 6 for cross C x D. This code is needed only for one input file for CD boars from technical reasons in the program; no stand-alone calculation is carried out for this cross.

- Number of the calculation ($calc$).

  - In Breeding System 1, this number is always 1 as the program is run only once for breed A.
  - In Breeding System 2, the first run is for breed A and the second run for breed C.
  - In Breeding System 3, the first run is for the cross AB, the second run is for breed C, the third run is for breed A and the fourth run is for breed B.
  - In Breeding System 4, the first run is for the cross AB, the second run is for breed C, the third run is for breed D, the fourth run is for breed A and the fifth run is for breed B.

The parameter cb which can take values 1 (only pure-bred progeny) or 2 (pure-bred and cross-bred progeny) is determined by the codes for breeding system and breed (see Tab. 3.1).

Table 3.1: Values of variable cb for individual breeding systems and breeds or crosses

Breeding System ($bsyst$)	Breed or cross ($breed$)	Variable cb
1	A (1)	1
2	A (1)	2
2	C (3)	1
3	A (1)	2
3	B (2)	1
3	C (3)	1
3	AB (5)	2
4	A (1)	2
4	B (2)	1
4	C (3)	2
4	D (4)	1
4	AB (5)	2

3.1.1.2 PARAP*.TXT

This file contains basic information for running the program EWPIG2. The symbol '*' in the file name must be replaced by 'A', 'B', 'C', 'D' or 'AB' in the calculations for breeds A, B, C, D or cross AB, respectively. At the beginning of the file (between the first two quotation marks) you can write any text characterizing your calculation. Then the value of a parameter is always followed by its description. Modify the values of the parameters according to your needs. Generally, the file PARAP*.TXT reads the parameters given below. ***In some situations, the file PARAP*.TXT may contain less parameters.*** For example, the file PARA-PAB.TXT used in the first calculation of Breeding System 3 reads only parameters $cast[1]$, $sperm$ and $teat$.

- Castration of surplus pure-bred male progeny ($cast[0]$)

    - 0: No surplus pure-bred male progeny are castrated
    - 1: A part of surplus pure-bred male progeny are castrated
    - 2: All surplus pure-bred male progeny are castrated

- Castration of surplus cross-bred male progeny ($cast[1]$, only read if there is cross-bred progeny)

    - 0: No surplus cross-bred male progeny are castrated
    - 1: A part of surplus cross-bred male progeny are castrated
    - 2: All surplus cross-bred male progeny are castrated

- Finishing of negatively selected breeding gilts after selection ($fin16$)

    - 0: No
    - 1: Yes

- Genetic standard deviations are available and are to be read from INPUTP20*.TXT (std). (This variable is of interest only for the case that program GFPIG is not running after the program EWPIG2, i.e if the variable gf in input file INPUTPBS#.TXT is zero.)

    - 0: No

- 1: Yes

- Input parameters for the calculation of the marginal economic value for sperm quality traits of boars used for pure-breeding are available and are to be read from INPUTP22*.TXT ($sperm[0]$)

  - 0: No
  - 1: Yes

- Input parameters for the calculation of the marginal economic value for sperm quality traits of boars used for cross-breeding are available and are to be read from INPUTP22**.TXT of the appropriate breed (designated with **) its boars are used for crossing in breed designated with * ($sperm[1]$)

  - 0: No
  - 1: Yes

- Input parameters for the calculation of the marginal economic value for the number of sow teats are available and are to be read from INPUTP21*.TXT ($teat$)

  - 0: No
  - 1: Yes

After reading the variables from PARAP*.TXT, the variable $pcast[i]$ is set to 0 for $cast[i] = 0$ and is set to 1 for $cast[i] = 2$. The value of $pcast[i]$ is read from INPUTP05*.TXT for $cast[i] = 1$.

   Notice that the values of parameters ($sperm[0]$) and ($sperm[1]$) must be in accordance with mating types $mtype[0]$ ***and*** $mtype[1]$ ***you have inserted in input files INPUTP04*.TXT.*** If mating type for boars of the appropriate breed is only natural mating, i.e. $mtype[j] = 3$, the variable $sperm[j]$ is set to zero regardless the values you have inserted in file PARAP*.TXT.

3.1.2 Data input files

The data input files must be prepared only for breed A in Breeding System 1, for breed A (dam breed) and breed C (sire breed) in Breeding System 2, for dam breeds A and B, sire breed C and crossbreed AB in Breeding System 3 and for all four breeds A, B, C and D and crossbreeds AB and CD in Breeding System 4. For a detailed list of files which are necessary for the individual breeding systems see Section . The names of most of the input files have the structure INPUTP#*.TXT where '#' = 01, 02, 03 etc. and '*' = A, B, C, D, AB or CD which refers to the corresponding breeds or crosses. Unless noted otherwise, the input files for all breeds and crosses have the same structure.

Input files with the name INPUTPBS#.TXT depend only on the breeding system where '#' = 1, 2, 3 or 4 is the number of the breeding system.

   Note please that most numbers are _averages_ **for the given population. Therefore, data which are integer for a given animal or within a given farm (e.g. number of re-inseminations) will often not be integer for the whole population.**

   Data not needed for a given calculation (for example, data for non-existing categories of animals or for cross-bred animals when there is no cross-breeding) are skipped when reading data. This is valid for all data input files.

Do never change the structure of input files (for example do never delete inputs which you do not need). This will cause the program to break down or to calculate nonsense. As mentioned above, data which are not needed are skipped when reading the input files.

3.1.2.1 Input files INPUTPBS#.TXT

These files depend on the breeding system and contain the numbers of sows of the individual breeds and of cross AB in the whole production system (not in Breeding system 1) and a parameter describing if the program for gene flow (GFPIG) should be run after running the program EWPIG2 or not.

Input file INPUTPBS1.TXT for Breeding System 1   This file contains only one parameter:

- Gene flow is used in the calculation of economic weights (variable gf)

  - 0: no
  - 1: yes

Input file INPUTPBS2.TXT for Breeding System 2   This file contains the following variables:

- Number of sows of breed A in the whole breeding system (nA)

- Number of sows of breed C in the whole breeding system (nC)

- Gene flow is used in the calculation of economic weights (variable gf)

  - 0: no
  - 1: yes

Input file INPUTPBS3.TXT for Breeding System 3   This file contains the following variables:

- Number of sows of breed A in the whole breeding system (nA)

- Number of sows of breed B in the whole breeding system (nB)

- Number of sows of breed C in the whole breeding system (nC)

- Number of sows of cross AB in the whole breeding system (nAB)

- Gene flow is used in the calculation of economic weights (variable gf)

  - 0: no
  - 1: yes

Input file INPUTPBS4.TXT for Breeding System 4   This file contains the
following variables:

- Number of sows of breed A in the whole breeding system (nA)

- Number of sows of breed B in the whole breeding system (nB)

- Number of sows of breed C in the whole breeding system (nC)

- Number of sows of breed D in the whole breeding system (nD)

- Number of sows of cross AB in the whole breeding system (nAB)

- Gene flow is used in the calculation of economic weights (variable gf)

    - 0: no
    - 1: yes

3.1.2.2   Input file INPUTP01*.TXT

This file contains input parameters for calculating the sow herd structure. *Notice*
please in which units the input parameters are given. Most of the frac-
tions are not given in per cent, but they are expressed as proportions
(i.e. as numbers less then one). They are:

- Maximal number of reproductive cycles a sow stays in the herd (RR, must
  take a value between 6 and 15)

- Maximal number of matings (inseminations) for a sow in reproductive cycle i
  ($mm[i]$, $i = 1, \ldots, RR - 1$). Do not use values greater than 7. (This number
  say how many matings are applied for a sow after the ith farrowing before this
  sow is culled for not conceiving.)

- Conception rate of sows after the jth mating (insemination) in reproductive
  cycle i ($conrateS[i][j]$)[1]. One row is one reproductive cycle, so that the num-
  ber of rows must be $RR - 1$. The number of columns in reproductive cycle i
  must be identical to the maximal number of matings in that cycle ($mm[i]$) as
  given in the input above. All values must be in the range from 0 to 1.

- Sows died in reproductive cycle i ($i = 1, \ldots, RR$) from farrowing to piglet
  weaning as proportion of sows farrowed in reproductive cycle i ($pdfwS[i]$).
  All values must be in the range from 0 to 1.

- Sows died in reproductive cycle i ($i = 1, \ldots, RR - 1$) from conception to next
  farrowing as proportion of sows conceived in reproductive cycle i ($pdcfS[i]$).
  All values must be in the range from 0 to 1.

- Sows culled in reproductive cycle i ($i = 1, \ldots, RR - 1$) after piglet weaning
  for health problems or low litter size as proportion of sows at weaning in
  reproductive cycle i ($pcwS[i]$). All values must be in the range from 0 to 1.

- Average interval (in days) between two subsequent matings in reproductive cy-
  cle i ($intmS[i]$, $i = 1, \ldots, RR - 1$); the custom interval between two oestruses
  should not be inserted here, because the oestrus detection rate is hardly equal
  to 1 so that this interval is generally longer than 21 days.

---

[1]Conception rate is defined as the number of sows conceived after the jth mating (insemination)
as proportion of the number of sows mated in the jth mating.

- Sows crossed with other breeds in reproductive cycle i as proportion of sows mated in cycle i ($pcrossS[i]$, $i = 1, \ldots, RR-1$). All values must be in the range from 0 to 1. *This input is absent in Breeding Systems 3 and 4 for the cross AB (i.e. in file INPUTP01AB.TXT) where $pcrossS[i] = 1$ is automatically set for all i. This input is not read in Breeding System 1 and is also not read for breed C in Breeding systems 2 and 3, for bred B in Breeding systems 3 and 4 and for breed D.*

3.1.2.3   Input file INPUTP02*.TXT

The file contains input parameters describing the management within the reproductive cycles of sows. The values should represent average values over all reproductive cycles in the sow herds. The following parameters are read:

- Age of piglets at weaning ($agew$)

- Interval from farrowing to death for sows died in the period between farrowing and piglets weaning ($indfw$)

- Interval from weaning to culling for sows negatively selected after weaning (e.g. for health problems, low litter size, bad mothering ability, not showing heat) or culled for age (in the last reproductive cycle) ($inwc[i]$, $i = 1, \ldots, RR$)

- Interval from weaning to the first mating ($inwm$)

- Interval from last mating to culling for sows not being pregnant after the maximal number of matings ($inmc$)

- Interval from weaning to death for sows died in the period from conception to farrowing ($indcf$)

- Length of pregnancy ($lpreg$)

- Average weight of sows at weaning/mating ($wwS[i]$) in reproductive cycles $i = 1, \ldots, RR$ (averaged over sows bearing pure-bred and cross-bred litters). The weight at weaning must not be higher than the weight at previous farrowing.

- Average weight of sows at i^{th} farrowing ($wfS[i]$, $i = 2, \ldots, RR$), averaged over sows bearing pure-bred and cross-bred litters (***Notice that the first value is for the 2nd farrowing***[2])

- Average weight of sows culled ($wS[5 \times (i-1) + 3]$) after the maximal number of matings for failure to conceive in reproductive cycles $i = 1, \ldots, RR - 1$. The weight must be between the sow weight at weaning and the sow weight at next farrowing.

- Average weight of sows culled after piglet weaning in reproductive cycles 1 to RR-1 for health problems or low litter size and sows culled after piglet weaning in reproductive cycles RR for age ($wS[2 + 5 \times (i1 - 1)]$ where $i1 = 1, \ldots, RR$). The weight must not be lower than the weight at weaning.

3.1.2.4   Input file INPUTP03*.TXT

This file contains input parameters describing management and performance of replacement gilts. The following inputs are read:
Remark: The following 3 inputs ($pdiedG$, $pcullG[i]$ and $pmatG$) are not contained in INPUTP03AB.TXT.

---

[2]The weight at the first farrowing is a parameter which describes gilts

- Gilts died (mortality rate) during rearing (from the end of the nursery phase to including in the herd as replacement or to selling, i.e. during a period of about 5 months) expressed as proportion of female piglets intended for rearing as breeding animals after the nursery phase ($pdiedG$). The same mortality rate is assumed for pure-bred and cross-bred gilts.

- Pure-bred ($i = 0$) or cross-bred ($i = 1$) gilts negatively selected for different reasons (e.g. bad legs, low performance) before including in the herd as replacement or before selling, expressed as proportion of female piglets of the appropriate genotype intended for rearing as breeding animals after the nursery phase ($pcullG[i]$)

- Gilts firstly mated as proportion of gilts included in the herd as replacement ($pmatG$) (some gilts do not show head, can not be mated and must be culled)

- Maximal number of matings for replacement gilts (mmG). (This number say how many matings are applied for a gilts before this gilts is culled for not conceiving.)

- Conception rate of gilts after the ith mating or insemination[3] ($conrateG[i]$, $i = 1, \ldots, mmG$)

- Average interval (in days) between two subsequent matings of gilts ($intmG$); the custom interval between two oestruses should not be inserted here, because the oestrus detection rate is hardly equal to 1 so that this interval is generally longer than 21 days.

Remark: The next input ($pcrossG$) is also not contained in INPUTP03AB.TXT. In the calculation for cross AB, $pcrossG = 1$ is automatically set in the program. This input is not read in Breeding System 1 and is also not read for bred C in Breeding systems 2 and 3, for bred B in Breeding systems 3 and 4 and for breed D.

- Gilts mated with boars with genotypes different from the gilt genotype as proportion of gilts firstly mated ($pcrossG$)

After reading the last parameter of the file, $pcrossS[0] = pcrossG$ is set.

3.1.2.5 Input file INPUTP04*.TXT

This file contains parameters connected with mating management and breeding boars. Boars of two different genotypes may be used for mating in sow herds:

- Boars for pure-bred mating, i.e. boars of the breed of the sows, index $i = 0$, and

- Boars for cross-bred mating, i.e. boars of a breed or cross different from the breed of the sow, index $i = 1$.

In the first part of the file, values for the boars of the breed of the sows are read. If only pure-breeding is applied ($bsyst = 1$) , those inputs are the only ones which are read from the file. Otherwise inputs for the boars of a breed or cross different from the breed of the sows are read from the second part of the file too.

Attention! INPUTP04AB.TXT which reads data for the cross AB is shortened and contains only the second part of the file for boars for cross-bred mating. INPUTP04B.TXT which reads data for breed B and INPUTP04D.TXT which reads data for breed D are shortened too and contain only the first part of the file for boars for pure-bred mating.

---

[3]Conception rate is defined as the number of gilts conceived after the ith mating (insemination) as proportion of the number of gilts mated in the ith mating.

The following variables are read:

- Boars of the breed of the sows died (mortality rate) during rearing (from the end of the nursery phase to including in the herd or in AI stations as replacement or to selling; i.e. during a period of about 5 months), expressed as proportion of male piglets intended for rearing as breeding animals after the nursery phase ($pdiedB[0]$)

- Boars of the breed of the sows negatively selected for different reasons (e.g. bad legs, low performance, bad libido) before including them in the herd or in AI stations as replacement or before selling, expressed as proportion of male piglets intended for rearing as breeding animals after the nursery phase ($pcullB[0]$)

- Type of mating for boars of the breed of the sows ($mtype[0]$) (i.e. the mating type for pure-bred matings):

    - 0: artificial insemination (AI) is used throughout and no boars are used for oestrus stimulation
    - 1: AI is used throughout and boars are used for oestrus stimulation
    - 2: AI and natural mating is applied
    - 3: natural mating is used throughout

The following 7 inputs are read if the type of mating for boars of the breed of the sows is less than 3 ($mtype[0] < 3$).

- Number of boars of the breed of the sows imported for sperm production, per sow per reproductive cycle (i.e. per average farrowing interval) ($imspB[0]$)

- Young boars of the breed of the sows purchased to AI stations (or intended for sperm production on farms) which were culled because of unsuitability for sperm collection as proportion of young boars purchased to AI stations or included in the herd for sperm production ($cullyB[0]$)

- Number of sperm doses per young boar of the breed of the sows (age 7 to 13 months) produced per a time interval of 6 months ($spermyB[0]$)

- Number of sperm doses per mature boar of the breed of the sows (age > 13 months) produced per a time interval of 6 months ($spermoB[0]$)

- Number of re-inseminations[4] per sow per oestrus for boars of the breed of the sows ($reinS[0]$)

- Number of re-inseminations per gilt per oestrus for boars of the breed of the gilts ($reinG[0]$)

- Average productive lifetime of boars of the breed of the sows used for sperm collection on AI stations or on farms ($lifespB[0]$)

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[4]The number of re-inseminations is defined as the number of repeated AI within one oestrus of a female. For example, if a sow is inseminated only once, there is no (0) re-insemination. If a sow is inseminated twice, then the first insemination is repeated once so that the number of re-inseminations is 1. Have in mind that average values have to be inserted. Assume that there is a population of 5 sows. Three of them have 2 inseminations (1 re-insemination) and two sows have 3 inseminations, i.e. 2 re-inseminations. The average number of re-inseminations is then $(3 \times 1 + 2 \times 2)/5 = 7/5 = 1.4$.

The following 2 inputs are read if the type of mating for boars of the breed of the sows is 1 ($mtype[0] = 1$).

- Sow (and gilt) to boar ratio for boars of the breed of the sows used only for oestrus stimulation ($sowb[0]$)

- Average productive lifetime of boars of the breed of the sows used only for oestrus stimulation ($lifeosB[0]$)

The following 6 inputs are read if the type of mating for boars of the breed of the sows is 2 ($mtype[0] = 2$).

- Number of boars of the breed of the sows imported for natural mating per sow per reproductive cycle ($imnmB[0]$)

- Maximal number of artificial inseminations per sow in reproductive cycle i ($i = 1, \ldots, RR - 1$) within a mating period with sperm of boars of the breed of the sow ($maxAIS[i][0]$); for further matings, natural service boars is used. The values must be less than the appropriate values $mm[i]$, $i = 1, \ldots, RR - 1$ given in INPUTP01*.TXT.

- Maximal number of artificial inseminations per gilt within a mating period with sperm of boars of the breed of the gilts ($maxAIG[0]$); for further matings, natural service boars are used. The value must be less than mmG given in INPUTP03*.TXT.

- Sow (and gilt) to young boar (7 to 13 months of age) ratio for boars of the breed of the sows when boars are used for natural mating next to AI and eventually simultaneously for oestrus stimulation ($sowyB[0]$)

- Sow (and gilt) to mature boar (older than 13 months) ratio for boars of the breed of the sows when boars are used for natural mating next to AI and eventually simultaneously for oestrus stimulation ($sowoB[0]$)

- Average productive lifetime of boars of the breed of the sows used for natural mating and eventually simultaneously for oestrus stimulation ($lifenmB[0]$)

The following 4 inputs are read if the type of mating for boars of the breed of the sows is 3 ($mtype[0] = 3$).

- Number of boars of the breed of the sows imported for natural mating per sow per reproductive cycle ($imnmB[0]$)

- Sow (and gilt) to young boar (7 to 13 months of age) ratio for boars of the breed of the sows when boars are used for natural mating ($sowyB[0]$)

- Sow (and gilt) to mature boar (older than 13 months) ratio for boars of the breed of the sows when boars are used for natural mating ($sowoB[0]$)

- Average productive lifetime of boars of the breed of the sows used for natural mating ($lifenmB[0]$)

The following 7 inputs are read only if the type of mating for boars of the breed of the sows is 1, 2 or 3 ($mtype[0] > 0$). The first 2 of those 7 inputs are read only if there is import of boars for natural mating ($imnmB[0] > 0$).

- Average age of boars of the breed of the sows imported as replacement for natural mating ($ageimB[0]$). This age is expected to be lower than 2 years.

- Average weight of boars of the breed of the sows imported as replacement for natural mating ($wimB[0]$)

- Target average daily gain of boars of the breed of the sows till 12 months of age ($adg12B[0]$)

- Target average daily gain of boars of the breed of the sows between 12 to 24 months of age ($adg24B[0]$)

- Target weight of boars of the breed of the sows (the weight after which no further growth of boars is required, $mwB[0]$)

- Amount of protein in 1 kg weight gain of boars of the breed of the sows older than 12 months ($protpB[0]$)

- Amount of lipid in 1 kg weight gain of boars of the breed of the sows older than 12 months ($lippB[0]$)

If you do not have information about the values for the last two parameters (for protein and lipid mass in 1 kg gain of boars) for your breed, use the default values from our example inputs. (For references from which these values were taken, see the manual of EWPIG2.)

Here start data for boars of a breed or cross different from the breed of the sows. Files INPUTP04B and INPUTP04D end here. File INPUT04AB starts here.

- Type of mating for boars of a breed or cross different from the breed of the sows ($mtype[1]$) (i.e. mating type used for cross-bred mating):

    - 0: artificial insemination (AI) is used throughout and no boars are used for oestrus stimulation
    - 1: AI is used throughout and boars are used for oestrus stimulation
    - 2: AI and natural mating is applied
    - 3: natural mating is used throughout

The following 2 inputs are read if the type of mating for boars of a breed or cross different from the breed of the sows is less than 3 ($mtype[1] < 3$).

- Number of re-inseminations[5] per sow per oestrus for boars of a breed or cross different from the breed of the sows ($reinS[1]$)

- Number of re-inseminations per gilt per oestrus for boars of a breed or cross different from the breed of the gilts ($reinG[1]$)

The following 2 inputs are read if the type of mating for boars of a breed or cross different from the breed of the sows is 1 ($mtype[1] = 1$).

- Sow (and gilt) to boar ratio for boars of a breed or cross different from the breed of the sow used only for oestrus stimulation ($sowb[1]$)

- Average productive lifetime of boars of a breed or cross different from the breed of the sows used only for oestrus stimulation ($lifeosB[1]$)

The following 6 inputs are read if the type of mating for boars of a breed or cross different from the breed of the sows is 2 ($mtype[1] = 2$).

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[5]See footnote 4 on page 34

- Number of boars of a breed or cross different from the breed of the sows imported for natural mating per sow per reproductive cycle ($imnmB[1]$)

- Maximal number of artificial inseminations per sow in reproductive cycle i ($i = 1, \ldots, RR - 1$) within a mating period with sperm of boars of a breed or cross different from the breed of the sows ($maxAIS[i][1]$); for further matings, natural service boars is used. The values must be less than the appropriate values $mm[i]$, $i = 1, \ldots, RR - 1$ given in INPUTP01*.TXT.

- Maximal number of artificial inseminations per gilt within a mating period with sperm of boars of a breed or cross different from the breed of the gilts ($maxAIG[1]$); for further matings, natural service boars are used. The value must be less than mmG given in INPUTP03*.TXT.

- Sow (and gilt) to young boar (7 to 13 months of age) ratio for boars of a breed or cross different from the breed of the sows when boars are used for natural mating next to AI and eventually for oestrus stimulation ($sowyB[1]$)

- Sow (and gilt) to mature boar (older than 13 months) ratio for boars of a breed or cross different from the breed of the sows when boars are used for natural mating next to AI and eventually for oestrus stimulation ($sowoB[1]$)

- Average productive lifetime of boars of a breed or cross different from the breed of the sows used for natural mating and eventually for oestrus stimulation ($lifenmB[1]$)

The following 4 inputs are read if the type of mating for boars of a breed or cross different from the breed of the sows is 3 ($mtype[1] = 3$).

- Number of boars of a breed or cross different from the breed of the sows imported for natural mating per sow per reproductive cycle ($imnmB[1]$)

- Sow (and gilt) to young boar (7 to 13 months of age) ratio for boars of a breed or cross different from the breed of the sows when boars are used for natural mating ($sowyB[1]$)

- Sow (and gilt) to mature boar (older than 13 months) ratio for boars of a breed or cross different from the breed of the sows when boars are used for natural mating ($sowoB[1]$)

- Average productive lifetime of boars of a breed or cross different from the breed of the sows used for natural mating ($lifenmB[1]$)

The following 7 inputs are read only if the type of mating for boars of a breed or cross different from the breed of the sows is 1, 2 or 3 ($mtype[1] > 0$). The first 2 of those 7 inputs are read only if there is import of boars for natural mating ($imnmB[1] > 0$).

- Average age of boars of a breed or cross different from the breed of the sows imported as replacement for natural mating ($ageimB[1]$). This age is expected to be lower than 2 years.

- Average weight of boars of a breed or cross different from the breed of the sows imported as replacement for natural mating ($wimB[1]$)

- Target average daily gain of boars of a breed or cross different from the breed of the sows till 12 months of age ($adg12B[1]$)

- Target average daily gain of boars of a breed or cross different from the breed of the sows between 12 to 24 months of age ($adg24B[1]$)

- Target weight of boars of a breed or cross different from the breed of the sows (the weight after which no further growth of boars is required, $mwB[1]$)

- Amount of protein in 1 kg weight gain of boars of a breed or cross different from the breed of the sows older than 12 months ($protpB[1]$)

- Amount of lipid in 1 kg weight gain of boars of a breed or cross different from the breed of the sows older than 12 months ($lippB[1]$)

If you do not have information about the values for the last two parameters (for protein and lipid mass in 1 kg gain of boars) for your breed, use the default values from our example inputs. (For references from which these values were taken, see the manual of EWPIG2.)

Special form for cross CD: INPUTP04CD.TXT   This file is needed in Breeding System 4 in the program run for cross AB. The following inputs are read for boars of cross CD:

- Boars CD died (mortality rate) during rearing (from the end of the nursery phase to including in the herd or in AI stations as replacement or to selling; i.e. during a period of about 5 months), expressed as proportion of male piglets intended for rearing as breeding animals after the nursery phase ($pdiedB[1]$)

- Boars CD negatively selected for different reasons (e.g. bad legs, low performance, bad libido) before including them in the herd or in AI stations as replacement or before selling, expressed as proportion of male piglets intended for rearing as breeding animals after the nursery phase ($pcullB[1]$)

The following 4 inputs are read if the type of mating for boars CD is 0, 1 or 2:

- Young boars of the cross CD purchased to AI stations (or intended for sperm production on farms) which were culled because of unsuitability for sperm collection as proportion of young boars purchased to AI station or included in the herd for sperm production ($cullyB[1]$)

- Number of sperm doses per young boar of the cross CD (age 7 to 13 months) produced per a time interval of 6 months ($spermyB[1]$)

- Number of sperm doses per mature boar of the cross CD (age > 13 months) produced per a time interval of 6 months ($spermoB[1]$)

- Average productive lifetime of boars of the cross CD used for sperm collection on AI stations or on farms ($lifespB[1]$)

3.1.2.6 Input file INPUTP05*.TXT

This file contains parameters for the progeny of the sows from birth until the end of the nursery phase. The first part of the file refers to progeny of the same genotype as the genotype of sows (pure-bred progeny), the second part of the file refers to cross-bred progeny and is read only if cross-breeding is applied. This file has a special form for cross AB (see Paragraph 3.1.2.6). The files INPUTP05B.TXT for breed B and INPUTP05D.TXT for breed D contain only the inputs for pure-bred progeny.

The following inputs are read for the progeny of the same genotype as the genotype of sows (**pure-bred progeny**).

- Total number of piglets born in pure-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nb[i][0]$)

- Number of piglets born alive in pure-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nba[i][0]$)

- Number of piglets weaned in pure-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nw[i][0]$)

- Pure-bred piglets of all sexes died in the nursery phase as proportion of weaned piglets (mortality rate in piglet rearing, $pdiedPP[0]$)

- Female (pure-bred) piglets alive at the end of the nursery phase as proportion of all (pure-bred) piglets (of all sexes) alive at that time ($pfP[0]$)

The following three parameters must sum to 1:

- Surplus female (pure-bred) piglets exported after the nursery phase expressed as proportion of all surplus female (pure-bred) piglets (which are not needed within the system) at the end of the nursery phase ($pexfP[0]$). The given input value together with the values of the following two inputs must sum to 1.

- Surplus female (pure-bred) piglets intended for export as breeding gilts after rearing expressed as proportion of all surplus female (pure-bred) piglets at the end of the nursery phase ($pexG[0]$)

- Surplus female (pure-bred) piglets finished to target slaughter weight expressed as proportion of all surplus female (pure-bred) piglets at the end of the nursery phase ($pfin[0][0]$)

The following three parameters are read only if there are surplus entire pure-bred male piglets, i.e. if the first parameter in the input file PARAP*.TXT $cast[0] < 2$. These three parameters must sum to 1:

- Surplus entire male (pure-bred) piglets exported after the nursery phase expressed as proportion of all surplus male (pure-bred) piglets (which are not needed within the system) at the end of the nursery phase ($pexmP[0]$). The given input value together with the values of the following two inputs must sum to 1.

- Surplus entire male (pure-bred) piglets intended for export as breeding boars after rearing expressed as proportion of all surplus male (pure-bred) piglets at the end of the nursery phase ($pexB[0]$)

- Surplus entire male (pure-bred) piglets finished to target slaughter weight expressed as proportion of all surplus male (pure-bred) piglets at the end of the nursery phase ($pfin[1][0]$)

The following two parameters are read only if there are surplus pure-bred castrated piglets, i.e. if the first parameter in the input file PARAP*.TXT $cast[0] > 0$. These two parameters must sum to 1:

- Castrated (pure-bred) piglets exported after the nursery phase expressed as proportion of castrated (pure-bred) piglets at the end of the nursery phase ($pexcP[0]$). The sum of the given and the following input must be 1.

- Castrated (pure-bred) piglets finished to target slaughter weight expressed as proportion of castrated (pure-bred) piglets at the end of the nursery phase ($pfin[2][0]$)

The following parameter is read only if the first parameter in the input file PARAP*.TXT $cast[0] = 1$.

- Castrated (pure-bred) piglets as proportion of all surplus (pure-bred) males (entire and castrated) alive at the end of the nursery phase

> **INPUTP05B.TXT and INPUTP05D.TXT end here.   The following inputs are not read for breed A in Breeding system 1 and for breed C in Breeding systems 2 and 3.**

The following inputs (until the end of the file) are read for **cross-bred progeny**.

- Total number of piglets born in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nb[i][1]$)

- Number of piglets born alive in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nba[i][1]$)

- Number of piglets weaned in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nw[i][1]$)

- Cross-bred piglets of all sexes died in the nursery phase as proportion of weaned piglets (mortality rate in piglet rearing, $pdiedPP[1]$)

- Female (cross-bred) piglets alive at the end of the nursery phase as proportion of all (cross-bred) piglets (of all sexes) alive at that time ($pfP[1]$)

The following three parameters must sum to 1:

- Surplus female (cross-bred) piglets exported after the nursery phase expressed as proportion of all surplus female (cross-bred) piglets (which are not needed within a Breeding system) at the end of the nursery phase ($pexfP[1]$). The given input value together with the values of the following two inputs must sum to 1.

- Surplus female (cross-bred) piglets intended for export as breeding gilts after rearing expressed as proportion of all surplus female (cross-bred) piglets at the end of the nursery phase ($pexG[1]$)

- Surplus female (cross-bred) piglets finished to target slaughter weight expressed as proportion of all surplus female (cross-bred) piglets at the end of the nursery phase ($pfin[0][1]$)

The following three parameters are read only if there are surplus entire cross-bred male piglets, i.e. if the second parameter in the input file PARAP*.TXT $cast[1] < 2$. These three parameters must sum to 1:

- Surplus entire male (cross-bred) piglets exported after the nursery phase expressed as proportion of all surplus male (cross-bred) piglets (which are not needed within a Breeding system) at the end of the nursery phase ($pexmP[1]$). The given input value together with the values of the following two inputs must sum to 1.

- Surplus entire male (cross-bred) piglets intended for export as breeding boars after rearing expressed as proportion of all surplus male (cross-bred) piglets at the end of the nursery phase ($pexB[1]$)

- Surplus entire male (cross-bred) piglets finished to target slaughter weight expressed as proportion of all surplus male (cross-bred) piglets at the end of the nursery phase ($pfin[1][1]$)

The following two parameters are read only if there are pure-bred castrated piglets, i.e. if the second parameter in the input file PARAP*.TXT $cast[1] > 0$. These two parameters must sum to 1:

- Castrated (cross-bred) piglets exported after the nursery phase expressed as proportion of all castrated (cross-bred) piglets at the end of the nursery phase ($pexcP[1]$). The sum of the given and the following input must be 1.

- Castrated (cross-bred) piglets finished to target slaughter weight expressed as proportion of all castrated (cross-bred) piglets at the end of the nursery phase ($pfin[2][1]$)

The following parameter is read only if the second parameter in the input file PARAP*.TXT $cast[1] = 1$.

- Castrated (cross-bred) piglets as proportion of all surplus (cross-bred) males (entire and castrated) alive at the end of the nursery phase

Special form for cross AB: INPUTP05AB.TXT This file contains parameters for the progeny of the cross-bred sows AB from birth until the end of the nursery phase. All progeny is cross-bred progeny with a third breed or cross.

The following inputs (until the end of the file) are read for **cross-bred progeny** AB x C in Breeding System 3 or AB x CD in Breeding System 4:

- Total number of piglets born in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nb[i][1]$)

- Number of piglets born alive in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nba[i][1]$)

- Number of piglets weaned in cross-bred litters, per sow in reproductive cycle i where $i = 1, \ldots, RR$ ($nw[i][1]$)

- Cross-bred piglets of all sexes died in the nursery phase as proportion of weaned piglets (mortality rate in piglet rearing, $pdiedPP[1]$)

- Female (cross-bred) piglets alive at the end of the nursery phase as proportion of all (cross-bred) piglets (of all sexes) alive at that time ($pfP[1]$)

The following two parameters must sum to 1:

- Female (cross-bred) piglets exported after the nursery phase expressed as proportion of female (cross-bred) piglets at the end of the nursery phase ($pexfP[1]$). The given input value together with the values of the following two inputs must sum to 1.

- Female (cross-bred) piglets finished to target slaughter weight expressed as proportion of female (cross-bred) piglets at the end of the nursery phase ($pfin[0][1]$)

The following two parameters are read only if there are entire cross-bred male piglets, i.e. if the parameter in the input file PARAPAB.TXT $cast[1] < 2$. These two parameters must sum to 1:

- Entire male (cross-bred) piglets exported after the nursery phase expressed as proportion of male (cross-bred) piglets at the end of the nursery phase ($pexmP[1]$). The given input value together with the values of the following two inputs must sum to 1.

- Entire male (cross-bred) piglets finished to target slaughter weight expressed as proportion of male (cross-bred) piglets at the end of the nursery phase ($pfin[1][1]$)

The following two parameters are read only if there are pure-bred castrated piglets, i.e. if the parameter in the input file PARAPAB.TXT $cast[1] > 0$. These two parameters must sum to 1:

- Castrated (cross-bred) piglets exported after the nursery phase expressed as proportion of castrated (cross-bred) piglets at the end of the nursery phase ($pexcP[1]$). The sum of the given and the following input must be 1.

- Castrated (cross-bred) piglets finished to target slaughter weight expressed as proportion of castrated (cross-bred) piglets at the end of the nursery phase ($pfin[2][1]$)

The following parameter is read only if the parameter in the input file PARA-PAB.TXT $cast[1] = 1$.

- Castrated (cross-bred) piglets as proportion of all (cross-bred) males (entire and castrated) alive at the end of the nursery phase

After reading the file, the following two parameters are automatically set to zero for progeny of sows AB: $pexG[1] = pexB[1] = 0$.

3.1.2.7   Input file INPUTP06*.TXT

This file contains parameters for the progeny of the sows in the finishing phase. The first part of the file refers to progeny of the same genotype as the genotype of the sows (pure-bred progeny), the second part of the file refers to cross-bred progeny and is read only if cross-breeding is applied. (Inputs for cross-bred progeny are not read for breed A in Breeding system 1, for breed C in Breeding systems 2 and 3, for breed B in Breeding systems 3 and 4 and for breed D in Breeding system 4). These inputs are read only if there is finishing of the appropriate progeny group (gilts, boars and castrates).

The following 3 inputs ($pdiedPG[0]$, $pdiedPC[0]$ and $pdiedPB[0]$) are read for the progeny of the same genotype as the genotype of the sows (**pure-bred progeny**). *They are not contained in INPUTP06AB.TXT.*

- Pure-bred gilts died during the finishing phase expressed as proportion of pure-bred gilts which entered finishing ($pdiedPG[0]$)

- Pure-bred castrates died during the finishing phase expressed as proportion of pure-bred castrates which entered finishing ($pdiedPC[0]$)

- Pure-bred boars died during the finishing phase expressed as proportion of pure-bred boars which entered finishing ($pdiedPB[0]$)

The following 3 inputs ($pdiedPG[1]$, $pdiedPC[1]$ and $pdiedPB[1]$) are read for the **cross-bred progeny**. *They are the only inputs in INPUTP06AB.TXT.*

- Cross-bred gilts died during the finishing phase expressed as proportion of cross-bred gilts which entered finishing ($pdiedPG[1]$)

- Cross-bred castrates died during the finishing phase expressed as proportion of cross-bred castrates which entered finishing ($pdiedPC[1]$)

- Cross-bred boars died during the finishing phase expressed as proportion of cross-bred boars which entered finishing ($pdiedPB[1]$)

3.1.2.8 Input file INPUTP07*.TXT

This input file contains the parameters a and b for the allometric function which is used for the calculation of the protein and lipid mass in animals. The coefficients are specific for each sex of animals (females, entire males and castrated males). Furthermore, the input file contains values of parameters c and d for calculating the intestinal contents (for details see Manual for EWPIG2, Chapter 4). All these coefficients are read, but the coefficients for animal groups which do not exists in the given calculations are not used by the program (e.g. if there are no castrates, the coefficients for castrates are not used, but do not delete these inputs, just ignore them). **If these coefficients are not known for your breeds, used the default values which are given in the example inputs.** *The references from which these coefficients were taken are given in the manual for EWPIG2.*

- Coefficient a for protein mass in females ($ap[0]$)

- Coefficient b for protein mass in females ($bp[0]$)

- Coefficient a for lipid mass in females ($al[0]$)

- Coefficient b for lipid mass in females ($bl[0]$)

- Coefficient a for protein mass in entire males ($ap[1]$)

- Coefficient b for protein mass in entire males ($bp[1]$)

- Coefficient a for lipid mass in entire males ($al[1]$)

- Coefficient b for lipid mass in entire males ($bl[1]$)

- Coefficient a for protein mass in castrates ($ap[2]$)

- Coefficient b for protein mass in castrates ($bp[2]$)

- Coefficient a for lipid mass in castrates ($al[2]$)

- Coefficient b for lipid mass in castrates ($bl[2]$)

- Coefficient c for the calculation of intestinal contents for all sexes (cgf)

- Coefficient d for the calculation of intestinal contents for all sexes (dgf)

3.1.2.9 Input file INPUTP08*.TXT

This input file contains parameters describing the growth of progeny except of growth in finishing. The values for the percentages of protein and lipid mass in the piglet body at birth and at weaning used in the distributed input files are taken from literature (see references in Manual for EWPIG2). **If these values are not known for your breeds, used the default values which are given in the example inputs.** The input values are read only for animal categories which exist in the given calculation. But do not delete values which are not of interest for you, just ignore them. This file has a special form for the cross AB (see last Paragraph in this file).

Values for pure-bred piglets:

- Average birth weight of pure-bred piglets ($bw[0]$)

- Percentage of protein mass in pure-bred piglets at birth ($pmassb[0]$)

- Percentage of lipid mass in pure-bred piglets at birth ($lmassb[0]$)

- Average weight of pure-bred piglets at weaning ($wP[3][0]$)

- Percentage of protein mass in pure-bred piglets at weaning ($pmassw[0]$)

- Percentage of lipid mass in pure-bred piglets at weaning ($lmassw[0]$)

- Average age of pure-bred piglets died from birth till weaning ($ageP[2][0]$)

- Average age of pure-bred piglets died from weaning till the end of the nursery phase ($ageP[4][0]$)

- Average age of pure-bred piglets at the end of the nursery phase ($ageP[5][0]$)

- Average weight of pure-bred piglets at the end of the nursery phase ($wP[5][0]$)

The following values are for cross-bred piglets and are read only if cross-breeding is applied (i.e. the following values are not read for breed A in Breeding system 1, for breed C in Breeding systems 2 and 3, for breed B in Breeding systems 3 and 4 and for breed D in Breeding system 4) :

- Average birth weight of cross-bred piglets ($bw[1]$)

- Percentage of protein mass in cross-bred piglets at birth ($pmassb[1]$)

- Percentage of lipid mass in cross-bred piglets at birth ($lmassb[1]$)

- Average weight of cross-bred piglets at weaning ($wP[3][1]$)

- Percentage of protein mass in cross-bred piglets at weaning ($pmassw[1]$)

- Percentage of lipid mass in cross-bred piglets at weaning ($lmassw[1]$)

- Average age of cross-bred piglets died from birth till weaning ($ageP[2][1]$)

- Average age of cross-bred piglets died from weaning till the end of the nursery phase ($ageP[4][1]$)

- Average age of cross-bred piglets at the end of the nursery phase ($ageP[5][1]$)

- Average weight of cross-bred piglets at the end of the nursery phase ($wP[5][1]$)

The following inputs are for pure-bred gilts:

- Average age of pure-bred breeding gilts died during rearing ($ageP[15][0]$)

- Average weight of pure-bred breeding gilts died during rearing ($wP[15][0]$)

- Average age of pure-bred breeding gilts at selection ($ageP[16][0]$)

- Average weight of pure-bred breeding gilts at selection ($wP[16][0]$)

The following two inputs are read only if there is finishing of negatively selected gilts after selection. If there is no finishing of negatively selected gilts, the age and weight for culled gilts should be equal to the age and weight of gilts at selection (i.e . $ageP[29][0] = ageP[16][0]$ and $wP[29][0] = wP[16][0]$).

- Average age at culling of pure-bred breeding gilts negatively selected during rearing ($ageP[29][0]$)

- Average weight at culling of pure-bred breeding gilts negatively selected during rearing ($wP[29][0]$)

- Average age of pure-bred breeding gilts exported outside the breeding system $(ageP[18][0])$[6]

- Average weight of pure-bred breeding gilts exported outside the breeding system $(wP[18][0])$

- Average age of pure-bred breeding gilts when including in the herd as replacement $(ageP[19][0])$. (If gilts are included in the herd as replacement immediately after selection this age will be equal to the age at selection, i.e. $(ageP[19][0] = ageP[16][0])$)

- Average weight of pure-bred breeding gilts when including in the herd as replacement $(wP[19][0])$. (If gilts are included in the herd as replacement immediately after selection this weight will be equal to the weight at selection, i.e. $(wP[19][0] = wP[16][0])$)

- Average age of pure-bred breeding gilts at first mating $(age1matG[0])$

- Average weight of pure-bred breeding gilts at first mating (target weight for first mating) $(w1matG[0])$

- Average age of pure-bred breeding gilts included in the herd as replacement, but culled for not showing heat $(ageP[20][0])$

- Average weight of pure-bred breeding gilts included in the herd as replacement, but culled for not showing heat $(wP[20][0])$

- Interval from last mating to culling for gilts not being pregnant after the maximal number of matings $(inmcG)$

- Average weight of pure-bred breeding gilts at first farrowing $(wP[22][0])$

The following inputs are read for breeding boars in rearing[7]:

- Average age of pure-bred breeding boars died during rearing $(ageP[23][0])$

- Average weight of pure-bred breeding boars died during rearing $(wP[23][0])$

- Average age at culling of pure-bred breeding boars negatively selected during rearing $(ageP[24][0])$

- Average weight at culling of pure-bred breeding boars negatively selected during rearing $(wP[24][0])$

- Average age of pure-bred breeding boars sold to another link of the breeding system $(ageP[25][0])$

- Average weight of pure-bred breeding boars sold to another link of the breeding system $(wP[25][0])$

- Average age of pure-bred breeding boars sold to insemination stations $(ageP[26][0])$

- Average weight of pure-bred breeding boars sold to insemination stations $(wP[26][0])$

- Average age of pure-bred breeding boars exported outside the breeding system $(ageP[27][0])$

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[6]This input and the following one are read only if there is export of breeding gilts.

[7]Certain categories may not exist in a given system. Then, the inputs referring to those categories are skipped when reading the file.

- Average weight of pure-bred breeding boars exported outside the breeding system ($ageP[27][0]$)

- Average age of pure-bred breeding boars included in the herd as replacement for natural mating or for oestrus stimulation ($ageP[28][0]$)

- Average weight of pure-bred breeding boars included in the herd as replacement for natural mating or for oestrus stimulation ($wP[28][0]$)

The following two values are for cross-bred boars and are read only if cross-breeding is applied (i.e. the following values are not read for breed A in Breeding system 1, for breed C in Breeding systems 2 and 3, for breed B in Breeding systems 3 and 4 and for breed D in Breeding system 4) :

- Average age of cross-bred breeding boars exported outside the breeding system ($ageP[27][1]$)

- Average weight of cross-bred breeding boars exported outside the breeding system ($ageP[27][1]$)

Input files INPUTP08B.TXT and INPUTP08D.TXT end here. The following inputs until the end of the file are different for IN-PUTP08A.TXT and INPUTP08C.TXT. Here are the inputs for IN-PUTP08A.TXT which are read only in Breeding Systems 3 and 4.

The following inputs are for cross-bred gilts AB:

- Average age of cross-bred breeding gilts died during rearing ($ageP[15][1]$)

- Average weight of cross-bred breeding gilts died during rearing ($wP[15][1]$)

- Average age of cross-bred breeding gilts at selection ($ageP[16][1]$)

- Average weight of cross-bred breeding gilts at selection ($wP[16][1]$)

The following two inputs are read only if there is finishing of negatively selected gilts after selection. If there is no finishing of negatively selected gilts, the age and weight for culled gilts should be equal to the age and weight of gilts at selection (i.e . $ageP[29][1] = ageP[16][1]$ and $wP[29][1] = wP[16][1]$).

- Average age at culling of cross-bred breeding gilts negatively selected during rearing ($ageP[29][1]$)

- Average weight at culling of cross-bred breeding gilts negatively selected during rearing ($wP[29][1]$)

- Average age of cross-bred breeding gilts exported outside the breeding system ($ageP[18][1]$)[8]

- Average weight of cross-bred breeding gilts exported outside the breeding system ($wP[18][1]$)

Here are the inputs for INPUTP08C.TXT which are read only in Breeding System 4. They are for cross-bred boars CD which are progeny of sows C.

- Average age of cross-bred breeding boars CD died during rearing ($ageP[23][1]$)

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[8]This input and the following one are read only if there is export of breeding gilts.

- Average weight of cross-bred breeding boars CD died during rearing ($wP[23][1]$)

- Average age at culling of cross-bred breeding boars CD negatively selected during rearing ($ageP[24][1]$)

- Average weight at culling of cross-bred breeding boars CD negatively selected during rearing ($wP[24][1]$)

- Average age of cross-bred breeding boars CD sold to another link of the breeding system (read as $ageP[25][1]$ in the program run for breed C where those boars are sold and read as $ageP[28][1]$ in the program run for cross AB where those boars are purchased)

- Average weight of cross-bred breeding boars CD sold to another link of the breeding system (read as $wP[25][1]$ in the program run for breed C where those boars are sold and read as $wP[28][1]$ in the program run for cross AB where those boars are purchased)

The following inputs are read only if the given boar category exists (i.e. if there is artificial insemination in herds with sows AB):

- Average age of cross-bred breeding boars CD sold to insemination stations ($ageP[26][1]$)

- Average weight of cross-bred breeding boars CD sold to insemination stations ($wP[26][1]$)

Special form for cross AB: INPUTP08AB.TXT   This input file contains parameters describing the growth of progeny except of growth in finishing for the cross AB. The values for the percentages of protein and lipid mass in the piglet body at birth and at weaning used in the distributed input files are taken from literature (see references in Manual for EWPIG2). *If these values are not known for your crosses, used the default values which are given in the example inputs.*
The following values are for piglets of the cross AB x C (in Breeding System 3) or AB x CD (in Breeding System 4):

- Average birth weight of cross-bred piglets ($bw[1]$)

- Percentage of protein mass in cross-bred piglets at birth ($pmassb[1]$)

- Percentage of lipid mass in cross-bred piglets at birth ($lmassb[1]$)

- Average weight of cross-bred piglets at weaning ($wP[3][1]$)

- Percentage of protein mass in cross-bred piglets at weaning ($pmassw[1]$)

- Percentage of lipid mass in cross-bred piglets at weaning ($lmassw[1]$)

- Average age of cross-bred piglets died from birth till weaning ($ageP[2][1]$)

- Average age of cross-bred piglets died from weaning till the end of the nursery phase ($ageP[4][1]$)

- Average age of cross-bred piglets at the end of the nursery phase ($ageP[5][1]$)

- Average weight of cross-bred piglets at the end of the nursery phase ($wP[5][1]$)

The following inputs are for breeding gilts AB:

- Average age of breeding gilts AB purchased as replacement ($ageP[19][0]$)

- Average weight of breeding gilts AB purchased as replacement ($wP[19][0]$)

- Average age of breeding gilts AB at first mating ($age1matG[0]$)

- Average weight of breeding gilts AB at first mating (target weight for first mating) ($w1matG[0]$)

- Average age of breeding gilts AB included in the herd as replacement, but culled for not showing heat ($ageP[20][0]$)

- Average weight of breeding gilts AB included in the herd as replacement, but culled for not showing heat ($wP[20][0]$)

- Interval from last mating to culling for gilts not being pregnant after the maximal number of matings ($inmcG$)

- Average weight of breeding gilts AB at first farrowing ($wP[22][0]$)

3.1.2.10   Input file INPUTP09*.TXT

This input file contains parameters describing the growth of progeny in finishing. A maximum of 3 feeding phases are assumed. If there are less than 3 feeding phases, the inputs for the feeding phases not used are skipped.

In the special case of INPUTP09AB.TXT, "cross-bred progeny" refers to three-way or four-way crosses (i.e. to AB x C in Breeding System 3 or to AB x CD in Breeding System 4). "Pure-bred progeny" would refer to progeny of the type AB which is not present. Therefore, all inputs referring to "pure-bred" progeny are omitted in INPUTP09AB.TXT.

In the run for breeds B and D, there is no cross-bred progeny and all inputs referring to cross-bred animals are not read from INPUTP09B.TXT and INPUTP09D.TXT, respectively.

The following inputs are read if there is finishing of pure-bred gilts (omitted in INPUTP09AB.TXT):

- Number of feeding phases in finishing of pure-bred gilts ($nfin[0][0]$). Insert 1, 2 or 3.

- Average age of pure-bred gilts at the end of the first feeding phase in finishing ($agefin[1][0][0]$)

- Average weight of pure-bred gilts at the end of the first feeding phase in finishing ($wfin[1][0][0]$)

- Average age of pure-bred gilts at the end of the second feeding phase in finishing ($agefin[2][0][0]$)

- Average weight of pure-bred gilts at the end of the second feeding phase in finishing ($wfin[2][0][0]$)

- Average age of pure-bred gilts at the end of the third feeding phase in finishing ($agefin[3][0][0]$)

- Average weight of pure-bred gilts at the end of the third feeding phase in finishing ($wfin[3][0][0]$)

- Average age of pure-bred gilts died in finishing ($ageP[9][0]$)

The following inputs are read if there is finishing of cross-bred gilts (not read for breed A in Breeding system 1, for breed C in Breeding system 2 and 3, for breed B and for breed D):

- Number of feeding phases in finishing of cross-bred gilts ($nfin[0][1]$). Insert 1, 2 or 3.

- Average age of cross-bred gilts at the end of the first feeding phase in finishing ($agefin[1][0][1]$)

- Average weight of cross-bred gilts at the end of the first feeding phase in finishing ($wfin[1][0][1]$)

- Average age of cross-bred gilts at the end of the second feeding phase in finishing ($agefin[2][0][1]$)

- Average weight of cross-bred gilts at the end of the second feeding phase in finishing ($wfin[2][0][1]$)

- Average age of cross-bred gilts at the end of the third feeding phase in finishing ($agefin[3][0][1]$)

- Average weight of cross-bred gilts at the end of the third feeding phase in finishing ($wfin[3][0][1]$)

- Average age of cross-bred gilts died in finishing ($ageP[9][1]$)

The following inputs are read if there is finishing of pure-bred boars, i.e. if the first parameter in file PARAP*.TXT $cast[0] < 2$, (omitted in INPUTP09AB.TXT):

- Number of feeding phases in finishing of pure-bred boars ($nfin[1][0]$). Insert 1, 2 or 3.

- Average age of pure-bred boars at the end of the first feeding phase in finishing ($agefin[1][1][0]$)

- Average weight of pure-bred boars at the end of the first feeding phase in finishing ($wfin[1][1][0]$)

- Average age of pure-bred boars at the end of the second feeding phase in finishing ($agefin[2][1][0]$)

- Average weight of pure-bred boars at the end of the second feeding phase in finishing ($wfin[2][1][0]$)

- Average age of pure-bred boars at the end of the third feeding phase in finishing ($agefin[3][1][0]$)

- Average weight of pure-bred boars at the end of the third feeding phase in finishing ($wfin[3][1][0]$)

- Average age of pure-bred boars died in finishing ($ageP[13][0]$)

The following inputs are read if there is finishing of cross-bred boars, i.e. if the second parameter in file PARAP*.TXT $cast[1] < 2$, and not read for breed A in Breeding system 1, for breed C in Breeding system 2 and 3, for breed B and for breed D):

- Number of feeding phases in finishing of cross-bred boars ($nfin[1][1]$). Insert 1, 2 or 3.

- Average age of cross-bred boars at the end of the first feeding phase in finishing ($agefin[1][1][1]$)

- Average weight of cross-bred boars at the end of the first feeding phase in finishing ($wfin[1][1][1]$)

- Average age of cross-bred boars at the end of the second feeding phase in finishing ($agefin[2][1][1]$)

- Average weight of cross-bred boars at the end of the second feeding phase in finishing ($wfin[2][1][1]$)

- Average age of cross-bred boars at the end of the third feeding phase in finishing ($agefin[3][1][1]$)

- Average weight of cross-bred boars at the end of the third feeding phase in finishing ($wfin[3][1][1]$)

- Average age of cross-bred boars died in finishing ($ageP[13][1]$)

The following inputs are read if there is finishing of pure-bred castrates, i.e. if the first parameter in file PARAP*.TXT $cast[0] > 0$, (omitted in INPUTP09AB.TXT):

- Number of feeding phases in finishing of pure-bred castrates ($nfin[2][0]$). Insert 1, 2 or 3.

- Average age of pure-bred castrates at the end of the first feeding phase in finishing ($agefin[1][2][0]$)

- Average weight of pure-bred castrates at the end of the first feeding phase in finishing ($wfin[1][2][0]$)

- Average age of pure-bred castrates at the end of the second feeding phase in finishing ($agefin[2][2][0]$)

- Average weight of pure-bred castrates at the end of the second feeding phase in finishing ($wfin[2][2][0]$)

- Average age of pure-bred castrates at the end of the third feeding phase in finishing ($agefin[3][2][0]$)

- Average weight of pure-bred castrates at the end of the third feeding phase in finishing ($wfin[3][2][0]$)

- Average age of pure-bred castrates died in finishing ($ageP[11][0]$)

The following inputs are read if there is finishing of cross-bred castrates, i.e. if the second parameter in file PARAP*.TXT $cast[1] > 0$, and not read for breed A in Breeding system 1, for breed C in Breeding system 2 and 3, for breed B and for breed D):

- Number of feeding phases in finishing of cross-bred castrates ($nfin[2][1]$). Insert 1, 2 or 3.

- Average age of cross-bred castrates at the end of the first feeding phase in finishing ($agefin[1][2][1]$)

- Average weight of cross-bred castrates at the end of the first feeding phase in finishing ($wfin[1][2][1]$)

- Average age of cross-bred castrates at the end of the second feeding phase in finishing ($agefin[2][2][1]$)

- Average weight of cross-bred castrates at the end of the second feeding phase in finishing ($wfin[2][2][1]$)

- Average age of cross-bred castrates at the end of the third feeding phase in finishing ($agefin[3][2][1]$)

- Average weight of cross-bred castrates at the end of the third feeding phase in finishing ($wfin[3][2][1]$)

- Average age of cross-bred castrates died in finishing ($ageP[11][1]$)

3.1.2.11   Input file INPUTP10*.TXT

This file contains general parameters and parameters for progeny needed for the calculation of nutrition costs. ***If you have no other estimations for net energy value of body protein and lipid, for the coefficients for the efficiency utilization of metabolisable energy for protein and lipid gain and for other parameters connected with the calculation of metabolisable energy requirement use default values as given in example input files.*** *You find the references from which these values were taken in the manual for EWPIG2.*
General parameters:

- Net energy value of body protein (pne)

- Net energy value of body lipid (lne)

- Coefficient for the efficiency of utilization of metabolisable energy for protein gain (kp)

- Coefficient for the efficiency of utilization of metabolisable energy for lipid gain (kl)

- Price for water (prw)

- Number of different feed rations for piglets during the nursery phase ($nnur$). Insert 1, 2 or 3.

The following parameter is read only if the number of feed rations in the nursery phase is greater than 1 ($nnur > 1$):

- Length of the 1st feeding period in nursery ($dfP[5][j][2]$). The same value is expected both for pure-bred ($j = 0$) and cross-bred progeny ($j = 1$).

The following parameter is read only if the number of feed rations in the nursery phase is greater than 2 ($nnur > 2$):

- Length of the 2nd feeding period in nursery ($dfP[5][j][3]$). The same value is expected both for pure-bred ($j = 0$) and cross-bred progeny ($j = 1$).

- Day of pregnancy when gilts are starting to get a special feed ration (feed ration 6 for pregnant gilts, $dfP6$)

Parameters for piglets until weaning:

- Amount of supplementary feed (next to sow milk) until weaning per piglet ($fP1$). Insert zero if no supplementary feed is given. The following 3 inputs will then be ignored.

- Metabolisable energy content in fresh feed matter of supplementary feed for piglets until weaning (feed ration 1 for progeny[9], $mefP[1]$)

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[9]For numbering of feed rations for progeny, see page ......

- Price of fresh feed matter of supplementary feed for piglets until weaning (feed ration 1 for progeny, $prfP[1]$)

- Coefficient of efficiency of utilization of metabolisable energy from supplementary feed for growth of piglets until weaning (kgw)

- Average daily amount of water for piglets until weaning ($watw$)

Parameters for young growing pigs (for the categories of progeny after weaning, in the nursery phase):

- Exponent for the calculation of metabolic body weight from body weight of young growing pigs (bmP)

- Standard metabolisable energy per kg metabolic body weight and per d for growing pigs housed in thermoneutral environment and standing or walking on average 4 hours per day (smP)

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in the nursery phase (amn). (e.g. the ratio of the standard energy requirement for maintenance for piglets (during nursery phase) kept in outdoor systems and of the standard energy requirement for maintenance for piglets kept indoor)

- Number of degrees centigrade below the lower critical temperature for piglets in nursery ($tdiffn$) (**Insert zero for this parameter if you have no knowledge about it**)

- Metabolisable energy requirement for thermogenesis needed per kg metabolic weight, per d and per °C below the lower critical temperature for piglets in nursery (tmn)

- Metabolisable energy content in the fresh feed matter in feed ration 2 (i.e. in the feed ration for the first feeding phase of nursery piglets, $mefP[2]$)

- Dry matter content in fresh feed matter of feed ration 2 ($dryfP[2]$)

- Price of fresh feed matter of feed ration 2 ($prfP[2]$)

The following 3 parameters are read only if the number of feed rations in the nursery phase is greater than 1 ($nnur > 1$):

- Metabolisable energy content in the fresh feed matter in feed ration 3 (i.e. in the feed ration for the second feeding phase of nursery piglets, $mefP[3]$)

- Dry matter content in the fresh feed matter of feed ration 3 ($dryfP[3]$)

- Price of fresh feed matter of feed ration 3 ($prfP[3]$)

The following 3 parameters are read only if the number of feed rations in the nursery phase is greater than 2 ($nnur > 2$):

- Metabolisable energy content in the fresh feed matter in feed ration 4 (i.e. in the feed ration for the third feeding phase of nursery piglets, $mefP[4]$)

- Dry matter content in the fresh feed matter of feed ration 4 ($dryfP[4]$)

- Price of fresh feed matter of feed ration 4 ($prfP[4]$)

- Coefficient for feed wasting in the nursery phase ($kfwn$). (Ratio of the amount of feed given to animals and of the amount of feed really consumed.)

- Coefficient for water wasting in the nursery phase ($kwatn$). (Ratio of the amount of water given to animals and of the amount of water really consumed.)

The following 3 parameters are read only if there is finishing of gilts, boars or castrates:

- Coefficient for feed wasting in finishing ($kfwf$) (Ratio of the amount of feed given to animal and of the amount of feed really consumed)

- Amount of water used per kg dry matter of feed in finishing ($watfin$). (This amount should include water wasting)

- Metabolisable energy requirement for thermogenesis per degree centigrade below the lower critical temperature for animals in finishing (tmf)

The following 11 parameters are read only if there is finishing of gilts:

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in finishing gilts ($amf[0]$) (e.g. the ratio of the standard energy requirement for maintenance for gilts kept in outdoor systems and of the standard energy requirement for maintenance for gilts kept indoor)

- Number of degrees centigrade below the lower critical temperature in finishing gilts ($tdifff[0]$). (**Insert zero for this parameter if you have no knowledge about it**)

- Metabolisable energy content in fresh feed matter of the feed ration for gilts in the first finishing phase (feed ration 8 for progeny, $mefP[8]$)

- Dry matter content in fresh feed matter of the feed ration for gilts in the first finishing phase (feed ration 8 for progeny, $dryfP[8]$)

- Price of fresh feed matter of the feed ration for gilts in the first finishing phase (feed ration 8 for progeny, $prfP[8]$)

The following 3 parameters are read if the number of feeding phases in finishing gilts is > 1:

- Metabolisable energy content in fresh feed matter of the feed ration for gilts in the second finishing phase (feed ration 9 for progeny, $mefP[9]$)

- Dry matter content in fresh feed matter of the feed ration for gilts in the second finishing phase (feed ration 9 for progeny, $dryfP[9]$)

- Price of fresh feed matter of the feed ration for gilts in the second finishing phase (feed ration 9 for progeny, $prfP[9]$)

The following 3 parameters are read if the number of feeding phases in finishing gilts is > 2:

- Metabolisable energy content in fresh feed matter of the feed ration for gilts in the third finishing phase (feed ration 10 for progeny, $mefP[10]$)

- Dry matter content in fresh feed matter of the feed ration for gilts in the third finishing phase (feed ration 10 for progeny, $dryfP[10]$)

- Price of fresh feed matter of the feed ration for gilts in the third finishing phase (feed ration 10 for progeny, $prfP[10]$)

The following 11 parameters are read only if there is finishing of boars:

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in finishing boars ($amf[1]$) (e.g. the ratio of the standard energy requirement for maintenance for boars kept in outdoor systems and of the standard energy requirement for maintenance for boars kept indoor)

- Number of degrees centigrade below the lower critical temperature in finishing boars ($tdifff[1]$). (***Insert zero for this parameter if you have no knowledge about it***.)

- Metabolisable energy content in fresh feed matter of the feed ration for boars in the first finishing phase (feed ration 14 for progeny, $mefP[14]$)

- Dry matter content in fresh feed matter of the feed ration for boars in the first finishing phase (feed ration 14 for progeny, $dryfP[14]$)

- Price of fresh feed matter of the feed ration for boars in the first finishing phase (feed ration 14 for progeny, $prfP[14]$)

The following 3 parameters are read if the number of feeding phases in finishing of boars is > 1:

- Metabolisable energy content in fresh feed matter of the feed ration for boars in the second finishing phase (feed ration 15 for progeny, $mefP[15]$)

- Dry matter content in fresh feed matter of the feed ration for boars in the second finishing phase (feed ration 15 for progeny, $dryfP[15]$)

- Price of fresh feed matter of the feed ration for boars in the second finishing phase (feed ration 15 for progeny, $prfP[15]$)

The following 3 parameters are read if the number of feeding phases in finishing of boars is > 2:

- Metabolisable energy content in fresh feed matter of the feed ration for boars in the third finishing phase (feed ration 16 for progeny, $mefP[16]$)

- Dry matter content in fresh feed matter of the feed ration for boars in the third finishing phase (feed ration 16 for progeny, $dryfP[16]$)

- Price of fresh feed matter of the feed ration for boars in the third finishing phase (feed ration 16 for progeny, $prfP[16]$)

The following 11 parameters are read only if there is finishing of castrates (castrates):

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in finishing castrates ($amf[2]$) (e.g. the ratio of the standard energy requirement for maintenance for castrates kept in outdoor systems and of the standard energy requirement for maintenance for castrates kept indoor)

- Number of degrees centigrade below the lower critical temperature in finishing castrates ($tdifff[2]$). (***Insert zero for this parameter if you have no knowledge about it***.)

- Metabolisable energy content in fresh feed matter of the feed ration for castrates in the first finishing phase (feed ration 11 for progeny, $mefP[11]$)

- Dry matter content in fresh feed matter of the feed ration for castrates in the first finishing phase (feed ration 11 for progeny, $dryfP[11]$)

- Price of fresh feed matter of the feed ration for castrates in the first finishing phase (feed ration 11 for progeny, $prfP[11]$)

The following 3 parameters are read if the number of feeding phases in finishing of castrates is > 1:

- Metabolisable energy content in fresh feed matter of the feed ration for castrates in the second finishing phase (feed ration 12 for progeny, $mefP[12]$)

- Dry matter content in fresh feed matter of the feed ration for castrates in the second finishing phase (feed ration 12 for progeny, $dryfP[12]$)

- Price of fresh feed matter of the feed ration for castrates in the second finishing phase (feed ration 12 for progeny, $prfP[12]$)

The following 3 parameters are read if the number of feeding phases in finishing of castrates is > 2:

- Metabolisable energy content in fresh feed matter of the feed ration for castrates in the third finishing phase (feed ration 13 for progeny, $mefP[13]$)

- Dry matter content in fresh feed matter of the feed ration for castrates in the third finishing phase (feed ration 13 for progeny, $dryfP[13]$)

- Price of fresh feed matter of the feed ration for castrates in the third finishing phase (feed ration 13 for progeny, $prfP[13]$)

The following parameters are for breeding animals in rearing:

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in rearing breeding gilts ($amb[0]$) (e.g. the ratio of the standard energy requirement for maintenance for breeding gilts kept in outdoor systems and of the standard energy requirement for maintenance for breeding gilts kept indoor)

- Number of degrees centigrade below the lower critical temperature in rearing breeding gilts ($tdiffb[0]$). (***Insert zero for this parameter if you have no knowledge about it***.)

- Metabolisable energy requirement for thermogenesis per degree centigrade below the lower critical temperature for breeding gilts in rearing ($tmb[0]$)

- Dry matter content in the mammary tissue at the end of pregnancy (for pregnant gilts and sows, $drylg$)

- Net energy content in the dry matter of mammary tissue at the end of pregnancy (for pregnant gilts and sows, $nedrylg$)

- Number of degrees centigrade below the lower critical temperature in housing barren or pregnant sows or pregnant gilts ($tdiffS$) (***Insert zero for this parameter if you have no knowledge about it***.)

- Metabolisable energy requirement for thermogenesis per degree centigrade below the lower critical temperature for barren or pregnant sows or pregnant gilts ($tmpS$)

- Standard maintenance energy adjustment coefficient for higher activity of barren or pregnant sows or pregnant gilts (e.g. in group housing of pregnant sows) ($ampS$) (e.g. the ratio of the standard energy requirement for maintenance for gilts housed in group and of the standard energy requirement for maintenance for gilts housed individually)

- Standard metabolisable energy needed per kg metabolic body weight and per day for barren and pregnant sows or pregnant gilts housed in thermoneutral environment and standing or walking on average 4 hours per day ($smpS$)

- Efficiency of metabolisable energy from feed for pregnancy product ($kpreg$)

- Metabolisable energy content in fresh feed matter of the feed ration for rearing gilts (barren gilts, feed ration 5 for progeny, $mefP[5]$)

- Dry matter content in fresh feed matter of the feed ration in rearing gilts (barren gilts, feed ration 5 for progeny, $dryfP[5]$)

- Price of fresh feed matter of the feed ration in rearing of gilts (barren gilts, feed ration 5 for progeny, $prfP[5]$)

- Metabolisable energy content in fresh feed matter of the feed ration for pregnant gilts (feed ration 6 for progeny, $mefP[6]$)

- Dry matter content in fresh feed matter of the feed ration for pregnant gilts (feed ration 6 for progeny, $dryfP[6]$)

- Price of fresh feed matter of the feed ration for pregnant gilts (feed ration 6 for progeny, $prfP[6]$)

- Coefficient for feed wasting in rearing breeding gilts ($kfwbG$). (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

- Amount of water used per kg dry matter of feed in rearing breeding animals ($watb$). This amount should included water wasting.

- Daily amount of water for pregnant gilts fed with feed ration 6 ($watpG$). This amount should included water wasting.

The following three parameters are read only if there is finishing of negatively selected breeding gilts:

- Metabolisable energy content of fresh feed matter of the feed ration for negatively selected breeding gilts in finishing (feed ration 17 for progeny, $mefP[17]$)

- Dry matter content in fresh feed matter of the feed ration for negatively selected breeding gilts in finishing (feed ration 17 for progeny, $dryfP[17]$)

- Price of fresh feed matter of the feed ration for negatively selected breeding gilts in finishing (feed ration 17 for progeny, $prfP[17]$)

The following parameters until the end of the file are for rearing breeding boars:

- Standard maintenance energy adjustment coefficient for higher animal activity (e.g. in outdoor systems) in rearing breeding boars ($amb[1]$) (e.g. the ratio of the standard energy requirement for maintenance for breeding boars kept in outdoor systems and of the standard energy requirement for maintenance for breeding boars kept indoor)

- Number of degrees centigrade below the lower critical temperature in rearing breeding boars ($tdiffb[1]$). (***Insert zero for this parameter if you have no knowledge about it***.)

- Metabolisable energy requirement for thermogenesis per degree centigrade below the lower critical temperature for breeding boars in rearing $tmb[1]$

- Metabolisable energy content in fresh feed matter of the feed ration for breeding boars in rearing (feed ration 7 for progeny, $mefP[7]$)

- Dry matter content in fresh feed matter of the feed ration for breeding boars in rearing (feed ration 7 for progeny, $dryfP[7]$)

- Price of fresh feed matter of the feed ration for breeding boars in rearing (feed ration 7 for progeny, $prfP[7]$)

- Coefficient for feed wasting in rearing breeding boars ($kfwbB$). (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

3.1.2.12   Input file INPUTP11*.TXT

This file contains parameters needed for the calculation of nutrition costs for sows and boars in the herd. ***If you have no other estimations for the parameters connected with the calculation of metabolisable energy requirement use default values as given in example input files.***
First, the input parameters for sows are listed:

- Standard metabolisable energy needed per kg metabolic body weight and per day for lactating sows ($smlS$)

- Exponent for the calculation of metabolic body weight from body weight of sows (bmS)

- Efficiency of metabolisable energy from feed for milk production ($kmilk$)

- Efficiency of net energy from body reserves for milk production ($kbrl$)

- Efficiency of metabolisable energy from feed for body weight gain of sows ($kgain$)

- Efficiency of net energy from body reserves for pregnancy ($kbrp$)

- Dry matter content in the mammary tissue at death of pregnant sows ($drylgdS$)

- Net energy content in the dry matter of mammary tissue at death of pregnant sows ($nedrylgdS$)

- Metabolisable energy content in fresh feed matter of the feed ration for barren and pregnant sows (feed ration 1 for sows, $mefS[1]$)

- Dry matter content in fresh feed matter of the feed ration for barren and pregnant sows (feed ration 1 for sows, $dryfS[1]$)

- Price of fresh feed matter of the feed ration for barren and pregnant sows (feed ration 1 for sows, $prfS[1]$)

- Average amount of water used for sows fed with feed ration 1 (barren and pregnant sows, $watS[1]$)

- Coefficient for feed wasting in barren and pregnant sows (fed with feed ration 1, $kfS[1]$). (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

- Metabolisable energy content in fresh feed matter of the feed ration for lactating sows (feed ration 2 for sows, $mefS[2]$)

- Dry matter content in the fresh feed matter of the feed ration for lactating sows (feed ration 2 for sows, $dryfS[2]$)

- Price of fresh feed matter of the feed ration for lactating sows (feed ration 2 for sows, $prfS[2]$)

- Average amount of water used for lactating sows fed with feed ration 2 ($watS[2]$)

- Coefficient for feed wasting of lactating sows fed with feed ration 2 ($kfS[2]$) (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

- Metabolisable energy content in fresh feed matter of the feed ration for barren sows determined for culling (feed ration 3 for sows, $mefS[3]$)

- Dry matter content in the fresh feed matter of the feed ration for barren sows determined for culling (feed ration 3 for sows, $dryfS[3]$)

- Price of fresh feed matter of the feed ration for barren sows determined for culling (feed ration 3 for sows, $prfS[3]$)

- Average amount of water used for barren sows determined for culling fed with feed ration 3 ($watS[3]$)

- Coefficient for feed wasting of barren sows determined for culling fed with feed ration 3 ($kfS[3]$) (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

The following parameters are for breeding boars which are used for natural mating or oestrus stimulation:

- Exponent for the calculation of metabolic body weight from body weight of boars (bmB)

- Standard metabolisable energy needed per kg metabolic body weight and per day for breeding boars used for natural mating or oestrus stimulation, housed in thermoneutral environment and standing or walking on average 4 hours per day (smB)

- Standard maintenance energy adjustment for higher activity of boars according to housing technology (amB) (e.g. the ratio of the standard energy requirement for maintenance for boars kept in outdoor systems and of the standard energy requirement for maintenance for boars kept indoor)

- Number of degrees centigrade below the lower critical temperature in housing boars kept for natural mating or oestrus stimulation ($tdiffB$). (**Insert zero for this parameter if you have no knowledge about it**.)

- Metabolisable energy requirement for thermogenesis per degree centigrade below the lower critical temperature for boars kept for natural mating or oestrus stimulation (tmB)

- Metabolisable energy requirement for the production of an ejaculate for boars used for natural mating ($meejB$)

- Additional metabolisable energy requirement for higher activity of boars at mating ($amacB$)

- Average number of matings per young boar (until the age of one year) used in the herd for natural mating per week ($nmyB$)

- Average number of matings per mature boar (older than one year) used in the herd for natural mating per week ($nmoB$)

- Metabolisable energy content in fresh feed matter of the feed ration for boars kept for natural mating (feed ration 1 for boars, $mefB[1]$)

- Dry matter content in fresh feed matter of the feed ration for boars kept for natural mating (feed ration 1 for boars, $dryfB[1]$)

- Price of fresh feed matter for boars kept for natural mating (feed ration 1 for boars, $prfB[1]$)

- Metabolisable energy content in fresh feed matter of the feed ration for boars kept only for oestrus stimulation (feed ration 2 for boars, $mefB[2]$)

- Dry matter content in fresh feed matter of the feed ration for boars kept only for oestrus stimulation (feed ration 2 for boars, $dryfB[2]$)

- Price of fresh feed matter for boars kept only for oestrus stimulation (feed ration 2 for boars, $prfB[2]$)

- Daily amount of water for boars ($watB$)

- Coefficient for feed wasting of boars (kfB) (Ratio of the amount of feed given to animals and of the amount of feed really consumed)

3.1.2.13   Input file INPUTP12*.TXT

This file contains general parameters for calculating non-feed costs and cost parameters for the breeding unit, the nursery unit and the unit for rearing breeding animals. For definition of non-specific and specific non-feed costs see the Manual of EWPIG2, Chapter 6):

- Non-specific non-feed costs in the breeding unit ($cfixS$)

- Number of farrowing places per farrowing ($nfpS$)[10]

- Costs for disposal of dead animals ($cdead$)

- Price for one insemination dose from boars of the same breed as the breed of the sows ($prID[0]$) (read only if AI is applied for this boars)

- *Only if there is crossing:* Price for one insemination dose from boars of a breed or cross different from the breed of the sows ($prID[1]$) (read only if AI is applied for this boars)

- Costs for service making AI (**if external workers make the AI, otherwise set zero for this parameter**) ($cservAI$)

- Specific costs for health care for piglets until weaning ($prhcw$)

- Specific costs for health care for sows staying in the herd for the whole farrowing interval ($prhcS$)

- Specific costs for health care for sows died in the period from farrowing to piglet weaning as proportion of the specific costs for health care for sows staying in the herd for the whole farrowing interval ($khcS[1]$)

- Specific costs for health care for sows died in the period from piglet weaning to the next farrowing as proportion of the specific costs for health care for sows staying in the herd for the whole farrowing interval ($khcS[4]$)

---

[10]This parameter depends on the time interval between the time when one sow batch is leaving the farrowing barn and the time when the next batch is coming in.

- Specific costs for health care for sows culled after piglet weaning for health problems or low litter size without being mated as proportion of the specific costs for health care for sows staying in the herd for the whole farrowing interval ($khcS[2]$)

- Specific costs for health care for sows culled after piglet weaning for failure to conceive as proportion of the specific costs for health care for sows staying in the herd for the whole farrowing interval ($khcS[3]$)

- Specific costs for health care of replacement gilts from including in the herd to first farrowing ($prhcG$)

- Specific costs for health care of replacement gilts negatively selected for not showing heat and culled (progeny category 20) as proportion of the specific costs for health care of replacement gilts from including in the herd to first farrowing ($khcG[0]$)

- Specific costs for health care of replacement gilts culled for failure to conceive (progeny category 21) as proportion of the specific costs for health care of replacement gilts from including in the herd to first farrowing ($khcG[1]$)

- Specific costs for health care of boars used in the breeding unit for natural mating and/or oestrus stimulation ($prhcB$) (read only if these boars exist)

- Costs for piglet castration ($ccasP$). (Read only if there is piglet castration.)

- Piglets transferred after weaning to the nursery unit which does not belong to the enterprise where piglets were born as proportion of all weaned piglets ($ptrawnu$). (Insert zero if piglet nursery belong to enterprises with breeding units.)

- Costs for transferring piglets after weaning to the nursery unit when piglets are reared in specific enterprises (transport costs and marketing levy, $ctrawnu$). (Insert zero if piglet nursery belong to enterprises with breeding units.)

- Marketing costs for culled sows (transport costs to abattoir and marketing levy, $cmarbuS$)

- Price for boars of the same breed as the breed of the sows imported for natural mating ($prnimB[0]$, only read if there is natural mating and if some boars are imported)

The following two parameters are read only if there is natural mating and crossing:

- Price for boars of a breed or cross different from the breed of the sows purchased within the evaluated breeding system for natural mating or oestrus stimulation ($prnB$)

- Price for boars of a breed or cross different from the breed of the sows imported for natural mating or oestrus stimulation ($prnimB[1]$)

The inputs for the nursery unit start here.

- Non-specific non-feed costs in the nursery unit ($cfixnu$)

- Empty nursery unit days per cycle (i.e. the time interval between the time when one piglet batch is leaving and the time when the next batch is coming in, $ednu$)

- Specific costs for health care for piglets in the nursery unit for piglets alive at the end of the nursery phase (*prhcnu*)

- Specific costs for health care for piglets died in the nursery phase as proportion of the specific costs for health care for piglets alive at the end of the nursery phase (*khc4P*)

- Costs for exporting piglets after the nursery phase (transport costs and marketing levy, *cexpnu*). (Read only if there is export of piglets any sexes after nursery)

- Costs for transferring piglets from the nursery to the finishing unit when finishing is made in specific enterprises (transport costs and marketing levy, *ctrafnu*). (Insert zero if finishing units belong to enterprises with nursery units.)

- Piglets transferred from the nursery to the finishing unit which does not belong to the enterprise where piglets are reared as proportion of all piglets determined for finishing (*ptrafnu*). (Insert zero if finishing units belong to enterprises with nursery units.)

> **Here ends the file INPUTP12AB.TXT for cross AB which is used in Breeding Systems 3 and 4.**

- Costs for transferring piglets from the nursery unit to the unit for rearing breeding animals when rearing is made in specific enterprises (transport costs and marketing levy, *ctrabnu*). (**Insert zero if rearing units belong to enterprises with nursery units.**)

- Piglets transferred from the nursery unit to the unit for rearing breeding animals which does not belong to the enterprise where piglets are reared as proportion of all piglets determined for rearing as breeding animals (*ptrabnu*) (**Insert zero if rearing units belong to enterprises with nursery units.**)

The inputs for the unit for rearing breeding animals start here.

- Non-specific non-feed costs in the unit for rearing breeding gilts and boars (*cfixbr*)

- Empty rearing unit days per cycle (i.e. the time interval between the time when one animal batch is leaving and the time when the next batch is coming in, *edru*)

- Specific costs for health care of gilts and boars in the unit for rearing breeding animals for breeding animals alive at the end of rearing (*prhcbr*)

- Specific costs for health care for breeding animals died during rearing as proportion of the specific costs for health care for breeding animals alive at the end of rearing (*khcdbr*)

- Costs for transferring replacement gilts from the rearing to the breeding unit when gilts are reared in specific enterprises (transport costs and marketing levy, *ctraG*). (**Insert zero if rearing units belong to enterprises with breeding units.**)

- Replacement gilts transferred from the rearing unit to the breeding unit which does not belong to the enterprise where the rearing unit is located as proportion of all replacement gilts (*ptraG*). (**Insert zero if rearing units belong to enterprises with breeding units.**)

The following two inputs are read only if boars are used for oestrus stimulation and/or natural mating:

- Costs for transferring replacement boars for natural mating (or oestrus stimulation) from the rearing unit to the breeding unit when boars are reared in specific enterprises (transport costs and marketing levy, $ctraB$). **(Insert zero if rearing units belong to enterprises with breeding units.)**

- Replacement boars for natural mating (or oestrus stimulation) transferred from the rearing unit to the breeding unit which does not belong to the enterprise where the rearing unit is located as proportion of all replacement boars ($ptraB$). **(Insert zero if rearing units belong to enterprises with breeding units.)**

- Costs for selling replacement boars for natural mating (or oestrus stimulation) to another link of the breeding system (transport cost and marketing levy, $cselB$). This variable is not read in pure-bred breeding systems.

- Costs for transferring replacement boars from the rearing unit to AI stations (transport cost and marketing levy, $ctraAIB$). This variable is only read if there is AI.

- Costs for exporting young breeding boars (transport cost and marketing levy, $cexpB$). This variable is read only if there is export of boars.

- Costs for exporting breeding gilts (transport cost and marketing levy, $cexpG$). This variable is read only if there is export of gilts.

- Marketing costs for negatively selected and culled breeding gilts or boars (transport costs to abattoir and marketing levy, $cmarbr$)

- Extra costs for testing and evaluating breeding gilts ($ctestbrG$)

- Extra costs for testing and evaluating young breeding boars ($ctestbrB$)

The following parameter is only read if there is finishing of negatively selected gilts:

- Non-feed costs in finishing of negatively selected breeding gilts ($cnf29$)

3.1.2.14 Input file INPUTP13*.TXT

This file contains parameters for calculating non-feed costs connected with the finishing unit of the integrated production system.

- Non-specific non-feed costs in the finishing unit for finishing gilts and castrates ($cfixfGC$)

- Empty finishing unit days per cycle (i.e. the time interval between the time when one animal batch is leaving and the time when the next batch is coming in, $edfu$)

- Specific costs for health care of gilts or castrates alive at the end of finishing ($prhcfGC$)

- Specific costs for health care for gilts or castrates died during finishing as proportion of the specific costs for health care for gilts or castrates alive at the end of finishing ($khcdfGC$)

- Marketing costs for finished gilts or castrates including transport of finished pigs to abattoir, meat inspection and carcass classification charges ($cmarfGC$)

The following parameters until the end of the file are read only if there is finishing of boars:

- Non-specific non-feed costs in the finishing unit for finishing boars ($cfixfB$)

- Specific costs for health care of boars alive at the end of finishing ($prhcfB$)

- Specific costs for health care for boars died during finishing as proportion of the specific costs for health care for boars alive at the end of finishing ($khcdfB$)

- Costs for immuno-castration of fattened boars ($ccasB$). (This input is read only if there is immuno-castration of fattened boars.)

- Marketing costs for finished boars including transport of finished boars to abattoir, meat inspection and carcass classification charges ($cmarfB$)

3.1.2.15 Input file INPUTP14*.TXT

This file contains parameters for the calculation of revenues from culled sows and culled end-of-cycle boars:

- Total governmental subsidies in the whole production system of a breed (in pure-bred systems) or of a link of a breeding system per sow per year ($dotS$)

The following inputs are for culled sows including culled breeding gilts already included in the sow herd:

- Pricing system for culled sows. Insert an integer value between 1 and 4:

    - 1: The price is given per kg live weight (LW) and does not change with LW
    - 2: The price is given per kg carcass weight (CW) and does not change with CW
    - 3: The price is given per kg LW and depends on LW classes
    - 4: The price is given per kg CW and depends on CW classes

Input for Pricing System 1:

- Price for culled sows ($prbS$)

Inputs for Pricing System 2:

- Price for carcasses of culled sows ($prbS$)

- Average dressing percentage of culled sows ($dressS0$)

Inputs for Pricing System 3:

- Price for live weight in the base class in the classification system according to live weight for sows ($prbS$)

- Number of live weight classes for culled sows ($nwcS$)

- Upper limits in live weight classes $1, \ldots, nwcS - 1$ for culled sows ($nwcS$ is the number of classes) starting with the class with the lowest live weight ($upS[i]$, $i = 1, \ldots, nwcS - 1$)

- Relative prices for live weight ($kprS[i]$) in live weight classes $1, \ldots, nwcS$ for culled sows ($nwcS$ is the number of classes) expressed as proportion of the absolute price in the base class (**i.e. the relative price in the base class must be 1**)

Inputs for Pricing System 4:

- Price for carcass weight in the base class in the classification system according to carcass weight for sow ($prbS$)

- Number of carcass weight classes for culled sows ($nwcS$)

- Upper limits in carcass weight classes $1, \ldots, nwcS - 1$ for culled sows ($nwcS$ is the number of classes) starting with the class with the lowest carcass weight ($upS[i]$, $i = 1, \ldots, nwcS - 1$)

- Relative prices for carcass weight ($kprS[i]$) in carcass weight classes $1, \ldots, nwcS$ for culled sows ($nwcS$ is the number of classes) expressed as proportion of the absolute price in the base class (**i.e. the relative price in the base class must be 1**)

- Dressing percent of culled sows averaged over different weights ($dressS0$)

The following inputs are for culled end-of-cycle boars[11]. Insert an integer value 1 or 2:

- Pricing system for culled end-of-cycle boars ($prcB$).

    - 1: The price is given per kg live weight (LW)
    - 2: The price is given per kg carcass weight (CW)

Input for Pricing System 1:

- Price for culled end-of-cycle boars ($preB$)

Inputs for Pricing System 2:

- Price for carcasses of culled end-of-cycle boars ($preB$)

- Average dressing percentage of culled end-of-cycle boars ($dressB$)

3.1.2.16   Input file INPUTP15*.TXT

This file contains parameters for the calculation of revenues from culled young breeding animals (gilts and young boars). The file is not needed for cross AB in Breeding Systems 3 and 4.
The following inputs are for culled breeding gilts which where negatively selected:

- Pricing system for culled breeding gilts which where negatively selected ($prcG$). Insert an integer value between 1 and 4:

    - 1: The price is given per kg live weight (LW) and does not change with LW
    - 2: The price is given per kg carcass weight (CW) and does not change with CW
    - 3: The price is given per kg LW and depends on LW classes
    - 4: The price is given per kg CW and depends on CW classes

Input for Pricing System 1:

- Price for culled negatively selected breeding gilts ($prbcG$)

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[11]The following inputs until the end of the file are read only if there are boars for natural mating or for oestrus stimulation.

Inputs for Pricing System 2:

- Price for carcasses of culled negatively selected breeding gilts ($prbcG$)

- Average dressing percentage of culled negatively selected breeding gilts ($dresscG$)

Inputs for Pricing System 3:

- Price for live weight in the base class in the classification system according to live weight for culled negatively selected breeding gilts ($prbcG$)

- Number of live weight classes for culled negatively selected breeding gilts ($nwcG$)

- Upper limits in live weight classes $1, \ldots, nwcG-1$ for culled negatively selected breeding gilts ($nwcG$ is the number of classes) starting with the class with the lowest live weight ($upcG[i]$, $i = 1, \ldots, nwcG - 1$)

- Relative prices for live weight ($kprcG[i]$) in live weight classes $1, \ldots, nwcG$ for culled negatively selected breeding gilts ($nwcG$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

Inputs for Pricing System 4:

- Price for carcass weight in the base class in the classification system according to carcass weight for culled negatively selected breeding gilts ($prbcG$)

- Number of carcass weight classes for culled negatively selected breeding gilts ($nwcG$)

- Upper limits in carcass weight classes $1, \ldots, nwcG - 1$ for culled negatively selected breeding gilts ($nwcG$ is the number of classes) starting with the class with the lowest carcass weight ($upcG[i]$, $i = 1, \ldots, nwcG - 1$)

- Relative prices for carcass weight ($kprcG[i]$) in carcass weight classes $1, \ldots, nwcG$ for culled negatively selected breeding gilts ($nwcG$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Average dressing percentage of culled negatively selected breeding gilts ($dresscG$)

The following inputs are for culled young breeding boars which where negatively selected:

- Pricing system for culled young breeding boars which where negatively selected ($prcyB$). Insert an integer value between 1 and 4:

  - 1: The price is given per kg live weight (LW) and does not change with LW
  - 2: The price is given per kg carcass weight (CW) and does not change with CW
  - 3: The price is given per kg LW and depends on LW classes
  - 4: The price is given per kg CW and depends on CW classes

Input for Pricing System 1:

- Price for culled negatively selected young breeding boars ($prbcB$)

Inputs for Pricing System 2:

- Price for carcasses of culled negatively selected young breeding boars ($prbcB$)

- Average dressing percentage of culled negatively selected young breeding boars ($dressyB$)

Inputs for Pricing System 3:

- Price for live weight in the base class in the classification system according to live weight for culled negatively selected young breeding boars ($prbcB$)

- Number of live weight classes for culled negatively selected young breeding boars ($nwcB$)

- Upper limits in live weight classes $1, \ldots, nwcB-1$ for culled negatively selected young breeding boars ($nwcB$ is the number of classes) starting with the class with the lowest live weight ($upcB[i]$, $i = 1, \ldots, nwcB - 1$)

- Relative prices for live weight ($kprcB[i]$) in live weight classes $1, \ldots, nwcB$ for culled negatively selected young breeding boars ($nwcB$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

Inputs for Pricing System 4:

- Price for carcass weight in the base class in the classification system according to carcass weight for culled negatively selected young breeding boars ($prbcB$)

- Number of carcass weight classes for culled negatively selected young breeding boars ($nwcB$)

- Upper limits in carcass weight classes $1, \ldots, nwcB - 1$ for culled negatively selected young breeding boars ($nwcB$ is the number of classes) starting with the class with the lowest carcass weight ($upcB[i]$, $i = 1, \ldots, nwcB - 1$)

- Relative prices for carcass weight ($kprcB[i]$) in carcass weight classes $1, \ldots, nwcB$ for culled negatively selected young breeding boars ($nwcB$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Average dressing percentage of culled negatively selected young breeding boars ($dressyB$)

3.1.2.17 Input file INPUTP16*.TXT

This file contains parameters for the calculation of revenues from animals slaughtered after finishing. A special form of the input file is used for the cross AB (see last Paragraph in this file. **It must be ensured that *all* inputs connected with carcass weight refer either to hot or to cold carcass weight. Only values for those animal categories are read which exist in the specific breed and Breeding system. Do not delete inputs you do not need, just ignore them.**

- Pricing system for animals slaughtered after finishing ($prfsP$). Insert an integer value between 1 and 6:

    - 1: The price is given per kg live weight (LW) and does not change with LW

  - 2: The price is given per kg carcass weight (CW) and does not change with CW
  - 3: The price is given per kg LW and depends on LW classes
  - 4: The price is given per kg CW and depends on CW classes
  - 5: The price is given per kg CW and depends on classes according to lean meat content in carcass
  - 6: The price is given per kg CW and depends on CW classes and on classes according to lean meat content in carcass (a combination of 4 and 5)

Inputs for Pricing System 1:

- Price per kg LW for finished gilts ($prb[0]$)

- Price per kg LW for finished castrates ($prb[2]$, only read if there is finishing of castrates)

- Price per kg LW for finished boars ($prb[1]$, only read if there is finishing of boars)

Inputs for Pricing System 2:

- Price per kg CW for finished gilts ($prb[0]$)

- Dressing percentage of pure-bred finished gilts ($dress[0][0]$)

- Dressing percentage of cross-bred finished gilts ($dress[0][1]$)
  The following three inputs are read only if there is finishing of castrates:

- Price per kg CW for finished castrates ($prb[2]$)

- Dressing percentage of pure-bred finished castrates ($dress[2][0]$)

- Dressing percentage of cross-bred finished castrates ($dress[2][1]$)
  The following three inputs are read only if there is finishing of boars:

- Price per kg CW for finished boars ($prb[1]$)

- Dressing percentage of pure-bred finished boars ($dress[1][0]$)

- Dressing percentage of cross-bred finished boars ($dress[1][1]$)

Inputs for Pricing System 3:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for live weight in the base class in the classification system according to live weight for gilts ($prb[0]$) and castrates ($prb[2]$)

- Number of live weight classes for finished gilts ($nwcf[0]$) and castrates ($nwcf[2]$)

- Upper limits in live weight classes $1, \ldots, nwcf[0] - 1$ for finished gilts or castrates ($nwcf[0] = nwcf[2]$ is the number of classes) starting with the class with the lowest live weight ($upf[0][i] = upf[2][i]$, $i = 1, \ldots, nwcf[0] - 1$)

- Relative prices for live weight of gilts ($kprwf[0][i]$) and castrates ($kprwf[2][i]$) in live weight classes $1, \ldots, nwcf[0]$ ($nwcf[0] = nwcf[2]$ is the number of classes) expressed as proportion of the absolute price in the base class (**i.e. the relative price in the base class must be 1**)

- Relative frequencies ($pwcf[0][0][i]$) of finished pure-bred gilts in live weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Relative frequencies ($pwcf[0][1][i]$) of finished cross-bred gilts in live weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Relative frequencies ($pwcf[2][0][i]$) of finished pure-bred castrates in live weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

- Relative frequencies ($pwcf[2][1][i]$) of finished cross-bred castrates in live weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

Finished boars (only read if there is finishing of boars; only relevant data are read):

- Price for live weight in the base class in the classification system according to live weight for finished boars ($prb[1]$)

- Number of live weight classes for finished boars ($nwcf[1]$)

- Upper limits in live weight classes $1, \ldots, nwcf[0]-1$ for finished boars ($nwcf[1]$ is the number of classes) starting with the class with the lowest live weight ($upf[1][i]$, $i = 1, \ldots, nwcf[1] - 1$)

- Relative prices for live weight of boars ($kprwf[1][i]$) in live weight classes $1, \ldots, nwcf[1]$ ($nwcf[1]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Relative frequencies ($pwcf[1][0][i]$) of finished pure-bred boars in live weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

- Relative frequencies ($pwcf[1][1][i]$) of finished cross-bred boars in live weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

Inputs for Pricing Systems 4 and 6:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight in the base class in the classification system according to carcass weight for gilts ($prb[0]$) and castrates ($prb[2]$)

- Number of carcass weight classes for finished gilts ($nwcf[0]$) and castrates ($nwcf[2]$)

- Upper limits in carcass weight classes $1, \ldots, nwcf[0] - 1$ for finished gilts or castrates ($nwcf[0] = nwcf[2]$ is the number of classes) starting with the class with the lowest carcass weight ($upf[0][i] = upf[2][i]$, $i = 1, \ldots, nwcf[0] - 1$)

- Relative prices for carcass weight of gilts ($kprwf[0][i]$) and castrates ($kprwf[2][i]$) in carcass weight classes $1, \ldots, nwcf[0]$ ($nwcf[0] = nwcf[2]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of pure-bred finished gilts ($dress[0][0]$)

- Relative frequencies ($pwcf[0][0][i]$) of finished pure-bred gilts in carcass weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished gilts ($dress[0][1]$)

- Relative frequencies ($pwcf[0][1][i]$) of finished cross-bred gilts in carcass weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Dressing percentage of pure-bred finished castrates ($dress[2][0]$)

- Relative frequencies ($pwcf[2][0][i]$) of finished pure-bred castrates in carcass weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished castrates ($dress[2][1]$)

- Relative frequencies ($pwcf[2][1][i]$) of finished cross-bred castrates in carcass weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

Finished boars (only read if there is finishing of boars; only relevant data are read):

- Price for carcass weight in the base class in the classification system according to carcass weight for finished boars ($prb[1]$)

- Number of carcass weight classes for finished boars ($nwcf[1]$)

- Upper limits in carcass weight classes $1, \ldots, nwcf[1] - 1$ for finished boars ($nwcf[1]$ is the number of classes) starting with the class with the lowest carcass weight ($upf[1][i]$, $i = 1, \ldots, nwcf[1] - 1$)

- Relative prices for carcass weight of boars ($kprwf[1][i]$) in carcass weight classes $1, \ldots, nwcf[1]$ ($nwcf[1]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of pure-bred finished boars ($dress[1][0]$)

- Relative frequencies ($pwcf[1][0][i]$) of finished pure-bred boars in carcass weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished boars ($dress[1][1]$)

- Relative frequencies ($pwcf[1][1][i]$) of finished cross-bred boars in carcass weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

Inputs for Pricing Systems 5 and 6:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight of gilts or castrates in the base class in the classification system according to lean meat content in the carcass ($prblm[0] = prblm[2]$)

- Number of classes for gilts ($nlm[0]$) or castrates ($nlm[2]$) according to lean meat content in the carcass

- Upper limits in lean meat classes $1, \ldots, nlm[0] - 1$ for finished gilts or castrates ($nlm[0] = nlm[2]$ is the number of classes) starting with the class with the lowest lean meat content

- Relative prices for carcass weight of gilts ($kprlm[0][i]$) in lean meat classes $1, \ldots, nlm[0]$ ($nlm[0] = nlm[2]$ is the number of classes) expressed as proportion of the absolute price in the base class (i.e. the relative price in the base class must be 1)

- Dressing percentage of pure-bred finished gilts ($dress[0][0]$)

- Relative frequencies ($plm[0][0][i]$) of finished pure-bred gilts in lean meat classes $i = 1, \ldots, nlm[0]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished gilts ($dress[0][1]$)

- Relative frequencies ($plm[0][1][i]$) of finished cross-bred gilts in lean meat classes $i = 1, \ldots, nlm[0]$ (The values must sum to 100)

- Dressing percentage of pure-bred finished castrates ($dress[2][0]$)

- Relative frequencies ($plm[2][0][i]$) of finished pure-bred castrates in lean meat classes $i = 1, \ldots, nlm[2]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished castrates ($dress[2][1]$)

- Relative frequencies ($plm[2][1][i]$) of finished cross-bred castrates in lean meat classes $i = 1, \ldots, nlm[2]$ (The values must sum to 100)

Finished boars (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight of boars in the base class in the classification system according to lean meat content in the carcass ($prblm[1]$)

- Number of classes for boars ($nlm[1]$) according to lean meat content in the carcass

- Upper limits in lean meat classes $1, \ldots, nlm[1] - 1$ for finished boars ($nlm[1]$ is the number of classes) starting with the class with the lowest lean meat content

- Relative prices for carcass weight of boars ($kprlm[1][i]$) in lean meat classes $1, \ldots, nlm[1]$ ($nlm[1]$ is the number of classes) expressed as proportion of the absolute price in the base class (i.e. the relative price in the base class must be 1)

- Dressing percentage of pure-bred finished boars ($dress[1][0]$)

- Relative frequencies ($plm[1][0][i]$) of finished pure-bred boars in lean meat classes $i = 1, \ldots, nlm[1]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished boars ($dress[1][1]$)

- Relative frequencies ($plm[1][1][i]$) of finished cross-bred boars in lean meat classes $i = 1, \ldots, nlm[1]$ (The values must sum to 100)

Special form for cross AB: INPUTP16AB.TXT This file contains parameters for the calculation of revenues from animals slaughtered after finishing for the cross AB. **It must be ensured that *all* inputs connected with carcass weight refer either to hot or to cold carcass weight. Only values for those animal categories are read which exist in the link with cross AB. Do not delete inputs you do not need, just ignore them.**

- Pricing system for animals slaughtered after finishing ($prfsP$). Insert an integer value between 1 and 6:

    - 1: The price is given per kg live weight (LW) and does not change with LW
    - 2: The price is given per kg carcass weight (CW) and does not change with CW
    - 3: The price is given per kg LW and depends on LW classes
    - 4: The price is given per kg CW and depends on CW classes
    - 5: The price is given per kg CW and depends on classes according to lean meat content in carcass
    - 6: The price is given per kg CW and depends on CW classes and on classes according to lean meat content in carcass (a combination of 4 and 5)

Inputs for Pricing System 1:

- Price per kg LW for finished gilts ($prb[0]$)

- Price per kg LW for finished castrates ($prb[2]$, only read if there is finishing of castrates)

- Price per kg LW for finished boars ($prb[1]$, only read if there is finishing of boars)

Inputs for Pricing System 2:

- Price per kg CW for finished gilts ($prb[0]$)

- Dressing percentage for finished gilts ($dress[0][1]$)

    The following three inputs are read only if there is finishing of castrates:

- Price per kg CW for finished castrates ($prb[2]$)

- Dressing percentage for finished castrates ($dress[2][1]$)

    The following three inputs are read only if there is finishing of boars:

- Price per kg CW for finished boars ($prb[1]$)

- Dressing percentage for finished boars ($dress[1][1]$)

Inputs for Pricing System 3:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for live weight in the base class in the classification system according to live weight for gilts ($prb[0]$) and castrates ($prb[2]$)

- Number of live weight classes for finished gilts ($nwcf[0]$) and castrates ($nwcf[2]$)

- Upper limits in live weight classes $1, \ldots, nwcf[0] - 1$ for finished gilts or castrates ($nwcf[0] = nwcf[2]$ is the number of classes) starting with the class with the lowest live weight ($upf[0][i] = upf[2][i]$, $i = 1, \ldots, nwcf[0] - 1$)

- Relative prices for live weight of gilts ($kprwf[0][i]$) and castrates ($kprwf[2][i]$) in live weight classes $1, \ldots, nwcf[0]$ ($nwcf[0] = nwcf[2]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Relative frequencies ($pwcf[0][1][i]$) of finished gilts in live weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Relative frequencies ($pwcf[2][1][i]$) of finished castrates in live weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

Finished boars (only read if there is finishing of boars; only relevant data are read):

- Price for live weight in the base class in the classification system according to live weight for finished boars ($prb[1]$)

- Number of live weight classes for finished boars ($nwcf[1]$)

- Upper limits in live weight classes $1, \ldots, nwcf[0] - 1$ for finished boars ($nwcf[1]$ is the number of classes) starting with the class with the lowest live weight ($upf[1][i]$, $i = 1, \ldots, nwcf[1] - 1$)

- Relative prices for live weight of boars ($kprwf[1][i]$) in live weight classes $1, \ldots, nwcf[1]$ ($nwcf[1]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Relative frequencies ($pwcf[1][1][i]$) of finished boars in live weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

Inputs for Pricing Systems 4 and 6:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight in the base class in the classification system according to carcass weight for gilts ($prb[0]$) and castrates ($prb[2]$)

- Number of carcass weight classes for finished gilts ($nwcf[0]$) and castrates ($nwcf[2]$)

- Upper limits in carcass weight classes $1, \ldots, nwcf[0] - 1$ for finished gilts or castrates ($nwcf[0] = nwcf[2]$ is the number of classes) starting with the class with the lowest carcass weight ($upf[0][i] = upf[2][i]$, $i = 1, \ldots, nwcf[0] - 1$)

- Relative prices for carcass weight of gilts ($kprwf[0][i]$) and castrates ($kprwf[2][i]$) in carcass weight classes $1, \ldots, nwcf[0]$ ($nwcf[0] = nwcf[2]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of finished gilts ($dress[0][1]$)

- Relative frequencies ($pwcf[0][1][i]$) of finished gilts in carcass weight classes $i = 1, \ldots, nwcf[0]$ (The values must sum to 100)

- Dressing percentage of finished castrates ($dress[2][1]$)

- Relative frequencies ($pwcf[2][1][i]$) of finished castrates in carcass weight classes $i = 1, \ldots, nwcf[2]$ (The values must sum to 100)

Finished boars (only read if there is finishing of boars; only relevant data are read):

- Price for carcass weight in the base class in the classification system according to carcass weight for finished boars ($prb[1]$)

- Number of carcass weight classes for finished boars ($nwcf[1]$)

- Upper limits in carcass weight classes $1, \ldots, nwcf[1] - 1$ for finished boars ($nwcf[1]$ is the number of classes) starting with the class with the lowest carcass weight ($upf[1][i]$, $i = 1, \ldots, nwcf[1] - 1$)

- Relative prices for carcass weight of boars ($kprwf[1][i]$) in carcass weight classes $1, \ldots, nwcf[1]$ ($nwcf[1]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of cross-bred finished boars ($dress[1][1]$)

- Relative frequencies ($pwcf[1][1][i]$) of finished cross-bred boars in carcass weight classes $i = 1, \ldots, nwcf[1]$ (The values must sum to 100)

Inputs for Pricing Systems 5 and 6:

Finished gilts and castrates (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight of gilts or castrates in the base class in the classification system according to lean meat content in the carcass ($prblm[0] = prblm[2]$)

- Number of classes for gilts ($nlm[0]$) or castrates ($nlm[2]$) according to lean meat content in the carcass

- Upper limits in lean meat classes $1, \ldots, nlm[0] - 1$ for finished gilts or castrates ($nlm[0] = nlm[2]$ is the number of classes) starting with the class with the lowest lean meat content

- Relative prices for carcass weight of gilts ($kprlm[0][i]$) in lean meat classes $1, \ldots, nlm[0]$ ($nlm[0] = nlm[2]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of cross-bred finished gilts ($dress[0][1]$)

- Relative frequencies ($plm[0][1][i]$) of finished cross-bred gilts in lean meat classes $i = 1, \ldots, nlm[0]$ (The values must sum to 100)

- Dressing percentage of pure-bred finished castrates ($dress[2][0]$)

- Relative frequencies ($plm[2][0][i]$) of finished pure-bred castrates in lean meat classes $i = 1, \ldots, nlm[2]$ (The values must sum to 100)

- Dressing percentage of cross-bred finished castrates ($dress[2][1]$)

- Relative frequencies ($plm[2][1][i]$) of finished cross-bred castrates in lean meat classes $i = 1, \ldots, nlm[2]$ (The values must sum to 100)

Finished boars (Only data which are of relevance to the given situation are read; e.g. data for non-existent groups of animals are skipped):

- Price for carcass weight of boars in the base class in the classification system according to lean meat content in the carcass ($prblm[1]$)

- Number of classes for boars ($nlm[1]$) according to lean meat content in the carcass

- Upper limits in lean meat classes $1, \ldots, nlm[1] - 1$ for finished boars ($nlm[1]$ is the number of classes) starting with the class with the lowest lean meat content

- Relative prices for carcass weight of boars ($kprlm[1][i]$) in lean meat classes $1, \ldots, nlm[1]$ ($nlm[1]$ is the number of classes) expressed as proportion of the absolute price in the base class **(i.e. the relative price in the base class must be 1)**

- Dressing percentage of finished boars ($dress[1][1]$)

- Relative frequencies ($plm[1][1][i]$) of finished boars in lean meat classes $i = 1, \ldots, nlm[1]$ (The values must sum to 100)

3.1.2.18 Input file INPUTP17*.TXT

This file contains parameters for the calculation of revenues from *pure-bred* animals exported or sold to other links of the breeding system (progeny categories 6, 7, 8, 17, 18, 25, 26 and 27). **Data are read only for categories which exist and for the appropriate pricing system. Do not delete inputs which you do not need, just ignore them**. The file is not needed for cross AB in Breeding Systems 3 and 4. The file contains the following inputs:
Inputs for progeny category 6[12]:

- Pricing system for pure-bred female piglets exported after the nursery phase ($prsP[6][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred female piglets exported after the nursery phase (if Pricing System is 1, $prP[6][0]$)

- Price (per kg LW) for pure-bred female piglets exported after the nursery phase (if Pricing System is 2, $prP[6][0]$)

Inputs for progeny category 7:

- Pricing system for pure-bred entire male piglets exported after the nursery phase ($prsP[7][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

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[12]See Subsection 107 for categories of progeny.

- Price (per animal) for pure-bred entire male piglets exported after the nursery phase (if Pricing System is 1, $prP[7][0]$)

- Price (per kg LW) for pure-bred entire male piglets exported after the nursery phase (if Pricing System is 2, $prP[7][0]$)

Inputs for progeny category 8:

- Pricing system for pure-bred castrated male piglets exported after the nursery phase ($prsP[8][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred castrated male piglets exported after the nursery phase (if Pricing System is 1, $prP[8][0]$)

- Price (per kg LW) for pure-bred castrated male piglets exported after the nursery phase (if Pricing System is 2, $prP[8][0]$)

Inputs for progeny category 17:

- Pricing system for pure-bred breeding gilts sold to another link of the breeding system ($prsP[17][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred breeding gilts sold to another link of the breeding system (if Pricing System is 1, $prP[17][0]$)

- Price (per kg LW) for pure-bred breeding gilts sold to another link of the breeding system (if Pricing System is 2, $prP[17][0]$)

Inputs for progeny category 18:

- Pricing system for pure-bred breeding gilts exported ($prsP[18][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred breeding gilts exported (if Pricing System is 1, $prP[18][0]$)

- Price (per kg LW) for pure-bred breeding gilts exported (if Pricing System is 2, $prP[18][0]$)

Inputs for progeny category 25:

- Pricing system for pure-bred breeding boars sold to another link of the breeding system ($prsP[25][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred breeding boars sold to another link of the breeding system for natural mating (if Pricing System is 1, $prP[25][0]$)

- Price (per kg LW) for pure-bred breeding boars sold to another link of the breeding system for natural mating (if Pricing System is 2, $prP[25][0]$)

- Price (per animal) for pure-bred breeding boars sold to another link of the breeding system for oestrus stimulation (if Pricing System is 1, $prP[25][0]$)

- Price (per kg LW) for pure-bred breeding boars sold to another link of the breeding system for oestrus stimulation (if Pricing System is 2, $prP[25][0]$)

Inputs for progeny category 26:

- Pricing system for pure-bred breeding boars sold to AI stations ($prsP[26][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred breeding boars sold to AI stations (if Pricing System is 1, $prP[26][0]$)

- Price (per kg LW) for pure-bred breeding boars sold to AI stations (if Pricing System is 2, $prP[26][0]$)

Inputs for progeny category 27:

- Pricing system for pure-bred breeding boars exported ($prsP[27][0]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for pure-bred breeding boars exported (if Pricing System is 1, $prP[27][0]$)

- Price (per kg LW) for pure-bred breeding boars exported (if Pricing System is 2, $prP[27][0]$)

3.1.2.19 Input file INPUTP18*.TXT

This file contains parameters for the calculation of revenues from *cross-bred* animals exported or sold to other links of the breeding system (progeny categories 6, 7, 8, 17, 18, 25, 26 and 27). **Data are read only for categories which exist and for the appropriate pricing system. Do not delete inputs you do not need, just ignore them.** The file contains the following inputs:
Inputs for progeny category 6[13]:

- Pricing system for cross-bred female piglets exported after the nursery phase ($prsP[6][1]$). Insert 1 or 2:

    - 1: The price is given per animal
    - 2: The price is given per kg live weight

- Price (per animal) for cross-bred female piglets exported after the nursery phase (if Pricing System is 1, $prP[6][1]$)

- Price (per kg LW) for cross-bred female piglets exported after the nursery phase (if Pricing System is 2, $prP[6][1]$)

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[13]See Subsection 6.3 for categories of progeny.

Inputs for progeny category 7:

- Pricing system for cross-bred entire male piglets exported after the nursery phase ($prsP[7][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred entire male piglets exported after the nursery phase (if Pricing System is 1, $prP[7][1]$)

- Price (per kg LW) for cross-bred entire male piglets exported after the nursery phase (if Pricing System is 2, $prP[7][1]$)

Inputs for progeny category 8:

- Pricing system for cross-bred castrated male piglets exported after the nursery phase ($prsP[8][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred castrated male piglets exported after the nursery phase (if Pricing System is 1, $prP[8][1]$)

- Price (per kg LW) for cross-bred castrated male piglets exported after the nursery phase (if Pricing System is 2, $prP[8][1]$)

> **Here ends the file INPUTP18AB.TXT for cross AB which is used in Breeding Systems 3 and 4.**

Inputs for progeny category 17 or 19[14]:

- Pricing system for cross-bred breeding gilts sold to another link of the breeding system ($prsP[17][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred breeding gilts sold to another link of the breeding system (if Pricing System is 1, $prP[17][1]$)

- Price (per kg LW) for cross-bred breeding gilts sold to another link of the breeding system (if Pricing System is 2, $prP[17][1]$)

Inputs for progeny category 18:

- Pricing system for cross-bred breeding gilts exported ($prsP[18][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred breeding gilts exported (if Pricing System is 1, $prP[18][1]$)

---

[14]In the calculation for the cross AB, the variables $prsP[17][1]$ and $prP[17][1]$ are read from INPUTP18A.TXT as $prsP[19][0]$ and $prP[19][0]$, i.e. as pricing system for *purchased* breeding gilts of the genotype of the sows and as price for these gilts.

- Price (per kg LW) for cross-bred breeding gilts exported (if Pricing System is 2, $prP[18][1]$)

Inputs for progeny category 25:

- Pricing system for cross-bred breeding boars sold to another link of the breeding system ($prsP[25][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred breeding boars sold to another link of the breeding system for natural mating (if Pricing System is 1, $prP[25][1]$)

- Price (per kg LW) for cross-bred breeding boars sold to another link of the breeding system for natural mating (if Pricing System is 2, $prP[25][1]$)

- Price (per animal) for cross-bred breeding boars sold to another link of the breeding system for oestrus stimulation (if Pricing System is 1, $prP[25][1]$)

- Price (per kg LW) for cross-bred breeding boars sold to another link of the breeding system for oestrus stimulation (if Pricing System is 2, $prP[25][1]$)

Inputs for progeny category 26:

- Pricing system for cross-bred breeding boars sold to AI stations ($prsP[26][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred breeding boars sold to AI stations (if Pricing System is 1, $prP[26][1]$)

- Price (per kg LW) for cross-bred breeding boars sold to AI stations (if Pricing System is 2, $prP[26][1]$)

Inputs for progeny category 27:

- Pricing system for cross-bred breeding boars exported ($prsP[27][1]$). Insert 1 or 2:

  - 1: The price is given per animal
  - 2: The price is given per kg live weight

- Price (per animal) for cross-bred breeding boars exported (if Pricing System is 1, $prP[27][1]$)

- Price (per kg LW) for cross-bred breeding boars exported (if Pricing System is 2, $prP[27][1]$)

3.1.2.20 Input file INPUTP19*.TXT

This file is necessary for the selection of traits for which the relative economic values are calculated (For explanation why this selection is needed, see Manual for EWPIG2 Subsection 8.7.1). **The file is not read in the program run for cross AB and is also skipped for the option** $gf = 1$ **in input file INPUTPBS#.TXT (see Section 3.1.2.1).** The following selections are made:

- Select between the following options for growth traits in pigs ($flag[0]$):

  - (0) Separate traits for individual growth phases of young animals are defined and used (traits 1 to 6) or

  - (1) Only one lifetime growth trait from birth until slaughter is used (traits 7 or 8)

- Select ($flag[1]$):

  - (1) Average piglet weight at weaning at fixed age or

  - (2) Average daily gain of piglets until weaning

- Select ($flag[2]$):

  - (3) Weight of piglets at the end of the nursery phase or

  - (4) Average daily gain of piglets in nursery until fixed age

- Select ($flag[3]$):

  - (5) Average daily gain of of pigs in finishing to fixed slaughter weight or

  - (6) Length of the finishing period until reaching target slaughter weight

- Select ($flag[4]$):

  - (7) Average lifetime daily gain of animals from birth to slaughter after finishing or

  - (8) Age at reaching target slaughter weight

- Select a litter size trait ($flag[5]$):

  - (9) Total number of piglets born or

  - (10) Number of piglets born alive or

  - (11) Number of piglets weaned

- Select a fertility trait for gilts ($flag[6]$):

  - (15) Conception rate of gilts after the first mating or

  - (16) Total conception rate of gilts or

  - (17) Average age at first farrowing

- Select a fertility trait for sows ($flag[7]$):

  - (18) Conception rate of sows after the first mating averaged over all parities or

  - (19) Total conception rate of sows averaged over all matings and all parities or

  - (20) Average farrowing interval

- Select a trait for productive lifetime ($flag[8]$):

  - (23) Average productive lifetime of sows measured in number of farrowings or
  - (24) Average productive lifetime of sows measured in years

- Select a trait for feed efficiency in nursery ($flag[9]$):

  - (27) Residual feed intake in nursery or
  - (28) Feed conversion in nursery

- Select a trait for feed efficiency in finishing ($flag[10]$):

  - (29) Residual feed intake in finishing or
  - (30) Feed conversion in finishing

3.1.2.21 Input file INPUTP20*.TXT

The file contains the genetic standard deviations of all traits. It is read if these standard deviations are known which is controlled via the parameter *std* read in the parameter file PARAP*.TXT (see Subsection 3.1.1.2 on page 28). The genetic standard deviations are read only for those traits which are selected on the basis of INPUTP19*.TXT. **Keep attention that the genetic standard deviations are given in the correct units.** *The file is not read in the program run for cross AB and is also skipped for the option $gf = 1$ in input file INPUTPBS#.TXT (see Section 3.1.2.1).* The file contains the following inputs (the number of trait according to Appendix ... is given in parentheses):

- (1) Genetic standard deviation for average piglet weight at weaning ($gsd\_d[1]$)

- (2) Genetic standard deviation for average daily gain of piglets until weaning ($gsd\_d[2]$)

- (3) Genetic standard deviation for weight of piglets at the end of the nursery phase ($gsd\_d[3]$)

- (4) Genetic standard deviation for average daily gain of piglets in nursery ($gsd\_d[4]$)

- (5) Genetic standard deviation for average daily gain of pigs in finishing ($gsd\_d[5]$)

- (6) Genetic standard deviation for the length of the finishing period ($gsd\_d[6]$)

- (7) Genetic standard deviation for average lifetime daily gain of animals from birth to slaughter ($gsd\_d[7]$)

- (8) Genetic standard deviation for age at reaching target slaughter weight ($gsd\_d[8]$)

- (9) Genetic standard deviation for total number of piglets born ($gsd\_d[9]$)

- (10) Genetic standard deviation for number of piglets born alive ($gsd\_d[10]$)

- (11) Genetic standard deviation for number of piglets weaned ($gsd\_d[11]$)

- (12) Genetic standard deviation for piglet survival rate at birth ($gsd\_d[12]$)

- (13) Genetic standard deviation for survival rate of piglets born alive until weaning ($gsd\_d[13]$)

- (14) Genetic standard deviation for age of gilts at first mating ($gsd\_d[14]$)

- (15) Genetic standard deviation for conception rate of gilts after the first mating ($gsd\_d[15]$)

- (16) Genetic standard deviation for total conception rate of gilts ($gsd\_d[16]$)

- (17) Genetic standard deviation for average age at first farrowing ($gsd\_d[17]$)

- (18) Genetic standard deviation for conception rate of sows after the first mating averaged over all parities ($gsd\_d[18]$)

- (19) Genetic standard deviation for total conception rate of sows averaged over all matings and all parities ($gsd\_d[19]$)

- (20) Genetic standard deviation for average farrowing interval ($gsd\_d[20]$)

- (21) Genetic standard deviation for survival rate of piglets in nursery ($gsd\_d[21]$)

- (22) Genetic standard deviation for survival rate of animals in finishing ($gsd\_d[22]$)

- (23) Genetic standard deviation for average productive lifetime of sows measured in number of farrowings ($gsd\_d[22]$)

- (24) Genetic standard deviation for average productive lifetime of sows measured in years ($gsd\_d[24]$)

- (25) Genetic standard deviation for dressing percentage of finished animals ($gsd\_d[25]$)

- (26) Genetic standard deviation for average lean meat content in carcass ($gsd\_d[26]$)

- (27*) Genetic standard deviation for residual **daily** feed intake of piglets in nursery ($gsd\_d[27]$) (see Remark below)

- (28) Genetic standard deviation for feed conversion of piglets in nursery ($gsd\_d[28]$)

- (29*) Genetic standard deviation for residual **daily** feed intake of gilts in finishing ($gsd\_d[29]$) (see Remark below)

- (30) Genetic standard deviation for feed conversion of gilts in finishing ($gsd\_d[30]$)

- (31) Genetic standard deviation for number of sow teats ($gsd\_d[31]$)

- (32) Genetic standard deviation for semen volume ($gsd\_d[32]$)

- (33) Genetic standard deviation for sperm concentration ($gsd\_d[33]$)

- (34) Genetic standard deviation for percentage of spermatozoa with progressive motion (for motility) ($gsd\_d[34]$)

- (35) Genetic standard deviation for percentage of abnormal spermatozoa ($gsd\_d[35]$)

Remark to traits 27 and 29. The genetic standard deviations for traits 27 and 29 are per day whereas in the calculation of the economic values residual feed intake is defined for the whole nursery period or the whole finishing period. Therefore, the genetic standard deviations of these two traits must be converted to be in accordance with the units of the corresponding economic weights which is done automatically in the program after reading the input file and after the calculation of the length of the nursery period (variable $dP[5][0]$) and of the length of gilts finishing period (variable $dP[10][0]$):

$$
\begin{aligned}
gsd\_d[27] &= gsd\_d[27] \times dP[5][0] \\
gsd\_d[29] &= gsd\_d[29] \times dP[10][0]
\end{aligned}
\tag{3.1}
$$

. These converted values are printed only in file CHECKP*.

3.1.3 Files for data transfer between EWPIG2 runs for different breeds

These files are created automatically in breeding systems with crossing where more than one breed participate and a separate run of EWPIG2 is carried out for each breed and for the cross AB. **Do not edit these files.** They are both output and input files. Their detailed description is given in the manual for the program EWPIG2. There are files: BS2_AtoC, BS3_ABtoC,BS3_ABtoA, BS3_ABtoB, BS3_AtoB, BS4_ABtoC, BS4_ABtoA, BS4_ABtoB, BS4_ABtoD, BS4_CtoD and BS4_AtoB.

ERR.TXT is a special file which transfers the message if there has occurred an error in one of the preceding runs to the subsequent runs (see Subsection 3.3 for details).

3.1.4 TEXTP_OUT.TXT

This file contains text which is used for printing the results. It contains headings of sections of the results files, comments and names of variables the values of which are printed in the results files. For editing the file read carefully the remarks at the beginning of Chapter 3.

3.2 Input files for the program GFPIG

3.2.1 File PARAGFP.TXT

This file contains informations about breed the gene flow is run for and information for the calculation of relative economic weights for all breeds in all Breeding systems. The value of the parameter is always followed by its description. Modify the values of the parameter(s) according to your needs. The following parameters are read:

- Breed for which the number of discounted expressions and economic weights are calculated (variable *breed*)

  - 1: breed A
  - 2: breed B
  - 3: breed C
  - 4: breed D

/*The following parameter is read in all Breeding systems for breed A*/

- Genetic standard deviations (variable *gstdA*)

  - 0: of traits are not known or are not intended to be used for the calculation of relative economic weights
  - 1: for the direct and maternal traits and direct and maternal trait components are known and given in INPUTGFP03A.TXT
  - 2: of traits are known but only one value for each trait is given in IN-PUTGFP04A.TXT

/*The following parameter is read in Breeding systems 3 and 4 for breed B*/

- Genetic standard deviations (variable *gstdB*)

  - 0: of traits are not known or are not intended to be used for the calculation of relative economic weights
  - 1: for the direct and maternal traits and direct and maternal trait components are known and given in INPUTGFP03B.TXT
  - 2: of traits are known but only one value for each trait is given in IN-PUTGFP04B.TXT

/*The following parameter is read in Breeding systems 2 to 4 for breed C*/

- Genetic standard deviations (variable *gstdC*)

  - 0: of traits are not known or are not intended to be used for the calculation of relative economic weights
  - 1: for the direct and maternal traits and direct and maternal trait components are known and given in INPUTGFP03C.TXT
  - 2: of traits are known but only one value for each trait is given in IN-PUTGFP04C.TXT

/*The following parameter is read in Breeding system 4 for breed D*/

- Genetic standard deviations (variable *gstdD*)

  - 0: of traits are not known or are not intended to be used for the calculation of relative economic weights
  - 1: for the direct and maternal traits and direct and maternal trait components are known and given in INPUTGFP03D.TXT
  - 2: of traits are known but only one value for each trait is given in IN-PUTGFP04D.TXT

3.2.2 Input file INPUTGFP01.TXT for all breeds and all Breeding systems

This file contains general input parameters which are valid for all breeds (A, B, C and D) in the appropriate Breeding system. This file contains parameters needed for the calculation of relative economic weights of traits. The following selections are to be made (for explanation why this selection is needed see the Manual for EWPIG2, Subsection 8.7.1):

- Select between the following options for growth traits in pigs:

  - 0: Separate traits for individual growth phases of young animals are defined and used (traits 1 to 6)

- – 1: Only one lifetime growth trait from birth until slaughter is used (traits 7 or 8)

/*The following three selections should be made if the first selection was 0*/

- Select:

  - – 1: Average piglet weight at weaning at fixed age or
  - – 2: Average daily gain of piglets until weaning

- Select:

  - – 3: Weight of piglets at the end of the nursery phase or
  - – 4: Average daily gain of piglets in nursery until fixed age

- Select:

  - – 5: Average daily gain of of pigs in finishing to fixed slaughter weight or
  - – 6: Length of the finishing period until reaching target slaughter weight

/*The following selection should be made if the first selection was 1*/

- Select:

  - – 7: Average lifetime daily gain of animals from birth to slaughter after finishing or
  - – 8: Age at reaching target slaughter weight

/*The following selection should be always made*/

- Select a litter size trait:

  - – 9: Total number of piglets born or
  - – 10: Number of piglets born alive or
  - – 11: Number of piglets weaned

- Select a fertility trait for gilts:

  - – 15: Conception rate of gilts after the first mating
  - – 16: Total conception rate of gilts or
  - – 17: Average age at first farrowing

- Select a fertility trait for sows:

  - – 18: Conception rate of sows after the first mating averaged over all parities or
  - – 19: Total conception rate of sows averaged over all matings and all parities or
  - – 20: Average farrowing interval

- Select a trait for productive lifetime::

  - – 23: Average productive lifetime of sows measured in number of farrowings
  - – 24: Average productive lifetime of sows measured in years

- Select a trait for feed efficiency in nursery:

    - 27: Residual feed intake in nursery or
    - 28: Feed conversion in nursery

- Select a trait for feed efficiency in finishing:

    - 29: Residual feed intake in finishing or
    - 30: Feed conversion in finishing

3.2.3 Input file INPUTGFP02.TXT for all breeds within a Breeding system

This file contains general input parameters which are valid for all breeds (A, B, C, D) in all Breeding systems (1, 2, 3 and 4). The following variables are read:

- Discount rate per half a year (r)

- Length of the investment period (in numbers of half year periods) (l_inv)

3.2.4 Input files for breed A (for Breeding systems 1 to 4)

3.2.4.1 Input file INPUTGFP01A.TXT

This file is produced by the run of the program EWPIG2 for breed A in the appropriate Breeding system. It contains only numbers, no text. **Do not edit this file.** (For the description of these numbers see the Manual for GFPIG, Subsection 8.3.1.1.)

3.2.4.2 Input file INPUTGFP02A.TXT

This file contains input parameters for calculating the transmission matrix **P** for gene flow for all Breeding systems for breed A. When filling in the numbers you must know the number of age classes for sires and dams of breed A in the appropriate Breeding system, which you can easily calculated as described in the Manual for GFPIG, subsection 2.2.2. The following variables are read from the input file (for detailed description of these variables see the Manual GFPIG):

- Number of sex and age class within breed A for which the gene flow will be calculated (n_sac)

- Indicator variable #1 ($pgssA$). Insert 1, if the proportion of genes from the individual age classes of sires in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires in male progeny are calculated and automatically inserted by the program.

- Indicator variable #2 ($pgdsA$). Insert 1, if the proportion of genes from the individual age classes of dams in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams in male progeny are calculated and automatically inserted by the program.

- Proportions of genes from individual age classes of sires in male progeny (the path sires to sires, the numbers must sum to 0.5 ($P[1][1]$ to $P[1][acsAp]$). These values are only read if indicator variable #1 is set to 1. The number of values must be in accordance with the number of classes for sires used for pure-breeding (variable acsAp, see Subsection 2.2.2 in the Manual GFPIG).

- Proportions of genes from individual age classes of dams in male progeny (the path dams to sires, the numbers must sum to 0.5 ($P[1][acsAp + 1]$ to $P[1][acsAp+acdA]$). These values are only read if indicator variable #2 is set to 1. The number of values must be in accordance with the number of classes for dams (variable acdA, see Subsection 2.2.2 in the Manual GFPIG).

3.2.5 Input files for breed B (for Breeding systems 3 and 4)

3.2.5.1 Input file INPUTGFP01B.TXT

This file is produced by the run of the program EWPIG2 for breed B in Breeding systems 3 or 4. It contains only numbers, no text. **Do not edit this file.** (For the description of these numbers see the Manual for GFPIG, Subsection 8.3.2.1.).

3.2.5.2 Input file INPUTGFP02B.TXT

This file contains input parameters for calculating the transmission matrix **P** for gene flow for Breeding systems 3 and 4 for breed B. When filling in the numbers you must know the number of age classes for sires and dams of breed B in the appropriate Breeding system, which you can easily calculated as described in the Manual for GFPIG, subsection 2.2.2. The following variables are read from the input file (for detailed description of these variables see the Manual GFPIG):

- Number of sex and age class for which the gene flow will be calculated (n_sac) within the blocks of sub-matrices for breed B[15]

- Indicator variable #1 ($pgssB$). Insert 1, if the proportion of genes from the individual age classes of sires in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires in male progeny are calculated and automatically inserted by the program.

- Indicator variable #2 ($pgdsB$). Insert 1, if the proportion of genes from the individual age classes of dams in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams in male progeny are calculated and automatically inserted by the program.

- Proportions of genes from individual age classes of sires in male progeny (the path sires to sires, the numbers must sum to 0.5. ($P[acsAp+acdA+1][acsAp+ acdA + 1]$ to $P[acsAp + acdA + 1][acsAp + acdA + acsBp]$). These values are only read if indicator variable #1 is set to 1. The number of values must be in accordance with the number of classes for sires used for pure-breeding (variable acsBp, see Subsection 2.2.2 in the Manual GFPIG).

- Proportions of genes from individual age classes of dams in male progeny (the path dams to sires, the numbers must sum to 0.5. ($P[acsAp + acdA + 1][acsAp+acdA+acsBp+1]$ to $P[acsAp+acdA+1][acsAp+acdA+acsBp+ acdB]$). These values are only read if indicator variable #2 is set to 1. The number of values must be in accordance with the number of classes for dams (variable acdB, see Subsection 2.2.2 in the Manual GFPIG).

---

[15]E.g. if there are 5 sex-age-classes for sires B and 14 sex-age-classes for dams B, the number for n_sac must be in the range from 1 to 19.

3.2.6 Input files for breed C (for Breeding systems 2, 3 and 4)

3.2.6.1 Input file INPUTGFP01C.TXT

This file is produced by the run of the program EWPIG2 for breed C in the appropriate Breeding system. It contains only numbers, no text. **Do not edit this file.** (For the description of these numbers see the Manual for GFPIG, Subsection 8.3.3.1.).

3.2.6.2 Input file INPUTGFP02C.TXT

This file contains input parameters for calculating the transmission matrix **P** for gene flow for Breeding systems 2, 3 and 4 for breed C. When filling in the numbers you must know the number of age classes for sires and dams of breed C in the appropriate Breeding system, which you can easily calculated as described in the Manual for GFPIG, subsection 2.2.2. The following variables are read from the input file (for detailed description of these variables see the Manual GFPIG):

- Number of sex and age class for which the gene flow will be calculated (n_sac) within the blocks of sub-matrices for breed C[16]

- Indicator variable #1 ($pgssC$). Insert 1, if the proportion of genes from the individual age classes of sires in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires in male progeny are calculated and automatically inserted by the program.

- Indicator variable #2 ($pgdsC$). Insert 1, if the proportion of genes from the individual age classes of dams in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams in male progeny are calculated and automatically inserted by the program.

- Proportions of genes from individual age classes of sires in male progeny (the path sires to sires, the numbers must sum to 0.5. In Breeding system 2, these values are the following elements in matrix P: $P[acsAp + acdA + 1][acsAp + acdA + 1]$ to $P[acsAp + acdA + 1][acsAp + acdA + acsCp]$. In Breeding systems 3 and 4, these values are the following elements in matrix P: $P[acsAp + acdA + acsBp + acdB + 1][acsAp + acdA + acsBp + acdB + 1]$ to $P[acsAp + acdA + acsBp + acdB + 1][acsAp + acdA + acsBp + acdB + acsCp]$. These values are only read if indicator variable #1 is set to 1. The number of values must be in accordance with the number of classes for sires used for pure-breeding (variable acsCp, see Subsection 2.2.2 in the Manual GFPIG).

- Proportions of genes from individual age classes of dams in male progeny (the path dams to sires, the numbers must sum to 0.5. In Breeding system 2, these values are the following elements in matrix P: $P[acsAp + acdA + 1][acsAp + acdA + acsCp + 1]$ to $P[acsAp + acdA + 1][acsAp + acsCp + acdC]$. In Breeding systems 3 and 4, these values are the following elements in matrix P: $P[acsAp + acdA + acsBp + acdB + 1][acsAp + acdA + acsBp + acsCp + 1]$ to $P[acsAp + acdA + acsBp + acdB + 1][acsAp + acdA + acsBp + acsCp + acdC]$. These values are only read if indicator variable #2 is set to 1. The number of values must be in accordance with the number of classes for dams (variable acdC, see Subsection 2.2.2 in the Manual GFPIG).

---

[16]E.g. if there are 6 sex-age-classes for sires C and 10 sex-age-classes for dams C, the number for n_sac must be in the range from 1 to 16.

3.2.7   Input files for breed D (for Breeding system 4)

3.2.7.1   Input file INPUTGFP01D.TXT

This file is produced by the run of the program EWPIG2 for breed D in Breeding system 4. It contains only numbers, no text. **Do not edit this file.** (For the description of these numbers see the Manual for GFPIG, Subsection 8.3.4.1.).

3.2.7.2   Input file INPUTGFP02D.TXT

This file contains input parameters for calculating the transmission matrix $\mathbf{P}$ for gene flow for Breeding systems 4 for breed D. When filling in the numbers you must know the number of age classes for sires and dams of breed D in the appropriate Breeding system, which you can easily calculate from equations (**??**) and (**??**).

The following values are read from the input file:

- Number of sex and age class for which the gene flow will be calculated (n_sac) within the blocks of the sub-matrices for breed D [17]

- Indicator variable #1 ($pgssD$). Insert 1, if the proportion of genes from the individual age classes of sires in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires in male progeny are calculated and automatically inserted by the program.

- Indicator variable #2 ($pgdsD$). Insert 1, if the proportion of genes from the individual age classes of dams in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams in male progeny are calculated and automatically inserted by the program.

- Proportions of genes from individual age classes of sires in male progeny (the path sires to sires, the numbers must sum to 0.5. ($P[acsAp + acdA + acsBp + acdB + acsCp + acdC + 1][acsAp + acdA + acsBp + acdB + acsCp + acdC + 1]$ to $P[acsAp + acdA + acsBp + acdB + acsCp + acdC + 1][acsAp + acdA + acsBp + acdB + acsCp + acdC + acsDp]$). These values are only read if indicator variable #1 is set to 1. The number of values must be in accordance with the number of classes for sires used for pure-breeding (variable acsDp, see Subsection 2.2.2 in the Manual GFPIG).

- Proportions of genes from individual age classes of dams in male progeny (the path dams to sires, the numbers must sum to 0.5. ($P[acsAp + acdA + acsBp + acdB + acsCp + acdC + 1][acsAp + acdA + acsBp + acsCp + acdC + acsDp + 1]$ to $P[acsAp + acdA + acsBp + acdB + acsCp + acdC + 1][acsAp + acdA + acsBp + acsCp + acdC + acsDp + acdD]$). These values are only read if indicator variable #2 is set to 1. The number of values must be in accordance with the number of classes for dams (variable acdD, see Subsection 2.2.2 in the Manual GFPIG).

3.2.8   Input files for cross AB (for Breeding systems 3 and 4)

3.2.8.1   Input file INPUTGFP01AB.TXT

This file is produced by the run of the program EWPIG2 for cross AB in the appropriate Breeding system. It contains only numbers, no text. **Do not edit this file.** (For the description of these numbers see the Manual for GFPIG, Subsection 8.3.5.1.).

---

[17]E.g. if there are 5 sex-age-classes for sires D and 10 sex-age-classes for dams D, the number for n_sac must be in the range from 1 to 15.

3.2.9 Input files with general structure for all breeds

These input files are read for all breeds (A, B, C and D) in all Breeding system, but they are not read for cross AB.

3.2.9.1 Input files INPUTGFP03*.TXT

This file is read if the the parameter $std*$ in the input file PARAGFP.TXT is equal to 1. Structure of these files is the same for all breeds in all Breeding system. This file contains genetic standard deviation for direct ($gstd\_d[i]$) and maternal ($gstd\_m[i]$) traits or direct and maternal trait components for breed * (where * means breeds A, B, C and D). **Fill in genetic standard deviations for the traits you have selected in INPUTGFP01.TXT (see Subsection3.2.2) or which are calculated according the options in file PARAP*.TXT (trait number of teats and sperm quality traits, see Subsection 3.1.1.2) and ignore the genetic standard deviations for not selected traits (but do not delete the values you do not need).** If a trait has direct and maternal components, two values should be inserted, the first value for direct and the second value for maternal trait component. Otherwise one value should be given. The number of trait is given in parentheses.

- (1) Genetic standard deviations for direct and maternal components of the average piglet weight at weaning ($gstd\_d[1], gstd\_m[1]$)

- (2) Genetic standard deviation for direct and maternal component of the average daily gain of piglets until weaning ($gstd\_d[2], gstd\_m[2]$)

- (3) Genetic standard deviation for weight of piglets at the end of the nursery phase ($gstd\_d[3]$)

- (4) Genetic standard deviation for average daily gain of piglets in nursery ($gstd\_d[4]$)

- (5) Genetic standard deviation for average daily gain of pigs in finishing ($gstd\_d[5]$)

- (6) Genetic standard deviation for the length of the finishing period ($gstd\_d[6]$)

- (7) Genetic standard deviation for average lifetime daily gain of animals from birth to slaughter ($gstd\_d[7]$)

- (8) Genetic standard deviation for age at reaching target slaughter weight ($gstd\_d[8]$)

- (9) Genetic standard deviation for direct and maternal trait components of the trait total number of piglets born ($gstd\_d[9], gstd\_m[9]$)

- (10) Genetic standard deviation for direct and maternal trait components of the trait number of piglets born alive ($gstd\_d[10], gstd\_m[10]$)

- (11) Genetic standard deviation for direct and maternal trait components of the trait number of piglets weaned ($gstd\_d[11], gstd\_m[11]$)

- (12) Genetic standard deviation for direct and maternal trait components of the trait piglet survival rate at birth ($gstd\_d[12], gstd\_m[12]$)

- (13) Genetic standard deviation for direct and maternal trait components of the trait survival rate of piglets born alive until weaning ($gstd\_d[13], gstd\_m[13]$)

- (14) Genetic standard deviation for age of gilts at first mating ($gstd\_d[14]$)

- (15) Genetic standard deviation for conception rate of gilts after the first mating ($gstd\_d[15]$)

- (16) Genetic standard deviation for total conception rate of gilts ($gstd\_d[16]$)

- (17) Genetic standard deviation for average age at first farrowing ($gstd\_d[17]$)

- (18) Genetic standard deviation for conception rate of sows after the first mating averaged over all parities ($gstd\_m[18]$)

- (19) Genetic standard deviation for total conception rate of sows averaged over all matings and all parities ($gstd\_m[19]$)

- (20) Genetic standard deviation for average farrowing interval ($gstd\_m[20]$)

- (21) Genetic standard deviation for survival rate of piglets in nursery ($gstd\_d[21]$)

- (22) Genetic standard deviation for survival rate of animals in finishing ($gstd\_d[22]$)

- (23) Genetic standard deviation for average productive lifetime of sows measured in number of farrowings ($gstd\_m[23]$)

- (24) Genetic standard deviation for average productive lifetime of sows measured in years ($gstd\_m[24]$)

- (25) Genetic standard deviation for dressing percentage of finished animals ($gstd\_d[25]$)

- (26) Genetic standard deviation for average lean meat content in carcass ($gstd\_d[26]$)

- (27*) Genetic standard deviation for residual daily feed intake of piglets in nursery ($gstd\_d[27]$)

- (28) Genetic standard deviation for feed conversion of piglets in nursery ($gstd\_d[28]$)

- (29*) Genetic standard deviation for residual daily feed intake of gilts in finishing ($gstd\_d[29]$)

- (30) Genetic standard deviation for feed conversion of gilts in finishing ($gstd\_d[30]$)

- (31) Genetic standard deviation for number of sow teats ($gstd\_m[31]$)

- (32) Genetic standard deviation for semen volume ($gstd\_d[32]$)

- (33) Genetic standard deviation for sperm concentration ($gstd\_d[33]$)

- (34) Genetic standard deviation for percentage of spermatozoa with progressive motion (for motility) ($gstd\_d[34]$)

- (35) Genetic standard deviation for percentage of abnormal spermatozoa ($gstd\_d[35]$)

3.2.9.2   Input file INPUTGFP04*.TXT

This file is read if the the parameter $gstd*$ in the input file PARAGFP.TXT is equal to 2. This file contains genetic standard deviations of traits for breed * (where * means breeds A, B, C and D) when not differentiated in maternal and direct trait components. These genetic standard deviations are read as $gstd\_d[i]$ if the value of the variable $tt[i]$ is equal to 0 for trait i and as $gstd\_m[i]$ if the value of $tt[i]$ is equal to 1 for trait i (see Table 2.2 in the Manual GFPIG). The number of trait (index i) is given in parentheses. **Fill in genetic standard deviations for the traits**

you have selected in INPUTGFP01.TXT (see Subsection 3.2.2) or which are calculated according the options in file PARAP*.TXT (trait number of teats and sperm quality traits, see Subsection 3.1.1.2) and ignore the genetic standard deviations for not selected traits (but do not delete the values you do not need).

- (1) Genetic standard deviation for average piglet weight at weaning ($gstd\_m[1]$)

- (2) Genetic standard deviation for average daily gain of piglets until weaning ($gstd\_m[2]$)

- (3) Genetic standard deviation for weight of piglets at the end of the nursery phase ($gstd\_d[3]$)

- (4) Genetic standard deviation for average daily gain of piglets in nursery ($gstd\_d[4]$)

- (5) Genetic standard deviation for average daily gain of pigs in finishing ($gstd\_d[5]$)

- (6) Genetic standard deviation for the length of the finishing period ($gstd\_d[6]$)

- (7) Genetic standard deviation for average lifetime daily gain of animals from birth to slaughter ($gstd\_d[7]$)

- (8) Genetic standard deviation for age at reaching target slaughter weight ($gstd\_d[8]$)

- (9) Genetic standard deviation for total number of piglets born ($gstd\_m[9]$)

- (10) Genetic standard deviation for number of piglets born alive ($gstd\_m[10]$)

- (11) Genetic standard deviation for number of piglets weaned ($gstd\_m[11]$)

- (12) Genetic standard deviation for piglet survival rate at birth ($gstd\_m[12]$)

- (13) Genetic standard deviation for survival rate of piglets born alive until weaning ($gstd\_m[13]$)

- (14) Genetic standard deviation for age of gilts at first mating ($gstd\_d[14]$)

- (15) Genetic standard deviation for conception rate of gilts after the first mating ($gstd\_d[15]$)

- (16) Genetic standard deviation for total conception rate of gilts ($gstd\_d[16]$)

- (17) Genetic standard deviation for average age at first farrowing ($gstd\_d[17]$)

- (18) Genetic standard deviation for conception rate of sows after the first mating averaged over all parities ($gstd\_m[18]$)

- (19) Genetic standard deviation for total conception rate of sows averaged over all matings and all parities ($gstd\_m[19]$)

- (20) Genetic standard deviation for average farrowing interval ($gstd\_m[20]$)

- (21) Genetic standard deviation for survival rate of piglets in nursery ($gstd\_d[21]$)

- (22) Genetic standard deviation for survival rate of animals in finishing ($gstd\_d[22]$)

- (23) Genetic standard deviation for average productive lifetime of sows measured in number of farrowings ($gstd\_m[23]$)

- (24) Genetic standard deviation for average productive lifetime of sows measured in years ($gstd\_m[24]$)

- (25) Genetic standard deviation for dressing percentage of finished animals ($gstd\_d[25]$)

- (26) Genetic standard deviation for average lean meat content in carcass ($gstd\_d[26]$)

- (27) Genetic standard deviation for residual daily feed intake of piglets in nursery ($gstd\_d[27]$)

- (28) Genetic standard deviation for feed conversion of piglets in nursery ($gstd\_d[28]$)

- (29) Genetic standard deviation for residual daily feed intake of gilts in finishing ($gstd\_d[29]$)

- (30) Genetic standard deviation for feed conversion of gilts in finishing ($gstd\_d[30]$)

- (31) Genetic standard deviation for number of sow teats ($gstd\_m[31]$)

- (32) Genetic standard deviation for semen volume ($gstd\_d[32]$)

- (33) Genetic standard deviation for sperm concentration ($gstd\_d[33]$)

- (34) Genetic standard deviation for percentage of spermatozoa with progressive motion (for motility) ($gstd\_d[34]$)

- (35) Genetic standard deviation for percentage of abnormal spermatozoa ($gstd\_d[35]$)

3.2.10   TEXTGFP_OUT.TXT

This file contains texts which are used for printing the results. It contains headings of sections of the results files, comments and names of variables the values of which are printed in the results files. For editing the file read carefully the remarks at the beginning of Chapter 3 on page 26.

3.3   File ERR.TXT in programs EWPIG and GFPIG

This file contains only the value of the variable *errmess*. At the start of each calculation of the program EWPIG2 this file is read with the value 0 for *errmess*. If there occurs an error during the calculation of the program EWPIG2, the value of *errmess* is changed to 1 and written to the file ERROR.TXT. In the next run of EWPIG2 or in the run of the program GFPIG, the file ERR.TXT is read again. If *errmess* = 1, all subsequent programs including GFPIG will stop and write an error message.

Then ERR.TXT causes the following runs to stop and to give the following message:

```
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
The calculation has stopped because there was an error in the run for
   breed (cross) x[18].
Correct the input files for this breed or cross and restart the program.
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

---

[18]x stands for the name of the breed or cross which may be A, B, C, D or AB.

The file contains the following two variables:

- *err*1: Indicator variable, if there was an error in the given run or in a preceding run of EWPIG2; the variable takes two values:

  - 0: no error

  - 1: error

- *breed*1: Breed where the error occurred; this variable may take the same values as the variable *breed* (see the codes for *breed* in Subsection 3.1.1.1).

Chapter 4

Output files from EWPIG2 and GFPIG

4.1 Results files from the program EWPIG2

The name of the file the results are written to is automatically generated. It has the structure reP*# where '*' is the breed or cross for which the calculation is carried out (A, B, C, D or AB) and '#' is the number of the run of EWPIG2 (01 in Breeding System 1, 01 to 02 in Breeding System 2, 01 to 04 in Breeding System 3 and 01 to 05 in Breeding System 4). Therefore, in Breeding System 1 only the results file rePA01 is generated, in Breeding System 2 the files rePA01 and rePC02 are produced etc. See Table 4.1 for a survey of results files printed for the individual breeding systems.

If you want to carry out more calculations in the same directory, copy the results files first to a secure place before starting a new calculation, otherwise they will be overwritten by the new results.

The first part of the results file contains information on the version of the program, copyright and contact to the authors and the values of the system variables read from P00P.TXT and PARAP*.TXT (see Section 3.1.1). The second part of the file copies more or less the data input files INPUTP#*.TXT where '#' is to be replaced by the corresponding numbers (01, 02, 03 etc.) and '*' by the breed or cross (A, B, C, D, AB or CD). The information read from the input files is selected according to the parameters given in the parameter file and in certain data input files. Therefore, the results file does not contain a simple copy of the input files, but only data from input files which will be needed for the given calculation.

The third part of the results file contains the results in the following order (values for animal groups which do not exist in the specific calculation are not printed):

- Structure of the sow herd

  - Relative frequencies of sow categories (i.e. number of sows of each category per sow per reproductive cycle; for the explanation of the categories see Section 6.2)

  - Relative frequencies of sows in individual reproductive cycles (i.e. number of sows on each parity per sow per reproductive cycle)

- Survival and reproduction characteristics of the sow herd

  - Sow mortality and culling rate, productive lifetime etc.

- – Litter size (i.e. number of piglet born total, born alive, weaned) in each parity and averaged over parities

- – Average number of litters per sow per year

- – Average number of piglet born total, born alive and weaned per sow per year

- – Survival rate of piglets

- – Sow conception rate after each farrowing andconception rate averaged over parities

- Survival and reproduction characteristics of replacement gilts

- Structure and characteristics of the boar population

- Structure and survival characteristics of progeny (for the explanation of progeny categories see Section 6.3).

- Growth of animals in individual time periods

  - – Growth of piglets

  - – Growth of breeding gilts

  - – Growth of breeding boars in rearing

  - – Growth of animals in finishing

  - – Growth of sows in the herd and change in body weight during lactation and pregnancy

  - – Further variables useful for a validity check of input parameters (protein and lipid content in empty body weight of the individual progeny and sow categories and in boars if they exist in breeding units)

  - – Feed conversion rations in nursery and in finishing

  - – Lean meat content in carcasses of finished animals calculated from the slaughterhouse data

- Daily metabolisable energy, dry matter and fresh feed matter requirements, total metabolisable energy and feed requirements from all feeding ration which exist in the specific calculation (for the definition of feeding rations for all animal groups see Section ...), the length of the periods these feeding rations are given to the animals, feed and water costs and the total length of period these costs are calculated for all categories (groups) of

  - – progeny

  - – pregnant, lactating and open sows

  - – boars in the herds (used for natural mating and oestrus stimulation)

- Total nutrition (feed and water) costs for the individual facilities of the production system (breeding, nursery, finishing units and unit for rearing of breeding animals) expressed per farrowed sow per reproductive cycle

- Non-feed costs and total costs

  - – Non-feed costs items for different animal groups and for all facilities of the production system

  - – Total costs for all facilities

  - – Several cost items expressed in different ways (e.g. per sow, per finished animal, per kg carcass weight)

- Revenues

  - – Revenues from culled sows
  - – Revenues from culled end-of-cycle boars
  - – Revenues from progeny
    - ∗ Revenues from culled breeding animals
    - ∗ Revenues from finished animals
    - ∗ Revenues from animals exported or sold to other links of the breeding system
  - – Total revenues
  - – Several revenue items expressed in different ways (e.g. per sow, per finished animal, per kg carcass weight)

- Total profit and profitability

- Marginal economic values

- Approximate economic weights (***not printed in the run for cross AB and not printed for the option*** $gf = 1$ in files INPUTPBS#.TXT, see Section 3.1.2.1)

  - – Absolute approximate economic weights
  - – Standardized approximate economic weights
  - – Relative approximate economic weights

4.2 Files listing the values of all variables at the end of the program EWPIG2 and before calculating economic values with this program

A further output of each program run is a file where the values of all variables and constants (except some index variables and temporary variables) of the program are listed in alphabetic order. (The names of all variables are given in Appendix B in the Manual of the program EWPIG2). The name of the file is automatically generated and has the form CHECKP*# where '*' is the breed or cross for which the calculation is carried out (A, B, C, D or AB) and '#' is the number of the run of EWPIG2 (01 in Breeding System 1, 01 to 02 in Breeding System 2, 01 to 04 in Breeding System 3 and 01 to 05 in Breeding System 4). See Table 4.1 for a survey of those files printed for the individual breeding systems.

The files CHECKP*# deliver more complete information than the results files, but the information given in the results files should normally be sufficient for the user. However, the files CHECKP*# may be useful for a further development of the program. For more details about these files see Manual of the program EWPIG2, Section 11.5.

Finally, there is an output of each program run where the values of all variables and constants (except some index variables and temporary variables) of the program listed in alphabetic order are printed before starting the calculation of economic values. The name of the file is automatically generated and has the form CHECKP*#a where '*' is the breed or cross for which the calculation is carried out

Table 4.1: Survey of the names of files printing the results (the files reP*# print the results in a form easily readable; the files CHECKP*# print the values of all variables at the end of the calculations in alphabetic order; the files CHECKP*#a print the values of all variables before the calculation of economic values in alphabetic order)

Breeding System	Breed or cross	File names
1	A	rePA01, CHECKPA01, CHECKPA01a
2	A	rePA01, CHECKPA01, CHECKPA01a
	C	rePC02, CHECKPC02, CHECKPC02a
3	AB	rePAB01, CHECKPAB01, CHECKPAB01a
	C	rePC02, CHECKPC02, CHECKPC02a
	A	rePA03, CHECKPA03, CHECKPA03a
	B	rePB04, CHECKPB04, CHECKPB04a
4	AB	rePAB01, CHECKPAB01, CHECKPAB01a
	C	rePC02, CHECKPC02, CHECKPC02a
	D	rePD03, CHECKPD03, CHECKPD03a
	A	rePA04, CHECKPA04, CHECKPA04a
	B	rePB05, CHECKPB05, CHECKPB05a

(A, B, C, D or AB) and '#' is the number of the run of EWPIG2 (01 in Breeding System 1, 01 to 02 in Breeding System 2, 01 to 04 in Breeding System 3 and 01 to 05 in Breeding System 4). See Table 4.1 for a survey of those files printed for the individual breeding systems. The files CHECKP*#a may be of interest for people who want to work on a further development of the program (for details see Manual of the program EWPIG2, Section 11.6).

4.3   Results files from the program GFPIG

The name of the file the results are written to is fixed to *reGFP* within each Breeding system.

> *If you want to carry out more calculations for different breed in a Breeding system, copy the results files first to a secure place or rename it before starting a new calculation, otherwise they will be overwritten by the new results.*

The first part of the file contains information on the version of the program, copyright and contact to the authors and the values of the system variables read from P00P.TXT and PARAGFP.TXT. The second part of the file copies more or less the data input files INPUTGFP01.TXT, INPUTGFP02.TXT and files INPUT-GFP#*.TXT where # is to be replaced by the corresponding numbers 01 to 04 and * stand for sow breed A, B, C, D. For cross-bred sows AB only files 01 and 02 exist. The information read from the input files is selected according to the parameters given in the parameter files. Therefore, the results file does not contain a simple copy of the input files, but only data from input files which will be needed for the given calculation.

The third part of the results file contains the results in the following order:

- Number of Breeding system, sex and age class of breed, economic weights are calculated for, and the length of investment period

- Cumulative number of discounted expressions in all sex and age classes of the selected breed at the end of the investment period

- Economic weights for direct and maternal traits or direct and maternal components of the individual traits expressed in monetary units per unit of trait and per sow in the whole Breeding system

- Economic weights per genetic standard deviation for direct and maternal traits or direct and maternal components of the individual traits and per sow in the whole breeding system

- Relative economic weights

  - Standardized economic weights for for direct and maternal traits or direct and maternal trait components as percentage of the sum of absolute values of standardized economic values for direct and maternal traits or direct and maternal trait components, respectively

  - Standardized economic weights for direct or maternal trait components as percentage of the sum of absolute values of standardized economic values for both direct and maternal traits or direct and maternal trait components

The last two values are printed only if genetic standard deviations for direct and maternal traits or direct and maternal components are known, i.e. for the option in file PARAGFP $std* > 0$, where * stand for the sow breed A, B, C or D).

4.4   File listing the values of all variables at the end of the program GFPIG

The file CHECKGFP is mainly thought as a help in programming. The file contains only the names and the values of all variables in alphabetic order without further explaining text. The names of all variables are given in Appendix B in the Manual of GFPIG.

Remark.   A dense network of conditions was used in both programs to ensure printing out only the items relevant for the given production systems. But it cannot fully be guaranteed that no variables not meaningful for the given calculation slipped through the meshes. In these cases don't worry, as the values of these variables are (hopefully) ignored in the calculation.

Chapter 5

Basic description of the modeled breeding systems

The program EWPIG2 serves for the calculation of economic values and approximate or true economic weights for breeds involved in four different breeding systems. Next to a pure-bred system, cross-bred systems with two-way, three-way and four-way crosses are handled. Throughout, capital letters A and B are used for dam breeds and C and D for sire breeds.

When modeling the (sub)system for any breed involved in a particular breeding system, it is assumed that replacement gilts and boars may be purchased (only cross-bred gilts or boars for crossing) or reared within the system (pure-breed gilts and boars for pure-breeding). The pig breeding systems are often composed of different breeding levels (e.g. nucleus, multiplier and commercial tiers). However, in the model for the calculation of marginal economic values of traits, all sows of a breed (whether kept in one or more tiers) or cross-bred sows of a given combination of breeds build a single unit (one link of the whole pork production chain). That means, within each breed, at least a part of the pure-bred sows always produce pure-bred female and male replacements and a part of them can produce cross-bred females and/or males used as breeding stocks in other links of the pork production chain or as grow-finishing pigs. No import of breeding females for replacement from outside the system is assumed, but import of some breeding boars can be considered. The possibility to export surplus breeding gilts or boars or nursery pigs (feeder pigs) is included in the model.

5.1   Breeding System 1: Pure-bred system

Only one breed is considered in this breeding system and, without loss of generality, the capital letter "A" is used to designate this breed; this letter is used at the end of the names of input files and of several variables to make clear that these variables refer to breed A. Considering this breeding system, the sow population can be kept in one or more tiers (nucleus, multiplier and commercial herds can be distinguished). Fattening of pigs can be integrated with production of weaner and nursery piglets or can be done in separate units (fattening enterprises). However, as stated in the introduction to this Chapter, all breeding tiers and production units are considered as one closed population producing gilts for own replacement, boars for natural mating or artificial insemination and grow-finishing pigs for pork production when calculating the economic values of traits (see Fig. 5.1).

Calculating the economic values and approximate economic weights of traits for this system, only one run of program EWPIG2 is needed. Calculating the

../../DOCUME\unhbox \voidb@x \penalty \@M \ 1/EW/TEXT/FIGURES/fig1.eps
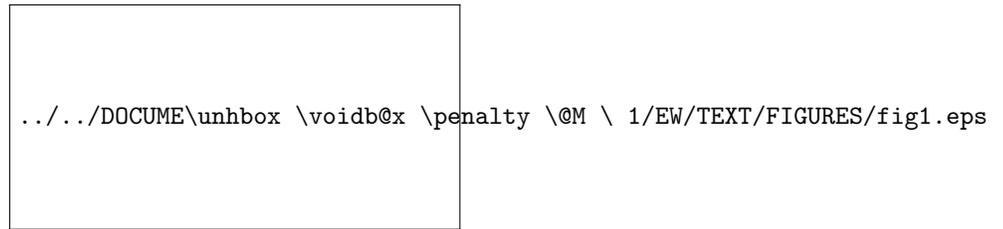
Figure 5.1: Pure-bred system of breed A

true economic weights of traits or of direct and maternal trait components for this system, after running EWPIG2, the program GFPIG must be run which is controlled by the users with variable gf in INPUTPBS1.TXT.

5.2 Breeding System 2: Two-way terminal crossing

In this breeding system, a specialized dam breed (designated as breed A) and a sire breed (designated as breed C) are assumed. The numbers of sows of breeds A and C are not calculated by the program (i.e. the crossing system is not optimized), but are given by the user of the program in the file INPUTPBS2.TXT (see Subsection 3.1.2.1) on the basis of the real sizes of these breeds in the evaluated pork production chain. For each breed, separate input files are used the names of which end with capital letters A and C to refer to the appropriate breed.

A part of sows of breed A produce pure-bred gilts and boars for own replacement (again, more tiers than one can be distinguished) and a part of sows A are mated with purchased boars (or inseminated with sperm from boars) of breed C to produce cross-bred offspring for fattening. Surplus pure-bred offspring are also fattened. The sows of the sire breed C produce gilts and boars for own replacement and boars for terminal crossing with sows of breed A (see Figure 5.2).

../../DOCUME\unhbox \voidb@x \penalty \@M \ 1/EW/TEXT/FIGURES/fig2.eps
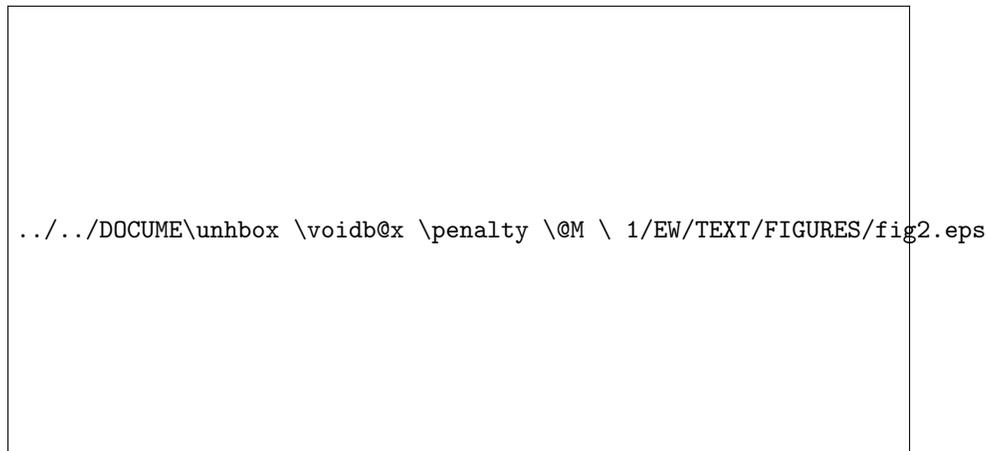
Figure 5.2: Two-way crossing system

Two runs of the program EWPIG2 are needed in this breeding system, the first run is for breed A and the second one for breed C. The input parameters age and weight for boars of breed C, which are used in the program run for breed A, are directly read from the input files for breed C. The numbers of boars or sperm doses needed for crossing are calculated running program EWPIG2 for breed A and

written to the transfer file BS2_AtoC.TXT which is read in the following run of EWPIG2 which is for breed C.

Because a separate marketing chain can exist between breed C and breed A, i.e. the price for selling boars C in production system with sows C can differ from the price for purchasing boars in production system with sows A, both prices are input parameters (in INPUTP12A.TXT or INPUTP17C.TXT, respectively) as they may differ from each other.

If artificial insemination is the only mating system used, the numbers of boars A and C that must be sold to AI stations is calculated on the basis of the number of sperm doses produced per boar of both breeds per time unit. The prices of sperm doses are input parameters in both subsystems with breed A and C. A combination of natural mating and AI is allowed.

Calculating the economic values and approximate economic weights of traits for this system, only runs of program EWPIG2 are needed. Calculating the true economic weights of traits or for direct and maternal trait components for this system, after running EWPIG2, the program GFPIG must be run which is controlled by the users with variable gf in INPUTPBS2.TXT.

5.3 Breeding System 3: Three-way crossing

In this breeding system, two specialized dam breeds, designated as A and B are used. These two breeds are crossed to produce AB sows, where breed A is assumed to be in dam position and breed B in sire position. A sire breed (designated as C) is then used to produce the final three-way crosses (slaughter animals). The numbers of sows of breeds A, B, C and of cross-bred sows AB are not calculated by the program (i.e. the crossing system is not optimized), but are input parameters in file INPUTBS3.TXT (see Subsection 3.1.2.1); they should reflect the real sizes of these breeds and crosses in the evaluated pork production chain.

Sows of dam breed B produce gilts and boars for own replacement and boars for crossing with sows of breed A. A part of sows of dam breed A produce pure-bred gilts and boars for own replacement and a second part of sows A are mated with purchased boars (or inseminated with sperm) of breed B to produce AB breeding females for the last link of the pork production chain, i.e. for herds with cross-bred sows AB which are used for terminal crossing with boars of sire breed C. Sows of sire breed C produce gilts and boars for own replacement and boars for crossing with sows AB. All offspring of AB sows are fattened. The surplus pure-bred offspring of breeds A, B and C and the cross-bred male offspring or surplus cross-bred female offspring of breed A are also fattened (see Fig. 5.3). In each breed, again more than one breeding tiers can be distinguished, but all these tiers within a breed are handled as one unit of the whole pork production chain.

In the program, for each breed and for the system with AB sows, separate input files are used which names end with capital letters A, B, C and AB. Four runs of the program EWPIG2 are needed to create connections among the four links of the pork production chain:

- The first run is done for cross AB, while some input parameters (i.e. age, weight and price for boars) needed for this run are also read from two input files for breed C (INPUTP04C.TXT and INPUTP08C.TXT). The price of purchased AB gilts is read from input file INPUTP18A.TXT for breed A. Several parameters calculated in this run are written to files BS3_ABtoC, BS3_ABtoA and BS3_ABtoB (see Subsections ??, ?? and ??, respectively, for details) to transfer them to the subsequent runs for breeds C, A and B, respectively.

../../DOCUME\unhbox \voidb@x \penalty \@M \ 1/EW/TEXT/FIGURES/fig3.eps
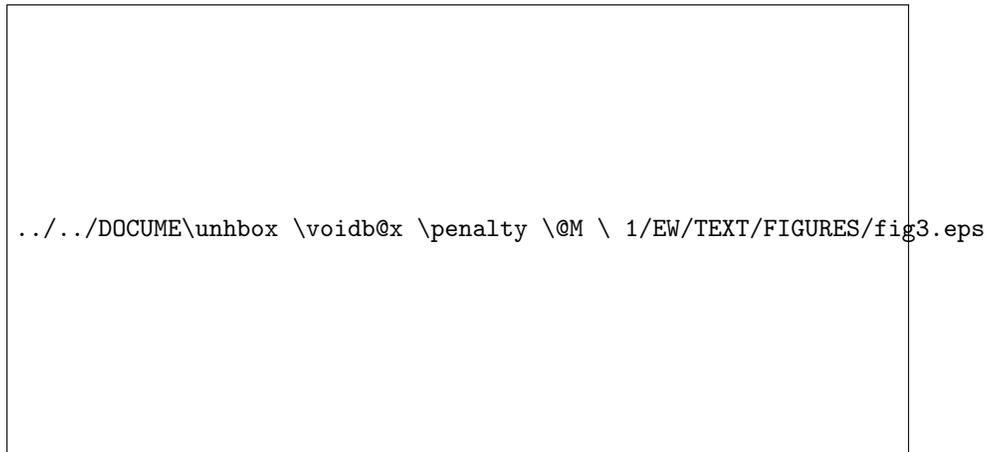
Figure 5.3: Three-way crossing system. A and B are dam breeds, B is used in sire position for the production of AB sows, boars of the sire breed C are used to produce the final three-way crosses ABxC (slaughter animals).

- The second run is for breed C.

- The third run is for breed A where some input parameters concerning boars of breed B are also read from two input files for breed B (INPUTP04B.TXT and INPUTP08B.TXT). Several parameters calculated in this run are written to file BS3_AtoB (see Subsection **??** for details) to transfer them to the subsequent run for breed B.

- The fourth and last run is for breed B.

Calculating the economic values and approximate economic weights of traits for this system, only runs of program EWPIG2 are needed. Calculating the true economic weights of traits or for direct and maternal trait components for this system, after running EWPIG2, the program GFPIG must be run which is controlled by the users with variable gf in INPUTPBS3.TXT.

5.4   Breeding System 4: Four-way crossing

In this breeding system, again two specialized dam breeds, designated as A and B, are used. These two breeds are crossed to produce AB sows, where breed A is assumed to be in dam position and breed B in sire position. Instead of one sire breed as in the three-way crossing system, two specialized sire breeds, say C and D, are used. They are crossed to produce CD boars where animals of breed C are in dam position and animals of breed D are in sire position. The final four-way slaughter animals are produced by crossing AB sows with CD boars (see Fig. 5.4). The numbers of sows of breeds A, B, C and D and of cross AB are not calculated by the program (i.e. the crossing system is not optimized), but are given by the user of the program on the basis of the real sizes of these breeds in the evaluated pork production chain in file INPUTPBS4.TXT (see Subsection 3.1.2.1).

In the program, for each breed and for the system with AB sows, separate input files are used which names end with capital letters A, B, C, D and AB. Some inputs needed for CD boars are given in a file ending with capital letters CD. Five runs of the program EWPIG2 are needed to create connections among the five links of the pork production chain:

../../DOCUME\unhbox \voidb@x \penalty \@M \ 1/EW/TEXT/FIGURES/fig4.eps
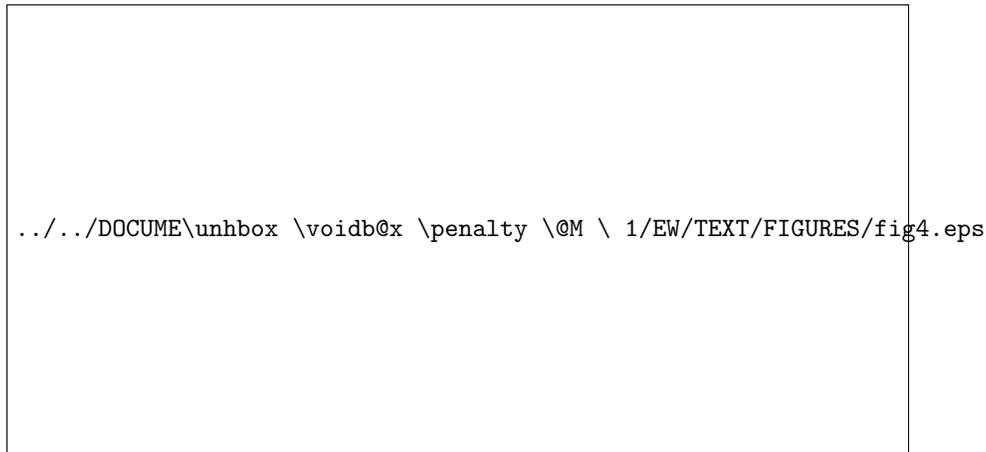
Figure 5.4: Four-way crossing system. A and B are dam breeds, C and D are sire breeds

- The first run is done for cross AB, while some input parameters (i.e. age, weight and price for boars) needed for this run are also read from an input files for breed C (INPUTP08C.TXT) and a special file for CD boars (IN-PUTP04CD.TXT). The price of purchased AB gilts is read from input file INPUTP18A.TXT for breed A. Several parameters calculated in this run are written to files BS4_ABtoC, BS4_ABtoA, BS4_ABtoB and BS4_ABtoD (see Subsections **??**, **??**, **??** and **??**, respectively, for details) to transfer them to the subsequent runs for breeds C, D, A and B, respectively.

- The second run is for breed C. Several parameters calculated in this run are written to file BS4_CtoD (see Subsection **??**) for the subsequent run of breed D.

- The third run is for breed D.

- The fourth run is for breed A where some input parameters concerning boars of breed B are also read from two input files for breed B (INPUTP04B.TXT and INPUTP08B.TXT). Several parameters calculated in this run are written to file BS4_AtoB (see Subsection **??** for details) to transfer them to the subsequent run for breed B.

- The fifth and last run is for breed B.

Calculating the economic values and approximate economic weights of traits for this system, only runs of program EWPIG2 are needed. Calculating the true economic weights of traits or for direct and maternal trait components for this system, after running EWPIG2, the program GFPIG must be run which is controlled by the users with variable gf in INPUTPBS4.TXT.

Chapter 6

Description of the production system

The bio-economic model of the integrated pig production system includes the whole production system in the case of pure-breeding. In the case of cross-breeding, each link of the whole pork production chain (each breed) is first modeled separately and later on connected. The model is mostly deterministic and static; performances of animals of each involved breed are represented by their population means, only phenotypic variations in slaughter weight, carcass weight and carcass quality (described by the distribution over commercial classes) are included. In all breeding systems, a fixed number of sow farrowing places in each breed is assumed. The model is non-integer, that means, fractions of animals are allowed.

6.1 Structure of the integrated production system

The assumed structure of an integrated pure-bred production system is shown in Fig. 6.1. The structure of a single production link (with specific breed) in a cross-breeding system is similar to the structure of a pure-bred system as shown in Fig. 6.1, but in some links of the production chain (e.g. in the last link of the production chain with cross-bred females AB), gilts for replacement and/or boars (or their sperm) for crossing are purchased from other links of the cross-breeding system.

Generally, each production system comprises four production units: breeding unit, nursery unit, finishing unit, and a unit for rearing breeding gilts and boars, although this last unit is absent from the link with crossbred sows in the three-way and four-way crossing systems. The breeding unit is visualized on the left side of Fig. 6.1. It includes mainly farrowing, service, and gestation facilities. When boars are used for natural mating or estrus stimulation and replacement gilts are reared at separate farms, facilities for housing boars and quarantine facilities are parts of the breeding unit. The main events in breeding unit, illustrated in Fig. 6.1, are farrowing, weaning, the first and the following matings, conception, culling sows and gilts for different reasons, and dying of animals. On the right side of Fig. 6.1, the nursery unit (for feeder pigs), the finishing unit and the unit for rearing of breeding gilts and boars (replacements) are illustrated. Thus, each link of a breeding system is treated as an integrated production system regardless of whether the mentioned units are located at one or more farms or enterprises. Each link's breeding unit includes sows with piglets until weaning, replacement gilts from the moment of their introducing in the sow herd, and boars for natural mating and estrus stimulation. After piglet weaning, sows that have reached the maximum number of farrowings specified by farmers, sows with health problems or with low litter size, and sows

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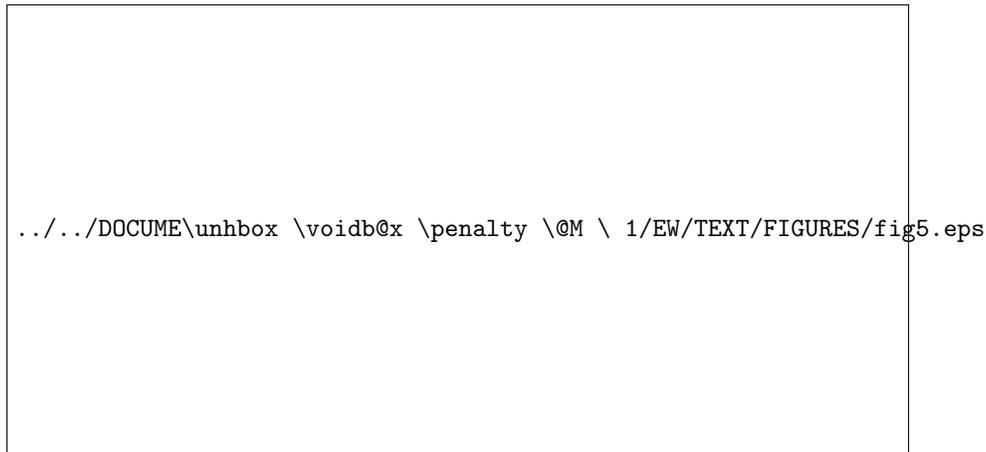
Figure 6.1: Integrated pork production system

that do not display heat are culled. The remaining sows are mated in their first heat after weaning and those that are not pregnant are mated repeatedly until the maximum number of matings allowed for a sow by farmers is reached. The average interval between two subsequent matings is an input parameter which depends on the interval between two oestruses (its length is assumed to be 21 days), on the oestrus detection rate and on the rate of embryonic mortality causing sows to return to oestrus after some months of pregnancy. To replace sows that died or were culled, replacement gilts are included in the breeding unit and mated in their second or third heat. Culled or dead sows are not replaced immediately, but after some delay until a new reproductive cycle restarts, to synchronize breeding and farrowing. Gilts that return to estrus after the first mating are mated repeatedly until the maximum number of matings allowed per gilt by farmers is reached. Gilts not showing heat and gilts that fail to conceive are culled. Sows and gilts determined for culling can remain on the farm until they are sent to the slaughterhouse.

The number of replacement gilts entering the breeding unit per farrowing interval is therefore a function of the conception rate of gilts and sows and of sow mortality and culling rates. The breeding of females can be done by artificial insemination, natural mating or by combination of both. Within one heat, one or more re-inseminations can be applied. Besides of natural mating, boars can be kept in the herds also for oestrus stimulation.

For the offspring of sows, the following stages are distinguished: weaner (from birth to weaning at constant weaning age), nursery or feeder pigs (from weaning to constant feeder pig age), grow-finish pigs (from nursery to slaughter at constant slaughter weight, i.e. fattening of females, males or castrates[1]), raising of breeding stock (breeding females and males for replacement from nursery to entering breeding units of sow herds or to sale).

The production facility can be based on 2 or 3 sites (in one or more enterprises). A two-site facility has nurseries attached to or on the same site as the breeding unit, whereas a 3-site production unit has nurseries in a separate location to both breeding and growing-finishing. In our bio-economic model, all these sites are taken as one integrated production unit (one link in a cross-breeding system).

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[1]The name castrates is used in this manual and in the program for castrated male pigs, i.e. for barrows

6.2   Structure of the sow herds

The structure of the sow population (sow herds) of a breed or crossbreed in the stationary state was calculated using a simple Markov chain model with culling probabilities as found empirically and not as a result of optimization (for details see Manual for EWPIG2). Herd dynamics were described in terms of the states a sow can pass during her life (these states are called sow categories in the program) and the probabilities of possible transitions between them.

The sow categories (sow states) are related to each reproductive cycle of sows that cover the interval between two subsequent farrowings. The maximal number of reproductive cycles (i.e the maximal number of farrowings) is an input parameter (RR) which is expected to be in the range between 6 to 15. A replacement female enters the farrowing group of sows at her first farrowing and stays in the herd until she is replaced or has reached the maximum number of reproductive cycles.

Each sow category (sow state) is characterised by a combination of two state-variables: *reproductive-cycle-number (parity number)* i $(i = 1, ..., RR)$ and *survival-class* j the sow is in within the given reproductive cycle.

The five survival classes of sows within reproductive cycle i $(i = 1, ...RR - 1)$ are defined as follows (the time a sow in the given survival class is staying in the herd is given in parentheses):

1   Sows that died between farrowing and piglet weaning (from farrowing to death)

2   Sows culled after piglet weaning for health problems or low litter size, without being mated (from farrowing to culling)

3   Sows culled after the maximal number of matings for failure to conceive (from farrowing to culling)

4   Sows that conceived but died within the period from conception to farrowing (from farrowing to death)

5   Sows conceiving and completing the current reproductive cycle and be-ginningentered a new reproductive cycle at farrowing (whole farrowing interval)

In the last reproductive cycle $(i = RR)$, only two survival-classes are defined:

1   Sows that died between farrowing and piglet weaning (from farrowing to death)

2   Barren sows culled after piglet weaning for age (from farrowing to culling)

The total number of states (i.e. total number of sow categories) (TS) is therefore

$$TS = 5 \times (RR - 1) + 2 \ . \tag{6.1}$$

There is a farrowing at the beginning of each possible state. At the end of a state, the sow is either died (or culled), followed by a transition of the system to parity number one (i.e. replacement of the sow by a gilt) or, alternatively, farrowing interval is completed and a transition of the system to the next parity number takes place (i.e. the same sow start a new parity). Because the died or culled sows are not replaced immediatelly (a synchronisation of farrowings is assumed), the amount of thime needed for a transition from one state to the next (the stage length) is the average farrowing interval.

The definition of the categories (states) of sows is the first step on the way to the structure of the sow herd. In the next step, the probabilities of possible transitions between the sow categories (sow states) must be calculated which are the elements $ts[i][j]$ of the transition matrix $\mathbf{T_S}$. For details see Manual of the program EWPIG2 version 3.0.0 (Section 3.2)

The number of sows of each category (expressed as relative frequencies per sow in the herd) is the first result of the calculation of the program EWPIG, which is printed in the result file in Section 3.1.1. From these numbers, the relative frequencies of sows in individual reproductive cycles is calculated, which is printed in the next Section of the result file (3.1.2). See also the description of the results files in Section 4.1.

6.3   Structure of progeny born in sow herds and of purchased gilts or boars

Categories of progeny are formed in accordance with the phases of pork production, i.e. piglets till weaning, piglets in nursery, grow-finish pigs, breeding gilts and boars are distinguished. The sex ratio and the fraction of castrated male piglets (castrates) in the litters at the end of the nursery phase are input parameters (see input file INPUTP05*.TXT on page 38). The frequency of stillborn piglets, piglet losses till weaning and in nursery is not distinguished between sexes. Each progeny can be of two breeding types (genotypes), pure-bred ($j = 0$) or cross-bred ($j = 1$). Some categories of progeny are missing in specific breeding systems (e.g. in Breeding System 1, only pure-bred categories exist). The following progeny categories born in the sow herds are defined (the time in which the category exists is given in parentheses. The number of the category is printed in the results file in Section 3.5.1:

1. Stillborn piglets (0)

2. Piglets died from birth till weaning (birth to death)

3. Piglets survived from birth until weaning at fixed age (birth to weaning)

4. Piglets died in the nursery phase (weaning to death)

5. Piglets alive from weaning to the end of the nursery phase (from weaning to the end of the nursery phase)

6. Female piglets sold (exported) after the nursery phase outside the evaluated breeding system (0)

7. Male piglets sold (exported) after the nursery phase outside the evaluated breeding system (0)

8. Castrated piglets sold (exported) after the nursery phase outside the evaluated breeding system (0)

9. Gilts died in the finishing phase (from the end of the nursery phase to death)

10. Gilts finished to target slaughter weight (from the end of the nursery phase to slaughter)

11. Castrates died in the finishing phase (from the end of the nursery phase to death)

12. Castrates finished to target slaughter weight (from the end of the nursery phase to slaughter)

13. Male pigs (boars) died in the finishing phase (from the end of the nursery phase to death)

14. Male pigs (boars) finished to target slaughter weight (from the end of the nursery phase to slaughter)

15. Breeding gilts died during the rearing phase (from the end of the nursery phase to death)

16. Breeding gilts negatively selected (before inclusion in the herd as replacement or before selling) for different reasons (bad legs, low performance) (from the end of the nursery phase to selection)

17. Breeding gilts sold to other links of the evaluated breeding system (from the end of the nursery phase to selling)

18. Breeding gilts sold (exported) outside the evaluated breeding system (from the end of the nursery phase to selling)

19. Breeding gilts included in the herd as replacement (from the end of the nursery phase to inclusion in the herd). In cross AB in Breeding Systems 3 and 4: purchased breeding gilts immediately included in the herd (0)

20. Breeding gilts negatively selected during the mating period for not showing heat and slaughtered (from inclusion in the herd to culling)

21. Breeding gilts included in the herd as replacement but culled after the maximal number of matings for failure to conceive (from inclusion in the herd to culling)

22. Breeding gilts included in the herd as replacement which became pregnant and farrowed (from inclusion in the herd to the 1st farrowing)

23. Breeding boars died during the rearing phase (from the end of the nursery phase to death)

24. Breeding boars negatively selected (before inclusion in the herd as replacements or before selling) for different reasons (e.g. bad legs, low performance, low libido) and culled (from the end of the nursery phase to culling)

25. Breeding boars sold to other links of the evaluated breeding system for natural mating (from the end of the nursery phase to selling)

26. Breeding boars sold to insemination stations (from the end of the nursery phase to selling)

27. Breeding boars sold (exported) outside the evaluated breeding system (from the end of the nursery phase to selling)

28. Breeding boars included in the herd as replacement for natural mating or oestrus stimulation (from the end of the nursery phase to inclusion in the herd). In systems with crossing and natural mating: purchased breeding boars immediately included in the herd (0)

29. Breeding gilts negatively selected for different reasons (bad legs, low performance) and finished (from selection to culling)

Structure of progeny is calculated based on the litter size, survival parameters of piglets until weaning and in nursery phase, on the base on number of female and male piglets needed for replacement of sows and boars and on further management and biological input parameters defined by the users. Structure of progeny calculated from these parameters is printed in the results files in Section 3.5.

6.4 Growth of animals and feed requirement

6.4.1 General strategy of modeling growth

Generally, there are not enough weighings during the life of pigs in production enterprises to construct a non-linear growth curve for a specific breed or for cross-bred progeny. Therefore, the growth pattern of pigs is approximated by a multi-phase growth curve assuming linear functions for the individual phases. The following phases of growth are distinguished:

- Growth of piglets from birth till weaning (average growth rate for both sexes)

- Growth of piglets in the nursery phase (average growth rate for both sexes)

- Growth in finishing for each sex (entire males, castrates, females)

- Growth in raising breeding animals for each sex (gilts and boars)

- Growth of sows at different parities

- Growth of boars at different ages until the age at which target weight is reached

Growth of animals is characterized by the rate of protein and lipid (fat) deposition. In practice, the real protein and lipid gain of animals of a special breed is often unknown. Therefore, to estimate the protein and lipid mass at a given animal weight (and consecutively the protein and lipid gain in the partial growth phases), the procedures described by Whittemore [18] were applied for the growth model in our program. For the early growth phase until weaning, the values given by Whittemore [17] cited in Table 4.3 in [18] on page 57 were inserted in input files INPUTP08*.TXT for all breeds. The following chemical composition of the piglets at birth was assumed: 18% protein, 2% lipid, 3% ash and 77% water. The composition at weaning at about 28 days of age was assumed to be: 16% protein, 15% lipid, 3% ash and 66% water. These proportions can be changed by the user of the program if appropriate data are available for the pig population modeled.

For the estimation of the protein and lipid mass in the empty body weight of growing pigs between body weight 20 and 200 kg (for entire males, castrates and gilts), the allometric function was used[2]:

$$Y = a \times X^b \tag{6.2}$$

where Y is the component of the whole body of the growing pigs (protein or lipid mass in kg), X is the empty body weight in kg and a and b are coefficients of the function specific for each breed and sex. These coefficients are input parameters in INPUTP07*.TXT and can be changed if these values are known for the evaluated breeds. Empty body weight is calculated as

$$X = W - G \tag{6.3}$$

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[2]In this Section, equations are given in general terms. The symbols used here are mostly different from the variables used in the source code of the program in concrete situations.

where W is body weight in kg and G (gut fill) is the intestinal contents calculated according to [12] as

$$G = c \times W^d .\tag{6.4}$$

where the values $c = 0.277$ and $d = 0.612$ are assumed in [12], but different values for c and d may be inserted in input file INPUTP07*.TXT.

Growth of pregnant females (gilts, sows) is given by the growth of conceptus (uterus contents, i.e. foetuses, fluids, placenta), growth of empty uterus, mammary tissue and by the growth of body tissues of females. The equation for the calculation of the weight of conceptus (kg) at day t of pregnancy ($WC(t)$) was taken from [12]:

$$WC(t) = \frac{1}{1000} \, e^{8.621 + 0.114 TNB - 21.02 \, e^{-0.053t}}\tag{6.5}$$

where TNB is the total number of piglets born.

For modeling the weight (kg) of the empty uterus as function of day t of pregnancy ($WU(t)$), an equation given in [15] was used:

$$WU(t) = 0.47 + 0.0319t .\tag{6.6}$$

The following equation was used for modeling the weight (kg) of the mammary gland as function of day t of pregnancy ($WMG(t)$) [15]:

$$WMG(t) = \begin{cases} 8.43 - 0.1626t + 0.001158t^2 & \text{for 1st pregnancy} \\ 6.95 - 0.1319t + 0.001167t^2 & \text{for 2nd pregnancy} \\ 7.40 - 0.1398t + 0.001244t^2 & \text{for pregnancy} \geq 3 . \end{cases}\tag{6.7}$$

Remark The users of the program will often not known parameters needed for the calculation of protein and lipid gain in animals of their specific breed. In this case, we recommend the users to apply the parameters given in the example files. All you have to know and to insert in the appropriate input files for the calculation of growth are then the weights of different animal categories at their specific age (read the explanations for input files INPUTP08.TXT and INPUTP09*.TXT in Sections 3.1.2.9 and 3.1.2.10).*

6.4.2 Calculation of energy and feed requirements and feeding costs

Feeding costs include costs for feed and water. The amount of feed of each feed ration for all animal categories is calculated on the basis of metabolisable energy requirement (in MJ) for maintenance, growth, gestation, lactation and change in sow body weight during lactation. Using this normative approach, it is assumed that feed intake of animals changes with performance (e.g. depends on growth rates, weights, litter size etc.). **For detailed description of the calculation see the Manual for EWPIG2, Chapter 5.**

6.5 Feed rations

For each feed ration defined below, it is assumed that the amount of amino acids and minerals is optimized for each stage of animal life. Because feed rations in different countries can be composed from many different ingredients, the following information should be known for each feed ration:

- metabolisable energy in MJ per kg fresh matter,

- amount of dry matter per kg fresh matter and

- price per kg fresh matter of each feed ration.

In the program, the number of the feed ration given in the following text is used as index for variables which refer to the appropriate feed ration. ***The numbers of feed rations given below for specific animal groups are those printed in the results files for the amount of energy, dry matter and fresh feed requirement from these rations.***

Feed rations for progeny.   Different feed rations are expected for the following feeding periods:

1. Birth to weaning

2. First feeding phase in nursery

3. Second feeding phase in nursery

4. Third feeding phase in nursery

5. Rearing of breeding gilts

6. Gilts during pregnancy

7. Rearing of breeding boars

8. First feeding phase in finishing gilts

9. Second feeding phase in finishing gilts

10. Third feeding phase in finishing gilts

11. First feeding phase in finishing castrates

12. Second feeding phase in finishing castrates

13. Third feeding phase in finishing castrates

14. First feeding phase in finishing boars

15. Second feeding phase in finishing boars

16. Third feeding phase in finishing boars

17. Finishing of negatively selected breeding gilts

Several feeding periods are optional so that the number of different feed rations will be less than 17.

Feed rations for sows.   Three feed rations are expected to be used for sows:

1. For barren and pregnant sows

2. For lactating sows

3. For barren sows which are candidates for being culled

Feed rations for boars.   Two feed rations are expected to be used for boars:

1. For breeding boars used for natural mating

2. For breeding boars used only for oestrus stimulation

6.6   Calculation of total costs, revenues and profit of the production system and calculation of marginal economic values of traits.

For the calculation of economic efficiency of the integrated production system of a breed (in Breeding system 1) or of each link of a cross-breeding system, see Chapters 6 and 7 of the Manual for EWPIG2. The economic efficiency is defined as a net profit (difference between total revenues and total costs) in this production system per farrowed sow and per year.

The general principles of the calculation of the marginal economic values of traits and the description of all traits which can be evaluated with the programs EWPIG2 and GFPIG are given in Chapter 8 of the Manual for EWPIG2.

Marginal economic value of a trait in our program is defined as a change in the net profit of the specified production system of a breed or crossbreed (per sow per year) caused by a change in the evaluated trait by defined unit.

The list of these traits and their numbers (which are printed in the results files) are given in the Appendix of this manual.

6.7   Calculation of economic weights of traits

6.7.1   Approximate and true economic weights

Approximate economic weights of traits are calculated by the program EWPIG2 when using it as a stand alone program (not applying method gene flow, i.e if the variable gf in files INPUTBS*.TXT is equal to 0, see also the description in Section 3.1.2.1). The calculated approximate economic weights consider the proportions of genes from the individual breeds or lines in all links of a breeding system which are expressed in one generation of progeny., The timing of expected genetic changes in the individual genotypes in all links of a breeding system is not considered (the numbers of gene expressions of the individual breeds or lines in different links of a breeding system are not discounted). Approximate economic weights are calculated as absolute, standardized and relative economic weights (see Section 8.7 in the Manual for EWPIG2).

The true economic weights of traits are calculated from the marginal economic values from the program EWPIG2 using gene flow methods incorporated in the program GFPIG which is run automatically after running EWPIG2 if the variable gf in files INPUTBS*.TXT is equal to 1 (see also the description in Section 3.1.2.1). You find the detailed description of the algorithm used for gene flow and for the calculation of true economic weights of traits in the Manual for the program GFPIG.

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Appendix A

Numbering of traits in program EWPIG2

1. Average piglet weight at weaning at fixed age (kg)

2. Average daily gain of piglets until weaning (g/d, alternative trait to weaning weight)

3. Weight at the end of the nursery phase (kg)

4. Average daily gain of piglets in nursery until fixed age (g/d, alternative trait to weight at the end of the nursery phase)

5. Average daily gain of pigs in finishing to fixed slaughter weight (g/d)

6. Length of the finishing period until reaching target slaughter weight (d, alternative trait to average daily gain in finishing)

7. Average lifetime daily gain of finished animals (g/d)

8. Age at reaching target slaughter weight (d, alternative trait to average lifetime daily gain)

9. Total number of piglets born (TNB)

10. Number of piglets born alive (NBA)

11. Number of piglets weaned (NW)

12. Survival rate at birth (%)

13. Survival rate of piglets born alive until weaning (%)

14. Average age of gilts at first mating (d)

15. Conception rate of gilts after the first mating (%)

16. Total conception rate of gilts (%)

17. Average age (d) at first farrowing (alternative trait to conception rate of gilts)

18. Conception rate of sows after the first mating averaged over all parities (%)

19. Total conception rate of sows averaged over all matings and all parities (%)

20. Farrowing interval (in d, alternative trait to conception rate of sows)

21. Survival rate of piglets in nursery (%)

22. Survival rate of young animals after nursery (%)

23. Average productive lifetime of sows measured in number of farrowings

24. Average productive lifetime of sows measured in years

25. Dressing percentage (%) of finished animals

26. Lean meat content (%) in finished animals

27. Residual feed intake (kg) in nursery

28. Feed conversion (kg feed/kg weight gain) in nursery

29. Residual feed intake (kg) in finishing

30. Feed conversion (kg feed/kg weight gain) in finishing

31. Number of functional sow teats (calculated only for maternal breed and breed cross, A, B and AB)

32. Semen volume

33. Sperm concentration

34. Percentage of progressive motion of spermatozoa (motility)

35. Percentage of abnormal spermatozoa