

A PopREP crash course

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The within breeds view

Objectives

Control inbreeding

- Loss of alleles → genetic variability
- Reduces future selection options
- Increases homozygosity → genetic defects
- Critical factor: rate of inbreeding ΔF
- Magical figure: keep ΔF below 1%/generation

Factors affecting Rate of Inbreeding

- Population size
- Sex ratio
- Variance of family size
- Generation interval ($\Delta F/\text{year}$)

Factors affecting Rate of Inbreeding

- There are simple procedures
- And more complicated ones
- Here: deal with the simple
- Later the day: the more complicated ones (OC)
- Now: pick the low hanging fruits

Inbreeding population size

- Population size $\sim 1/\Delta F$
- Consider 1 male x 1 female
 - Offspring: $\frac{1}{2}$ from sire + $\frac{1}{2}$ from dam
 - \rightarrow half of the alleles get lost
- Consider 1 male x 10000 females
 - ALL offspring will have half of its genes from that one sire
- \rightarrow Sex ratio matters

Inbreeding

effective population size

- Sewall Wright: "....the number of breeding individuals in an idealized population that would show the same amount of dispersion of allele frequencies under random genetic drift or the same amount of inbreeding as the population under consideration"
- A commonly used figure to compare populations of different structures

Inbreeding effective population size

- Assumptions:
 - all contribute equally to gene pool
 - distinct generations
 - random mating (incl selfing)
 - no selection
 - no mutation

Inbreeding effective population size

- $N_e = (4 * N_m * N_f) / (N_m + N_f)$
- $\Delta F = 1/2N_e$



Nf	Nm	Ne	ΔF
100	50	133.33	0.38
100	40	114.29	0.44
100	30	92.31	0.54
100	25	80	0.63
100	20	66.67	0.75
100	15	52.17	0.96
100	10	36.36	1.38
100	5	19.05	2.63
100	4	15.38	3.25
100	3	11.65	4.29

Inbreeding

- Number of females often a given
- Number of males prime importance!
- What is lost here, cannot be gained through trickery!!

Population management: defining targets

1. Definition of maximum rate of inbreeding
2. Definition of the target population structure
 1. Number of males
 2. Number of females
3. Definition of the generation interval

Population management: targets achieved?

- Assuming availability of pedigree data
- All information on targets is contained in pedigree:

■ Animal ID	Sire ID	Dam ID	birth dt	sex
73400	70335	358651	1951-01-21	F
398242	16590	7756462	1952-01-21	F
57700	47180	333654	1953-01-21	M
501215	147114	733141	1954-01-21	F
413520	772451	7756418	1955-01-21	M
8271925	501222	8539836	1956-01-21	M

- WEBSITE
- Accessible by standard browsers
- → upload pedigree
- ← Receive results through email
- Use for population management

poprep.tzv.fal.de

Service PopReport at Institute of Farm Animal Genetics

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The Popreport Homepage

Get a population report from your pedigree data

Breed:	EastFriesianMilkShee
Email:	eg@tzv.fal.de
Code for Male:	M
Code for Female:	F
Date Format:	YYYY-MM-DD
Date Separator:	-
Get compressed archive of files to postprocess?:	<input type="radio"/> no <input checked="" type="radio"/> yes
We kindly would ask you to also fill out the following fields. They are not required for getting a PopReport but just to satisfy our curiosity, who is using this software.	
Your Name:	Eildert Groeneveld
Your Institute/Company:	FLI
Your Country:	Ostfriesland
Thanks for filling out these optional fields.	
Your Pedigree File:	/home/eg/datafile.txt <input type="button" value="Browse..."/>
	<input type="button" value="Upload"/>

We started some [documentation](#) about how to use the PopReport Service at the Institute of Farm Animal Genetics.
You can download an [example datafile](#) to have a look at it and re-upload it again for testing.

Reset the [Popreport Homepage](#)

In case of problems contact the [Popmaster](#)
Last modified: 2009-08-20 13:35:32 GMT



The Popreport Homepage

Get a population report from your pedigree data

Some notes concerning your upload:

- Your upload succeeded.
- You are lucky, there are no pending requests for a popreport. Yours will be served immediately.
- Email will be sent to eg@tzv.fal.de

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Subject	Sender	Date	Size
Termin GSA	Herman...	Friday 16:3...	4.8 KiB
HV 2011 - 81201	Susanne...	Today 09:0...	78.6 KiB
Your popreport request (breed: EastFriesianMilkShee)	Poprepo...	Today 09:1...	1.4 MiB

Description:

Description	Type	Encoding	Size
Your popreport request (breed: E...	multipart/...	7bit	1.4 MiB
body part	plain text ...	7bit	83 B

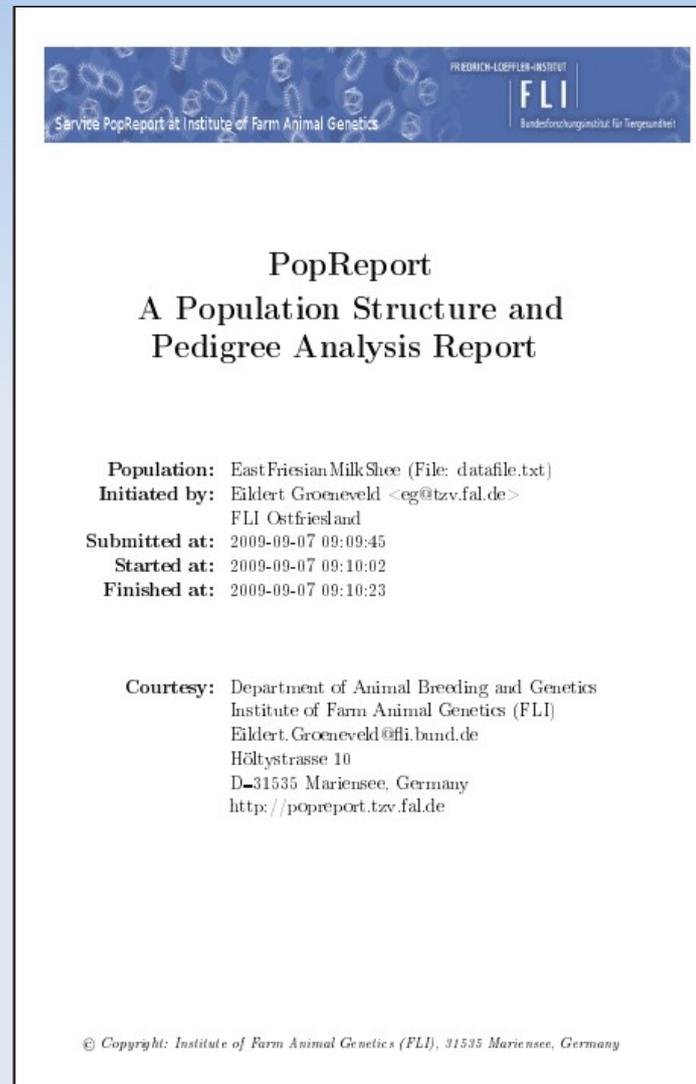
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From: Popreporter <popreport@tzv.fal.de>
To: eg@tzv.fal.de
Date: Today 09:10:25
Attachments: ☺

- PopulationEastFriesianMilkShee+.pdf
- InbreedingEastFriesianMilkShee+.pdf
- Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip

Find attached the files from your popreport request for breed EastFriesianMilkShee

- PopulationEastFriesianMilkShee+.pdf
- InbreedingEastFriesianMilkShee+.pdf
- Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip



Service PopReport at Institute of Farm Animal Genetics

FRIEDRICH-LOEFFLER-INSTITUT
FLI
Bundesforschungsinstitut für Tiergesundheit

PopReport

A Population Structure and Pedigree Analysis Report

Population: EastFriesian MilkShee (File: datafile.txt)
Initiated by: Eildert Groeneveld <eg@tzv.fal.de>
FLI Ostfriesland
Submitted at: 2009-09-07 09:09:45
Started at: 2009-09-07 09:10:02
Finished at: 2009-09-07 09:10:23

Courtesy: Department of Animal Breeding and Genetics
Institute of Farm Animal Genetics (FLI)
Eildert.Groeneveld@fli.bund.de
Höltystrasse 10
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<http://popreport.tzv.fal.de>

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Populations Structure

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Helmut Lichtenberg: Integration and WEB service, FLI, Germany

Eildert Groeneveld: Project Leader, FLI, Germany

Populations Structure

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Populations Structure

number of breeding animals

Number of breeding animals

1

1 Number of breeding males and females by year

The number of breeding animals at a given time determines the genetic structure of the population in subsequent generations. Under simplified conditions (*e.g.* ratio of males to females is 1:1, random selection, distribution of family size is Poisson, *etc*), the number of breeding males and females can be used to calculate the effective population size (to be defined later). In the context of this report, the term breeding refers to year of *actual* service (if date of natural or artificial insemination is available in the database). Also, a selected animal is defined as an animal that has participated in first service (if service data is available) or has already become a parent. The number of breeding males and females

used in the population in a given year is presented in the table. For ease of presentation the table is partitioned into two parts *i.e.* for the males and the females. Each part is further subdivided into three columns. The description for each column is:

Services: The number of males/females that participated in services in a given year the corresponding year.

Births: The number of males/females with offspring in a given year.

Select: The number of males/females that have selected offspring in a given year.

For example: For the EastFriesianMilkShee breed in 1988, 11 males produced 22 offspring while offspring of 12 males were selected to become parents in the next generations. Similarly, 18 females produced 22 offspring during the same year while offspring of 20 females were selected to become parents in the generations to follow.

Note: No service data were used in the calculations for this section.

Population Structure

number of breeding animals

For example: For the EastFriesianMilkShee breed in 1988, 11 males produced 22 offspring while offspring of 12 males were selected to become parents in the next generations. Similarly, 18 females produced 22 offspring during the same year while offspring of 20 females were selected to become parents in the generations to follow.

Table 1: Number of males and females in reproduction by year of birth of offspring

(select=the number of males/females whose offspring become parents in following generations)

Year	males			females			Number of animals born
	services	births	select	services	births	select	
1953	-	2	8				
1988	-	11	12	-	18	20	22
1989	-	7	6	-	12	15	21
1990	-	8	9	-	13	21	26
1991	-	12	11	-	17	24	31
1992	-	12	12	-	28	30	47
1993	-	24	13	-	40	28	61

Did we use the number of females and males that we wanted to?

Population Structure

age structure

Table 2: Age distribution of males in reproduction by year of birth of their offspring

Year	age of males in years																Avg
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	≥ 16	
1953	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0
1954	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.0
1955	2	5	1	-	-	-	-	-	-	-	-	-	-	-	-	-	1.9
1988	1	1	-	-	-	-	-	-	2	1	1	-	-	-	1	4	14.2
1989	-	1	-	-	1	-	-	-	1	1	-	1	-	-	1	1	10.4
1990	-	-	-	-	-	1	-	-	1	1	-	1	-	1	-	3	14.0
1991	-	-	2	1	-	-	-	1	-	-	1	2	-	-	-	5	14.4
1992	-	2	1	1	-	-	-	1	1	-	-	-	-	1	-	5	12.8
1993	-	1	2	1	3	-	-	-	2	-	-	-	-	1	2	12	15.8
1994	-	3	2	-	2	1	-	-	-	-	-	-	1	-	1	8	14.5
1995	-	-	3	2	-	1	-	-	-	-	-	-	-	-	2	8	15.1
1996	-	2	6	1	3	-	2	-	-	-	-	-	-	-	1	10	13.3
1997	-	1	3	5	2	2	-	2	-	-	-	-	-	-	-	-	4.6
1998	-	-	1	3	4	1	2	1	1	1	-	-	-	-	-	-	5.9
1999	-	-	-	1	2	4	1	3	-	-	-	-	-	-	-	-	6.3
2000	-	-	-	-	-	3	1	1	1	-	-	-	-	-	-	-	7.0
2001	-	-	-	-	-	-	2	1	1	1	-	-	-	-	-	-	8.2
2002	-	-	-	-	-	-	1	3	1	3	1	-	-	-	-	-	9.0
2003	-	-	-	-	-	-	1	3	1	3	2	1	-	-	-	-	9.5
2004	-	-	-	-	-	-	-	-	3	3	1	1	1	-	-	-	10.3
2005	-	-	-	-	-	1	-	-	2	4	4	-	-	1	-	-	10.2

Does the age structure correspond to the target generation interval?

Population Structure

Generation interval

Average age of parents at birth of their selected offspring (Falconer)

1. All animals born in a given year are considered
2. Animals in 1. that became parents in the later years were identified
3. The parents of animals in 2. were identified
4. The generation interval was calculated as the average age of animals identified in 3. at the birth date of their offspring

Population Structure

Generation interval

Table 5: Generation interval and number of animals by year of birth for different selection paths

(*ss=sire to son, Nss=number of selected males for ss, sd=sire to daughter, Nsd=number of females for sd, ms=dams to sons, Nms=number of males for ms, md=dams to daughters and Nmd=number of females for md, male=avg age of sires, Nmale=number of sires where age is known, female=avg age of dams, Nfemale=number of dams where age is known, pop=interval for the population, Npop=number of selected offspring*)

Year	Generation interval and number of animal													
	ss	Nss	sd	Nsd	ms	Nms	md	Nmd	male	Nmale	female	Nfemale	pop	Npop
1961	5.7	3	6.3	2	3.6	2	3.9	1	6.0	5	3.7	3	5.0	7
1968	9.0	5	8.8	3	4.9	2	6.2	1	8.9	8	5.3	3	8.2	8
1970	9.0	5	6.6	2	6.7	3	4.9	1	8.3	7	6.2	4	7.5	8
1971	7.0	1	11.1	2	3.3	1	2.9	1	9.7	3	3.1	2	7.6	4
1972	8.1	3	9.1	1	2.3	1	3.2	3	8.4	4	3.0	4	6.0	6
1978	9.2	3	8.6	7	6.9	3	2.9	3	8.7	10	4.9	6	7.3	10
1980	9.0	3	7.0	7	8.2	1	3.4	4	7.6	10	4.4	5	7.2	10
1983	7.9	2	8.1	9	8.1	2	3.6	6	8.1	11	4.7	8	7.5	12
1987	6.6	1	7.8	14	6.2	1	4.9	9	7.7	15	5.0	10	6.8	15
1988	23.7	6	11.2	13	3.6	4	4.4	13	15.1	19	4.2	17	11.0	19
1989	14.4	3	10.6	11	8.1	1	3.2	8	11.4	14	3.7	9	9.4	14
1990	13.6	4	14.8	16	5.4	2	3.2	9	14.5	20	3.6	11	11.9	21
1991	22.1	5	6.5	19	6.6	3	3.9	10	9.7	24	4.5	13	8.2	24
1992	7.9	4	13.9	25	5.2	4	4.4	15	13.1	29	4.5	19	10.6	30
1993	16.9	8	7.6	21	7.3	7	5.4	14	10.2	29	6.1	21	8.4	29
1994	17.0	5	12.0	17	6.3	5	5.3	14	13.1	22	5.6	19	9.3	22
1995	23.0	6	15.4	13	6.0	6	4.9	12	17.8	19	5.3	18	12.0	19
Total	14.3	-	10.5	-	6.0	-	4.4	-	11.5	-	4.8	-	9.1	-

Has the target generation interval been reached?

Population Structure

Variance of family size

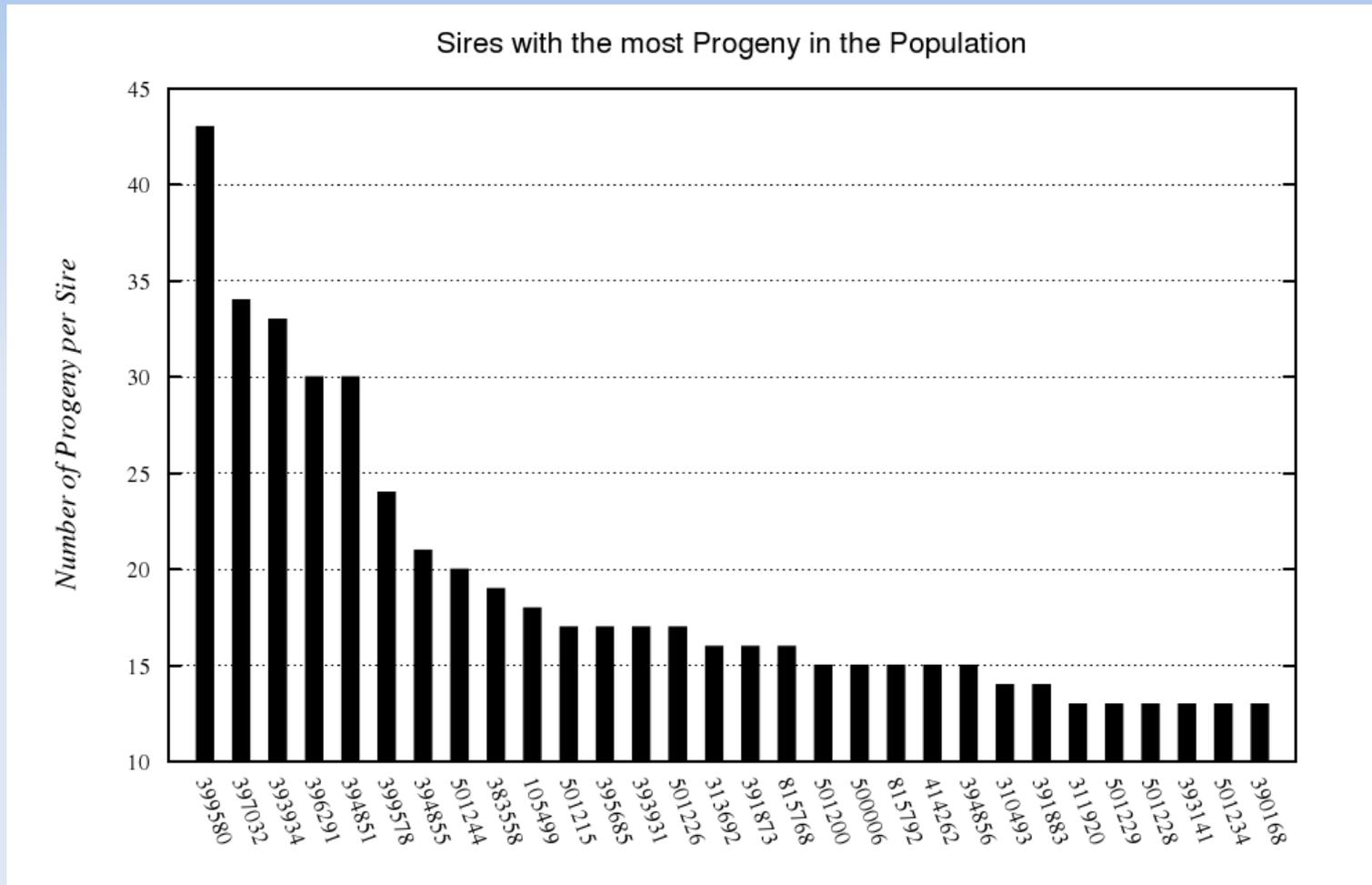
Table 6: The maximum and average number of family sizes

Year	All offspring				Selected offspring				Selected sons				Selected daughters			
	sires		dams		sires		dams		sires		dams		sires		dams	
	max	avg	max	avg	max	avg	max	avg	max	avg	max	avg	max	avg	max	avg
1950	1	1.0	1	1.0	1	1.0	-	-	1	1.0	-	-	-	-	-	-
1951	1	1.0	-	-	1	1.0	-	-	1	1.0	-	-	1	1.0	-	-
1952	2	1.3	-	-	1	1.0	-	-	1	1.0	-	-	-	-	-	-
1953	2	1.3	2	1.5	2	1.2	1	1.0	1	1.0	1	1.0	1	1.0	-	-
1954	1	1.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1955	8	1.9	-	-	8	2.0	-	-	5	1.7	-	-	3	2.0	-	-
1956	10	4.0	-	-	9	3.7	-	-	7	4.0	-	-	2	1.5	-	-
1957	4	2.7	2	1.7	3	2.0	2	1.7	2	1.7	2	2.0	1	1.0	1	1.0
1958	1	1.0	1	1.0	1	1.0	1	1.0	1	1.0	1	1.0	-	-	1	1.0
1959	2	1.2	1	1.0	1	1.0	1	1.0	1	1.0	1	1.0	-	-	1	1.0
1960	2	1.3	1	1.0	2	1.3	1	1.0	1	1.0	1	1.0	2	1.5	-	-
1961	7	2.5	1	1.0	7	2.3	1	1.0	5	2.8	1	1.0	2	1.3	1	1.0
1962	5	3.0	1	1.0	3	2.3	1	1.0	2	1.7	1	1.0	2	2.0	-	-
1963	4	1.8	1	1.0	3	1.7	1	1.0	2	1.5	1	1.0	1	1.0	-	-
1964	10	3.0	1	1.0	2	1.4	1	1.0	2	1.6	1	1.0	1	1.0	1	1.0
1965	2	1.6	1	1.0	2	1.3	1	1.0	2	1.3	1	1.0	-	-	-	-
1966	14	5.5	1	1.0	9	3.5	1	1.0	3	2.0	1	1.0	6	3.3	1	1.0
1967	18	3.7	1	1.0	15	3.3	1	1.0	3	2.3	1	1.0	12	3.2	-	-
1968	13	4.0	1	1.0	9	3.0	1	1.0	5	3.0	1	1.0	4	2.0	1	1.0
1969	5	2.8	1	1.0	2	1.3	1	1.0	1	1.0	1	1.0	2	1.3	1	1.0

Are the offspring groups as even as intended?

Population Structure

Sires with most offspring



Are the offspring groups as even as intended?

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- PopulationEastFriesianMilkShee+.pdf
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Find attached the files from your popreport request for breed EastFriesianMilkShee

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- InbreedingEastFriesianMilkShee+.pdf** (circled in blue)
- Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip

Inbreeding Report

Pedigree Analysis Report for Population: EastFriesianMilkShee

ii

Developers

Frits Voordewind: PERL/SQL/GNU-Plot/Report, ARC, Irene, South Africa

Bobbie van der Westhuizen: PERL/SQL/GNU-Plot/Report, ARC, Irene, South Africa

Norman Maiwashe: Report/Descriptions, ARC, Irene, South Africa

Ralf Fischer: Computation of Inbreeding, LfULG , Köllitsch, Germany

Didier Boichard: PEDIG software, INRA, France

Lina Yordanova: SQL, University of Stara Zagora, Bulgaria

Helmut Lichtenberg: Integration and WEB service, FLI, Germany

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Inbreeding Report

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Pedigree Completeness

The following formula was used to compute pedigree completeness (MacCluer *et al.*, 1983):

$$I_d = \frac{4I_{d_{pat}}I_{d_{mat}}}{I_{d_{pat}} + I_{d_{mat}}}$$

and

$$I_{d_k} = \frac{1}{d} \sum_{i=1}^d a_i \quad k = pat, mat$$

Pedigree Completeness

Table 1: The average pedigree completeness (%) for 1 to 6 generations deep by year

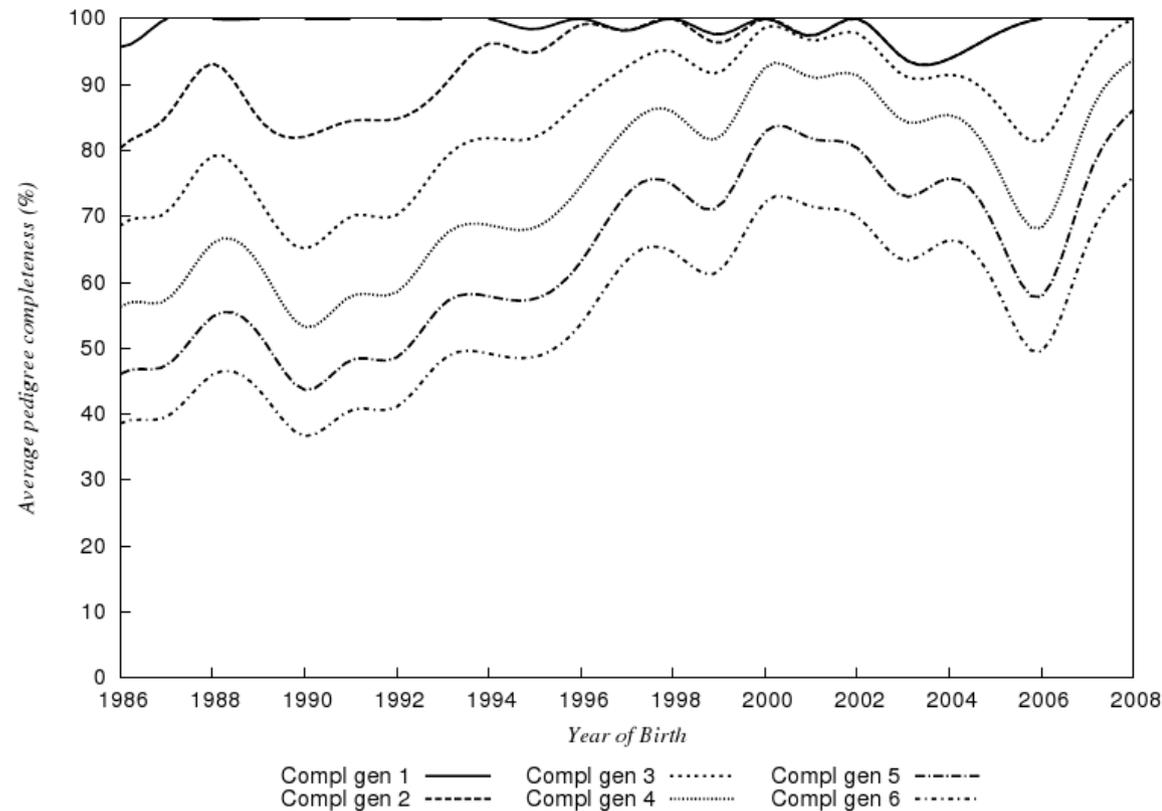
Year	No of Animals	Compl. gen 1	Compl. gen 2	Compl. gen 3	Compl. gen 4	Compl. gen 5	Compl. (%) gen 6(%)
1950	4	100.0	50.0	33.3	25.0	20.0	16.7
1951	3	100.0	50.0	33.3	25.0	20.0	16.7
1952	10	90.0	46.7	31.1	23.3	18.7	15.6
1953	10	100.0	53.3	35.6	26.7	21.3	17.8
1954	4	100.0	54.2	36.1	27.1	21.7	18.1
1955	10	100.0	63.3	42.5	31.9	25.5	21.3
1956	6	100.0	69.4	49.3	37.4	29.9	24.9
1957	8	100.0	58.3	40.1	30.1	24.0	20.0
1958	4	100.0	54.2	36.9	27.7	22.1	18.4
1959	9	100.0	63.0	44.9	34.2	27.4	22.8
1960	7	100.0	57.1	39.0	29.4	23.5	19.6
1961	12	83.3	51.4	35.4	26.8	21.4	17.8

2000	35	100.0	100.0	98.7	92.6	82.9	72.2
2001	38	97.4	97.4	96.7	91.1	81.8	71.5
2002	42	100.0	100.0	97.8	91.4	80.4	70.0
2003	50	94.0	94.0	91.4	84.5	73.1	63.4
2004	33	93.9	93.9	91.5	85.4	75.8	66.4
2005	41	97.6	97.6	87.4	77.9	68.2	59.5
2006	27	100.0	100.0	81.5	68.2	57.8	49.5
2007	22	100.0	100.0	93.7	84.8	75.6	66.0
2008	1	100.0	100.0	100.0	93.8	86.2	76.0

Pedigree Completeness

The average pedigree completeness for animals born within the last 10 years: 1 generations deep = 97.6%. 2 generations deep = 97.4%. 3 generations deep = 92.5%. 4 generations deep = 84.6%. 5 generations deep = 74.5%. 6 generations deep = 64.8%.

Figure 1: Average pedigree completeness for 1 to 6 generations



Is this what you think you have?

Level of Inbreeding

Table 2: Distribution of animals by year and inbreeding levels

(Classes 1=0-5%, 2=6-10%, 3=11-15%, 4=16-20%, 5=21-25%, 6=26-30%, 7=31-35%, 8=36-40%, 9=41-45%, 10=46-50% and 11=>50%)

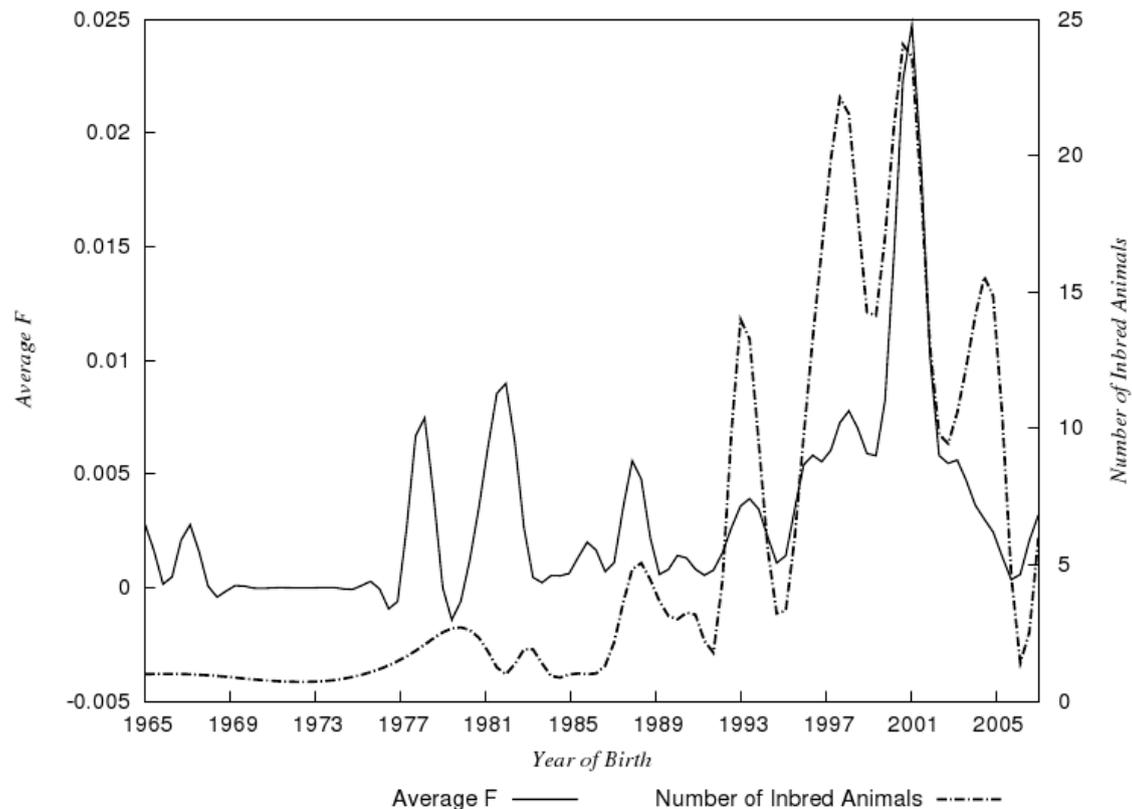
Year	Classes										
	1	2	3	4	5	6	7	8	9	10	11
1950	4	-	-	-	-	-	-	-	-	-	-
1951	3	-	-	-	-	-	-	-	-	-	-
1952	10	-	-	-	-	-	-	-	-	-	-
1953	10	-	-	-	-	-	-	-	-	-	-
1954	4	-	-	-	-	-	-	-	-	-	-
1955	10	-	-	-	-	-	-	-	-	-	-

1996	55	3	-	-	-	-	-	-	-	-	-
1997	54	2	-	-	-	-	-	-	-	-	-
1998	52	1	1	-	-	-	-	-	-	-	-
1999	40	1	-	-	-	-	-	-	-	-	-
2000	33	2	-	-	-	-	-	-	-	-	-
2001	32	5	-	-	-	1	-	-	-	-	-
2002	39	3	-	-	-	-	-	-	-	-	-
2003	48	-	2	-	-	-	-	-	-	-	-

Has close inbreeding been avoided?

Level of Inbreeding

Figure 2: Comparison between the average inbreeding coefficients (F) and the number of inbred animals by year



Has close inbreeding been avoided?

Effective Population Size

3.2 Effective population size based on the number of parents

This section presents effective population size calculated based on the number of parents. The following formula was used to calculate N_e (Falconer & Mackay, 1996):

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$

where N_m and N_f are the number of male and female parents, respectively. The columns in the table are:

Number of animals : born in a given year.

Number of sires : of animals born in a given year.

Number of dams : of animals born in a given year.

Number of parents : number of sires and dams of animals born in a given year.

N_e : effective population size.

Table 7: Effective population size by year via number of parents

Year	Number of				N_e
	Animals	Sires	Dams	Parents	
1950	4	3	4	7	7
1951	3	3	3	6	6
1952	10	6	10	16	15
1953	10	10	10	20	20
1954	4	4	4	8	8
1955	10	10	10	20	20
1956	6	6	6	12	12
1957	8	8	8	16	16
1958	4	4	4	8	8
1959	9	8	9	17	17
1960	7	7	7	14	14
1961	12	10	11	21	21

Effective Population Size

Method 1

Census based

Method 1: Assuming discrete generations and equal numbers of breeding males and females N_e can be determined directly as

$$N_e = \frac{4N_m N_f}{N_m + N_f} \quad (7)$$

The number of males and females are usually easy to determine, therefore this expression is often used where other ways of computing N_e are not possible. However, the assumptions that the ratio between breeding males and females is 1:1 and that all individuals in a real population have an equal chance to contribute genetically to next generation are usually not met. Therefore 7 tends to overestimate N_e considerably.

Effective Population Size

Method 2 - 6

All other methods are based on the rate of inbreeding

The relevant quantity for the assessment of inbreeding is the inbreeding coefficient F and its rate of change ΔF . The latter is defined as Falconer & Mackay (1996):

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}} \quad (2)$$

where t is the t^{th} generation. As has been stated the cohort are those animals born in a given year. To compute ΔF actually two cohorts i.e. sets of animals need to be defined: $cohort_t$ at generation t and $cohort_{t-1}$ at generation $t - 1$ have to be defined.

$$N_e = 1/2\Delta F$$

Effective Population Size

Method 2-6

- Method 2: based on actual parents of the current birth year (inbreeding F)
- Method 3: based on all animals of the year GI prior to the current (inbreeding F)
- Method 4: based on all animals of the year GI prior to the current (inbreeding f)

- Method 5:
$$\ln(1 - F_{u+t}) = t * \ln(1 - \Delta F) + \ln(1 - F_u)$$

- Method 6:
$$N_e = 1/2(1 - (1 - F_t)^{(1/t)})$$

Effective Population Sizes

Table 5: Effective population sizes based on the period 1990–2008

Breed ^a	method 1	method 2	method 3	method 4	method 5	method 6 ^b
Nellore	502	– ^c	–	–	476	1293
Bonsmara	6901	106	162	324	190	231
Jersey	3545	203	79	83	67	208
Holstein	4803	–	318	282	408	794
Duroc	247	40	119	99	219	143
Landrace	546	50	13??	44	222	102
Merino	861	241	562	5588	447	601
Skudden	280	–	528	391	–	210

^a5 generations with min PCI .8; based on arithmetic mean of ΔF_p ΔF_g Δf_g

^b N_e was taken from the most recent full birth year

^c– negative N_e

Reference

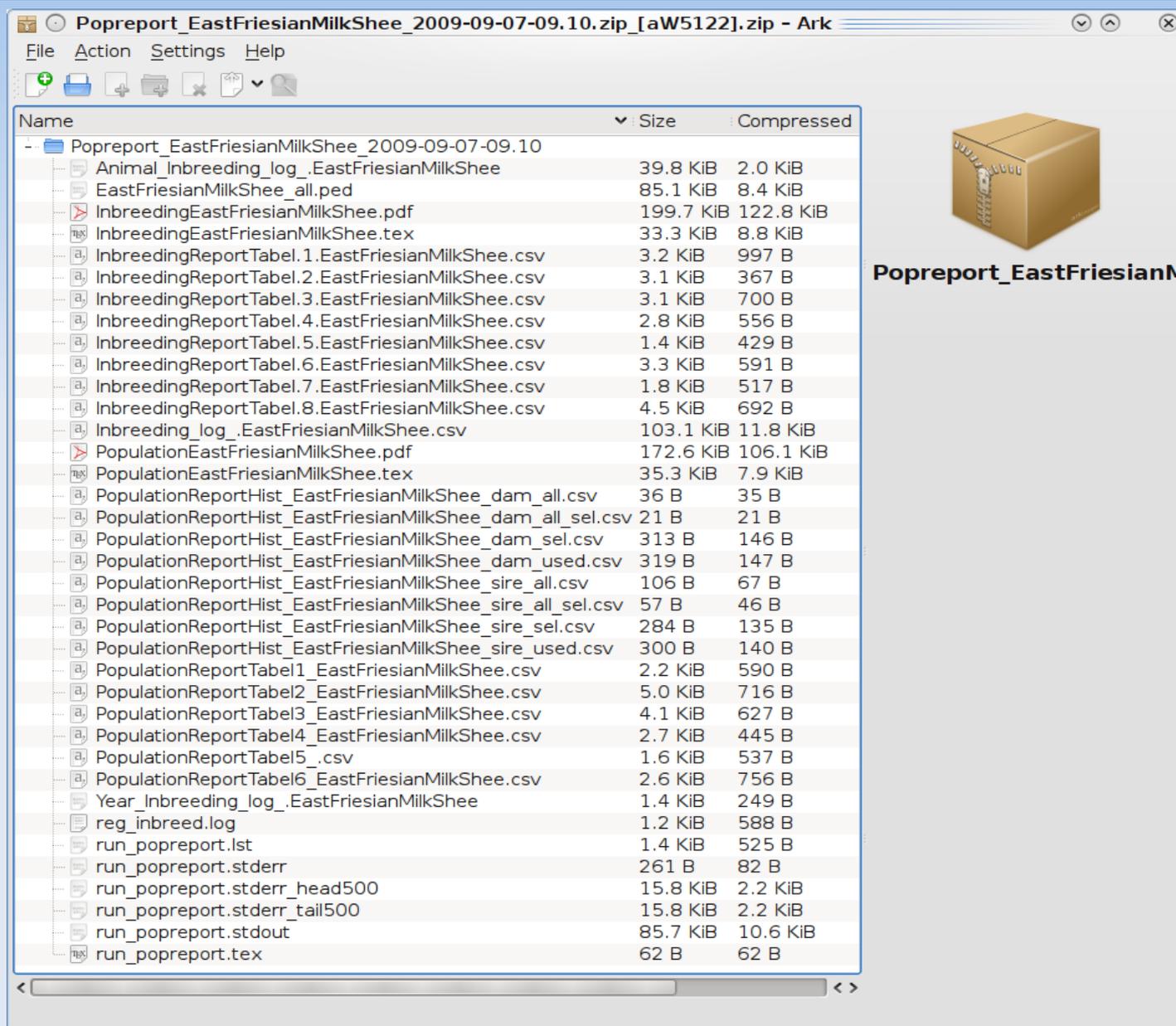
POPREP: A Generic Report for Population Management,
E Groeneveld, B v.d. Westhuizen A Maiwashe, F
Voordewind, JBS Ferraz
Genetics and Molecular Research (GMR) 2009, 8(3)

poprep.tzv.fal.de

The screenshot shows an email client window with the following components:

- Folder List:** Local Folders > inbox (selected). Other folders include 24-hours-shuttl..., Alejandro.Enge..., android-freeru..., Anne.Lueder, Begemann, bestellungen, Canh, cuc, Ernst.Kalm, Flavio, fp7, gfortan(4), gft, GMR, hackable1, hoersten, InternBuero, JoaoClaudio, John.Rocha, kate, magnatune, marcus.bauer, melvin, mettenleiter, Michael.Baudin, MolabisInstVN, MONItoring, poprep, Raul.Ponzoni, save, sentmail-old.ta., and silvia.wittin.
- Email List:** A table with columns Subject, Sender, Date, and Size. The selected email is "Your popreport request (breed: EastFriesianMilkShee)" from Popreporter, dated Today 09:10:25, with a size of 1.4 MiB.
- Description Table:** A table with columns Description, Type, Encoding, and Size. It shows "Your popreport request (breed: E..." as multipart/... (7bit, 1.4 MiB) and "body part" as plain text ... (7bit, 83 B).
- Email Content:**
 - Subject:** Your popreport request (breed: EastFriesianMilkShee)
 - From:** Popreporter <popreport@tzv.fal.de>
 - To:** eg@tzv.fal.de
 - Date:** Today 09:10:25
 - Attachments:**
 - PopulationEastFriesianMilkShee+.pdf
 - InbreedingEastFriesianMilkShee+.pdf
 - Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip
- Body Text:** Find attached the files from your popreport request for breed EastFriesianMilkShee
- Attachment List:** Three items are listed with icons: PopulationEastFriesianMilkShee+.pdf, InbreedingEastFriesianMilkShee+.pdf, and Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip. The zip file is circled in blue.

Data for post processing



Popreport_EastFriesianMilkShee_2009-09-07-09.10.zip [aW5122].zip - Ark

File Action Settings Help

Name	Size	Compressed
Popreport_EastFriesianMilkShee_2009-09-07-09.10		
Animal_Inbreeding_log_EastFriesianMilkShee	39.8 KiB	2.0 KiB
EastFriesianMilkShee_all.ped	85.1 KiB	8.4 KiB
InbreedingEastFriesianMilkShee.pdf	199.7 KiB	122.8 KiB
InbreedingEastFriesianMilkShee.tex	33.3 KiB	8.8 KiB
InbreedingReportTabel.1.EastFriesianMilkShee.csv	3.2 KiB	997 B
InbreedingReportTabel.2.EastFriesianMilkShee.csv	3.1 KiB	367 B
InbreedingReportTabel.3.EastFriesianMilkShee.csv	3.1 KiB	700 B
InbreedingReportTabel.4.EastFriesianMilkShee.csv	2.8 KiB	556 B
InbreedingReportTabel.5.EastFriesianMilkShee.csv	1.4 KiB	429 B
InbreedingReportTabel.6.EastFriesianMilkShee.csv	3.3 KiB	591 B
InbreedingReportTabel.7.EastFriesianMilkShee.csv	1.8 KiB	517 B
InbreedingReportTabel.8.EastFriesianMilkShee.csv	4.5 KiB	692 B
Inbreeding_log_EastFriesianMilkShee.csv	103.1 KiB	11.8 KiB
PopulationEastFriesianMilkShee.pdf	172.6 KiB	106.1 KiB
PopulationEastFriesianMilkShee.tex	35.3 KiB	7.9 KiB
PopulationReportHist_EastFriesianMilkShee_dam_all.csv	36 B	35 B
PopulationReportHist_EastFriesianMilkShee_dam_all_sel.csv	21 B	21 B
PopulationReportHist_EastFriesianMilkShee_dam_sel.csv	313 B	146 B
PopulationReportHist_EastFriesianMilkShee_dam_used.csv	319 B	147 B
PopulationReportHist_EastFriesianMilkShee_sire_all.csv	106 B	67 B
PopulationReportHist_EastFriesianMilkShee_sire_all_sel.csv	57 B	46 B
PopulationReportHist_EastFriesianMilkShee_sire_sel.csv	284 B	135 B
PopulationReportHist_EastFriesianMilkShee_sire_used.csv	300 B	140 B
PopulationReportTabel1_EastFriesianMilkShee.csv	2.2 KiB	590 B
PopulationReportTabel2_EastFriesianMilkShee.csv	5.0 KiB	716 B
PopulationReportTabel3_EastFriesianMilkShee.csv	4.1 KiB	627 B
PopulationReportTabel4_EastFriesianMilkShee.csv	2.7 KiB	445 B
PopulationReportTabel5_.csv	1.6 KiB	537 B
PopulationReportTabel6_EastFriesianMilkShee.csv	2.6 KiB	756 B
Year_Inbreeding_log_EastFriesianMilkShee	1.4 KiB	249 B
reg_inbreed.log	1.2 KiB	588 B
run_popreport.lst	1.4 KiB	525 B
run_popreport.stderr	261 B	82 B
run_popreport.stderr_head500	15.8 KiB	2.2 KiB
run_popreport.stderr_tail500	15.8 KiB	2.2 KiB
run_popreport.stdout	85.7 KiB	10.6 KiB
run_popreport.tex	62 B	62 B

Popreport_EastFriesianM

Post processing

- CSV file for each table and graph
- → do your own post processing

Summary

- Managing breeds for conservation (and production!)
 - set your targets
 - Use POPREP structure report to pick the low hanging fruits – and listen to following talks
 - Use POPREP inbreeding report for in depth inbreeding related analyses

Thank you for your attention