Use of genomic information for the determination of insemination doses per sire in a gene bank

C. Reimer[1,2], S. Weigend[1,2], T. Pook[2,3], J. Geibel[1,2]

[1] Friedrich-Loeffler-Institut, Institute for Farm Animal Genetics, Höltystraße 10, 31535 Neustadt, Germany
[2] University of Goettingen, Center for Integrated Breeding Research, Carl-Sprengel-Weg 1, 37075 Göttingen, Germany
[3] Wageningen University and Research, Animal Breeding and Genomics, Droevendaalsesteeg 1, 6700AH Wageningen, the Netherlands

Background

Important management considerations in gene banking of animal genetic resources

- How many and which specific breeders must be stored to represent the field population?
    - Core set
    - Proportion of segregating haplotypes

- How many insemination doses per sire should be stored?

- How is an insemination dose defined?
    - Number of motile sperms, defects etc.
    - AI technique used

Background

How many insemination doses per sire should be stored?

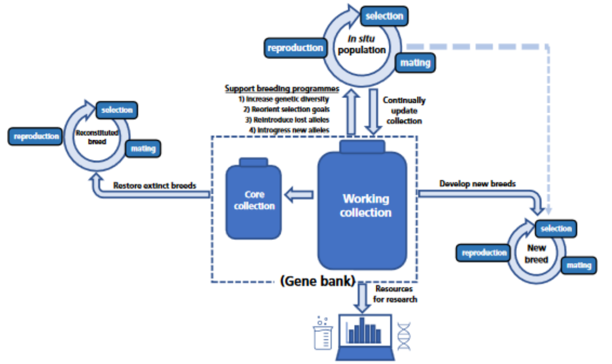
Dependent on the purpose:

1. Keeping a core collection in case of breed extinction
   - back-crossing on the basis of an alien breed
   - Storing gametes from both sexes

2. Supporting active breeding schemes from the cryo-conservation
   1. Increase diversity
   2. Reintroduce lost alleles
   3. …

➡ -Specific animals/ lines are wanted
-should be achieved in short term

FIGURE 5.1
Uses of gene bank collection (*ex situ in vitro* cryocollection)



Source: adapted from Berg P. & Windig J.J. 2017. Management of cryo-collections with genomic tools. In K. Oldenbroek, ed. *Genomic management of animal genetic diversity*, pp. 155–178. Wageningen, Netherlands, Wageningen Academic Publishers; and Tixier-Boichard, M. & Crooijmans, R. 2019. A universal tool to share knowledge about animal gene banks. Press release 5 of IMAGE project. Cited 22 September 2020. www.imageh2020.eu/Publications/PR5.pdf

FAO 2023

How many insemination doses per sire should be stored?

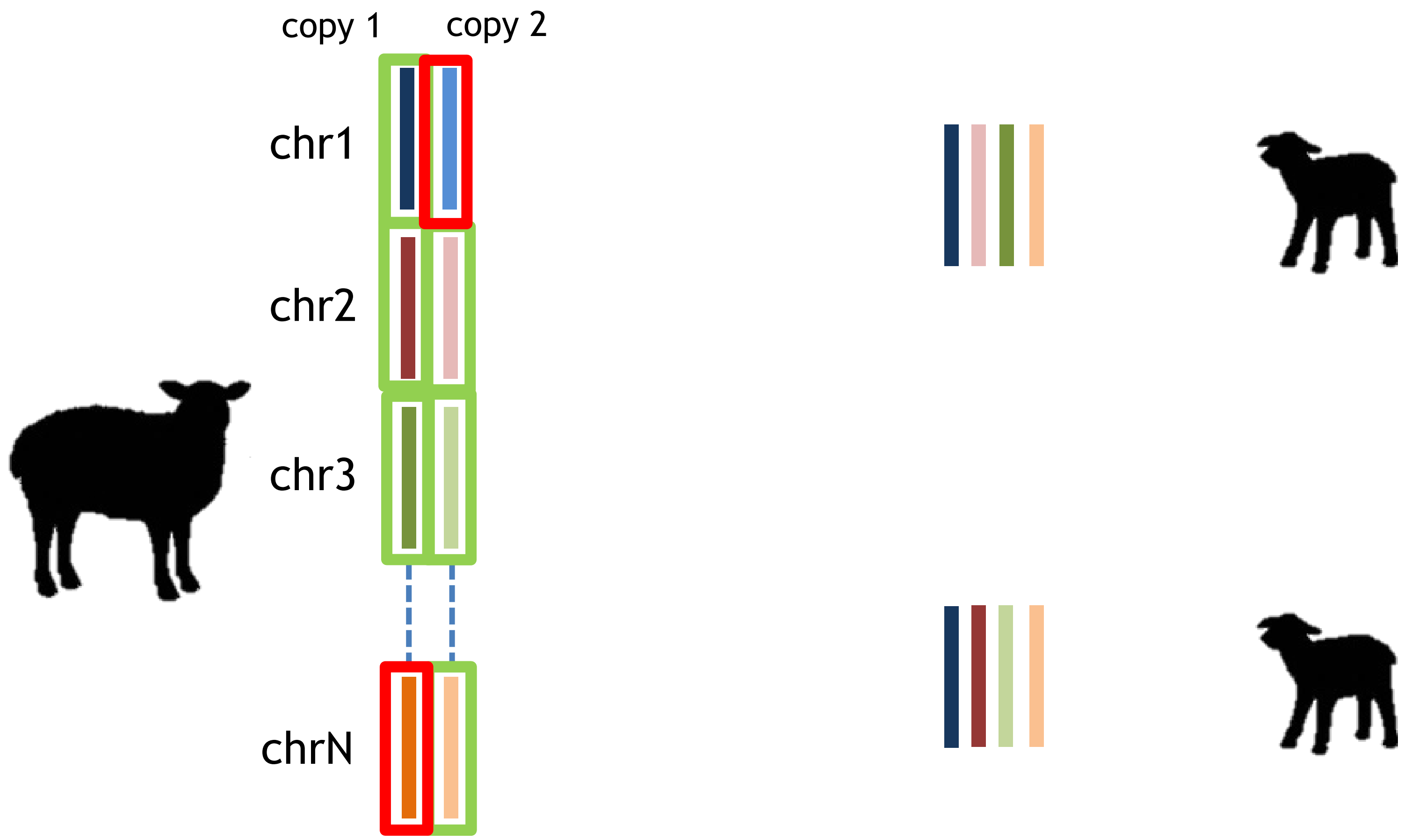
Aim:

A „simple“ formula to estimate how many doses are required to pass the whole genome of a gene-bank animal on to the next generation

e.g.: $$N_e = \frac{4N_m N_f}{N_m + N_f}$$

Reintroduction

Reintroduction of a sire:



Dependent on:

Number of offspring

- Inseminations
- Insemination success
- Litter size
- Survival till breeding age
- etc...

Number of chromosomes

Inbreeding

Theoretical probability

In diploid farm animals, every offspring carries 50 % of the paternal genome

The probility to inherit a certain chromosome copy is $p = 0.5$

The combined probability to find the same copy in N offspring is 0.5^N

The probability to find both copies in N offspring is one minus the probility to find either copy only

$$p = 1 - 0.5^N - 0.5^N = 1 - 2 * 0.5^N$$

Only copy 1   Only copy 2

Theoretical probability to transfer all chromosome copies

$$p = \left(1 - (1 - F) * 2 * 0.5^{N*B*W}\right)^{C}$$

- p: Probabilty to find all chromosome copies in offspring
- F: Inbreeding coefficient
- $N*B*W$: Number of offspring:
  - N = matings
  - B = insemination success
  - W = litter size
- C: Number of chromosomes

Simulation

Simulation with MoBPS (Pook et al., 2020)

Insemination success

Inseminations

litters
(binomial 0/1)

50 repeats

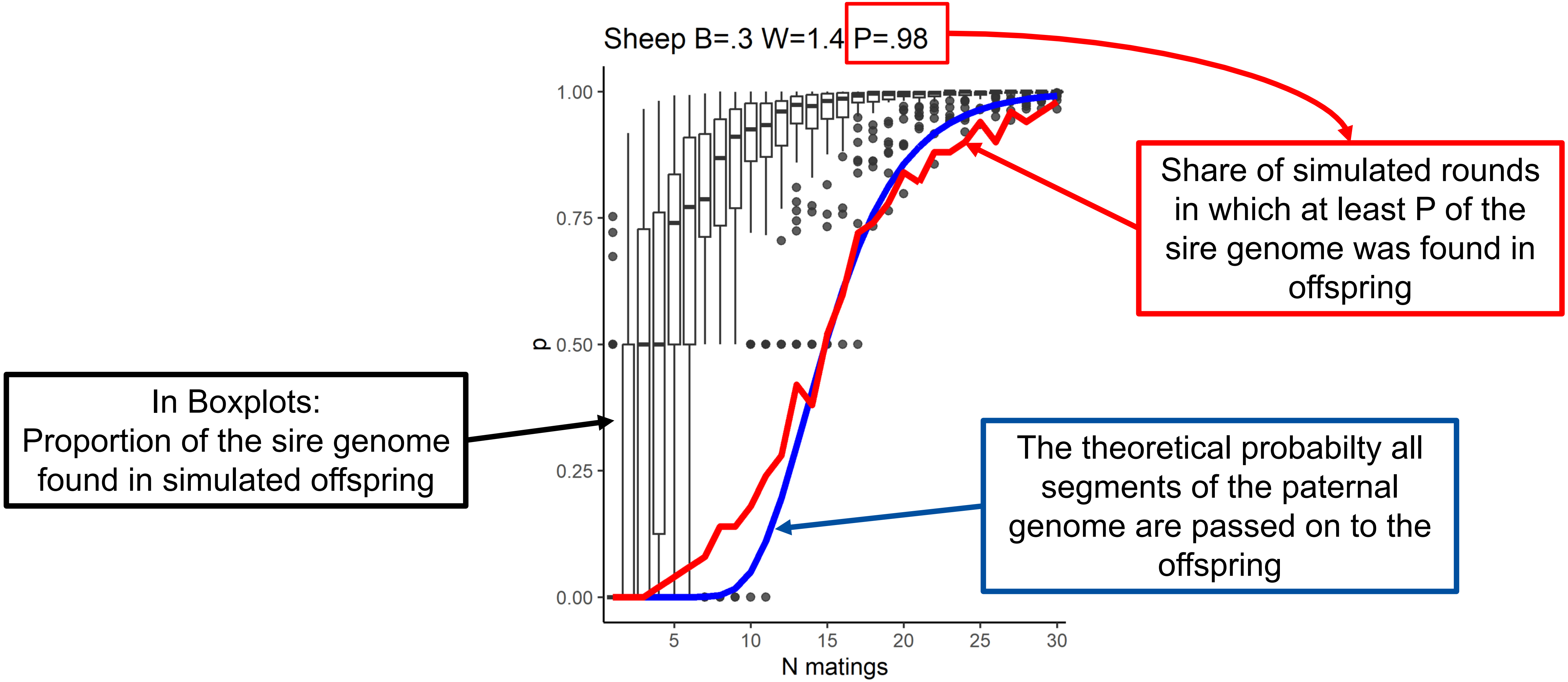
litter size

Litter size
(binomial, (μ, σ))

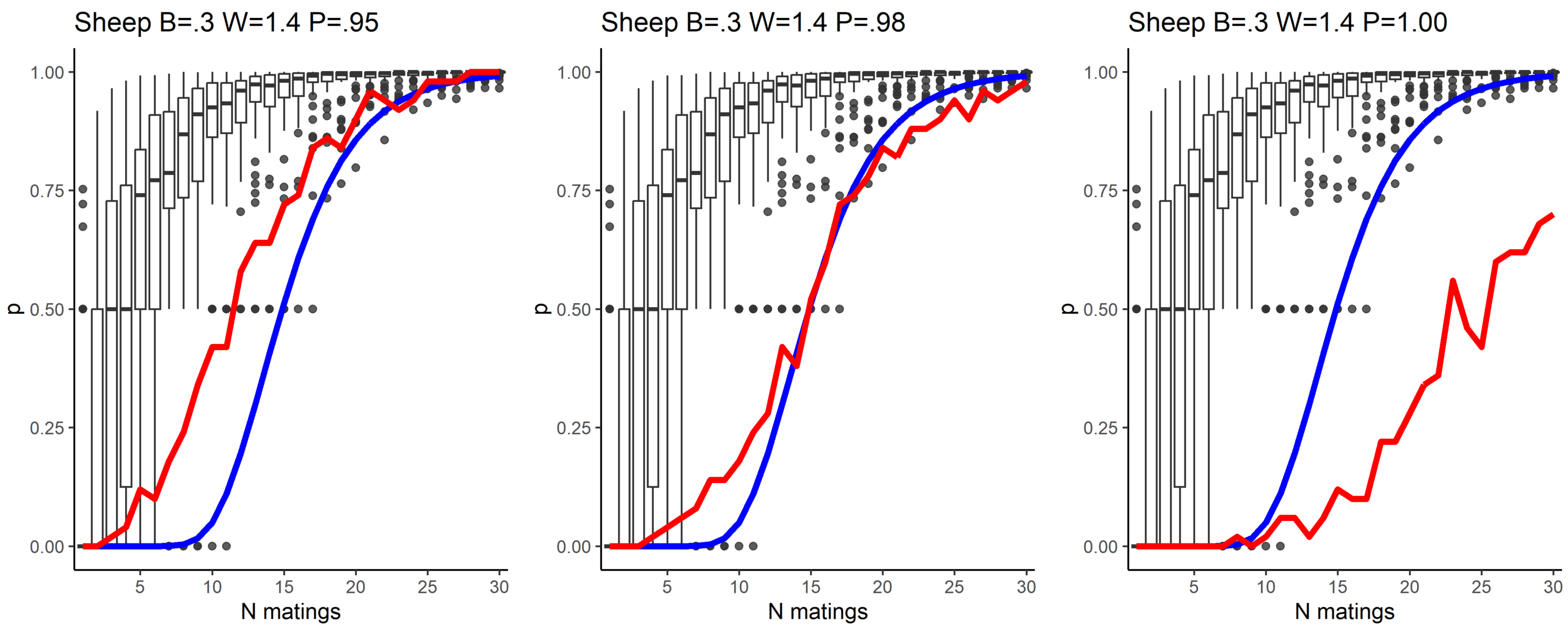
Percentage of simulations with minimum proportion P of genome sampled

Species and individual inbreeding coefficient

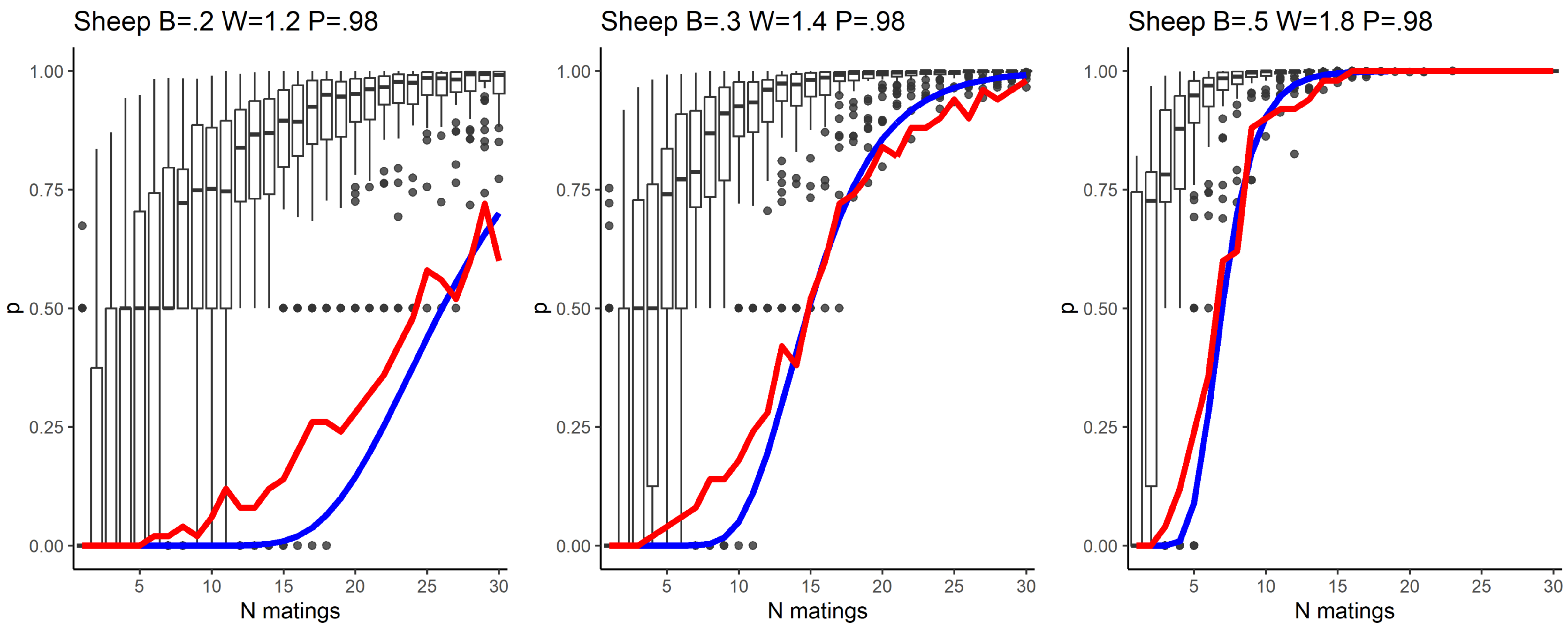
Simulation results



Simulation results

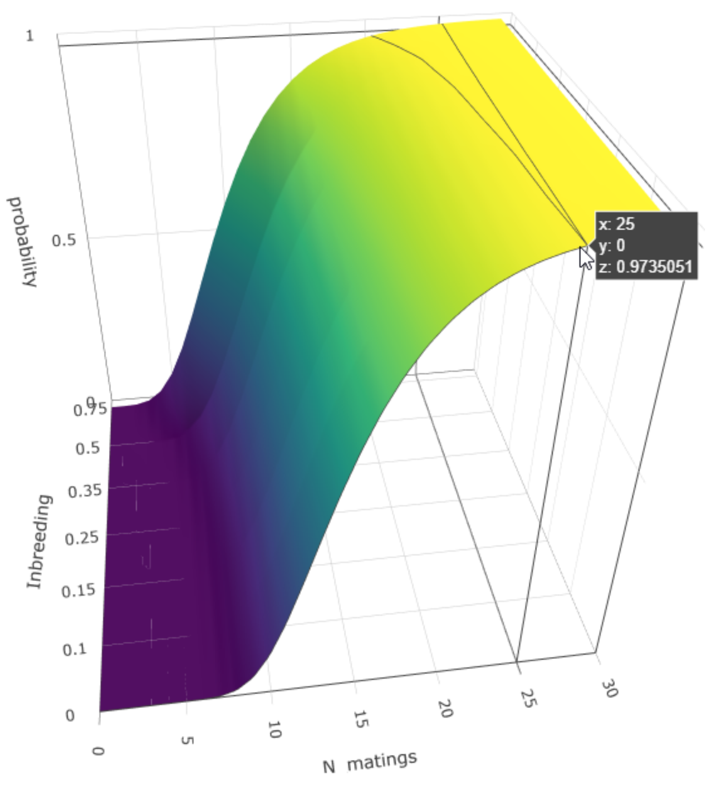


Simulation results

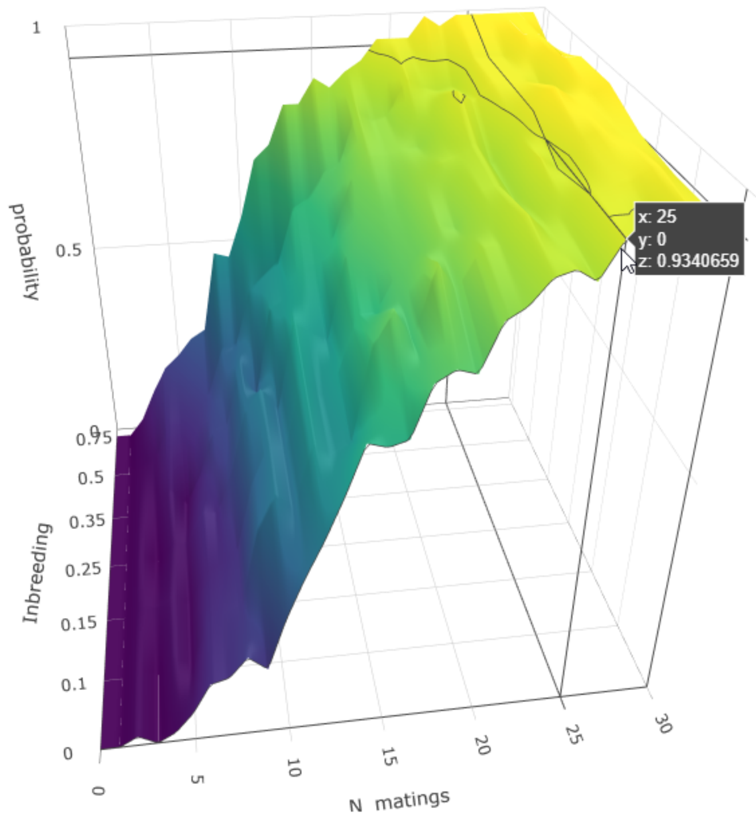


Simulation with inbreeding

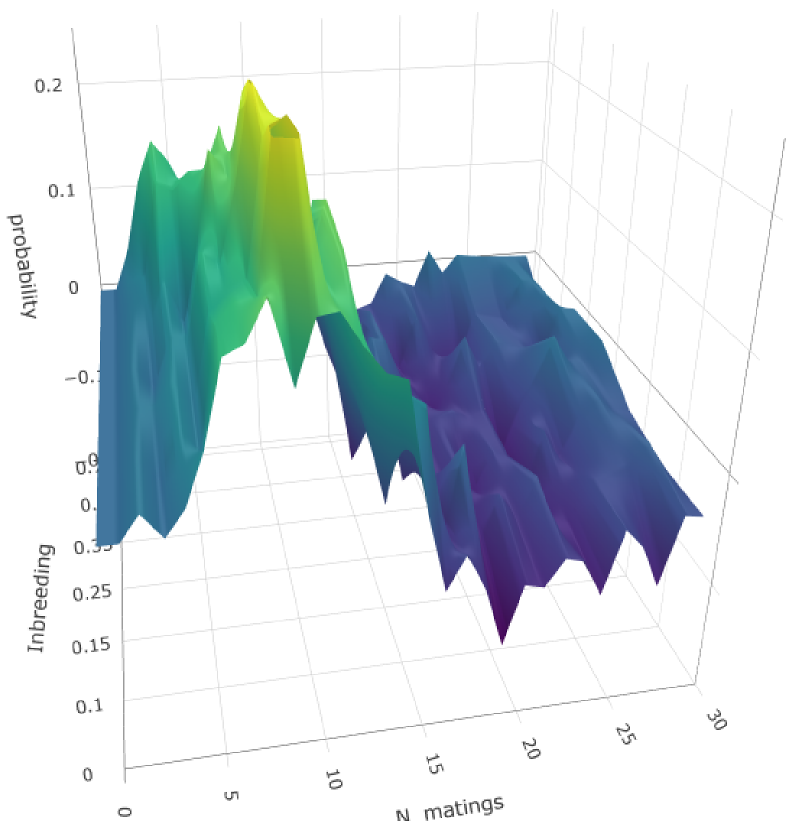
Expectation



Simulation



Simulation - Expectation



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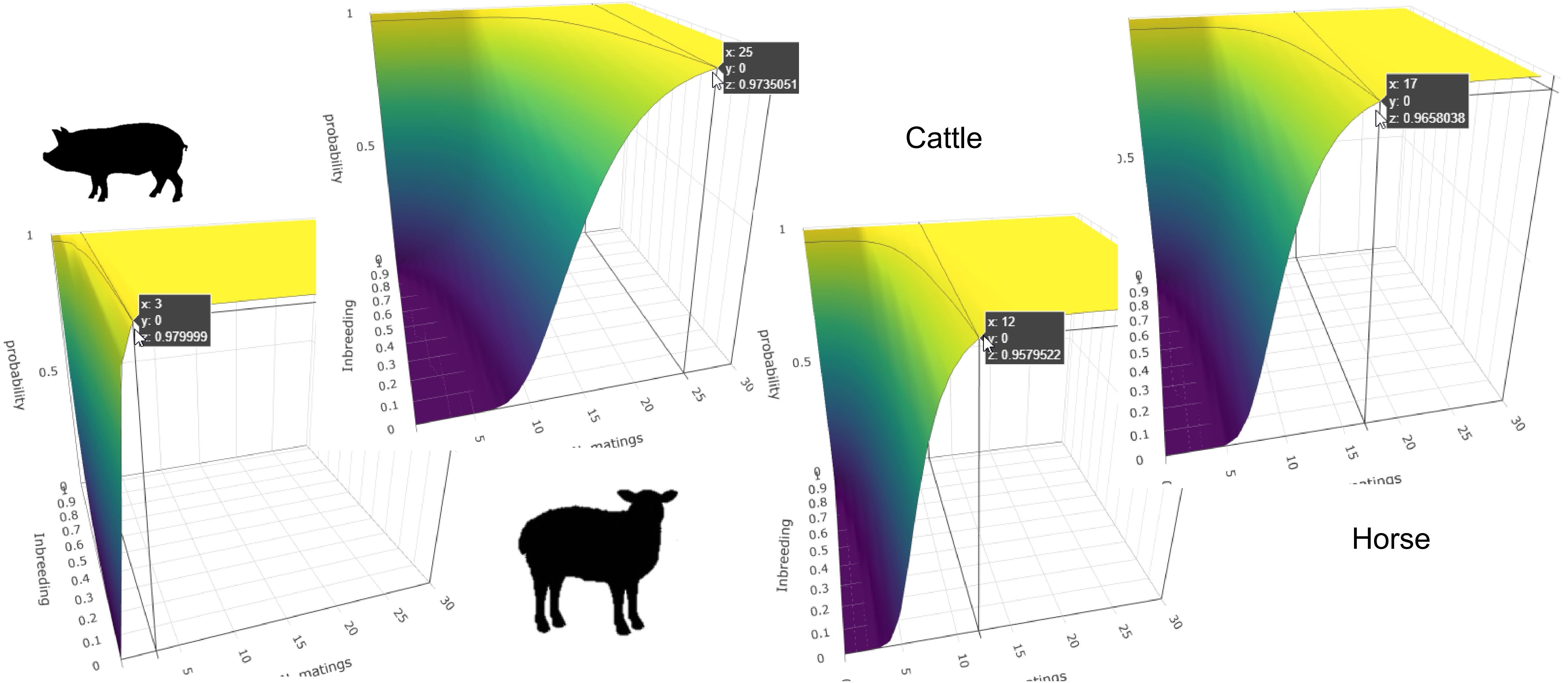
Application in active gene banking

Biological parameters used at the German Gene Bank

Factor	Pig	Sheep	Cattle	Horse
B(insemination success)	30%	30%	80%	60%
W(litter size)	6-12	1.4	1	1
Chromosomes	18	26	29	31
F(inbreeding)	?	?	?	?

Application in active gene banking



Conclusion

The developed formula is easily applicable under field conditions

The formula is supported by stochastic simulations addressing variation in insemination success, litter size and recombination

It predicts that reintroduction success is highly dependent on species characteristics, inbreeding, reproductive performance parameters and the number of inseminations.

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Thank you for your attention!

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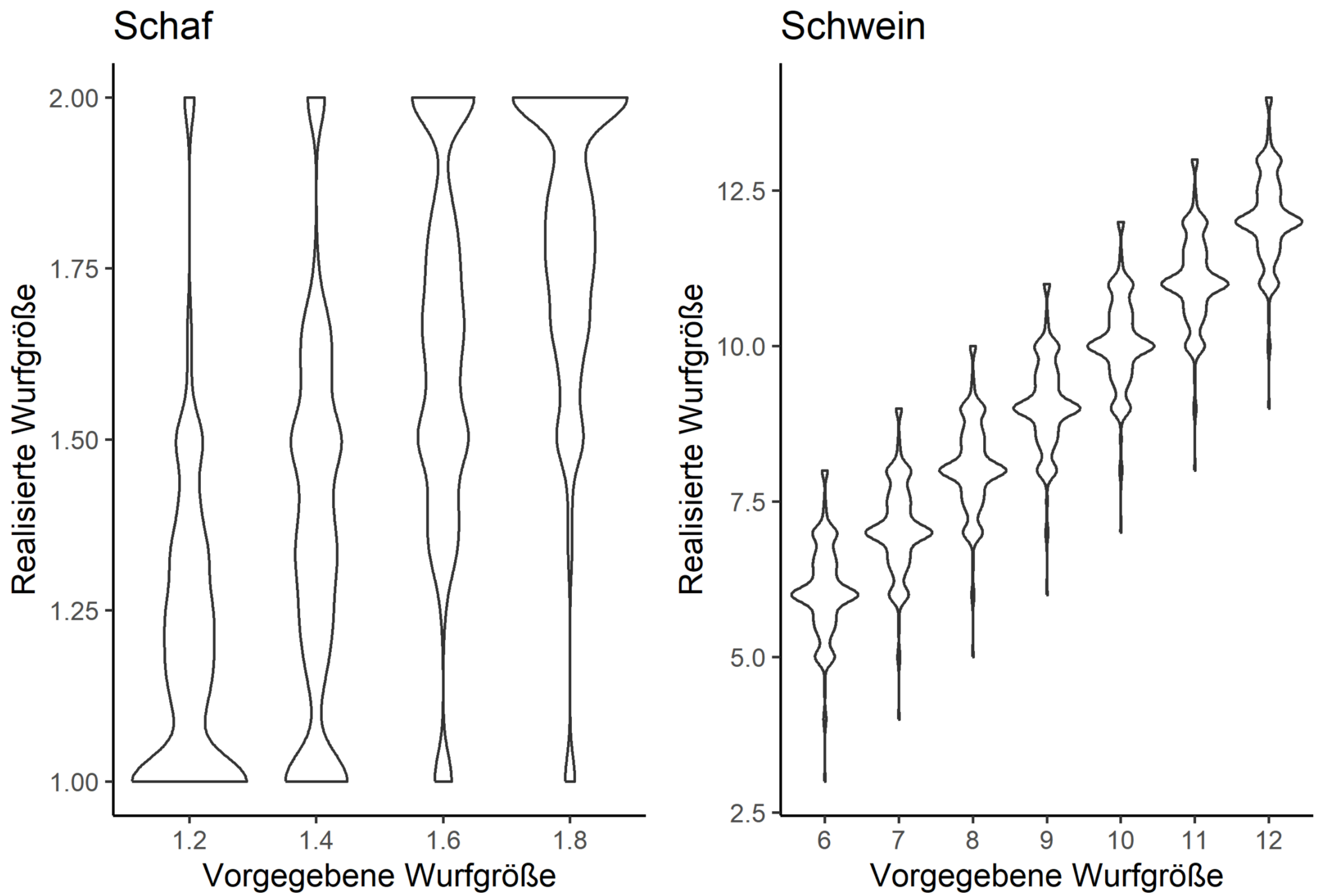
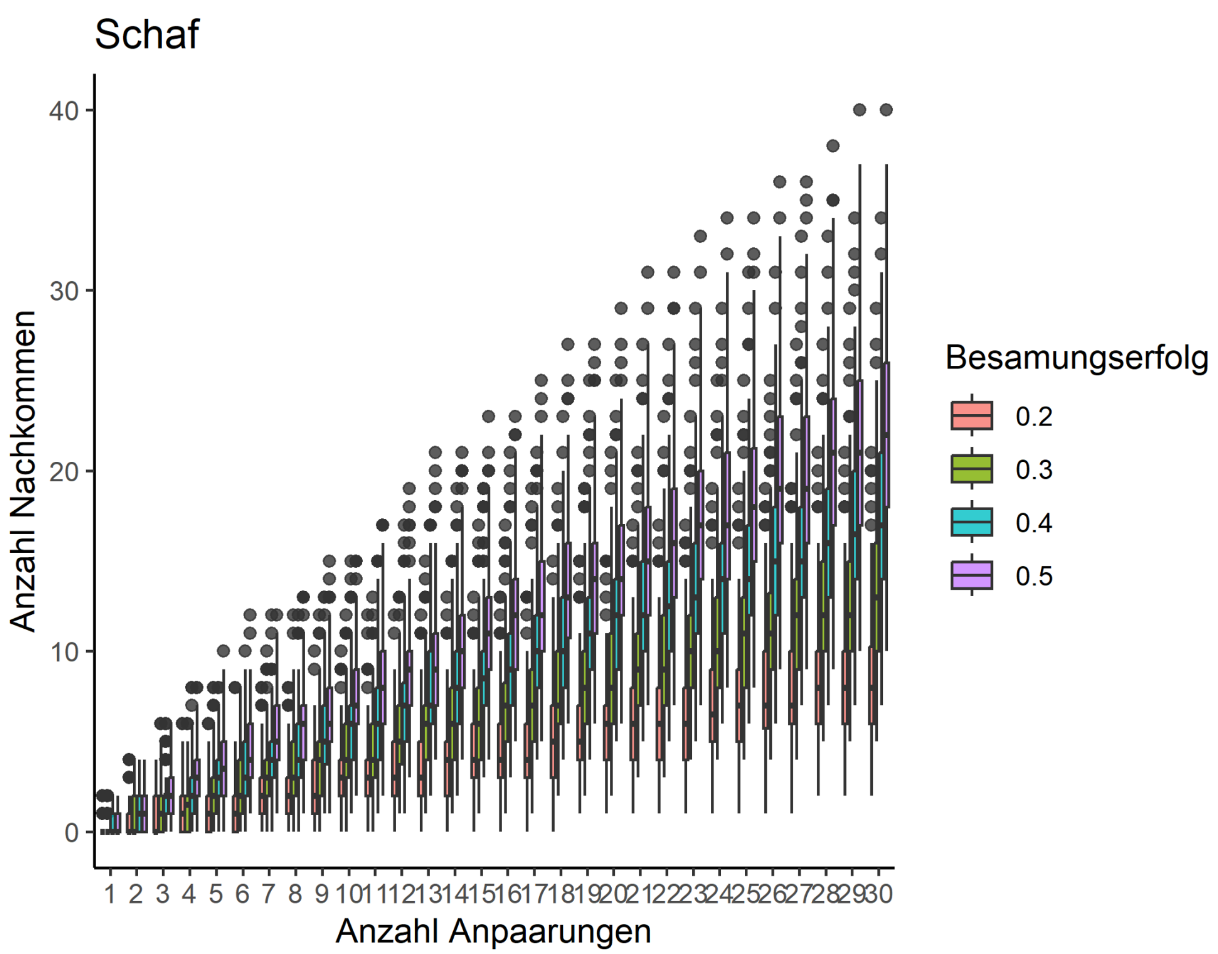
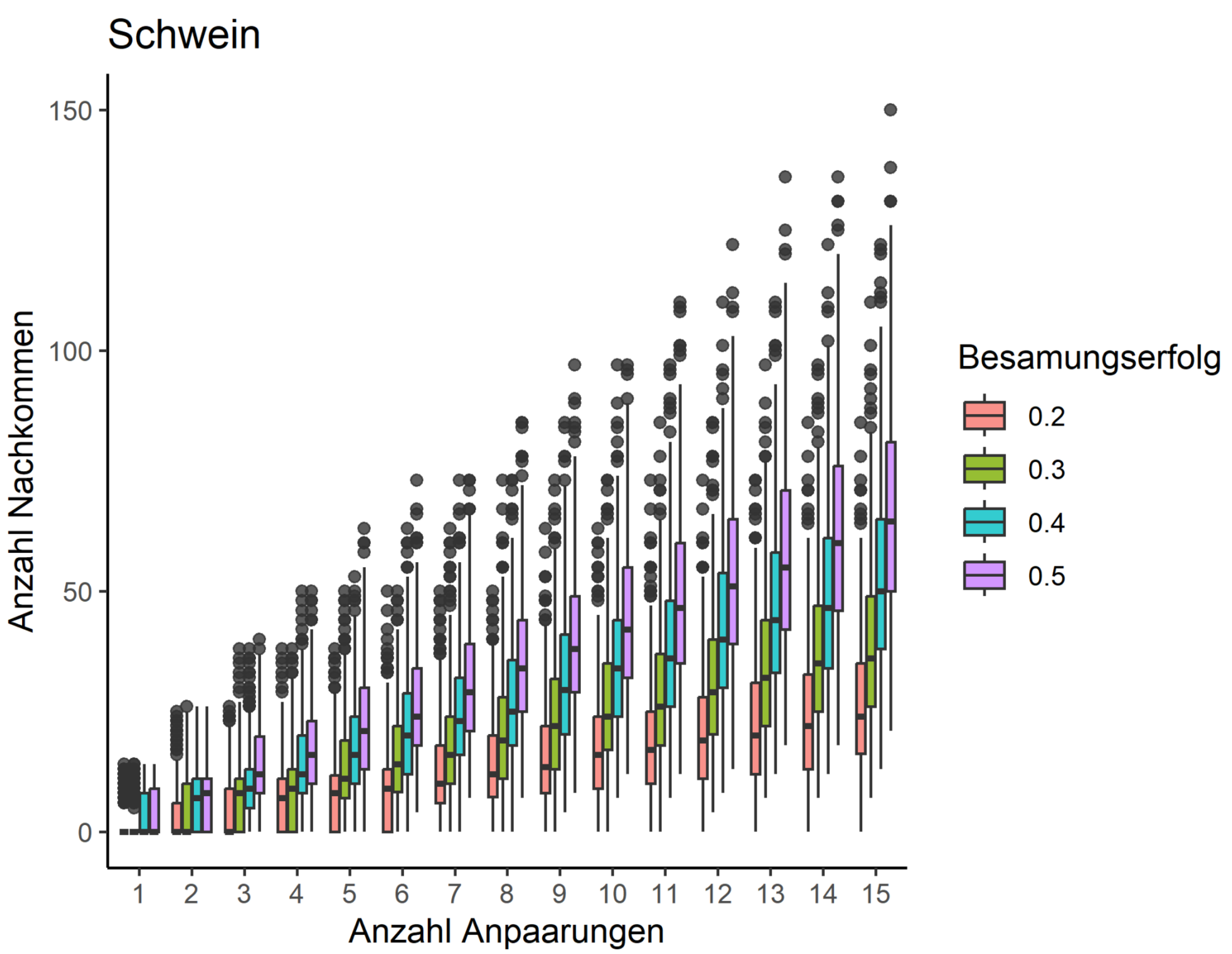
Simulation



Schaf
Realisierte Wurfgröße
2.00
1.75
1.50
1.25
1.00
1.2
1.4
1.6
1.8
Vorgegebene Wurfgröße
Schwein
Realisierte Wurfgröße
12.5
10.0
7.5
5.0
2.5
6
7
8
9
10
11
12
Vorgegebene Wurfgröße

Simulation


Schaf
Anzahl Nachkommen
40
30
20
10
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
Anzahl Anpaarungen
Besamungserfolg
0.2
0.3
0.4
0.5


Schwein
Anzahl Nachkommen
150
100
50
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Anzahl Anpaarungen
Besamungserfolg
0.2
0.3
0.4
0.5

Befruchtungserfolg (B) und Wurfgröße (W) haben direkten Einfluss auf die Anzahl erzeugter Nachkommen

$$p_{alles} = 1 - 2 * 0.5^{N*B*W}$$

Bei Inzucht $(Inzuchtkoeffizient\ F)$, entstehen zwei Fälle:

- Mit einer Wahrscheinlichkeit F sind beide Kopien gleich. Keine Kopie geht verloren
- Verlust kann nur $1 - F$ Fällen eintreten

$$p_{alles} = 1 - (1 - F) * 2 * 0.5^{N*B*W}$$

Erweiterung auf mehrere Chromosomen:

Die Wahrscheinlichkeit alle Chromosomen zu erhalten entspricht er kombinierten Wahrscheinlichkeit für jedes einzelne Chromosom jede Kopie zu erhalten.

$$p_{alles_{|}chr1} = 1 - (1 - F) * 2 * 0.5^{N*B*W}$$

$$\boldsymbol{p_{alleChr}} = p_{allesChr1} * pa_{llesChr2} * \dots * pall_{esChr\boldsymbol{C}} = \boldsymbol{(1 - (1 - F) * 2 * 0.5^{N*B*W})^{C}}$$