Poznań University of Life Sciences
FACULTY OF VETERINARY MEDICINE AND ANIMAL SCIENCE
Department of Genetics and Animal Breeding

WAGENINGEN UNIVERSITY & RESEARCH

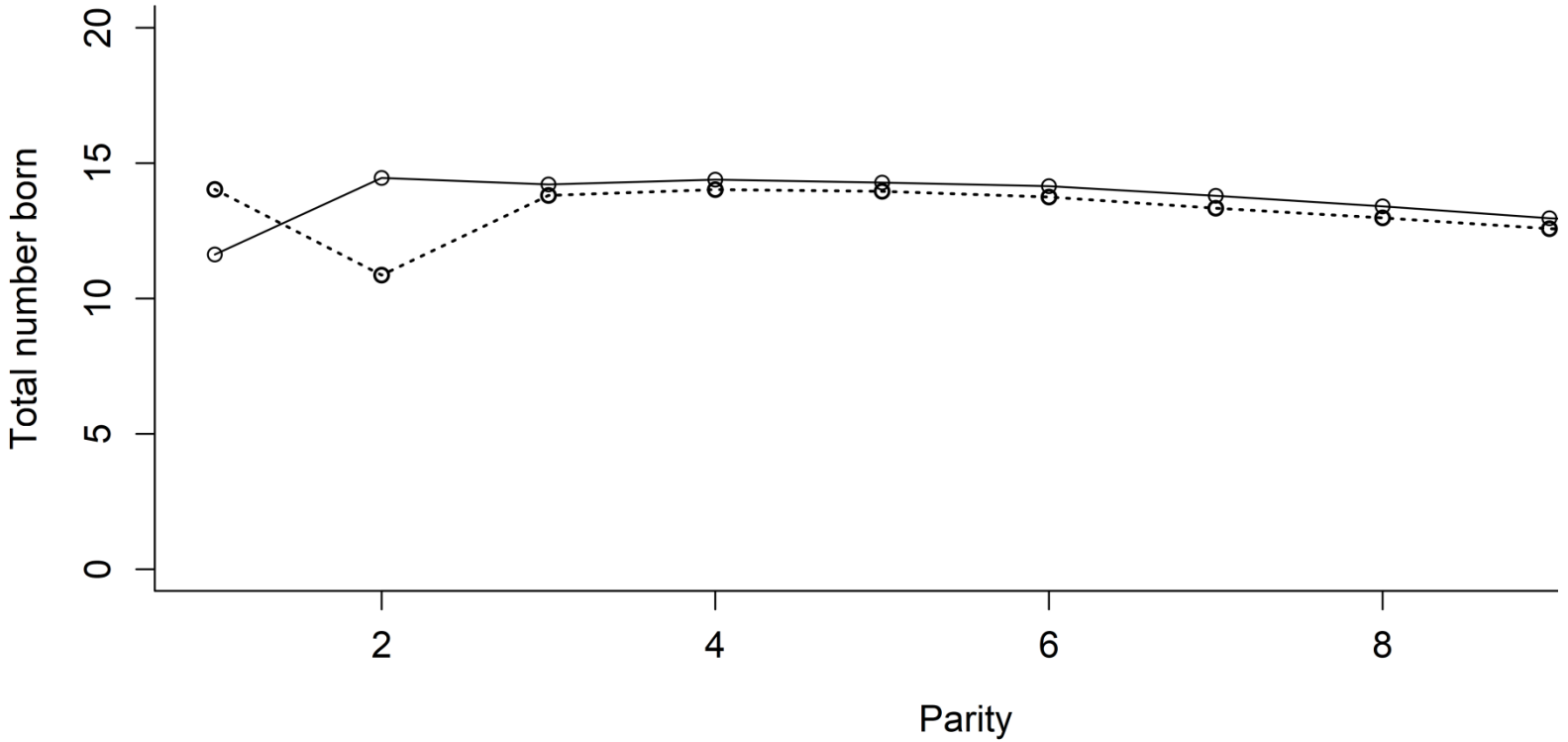
Topigs Norsvin

Verifying the existence of second litter syndrome in pigs

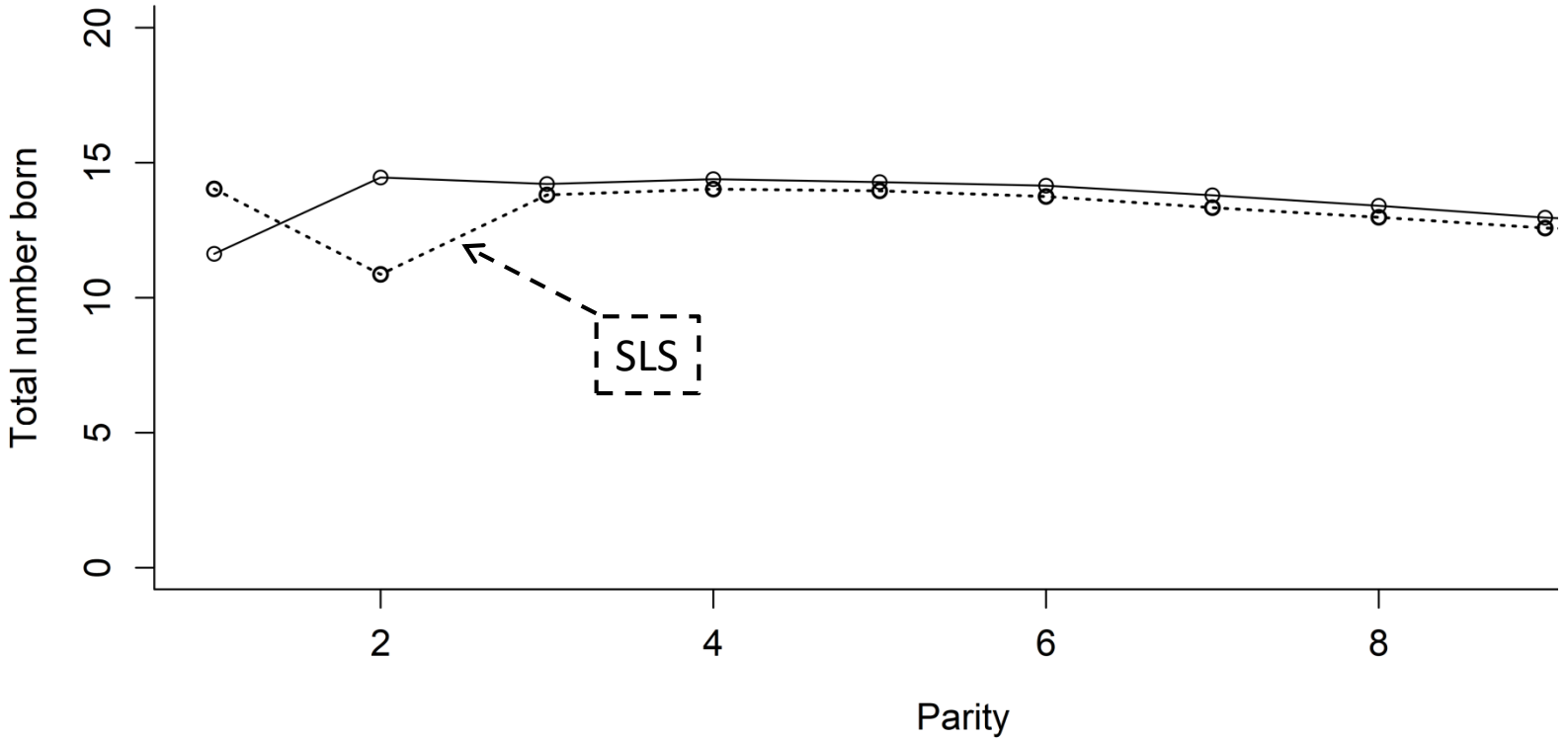
Marcin Pszczola, Egbert F. Knol, Han A. Mulder, Ewa Sell-Kubiak

twitter @marcinTHEbee

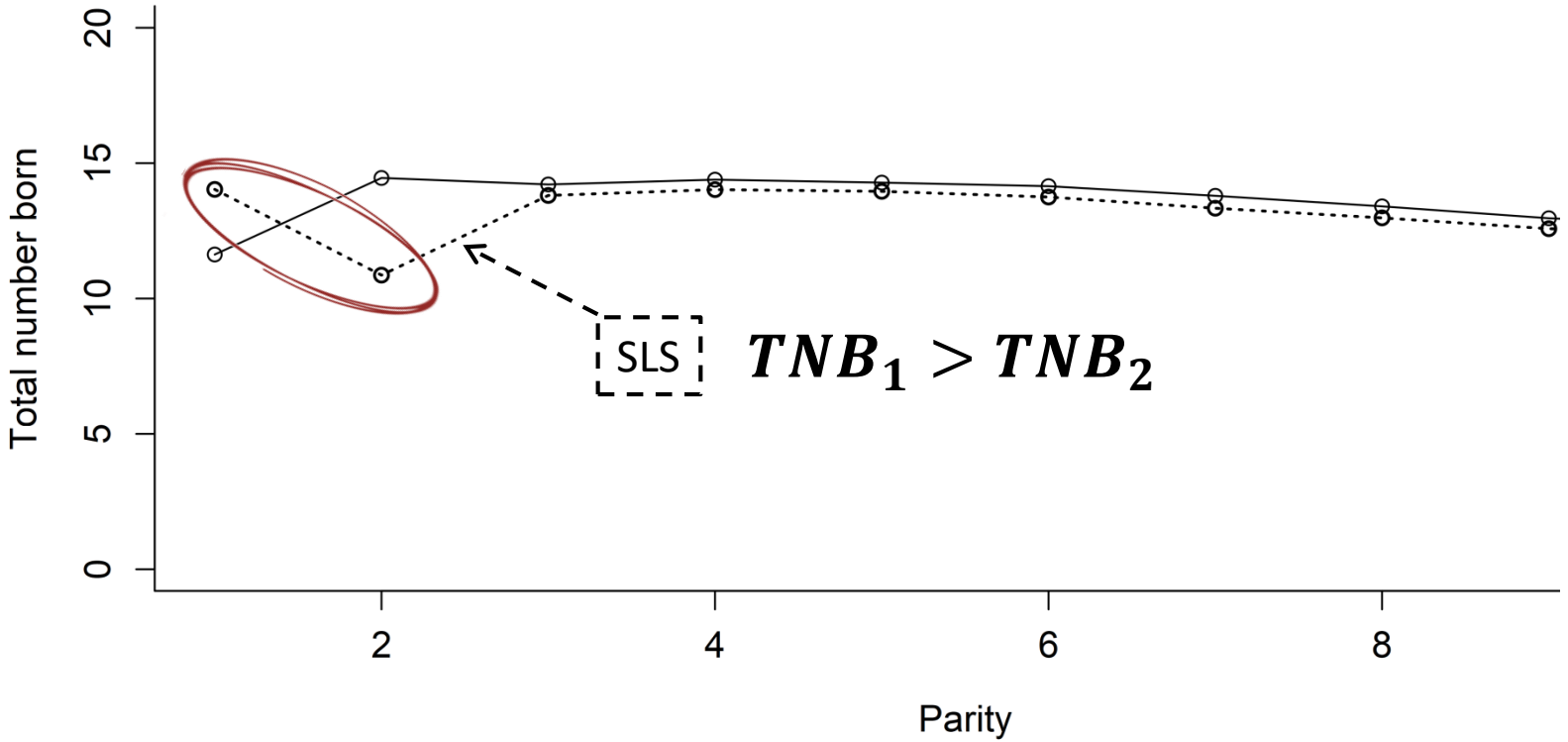
Total number of born piglets (TNB) in subsequent parities



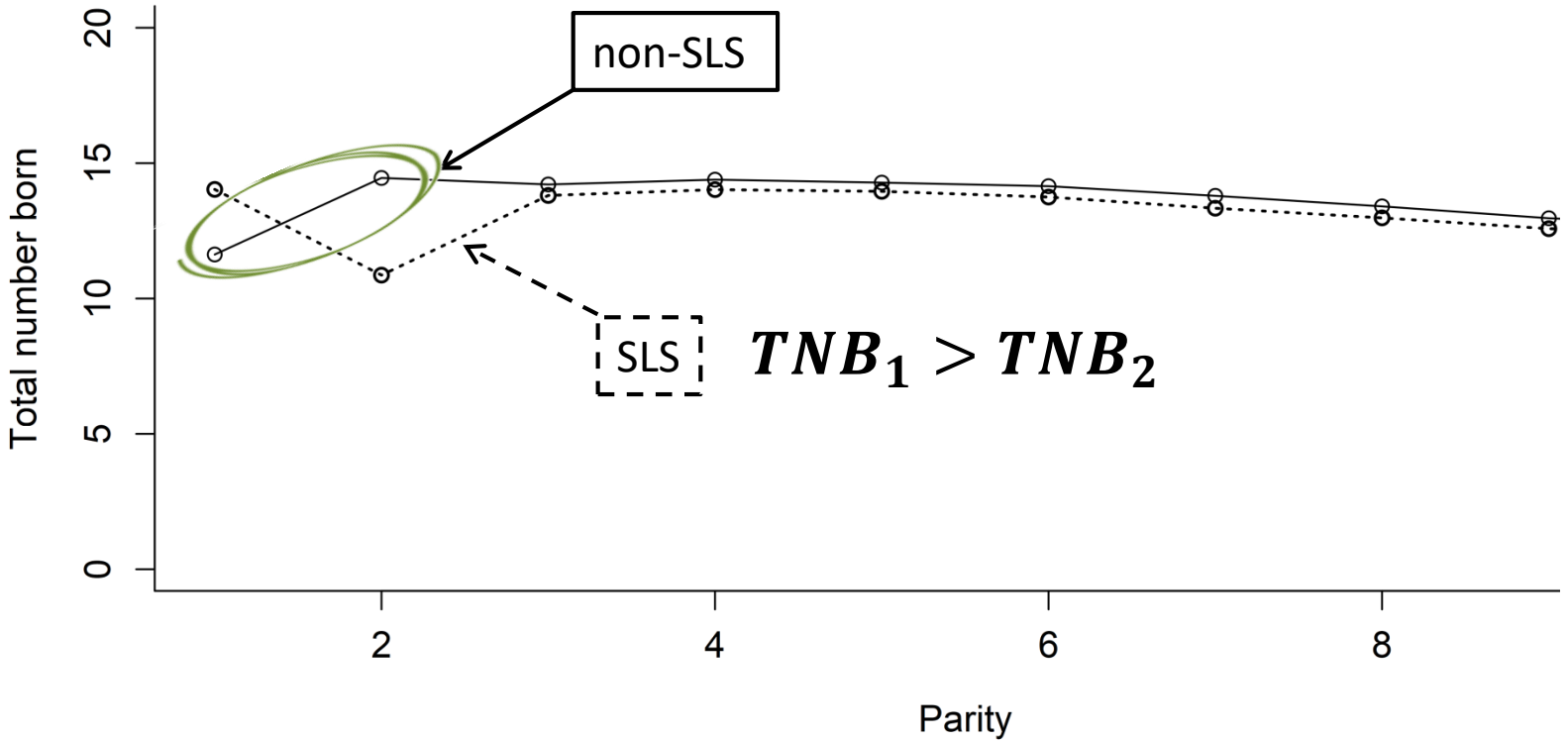
TNB in subsequent parities



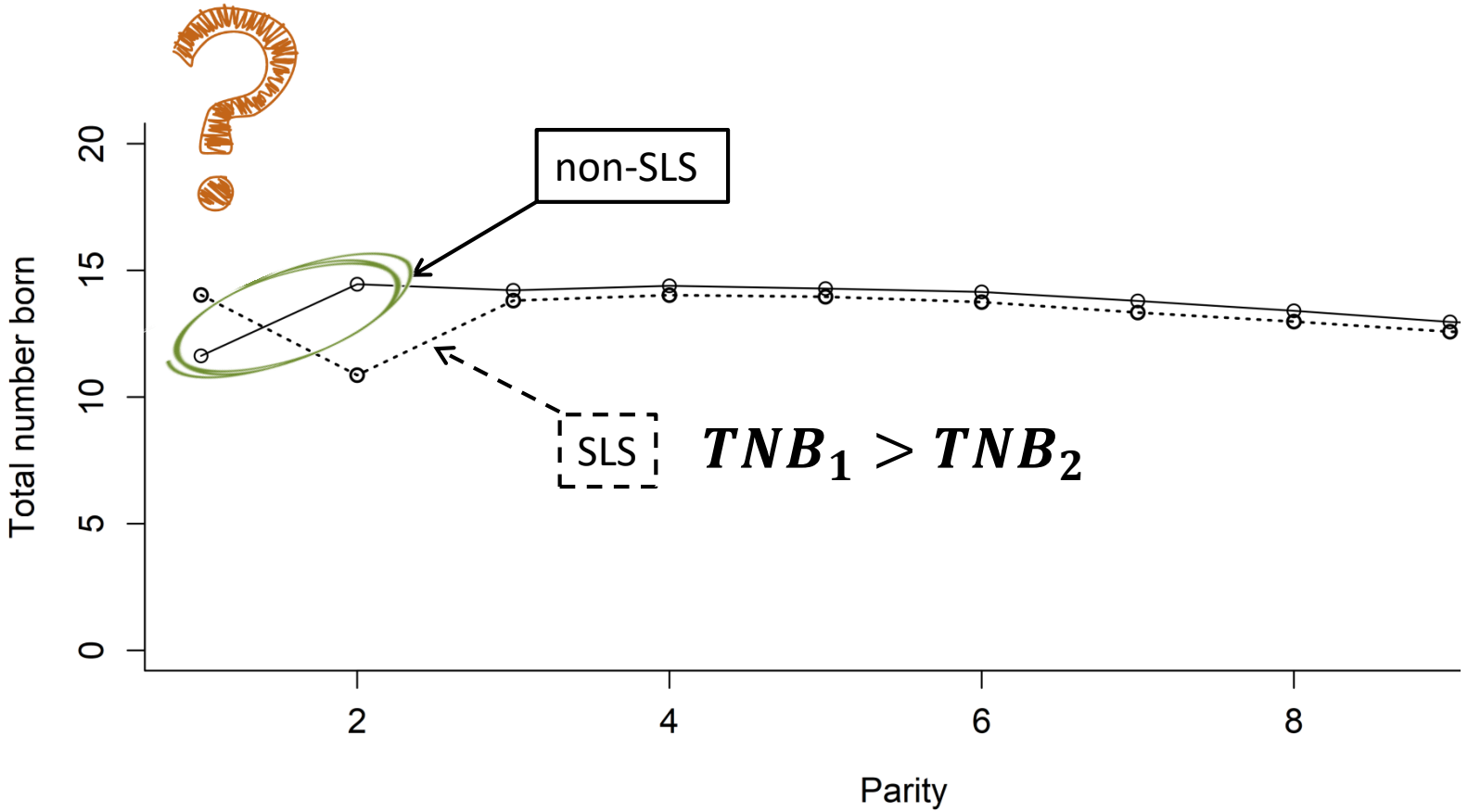
TNB in subsequent parities



TNB in subsequent parities



TNB in subsequent parities



DATA

46 218

SLS

15 398

non-SLS

30 820

Second litter syndrome (**SLS**)

does not exist!

SIMULATION

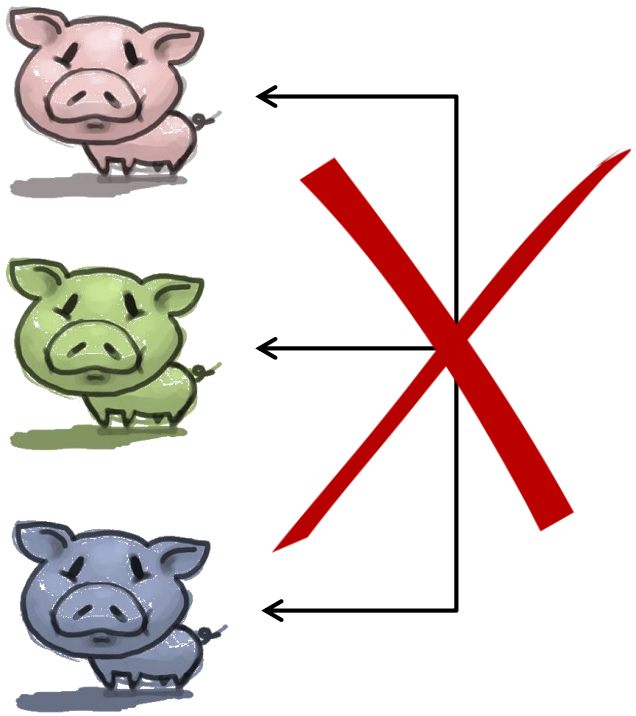
50k sows

9 correlated parities

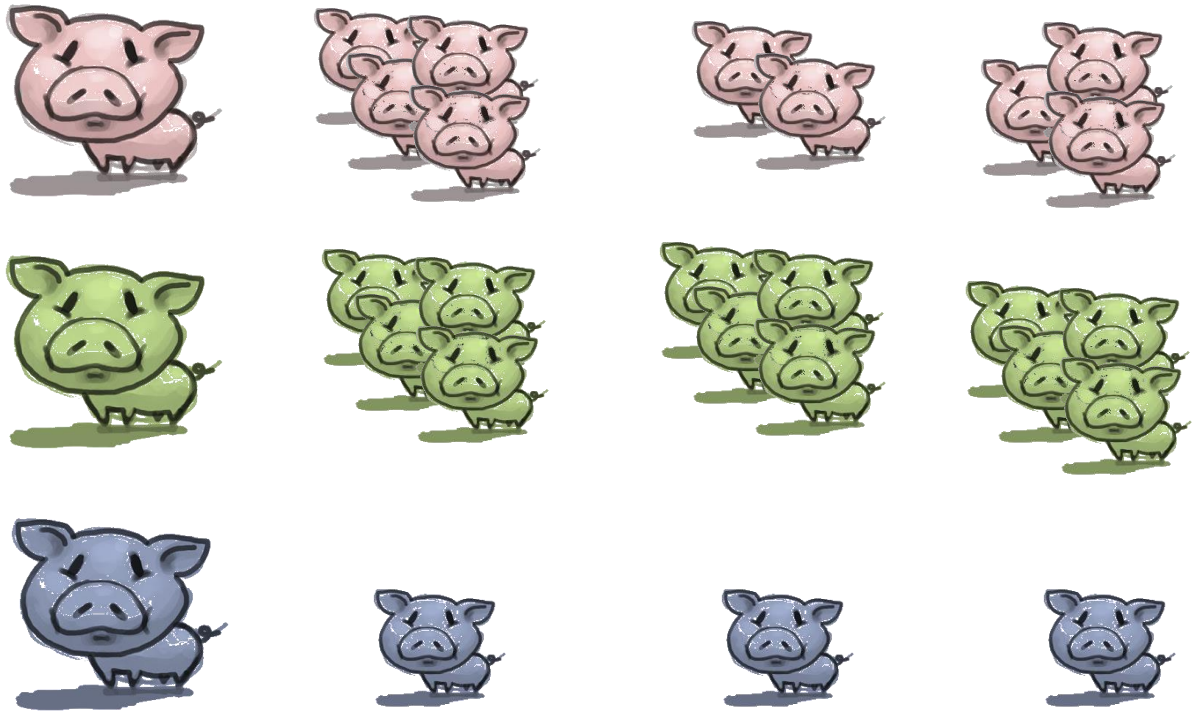
normal distribution of TNB

100 replicates

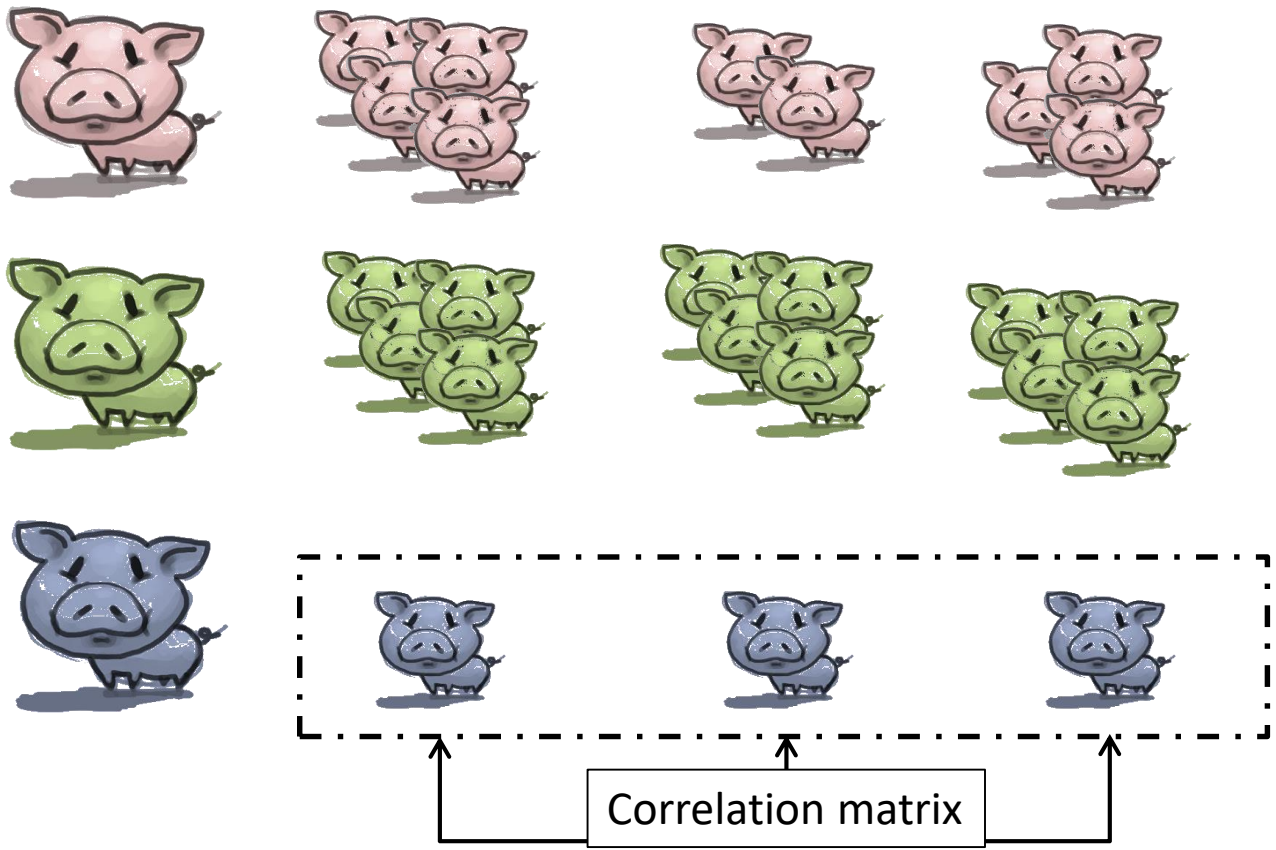
SIMULATION SETUP



SIMULATION SETUP



SIMULATION SETUP



Mean and SD of TNB across parities

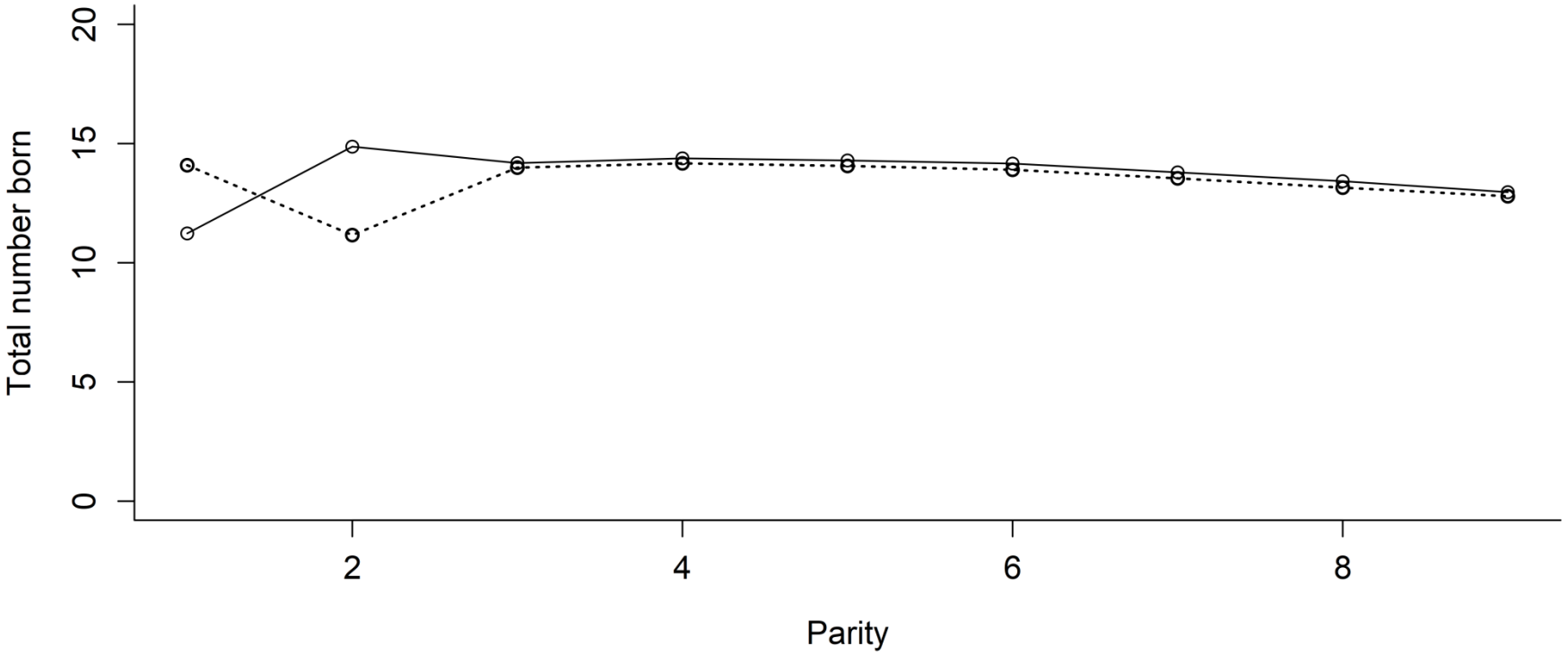
Parity	Mean	SD
1	12.40	3.03
2	13.33	3.37
3	14.09	3.42
4	14.29	3.66
5	14.19	3.55
6	14.04	3.56
7	13.68	3.52
8	13.30	3.45
9	12.87	3.31

Correlations between parities

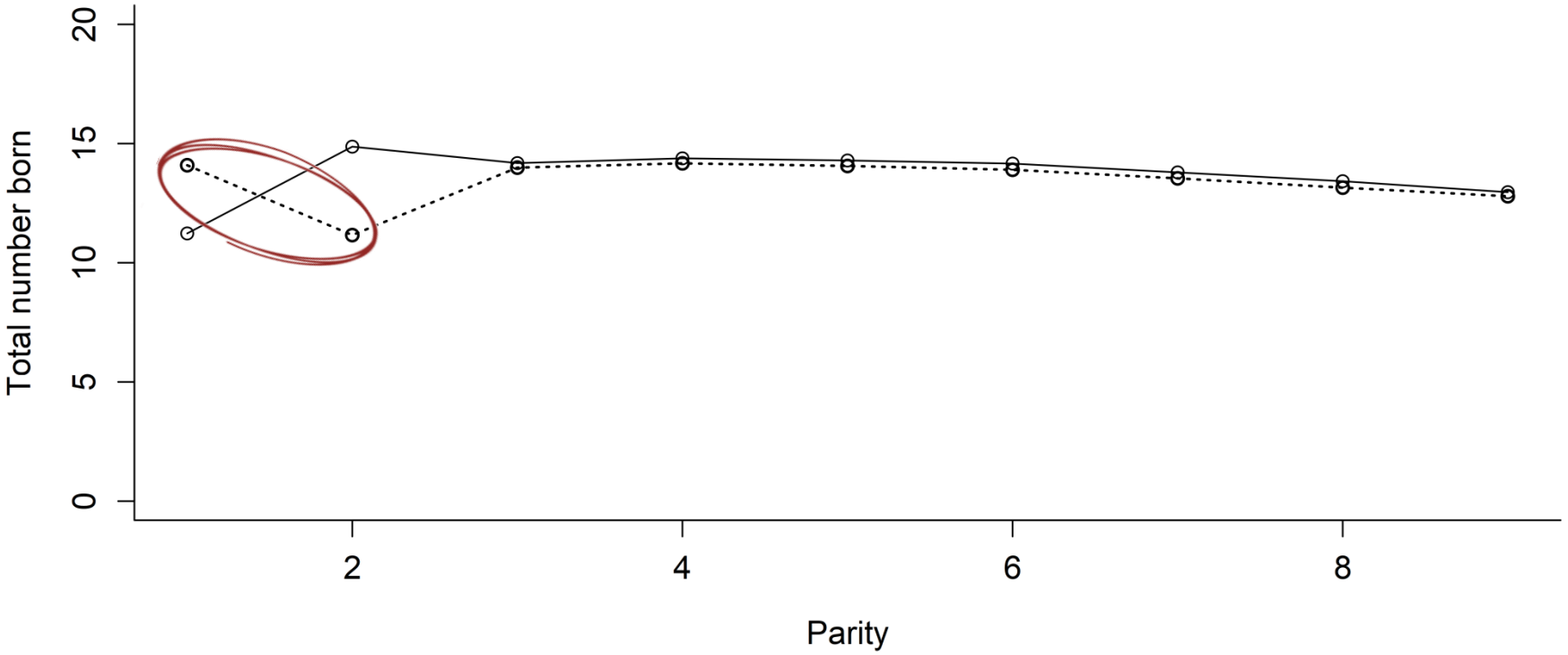
Parity	2	3	4	5	6	7	8	9
1	0.20							
2	0.19	0.21						
3	0.19	0.21	0.24					
4	0.18	0.21	0.25	0.26				
5	0.17	0.2	0.25	0.27	0.28			
6	0.16	0.2	0.24	0.27	0.28	0.30		
7	0.16	0.19	0.24	0.26	0.28	0.30	0.31	
8	0.15	0.19	0.23	0.26	0.28	0.30	0.31	0.33

Mean = 0.24, Min= 0.15, Max = 0.34

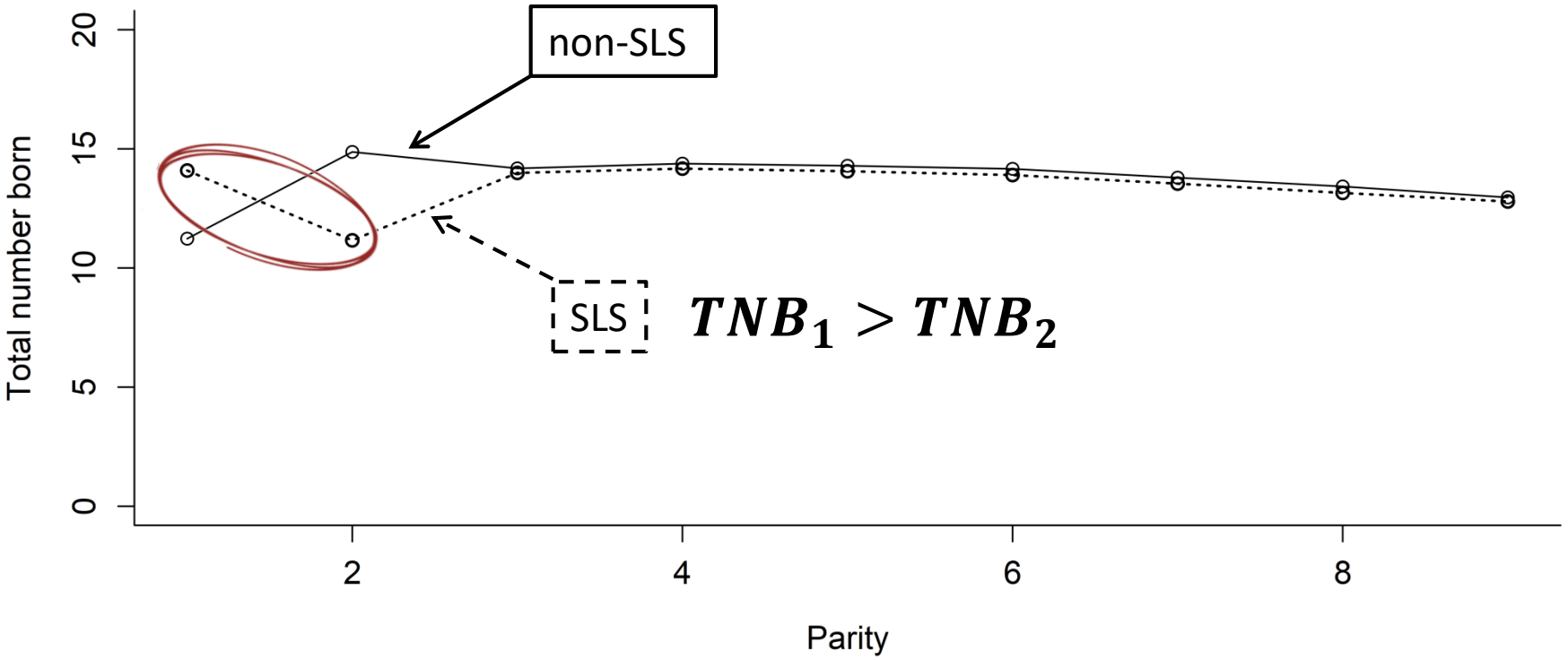
[**Simulated**] TNB in subsequent parities



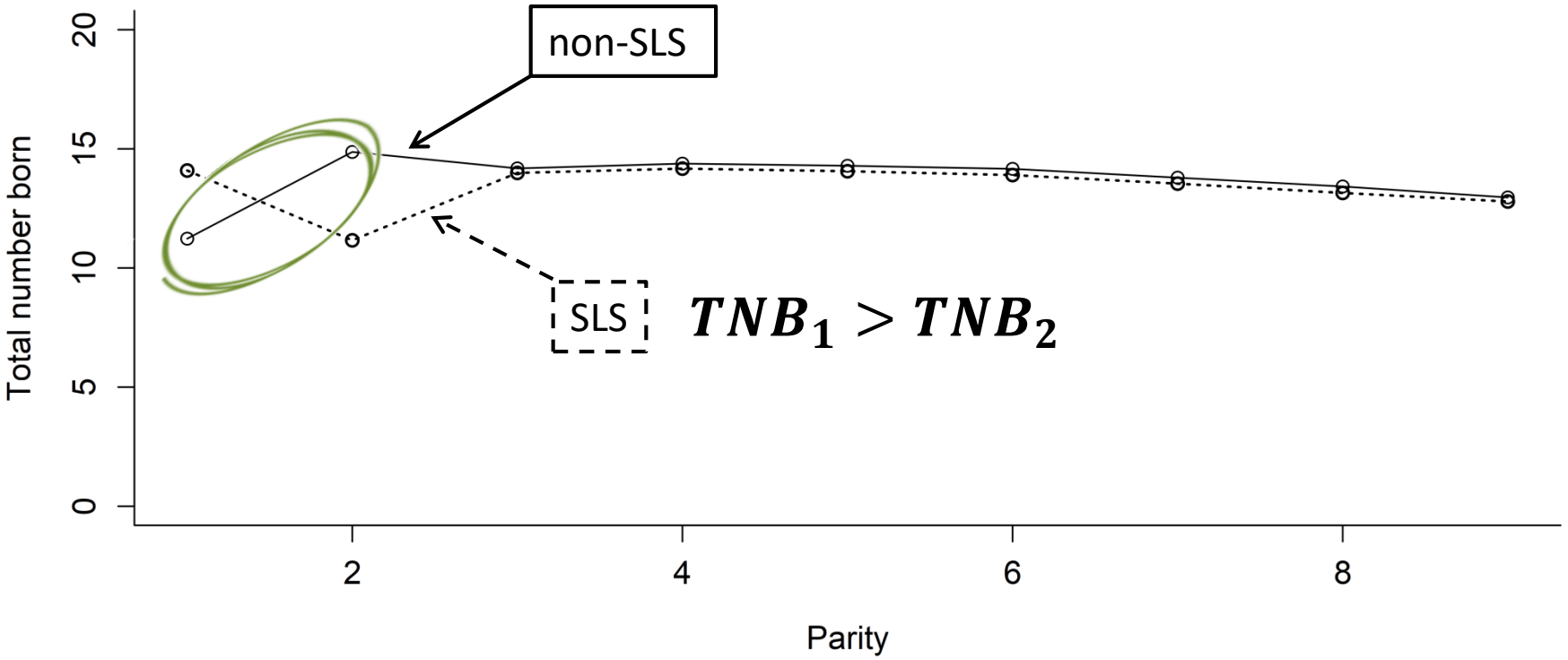
[**Simulated**] TNB in subsequent parities



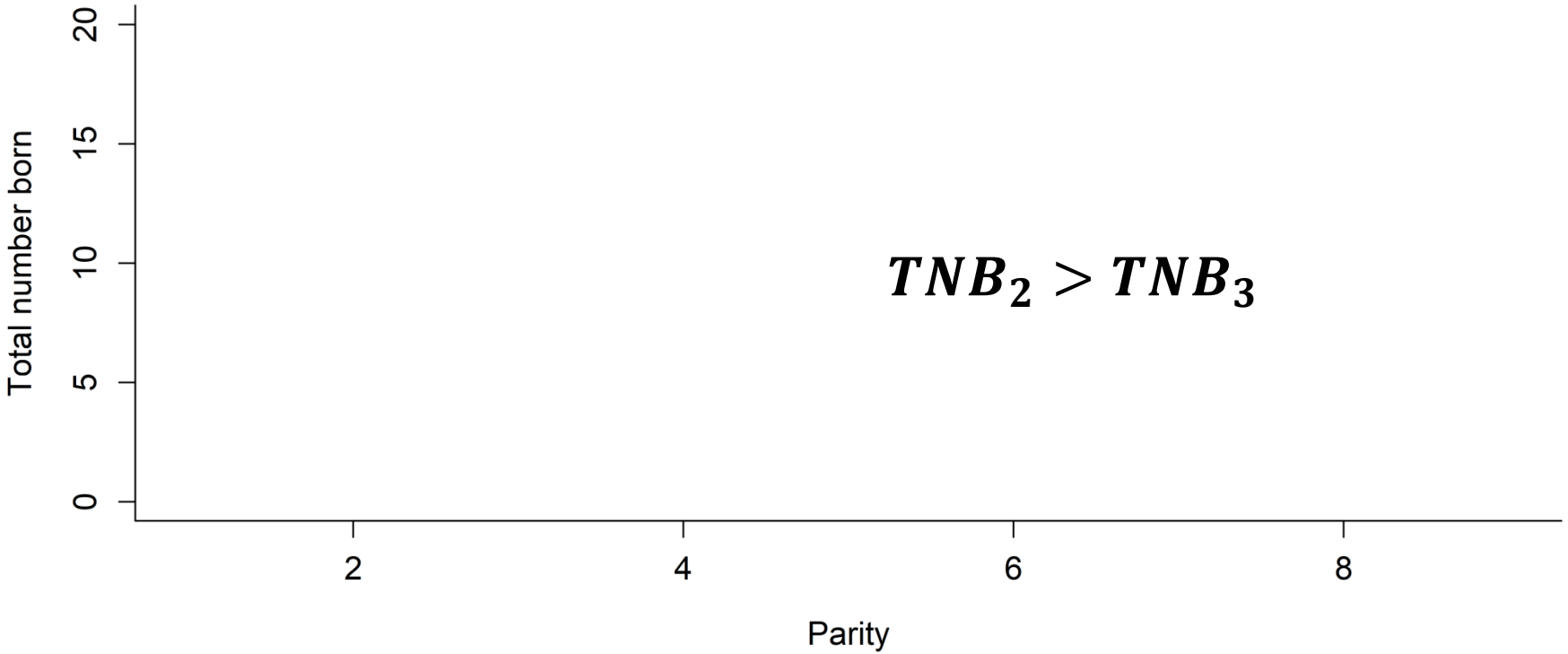
[**Simulated**] TNB in subsequent parities



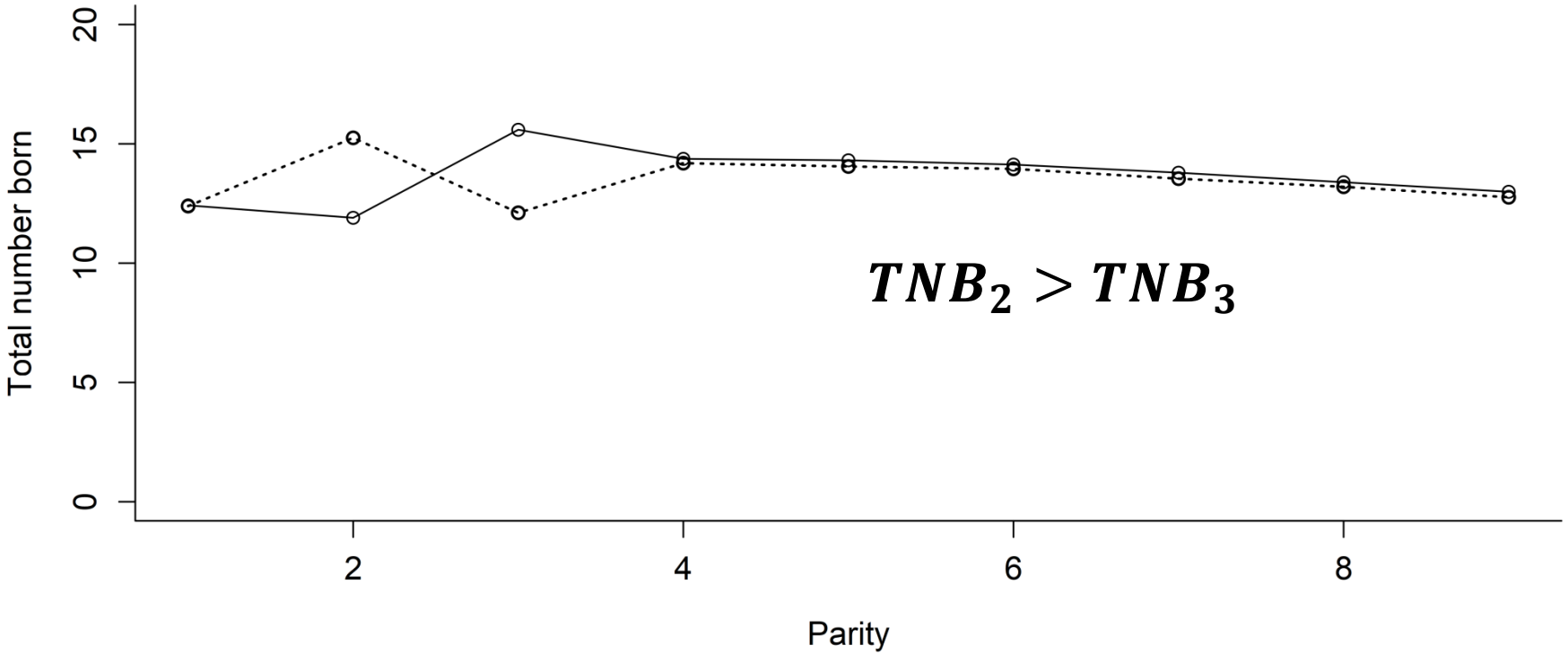
[**Simulated**] TNB in subsequent parities



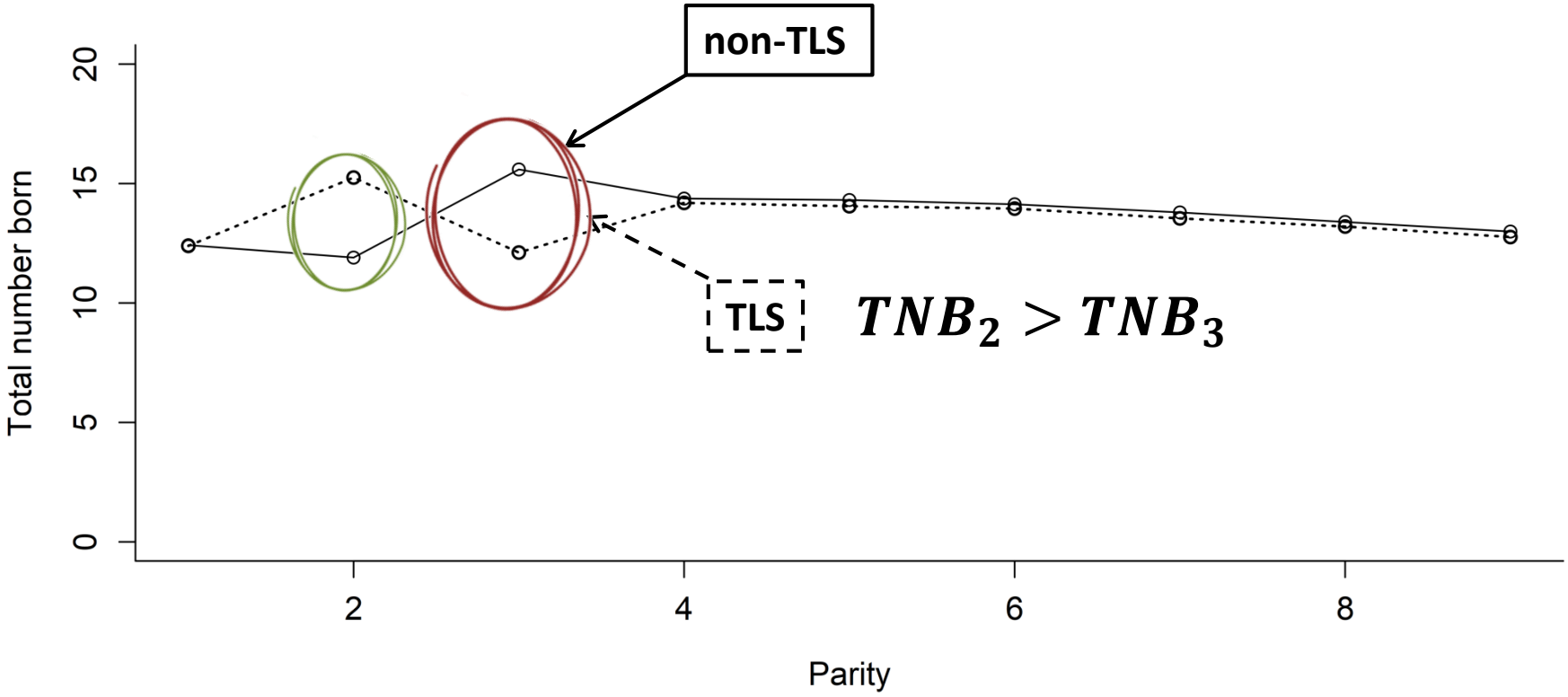
[**Simulated**] TNB in subsequent parities



[**Simulated**] TNB in subsequent parities

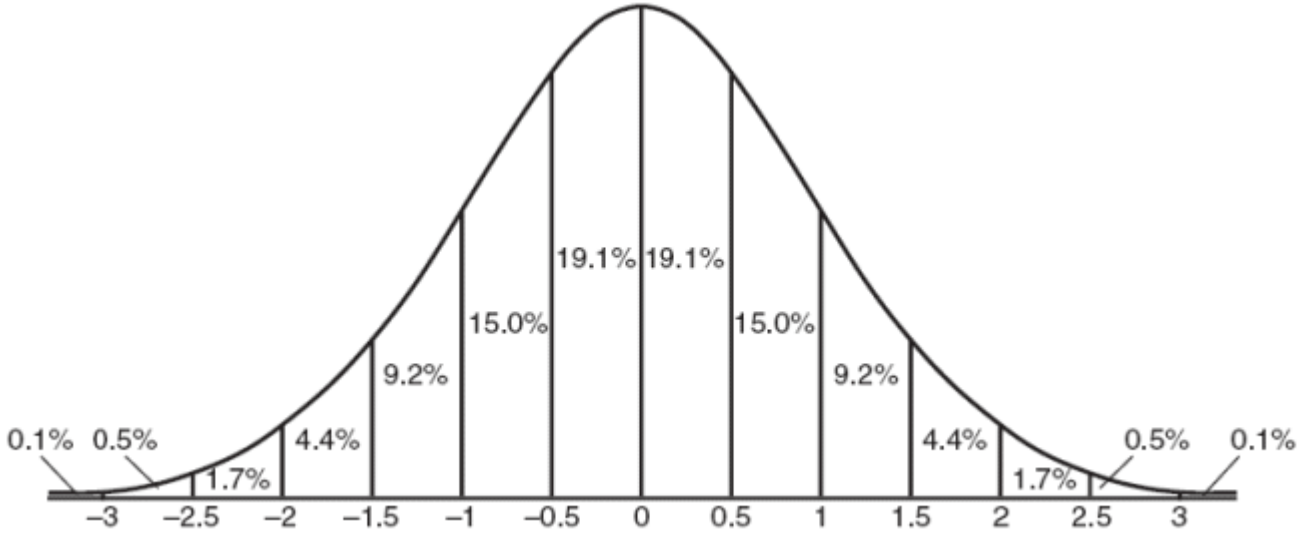


[**Simulated**] TNB in subsequent parities



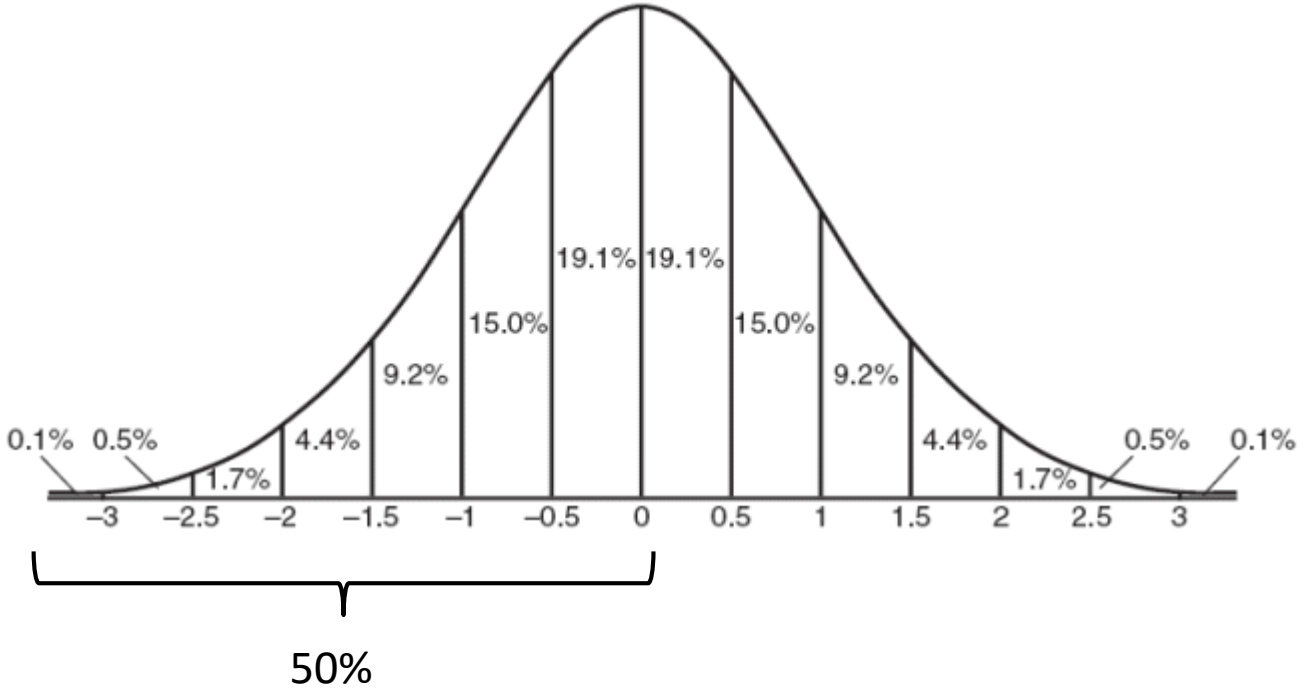
Let’s look at the statistical properties of the TNB

Distribution of TNB



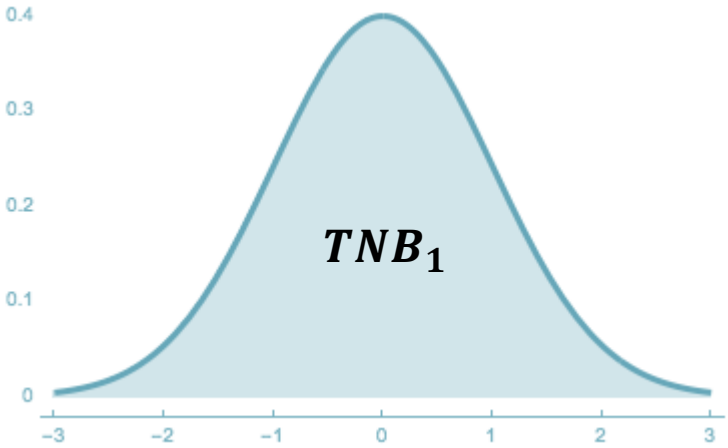
source: www.deeplytrivial.com

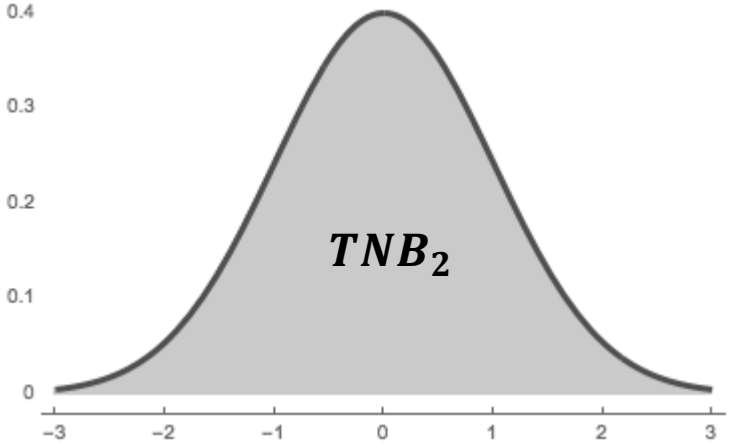
Distribution of TNB



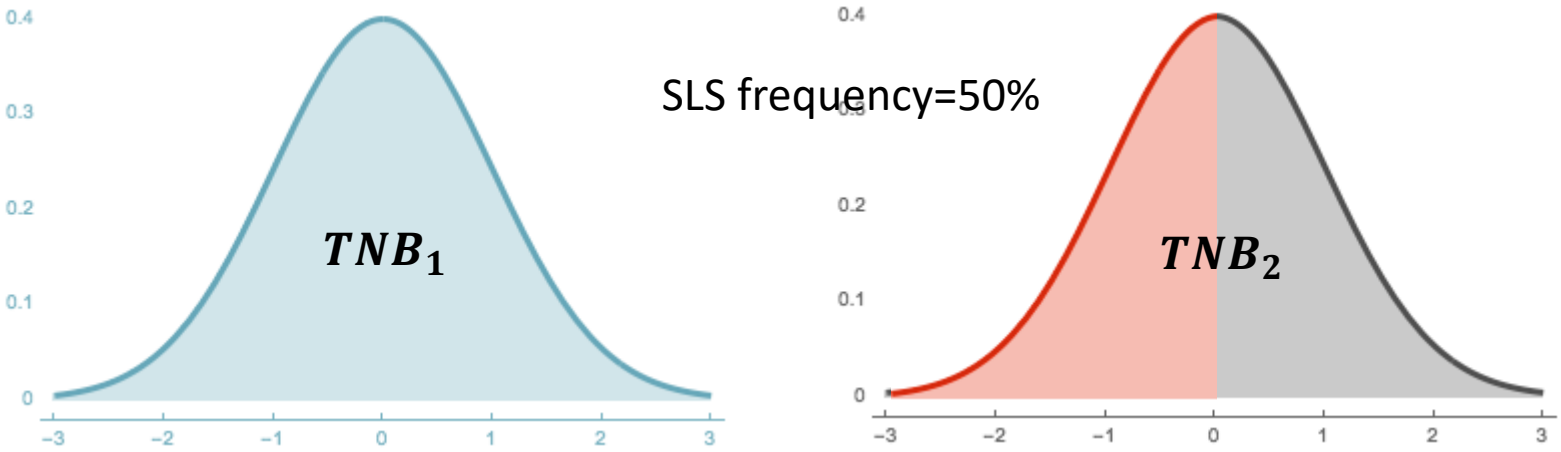
source: www.deeplytrivial.com

$\text{Mean}_{\text{TNB1}} = \text{Mean}_{\text{TNB2}}$



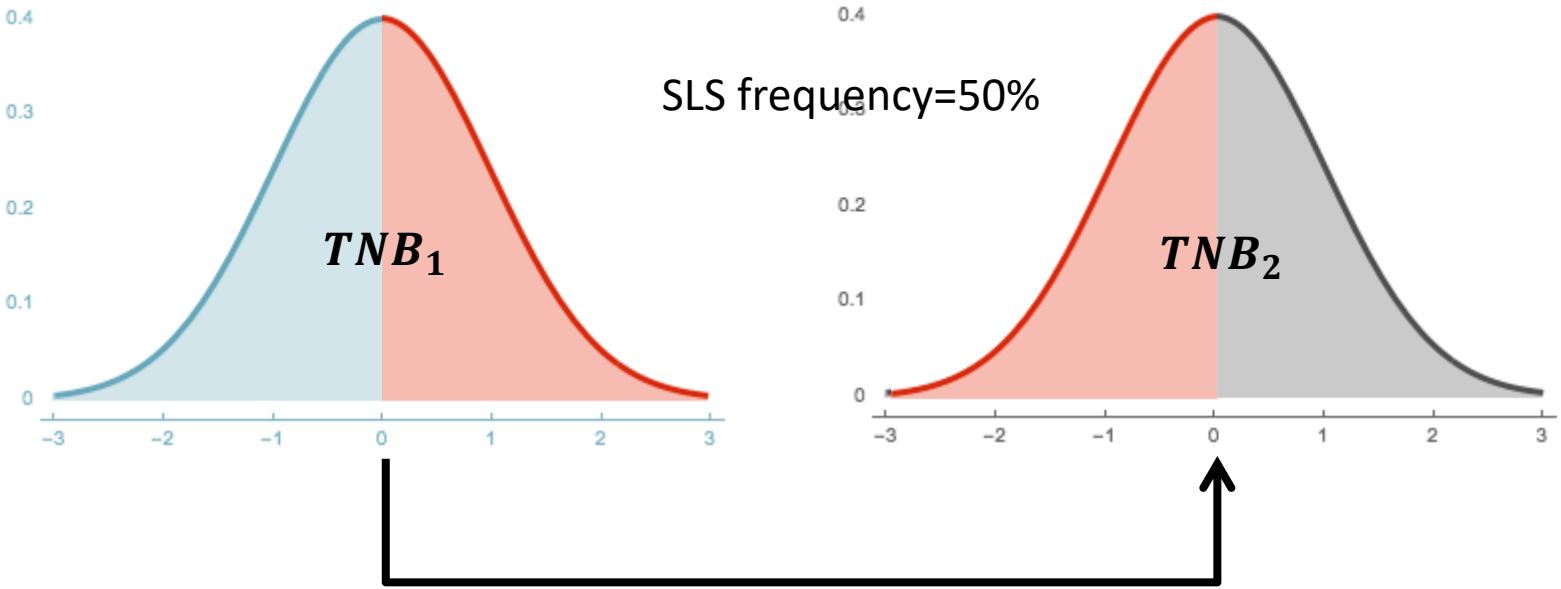


$$\text{Mean}_{\text{TNB1}} = \text{Mean}_{\text{TNB2}}$$



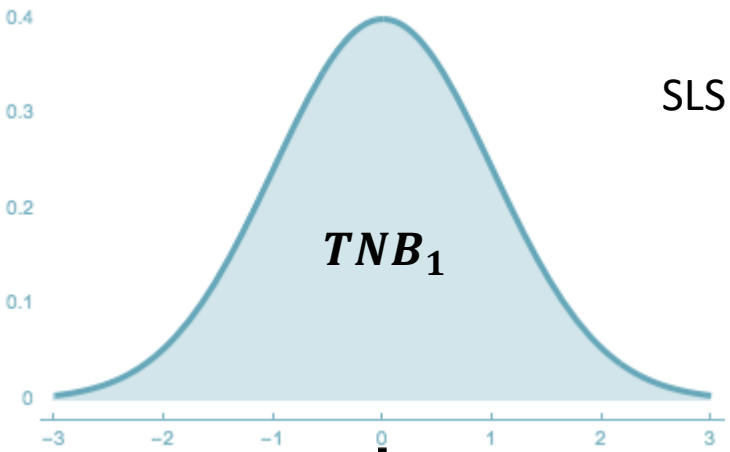
$$TNB_1 > TNB_2$$

$$\text{Mean}_{\text{TNB1}} = \text{Mean}_{\text{TNB2}}$$

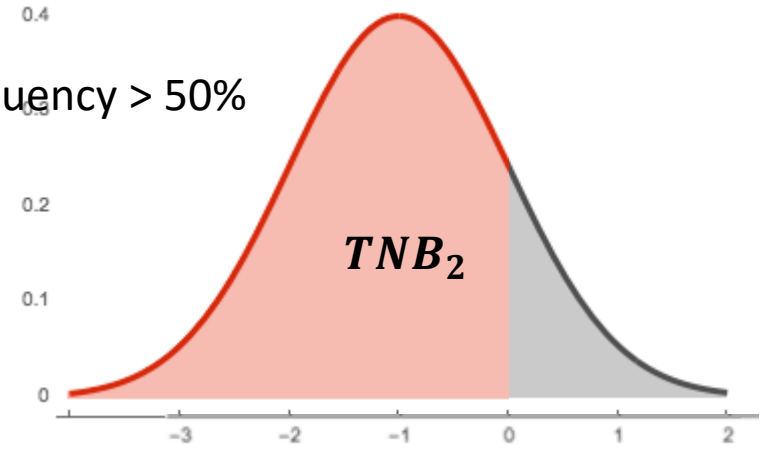


$$TNB_1 > TNB_2$$

$$\text{Mean}_{\text{TNB1}} > \text{Mean}_{\text{TNB2}}$$

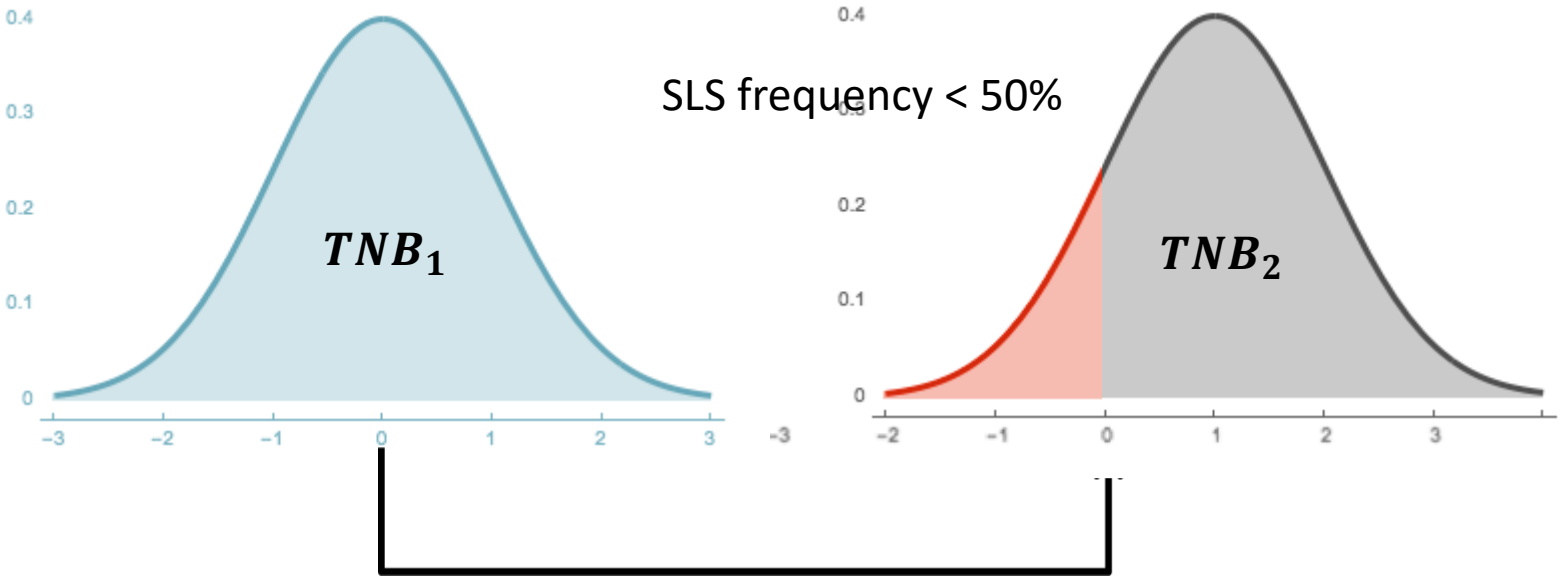


SLS frequency > 50%



$$TNB_1 > TNB_2$$

$\text{Mean}_{\text{TNB1}} < \text{Mean}_{\text{TNB2}}$



$$TNB_1 > TNB_2$$

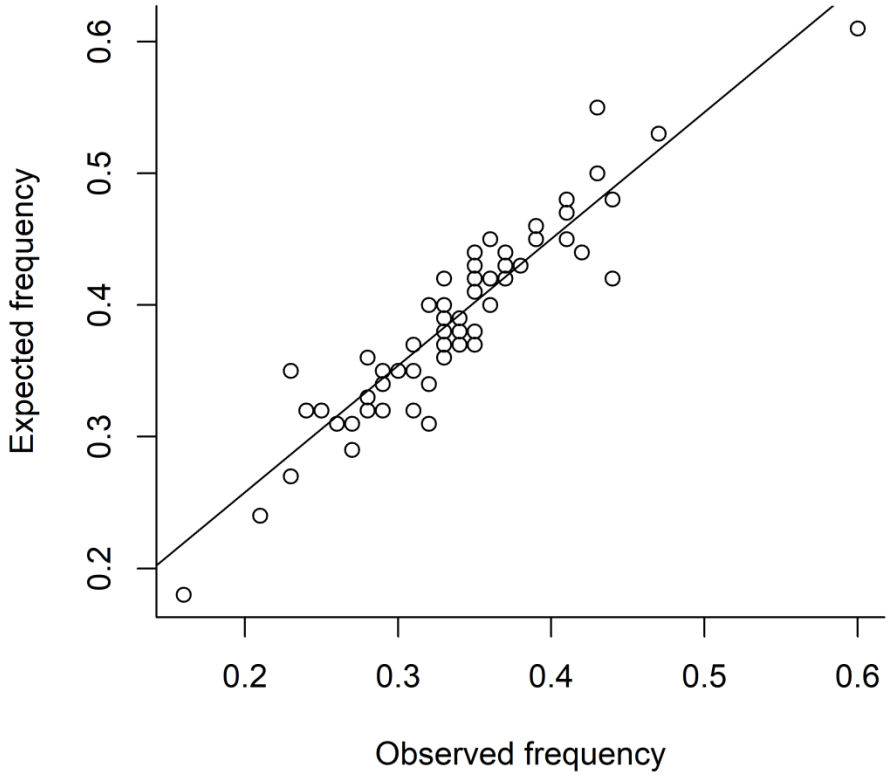
[real data] observed SLS frequency

Data from 67 herds

Min	0.16
Max	0.60
Mean	0.33
SD	0.07

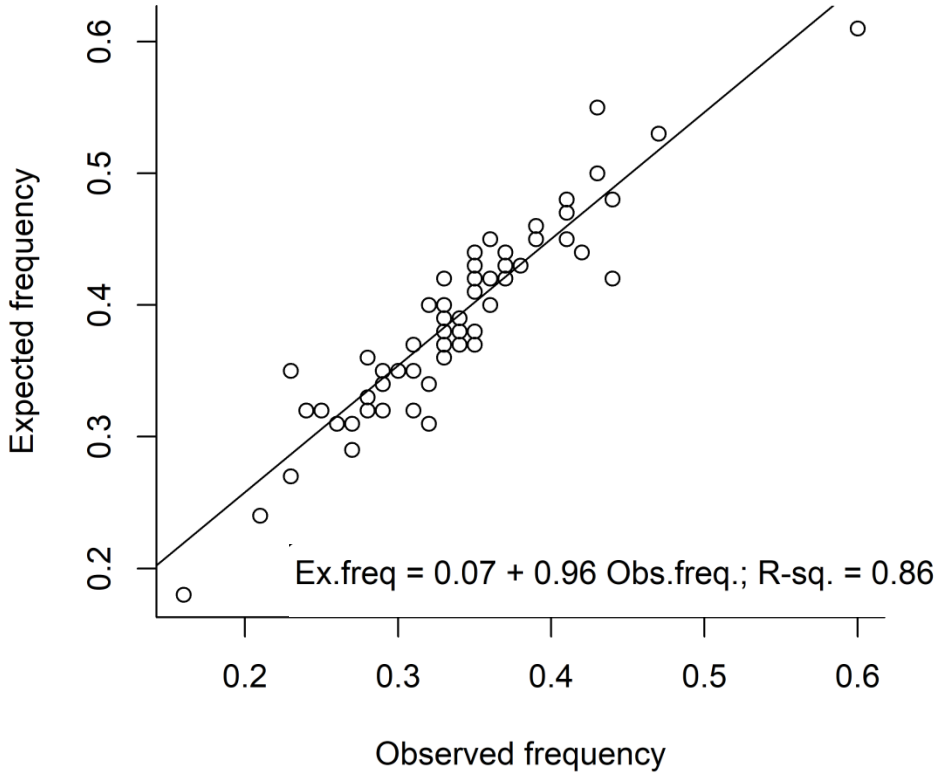
[real data] expected vs. observed SLS frequency

Data from 67 herds



[real data] expected vs. observed SLS frequency

Data from 67 herds



Second litter syndrome (**SLS**)

is the trait property!

How to minimize the frequency of

$$\boldsymbol{TNB_1 > TNB_2}$$

Solution 1:

Maximize mean differences

+

Minimize variability (more uniform litters)

Solution 2:

Accept high frequency of $TNB_1 > TNB_2$

+

Maximize mean litter size

+

Minimize variability (more uniform litters)

Poznań University of Life Sciences
FACULTY OF VETERINARY MEDICINE AND ANIMAL SCIENCE
Department of Genetics and Animal Breeding

SLS is due to the property of the data!

The frequency of SLS can be reduced by breeding for uniformity of the litter size.

marcin.pszczola@gmail.com

twitter **@marcinTHEbee**