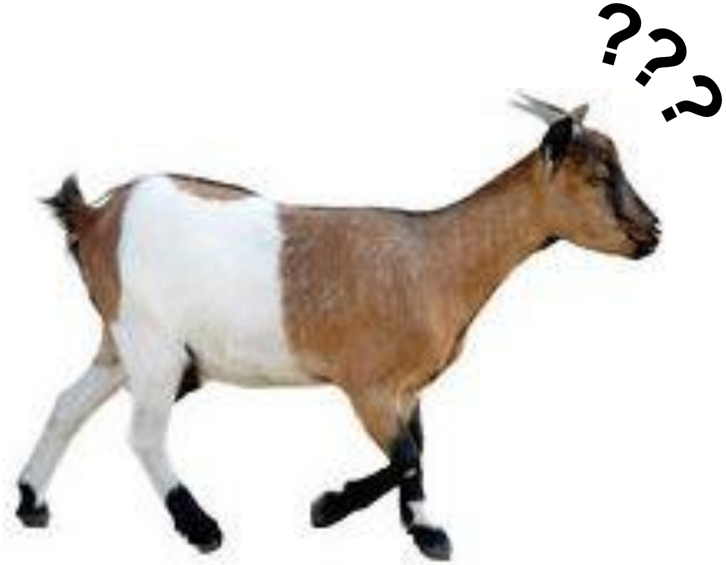
University of
Natural Resources and
Life Sciences, Vienna
Department of
Sustainable Agricultural Systems
Division of Livestock Sciences

A four-step approach for selecting a genetically diverse group of animals from pedigree data

by Michael Klaffenböck

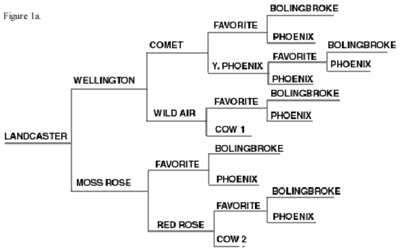


Or... which animals should I genotype?

Starting point:
We want to genotype a breed!

We have:

Samples in a gene bank



Pedigree

Not enough money to genotype all animals

Find a way to select a small group of animals that represents genetic diversity of the breed!

(In this case: 30 animals per breed)

Breeds


Chamois-coloured
Alpine goat (**GG**)


Blobe goat (**BB**)


Pinzgau goat (**PZ**)


Tauern pied goat (**TA**)

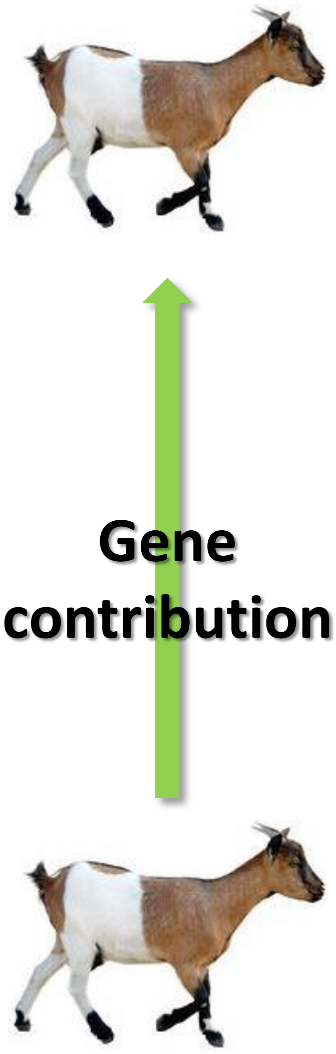

Styrian pied goat (**SS**)

Breed data

	BLZ	GG	PZ	SS	TA
Active female breeding goats	197	2,154	405	288	1,250
No. of animals in the pedigree	1,015	24,368	4,325	1,914	9,000
No. of samples available	63	541	240	150	702
Gene contribution of most important ten ancestors	0.32	0.17	0.30	0.42	0.62

Step 1: *Gene contribution*

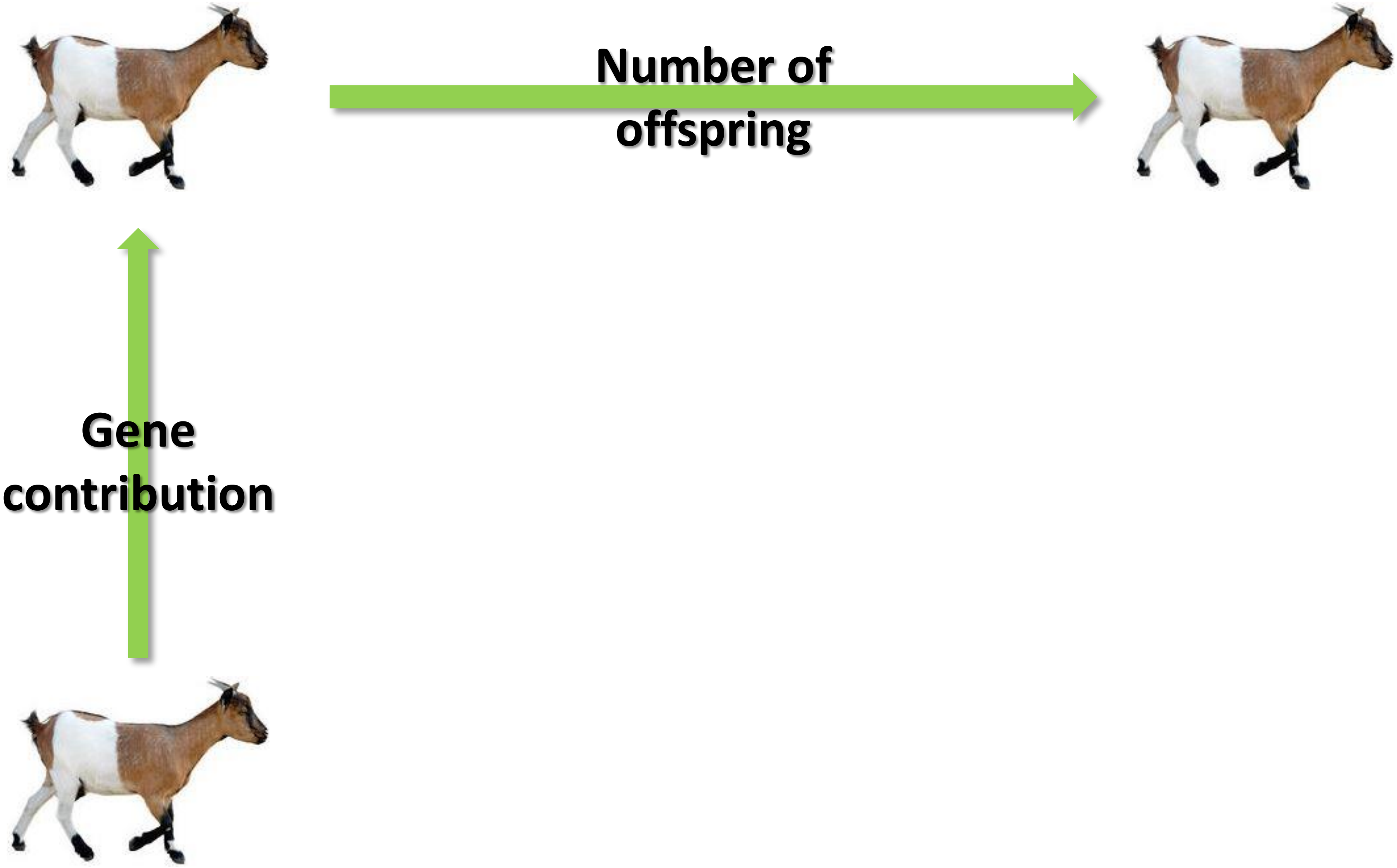
- Method: *prob_orig* from Fortran package PEDIG
  - calculates gene contribution for each ancestor
- Raw rather than marginal gene contribution was considered
  - Otherwise: influential animals are missed because their gene contributions were accounted for by un-available ancestors
- A **maximum of ten** animals with highest raw gene contribution was selected!



Gene contribution

Step 2: *Number of offspring*

- Method: in-house R script
- Counts **number of offspring** for each animal from pedigrees
  - Animals with less than 10 offspring excluded
- A **maximum of ten** animals with highest number of offspring selected

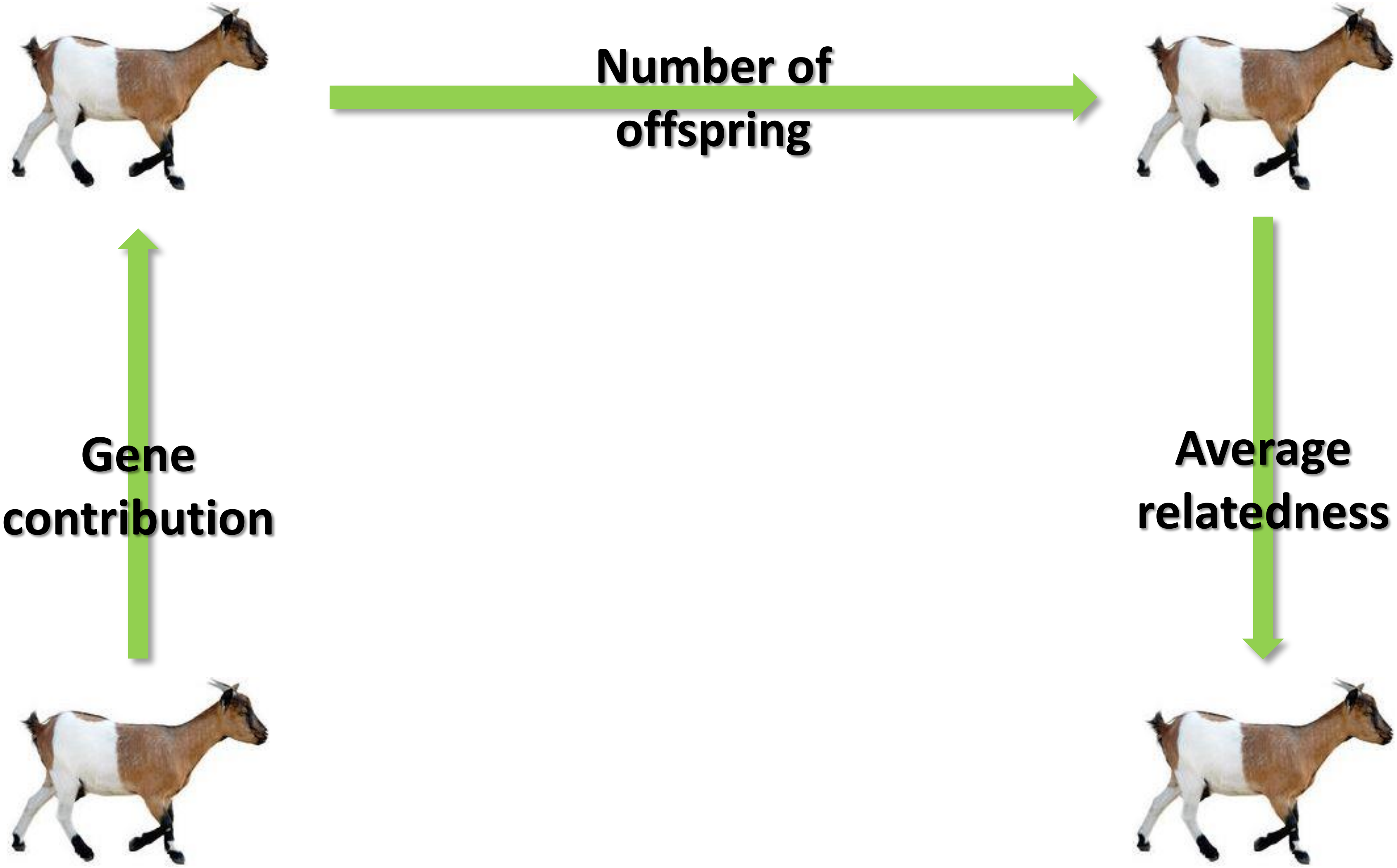


Number of offspring

Gene contribution

Step 3: *Average relatedness*

- Method: *par2* from Fortran package PEDIG
- **Average relatedness** of available animals to the **living population** was calculated
- Between **10 and 30** animals with lowest average relatedness selected
  (depending on how many selection spots are left)



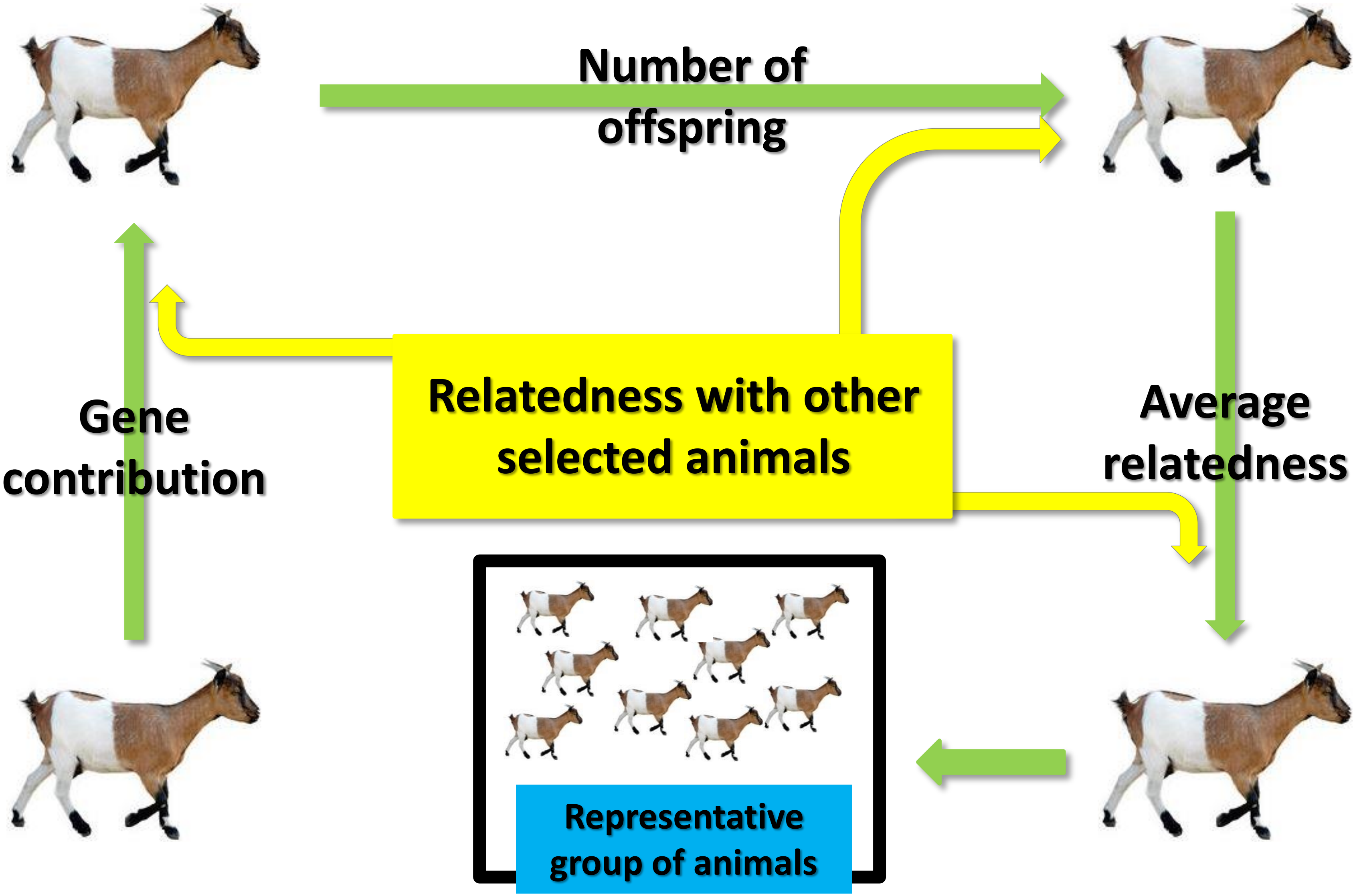
Number of offspring

Average relatedness

Gene contribution

Step 4: *Relatedness with other selected animals*

- Method: *parente* from Fortran package PEDIG
- **Relatedness** of each animal to **already selected animals** calculated
    - has to be below 0.15 to avoid half-sibs or closer
- If animals are closely related to other selection candidates, they are excluded even if they have e.g. high gene contribution



Number of offspring

Relatedness with other selected animals

Gene contribution

Average relatedness

Representative group of animals

Results

	Selection criteria			Inbreeding coefficient F	
	Raw gene contribution	**Most offspring**	**Average relatedness**	**Living population**	**Selected animals**
BLZ	0.028 (10)	- (0)	<0.001 (20)	0.007	0.000
GG	0.009 (10)	109 (10)	<0.001 (10)	0.014	0.006
PZ	0.020 (10)	30 (10)	0.005 (10)	0.023	0.001
SS	0.011 (9)	23 (10)	0.011 (11)	0.019	0.004
TA	0.019 (6)	40 (10)	0.087 (14)	0.100	0.061

- *In brackets: number of animals selected in this step*
- *F calculated using ‚meuw‘ program in PEDIG*

Drawback

- High relatedness in TA and SS
  - Not possible to select 30 unrelated animals
  - Small population sizes at time of sampling?
  - Samples don‘t represent current genetic diversity?
    - → *for SS: increase of* ***relatedness limit*** *from 0.15 to 0.25*
    - → *for TA: select animals with* ***lowest relatedness*** *to living population despite relation to selection candidates*

Conclusion

- Approach proposes a process that actually attempts to maximise genetic diversity in selection group from pedigree data alone
- Not all steps could be applied in all breeds (inbreeding, small sample size)
  - coping strategies tested

Genomic data of selected samples will **determine usefulness** of this approach

Thank you for your attention!

University of
Natural Resources and
Life Sciences, Vienna

Department of
Sustainable Agricultural Systems

Division of Livestock Sciences