Optimum contribution selection for populations with introgression from other breeds

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Classical optimum contribution selection

Animals with highest breeding values are closely related and only few of them are used for breeding

➔ Mean kinship and inbreeding coefficients may increase rapidely

Find the optimum contribution of each breeding animal to the next generation. These contributions are solutions of an optimization problem

Objective: **Maximize the mean breeding value**

Constraint: **Restrict the increase in mean kinship**

➔ Optimum contribution selection (OCS)

(Meuwissen, 1997)

Classical OCS applied to local breeds

Economically superior breeds have often been used for introgression.

Animals with high genetic contributions from these breeds have

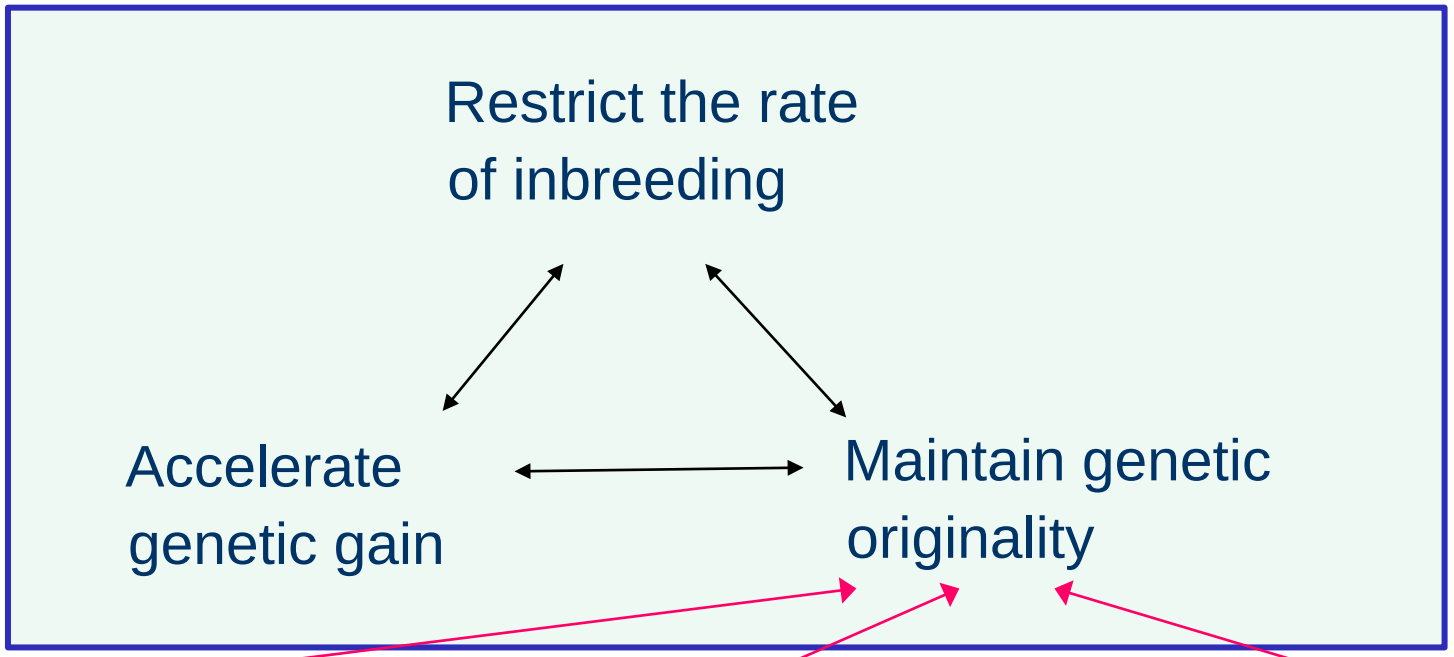
- high breeding values
- low relationship with the population

➔ Classical OCS uses predominantly these animals for breeding

➔ This could result in a great loss of genetic originality of endangered breeds

Conflicts of objectives

Conflicts of objectives in breeding programs for endangered breeds with historic introgression



The R package optiSel

The free R package **optiSel**

- enables to solve various OCS problems, e.g. to
    - maximize genetic gain
    - minimize pedigree-based or genomic kinship
    - minimize genetic contributions from other breeds
    - maximize genetic diversity of native alleles
- enables to use criteria not included in the objective function as constraints
- requires little R code
- provides functions for preparing and plotting pedigrees, for computing kinships, genetic contributions, native effective size, …

optiSel: Constraints relevant for OCS

x_i: optimum contribution of selection candidate *i*

(fraction of genes in the offspring originating from parent *i*)

<u>Constraints (Part 1)</u>

50% of genes originate from males

50% of genes originate from females

$x_i \geq 0$ or $x_i \geq lb_i$

$x_i \leq 0.5$ or $x_i \leq ub_i$

optiSel: Constraints relevant for OCS

Linear constraints (Part 2)

$BV^T x \geq lb.BV$ (BV = Vector with breeding values*)

$MC^T x \leq ub.MC$ (MC= Vector with migrant contributions*)

Quadratic constraints

$x^T f_A x \leq ub.fA$ ($\boldsymbol{f_A}$= Matrix with kinships*)

Rational constraints

$f_D(x) \leq ub.fD$ ($\boldsymbol{f_D(x)}$= Probability of native alleles to be IBD)

* of the selection candidates

Each criterion can either be optimized or restricted.

optiSel: Example for using the package

```
library(optiSel)
data(Kin)    #list of kinship matrices
data(Phen)  #data frame with breeding values and
migrant contributions

con <- list(ub.fA=0.03, ub.fD=0.073, ub.MC=0.55,
ub=c(M=NA, F=-1))
Res <- opticont("max BV", K=Kin, phen=Phen
```

	Sex	BV	MC	lb	oc	ub
276000891974272	1	2.3306090	1.0000000	0	3.315969e-07	0.5
276000891730313	1	3.1646864	1.0000000	0	1.366128e-03	0.5
276000892212506	1	0.9987306	1.0000000	0	4.615511e-08	0.5
276000891862786	1	-2.4614026	0.3835449	0	2.215463e-07	0.5
276000812497289	1	-0.2350507	0.2558594	0	2.125325e-02	0.5

optiSel: Example for using the package

```
summary(Res)[,c("valid","fA","fD","meanBV","meanMC")]
```

```
Checking constraints:
  min(oc) >= 0            : TRUE
  total male cont   = 0.5: TRUE
  total female cont = 0.5: TRUE
  females have equal cont: TRUE
  all male cont <= ub     : TRUE
  mean fA <= ub.fA        : TRUE
  mean fD <= ub.fD        : TRUE
  mean MC <= ub.MC        : TRUE

    valid         fA         fD    meanBV    meanMC
Res  TRUE 0.02413814 0.07299613 0.4577893 0.5499999
```

Materials

Pedigree of 10865 Hinterwald cattle

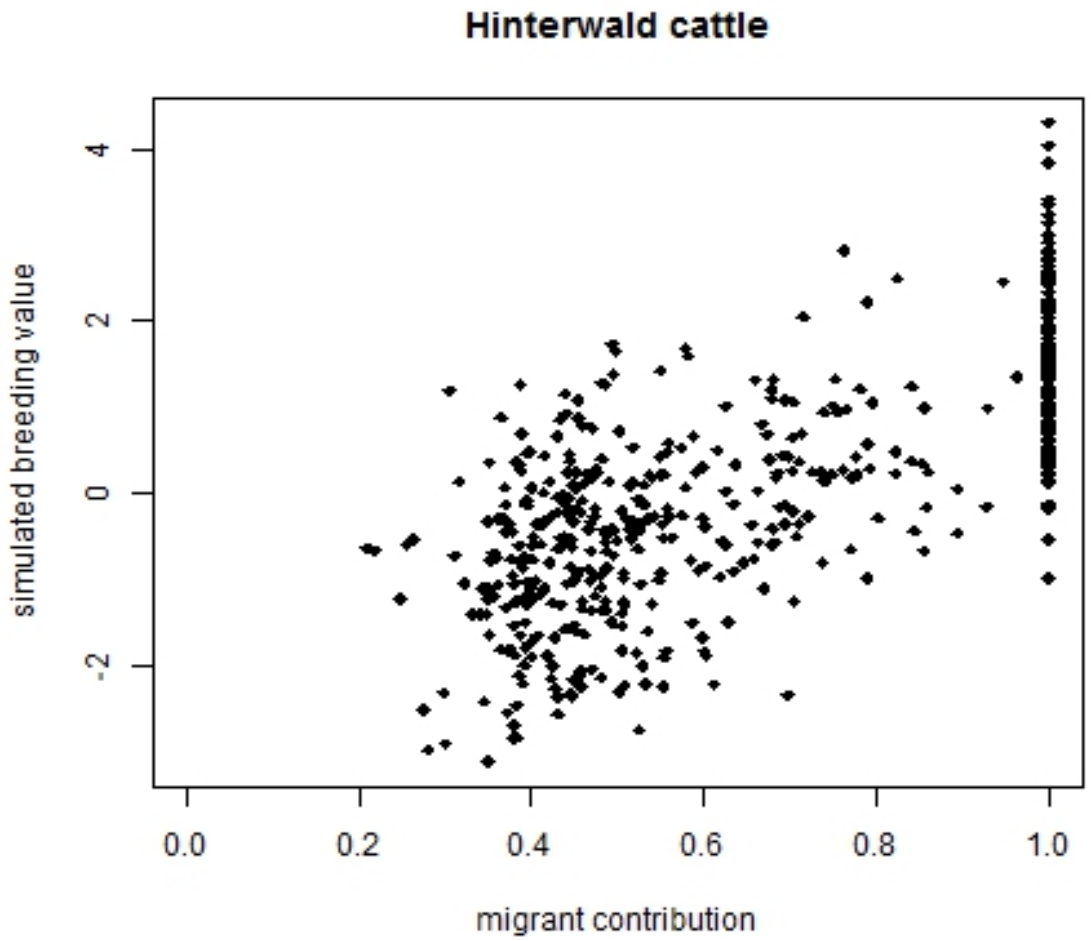
- Animals were born between 1947 and 2009.
- Founders born after 1970 were classified as migrants.
- Vector with migrant contributions (*MC*) was computed from pedigree.
- Breeding values (*BV*) were simulated as

$$BV \sim N(4(MC - \overline{MC}), A)$$

with additive relationship matrix *A*.

- 103 males and 414 females with offspring born in 2006 and 2007 were considered as selection candidates
- All females had equal contributions.

Materials



Simulated breeding values are affected by migrant contributions.

Results

Constraints settings:

fA: $x^T f_A x \leq 0.030$ (pedigree based kinship)

MC: $x^T MC \leq 0.550$ (migrant contributions)

fD: $f_D\,(x) \leq 0.074$ (similarity of native alleles)

Results:

obj. fun.	Constraints	BV	MC	fA	fD
maxBV	fA	1.031	0.778	0.030	0.089
maxBV	fA, MC	0.368	0.550	0.030	0.094
maxBV	fA, MC, fD	0.126	0.550	0.023	0.074
no optimization	equal cont.	-0.155	0.593	0.021	0.077

$\Rightarrow$ The additional constraints reduce genetic gain but contribute to recover the genetic background of endangered breeds.

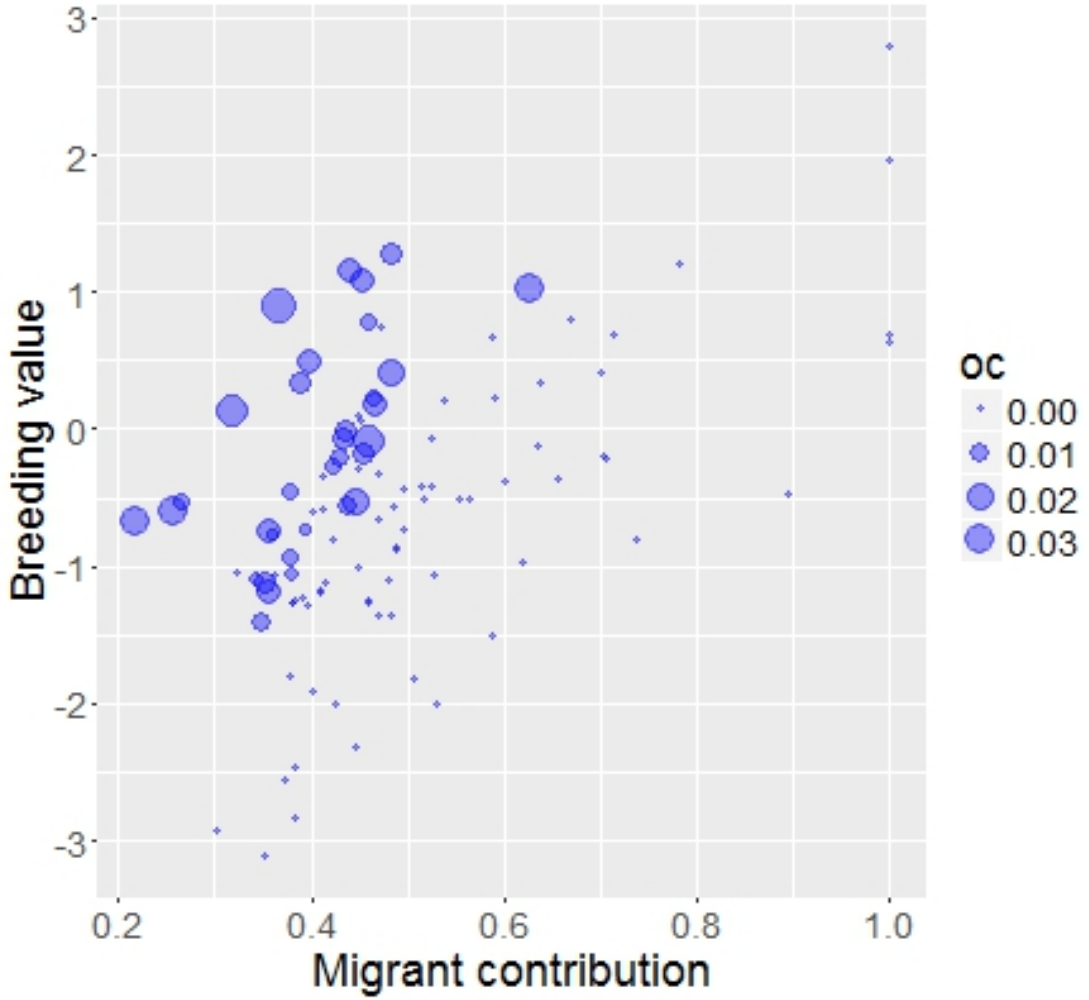
Results

Correlations between optimum contributions maximizing breeding values under various constraints:

	fA	fA, MC	fA, MC, fD
fA	1.000	0.077	0.002
fA, MC	0.077	1.000	0.807
fA, MC, fD	0.002	0.807	1.000

⇒ Adding constraints for reducing migrant contributions and conserving diversity of native alleles can lead to completely different selection decisions.

Results



Males with high optimum contributions have high BV and low MC.

Summary

- Optimum contribution selection applied to endangered breeds with historic migration requires special attention due to the conflicting objectives of their breeding programs.
- The free R package **optiSel** is an easy-to-use software taking these conflicting objectives into account.
- The package is described in detail in

Wellmann, R. (2016). Optimum Contribution Selection Methods for Animal Breeding: The **optiSel** R Package. *submitted*

Thank you for your attention!