Using Adaptive Simulated Annealing For Optimal Selection With Several Constraints

H. Chapuis[*], **C. Pincent**[†] and **J.J. Colleau**[‡].

[*]SYSAAF, Nouzilly, France, [†]Choice Genetics, Maixent, France, [‡]INRA, UR0631, Toulouse, France

ABSTRACT: An Adaptive Simulated Annealing (ASA) procedure was proposed to optimize genetic contributions, allowing for a maximal genetic gain on a main objective while reaching predefined values for an ancillary objective and for coancestry rate. As an illustration, a poultry population was simulated. The ASA procedure was compared with unconstrained selection on main objective and with an empirical procedure based on maximal numbers of selected sibs. The ASA procedure outperformed the empirical procedure for meeting the constraints *i.e.* a null genetic evolution of the ancillary objective and the chosen levels of coancestry rates, while providing a higher genetic gain for the main objective.

Keywords: Genetics, Simulated annealing, Genetic gain, Inbreeding, Coancestry

Introduction

Since the early nineties, numerous research works on population and quantitative genetics have been carried out in order to elucidate the appropriate concepts and methods for managing efficiently both genetic gains and evolution of genetic variability (Brisbane and Gibson (1994); Woolliams and Thompson (1994); Meuwissen and Woolliams (1994); Wray and Goddard (1994); Meuwissen (1997)). Here we described an Adaptive Simulated Annealing procedure which allowed optimization of genetic contributions for a maximal genetic gain on a main objective, given predefined values for a potentially antagonistic ancillary objective and for the coancestry coefficient between selected individuals (based on pre-defined coancestry rate).

Illustration was made with a simulated poultry population, simultaneously selected for both growth and reproductive traits.

The efficiency of the procedure was compared with an unconstrained BLUP selection index and with an empirical method.

Material and methods

Simulation features. The additive genetic values of founders were sampled as two-dimensional Gaussian variables. Heritabilities were set to 0.25 for the first trait and 0.5 for the second one, with an unfavourable value of -0.3 for both the genetic and residual correlations.

In our simulation, both traits were measured on both sexes. Each generation $N_m = 90$ sires were randomly mated to 3 dams in a hierarchic design. Thus the number of selected females per generation was $N_f = 270$. At birth, 2 male offspring and 6 female offspring were kept for each dam. 10 consecutive discrete generations were simulated, with 200 replicates.

The genetic additive value of offspring k from sire s and dam d was computed as $u_k = \frac{1}{2}(u_s + u_d) + \phi_k$ where ϕ_k stands for the Mendelian sampling deviation, accounting for inbreeding coefficients of sires and dams. The unconstrained (UNC) selection scenario aimed at improving trait 1, regardless of trait 2 or inbreeding. In the ASA_U scenario, an adaptive simulated annealing procedure, detailed below, was used to set a constraint on the second trait only (i.e., the coancestry coefficient was unconstrained). The second trait response was set to zero. In the ASA_U50 scenario, an additional constraint was set on the inbreeding rate, which should be half the one obtained with the ASA_U procedure.

A fourth scenario was an empirical procedure (EMP) where numbers of selected full sibs (FS) and half sibs (HS) were not allowed to exceed predefined values (2 FS and 3 HS for males, 4 FS and 11 HS for females) in order to limit inbreeding rate. In this scenario, the expected decrease of trait 2 was monitored in addition, as only individuals exhibiting an EBV above -0.5 standard genetic deviations for trait 2 were candidates.

ASA procedure. Simulated Annealing (Kirkpatrick et al. (1983)) is a Monte-Carlo approach for finding a global optimum in a discrete search space. Let us consider a function $f(x)$ where x denotes a vector of discrete variables. Adaptive (or Constrained) Simulated Annealing (ASA) empirically searches the optimum x giving the maximum value of function $f^*(x) = f(x) - \sum_i \lambda_i (h_i(x) - H_i)^2$, where $h_i(x)$ is a constraint function that should meet required value H_i. Parameters λ_i are counterparts of the conventional Lagrange multipliers used for constrained functions of continuous variables and are computed dynamically for each temperature of the annealing process. More details can be found in Colleau et al. (2009).

Here x was the vector of contributions (of size 2160 i.e., the number of selection candidates) taking 3 possible values: $x_i = \frac{1}{2N_m}$ for a selected male, $x_i = \frac{1}{2N_f}$ for a selected female and $x_i = 0$ otherwise. $f(x)$ was the mean EBV of selected candidates, H_1 was the desired level for trait 2 and H_2 the desired average coancestry among selected individuals. Alternative vectors were generated by two equiprobable permuta-

tion processes, between males or between females and were tested for variation of function f^*, according to the conventional annealing pattern. When variation was positive or null, the new vector was accepted. When variation was negative, the new vector was accepted with a probability decreasing over time, managed by the so called "temperature" parameter. The effect of this procedure was to avoid getting trapped in local maxima, less valuable than the global maximum that is looked for. The process was stopped when all the variations Δf^* were negative for a given temperature or when the computation time reached a predefined limit.

Results and Discussion

The genetic gains of both traits are displayed on Figure 1 and are expressed in standard genetic units. When selecting only on BLUP EBV for trait 1 (scenario UNC), the genetic gain achieved on this trait was maximal, with deleterious consequences on trait 2. The empirical procedure led to a lower (-24%) gain on trait 1, with an almost negligible increase on trait 2. Only ASA scenarios could actually provide null evolutions on trait 2. The constraint set on trait 2 only (ASA_U) led to slight reduction (-5%) of the genetic gain. When halving the expected inbreeding rate (ASA_U50) both constraints were actually met with a high accuracy and an additional decrease of the expected genetic gain was observed. Yet, it remained acceptable and scenario ASA_U50 outperformed the EMP procedure (-12% vs. -24% of the maximum gain).
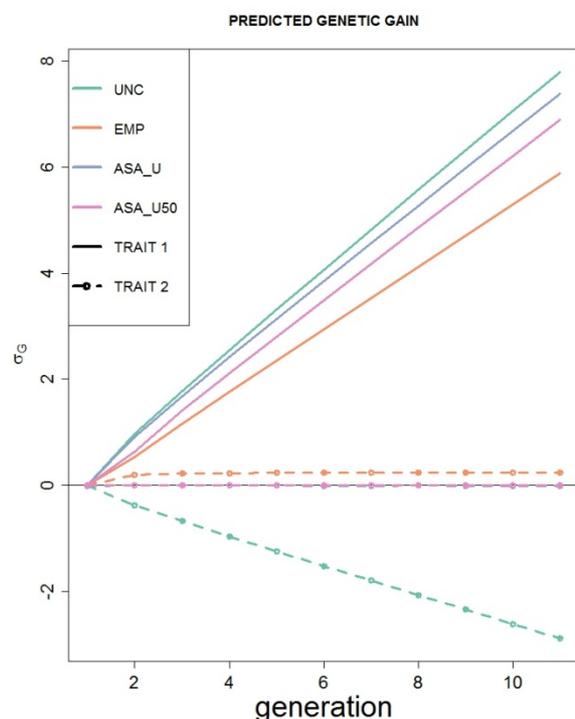

Figure 1: Observed genetic gain according to selection procedures: UNC=unconstrained selection on trait 1, EMP=empirical procedure setting a maximum number of selected sibs, ASA_U=optimized procedure setting to zero the second trait response,

ASA_U50=optimized procedure putting a constraint on the second trait and coancestry.

The observed evolutions of the mean inbreeding coefficient are displayed in Figure 2. The constraint set on trait 2 had no influence on the inbreeding rate (as UNC and ASA_U lines were merged). ASA_U50 and EMP scenario were roughly similar for inbreeding rate, the former being slightly better. The value of the ASA procedure was thus clearly demonstrated.
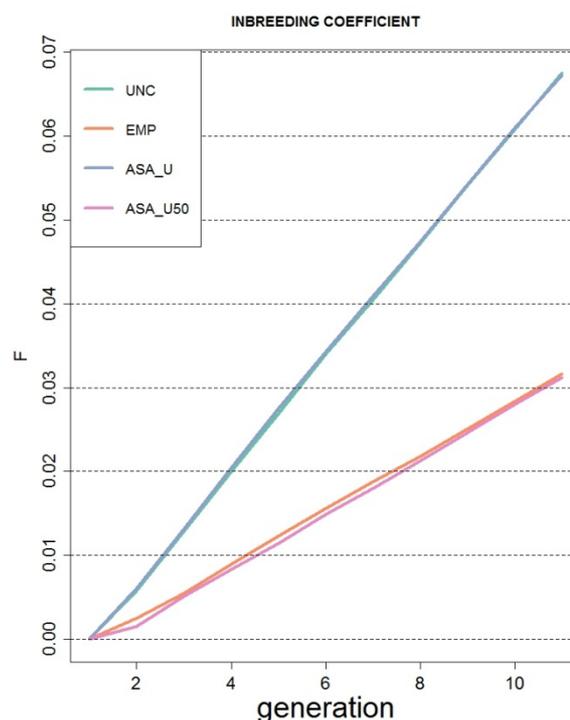

Figure 2: Evolution of the inbreeding coefficient across generations according to selection procedures: UNC=unconstrained selection on trait 1, EMP=empirical procedure setting a maximum number of selected sibs, ASA_U=optimized procedure setting to zero the second trait response, ASA_U50=optimized procedure putting a constraint on the second trait and coancestry.

Moreover the ASA algorithm was efficient, as each replicate (i.e. 10 selection cycles) took approximately 45 seconds on a 2.9 GHz Xeon processor.

Here, selected animals were randomly mated. As stated by numerous papers, an additional preservation of the genetic diversity could be achieved with an optimal design of the mating plan. Such a design could also be obtained using a simulated annealing algorithm.

Here the horizon was only 10 generations and the final inbreeding level was kept low. Should the number of simulated selected generations be increased, then the inbreeding depression should be accounted for with some deleterious effect compromising performance as a function of inbreeding level.

Conclusion

ASA procedures were able to meet constraints with a high accuracy. Furthermore, considering that EMP is a widely used method in poultry breeding schemes, one may consider that they improve genetic gains on an overall objective by 16%, while maintaining the genetic variability in an acceptable range. They are now used by French breeding companies affiliated with the SYSAAF organization (www.sysaaf.fr; Nouzilly, France). A similar procedure can be implemented to minimize coancestry while setting two or more objectives to given values. Such method could also be used to maintain small populations, such as local breeds.

Acknowledgments

Literature Cited

Brisbane, J. R., and Gibson J. P (1994). 5th WCGALP, 19 :135

Colleau, J. J., Tual K., de Préaumont H. et al. (2009). Gent. Sel. Evol., 41:7

Kirkpatrick S., Gelatt C.D., Vecchi M.P. (1983). Science 220 (4598): 671–680.

Meuwissen, T. H. E. and Wooliams J. A. (1994). J. Dairy Sci., 77:1905-1916

Meuwissen, T. H. E. (1997). J. Anim. Sci., 75:934-940

Wooliams J. A. and R. Thompson (1994). 5th WCGALP, 19:127

Wray N. R. and Goddard M. E. (1994). Genet. Sel. Evol. 26:431-451