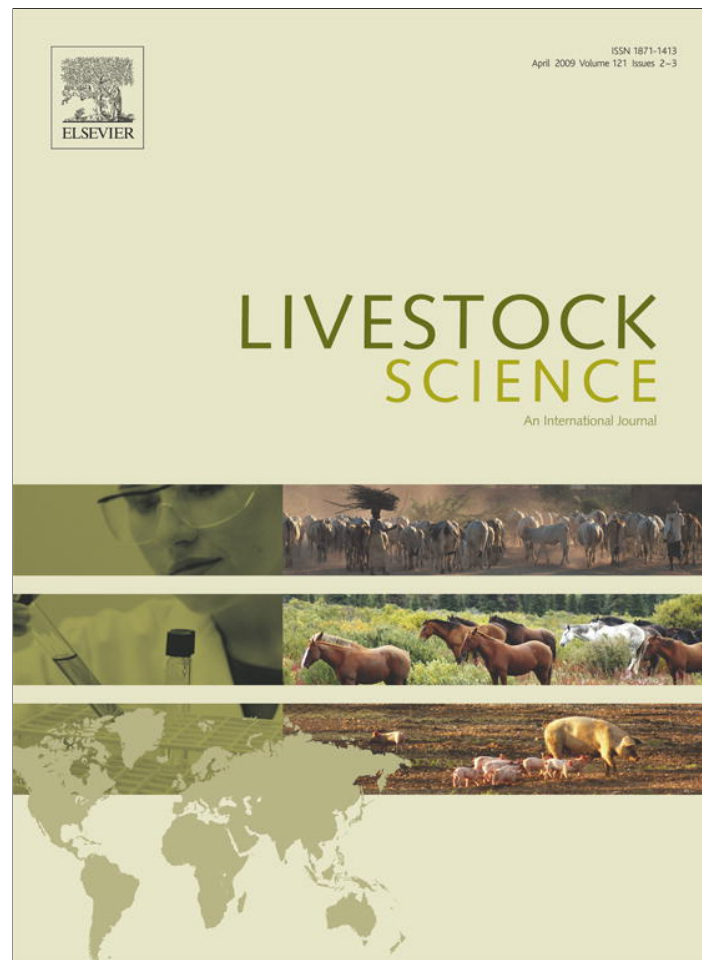


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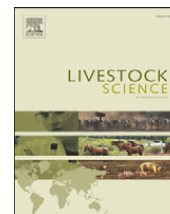
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## Short communication

## ADAM: A computer program to simulate selective breeding schemes for animals

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## ABSTRACT

ADAM is a computer program that models selective breeding schemes for animals using stochastic simulation. The program simulates a population of animals and traces the genetic changes in the population under different selective breeding scenarios. It caters to different population structures, genetic models, selection strategies, and mating designs. ADAM can be used to evaluate breeding schemes and generate genetic data to test statistical tools.

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ADAM has five major benefits when evaluating breeding schemes. First, it uses stochastic simulation, which is an accurate method when modelling complex breeding schemes. Second, it allows a plethora of breeding schemes to be evaluated. Third, ADAM uses new methods, such as marker and gene-assisted selection, selective genotyping (Ansari-Mahyari et al., 2008), MOET, and sexed semen. Fourth, ADAM allows new technologies and techniques to be tested under different breeding scenarios. Finally, the program can be easily expanded to include new methods and strategies because it has a modular design. To the best of our knowledge ADAM is the first program with such generality.

ADAM uses a set of user-defined parameters to specify the base population, genetic model, population structure, and selection and mating decisions when simulating breeding schemes.

*Base population and genetic model.* The program generates a base population and simulates descendant generations

through a series of time steps. The genetic model of the base population underlines the genetic makeup of the descendant generations. The model for single and multiple traits is based on one of the following:

- infinitesimal model, mimicking a polygenic makeup,
- finite-locus model, mimicking individual genes and/or genetic markers, and
- mixed-inheritance model, combining the infinitesimal and finite-locus models.

*Population structure.* The user-defined parameters specify the reproductive and life-cycle characteristics of the population. Such characteristics include the reproductive age of the animals, the age when traits are realised, the availability of germ plasm, and the number of herds in the population.

*Selection and mating decisions.* Selection and mating is carried out in each time step. Selection is carried out on single or multiple traits by random, truncation, or optimum contribution selection. Truncation and optimum contribution selection are based on one of the following criteria:

- phenotype,
- BLUP (best linear unbiased prediction based on phenotype and pedigree information),

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- c) MA-BLUP (BLUP including marker information), and
- d) GA-BLUP (BLUP including identified gene information).

Selection can be carried out in single or multiple stages within sex, age, herd, full-sib families or populations. The selection criteria can differ between stages.

Mating of the selected animals is carried out in a hierarchical or factorial mating design using one of the following mating criteria:

- a) random,
- b) minimum-coancestry, and
- c) minimum covariance of ancestral contributions (new method developed by Henryon et al., personal communication).

Mating takes place within or across herds.

The results that can be obtained include the true and estimated breeding values for each time step, overall and trait-wise genetic gain, generation interval and accuracy of the prediction. Inbreeding based on pedigree information and, optionally, inbreeding based on DNA information including the length of fixed regions on the genome is also calculated. Results are presented as summaries for all animals in each time step, and for each individual animal. The amount of output is optional as all data is stored in memory and can be printed if needed.

ADAM is written in FORTRAN 95. It is under continuous development at the Department of Genetics and Biotechnol-

ogy, Faculty of Agricultural Sciences, University of Aarhus. The program makes use of other programs for specific procedures: 'Randlib90' to generate random numbers (Randlib, 2002); 'DMU6' release 4.5 to estimate breeding values (Madsen and Jensen, 2008); 'EVA' for optimum contribution selection (Berg et al., 2006); and 'IBD' to calculate identity-by-descent matrices (Thomsen, 2006).

Further information is available at <http://adam.agrsci.dk> or by contacting one of the corresponding authors.

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