Appendix A
Controlling rate of inbreeding with overlapping generations

The contribution to average relationships in year t (t-> ∞) as a function of current genetic contributions c, equals in the case of discrete generations

$$c^T \cdot A \cdot c$$

With overlapping generations, animals contributions accumulates over time.
We need to describe the cumulated genetic contribution of animals over a generation.

Following the gene-flow theory of Hill (1974), we can define a transition matrix, P, with elements in row i and column j representing the proportion of genes from sex-age class j at time t contributed to sex-age class i at time t+1. The asymptotic contributions of sex-age classes is

$$\lim_{t \to \infty} P^t := 1 \cdot v^T \cdot \frac{1}{2L}$$

where the i'th element of v represents the expected contribution of sex-age class i, as the proportion of the cohorts contributions that are still to be realised.
Then the total contribution over a generation equals (see Grundy et al (2000) for details)

$$\left(c + \sum_{i=1}^{Na} v_i \cdot P^i \right) \cdot \frac{1}{2L}$$

where c is current contributions (by definition having a weight of 1) and P^i represents the contributions of anials in the i'th previous time period. Na is the maximum number of age classes.

This derivation assumes
1. constant age distribution of parents
2. asymptotic genetic contributions equals first generation genetic contributions (see Bijma & Wolliams 2000), such that selective advantage is not inherited.

Appendix B
Computational strategy used in EVA v1.4

The function of average relationships to be minimised can be written

$$\frac{1}{(2\cdot L)^2}\cdot(c + P\cdot w)^T\cdot A\cdot(c + P\cdot w)$$

where
c is a vector of contributions to the next generation
P is a matrix of contributions to previous generations, one period per columr
w is the lifetime breeding profile (Grundy et al 2000) weighing previous contributions and L is generation interval.

More specific, with two sexes P and w are defined as

$$P := \begin{pmatrix} P_m & 0 \\ 0 & P_f \end{pmatrix} \qquad w := \begin{pmatrix} w_m \\ w_f \end{pmatrix}$$

This can be rewritten as

$$\frac{1}{(2\cdot L)^2}\cdot\left(c^T\cdot A\cdot c + 2\cdot c^T\cdot A\cdot P\cdot w + w^T\cdot P^T\cdot A\cdot P\cdot w\right)$$

To evaluate a mating set a new c and w are computed conditional on the proposed matings and the mating set evaluated given formulas abiove. To simplify computations the following quantitties are computed once and stored

$A\cdot P\cdot 2$	with dimension number of candidates*number of age classes*2
$P^T\cdot A\cdot P$	square matrix with dimension 2*number of age classes

To further speed up computations, A and A*P are reduced to a dimension of number of candidates, i.e. animals that can have non-zero elements in c.

Including genetic merit (a) and inbreeding (F) in the function to be maximised results in

$$v_a \cdot c^T \cdot a + \frac{v_{rel}}{(2 \cdot L)^2} \cdot \left(c^T \cdot A \cdot c + 2 \cdot c^T \cdot A \cdot P \cdot w + w^T \cdot P^T \cdot A \cdot P \cdot w \right) + v_F \cdot F$$

where

a is a vector of predicted breeding values

F is the average coefficient of inbreeding of offspring

v_a is the weight on average merit of offspring

v_{rel} is the weight on the long-term rate of inbreeding

v_F is the weight on inbreeding in the next generation