

# Abstract: Session 13 Poster 25

## Strategic management of pig genetics

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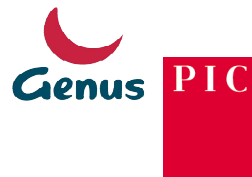
Genetic improvement has a wide range of actions but only two really critical control points – animal selection and mate allocation. The best animals to select depend on the pattern of mate allocation, and vice versa. Mate Selection allows this to be done simultaneously. The number of factors involved (e.g., breeding objectives, selection pressure, crossbreeding, inbreeding avoidance, migration) and the complexity of their interrelations require a strategic management approach. Mate Selection based on Optimal Contribution Theory (OCT) emerged in the late 1990s and established itself around 2000 as software became available for implementation. The information required to implement Mate Selection is collected in most animal breeding programs, including pedigree data; sex of the animal; trait EBVs and/or index value; candidate status; and, if available, marker/breed genotypes. Weekly analyses for each population include all current and future candidates (active animals, juveniles and unborns). The optimization system is customized for farm routines and requirements. The outcome is a proposed set of future virtual matings, based on OCT, farm management requirements and population-specific desired DeltaF and DeltaG as strategic target parameters. This paper shares the experience accumulated during this period within PIC and shows examples of achieved results. Factors contributing to the decision process and their interrelations are shown graphically. A balanced approach of managing short term system reactivity and long term objective targeting insures achievement of genetic gains over one genetic standard deviation per year as well as maintaining genetic diversity.

# Strategic management of pig genetics

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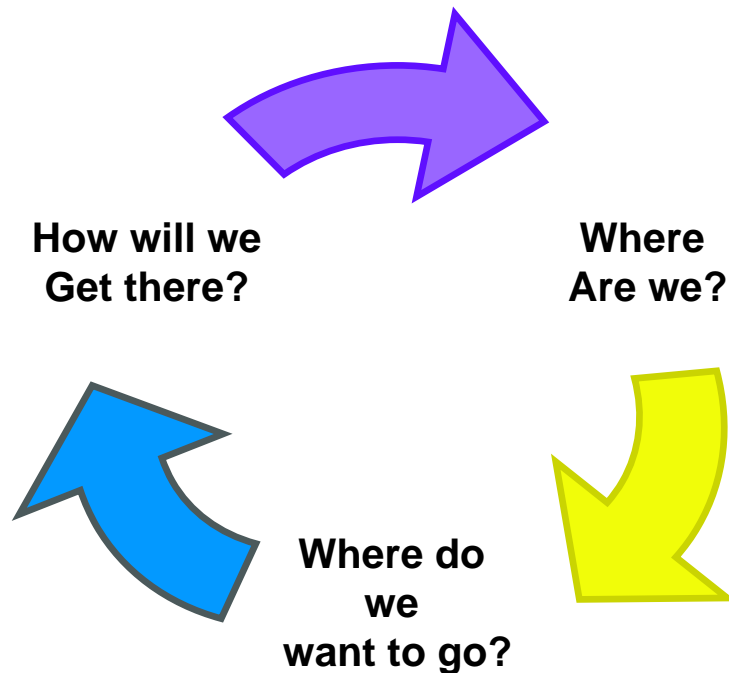
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# Rules-based Animal Breeding, e.g.

- **Sequential implementation**
  - Inbreeding rules
  - Crossbreeding rules
  - Constraint rules



- **Cull cows for age after 5 mating years**
- **Use this set of economic weightings**
- **Rank and select on EBV**
- **Use ten rams mated to 40 ewes each**
- **Set up a rotational cross**
- **Use no more than two boars out of any one sire**
- **Buy bulls in the \$2,000 to \$3,000 price range**
- **Don't mate full sibs**



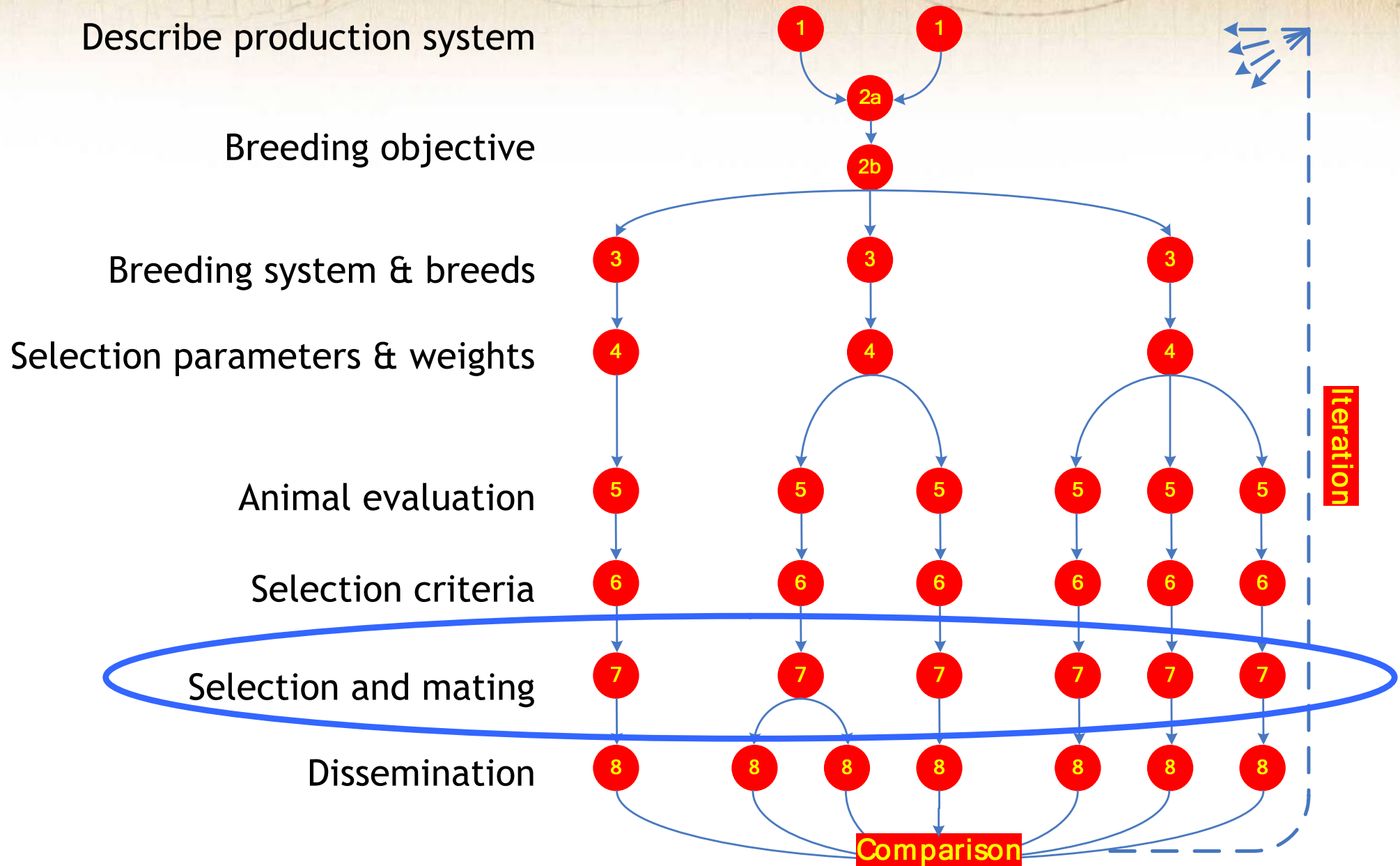
# Rules-based design

## Some problems ...



- Rules generally not flexible to exact prevailing conditions
- Sometimes simple rules need to be broken to exploit opportunities as they arise

# Systematic approach to animal breeding, e.g.



# Tactical Decisions for Animal Breeders

Critical control points:

- **SELECTION**
- **MATING**

**M  
A  
SELECTION  
E**

What to do?

- **Develop an objective function describing net utility as a function of selections and mate allocations, or, be able to evaluate the consequences of any action (any mate selection set)**
- **Develop and implement a mate selection algorithm that maximizes this objective function, or, find the action that maximizes the consequences**



## What do we improve?

- Maximize the index value of progeny

## What do we constrain?

- Coancestry of parents
- Average inbreeding of progeny



## How to do it?

- Evolutionary Algorithms - Create populations of candidate solutions and evolve these populations by selection based on some objective function which emulates natural selection

# Mate Selection Index

## The Objective Function

$$MSI = Index + \lambda_1 Coan + \lambda_2 F_{avg}$$

**Lambda values ( $\lambda$ ) are negative numbers/weights, thus, the Index gets adjusted (diminished) for the generated relationships**



# Coancestry

- Calculated as:

$$\text{Coan} = 0.5 \mathbf{x}^T \mathbf{A} \mathbf{x}$$

i.e., the additive relationship  $\mathbf{A}$  weighted by the optimal contributions  $\mathbf{x}$  of individuals

- $\mathbf{A}$  is the matrix of relationships among animals considered in the cohort (that is, the group of candidates proposed to become parents in the virtual mating list)
- $\mathbf{x}$  sums to 1 by gender and is simply the number of matings proposed for an individual divided by twice the total number of matings
- the "coancestry" calculated in this way refers to the "cohort coancestry"

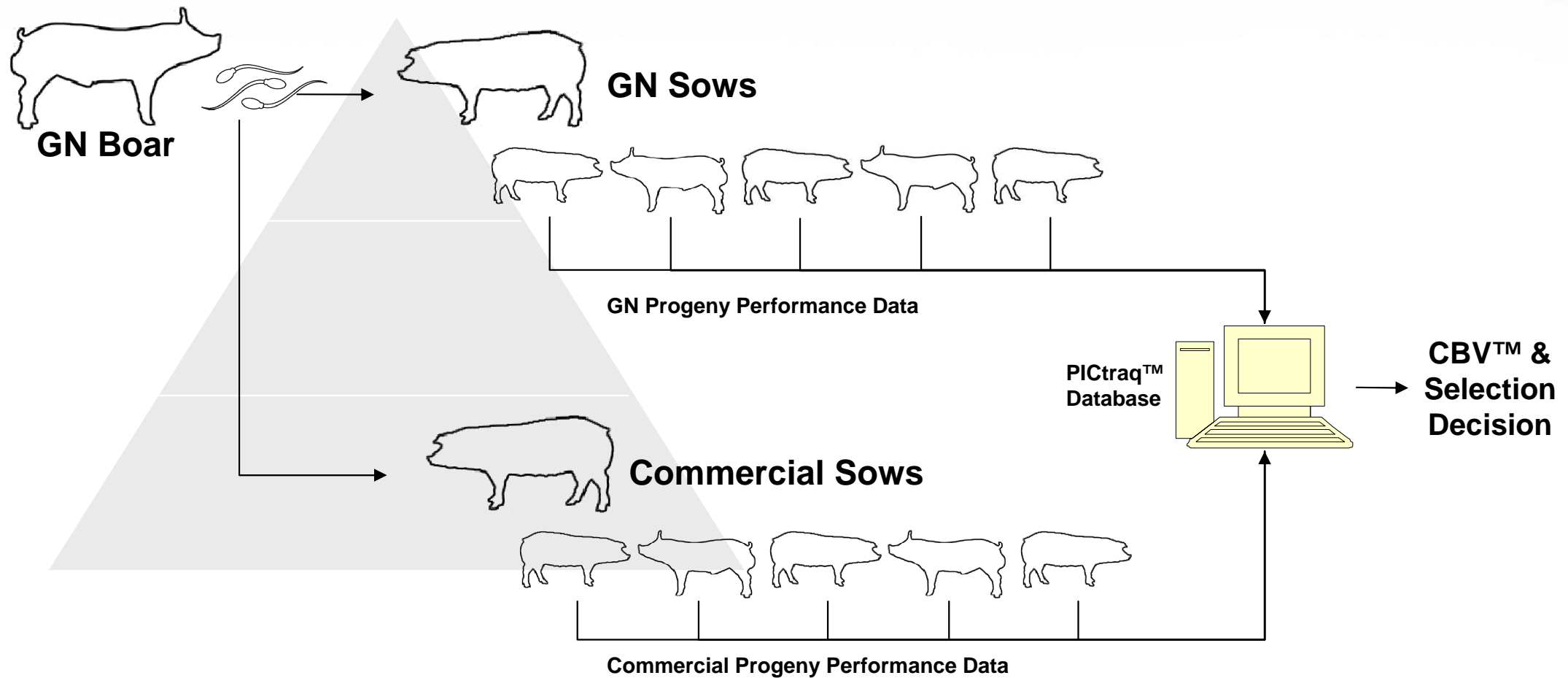
# Inbreeding coefficient

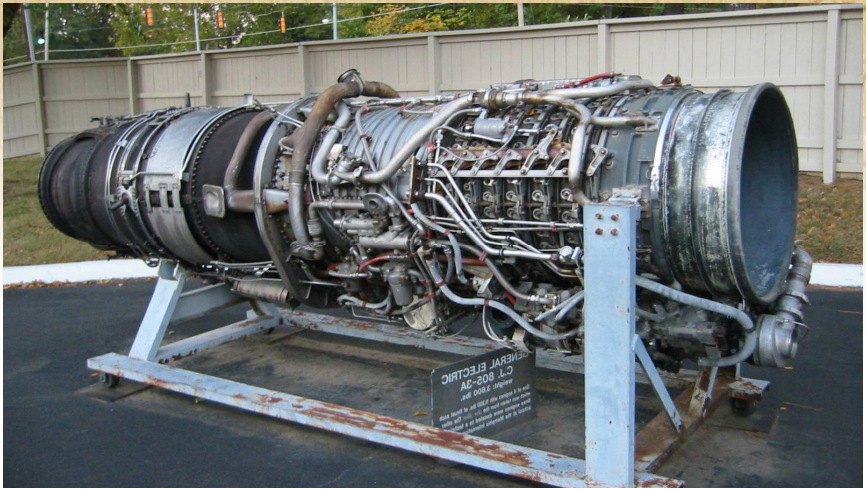
- It is usually computed from the diagonal of A:

$$F = \text{diag}(A) - 1$$

- We usually assess the inbreeding coefficient by looking at the average value of F of virtual progenies proposed by the virtual mating list:  $F_{\text{avg}} = \text{Average}(F)$
- F can also be computed as coancestry between the two parents of the individual concerned, hence a bit of a confusion with the “cohort coancestry”

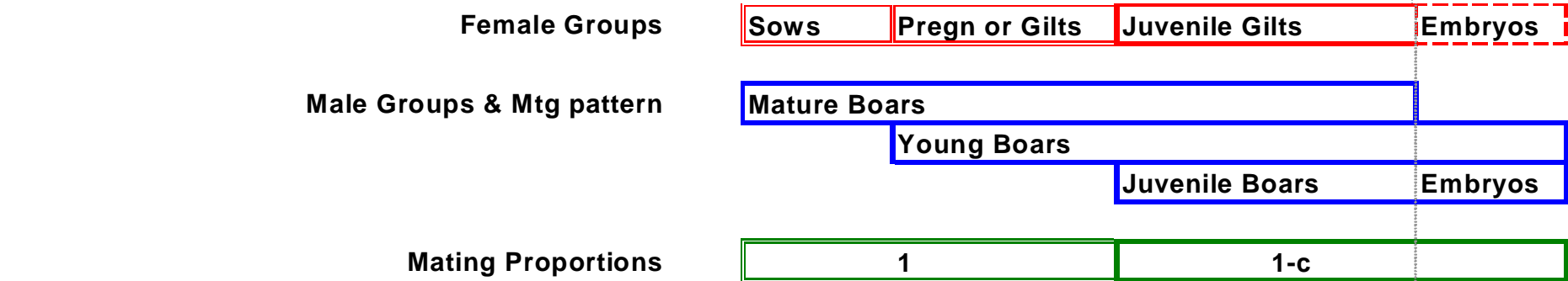
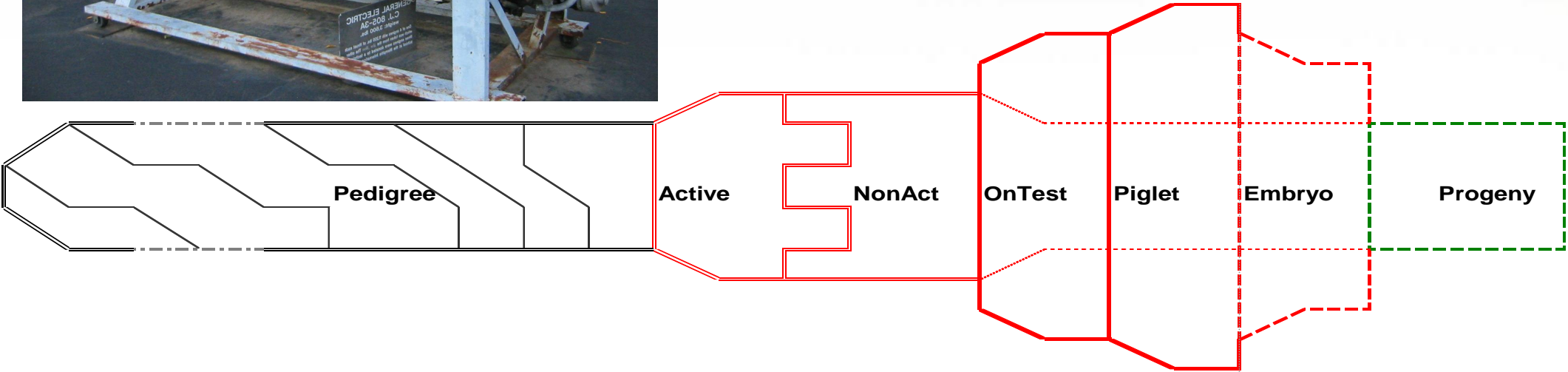
# The scheme in theory





# The scheme in practice

## "The Mate-Selection Turbine"





# Operational mate selection

*Maximize index value in progeny while managing coancestry*

**Being anywhere along this line maximizes predicted progeny genetic merit, while minimizing rate of inbreeding**

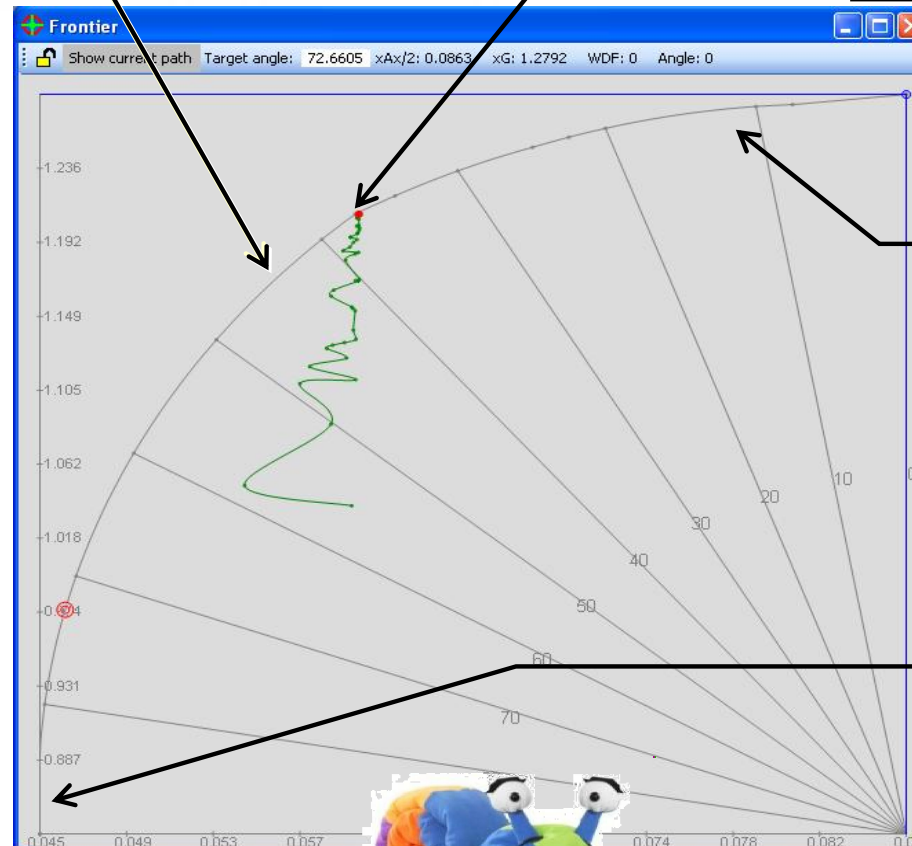
**The red dot represents the current mating set**

**Index  
(speed)**

**Few Sires  
High genetic gain  
High inbreeding rate**

**Many Sires  
Low genetic gain  
Low inbreeding rate**

**Coancestry  
(safety)**



# Rates of change

- **Rate of change in inbreeding coefficient ( $\Delta F$ )**
  - Traditional measure influenced by mating allocation
  - vary from one generation/cohort to another, from one time interval to another
  - makes life difficult when trying to make decisions based on shorter time intervals
- **Rate of change in coancestry ( $\Delta Coan$ )**
  - the change in coancestry does not suffer from the issues with  $\Delta F$
  - the “better measure” of risk associated to breeding of animals in selected populations

# Risk? What risk?

- Traditionally, risk in animal breeding is associated to reduction/erosion in genetic variance of the population
  - In practice this is actually a low risk due to the continuous imports of animals, merging of populations, change in economic scenarios (use of fashionable traits!), adding of new sources of information (new traits/ QTL and marker info), etc.
  - Thus, we may call this the “chronic issue”
- What is then the problem?
  - The risk of accumulation, in significantly important numbers, of (semi) deleterious alleles
  - Because this can happen relatively quickly in a population that is poorly managed in terms of relationships, this is to be considered the “acute issue”

# Results, e.g.

