



PEDIG : a fortran package for pedigree analysis suited to large populations

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General presentation

PEDIG is a set of programmes
to analyse pedigree information

- selects the information and recodes a pedigree file
- describes the quality/completeness of the pedigree
- computes inbreeding coefficients (complete or close)
relationship coefficients (complete or samples)
probabilities of gene origins, including ancestors,
founders or strains contributions



Pedig is suited to large populations

- RAM requirements proportional to population size
- Computationally efficient
example in the French Holstein (AIX system) :
 - 5 mn CPU for 15 million inbreeding coefficients**
 - one day CPU for 1 billion relationship coefficients**
(mating plan)



For the users...

- It is written in standard **fortran 77** and includes all necessary subroutines. It requires a fortran compiler (GNU is free)
- It also includes :
 - a **user's guide** in English and in French
 - several **examples** of small and medium size
- **Outputs** could be in English or in French (compilation option)
- http://www-sgqa.jouy.inra.fr/article.php3?id_article=94



Software demonstration content

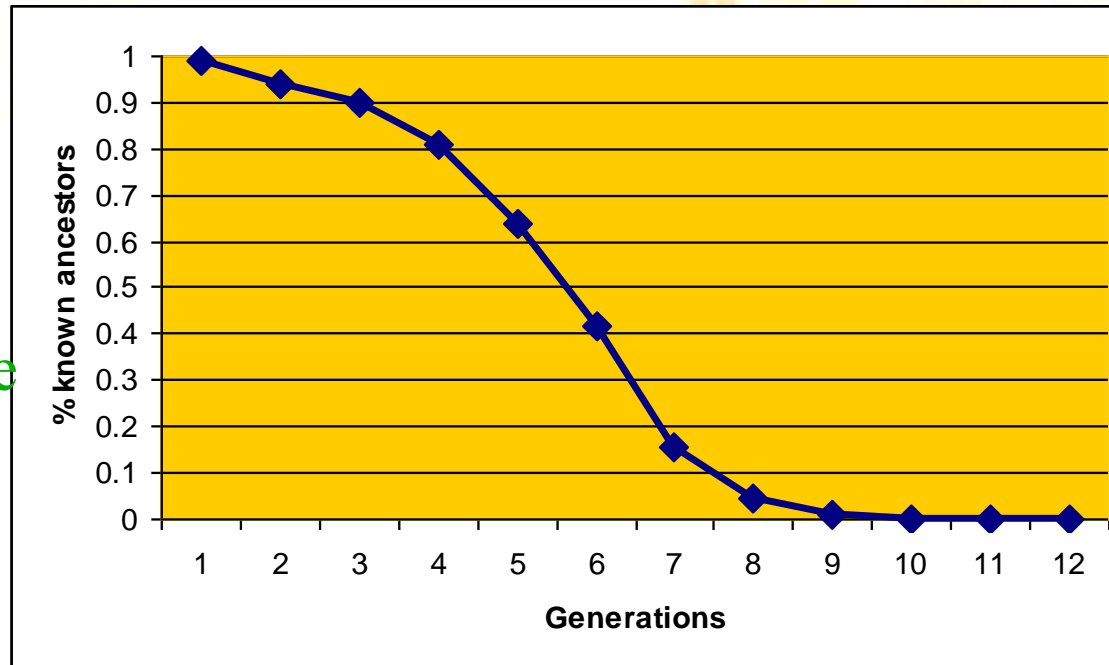
How to use **PEDIG** to

- extract necessary information from a pedigree file
- measure pedigree deepness
- compute inbreeding and relationships
- measure gene flow in cross-breeding
- find major ancestors contribution
- ...



Some results you can obtain (1)

Quality
of pedigree

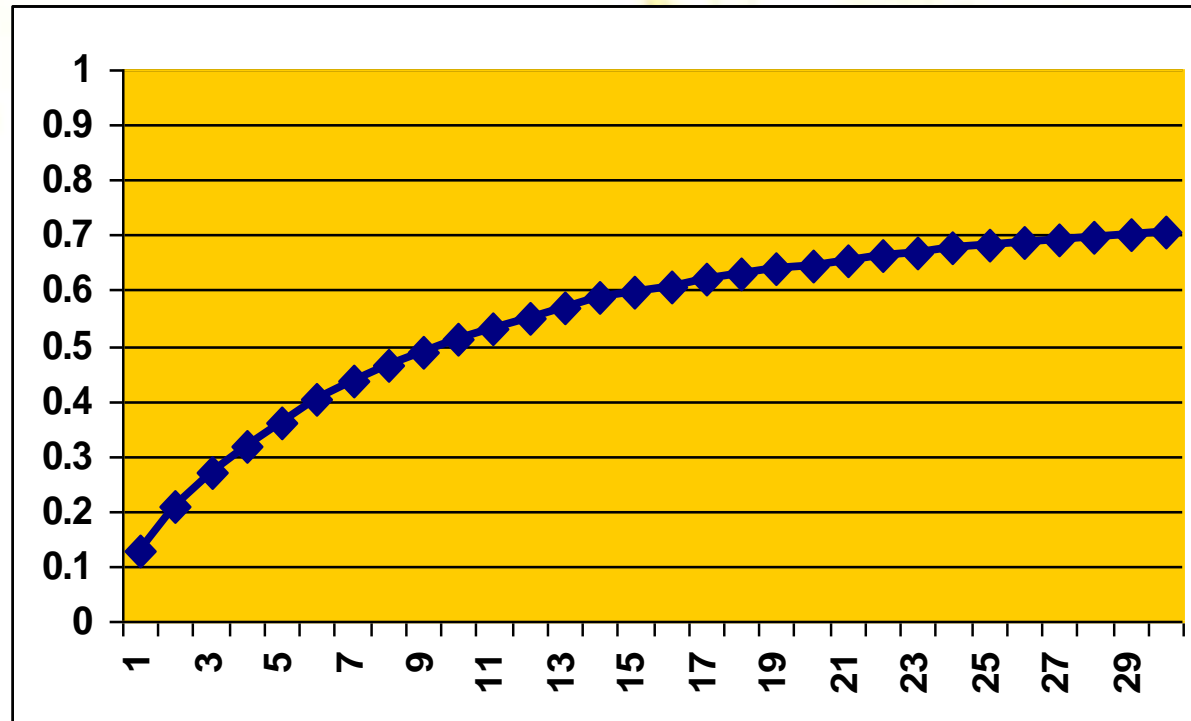


Number of
Equivalent
Complete
Generations = 4.91



Some results you can obtain (2)

Ancestors
contributions

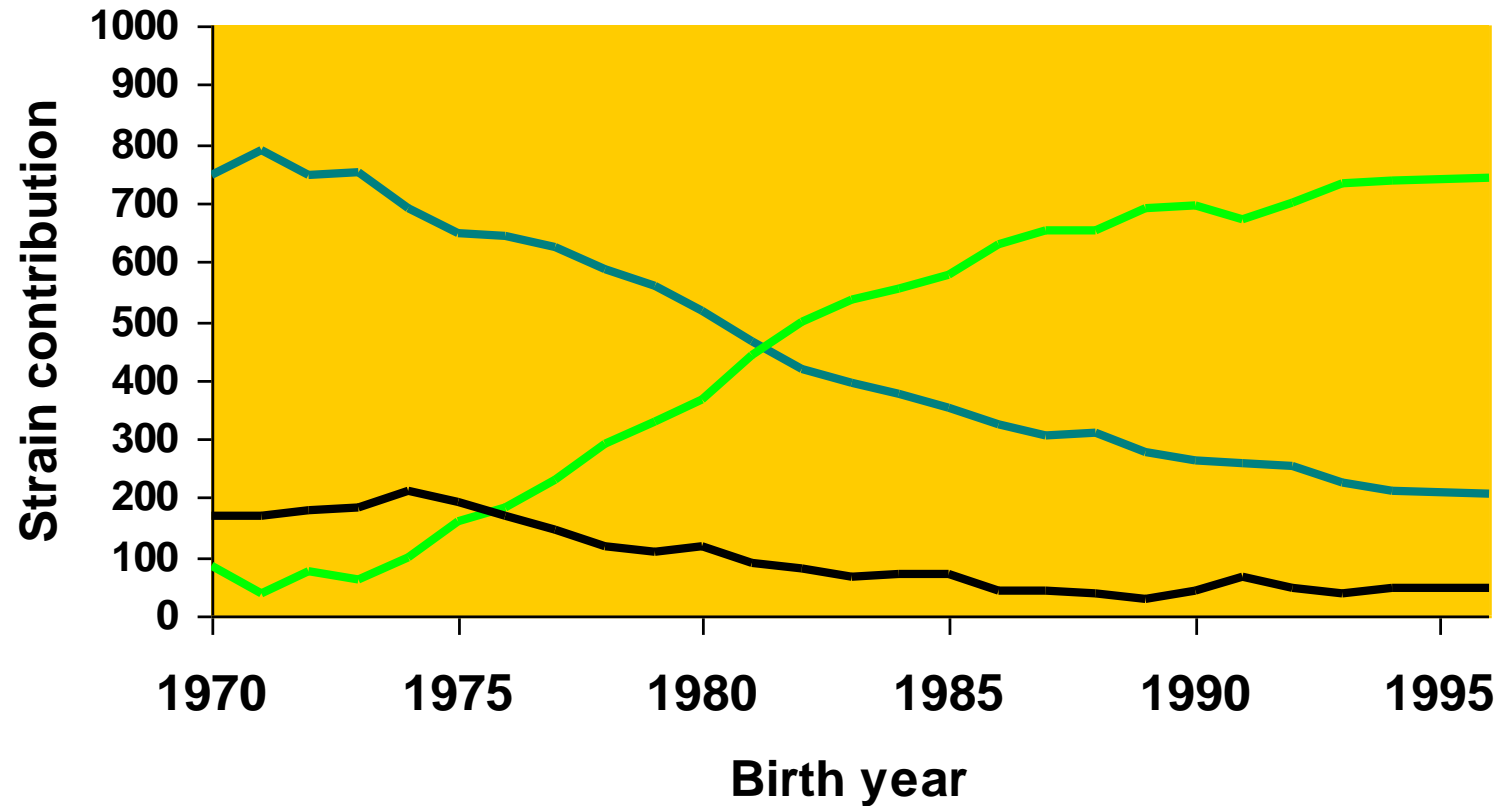


Effective
Number of
Ancestors
= 26



Some results you can obtain (3)

Strain
contributions





Some results you can obtain (4)

Relationships

(n=9730666
Coefficients
 $\mu=3.1\%$)

