



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

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# General presentation

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**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...

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- 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](http://www-sgqa.jouy.inra.fr/article.php3?id_article=94)



# Software demonstration content

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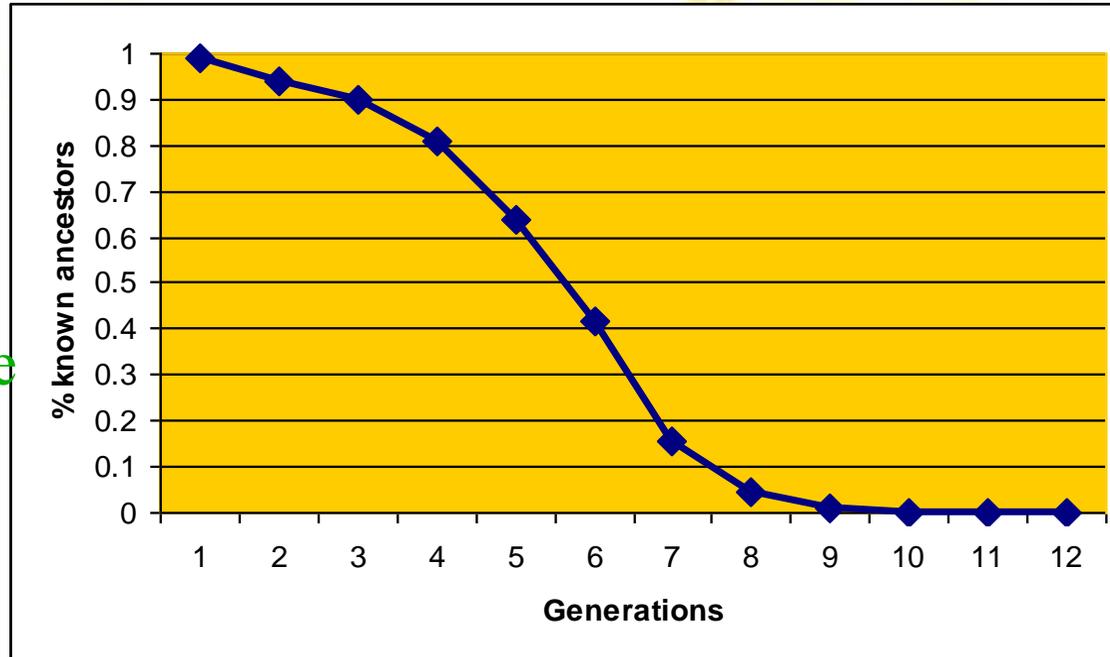
How to use **PEDIG** to ....

- **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

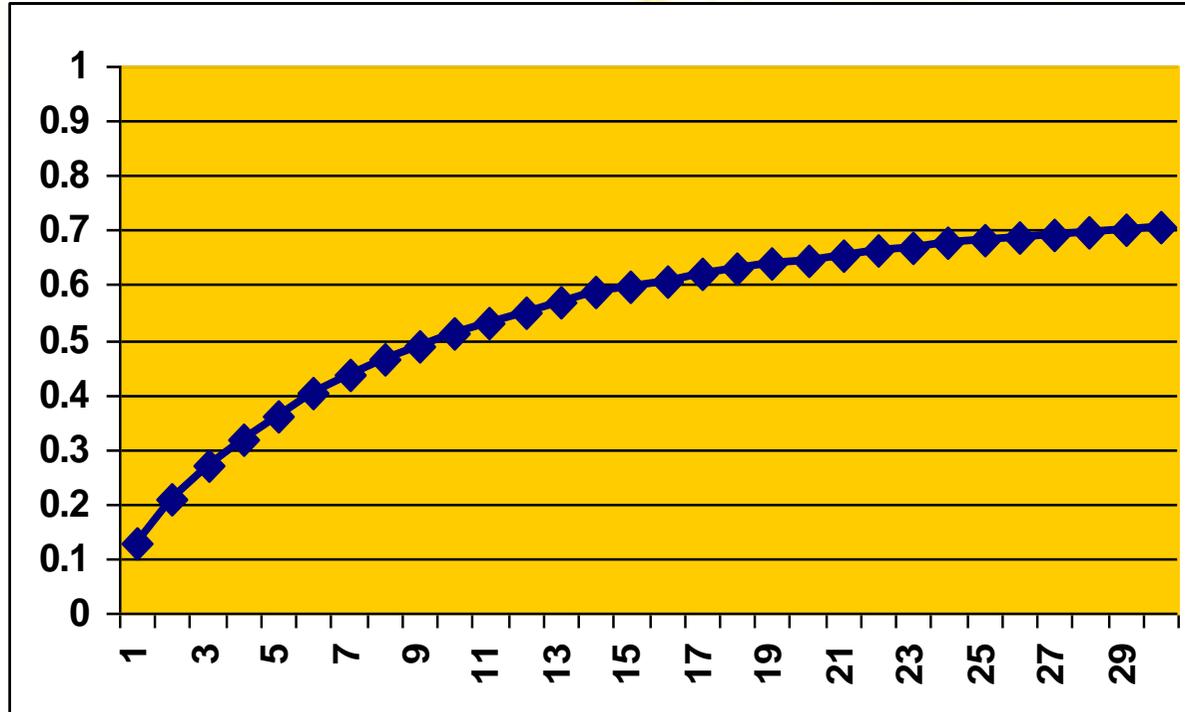


Number of  
Equivalent  
Complete  
Generations = 4.91



# Some results you can obtain (2)

Ancestors  
contributions

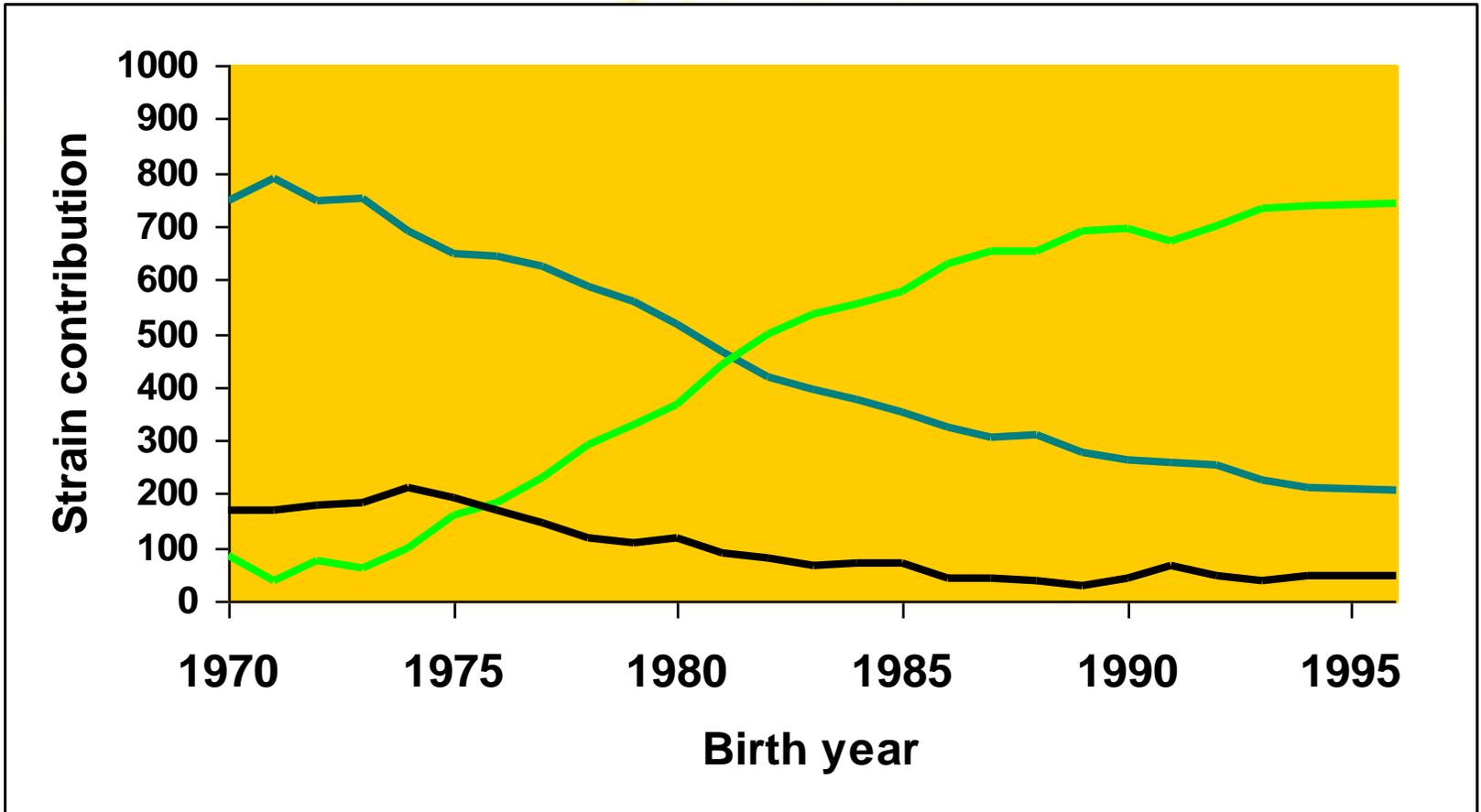


Effective  
Number of  
Ancestors  
= 26



# Some results you can obtain (3)

Strain contributions





# Some results you can obtain (4)

Relationships

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

