Population and Quantitative Genetics (PQgen): A Software Program For Teaching Animal Breeding.

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Introduction

The software program PQGen is developed as a complementary resource for an introductory course on Population and Quantitative Genetics oriented to animal breeding. The aim of the program is that the students use it either on guided sessions or privately. The program calculates the basic parameters and topics of population and quantitative genetics (Falconer and McKay, 1996; Lynch and Walsh, 1997) by using deterministic (infinite size populations) and stochastic (finite size populations) simulation.

The actual version of the program has been developed in Liberty Basic on Windows XP operating system. However, some inner calculations have been developed in Fortran 90, but they are completely hidden for the users. The program is shareware and can be downloaded from http://veterinaria.unizar.es/AVV/PQGen. Suggestions that allow to improve this program will be appreciated by the authors.

Dynamic of software execution

Activation of the software starts from a master window (Figure 1). From here, a graphical menu can be displayed and each unit can be activated with the subsequent submenus. After choosing a particular unit of the Population or Quantitative Genetics program, another window is opened on the right upper side of the screen to introduce the required parameters for data simulation. Acceptation of the introduced parameters activates one or several windows with text or graphics that can be moved, resized and closed independently. A first level of help about the active unit can be obtained by pressing "?" on the dialog window and a more detailed help in several languages can be always obtained. Contents of every text window can be edited, printed or saved.

Modules for population genetics:

1. Hardy-Weinberg Equilibrium. Visual description of gene and genotypic frequencies and HW equilibrium with autosomal loci with 2 alleles.
2. Gene frequencies and equilibrium HW. Estimation of gene frequencies and HW equilibrium with multiple alleles with up to three levels of dominance.
3. Gene frequency evolution of sex linked loci. Genetic equilibrium for loci located at sexual chromosomes.

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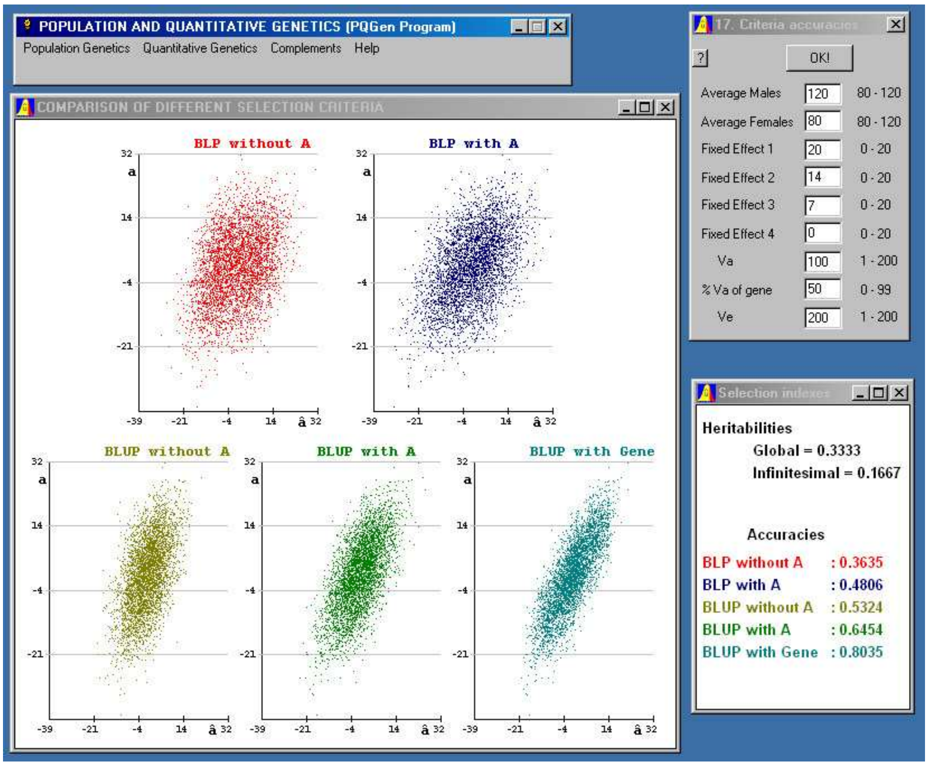
4. Map distances and recombination coefficients. Graphical and numerical expression of map functions. Efficiency of gametic samples with different sizes.



Average Males 120 80 - 120
Average Females 80 80 - 120
Fixed Effect 1 20 0 - 20
Fixed Effect 2 14 0 - 20
Fixed Effect 3 7 0 - 20
Fixed Effect 4 0 0 - 20
Va 100 1 - 200
% Va of gene 50 0 - 99
Ve 200 1 - 200

Heritabilities
Global = 0.3333
Infinitesimal = 0.1667

Accuracies
BLP without A : 0.3635
BLP with A : 0.4806
BLUP without A : 0.5324
BLUP with A : 0.6454
BLUP with Gene : 0.8035

Figure 1: Windows display when executing a didactic unit

5. Gametic frequencies evolution and linkage disequilibrium under different degrees of recombination between genes.
6. Linkage disequilibrium. Estimation of linkage disequilibrium from phenotypic counts for two loci with two alleles each.
7. Predictive ability of a marker. Verification of the predictive capacity to describe the genetic structure of a locus through a marker in linkage disequilibrium.
8. Assortative mating. Evolution of allele frequencies, variance and heterozygosis with positive and negative assortative mating.
9. Migration. Evolution of allele frequency on a population receiving a constant migration rate.

10. Mutation. Evolution of gene frequency on a population affected by constant rates of recurrent and reversible mutation.

11. Selection. Evolution of gene frequency under different selection rates on each genotype.

12. Hitchhiking effect on linked locus for selection. Displays the consequences of the selection from a locus marker on a locus of interest or QTL in linkage disequilibrium.

13. Mutation-Selection balance. Evolution of allele frequencies under simultaneous mutation and selection effect.

14. Selection for fitness defined by two loci. Evolution of allele and gametic frequencies, linkage disequilibrium (Bulmer effect) and correlation between gene frequencies.

15. Gene sampling - Genetic drift. Display the evolution of the genetic structure of subpopulations under finite size gene sampling in the idealized model context.

16. Genetic drift and selection. Evaluates the joint effect of selection and genetic drift on the evolution of gene frequencies.

17. Individual inbreeding. Evaluate a pedigree up to four generations backwards and calculates the inbreeding coefficient indicating the common antecessors.

18. Relationship matrices. Calculates the relationship coefficients between every individual on a given pedigree. Coefficients of coancestry and numerator and aditive relationship are computed.

19. Founder effects. Illustrate the contribution of each founder (allele or individual) to a population by gene dropping in a pedigree.

20. Effective size and population inbreeding. Relationship among effective population size and the evolution of inbreeding coefficient under HW equilibrium and different family size variances.

Modules for quantitative genetics:

1. Genetic structure of a quantitative trait. Simulation of the genetic components of a quantitative trait (G=A+D+I) defined by two loci in a random population of infinite size and genetic and haplotypic equilibrium.

2. Selection for components of the genotypic values. Simulation of changes on the genotypic values after selection on each genetic component of a quantitative trait.

3. Sampling of a quantitative trait. A stratified sampling is performed to illustrate the importance of sampling on the study of a quantitative trait.

4. Heritability estimation - Analysis of variance. Relationship between causal components involved on the infinitesimal model and the estimates from an analyisis of variance.

5. Heritability estimation - Regression analysis. Estimation of heritability is performed by linear regression between parents and progeny.

6. Effects of selection on the genetic structure of a population. Evolution of the population mean, genotypic variance and heterozygosis by positive, negative, or stabilizing selection for several generations.
7. Effects of inbreeding on the genetic structure of a population - Inbreeding depression. The consequences of the inbreeding caused by the repeated mating of parent and offspring are displayed, regarding the mean value of the trait, phenotypic variance, heterozygosis proportion and inbreeding coefficient.
8. Effects of crossbreeding on the genetic structure of populations - Heterosis. Consequences of crossbreeding on the population mean, the genotypic variance and heterozygosis.
9. Reciprocal recurrent selection. Dynamics and implementation of reciprocal recurrent selection on different steps.
10. Selection index and breeding values distributions. Expected distribution of selection indexes conditionally to the breeding values and vice versa.
11. Properties of the selection index as a selection criterion. Relationship between the components of expected selection response after one generation of selection via selection index.
12. Efficiency of selection indexes depending of the information source. Selection indexes calculated from individual, collateral, ascendancy and progeny data are compared in terms of expected and realized accuracy.
13. Best Linear Unbiased Prediction - Sire model. Construction and resolution of BLUP sire model with simulated data and a constant pedigree.
14. Best Linear Unbiased Prediction - Animal model. Construction and resolution of a BLUP animal model with up to 2 systematic effects with 5 levels each one and a total of 21 individuals on the pedigree.
15. Correlated response. Direct and correlated response to positive and negative selection during several generations.
16. Threshold model. Evolution of the incidence of a categorical trait after several generations of phenotypic selection.
17. Comparison between criteria of selection. Predicted and simulated breeding values are plotted by using different criteria of selection.
18. Marker assisted Selection. The efficiency of marker assisted selection is verified for several generations and compared with the results from the infinitesimal model**.**

References

Falconer D. S., McKay, T. F. C. (1996). Introduction to Quantitative Genetics, Longman.

Lynch M., Walsh, B. (1997). Genetics and Analysis of Quantitative Traits. Sinauer.