# A PACKAGE OF GENETIC-BREEDING STATISTICAL PROGRAMS FOR PERSONAL COMPUTERS

S.E. DROMASHKO

*Institute of Genetics and Cytology of the National Academy of Sciences of Belarus*
*Minsk, Republic of Belarus*
e-mail: `S.Dromashko@igc.bas-net.by`

**Abstract**

Packages of applied programs for personal computers AB-STAT and RISHON for different kinds of biometrical analysis directed at inquiries of geneticists and breeders were developed for operational system MS DOS in the middle of 1990s. Modernization of the packages by their uniting is supposed to be promising. Such a united package should be provided with new probabilistic and statistical methods for analysis of discrete data and modern user interface on MS Windows basis.

## 1 Introduction

At present there is no modern object-oriented software for processing genetic-breeding data, optimizing and promoting the process of quantitative estimation of a new gene pool for productivity parameters with due account of environmental factors (the productivity level depending on general and specific combinung ability, ecological stability and plasticity of plant varieties; resistance to main biotic and abiotic stresses, including soil-climatic factors; minimization of growing intensification procedures). The available statistic packages, for example, SYSTAT, STATGRAPH or STATISTICA are aimed at processing of pooled data and therefore do not include a block of genetic-statistical analysis taking into account specificity of breeder's demands. They are oriented to processing medical data, in the best case (see, for example, several issues of such a journal as Scientific Computing, 2005–2007).

## 2 Our previous experience

The Institute of Genetics and Cytology of the National Academy of Sciences of Belarus is a leading institution in the Republic of Belarus in the field of mathematical genetics and simulation of breeding process. Applied computer programs for genetic-statistical analyses of experimental data and mathematical simulation have been developed at the Institute for more than 30 years. The appearance of personal computers at the end of 1980s made it possible to raise a problem of integrating the stored programs into a single package corresponding to the modern level of demands for comfort and easiness of its application.

In the early 1990s a package of applied programs AB-STAT for statistical analysis of breeding, genetic and medical-biological experiments was developed at the Institute by Anoshenko (1994). It was a PC development of his program package SIGMA (1986).

By 1995 a package of applied programs for personal computers RISHON for different kinds of biometric analysis (elementary statistic, correlation, variance, multivariate, genetic methods) was developed for operating system MS DOS (Dromashko, Frenkel, Mats, 1995). In contrast to other program biometric products of that period, such as DAVP-PC (Germany), BIOSTAT (Moldova), the package RISHON is oriented to demands of geneticists and breeders, in the first place, of plant breeders (see, for example, Smiryaev et al., 1992). Its genetic block includes about 15 programs for computing parameters of conceptual genetic models (general and specific combining ability according to Griffing models, genetic parameters by Heumann method, Wright path coefficients, ecological stability and plasticity by Eberhardt and Russell, plant genotype adaptive ability by Kilchevsky and Khotyleva, etc.).

Orientation to genetics of agricultural plants allowed introduction of the package into practice of educational and research processes at the biological faculty of Gomel State University and at some chairs of Belarusian State Agricultural Academy. The package was also sent to the Experimental Station for Poultry Farming of the National Academy of Sciences of Belarus and to the Institute of Genetics and Physiology of Cotton of the Academy of Sciences of Tajikistan.

# 3   Prospect of modernization

However, over the past 10 years the design of the packages AB-STAT and RISHON oriented to MS DOS became morally out-of-date. A necessity for modernization arose. In 1995–2002 we made an attempt to develop a complex program of information theory analysis of genetic processes in agricultural plants taking into account the influence of environmental factors using MS DOS platform (Dromashko et al., 1998), then MS Excel formalities (Dromashko, Maschits, 2002). With due account of this experience, modernization of the package by equipping it with modern user interface on MS Windows basis seems promising.

Besides, there is a task of enlarging a genetic part of the package by addition of new models, such as: an express method of least squares for data grouping by a "template"; program for demonstration of genotypic difference between varieties groups classified by their ecologic-geographical origin; integral estimation of genotypes by complex of characters with taking into account "genotype-environment" interaction, etc. (Dromashko et al., 1997). We also suppose to provide genetic models with some new probabilistic and statistical methods for analysis of discrete data. This will allow users to realize a system approach in modern, convenient and usual environment, using up-to-date mathematical methods.

The approach makes it possible to carry out the entire complex of required computations, in particular, to perform statistical computer data processing for conceptual genetic models; to assess quantitatively the outlook of some or other genotypes for application in the breeding process; to plan optimum crop rotation; to compute the

most economic application of fertilizers and agents of chemical plant protection, etc.

# 4    Conclusion

Such a modified updated package will be required for educational, research and breeding institutions in the Republic of Belarus and other NIS countries. Particularly, there are above 10 thousand potential users – students and lecturers at institutes of higher education, universities and colleges in the field of biology and agriculture. We can also add no less than 1.5 thousand specialists at research and breeding institutions of our republic. Taking into account Russia, Ukraine, and Kazakhstan, this number can be enlarged at an order, at least. When translating interface into English, the package can be of interest for foreign distribution. It will be a good example of computer genetic data analysis in application to optimization and promotion of the breeding process.

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