



Statistical Evaluation and Interpretation of Data in Rice Plant Pathology

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DESCRIPTION

Across the past forty years, there has been a substantial increase in the use of statistical methods in plant pathology. Among these tools are multivariate analyses of disease dynamics, which involve principal component analysis, cluster analysis, factor analysis, pattern analysis, discriminant analysis, multivariate analyses of variance, correspondence analysis, canonical correlation analysis, redundancy analysis, genetic diversity analysis, and stability analysis, which involve joint regression, additive main effects and multiplicative interactions, and genotype-by-environment interaction. The analysis of disease dynamics makes use of advanced statistical techniques such as non-parametric analysis of disease association, meta-analysis, Bayesian analysis, and decision theory. Plant disease forecasting techniques using simulation models offer a lot of potential for use in real-world disease control tactics. In the study of disease epidemic development curves, common mathematical techniques including monomolecular, exponential, logistic, Gompertz, and linked differential equations play a significant role. It has been proposed to construct box and whisker plots as a highly informative method of displaying a variety of numerical data. The generalized linear model, linear mixed model, and generalized linear mixed models are some of the most current sophisticated tools for linear and non-linear mixed models. The most modern technologies, including micro-array analysis, require attention from molecular biologists since they provide estimates of the gene expressions for thousands of genes simultaneously while being cost-effective. Some of these advanced tools can be well employed in different disciplines of rice research, including crop development, crop production, crop protection, social sciences as well as agricultural engineering. The scientists conducting research on rice should make the most of these new chances by adopting new, highly advanced technology when they develop their experimental designs, gather data, analyze it, and interpret their study data sets [1].

The molecular biology area has expanded significantly over the past three decades, overshadowing the enormous progress made in the field of plant pathology during the 1960s major contribution

to the study of botanical epidemiology, which continues to be of the utmost relevance for the theoretical and practical underpinnings of disease management for the past fifty years. The use of the new statistical techniques in plant pathology is highlighted in a number of papers that were given at the 94th Annual Meeting of the American Phytopathological Society on July 29, 2002. Advanced statistical approaches such as multivariate analysis, meta-analysis, survival analysis, Bayesian analysis, and nonparametric study of disease dynamics predominate [2,3].

Although plant pathologists in North America and Europe have adopted these cutting-edge statistical tools, their use in Asia is still quite limited. The goal of this review is to familiarize rice research scientists in Asian nations with these incredibly important statistical methods so they can utilize them in various fields of rice research in general and rice pathology in particular.

For the analysis of data containing multiple variables, multivariate statistical techniques are available, such as Ordination, which combines Principal Component Analysis (PCA), principal coordinate analysis, discriminant analysis, correspondence analysis, multidimensional scaling, and Factor Analysis (FA); Classification/Discrimination; Consisting of multivariate analysis of variance, Multiple Logistic Regression, and Discriminant Analysis (MANOVA) including canonical correlation, correspondence, and redundancy; and Cluster Analysis (CA); . Ordination seeks to describe data by identifying a condensed data dimension comprising just a few variables that account for the majority of the data's variability. By using a collection of variables, discrimination seeks to distinguish between experimental groups or categorize observations into experimental groups. The goal of canonical is to explain and forecast how two sets of variables will interact [4,5].

Compared to the most popular forms of multiple regression analysis, the application of MVA to rice pathology is relatively new. The association between various injury levels brought on by rice insect pests and illnesses, as well as weed infestations and quantification of production losses, was examined for the first time using the MVA, Multiple Regression Analysis (MRA), and

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correspondence analysis. Three techniques were used in its application to categorize and identify rice genotypes with slow-blasting resistance and fast-blasting resistance. Analysis of the slow-blasting resistance's constituent parts, estimation of the parameters for resistance evaluation analysis of all disease progression curves during a nine-season span. A critical analysis of this method indicated that, despite providing the most precise data, it has some limitations in the data collection on each component of resistance, necessitating thorough research that are labour and resource expensive, costly, and time consuming. It is exceedingly challenging to evaluate a large number of varieties within a time frame that is conducive to the development of diseases, or alternatively, it requires controlled settings like a phytotron facility, which may not be feasible at all research labs.

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