Network Analysis of Cropping Practices and Injuries Profiles under Rice Agroecosystem

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Abstract

Here is the abstract.....

Introduction

The use of rice crop health survey at the field levels is ground truth database that allow one identify actual constraints due to pests in rice production. The database provide the overview of the complex relationships between crop stands, their management, pest injuries, may lead to better management, and guide researchers the new research hypotheses (6; 11).

Several previous studies (13; 12; 10; 2; 7) conducted the surveys have identified the relationships of individual production situation (a set of factors that determine agricultural production) and injury profiles (combination of disease and pest injuries that may occur in a given farmers field) using nonparametric multivariate analysis (9). Performing correspondence analysis, they characterized the relationships between categorized levels of variables: actual yield, production situations and injuries profiles . the results led to the conclusions that observed injuries profiles are strongly associated with production situations(6). However, the step of transform continuous data to categorized data by clustering approach is poor reproducibility and difficult interpretability of the individual cluster (5; 1).

The components of production situation and injury profiles, such as the amount of fertilizers applied, occurrence of leaf blast are biologically related. The relationships will be more complex when the number of their components will increase. A way to systemically model and intuitively interpret such relationships is the depiction as a graph or network. This approach has been widely used and proven very useful in biological studies. Networks typically consist of nodes, usually presenting components (), while links between the node depict their interactions. Correlation network is a type of network, which two nodes are connected if their respective correlation lies above a certain threshold. The construction of this network obtain from pairwise correlation methods. By using appropriate correlation measure, correlation network can capture biologically meaningful relationships, and discover the valuable information in crop health surveys.

Selecting the suitable association methods for crop health construction is important because the method that can capture the relationships with true concordance often determined the type and amount of knowledge we can gain from survey data. we have limited prior knowledge (positive relation and negative relation) for comparing the efficiency of different association methods in discovering true functionally associated variables.

The main aim of this article is to evaluate correlation methods including Pearson, Spearman, Kandell, Biweight to associate the components of cropping practices and the components of injuries profiles. Furthermore, we applied network theory and model to illustrate the pairwise relationships. Thus we hope to provide the necessary elements for a better comprehension of the methods and also the choice of a suitable dependence test method based on practical constrains and goals.

Materials and Methods

We inferred a interaction network by from survey project comprising 5 countries (India, Indonesia, the Philippines, Thailand, and Vietnam), 420 lowland farmers' fileds. Our study aimed to determine co-occurrence pattern among the incidence of injuries caused by animal pests and diseases and the cropping practices, potentially indicative of their occurrence relations. We thus construct the network from the surveys. The limitation of each measure are difference assumption and detach different patterns.

Survey datasets

Crop health survey data were collected through surveys comprising 420 farmers' fields from 2010 to 2012 for wet and dry seasons in different production environments across South and South East Asia representing irrigated lowland rice growing areas of India, Indonesia, the Philippines, Thailand, and Vietnam. The survey protocol described in the IRRI publication, "A survey portfolio to chatacterize yield-reducing factors in rice", was used for data collection (8). The variables collected included patterns of cropping practices, crop growth measurement and crop management status assessments, measurements of levels of injuries caused by pests, and direct measurements of actual yields from crop cuts. The data collected can be classified into three groups: cropping practices, injuries, and actual yield measurements.

Evaluation of association methods

The criteria of chosing correlation measures

Step one: Data exploratory Data were check the properties. There are three main properties to be determine before deciding the appropriate correlation measure.

Task check normality and data distribution This tesk can be achieved by significant test and visual methods. Each of varible in survery dataset was tested normality by Shipiro-Wilk test, which highly recommend (4). The Shapiro-Wilk test is based on the correlation between the data and the corresponding normal scores.

 H_0 : sample distribution is normal.

 H_a : sample distribution is not normal.

Thus if the p-value is less than the chosen alpha level, then the null hypothesis is rejected and there is evidence that the data tested are not from a normally distributed population. In other words, the data are not normal. On the contrary, if the p-value is greater than the chosen alpha level, then the null hypothesis that the data came from a normally distributed population cannot be rejected. However, for small sample sizes, normality tests have little power to reject the null hypothesis, so a QQ (quantile-quantile plot) plot and the freency distribution (histrogram) are required for verification in addition to check normality visually.

The R function for Shapiro-Wilk Normality test is shapiro.test (package stats). The stats package can be downloaded from the R Web page (http://www.r-project.org) (?).

Task check the independence Performing the distance correlation t-test(14) to check independence aims to select the pair of varibles which are able to be deteacted correlation. The distance correlation of two random variables is obtained by dividing their distance covariance by the product of their distance standard deviations. The distance correlation is

$$dCor(X,Y) = \frac{dCov(X,Y)}{\sqrt{dVar(X) \ dVar(Y)}}$$
(1)

- $0 \le dCor_n(X, Y) \le 1$ and $0 \le dCor(X, Y) \le 1$
- dCor(X, Y) = 0 if and only if X and Y are independent.
- $dCor_n(X,Y) = 1$ implies that dimensions of the linear subspaces spanned by X and Y samples respectively are almost surely equal and if we assume that these subspaces are equal, then in this subspace $Y = A + b \mathbf{C} X$ for some vector A, scalar b, and orthonormal matrix \mathbf{C} .

This test wes perform by R with fda.uss package (3).

Task check linearity or non-linearity

Step two: identify the most appropriate method

Pearsons product-moment correlation coefficient

The Pearsons product-moment correlation or simply Pearsons correlation is a measure of linear dependence, as the slope obtained by the linear regression of Y by X is Pearsons correlation multiplied by that ratio of standard deviations. Let $\overline{x} = \frac{\sum_{i=1}^n x_i}{n}$ and $\overline{y} = \frac{\sum_{i=1}^n y_i}{n}$ be the means of X and Y, respectively, then the Peasons's corrlation coefficient $\rho_{pearson}$ is defined as follows:

$$\rho_{pearson}(X,Y) = \frac{\sum_{i=1}^{n} (x_i - \overline{x})(y_i - \overline{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \overline{x})^2 \sum_{i=1}^{n} (y_i - \overline{y})^2}}$$
(2)

For joint normal distributions, Pearsons correl- at ion coefficient under H0 follows a Students t-distribution with n-2 degrees of freedom. The t statistic is as follows:

$$t = \frac{\rho_{pearson}(X, Y)\sqrt{n-2}}{\sqrt{1 - \rho_{pearson}^2(X, Y)}}$$
(3)

When the random variables are not jointly nor- mally distributed, the Fishers transformation is used to get an asymptotic normal distribution.

In the case of perfect linear dependence, we have $\rho_{pearson} = \pm 1$. The Pearson correlation is +1 in the case of a perfect positive (increasing) linear relationship and -1in the case of a perfect negative (decreasing) linear relationship. In the case of linearly independent random variables, $\rho_{pearson} = 0$, and in the case of imperfect linear dependence, $-1 < \rho_{pearson} < 1$. These last two cases are the ones for which misinterpretations of correlation are possible because it is usually assumed that non- correlated X and Y means independent variables, whereas in fact, they may be associated in a non-linear fashion that Pearsons correlation coefficient is not able to identify.

The R function for Pearsons test is cor.test with parameter method 'pearson' (package stats). The stats package can be downloaded from the R Web page (http://www.r-project.org).

Network Construction

Co-occurrence network construction

The matrix can be viewed as an adjacency matrix of a weighted network. The matrix contains the correlation coefficient between each node (i.e., the variable). Thus the matrix can be thought of as the population average of the network structure. Because we are looking at several specific links, we control for multiple testing by controlling the False Discovery Rate (FDR method) at 5%. The generated network structure can be visualized through the R package qgraph. Only connections that surpass the significance threshold are shown in the visual representation.

Network analysis

Important information about a network can be gained by analyzing its global structure, for example by looking at the relative centrality of different nodes. In a centrality analysis, nodes are ordered in terms of the degree to which they occupy a central place in the network. Global descriptors of the modules were obtained using package qgraph in R. The neighborhood of a given node n is the set of its neighbors. The connectivity is the size of its neighborhood. The average number of neighbors indicates the average connectivity of a node in the network. A normalized version of this parameter is the network density. Density ranges between 0 and 1. It shows how densely the network is populated with edges, A network which contains no edges and solely isolated nodes has a density of 0. In contrast, the density of a clique is 1. Another related parameter is the network centralization. Networks whose topologies resemble a star have a centralization close to 1, whereas decentralized networks are characterized by having a centralization close to 0.

In undirected networks, the clustering coefficient is the number of connected pairs between all neighbors of the network. The clustering coefficient of a node is always a number between 0 and 1. The network clustering coefficient is the average of the clustering coefficients for all nodes in the network. Nodes with less than two neighbors are assumed to have a clustering coefficient of 0. We then determined network centralities on the modules obtained from network analysis. Centralities were assessed using package in R. We calculated Degree centrality and Betweenness centrality.

Results

Discussion

References

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