

# Network Analysis of Cropping Practices and Injury Profiles in Irrigated Rice Agroecosystems

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## 2 ABSTRACT

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4 or **Table 1** for a summary according to article type.

5 **Keywords:** Text Text Text Text Text Text Text Text

## 1 INTRODUCTION

6 The use of in-field surveys is a useful tool to develop ground-truth databases that allow one identify  
7 actual constraints due to pests in an agricultural productions system. These sorts of databases provide  
8 an overview of the complex relationships between the crop, its management, pest injuries, yields.  
9 Understanding theses relationships may lead to better management, and guide researchers the new  
10 research hypotheses (Mew et al., 2004; Savary et al., 2006).

11 Several previous studies (Savary et al., 2005; Dong et al., 2010; ?) involved surveys that have  
12 been used to identify relationships in an individual production situation (a set of factors that determine  
13 agricultural production) and the injury profiles (combination of disease and pest injuries that may occur in  
14 a given farmer's field) using nonparametric multivariate analysis such as cluster analysis, correspondence  
15 analysis, multiple correspondence analysis. Performing correspondence analysis (?), they characterized  
16 the relationships between categorized levels of variables: actual yield, production situations, and injuries  
17 profiles. Their results led to the conclusions that observed injuries profiles were strongly associated with  
18 production situations and the level of actual yields.

19 The components of production situation and injury profiles are biologically related. For example, the  
20 excess amount of fertilizers applied in the rice files increases the susceptibility of rice to blast and directed  
21 seeded flooded rice fields with high seedling rate is the favorable condition for sheath blight (Ou, 1985).  
22 The relationships will be more complex when the number of their components increased. A way to  
23 systemically model and intuitively interpret such relationships is the depiction as a graph or network. This  
24 approach has been widely used and proven very useful in biological studies (Moslonka-Lefebvre et al.,

2011). Networks typically consist of nodes, usually representing components, while links between the nodes depict their interactions (Proulx et al., 2005). A correlation network is a type of network in which two nodes are connected if their respective correlation lies above a certain threshold. The construction of this network is obtained from pairwise correlation methods (Toubiana et al., 2013). By using appropriate correlation measure, correlation networks can capture biologically meaningful relationships, and discover valuable information in crop health surveys.

The main objective of this study is to apply network theory to the rice crop health survey data with the proposed methods for network construction. Selecting the suitable measure is important because the method should be able to capture the relationships with true concordance often determined the type and amount of knowledge we can gain from survey data, moreover it will affect the topological structure of network (the patterns of pairwise relationships between variables).

## 2 MATERIAL & METHODS

In the first step of the methods, we compute partial correlation coefficients between each edge and a behavioral measure of interest independently, by taking other behavioral measures as covariates. Either Pearson or Spearman correlation coefficients can be employed, though we employed Spearman rank correlation coefficient since the distribution of the brain connectivity data is unknown and often distribution not satisfy the normality condition. (copy from the)

Next, we inferred association network from surveys comprising five countries (India, Indonesia, Philippines, Thailand, and Vietnam), 420 lowland farmers' fields. We determine the correlation patterns among the incidence of injuries caused by animal pests and diseases and the cropping practices, potentially indicative of their occurrence relations. We then constructed the network from these pairwise correlations.

### 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. The survey protocol described in the IRRI publication, "A survey portfolio to characterize yield-reducing factors in rice", was used for data collection (Savary and Castilla, 2009). 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

#### One: Data exploration

There are three main properties to be determined before deciding the appropriate correlation measure for use in constructing the network.

##### 2.0.0.1 Check data distribution

This test can be achieved by significance test and visual methods. Each variable in survey dataset was tested normality using the Shapiro-Wilk test (?). The Shapiro-Wilk test is based on the correlation between the data and the corresponding normal scores.

$H_0$ : sample distribution is normal.

63  $H_a$ : sample distribution is not normal.

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

71 The R function for Shapiro-Wilk Normality test is `shapiro.test` (package stats), which is (?).

## 72 Network Construction

### 73 Correlation network construction

74 The matrix can be viewed as an adjacency matrix of a weighted network. The matrix contains the  
 75 correlation coefficient between each node (i.e., the variable). Thus, the matrix can be thought of as the  
 76 population average of the network structure. Because we are looking at several specific links, we control  
 77 for multiple testing by controlling the False Discovery Rate (FDR method) at 5%. The generated network  
 78 structure can be visualized through the R package qgraph (Epskamp et al., 2012). Only connections that  
 79 surpass the significance threshold are shown in the visual representation.

## 80 Evaluating Network properties

81 To evaluate the topological properties of both the interaction and the co-occurrence network, we used the  
 82 package igraph and qgraph in The R environment. Particularly we were interested in properties potentially  
 83 relevant for community roles and functioning as previously hypothesized in and reference therein m theres  
 84 are :

- 85 • Mean degree  $\langle k \rangle$ : the degree of a node counts the number of edges it has. The mean degree of nodes  
 86 calculate over all nodes in the network
- 87 • Degree distribution: the frequency of node vs. their (increasing) degree. item Average shortest path  
 88 length,  $l$ : the shortage path between any two nodes is the single path with fewest links between them.  
 89 Alternative paths are feasible. The average shortest path length is the mean over all shortest oaths  
 90 between any two nodes in the network.
- 91 • Mean clustering coefficients  $\langle c \rangle$ : a cluster of nodes a triangle of nodes. The clustering coefficient  
 92 calculates the fraction of observed vs possible triangles for each mode. The mean is subsequently  
 93 determined from all nodes in the network,
- 94 • Betweenness centrality  $\langle CB \rangle$
- 95 • Closeness centrality  $\langle CC \rangle$

96 Important information about a network can be gained by analyzing its global structure, for example by  
 97 looking at the relative centrality of different nodes. In a centrality analysis, nodes are ordered in terms  
 98 of the degree to which they occupy a central place in the network. Global descriptors of the modules  
 99 were obtained using package qgraph in R. The neighborhood of a given node  $n$  is the set of its neighbors.  
 100 The connectivity is the size of its neighborhood. The average number of neighbors indicates the average  
 101 connectivity of a node in the network. A normalized version of this parameter is the network density.

**Table 1.** Maximum size of the Manuscript

	Abstract max. length (incl. spaces)	Figures or tables	Manuscript max. length
Clinical Case Study Clinical Trial Hypothesis and Theory Methods Original Research Review Technology Report	2000 characters	15	12000 words
Focused Review	2000 characters	5	5000 words
CPC	1250 characters	6	2500 words
Perspective Mini Review	1250 characters	2	3000 words
Data Report	None	2	3000 words
Classification	1250 characters	10	2000 words
Editorial	None	None	1000 words
Frontiers Commentary General Commentary Book review	None	1	1000 words
Opinion Specialty Grand Challenge Field Grand Challenge	None	1	2000 words

102 Density ranges between 0 and 1. It shows how densely the network is populated with edges. A network,  
103 which contains no edges and solely isolated nodes has a density of 0.

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

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**3 RESULTS**

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## 4 DISCUSSION

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190 include software used, mass spectrometer type, sequence database and version, number of sequences in  
191 database, processing methods, mass tolerances used for matching, variable/fixed modifications, allowable  
192 missed cleavages, etc.

193 Authors should provide as supplementary material information used to identify proteins and/or peptides.  
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## AUTHOR CONTRIBUTIONS

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216 the References section.

## ACKNOWLEDGMENTS

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220 *Funding:* Text Text Text Text Text Text Text Text.

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223 found in the Frontiers LaTeX folder

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## FIGURES



**Figure 1.** Enter the caption for your figure here. Repeat as necessary for each of your figures