NETWORK ANALYSIS OF SURVEY DATA FOR CHARACTERIZATION OF YIELD REDUCING FACTORS AND YIELD LIMITING FACTORS OF TROPICAL RICE ECOSYSTEMS IN SOUTH AND SOUTHEAST ASIA

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Introduction

Pests and diseases to global rice production are significant yield reducing factors. Oerke (2006) estimated that rice pests potentially caused losses around 37 percent of global rice production. Additionally, future rice production will need to grow by 2.4 percent per year in order to meet the demands of a growing population (Ray et al., 2013). Addressing these yield-reducing factors is essential for food security not only in rice consuming societies, but also for other societies globally.

Rice is predominantly grown in Asia. So much so that thirty–one percent of the rice harvested globally comes from Southeast Asia alone (OECD/FAO, 2012). The highest levels of productivity are found in irrigated areas, the most intensified rice production system. Farmers can grow more than one rice crop per year here. Approximately 45 percent of the rice growing area in Southeast Asia is irrigated, with the largest irrigated areas being found in Indonesia, Vietnam, Philippines and Thailand (Mutert & Fairhurst, 2002). In South Asia, the two major rice-growing countries are India and Bangladesh. India has the largest rice growing area globally, approximately 43 million hectares, and contributes 25 percent of global rice production alone. Combined, rice production in South and Southeast Asia contributes around half of global rice production. If rice production in South and Southeast Asia is threatened, it will significantly affect global rice production.

Nowadays, developing the strategies of pest and disease management takes into

account sustainability, production efficiency, and environmental protection (Mew et al., 2004). To achieve this, interactions between pests and human activities must be studied. A survey may provide the necessary data and adequate methods for analyzing survey data can produce preliminary information on their behaviors including major interactions (Savary et al., 1995). Savary et al. (2000) concluded that the observed injury profiles (*i.e.*, the combination of disease and pest injury that may occur in a given farmer's field) were strongly dependent on production situation. The authors discussed that pest management strategies should be developed according to the patterns of cropping practices, and production situations. However, interactions among pests, cropping practices, and environments under different locations or over time are difficult to elucidate, which they are important to design the strategies of pest management.

To help visualize and understand these interactions, network analysis seems to provide a promising tool for revealing the interactions among entities within a complex system. It has been applied for many branches of science (*e.g.*, social science, computer science, and biology). A network model is an abstract model composed of a set of nodes or vertices and a set of edges, links or ties connected to the nodes. Nodes usually represent entities and the edges represent their relations. For example, an ecological network of a food web presents nodes as species (Krause et al., 2003) and edges as ecological relationships, or consider a social network of students in the school present where nodes are students and edges are friendships (Moody, 2001).

OBJECTIVES

My overall objective is to develop network approaches and apply them to analyze crop health survey data. My first objective for this research is to develop the network model based on crop health survey data and characterize relationships among

components of injuries and cropping practices. My second objective is to compare the differential relationships of network models under different seasons or locations. The third objective is to apply network analysis to compare differential interactions in networks under successive (from low to high) levels of estimated actual yields.

Once network models based on crop health survey data are constructed, they will be helpful for plant health authorities and the people who related to crop protection especially for rice. The models will support them to design specific strategies for rice pest and disease management and to limit the impacts of these yield reducing factors.

REVIEW OF LITERATURE

Introduction

The applications of network analysis have increased exponentially over the past two decades in various disciplines. Even though documented applications of network analysis in plant pathology are still relatively sparse, network applications in the social sciences, systems biology and ecology have been increasingly found. Here I review the empirical works that exist and argue that network analysis is a promising approach for exploring questions in the context of plant pathology.

This chapter contains four sections to thoroughly review of network analysis and its applications. In the first sections, I introduce a brief overview of the concepts and methods of network analysis, and I then discuss the unique values of network analysis that are not found in other approaches. In the third section I focus on the application of network analysis to current applications of plant pathology research, in particular, plant disease epidemiology and molecular plant pathology, for which network analysis has been broadly applied, and increasingly documented. In last section I will show a variety of applications of network analysis to study biological networks. Differential and dynamic network analysis are promising tools to understand biological responses to the different conditions or times.

Network Analysis

Introduction to network analysis

Network analysis is used for determining relationships between elements of interest. It offers toolkits for visualizing data in a network model and measuring its properties, and network thinkings (Proulx et al., 2005). It has been widely used by various branches of science, such as social science, ecology, biology, computer science, and many others to study the interactions between elements, e.g., the relationships of students in school (Moody, 2001), species in food webs (Krause et al., 2003), interactions of genes or proteins in cells (Guimera & Amaral, 2005), or the connections of computer in the network (Pastor-Satorras & Vespignani, 2001; Newman, 2006).

Newman (2003) loosely categorized four types of networks based on different complex data. The first category is social network, representing sets or groups of people forming some patterns of contacts or interactions between them such as the patterns of friendship or business relationships. Analyzing the structure of whole social entities gives us the perspectives from a social network, which enables us to explain the patterns observed. Moody (2001) analyzed the social behaviors in high school students using social network approaches. (Kasari et al., 2011) applied network analysis to compare the social relationships and friendships between children with and without autism spectrum disorder (ADS). The second type of network is an information network or knowledge network. The classic example of this network is the network of citations between academic papers (Newman, 2003). The articles cited other papers, which have related topics. They formed a citation network that has vertices as articles and direct links as citations. The citation network visualizes the structure and the movement of the

information. The third category, technological network, is object connected network, or man-made network which represents a physical connection between objects. This network is mostly applied for illustrating physical structures and systems such as the electrical power grid, the connections of rivers, transport systems, etc. The fourth category of network is a biological network. It represents the biological systems such as genes to genes, genes to protein, protein to protein interactions, which enable biologists understand the connections and interactions between individual constituents including genes, proteins, and metabolites at the level of the cell, tissue and organ to ultimately describe the entire organism system. Biologists use biological networks in various branches of biology at different levels (from a single molecule to an entire organism). For example, Yang et al. (2014); Barabási & Oltvai (2004) studied in the patterns of gene expression in different conditions and different types of cells (normal cells and cancer cells) in order to characterize the genes that change and do not change following the particular conditions; Freilich et al. (2010) applied a molecular ecological network analysis to study the communities of soil microorganisms. Networks revealed the complex relationships between microbial species in soils and their communities. Moreover, network analysis enables ecologists to understand ecological properties and predict the ecological roles of species in a soil ecosystem. Although the application of each type of network approach varies, all four categories of networks share a common empirical focus on relational structure and a similar set of mathematical analysis.

Network analysis can be a powerful tool to study plant disease. Moslonka-Lefebvre et al. (2011); Jeger et al. (2007) applied network models and concepts to study disease spreads in regional networks of plant nurseries and garden centers of *Phytophthora ramorum,* the oomycete causing Sudden Oak Death in the West Coast of the USA

and leaf blight and dieback in many ornamental shrubs both in America and Europe. The result could be applied to design measures to control plant disease epidemic from movement of infected material among plant nurseries. Shaw & Pautasso (2014) recently reviewed critically about network analysis to plant disease management (*i.e.*, to design ways to reduce the flow of disease in traded plants, to find the best sites to monitor as warning sites for annually reinvading diseases, to understand the fundamentals of how plant pathogen spreads in different structures of simulated trade network models). Windram et al. (2014) reviewed the applications of network analysis in molecular plant pathology. Network models were applied to reveal plant defense mechanism during plant-pathogen interactions.

Concepts, principles, and methods of network analysis

A network represents relationships between of elements of interest, which are defined by links (edges) among nodes (vertices). Nodes can be units of interests or studies, and links represent interactions between nodes. Network analysis aims to identify the patterns of associations among nodes, not only features or attributes of particular nodes.

Network analysis follows three principles. Nodes and their behaviors are mutually dependent, not autonomous; links between nodes can be channels for transmission of both material (*e.g.*, money, disease) and non-material (*e.g.*, information, knowledge, relationship, interaction) and; persistent pattern of association among nodes create structure that can define, enable, or restrict the behavior of a node.

Network models have two different organizational structures depending on goals of the representation and analysis (Borgatti et al., 2013). Flow models, commonly named directed graphs, represent the network as a system of pathways along which

something move such as transportation networks (*e.g.*, of highways, railways and airlines) or communication networks. Since flow networks show the directions of movement between nodes, thus these networks are interesting to study their behaviors. Analysis of flow networks can identify which nodes are more active or which ones are more important connectors. Jeger et al. (2007); Shaw & Pautasso (2014) applied such network models to study plant disease spread. Architectural models, or indirected graphs, are mainly used to determine the structure of the network, seeking to discern whether specific structures lead to similar outcomes or whether nodes in similar network positions behave in similar ways. Ecological applications related to the ecology and spatial structure of "community" tend to be organized and analyzed as architectural models. For example, Faust et al. (2012) studied networks of soil microbial interactions. Network models can describe how microbial populations change over time, which will require the use of dynamic models of microbial communities. Beyond these basic principles, network analysis enables the calculation of structural properties of nodes, groups, or the entire network.

Measuring network properties

A network is made up of nodes and links from relational data. It is constructed from an adjacency matrix, which is obtained from analysis using metric algebra techniques. The row and column headings for an adjacency matrix are identical, listing the names of the components involved in the network. In the simplest case, the cells of the matrix are coded with "1" if a link exists between the node or "0" if no edge exists. However, a link can be valued. Value indicates a characteristic of the relationship that the research has quantified. The values may be binary, such as whether two friends recognize each other, or variable strength (*e.g.*, the number of mutual friends between two

friends). A network link need not imply positive or cooperative interaction; they can also be a negative or competitive interaction between two individuals.

The distribution of links in a network suggests two important structural characteristics: centrality (importance) of nodes in the network and division of the network into subgroups. Variants of centrality in a network include degree, closeness, and betweenness. Degree centrality of a node is the sum of the value of the links between that node and every other node in the network. This measure tells us how well-connected a particular node is to the other nodes. Closeness centrality is calculated using the length of the path between a node and every other node. This measure could estimate the time required for information or resources to propagate to a given node in a network. Betweenness centrality corresponds to the number of paths in the network that pass through a particular node, and therefore measures the dependence of a network on a particular node for maintaining connectedness (Toubiana et al., 2013). Deng et al. (2012); Newman (2003); Toubiana et al. (2013) are recommended references for descriptions of the theory and uses, as well as the formal calculation of these measures.

The unique values of network analysis

There are four key points that will help to understand network analysis 1) how it differs from traditional approaches of scientific research; 2) how it relates to those traditional approaches; 3) how networks are constructed, manipulated and measured; and 4) what value network analysis offers beyond traditional approaches.

The first point of network analysis is that there are two types of data represented in the network graphs; technical and rational data. The first is data characterizing the actors or variables being studied referring to attributes. Attributes describe characteristics of individual actors or variables, for example their race, income or physical location,

and are the primary variables considered in traditional approaches. The second type of data is relational data, that is, data about the relationships between individual nodes. For example, Lazega & Pattison (1999) represented the network model of cooperation among lawyers in three law firms, through the exchange of various type of resources among them. This model consisted of over 70 lawyers in three different offices in three different cities. Rational data reflected to resources exchange and additional attribute information were included type of practice, genders, and seniority of each lawyers.

Relationships are also referred to as edges (links) in network analysis. Edges cannot be attributed to any single actor. Rather, edges only exist between nodes. This leads to the second point about network analysis that it requires a different conceptual approach. Because edges only exist between nodes, it is useful to think of edges existing in a separate dimension from nodes, who are connected in physical space. This dimension is sometimes referred to as relational space. To visualize the difference, think of someone far away with whom you correspond regularly, say using a phone, email, or Facebook. Even though the two of you are not physically close, you have a strong relationship. The two of you are distant in physical space but close in relational space. This notion of relational space is in part what means when he refers to the space of flows as something distinct from the space of places (Castells, 2001).

The third point that distinguishes network analysis from other approaches is it involves different methods of analysis. Because traditional research methods consider variable attributes in a wide variety of statistical analyses such as measures of center (*e.g.*, mean, median, etc.) and dispersion (*e.g.*, standard deviation, range, etc.), these methods are sometimes referred to as variable analysis, whereas, network analysis models relational data and to measure various characteristics of network structure. For

example, for lawyers data (Lazega & Pattison, 1999), it is natural to ask to what extend two lawyers that both work with third lawyer are likely to with each other as well. This notion corresponds to the social network concept of transitivity and can be captured numerically through an enumeration of proportion of vertex triples that form triangles, so-called cluster coefficient.

The idea that network structure may be correlated with variable attributes and behaviors is the fourth point to consider in comparing network analysis to other approaches. In network analysis, the arrangement of the network in relational space is basically correlated with the behavior and attributes of those variables. For example, in the network created by Lazega & Pattison (1999) lawyers of the same firm may share similar attributes such as office location or department, and lawyers in similar roles within that network may share similar behaviors. Basically, conventional approaches measure various attributes of variable (nodes in a network) and attempts to discern something about the relationships between actors (edges in a network) based on those attributes. When the network structure is simple and the differences in node attributes are clear, the conventional analytic approach is sufficient. However when relationships are complex or node attributes are more nuanced, clear answers using conventional analysis may prove elusive. As a result, network analysis offers a tool to help researchers visualize the large network and disentangle some of the relational complexities within the network, just as cluster analysis and multivariate analysis for help research disentangle the complex data.

Networks and Plant Pathology

Recently, a broad expansion of applications of network analysis has occurred across many disciplines. It has been evaluated as a promising tool to study a complex

system. Plant pathologists have applied network analysis for their research. Moslonka-Lefebvre et al. (2011); Jeger et al. (2007); Windram et al. (2014) supported that network analysis can be fruitful models in many applications relevant to plant pathology because of its generality and flexibility. For example, the network of main fresh cut flowers movements among European countries was determined the likelihood of introduction of new pathogens and other organisms associated with plants (Eagling, 2007), and plant-pathogen interaction network models were applied to present plant defense mechanisms (Dietz et al., 2010).

The development of network analysis challenges conventional approaches to uncover rational complexities of plant pathology studies. Two fields of research relevant to plant pathology presented particularly strong growth and proved that network analysis has significant potential to augment traditional analysis methods. The first is plant disease epidemiology, which investigates questions related to plant disease spread. The second is plant molecular biology, which investigates questions related to biological networks.

Using Network analysis to understand plant disease spread

Network analysis challenges conventional approaches of studies in plant disease epidemiology, especially underling the spatiotemporal flow of plants and their pathogens (Pautass et al., 2010). When plant pathological studies were restricted to a single geographical location, there was a limit to thinking about the connections or relationships between plants or fields in different locations. However, network analysis can enlarge the view of studies and can consider whether or not plant pathogens are moving from one field to others in the regions of interest. For example, networks of plant disease spread in trade networks presented the flows of plant disease from in-

fected units (infected plants or epidemic areas) to susceptible units (susceptible plants or areas).

Network models of epidemic development

The idea of plant epidemics is that the probability of infection embedded in the connection or the contact patterns between susceptible/infected plants, and it forms as the networks. Pautasso et al. (2010) showed a network model of epidemic development (susceptible-infected-susceptible model) in a directed network. In the network model, vertices were represented plant, and their attributes were presented the infectious status (healthy or infected). The epidemic is started at a single node, then nodes with a connection from the starting infected node will be infected at the next time step with a certain probability of transmission. In turn, already infected nodes will be infected at the next time step depending on their infection status and on a certain probability of persistence. The probability of infection transmission is the same for all connections between infected nodes and susceptible nodes over times. Similarly, the probability of infection persistence is the same for infected nodes in a certain network replicate. For each network structure, the two probabilities of persistence and transmission define an epidemic threshold, which is independent of the starting node of the epidemic. This epidemiological model does not result in either susceptible or infected nodes, as nodes will have a infection status along a continuum. Key quantities for epidemiological dynamics in networks were reviewed in Moslonka-Lefebvre et al. (2011).

Analysis of plant trade network

Phytophthora ramorum epidemic networks in the horticultural trade are an example of the application of network models in the study of plant disease spread (Harwood et al., 2009; Pautass et al., 2010). Simulations of spread of *P. ramorum* in dif-

ferent network structures (random, small–world and scale–free network) were found that epidemic threshold, the boundary between a no epidemic an epidemic outcome, is significantly lower for scale-free network, a network is dominated by a small number of nodes with many connections, compared to local, random and small-world network structure. Modeling suggested that was possible to control an epidemic by changing the structure of network, without having to decrease the probability of infection persistence at a nursery site and/or of transmission between sites. Simulation showed that correlation coefficient between link in and out nodes increased with connectivity level for all the structures investigated and underlined the importance of targeted control towards node with more connections than others.

Regardless of the network structure and connectivity level, epidemic threshold is negatively correlated to the correlation coefficient between link in and out nodes, (Moslonka-Lefebvre et al., 2009). In presence of high-connected nodes, the most effective way to control disease spread is to move from two-way to a one-way network. That is move from network where overall there is positive correlation among links-in and -out to one where the correlation are negative. In practice this would mean that a nursery network would be dominated by major node, which receives plant materials from many production sites but supply relatively few retail sites, or by major nodes which received plant materials from a few production sites but supply many retail sites. However, the scenario where there are major nodes which both receive plant material from many production sites and supply many retail sites is the most problematic control. The better way to control should target towards the cluster (group of nodes), not only to high-connected nodes.

The last point, the modeling of disease spread in small-size directed networks

showed that increasing the proportion of wholesalers (*i.e.*, traders without a preponderance of incoming or outgoing links) tends to decrease the epidemic threshold in local, random, and small-world network. The opposite result is obtained for the proportions of produces and retails. Scale free networks appear instead to be tolerant to changes in these hierarchical categories as the epidemic threshold in this case is governed by the presence of hub rather than by the features of the majority of nodes in the network (Pautass et al., 2010).

Network models to design strategies of plant disease management

Due to globalization, plant trades among countries are increasing and convenient. They potentially caused risks to plant health when they were not under good control. To control the risks of plant disease epidemic through plant trade, network models were applied to present the flows of trade network of plants and plant products across the world and within countries and to develop strategies of plant disease management (Pautasso, 2015). Networks could be found hubs or highly connected nodes, which represented locations or countries where imported and exported plants or plant parts. Hubs or highly connected nodes were targets for control disease flows in the scenarios that network presented because they were considered to the likelihood of pathogens actually infecting along particular links. Strategies for disease management should be designed by focusing on links to and from hubs, nodes which have high degree of connectivity, so that it increase efficiency to control plant pathogen spreads. The strategies may aim to remove them from the network (Jeger et al., 2007; Moslonka-Lefebvre et al., 2011). Alternatively, strategies may pay attention on them in order to prevent disease spreads. Shaw & Pautasso (2014) suggested placing quarantine efforts on hubs or on connections between major hubs.

Additionally, Pautasso et al. (2008) showed the good examples, which are co-occurrence networks of the *Phytophthora ramorum* infected plant genera different environments. The networks may be helpful in identifying host taxa playing an important role in spreading a certain disease in the seminatural environment, in crop plants, and plants in the trade. Combining genetic network analysis and data on trace forward and trace back on movement of plants nursery trade supported to identified confidentially *P. ramorum* migration. From this approach, it was clear that the pathogen was introduced originally from nurseries, which *P. ramorum* populations in nurseries are genetically ancestral to all Californian forest populations.

Using Network analysis to understand molecular plant pathology

For understanding mechanisms of plant-pathogen interactions, network analysis offers tools to visualize interactions of biological components including genes, proteins, and metabolites, which are related to plant-pathogen interactions. Network concepts enable us to characterize interplay of those components following the properties of network structure. Analyzing structural properties of networks may provide useful clues about the biological functions of individual genes, genes complexes, proteins, protein complexes, pathways they participate in.

Presenting biological data with network model

Networks are used in different contexts as ways to represent relationships between entities, such as interactions between genes, proteins or metabolites. Wu et al. (2007) gave the example of a network model built from gene-for-gene relationships between rice and various avirulence genes of the pathogen *Xanthomonas oryzae* pv. *oryzae* causing bacterial leaf blight of rice. Nodes represented isogenic lines of rice and weighted edges reflected the number of shared genes with high resistance (with respect

to avirulence genes) in the two isogenic lines of rice. For a plant breeder, this graph can help in identifying particularly promising genes for developing a disease resistant variety.

Network analysis to study biological systems

Network analyses have been applied to visualize the myriad information and analyze the complex relationships. To better understand the collective impact of genes on complex traits and determine what governs their organization, biologists are most likely to apply gene co-expression networks (Usadel et al., 2009). Co-expression networks most commonly use the Pearson's correlation coefficient to establish linear pairwise correlations between gene pairs in an adjacency matrix. Another associative metric that can be used is the Spearman correlation coefficient, which captures nonlinear correlations between genes to be uncovered (Usadel et al., 2009; Horvath, 2011). Once a co-expression network has been generated, identifying modules by clustering can help extract biological meaning from the network. Uncharacterized genes within such a module can be candidates for participating in the same process. Similarly, genes directly connected to (or co-expressed with) known central regulators of a developmental process are candidates within this co-functional framework.

Zheng & Zhao (2013) used co-expression network inference to investigate plant immunity system of citrus in response to *Candidatus* Liberibacter asiaticus. Gene co-expression networks based on Pearson's correlation coefficients using four transcriptomic data sets studies of citrus infected by *Candidatus* Liberibacter asiaticus bacterium were constructed. The result showed high degree of preservation of gene co-expression patterns across the networks based on different datasets. The network structures revealed hub genes, which have high connectivity. Highly connected nodes (genes) were

closely related to Arabidopsis SYP71 encoding a plant syntaxin which functions as a plasma membrane- associated protein transporter. Furthermore, in the study of Mukhtar et al. (2011), plant-pathogen interaction networks revealed the interactions of novel *Arabidopsis* protein-pathogen effectors, provided evidences that pathogen effectors target a limited number of host immune proteins, and demonstrated that effectors from very distantly related pathogens interact with the same host proteins.

The main use of co-expression networks with large collections of static expression data is gene discovery. However, many biologists have attempted to construct differential networks to measure differences in connectivity patterns from datasets with different conditions or targeted experiments (Toubiana et al., 2013). Lu et al. (2013) constructed networks of soil fungal communities. The fungal networks represented two different conditions; yield-invigorating and yield-debilitating soils under prolonged potato monoculture were compared. The authors discussed in differential network concepts that in healthy network three-eighths of fungal groups and soil organic matters were strongly correlated, and in diseases network two of four groups strongly correlated with soil electrical conductivity (EC) and ammonium nitrogen. Differential network analysis showed that average degrees of nodes belonging to *Sordariales* and *Hypocreales* in healthy network substantially were different in disease network. This indicated that they are key species of ecological communities.

A Variety of Network Construction Methods

Until this section, I gave the general information of network analysis with network concepts, network modeling and inference. Ultimately, most of the systems studied from a network–based perspective are dynamic in nature. This underscores the importance of developing tools to understand the interplay between network structures and

dynamic processes. I reviewed three network-based analyses: single network, differential network and dynamic network analysis. These techniques from network science have yielded many biological insights (Ideker & Krogan, 2012).

Single Network Analysis

Single-network analysis will be used for analyzing a network based on a single data set. It aims to model patterns of relationships between entities to a network, thereby determining its topological properties such as node degree, degree distribution, average path length, clustering coefficient, modularity index (Newman, 2006) to describe the patterns in the network model. These structural properties offer the potential to explore relationships within complex data sets and identify key factors or clusters.

Correlation based networks are widely used for studying biological networks based on pair–wise correlations between variables. Their edges are obtained using correlation-based measures removing spurious relationships. Correlation based measures include linear based correlation (Pearson's correlation, partial correlation) and rank based correlation (Spearman's correlation, Kendall's correlation). Removal of spurious relationships is particularly important when one attempts to establish causal relationships between entities (Toubiana et al., 2013). A correlation based network allows one to define modules (clusters), intramodular hubs, and network nodes with regard to module membership, to study the relationships between modules, and to compare the network topology of different network.

Differential Network Analysis

Networks can respond differently under various environments or with external signals. They can be simplified by focusing on key components and capture only the essential components differently responding between environments in which they play a

key role in the modeled response (Pe'er & Hacohen, 2011). Networks are examined by adding or deleting some variables. This allows predicting interactions or components that change following the changed structure of networks.

Differential network analysis is applied to identify and describe differences between two networks under different conditions. Differential networks from different data sets with different conditions might display different interactions from the single network based on the whole data set, which are disregarded the conditions. The strongest interactions in differential networks are not necessarily those that are strong in the single network. Conversely, they may be weak or absent in single network. Compared between differential networks under different environment conditions, the differential interactions can be implied that they are a result of response to environmental conditions. Moreover, it can be implied that environments influence on the interaction between pairs of nodes contributing to the differential interactions.

The objective of differential network analysis is to identify the different interactions, that may reveal when condition has changed. For example, the differential network analysis of gene co–expression networks to understand the differences between human and chimpanzee brain was focused on how expression patterns of genes were different in human and chimpanzee brains. These networks are contrasted to find a) non-preserved modules (group of genes with sharing similar expression profiles and presumably similar functions), b) differentially occurred genes, and c) differentially connected genes. The result showed that

Dynamic Network

Biological systems are highly dynamic. They must continuously respond to external signals or the internal state of the system. The responses can be altered slowly

or quickly over time (Pe'er & Hacohen, 2011). Thus, realistically the corresponding biological network models must evolve as well. It seems clear that dynamic networks enable us to see and understand the systems and how their dynamic effects change over time. Some understandings previously have been obtained from studies of dynamics of large networks, for example, gene expression or metabolic fluxes network (Ideker & Krogan, 2012).

The main goal of dynamic network analysis moves away from single network analysis, which characterizes absolute properties of the system. It aims to concentrate on a specific dynamic response. Rather than answer what the key factors in the system, it answers what parts of the system are most affected by perturbation. Most commonly, dynamic networks are applied when the edges among a set of vertices or the sets of vertices itself are changing as a function of time. For example,

Summary

This literature review presented a brief introduction of network analysis and concise concepts and methods. Briefly, a network is usually represented by sets of nodes (or vertices) connected by edges (or links) in various ways. Networks can be categorized to four types, social network, information, technology network, and biological network. Even though four types of networks are described and applied in different context, they share a common empirical focus on relational structure and a similar set of mathematical analyses. Network models are cable of presenting unique values, which traditional approaches cannot present. Network analysis was discussed as applied to two broad areas of study of plant diseases. It firstly was applied to study plant disease epidemics. For example, networks of *P. ramorum* spread through plant nurseries trade. The results enabled us to understand the directions and processes of disease spread.

Additionally, they could predict the movement of disease flows, and improve the implementation of plant disease policy. Secondly, molecular plant pathology showed two applications of network applications. The first use is to apply networks to model large and complex biological datasets. Another use is the consideration network structure to understand biological system. Emergent properties of network structure influences may be identified, measured and analyzed to yield better explanations of the experiments being observed. While numbers of documented plant pathological studies using network analysis are sparse, the literature presented in this review showed a clear and compelling case for plant pathologists to expand the understanding of and use network concepts and methods. Biological networks are context-specific and dynamic in nature. Under different conditions, the topology of the network changes. Network approaches (differential network, dynamic network analysis) are successful to yield insight on biological system under different conditions or dynamic processes. Network analysis concepts and methods augment existing approaches and provide tools for exploring complex relationships, which have been widely acknowledged as influential but difficult to measure using traditional methods.

MATERIALS AND METHODS

This research will use data collected from surveys of irrigated lowland rice growing areas in South and South East Asia to examine relationships between the injuries caused by pests and diseases, cropping practices (*e.g.*, rice variety grown, crop establishment method, fertilizer and chemicals applied). Their relationships will be constructed and analyzed through network analysis. I will develop and apply suitable methods of network analysis to characterize the associations of injuries and cropping practices. The resulting network of associations of injuries and cropping practices will thus provide a starting point for further investigations of their relationships (*i.e.*, characterization of relationships of cropping practices and injury profiles related to yields, comparison of networks under different production environments or examination of networks at different levels of yield gains).

In the following, I present three distinct network analysis approaches: single-network analysis, differential network analysis, and dynamic network analysis. These three approaches will answer different questions. I will apply single-network analysis to the data from all fields surveyed for identifying patterns of interactions between injuries and cropping practices and key components (*e.g.*, most connected variables). Second, differential network analysis will aim to uncover similarities and differences of networks constructed from the different data sets (*e.g.*, dry season versus wet season). Dynamic network analysis, the third type, will be applied to study how networks changed under at least two different aspects of an evolving complex system. Here, I will focus on dynamic

networks by dividing farms into different levels of yield attained.

Crop health survey data

Crop health survey data were collected through surveys of farmers' fields (approximately 800) from 2010 to 2015 for both wet and dry seasons in different production environments across South and South East Asia representing irrigated lowland rice growing areas West Java, Indonesia; Mekong River Delta and Red River Delta, Vietnam; Tamil Nadu and Odisha, India; and Suphanburi, Thailand. The survey protocol described in the IRRI publication, "A SURVEY PORTFOLIO TO CHARACTERIZE YIELD-REDUCING FACTORS IN RICE", (Savary & Castilla, 2009) was used for data collection. The variables collected included environmental attributes, 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.

Cropping practice data included information on the type of rice variety (traditional variety, modern variety, or hybrid rice), crop establishment methods used (direct seeded or transplanted rice) and were collected as categorical data. Pesticide usage (molluscicide, herbicide, insecticide and fungicide) were collected as discretized data, and accumulated organic, synthetic fertilizers were collected as continuous data.

Injury data were gathered on diseases, insects and weeds observed at two development stages of the growing crop: active tillering and active ripening. While injuries due to diseases and insects were specific to species (or species groups), information on weed infestation was the area covered by any weed species, either above or below the crop canopy. Information pertaining to injuries was collected in the form of number of

injured organs (tillers, leaves, and panicles), which later was made relative to the corresponding total number of organs present in the sampling units; 12 hills per field for transplanted rice crops, or 12×10 cm quadrat for direct seeded rice. As for weed infestation, the proportion of soil area covered at two levels of the crop canopy (below or above) was assessed in three points in the field of $1 \ mathrmm^2$ each. For this purpose, two types of injury indices were used: area under injury progress curves (AUIPC) or maximum level at any of the two observations, depending on the nature of the injury. Injuries which is occurred on tillers, hills and panicles were quantified as maximum level, whereas juries which occurred on leaf were quantified as AUIPC. The AUIPC was calculated by the mid- point method using the following equation: AUIPC $= \sum\limits_{i=1}^{n} \frac{1}{(x_i + x_{i-1})(T_i - T_{i-1})}$, where x_i is percentage (%) of leaves, tillers or panicles injured caused by pests (e.g., leaf blast, leaf folder), percentage (%) of weed infestation (ground coverage) at the ith observation, T_i is time in rice development stage units (DSU) on a 0 to 100 scale (10: seedling, 20: tillering, 30: stem elongation, 40: booting, 50: heading, 60: flowering, 70: milk, 80: dough, 90: ripening, 100: fully mature) at the ith observation where n is total number of observations.

Yield data were measured from three randomly selected crop cuts that were 5 m² (2×2.5 meters) and dried to 14% moisture content and weighed.

Single network analysis of crop health survey data

Cropping practices and injury profiles network will be constructed from the pair–wise correlation matrix between any variables of injuries (insect injuries and diseases) and cropping practices (fertilizer usage, pesticide applied, rice varieties and crop establishment methods). The edges of the network will correspond to the degree of correlation between two variables. A standard measurement of correlation between two

variable x and y, $cor(x, y)$, where values are between -1 to +1 depending on the level of relationship. $cor(x_i, x_j)$ is equal to -1 when there is a decreasing relationship between x and y, and +1 when there is a increasing relationship.

To identify the most suitable pairwise correlation methods, I will evaluate four correlation based measures, Pearson's correlation, Spearman's rank correlation, Kendall's correlation, and biweight midcorrealtion. The statistical programming language R will be employed to compute pairwise correlation (R Core Team, 2014). The `cor.test()` function will be applied for generating a correlation matrix, which describes the pairwise correlations between variables. This function allows users to choose types of correlation measures to perform such as Pearson's correlation, Spearman's rank correlation and Kendall's rank correlation. To compute biweight midcorrelation, I will apply the `bicor()` function from the **WGCNA** package (Langfelder & Horvath, 2008) in R.

When a correlation matrix is created, the next step is to construct the correlation based network. However, p values should be determined because correlation will be considered if its p value is less than p values at considered significant (*e.g.*, 0.01, 0.05). As with issues previously mentioned above, p values must be adjusted for multiple testing. Using a Benjamini-Hochberg adjustment or Bonferonni correction is recommended by Kolaczyk & Csárdi (2014). The `fdrtool()` function of **fdrtool** R package can calculate adjusted p values. These values are compared to a standard 0.05 significance level. The final correlation matrix contains pair-wise correlation coefficients, which have adjusted for p values lower than 0.05 significance level.

The R packages: **igraph** (Csardi & Nepusz, 2010); **qgraph** (Epskamp et al., 2012); **statnet** (Handcock et al., 2014) and **network** (Butts, 2008); and **sna** (Butts, 2014) will be used to construct and analyze network models.

Evaluating network properties

Once a network is constructed, several indices will be computed to convey information about network structure. To evaluate the topological properties of both the interaction and the correlation based network, I will use the packages **igraph** and **qgraph** in R (Epskamp et al., 2012). I am particularly interested in properties potentially relevant for biological roles and functioning as previously hypothesized in other biological networks (Strogatz, 2001; Horvath, 2011). For example, connected hub nodes are focused because they have high connectivity, which mean they have relationships with many nodes. In the following, there are some network indices used to describe the topological properties of single network and for comparing two or more networks (*e.g.* , differential , and dynamic network analysis)

1. Mean degree: the degree of a node counts the number of edges it has. The mean degree is calculated over all nodes in the network.

2. Degree distribution: the frequency of nodes vs. their (increasing) degree.

3. Average shortest path length: the shortest path between any two nodes is the single path with fewest edges between them. Alternative paths are feasible. The average shortest path length is the mean over all shortest paths between any two nodes in the network.

4. Mean clustering coefficient: a cluster of nodes is a triangle of nodes. The clustering coefficient calculates the fraction of observed vs. possible triangles for each node. The mean is subsequently determined from all nodes in the network.

5. Betweenness centrality: the betweenness centrality of a node is equal to the number of shortest paths between any two nodes in the graph passing through that

node. The mean is calculated from all nodes in the network.

6. Closeness centrality: the closeness centrality of a node is given by the average distance of this node to any other node. Again, the network-wide measure is an average over all nodes in the network.

Deng et al. (2012); Toubiana et al. (2013); Horvath (2011); Newman (2003) are recommended references for descriptions of the network properties as well as the formal calculation of these measures.

Differential network analysis of crop heath survey data

Differential networks will be constructed from the survey data with different groups of samples. With in my focuses, they will be produced from adjacency metrics, which are encoded with correlation coefficients of any variables under different conditions (dry and wet season). To analyze differential networks in different seasons, I will determine the differential relationships of any variables in cropping practices and injuries between dry season network and wet season network. Additionally I will construct differential networks under different production environments (locations).

For comparison with a standard differential network analysis, I will use the **WGCNA** (Horvath, 2011) and **dna** (Gill et al., 2014) packages in R. These packages provide several functions to analyze the different structures of two networks (Horvath, 2011). These functions include preprocessing tools for simultaneously preparing a pair of networks for analysis, procedures for computing connectivity scores between pairs of variables based on many available statistical techniques, and tools for handling modules of variables based on these scores. Also, procedures are provided for performing permutation tests based on these scores to determine if the connectivity of variables differs

between the two networks, to determine if the connectivity of a particular set of important variables differs between the two networks, and to determine if the overall module structure differs between the two networks. Several built-in options are available for the types of scores and distances used in the testing procedures, and additionally, the procedures provide flexible methods that allow the user to define custom scores and distances. For example, the `test.modular.structure()` function is used to compare between the connectivity measures of each network (Gill et al., 2014).

Dynamic network analysis of crop health survey data

Dynamic network analysis will be applied to study changes in networks with at least two different aspects of an evolving complex system. Dynamic networks of crop health survey data at three different levels of farmers' yields will be constructed. Surveys contain records of observed actual yields, various types of injuries and cropping practices. To generate the data set for constructing the dynamic network, I will group the data with successive levels of yields to obtain different yield data sets in order to construct a dynamic network of yield-varying behaviors. I then will employ **networkDynamic** (Butts et al., 2014) and **ndtv** (Bender-deMoll, 2015) packages to generate yield-varying networks. The dynamic graphs will be characterized following (Bilgin & Yener, 2006; Kolaczyk & Csárdi, 2014). From the network based perspectives, the results will show the patterns of interactions between nodes how they changed when levels of yield decreased or increased.
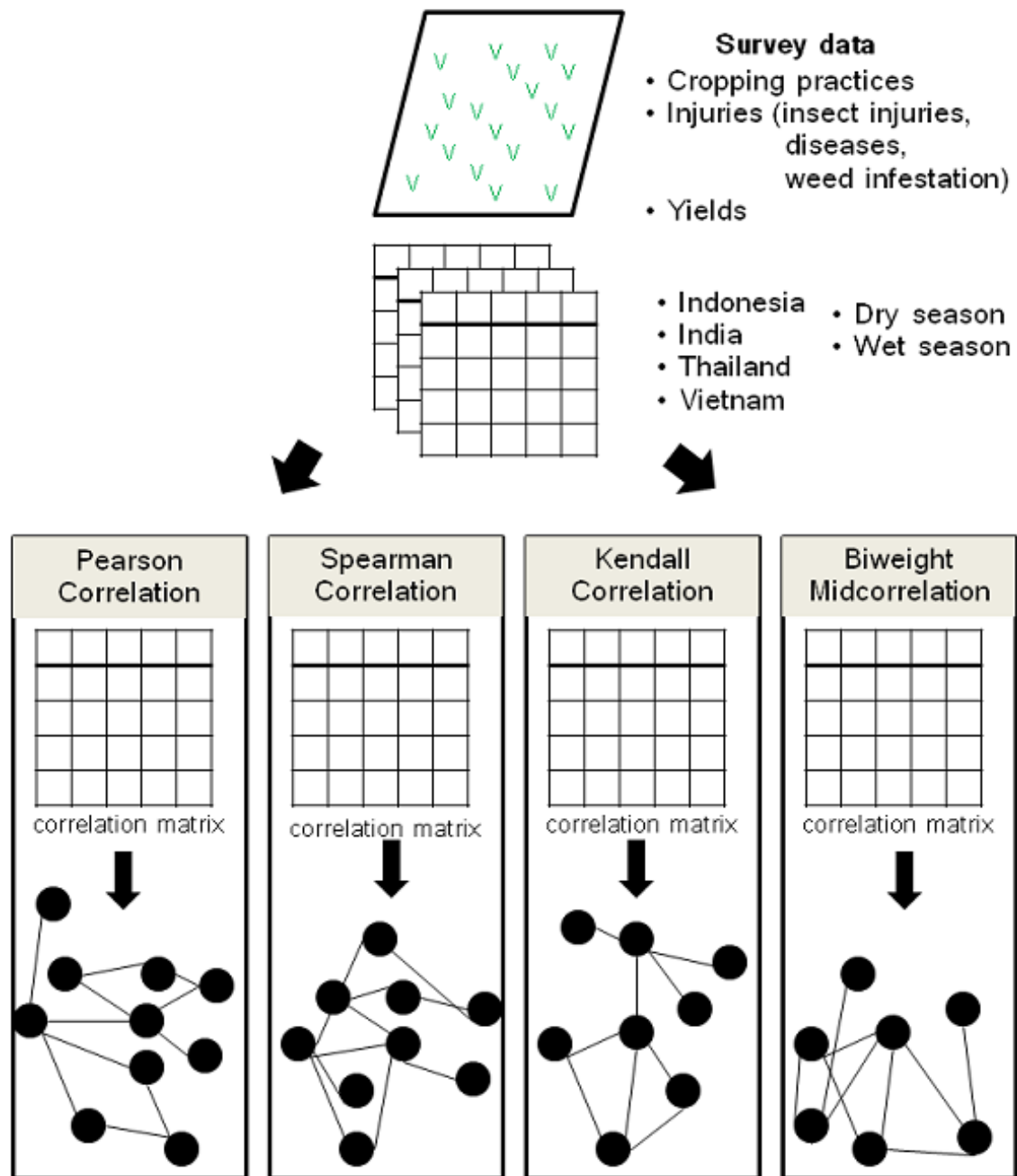
Figure 3-1: Crop health survey data that were collected include cropping practices, injuries, and yield data. These data were collected from farmers' fields in four countries: Indonesia, India, Thailand, and Vietnam. Correlation matrices will be produced using four individual methods; Pearson, Spearman, Kendall correlation and Biweight midcorrelation. The p values for all coefficients will be adjusted by FDR correction. The correlation coefficients with p values > 0.05 will be removed. The resulting network will be analyzed for structural properties and to infer biological meanings. This will provide the cropping practices and injury profiles network of crop health data.
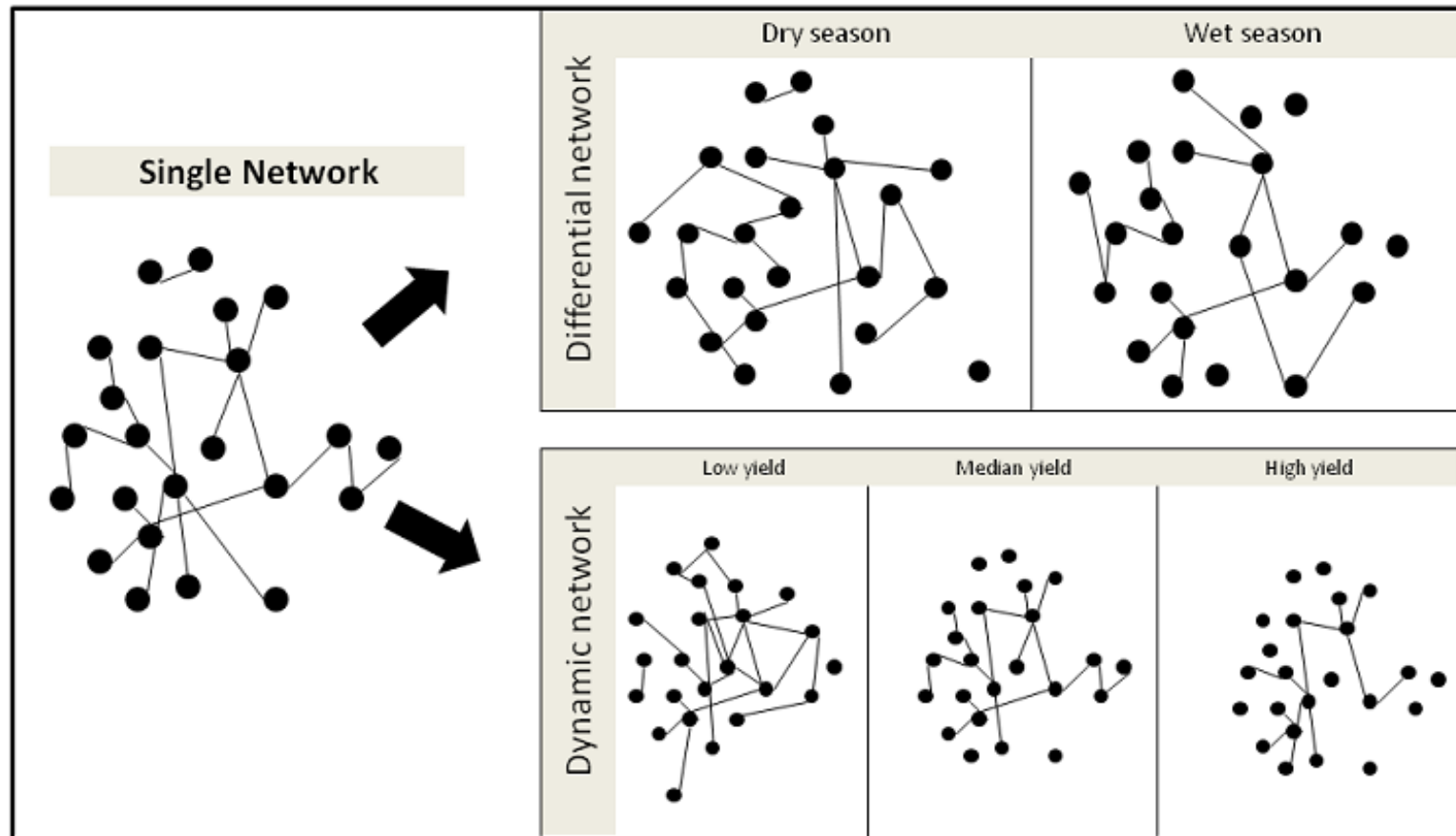
Figure 3-2: A single network will be created from the whole survey data set. Differential networks will be constructed using different data set, which may be different subgroups of samples from different seasons (*e.g.*, dry season and wet season) or different geographic locations, then differences in connectivity patterns between two networks will be measured. Dynamic networks will be produced from different subgroups of surveys by grouping consecutive yield levels, (*i.e.*, low, median, high yield).

LITERATURE CITED

BARABÁSI, A.-L. & OLTVAI, Z. N. (2004). Network biology: understanding the cell's functional organization. Nature Reviews Genetics, 5(2):101–113.

BENDER-DEMOLL, S. (2015). ndtv: Network dynamic temporal visualizations. R package version 0.6.1.

BILGIN, C. C. & YENER, B. (2006). Dynamic network evolution: models, clustering, anomaly detection. IEEE Networks.

BORGATTI, S. P., EVERETT, M. G., & JOHNSON, J. C. (2013). Analyzing social networks. SAGE Publications Limited.

BUTTS, C. T. (2008). network: a package for managing relational data in R. Journal of Statistical Software, 24(2):1–36.

BUTTS, C. T. (2014). sna: Tools for social network analysis. R package version 2.3-2.

BUTTS, C. T., LESLIE-COOK, A., KRIVITSKY, P. N., & BENDER-DEMOLL, S. (2014). networkDynamic: Dynamic extensions for network objects. R package version 0.7.1.

CASTELLS, M. (2001). The rise of network society. Oxford: Blackwell Publishers.

CSARDI, G. & NEPUSZ, T. (2010). Csardi: igraph: Network analysis and visualization. R package version 05.

DENG, Y., JIANG, Y.-H., YANG, Y., HE, Z., LUO, F., & ZHOU, J. (2012). Molecular ecological network analyses. BMC Bioinformatics, 13:113.

DIETZ, K. J., JACQUOT, J. P., & HARRIS, G. (2010). Hubs and bottlenecks in plant molecular signalling networks. New Phytologist, 188(4):919–938.

EAGLING, D. (2007). Australian trade in agricultural food products – the challenge for plant pathologists. Australasian Plant Pathology, 36(6):539–542.

EPSKAMP, S., CRAMER, A. O. J., WALDORP, L. J., SCHMITTMANN, V. D., & BORSBOOM, D. (2012). qgraph: Network visualizations of relationships in psychometric data. Journal of Statistical Software, 48(4):1–18.

FAUST, K., SATHIRAPONGSASUTI, J. F., IZARD, J., SEGATA, N., GEVERS, D., RAES, J., & HUTTENHOWER, C. (2012). Microbial co-occurrence relationships in the human microbiome. PLoS Computational Biology, 8(7):e1002606–e1002606.

FREILICH, S., KREIMER, A., MEILIJSON, I., GOPHNA, U., SHARAN, R., & RUP-

PIN, E. (2010). The large-scale organization of the bacterial network of ecological co–occurrence interactions. Nucleic Acids Research, 38(12):3857–3868.

GILL, R., DATTA, S., & DATTA, S. (2014). dna: Differential network analysis. R package version 1.1-1.

GUIMERA, R. & AMARAL, L. A. N. (2005). Functional cartography of complex metabolic networks. Nature, 433(7028):895–900.

HANDCOCK, M. S., HUNTER, D. R., BUTTS, C. T., GOODREAU, S. M., KRIVITSKY, P. N., BENDER-DEMOLL, S., & MORRIS, M. (2014). statnet: Software tools for the statistical analysis of network data. R package version 2014.2.0.

HARWOOD, T. D., XU, X., PAUTASSO, M., JEGER, M. J., & SHAW, M. W. (2009). Epidemiological risk assessment using linked network and grid based modelling: *Phytophthora ramorum* and *Phytophthora kernoviae* in the UK. Ecological Modelling, 220(23):3353–3361.

HORVATH, S. (2011). Weighted network analysis: applications in genomics and systems biology. Springer Science & Business Media.

IDEKER, T. & KROGAN, N. J. (2012). Differential network biology. Molecular Systems Biology, 8(1):565.

JEGER, M. J., PAUTASSO, M., HOLDENRIEDER, O., & SHAW, M. W. (2007). Modelling disease spread and control in networks: implications for plant sciences. New Phytologist, 174(2):279–297.

KASARI, C., LOCKE, J., GULSRUD, A., & ROTHERAM-FULLER, E. (2011). Social networks and friendships at school: comparing children with and without ASD. Journal of Autism and Developmental Disorders, 41(5):533–544.

KOLACZYK, E. D. & CSÁRDI, G. (2014). Statistical analysis of network data with R, volume 65. Springer.

KRAUSE, A. E., FRANK, K. A., MASON, D. M., ULANOWICZ, R. E., & TAYLOR, W. W. (2003). Compartments revealed in food-web structure. Nature, 426(6964):282–285.

LANGFELDER, P. & HORVATH, S. (2008). WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics, 9:559.

LAZEGA, E. & PATTISON, P. E. (1999). Multiplexity, generalized exchange and co-operation in organizations: a case study. Social Networks, 21(1):67–90.

LU, L., YIN, S., LIU, X., ZHANG, W., GU, T., SHEN, Q., & QIU, H. (2013). Fungal networks in yield-invigorating and -debilitating soils induced by prolonged potato monoculture. Soil Biology and Biochemistry, 65:186–194.

MEW, T. W., LEUNG, H., SAVARY, S., VERA CRUZ, C. M., & LEACH, J. E. (2004).

Looking ahead in rice disease research and management. Critical Reviews in Plant Sciences, 23(2):103–127.

MOODY, J. (2001). Race, school integration, and friendship segregation in America. American Journal of Sociology, 107(3):679–716.

MOSLONKA-LEFEBVRE, M., FINLEY, A., DORIGATTI, I., DEHNEN-SCHMUTZ, K., HARWOOD, T., JEGER, M. J., XU, X., HOLDENRIEDER, O., & PAUTASSO, M. (2011). Networks in plant epidemiology: from genes to landscapes, countries, and continents. Phytopathology, 101(4):392–403.

MOSLONKA-LEFEBVRE, M., MATHIEU PAUTASSO, M., & JEGER, M. J. (2009). Disease spread in small-size directed networks:epidemic threshold, correlation between links to and form nodes, and clustering. Journal of Theoretical Biology, 206:402–411.

MUKHTAR, M. S., CARVUNIS, A.-R., DREZE, M., EPPLE, P., STEINBRENNER, J., MOORE, J., TASAN, M., GALLI, M., HAO, T., NISHIMURA, M. T., PEVZNER, S. J., DONOVAN, S. E., GHAMSARI, L., SANTHANAM, B., ROMERO, V., POULIN, M. M., GEBREAB, F., GUTIERREZ, B. J., TAM, S., MONACHELLO, D., BOXEM, M., HARBORT, C. J., MCDONALD, N., GAI, L., CHEN, H., HE, Y., VANDENHAUTE, J., ROTH, F. P., HILL, D. E., ECKER, J. R., VIDAL, M., BEYNON, J., BRAUN, P., & DANGL, J. L. (2011). Independently evolved virulence effectors converge onto hubs in a plant immune system network. Science, 333(6042):596–601.

MUTERT, E. & FAIRHURST, T. (2002). Developments in rice production in Southeast Asia. Better Crops International, 15:12–17.

NEWMAN, M. E. J. (2003). The structure and function of complex networks. SIAM review, 45(2):167–256.

NEWMAN, M. E. J. (2006). Modularity and community structure in networks. Proceedings of the National Academy of Sciences, 103(23):8577–8582.

OECD/FAO (2012). OECD-FAO agricultural outlook 2012–2021.

OERKE, E. C. (2006). Crop losses to pests. The Journal of Agricultural Science, 144(1):31–43.

PASTOR-SATORRAS, R. & VESPIGNANI, A. (2001). Epidemic spreading in scale–free networks. Physical Review Letters, 86(14):3200.

PAUTASS, M., MOSLONKA-LEFEBVRE, M., & JEGER, M. J. (2010). The number of links to and from the starting node as a predictor of epidemic size in small-size directed networks. Ecological Complexity, 7:424–432.

PAUTASSO, M. (2015). Network simulations to study seed exchange for agrobiodiversity conservation. Agronomy for Sustainable Development, 35(1):145–150.

PAUTASSO, M., HARWOOD, T., SHAW, M., XU, X., & JEGER, M. (2008). Epidemiological modeling of *Phytophthora ramorum*: network properties of susceptible plant genera movements in the nursery sector of England and Wales. In Proceedings of the Sudden Oak Death Third Science Symposium.

PAUTASSO, M., MOSLONKA-LEFEBVRE, M., & JEGER, M. J. (2010). The number of links to and from the starting node as a predictor of epidemic size in small-size directed networks. Ecological Complexity, 7(4):424–432.

PE'ER, D. & HACOHEN, N. (2011). Principles and strategies for developing network models in cancer. Cell, 144(6):864–873.

PROULX, S., PROMISLOW, D., & PHILLIPS, P. (2005). Network thinking in ecology and evolution. Trends in Ecology & Evolution, 20(6):345–353.

R Core Team (2014). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

RAY, D. K., MUELLER, N. D., WEST, P. C., & FOLEY, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. PLoS ONE, 8(6):e66428.

SAVARY, S. & CASTILLA, N. (2009). A survey portfolio to characterize yield-reducing factors in rice. IRRI Discussion Paper No 18.

SAVARY, S., MADDEN, L., ZADOKS, J., & KLEIN-GEBBINCK, H. (1995). Use of categorical information and correspondence analysis in plant disease epidemiology. Advances in Botanical Research, 21:213–240.

SAVARY, S., WILLOCQUET, L., ELAZEGUI, F. A., TENG, P. S., VAN DU, P., ZHU, D., TANG, Q., HUANG, S., LIN, X., & SINGH, H. M. (2000). Rice pest constraints in tropical Asia: characterization of injury profiles in relation to production situations. Plant Disease, 84(3):341–356.

SHAW, M. W. & PAUTASSO, M. (2014). Networks and plant disease management: concepts and applications. Annual Review of Phytopathology, 52(1):477–493.

STROGATZ, S. H. (2001). Exploring complex networks. Nature, 410(6825):268–276.

TOUBIANA, D., FERNIE, A. R., NIKOLOSKI, Z., & FAIT, A. (2013). Network analysis: tackling complex data to study plant metabolism. Trends in Biotechnology, 31(1):29–36.

USADEL, B., OBAYASHI, T., MUTWIL, M., GIORGI, F. M., BASSEL, G. W., TANIMOTO, M., CHOW, A., STEINHAUSER, D., PERSSON, S., & PROVART, N. J. (2009). Co–expression tools for plant biology: opportunities for hypothesis generation and caveats. Plant, Cell & Environment, 32(12):1633–1651.

WINDRAM, O., PENFOLD, C. A., & DENBY, K. J. (2014). Network modeling to understand plant immunity. Annual Review of Phytopathology, 52(1):93–111.

WU, X. M., LI, Y. R., ZOU, L. F., & CHEN, G. Y. (2007). Gene–for–gene relationships between rice and diverse avrbs3/ptha avirulence genes in *Xanthomonas oryzae* pv.*oryzae*. Plant Pathology, 56(1):26–34.

YANG, Y., HAN, L., YUAN, Y., LI, J., HEI, N., & LIANG, H. (2014). Gene co–expression network analysis reveals common system-level properties of prognostic genes across cancer types. Nature Communications, 5.

ZHENG, Z. L. & ZHAO, Y. (2013). Transcriptome comparison and gene coexpression network analysis provide a systems view of citrus response to "*Candidatus* liberibacter asiaticus" infection. BMC Genomics, 14:27.