

Bio-Robustness and Fault Tolerance: A New Perspective on Reliable, Survivable and Evolvable Network Systems

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Abstract—Biological structures and organizations in nature, from gene, molecular, immune systems, and biological populations, to ecological communities, are built to stand against perturbations and biological robustness is therefore ubiquitous. Furthermore, it is intuitively obvious that the counterpart of bio-robustness in engineered systems is fault tolerance. With the objective to stimulate inspiration for building reliable and survivable computer networks, this paper reviews the state-of-the-art research on bio-robustness at different biological scales (level) including gene, molecular networks, immune systems, population, and community. Besides identifying the biological/ecological principles and mechanisms relevant to biological robustness, we also review major theories related to the origins of bio-robustness, such as evolutionary game theory, self-organization and emergent behaviors. Evolutionary game theory, which we present in a relative comprehensive introduction, provides an ideal framework to model the reliability and survivability of computer networks, especially the wireless sensor networks. We also present our perspectives on the reliability and survivability of computer networks, particularly wireless sensor and ad hoc networks, based on the principles and mechanisms of bio-robustness reviewed in the paper. Finally, we propose four open questions including three in engineering and one in DNA code robustness to demonstrate the bidirectional nature of the interactions between bio-robustness and engineering fault tolerance.

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1. INTRODUCTION

John von Neumann's (1956) paper in the context of automata theory introduced far-reaching new ideas including building reliable systems from unreliable components. Apparently, his idea was inspired by the studies of human and animal brains. He and other pioneers have already attempted to apply bio-robustness for building fault-tolerant systems.

By using the *new* in the title, we simply wish to express our opinions that the scientific advances in several fields outside computer science in the last few decades warrant a rethinking of the ways we approach the reliability and survivability of computer networks. In particular, the tradition of the interactions between biology and computing has been expanding, and the synergetic interplay has generated some remarkable new scientific fields such as bioinformatics, evolutionary computation, and computational biology. In this paper, we review a not yet conspicuous research topic: the biological robustness *vs.* engineering fault tolerance. Therefore, the use of *new* is simply to stimulate interests to this still largely unexplored field, and its usage will certainly be one-time in this paper.

The focus of this paper is to review and summarize literature on *biological robustness*, scattered in multiple subjects of biology, including molecular biology and system biology, ecology, evolutionary biology, ethology, evolutionary game theory, etc. We also present a comparative analysis of biological/ecological systems and fault tolerant systems engineered by human beings, in particular, the computer network systems. The term *biological robustness*, or *bio-robustness*, is used with various meanings in different fields of biology, and we still

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lack a commonly accepted definition. This is understandable for at least two obvious reasons. First, biological robustness may be demonstrated very differently in at various *scales*. At gene and molecular scale level, it is the redundancy of gene codes and various molecular networks involved in gene expression and metabolism controls. At the individual organism level, most obvious examples can be pairs of eyes, ears, and some crucial internal organs such as kidneys, which we often take for granted and do not necessarily associate with robustness or fault tolerance. In the population level, the population dynamics of animal species can endure catastrophic events in environment and exhibit chaotic fluctuations. Biological communities, ecosystems and landscape levels also exhibit remarkable resilience and stability. Bio-robustness also exists in many other systems scales. One more example would be the immune systems, which possesses extraordinary defense and offense mechanisms to foreign invasions. Therefore, despite the diverse *expressions* of robustness on different scales, biological robustness is universal and ubiquitous. We can say, biological system is built to survive perturbations, and it achieves robustness with extremely rich and diverse mechanisms from extremely parsimonious organizations or structures to extravagant redundancy. This makes it extremely difficult to have a unified bio-robustness theory or subject, unlike the fault tolerance or reliability theory we have in engineering. However, these highly diversified robustness mechanisms may hold enormous potential for engineering sciences to draw inspirations for designing reliable and survivable systems. The second reason for this lack of uniformness is that bio-robustness is often taken for granted in biology. Perhaps, except for biomedicine, bio-robustness has been treated as secondary in many fields of biology and ecology and often is not the focus of scientific research, until even recently.

This paper has three objectives: (1) Review the state-of-the-art research on bio-robustness at different scales including gene, molecular networks, immune systems, population, and community. We also briefly review the status of bio-robustness inspired engineering research, such as self-organization and emergent systems. (2) Present our perspective on the reliability and survivability of computer networks, especially the wireless sensor network and ad hoc networks, based on the principles and mechanisms of bio-robustness. (3) Propose four open problems in the fields of reliability, survivability and fault tolerance of computer networks.

2. RECENT ADVANCES IN THEORIES OF NETWORKS.

Newman, Barabasi and Watts (2006) compiled a selection of research papers covering what they believe to represent the most significant advances for what was suggested as a branch of new science -- *science of networks*. The study of networks, as Newman et al (2006) indicated, can be trace back to Euler's 1736 Kongigsberg Bridge Problem described

with a Graph model. They summarized three major features of the new *science of networks*, which to some extent, reflects their standard in selecting the papers for the collection. The three features they summarized are:

(1) Modeling of real-world networks from both theoretic and practical perspectives. Real-world networks are the networks that arise naturally—evolve in a manner that is typically unplanned and decentralized, such as social networks, biological networks, publications citations, Web, Internet, etc, in contrast of traditional pure Graph theory models.

(2) Networks as *evolving* structures— many networks are generated by the dynamic processes that add or remove edges or vertices dynamically. In other words, the structure of the network evolves with time. A major motivation of the new network science is to understand how local interactions influence global structures.

(3) Networks as dynamic systems: it appears that the term of dynamic systems used by Newman et al. (2006) is somewhat different from the dynamic systems in engineering and computer science. They refer to the notion that vertices of graphs are representative of discrete dynamic entities, and the edges of the interactions between the entities. One example is the application and expansion of the classical mathematical epidemic model (e.g., SIR model) to social networks.

It is obvious that this selection of research papers presents a comprehensive overview of the state-of-the-art of network theories. The dominant mathematical theory adopted is Random Graphs theory. The research is further fueled by decades of results from complexity science studies. The research fields are largely focused on social networks, and to a lesser extent to biological networks such as metabolism networks, gene control, etc. It almost touched every type of network organizations in social and natural sciences. The only major exception might be the theory of immune system networks, which was initiated with the name of idiotypic network by Jerne (1974) and has been expanded significantly in several fields (Perelson 1989, Dasgupta and Attoh-Okine 1997). Perhaps the most well known results from the new network theory are the study of the "small-world problem (Watts and Strogatz 1998, Barabasi and Albert's 1999). According to Durrett's (2006) query of Science Citation Index in early July 2005, both Watts and Strogatz's (1998) and Barabasi and Albert's (1999) papers had 1154 and 964 citations. Durrett (2006) commented on the explosion of the research spawned by these papers, and on the difference in how physicists and mathematicians approach problems differently.

Although the world-wide-web and Internet were two of the central objects in the research of new network theory, their abstract models seem to be more similar to social networks than to the strict computer networks such as LAN, WAN, or even the "Internet" from technical perspectives. Significant

differences between the real-world *computer networks* and the networks modeled by Random Graphs exist. For example, the real world computer networks are highly clustered and inhomogeneous, hierarchically structured, which seem to be very hard to capture with standard random graphs models where analytic solutions have been available. In spite of these difficulties, there have been quite a few applications of Random Graphs to communications networks, especially in the fields of wireless sensor and ad-hoc networks. Study of wireless capacity by Gupta & Kumar (2000) is one of the most cited studies, and Hekmat's (2006) monograph is a more comprehensive treatment of the applications of random graphs in wireless communications. Random geometric graphs, which also consider Euclidean distances between vertices, are more realistic in describing wireless networks (Kozat and Tassiulas 2005).

The biggest challenge of applying Random Graphs (Bollobás 2001) or Random Geometrical Graphs (Penrose 2003) is to formulate realistic graphs models that are still amenable for obtaining analytic solutions. In the field of wireless sensor networks, it seems that Random Geometrical Graphs are more flexible in capturing topology, but still not flexible enough to analytically model more realistic dynamic events such as *hybrid faults* in *agreement algorithms*. Despite the difficulties in modeling wireless networks, Random graphs theory is of significant importance to computer science. The two leading journals "*Random Structures and Algorithms*" and "*Combinatorics, Probability and Computing*" publish significant research papers of random graphs in theoretic computer science. Similarly, Percolation (Grimmett 1999) and Continuum Percolation (Meester & Roy 1996), which can be formulated as Random Graphs and Random Geometric Graphs, respectively, can also be applied to the study of networks, although it appears they are out of favor these days. However, Percolation models are more convenient for simulation study if analytic solutions are not available.

3. BIOLOGICAL ROBUSTNESS AT INDIVIDUAL LEVEL: GENETICS AND IMMUNOLOGY

3.1. Genetic Robustness

Before proceeding, it would be helpful to clarify a few terms first. In this paper, we use biological system to refer to any biological unit that has an identifiable functionality. In Wagner's words, a biological system is an assembly of parts that carries out well-defined biological functions (Wagner 2005). As Wagner pointed out, two questions should be asked to form a robustness problem of a biological system: (1) What feature of a biological system is robust? (2) What kind of change is this feature robust to? In addition, the use of networks is in the broadest sense and can refer to gene, metabolic, DNA, RNA, protein networks, population networks, food web, and immune networks. We use the term reliability loosely; especially in the context of

biological systems, reliability is used, by analogy, with that in engineering systems.

Biological robustness is the capability of a biological system to continue to function in the face of perturbations that can be genetic or non-genetic (e.g., environmental fluctuations). Again, there are many interchangeable terms for robustness and perturbations. The alternatives for robustness, such as stability, homeostasis, resilience, balance, buffering, canalization, tolerance, efficiency, are often used at different levels of biological organizations (systems). The alternatives for perturbation include disturbance (environment), impact (environment), mutation (gene), fragmentation (landscape) and regulation (population). Therefore, our biological reliability may be interchangeably used with different biological/ecological terms at various organizational levels: robustness at the individual level, stability and regulation for population, stability for community, and balance at the ecological system level.

Fitness has a clear definition in biology and it refers to the reproductive potential which natural selection acts on. One of the main goals of this paper is to draw inspiration from biological systems on how the fitness is maximized, and then apply the principles and mechanisms to improving the reliability of computer networks. Accordingly, a practical and convenient mapping for fitness is the measurement of reliability and survivability.

Wagner (2005) reviewed the biological robustness of gene and metabolism networks, which is probably the most comprehensive survey on biological reliability at the individual level. He summarized seven principles of robustness from the analyses of the studies in gene and metabolism networks. Those principles are (Wagner 2005):

- (1) Most problems living systems have solved have an astronomical number of equivalent solutions, explained by the now widely accepted neutral fitness space theory.
- (2) Living systems are generally robust to mutations for two fundamental reasons: the huge mutation neutral space and incremental evolution of mutation robustness. Furthermore, the immense mutational neutral space is inhomogeneous. The population is driven to high robust regions in the neutral space by natural selection.
- (3) Incremental evolution of mutational robustness can be caused by either mutation or environment selection pressure. However, the mutation-driven evolution is very limited in nature; the dominant selection pressure is from environment or non-genetic changes. This implies that the mutation robustness may be a by-product of the selection for robustness to environment.
- (4) Evolutionary innovations need robustness and neutral mutations. Robust systems can endure many neutral mutations, but these mutations also provide substrate for future evolutionary innovations, which may evolve the

detrimental features again. In other words, neutrality is changeable.

(5) Components redundancy of a system is lesser important than the distributed robustness in terms of the robustness to mutation. Wagner (2005) refers to the distributed robustness as "interactions of multiple system parts, each with a different role, can compensate for the effects of mutations".

The above notion that component redundancy is of the secondary importance seems counter-intuitive from the engineering perspective. However, the difficulty in quantitative study of robustness of biological systems, as Wagner pointed out, may actually hold the explanation for this seemingly counter-intuitive principle. The difficulty lies in the phenomenon that, as Wagner (2005) stated, "*redundancy and distributed robustness have indistinguishable signatures on the variables to understand a system's function and robustness*", which means it is near impossible to distinguish redundancy with distributed robustness. This principle might echo the redundancy management in engineering design; a system with multiple redundant components without proper coordinating mechanisms may render the system less reliable.

(6) Fragility in a biological system, the opposite of robustness, does exist in nature. There may be multiple evolutionary causes for being fragile. A fragile system can change its function or structure dramatically in the face of mutations. In some cases, being flexible to drastic changes might be advantageous, for example, the antibody diversities in immune system (Wagner 2005).

(7) Many natural systems below and beyond living organisms demonstrate remarkable robustness to changes in their system components. Wagner (2005) argued that such robustness is often caused by self-organization, rather than natural selection. Wagner (2005) cited the robustness of ecological community to species invasions as an example of self-organizations. We consider it might be a more complex issue to attribute all ecological stabilities or robustness to self-organizations. There are many sound examples of evolutionary mechanisms in the ecological community level, for example, co-evolution between insects and plants, or niche overlaps, or trophic relationships. We will return to this topic in sections 4 and 5.

Wagner (2005) also dedicated one chapter of his monograph to the robustness of the engineered system—the focus of this paper. In some sense, the present article is motivated by Wagner's (2005) pioneering work but we focus on what Wagner chose to leave out: the bio-robustness beyond gene and molecular levels as well as their implications to engineering fault tolerance. Specifically, we focus on biological population and community levels.

Here, we present an extremely brief summary of Wagner's (2005) engineering robustness chapter. One important argument Wagner (2005) made is that the evolved

robustness, which is often considered as unique to living systems, can be implemented in engineering systems. First, it is argued that although gene or genetic materials do not exist in engineered systems, the distinction between genetic and environmental perturbations are still highly relevant. Environmental perturbations may include changes that are not foreseen in the design stage. The counterparts of genetic changes in engineered systems can be components failures (Wagner 2005). Therefore, the counterpart of robustness in engineered systems is fault tolerance.

Wagner (2005) discussed the most conspicuous differences between living systems and engineered systems. The substrate of engineered systems, ceramics, steel, plastic, silicon, and arguably wood, are very different from protein and nucleic acids of living things. Biological systems are evolved through natural selection, which is similar to blind search mechanism to some extent, and engineered systems are from the rational design. Two features in living systems seem to be fundamentally different. The behaviors of most parts of living systems are best characterized as erratic. In contrast, most engineered systems behave much more orderly. In other words, the living systems are internally noisy. Often the noise suppression leads to mutational robustness as by-products. Wagner (2005) further concluded that despite the significant difference, no radically different new approaches are needed in living systems to deal with the internal noise inside organisms. Wagner (2005) cited two engineering examples (Carlson and Doyle 2002, Keymeulen et al. 2000), distributed robustness of telecommunication networks, and evolved integrated circuits with genetic algorithms. There are numerous similar examples in engineering fields and recently in evolutionary computation that further support Wagner's points.

Wagner (2005) noted seven open problems related to biological robustness. These open questions may be interesting in at least three fields: biology, evolutionary computing, and fault tolerant engineers. The significance in the first and third fields is obvious. As to the second field, the interactions between bio-robustness and evolutionary computing are bidirectional. Evolutionary computing tries to obtain inspiration from the evolution of bio-robustness; on the other hand, computer scientists also try to simulate evolution and offer insights to biology. Here, we briefly introduce four of the seven open questions Wagner (2005) identified (we preserve Wanger's original numbering).

Problem-1—Which of the two main evolutionary causes of robustness is more important: the vast mutation neutral space or the incremental evolution of mutation robustness? The first implies that the evolution process selects solutions that are more frequent among all solutions, that is, associated with large neutral space. Furthermore, such solutions lead to robust biological systems. If this is the case, then robustness is largely a by-product of the evolutionary discovery process. The second cause is the incremental evolution of robustness within a neutral space, which discovers regions within neutral space with

particularly high robustness.

While the answer to this question is still open in biology, analogically similar questions exist in computer science, specifically, the evolutionary computing (EC). It seems there is not a definite answer for it either in EC. If the first cause should be dominant, then the exploration should be favored over the exploitation and the opposite if the second cause is the primary cause.

Problem-4—Is robustness to mutation ever an adaptation to mutations? Or can mutations be the primary driving force for the evolution of mutational robustness? This is indeed a very interesting question, which could imply that organisms living under less stable environments should be more robust than those living under stable environments. If we think of the evolution of insects vs. vertebrates, the environments insects survive are often more severe and unstable, still they demonstrate remarkable robustness at both organism and population levels.

Problem-5—Is robustness always associated with other features that facilitate evolvability? For example, modularity promotes evolvability, so are the robustness and modularity always positively correlated? The answer seems yes in engineered systems, in our opinion.

Problem-7—Where has natural selection promoted fragility over robustness? Given individual-based selection do not promote fragility; does kin selection play any roles in it? This may have significance for evolutionary computation too, where *fragility* may be desirable.

3.2. Immune Network Theory and Artificial Immune System (AIS)

The artificial immune system (AIS) is a computation paradigm inspired by natural immune systems. The natural immune system is the most important defense system for animal and human individuals and plays crucial roles for the functional robustness of an individual body. Our body maintains a large number of immune cells, named lymphocytes that circulate throughout the body and forms a defense network. What is remarkable with the immune system is that it is very similar to nerve system. It is a highly adaptive, parallel and distributed system from the perspective of information processing. The immune system possesses remarkable capability to recognize and remember relevant patterns encountered previously, and use combinatorics to build pattern detectors. In addition, the overall system behavior is an emergent property of many local interactions (Dasgupta and Attoh-Okine 1997).

Jerne (1974) founded the immune network theory with a system of differential equations that describe the dynamics of lymphocytes, and later Perelson (1989) expanded Jerne (1974) theory with a stochastic approach including the study of phase transitions. The theory is also called *idiotypic network theory* since it is built on the hypothesis of *idiotypy*

cascading, analogous to neuron cascading in the nerve system. As Behn (2007) indicated in a review that the immune network theory has fallen out of fashion in parallel with the rapid advances in molecular immunobiology in biology fields, but seems returning due to the interests of system biologists and physicists. Part of the renewed interests also comes from the efforts of computer scientists in the fields of Immunological Computation or Artificial Immune Systems (AIS) (Hofmeyr and Forrest 1999), which were inspired by the natural immune network theory. The applications of AIS have been expanded to intrusion detection, pattern recognition, computer virus detection, fault diagnosis, machine learning, etc. For the latest status of AIS, Dasgupta (2006) surveyed the recent advances and Garrett (2005) presented a somewhat critical but confirmative review. There are quite a few applications to wireless ad hoc networking, including misbehavior nodes detection etc. (Balachandran 2006, Drozda and Szczerbicka 2006). Immune network systems have also inspired the strong interests in network survivability and fault tolerance research (e.g., Avizienis 2004).

4. BIOLOGICAL ROBUSTNESS AT POPULATION LEVEL: POPULATION DYNAMICS, DARWIN DYNAMICS AND EVOLUTIONARY GAME THEORY.

4.1. Biological Population Dynamics and Spatial Distribution Patterns.

4.1.1. Population and Metapopulation.

A biological *population* consists of individuals of the same species that distribute in specific habitats. Population is spatially and temporally dynamic, determined by the net effects of birth-death and immigration-emigration processes, under the constraints of environment conditions. Of course, species exist as populations, and a population is an information network carrying genome information, similar to a Local Area Network (LAN) vs. global Internet (species), in the analogy of computer networking. Historically it has been argued that geographical separation or environment is the major factors that lead to *reproduction isolation* and further *speciation*. Recent studies seem to show that intraspecies and intragenomic conflicts may lead to rapid evolution of genes and formation of reproductive barriers necessary for speciation. Genomic conflicts occur when natural selection favors alleles that may simultaneously raise fitness for some phenotype but lower for others (for example, in the other sex). This kind of conflicts may lead to tit-for-tat or arms race (Hey et al. 2005). This is clear evidence *at the gene level* that *speciation* is an *evolutionary game*, as we will discuss in section 4.3.

In nature, a species exists as evolving *metapopulation* lineages. In systematics and evolutionary biology, a metapopulation is the equivalent of a species; it is the set of

connected populations of the same species, or maximally inclusive populations (de Queiroz's 2005). In ecology, metapopulation means population of populations, and it becomes an established concept largely due to Levin's (1969) mathematical model, in which a metapopulation is described as a dynamic process of extinction and recolonization of local populations linked to one another by ongoing dispersal and gene flow (Hanski 1999).

4.1.2. Population Dynamics.

Population dynamics, the changes of population size over space and time, is the central topic of population ecology. The mathematical modeling of population dynamics can be traced back to Thomas Malthus's (1798) "*An Essay on the Principle of Populations*" (cited in Kot 2001). With his exponential growth model for human population, Malthus argued that human population grow geometrically while resources such as food grows arithmetically, and therefore fast population growth would lead to much human misery. Malthus's conclusion had significance influence for Darwin's formation of struggle for existence or natural selection. Verhulst (1845) derived the famous Logistic population growth model, which was re-discovered by Pearl and Read in 1920 (cited in Kot 2001). The Logistic population model is more realistic than Malthus's exponential growth model; it is the solution of a first-order nonlinear differential equation. The difference form of the Logistic model was found to possess rich and complex Chaos behaviors in the 1970s (May 1976).

Logistic differential equation and its discrete counterpart (difference equation) form the foundation for studying single species population dynamics deterministically. It has extraordinary rich and complex mathematical properties from stable growth, oscillation, attractors to chaos, and its applications have expanded well beyond biology. Logistic differential equation is also the basis for forming the famous Lotka-Volterra differential equations system for interspecific interactions such as predation and competition. The deterministic differential equations have traditionally been used to model population dynamics and are still one of the major approaches (Kingsland 1995, Hallman and Levin 1986, Kot 2001, Brauer and Castillo-Chavez 2001). An alternative to the differential equation modeling is the stochastic modeling with stochastic process models such as birth-death process (Lande and Engen 2003). The third group of analytic model is the matrix model which can be formed in either deterministic or stochastic (Caswell 2001), and it turns out that matrix is often equivalent to either differential equations or stochastic process models (such as Markov Chains). The fourth type of analytical model is the optimization and game theory model, which was initially applied to study animal behavior or ethology (Lendrem 1986). As we will discuss in the next two sections, recent studies show that the game theory is able to unify population dynamics and evolutionary dynamics, and the resulting evolutionary game theory is mathematically equivalent to the traditional differential and difference

equations for population dynamics (Nowak 2006, Vincent and Brown 2005, Hofbauer and Sigmund. 1998).

4.1.3. Population Regulation.

Population regulation was one of the most contested theory in the history of ecology (e.g., see Kingsland 1995 for a brief history) and the debates started in the 1950s and culminated in the 1960s, and even these days, the antagonistic arguments from both schools occasionally appear in ecological publications (e.g., Berryman 2002, White 2001). The debate sounds simple from an engineering perspective. The core of the debate is: is population *regulated* by feedback mechanisms such as density-dependent effects of natural enemies or is simply *limited* by its environment constraints. Within the regulation school, there are diverse theories on what factors (intrinsic such as competition, natural enemies, gene, behavior, movement, migration, etc) and how the population is regulated. Certainly, there are mixed hypothesis of two schools. About a dozen hypotheses have been advanced since the 1950s. The debates were "condemned" by some critics as "bankrupt paradigm", "a monumental obstacle to progress" (cited in Berryman 2002). However, there is no doubt that the debates kept population ecology as the central field for more than three decades, and is critical for shaping population ecology as the most quantitatively studied field in ecology. The *mathematical ecology* also known as *theoretic ecology* is often dominated by the contents of *population ecology* (Kot 2001). In addition, the important advances in ecology such as Chaos theory, spatially explicit modeling, agent or individual based modeling all initiated in population ecology.

The importance of population regulation cannot be emphasized more, since it reveals the mechanisms for population dynamics. Even more important is to treat population dynamics from the time-space paradigm, not just the temporal changes of population numbers. In addition, the concept of metapopulation is also crucial, which implies that local population extinction and recolonization happens in nature. Obviously, population regulation as control mechanisms for population size is very inspiring for the counterpart problem in evolutionary computation. As we will see, population regulation and population dynamics can be unified with evolutionary game theory, and even united with population genetics under same mathematical modeling framework such as Logistic model and Lotka-Volterra systems.

4.1.4. Population Spatial Distribution

In biology, the terms spatial distribution patterns, spatial distributions, and spatial patterns are used interchangeably for biological populations. Spatial distribution of population is one of the most fundamental ecological properties of species. As Taylor (1984) summarized, "*Spatial distribution yields characteristic parameters that segregate species. These parameters are the population*

expression of the individual behavior... This behavior determines their spatial patterns." Many researchers believe spatial distribution of animals is governed by self-organization, and the spatial distribution pattern is therefore an emergent property at population level. It was already known in the early 1960s that insect population distribution follows the Power Law (Taylor 1961, 1984, Ma 1988, 1990a,b).

Generally, there are three types of spatial distribution patterns: aggregated, random and regular. Random spatial distribution can be fitted with Poisson probability distribution, and the regular distribution (also termed uniform distribution) is totally regular with even spacing of individuals than random. Aggregated (also termed contagious, congregated, or clustered) distribution represents nonrandom and uneven density in space (non-randomly unequal spacing of individuals). The probability distributions (in mathematical term) for aggregated distributions (in biological term) are strongly skewed with very long right tails (Ma 1989, 1990a,b, 1991a,b,c).

Theoretical modeling of spatial distribution was started as early as the 1920s. Until around the 1950s, the dominant modeling approach was to fit *probability distributions* to the frequency distribution data from the field sampling investigation. This is often termed probability (frequency) distribution approach in literature. Taylor (1961) discovered that the Power Law model fits spatial distribution data ubiquitously well, $V = aM^b$, where M and V are population mean and variance, respectively, and a and b are parameters. According to Taylor (1961, 1984), $b > 1$ corresponds to aggregated distribution, $b = 1$ to random distribution and $b < 1$ to regular distribution. Ma (1988, 1990b, 1991c) extended Taylor's Power law model with his concept of population aggregation density (PACD), which was derived, based on the Power Law: $m_0 = \exp[\ln(a)/(1-b)]$, where a and b are the parameters of Power Law and m_0 is the PACD. According to Ma's (1988, 1990b, 1991c) reinterpreted Power Law, population spatial distributions are population density-dependent and form a continuum on the population density series. The PACD is the transition threshold (population density) between the aggregated, random and regular distributions. Ma and Krings (2008d) presented an engineering application inspired by the spatial distribution pattern mechanisms.

4.2. Evolution and Natural Selection.

The publication of Charles Darwin's "*On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*" published in 1859 firmly established evolution as the fundamental theory of biology. Lewontin (1974, cited in Vincent and Brown 2005) and Vincent and Brown (2005) summarize Darwin's postulates as three folds: (1) "Like tends to beget like" and there is heritable variation in traits associated with each type of organism. The best evidence for this postulate would be

Mendel's laws of heredity or *Mendelian inheritance*. (2) Organisms struggle for existence, often with the intra-specific struggle fiercer than the inter-specific. This postulate was strongly influenced by Malthus's (1798) "*An Essay on the Principle of Populations*." (3) The struggle for existence is affected by the heritable traits. The third postulate holds the key to understand the consequence of evolution. Obviously, the first postulate is the genetic dimension of evolution theory and the second is the ecological dimension, and the third postulate is a logical derivation for the consequences from natural selection upon inheritable traits (Vincent and Brown 2005). It is indeed true that Darwin formed his theory of evolution without invoking genes, which was first discovered by Mendel in 1866 but unnoticed until the rediscovery by Fisher (1930), Wright (1931) and others in the 1930s. The unification of Darwin's evolution with Mendelian was reached in the 1930s by the efforts of Fisher (1930) and others and the latter unification further into the well-known *Modern Synthesis* (Mayr and Provine 1980).

4.3. Evolutionary game theory.

Games can be classified as cooperative (in which two or more players can form coalitions) versus non-cooperative. Non-cooperative games are generally simpler to analyze than their cooperative counterparts are. Therefore, one approach to cooperative study is to reduce the cooperative to non-cooperative version. Another way to distinguish cooperative and non-cooperative games is by examining the number of objectives involved in decision-making, with cooperative games dealing with single objective, and non-cooperative ones dealing with multiple objectives (Bilbao 2000). Still another classification for conventional games is to divide them into the matrix (discrete), continuous static and differential. Matrix games have a finite number of strategy choices, and payoffs can be expressed with matrices. In continuous static games, payoffs and strategies are related in a continuous function; the game is static -- an individual's strategy is constant. Continuous games are characterized by continuously time-varying strategies and payoffs with a dynamic system modeled by differential equations.

Traditional game theory is normative rather than descriptive (or positive) from the viewpoints of rationality assumption, since it only prescribes what players should act if rationality prevails. In addition, it assumes that players always try to maximize their payoffs and behave consistently. It has been found that even intelligent players like human beings do not always follow rationality, and therefore the applicability of traditional game theory in real world has been seriously questioned. Those contradictions with reality put serious doubts on the relevancy and applicability of the corner stones of classical game theory such as Nash equilibrium, although the mathematical validity of Nash equilibrium is never in question (e.g., Mailath 1998). Another crucial weakness of traditional game theory, when applied to real world problems, is that it implies that the game is not

repeated. In practice, a typical decision-making problem is often dynamically interactive. Evolutionary game theory, largely, overcomes those restrictions associated with classical games, and understandably, was quickly embraced upon its invention, especially in the fields of economics and biology. As a side note but relevant to this article, Kumar and Marbukh (2003) seemed to be the first that proposed to model network survivability as a (traditional) game model.

Evolutionary game theory is co-advanced by John Maynard Smith and George Price (Maynard Smith and Price 1973, Maynard Smith 1976, 1982). It was reported that George Price's manuscript, rejected by the *Nature* magazine, inspired Maynard Smith to study the field systematically and led to their cooperative work. In the late 1960s, Price was puzzled by the evolution of ritualized non-injurious behaviors in animal conflicts, and even in the competing for the most valuable resources, animals rarely use their weaponry in the most effective way. The solution to the puzzle was the application of game theory.

Darwin and his contemporaries already recognized that life is a game; nevertheless, the formal tools of game theory was not available in their times (Vincent and Brown 2005). The so-called *tragedy of the commons* (the gains to individuals at the expenses of the group) encourages organisms invariably overexploit their common pool of resources (Vincent and Brown 2005). Darwin's "*struggle of life*" captures the conflicting nature of life. In evolving favorable traits, no organism is free from meddling with others. Therefore, individual organisms are the *players* of a game. Wright's fitness landscape (1931), Fisher's fundamental theorem (1930) of natural selection provided how natural selection drives the change of *fitness* (indication of *payoffs*) of traits (*strategies*).

As indicated by Vincent and Brown 2005, ever since Darwin, natural selection has been deemed as an optimization process. Prior to Maynard Smith and Price (1973), who recognized natural selection is better described with game theory than the simple optimization model, several scientists including Fisher (1930), Hamilton (1963), Hutchinson (1966), Levins (1962), were very close to achieve the fundamental breakthroughs. Hutchinson's (1966) treatise titled "*The Ecological Theater and the Evolutionary Play*" clearly pointed out the relationship between ecology and evolution. What made Maynard-Smith and Price's work particularly significant is that the nature of natural selection as a game induced the extension of traditional game theory. The extended version has to accommodate the ongoing dynamic populations, players come and go through birth-death process, but strategies are inheritable from generations to generations, etc.

Evolutionary game is different from any of the three traditional games mentioned previously: matrix (discrete games), continuous static and continuous dynamic games (differential games). It can be considered as a hybrid of the latter two. The players are the individuals and the strategies

are inheritable phenotypes. A player's strategy is the set of all evolutionarily feasible phenotypes; a strategy may be inherited from generation to generation. Payoffs of a game are expressed in terms of fitness, for example, the per capital growth rate of a strategy under specific ecological scenario. The fitness of a player then directly influences changes in the strategy's frequency within the population. The major differences between evolutionary games and traditional games are summarized by Vincent and Brown (2005) as follows:

(1) Evolutionary games focus on the sustainability or persistence of strategies from generation to generation, while traditional games focus on payoffs for individual players. Players are updated from generation to generation via birth-death processes, but the strategy is often preserved with occasional modification due to mutation. If we envision the analogy between a population of individual organisms and a wireless sensor network, the individual nodes will be the players; the game is played to maximize the persistence of the whole network, which can be "translated" into reliability or survivability. The advantage of evolutionary game model versus traditional game model is obvious in this case, since the traditional game model will be an individual payoff centric, which is not important for the reliability/survivability of the whole network.

(2) In classic games, players choose their strategies from well-defined strategy set rationally, which is defined as part of the game. In the evolutionary game, players inherit from their previous generation, and occasionally mutate a new strategy. The strategy set is determined by genetical, physical and environment constrains that may change over time. In the analogy of WSN, this is again advantageous over the traditional game model, since the evolutionary game model has built-in adaptability to environment (such as invasions from outside) and to the mutation (sabotages within a network).

(3) In the traditional games, rationality or self-interests provides the optimization agents that encourage players to behave rationally. In the case of WSN, this is not practical since the network is dynamic and step-wise strategy development is not feasible even if we can define rationality properly. In evolutionary games, the natural selection serves as the agent of optimization and there is no need for step-wise or generation-by-generation development of strategies, since strategies selection is automatically picked up by the natural selection, which represents the pressure from inside and outside of the WSN. With traditional games, the winners are the players, and with evolutionary games, winners are the strategies, or phenotypes. In the analogy of WSN design, the winner is the persistent strategy -- the schemes of network organizations and functionalities.

(4) Evolutionary games have *inner games* and *outer games*. Inner games are similar to classic games, and are played in ecological process (short term). Evolution plays outer

games; it is the game dynamics, via inheritance, that evolve strategies by assessing the payoffs.

Since the evolutionary game is a hybrid of the continuous static and continuous dynamic (differential games), classical matrix payoff model is not sufficient for the modeling purpose. On the other hand, a somewhat surprising reward for evolutionary game theory is that the mathematical modeling framework for it has already existed for almost a century. The population dynamics theory, as briefly introduced in section 4.1, provides this modeling framework. However, few of the many publications of mathematical ecology seem to note the connections with evolutionary theory. The situation is certainly changing with the excellent works such as Hofbauer and Sigmund (1998), Vincent and Brown (2005), Novak (2006).

The remarkable descriptive power, elegance, and flexibility, with the extension of the existing population dynamics models to the evolutionary game theory, lie in the fact that it provides a unified mathematical framework to describe all three cornerstones (postulates) of Darwin's evolution theory. Those cornerstones are, as mentioned previously, (1) the struggle of life — ecological dimension (the original objectives of those models), (2) natural selection — the replicator dynamics, (3) "Like tends to beget like" — gene frequency dynamics. All three dimensions can be modeled with the same set of differential equations. The resulting model parameters achieve the biological meanings exchangeable in all three aspects of evolution theory (Hofbauer and Sigmund 1998, Vincent and Brown 2005, Novak 2006). This unified framework is named as Darwin dynamics by Vincent and Brown (2005).

The development of evolutionary game theory by Maynard Smith and George Price (Maynard-Smith and Price 1973, Maynard Smith 1982) received immediate embracement from game theoreticians and practitioners in many fields. However, it seems that, the mathematical framework which evolutionary game theory borrowed from population ecology, has not received as much attention as it deserved. In other words, the principles and ideas of evolutionary game theory have been adopted in many game theory studies, but the specific differential equation models, borrowed from population dynamics, do not seem widely applied, perhaps due to the biological nature of those models. Therefore, this topic will be expanded in the next section (section 4.4), which we believe is particularly useful for studying dynamic systems such as wireless sensor networks.

With hundreds of papers on important games such as prisoner's dilemma already published, the literature of evolutionary game theory is still growing daily in multiple subjects across game theory, economics, sociology, psychology, computer science, mathematics, etc. Many of the studies in the above-mentioned fields adopted complex simulation models. The deterministic differential equation models from the classical mathematical ecology should

bring in very refreshing perspectives, as already demonstrated by Hofbauer and Sigmund (1998), Weibull's (1995), Vincent and Brown (2005), Novak (2006) and others.

4.4. *Unifying population and strategy dynamics — Darwin dynamics.*

The discussion in this section is mainly based on Hofbauer and Sigmund (1998), Vincent and Brown (2005), and Novak (2006).

4.4.1. *Evolutionary Stable Strategy (ESS)*

Evolutionary game theory started with the introduction of ESS and its applications to the matrix games (Maynard Smith and Price 1973). The role of ESS in evolutionary game theory is similar to that of the Nash equilibrium in classical games. ESS is *unbeatable* or *impregnable* in the sense that *mutants* or *dissidents* in a population cannot "invade" the population under natural selection, in terms of the reduction of fitness. In analogy, in a computer sensor network, the failures of some nodes either voluntarily (e.g., refuse to relay due to selfish behavior) or involuntarily (e.g., "neutral mutation" such as running out of batteries) will not reduce the overall reliability/survivability of the network.

As reviewed by Vincent and Brown (2005), the difference between the Nash equilibrium and ESS is that ESS requires both equilibrium and convergence-stability conditions. This additional requirement is significant, since evolutionary games are always dynamic and played repeatedly. It also reflects its original application domain, biological evolution, where one is interested in whether the extant properties should be evolutionarily stable. The equilibrium describes the resistance to invasion by a mutant strategy and equilibrium is a necessary condition for ESS. The convergence stability, which is the sufficient condition for ESS, implies that a population will evolve to the ESS when it is near the ESS.

The *co-evolutionary game* is a game that possesses the flavors of both cooperative and non-cooperative games; furthermore, it has been studied in both traditional game and evolutionary game domains (Vincent and Brown 2005). On the cooperative side, the game does not cause mutual destruction; on the contrary, it may promote the well-being of both parties, for example, the co-evolution between insects and plants. On the non-cooperative side, one party evolves the strategy that is tuned to deter the advantages of its counterparts. Since the co-evolutionary game has been approached in both traditional and evolutionary games, the terminologies could be confusing.

4.4.2. *Replicator Dynamics*

Replicator dynamics describes evolution of the frequencies of strategies in a population. In evolutionary game theory, replicator dynamics is described with differential equations.

For example, if a population consists of n types E_1, E_2, \dots, E_n with frequencies x_1, x_2, \dots, x_n . The fitness $f_i(x)$ of E_i will be a function of the population structure, or the vector, $x = (x_1, x_2, \dots, x_n)$. Following the basic tenet of Darwinism, one may define the success as the difference between the fitness $f_i(x)$ of E_i and the average fitness $f(x) = \sum x_i f_i(x)$ of the population. The simplest replicator model can be defined as: $dx_i/dt = x_i[f_i(x) - f(x)]$, for $i=1,2,\dots,n$. The population $x(t) \in S_n$, where S_n is a simplex, which is the space for population composition, is similar to mixed strategies in traditional games (Hofbauer and Sigmund 1998, Vincent and Brown 2005).

It has been shown that the replicator differential equations are equivalent to the classical population dynamics models such as Logistic differential equation and Lotka-Volterra equation. In the analogy of reliability modeling, we can use the net fitness change $[f_i(x) - f(x)]$ as a measure of reliability or survivability in a wireless sensor network.

4.4.3. Adaptation and co-adaptation

The *internal* debate within Darwinists is often focused on the role of adaptation, with the difference that adaptationists consider every characteristic is evolved from the adaptation to the natural selection. The opponents of adaptationists consider that some biological features are the by-products of natural selection, what Gould (1979) termed as "*Spandrels of San Marco*". In the game theoretic evolutionary school such as Maynard Smith (1982), Hofbauer & Sigmund 1998, Vincent and Brown (2005), an adaptation is the particular strategies that make up the ESS. With Vincent and Brown's (2005) words, the ESS is the end point of evolution by natural selection, which probably should not be taken literally, in our opinion, since evolution of living things is certainly still going on. With evolutionary game theory, adaptive dynamics is the changes of the frequencies of strategies within the population, and can be modeled with the replicator equations. Traditionally, adaptive dynamics refers to the change of gene frequencies in population genetics. Some researchers use adaptive dynamics to refer to the dynamics of phenotypes (e.g., McGhee 2007). Strategy dynamics refers to the strategy changes of a species and its difference with adaptation dynamics lies in the species *versus* population.

4.4.4. Fitness Generating Function: G-function

Fitness Generating Function (*G-function*) is invented by Vincent and Brown (2005) to specify groups of individuals within a population. Individuals are assigned same *G-functions* if they possess the same set of evolutionarily feasible strategies and experience the same fitness consequences within a given environment. This *G-function* has close connection with the German term *bauplan*, which

is used to classify organisms by what appears to be common design features or rules. *G-function* can be thought of as describing both an organism's bauplan and its environment. In the analogy with computer networks, we might define bauplan as the clusters of homogenous nodes, for example, all Linux workstations in a network. Hazard function model, which can be modeled with survival analysis, should be a good candidate for network *G-function*.

The motivation of proposing *G-function* by Vincent and Brown (2005) seem to capture both aspects of ESS, the necessary equilibrium conditions and the sufficient convergent stabilities. In practice, there is no single fixed form of *G-function*; instead, they are devised based on specific systems. For example, one of the simplest *G-function* can be defined based on the Logistic equation, $G = G[v, x]$, where v is the strategy vector and x is the vector of population dynamics. By studying dynamic properties of the *G-function*, one can obtain the models for both evolutionary equilibrium and convergent stability. The analytic procedures for *G-function* are very similar to the methodologies in Hofbauer and Sigmund's (1998), but the later just did not propose specific terms. *G-function* plays the similar roles of *fitness functions* in Hofbauer and Sigmund's (1998).

Multiple *G-functions* and multi-stage *G-functions* can be defined for an evolutionary system. Often, both differential and difference equations forms of *G-functions* are provided. It might be the difference equations that prompted the adoption of the term generating function, since generating function is another term for the z -transform that often involves with the solving of difference equations.

4.4.5. Darwin dynamics

For biologists, one of the most appealing advantages with evolutionary game theory is the unified modeling framework for population dynamics and strategy dynamics, both of which together is termed as *Darwin dynamics* in literature (Hofbauer & Sigmund 1998, Vincent and Brown (2005). This seems to be the first time in biology that ecology-based population dynamics modeling is united with evolution theory. What is more remarkable is that the newly unified framework of Darwin dynamics is interchangeable with the traditional genetics-based Modern Synthesis (Fisher 1930, Mayr 1980).

In the previous sections, we emphasized ESS. However, evolutionary game theory is not limited to study the games with ESS only. ESS may not exist in some evolutionary games. Actually, the existence of Nash equilibrium is not sufficient to guarantee the existence of ESS, since the existence of ESS depends on the convergent stability. The study of non-equilibrium is certainly complicated. Fortunately, the results from population dynamics, such as nonlinear dynamic models, provide valuable insights; the dynamic behaviors such as periodic, quasi-periodic, chaos, limit cycles and n -cycles (discrete cycles) can be analyzed

with those models. These analyses require the solutions from the models to be bounded (Hofbauer & Sigmund 1998, Vincent and Brown 2005).

In summary, evolutionary game theory, which itself is inspired by the evolution theory, provides an effective alternative to the traditionally genetics-centered statistical approach to the studies of evolution. Furthermore, it united population dynamics with evolution theory. In addition, the mathematical framework of evolutionary game theory still holds, when gene frequency is brought into the model, that is, it can replace the traditional genetics-centered evolution models.

5. BIOLOGICAL ROBUSTNESS AT COMMUNITY LEVEL

Generally, living systems can be classified vertically as the organizations of molecular, individual, population, community and eco-systems. Although this classification is not precise, it serves well for organizing research subjects. Each of the organizational levels may be further detailed. For example, at molecular level research, there are gene and protein, cell, metabolic networks, etc. The main subjects at the molecular level are molecular biology, biochemistry, and more recently, genome sequencing and bioinformatics. Research at the individual level is somewhat special and several subjects are deeply rooted at this level, including physiology (which also interfaces with biochemistry and metabolism at molecular biology level), autecology, and ethology. Population, community, and ecosystem traditionally are subjects of ecology. This imprecise classification is far from complete, for example, some important subjects do not fit into any single level or form their own level. Two outstanding examples are evolutionary biology and immunology. With the recent rapid advances in molecular biology, a few new subjects have been established, for example, bioinformatics, molecular ecology, and system biology. In addition, in recent years, the theories of metapopulation (ensemble of populations) and metacommunity (ensemble of communities) have been established solidly in ecology, which can be considered as organizational levels between population and community and between community and ecosystem, respectively.

In recent years, landscape ecology has emerged as a new and exciting level of ecological study. Environmental problems such as global climate change, land use, habitat fragmentation and decline of biodiversity have required ecologists to expand their traditional spatial and temporal scales. The widespread availability of remote imagery, GIS technology, has permitted the development of spatially explicit analyses (Turner et al. 2003). Due to the emergence of landscape organization level which is beyond community but vague with the ecosystem level, plus the ambiguity surrounding ecosystem itself, there is suggest to abandon the ecosystem concept (O'Neill 2001).

There is no doubt that biological robustness is ubiquitous at various levels. Some of the concepts are even deeply embedded into our daily lives, for example, the near ideological concepts of conservation of biodiversity, balance of ecosystems and global warming. One fundamental question implied by these concepts is how ecosystem or nature is resilient to human disturbance or how stable is the ecosystem? We are going to totally skip the ecosystem and landscape level robustness or stability and balance with its native terms, not because of the controversies around it, but for two reasons: (1) The field is too broad to summarize a meaningful definition of robustness. (2) Many of the ecological principles and mechanisms in ecosystem and landscape levels are the extension of community level theory. Therefore, from the practical point of view, focusing on community level should be sufficient for drawing ecological inspiration. Of course, our ignorance of these topics never implies these fields are unimportant in their own rights or in other fields. For example, there is very active research in software engineering that draws inspiration from ecosystem concept.

5.1. Ecological Communities

Ecology as a subject has more than 100 years of active research, and early ecological research was largely experimental and descriptive. Significant portions of the theoretic ecology described with mathematical models have been mainly accumulated since the 1960s. One significant difference between theoretic physics and theoretic ecology is that an ecological theory, presented with perfectly correct and logical mathematical models, does not guarantee that the theory is biologically valid, since the *law in ecology* is very difficult to verify with experiments, unlike in physics. In addition, our understanding of ecological systems, especially beyond population level, is very limited. It sounds unbelievable, that while we have the full knowledge of human gene sequence, we still do not have a reliable estimate for the number of species on earth, not to mention the controversies around collapsing biodiversity and global climate changes. Here we choose to briefly discuss two fields, which are more relevant to our topic—biological robustness. These two fields should also reflect the level of our understanding of ecological communities.

5.2. Community organization

The most common denominator for ecological communities is the ensemble of biological species. Beyond that commonality, differences emerge. One definition for *ecological community* adopted by Hubbell (2001) is "a group of trophically similar, sympatric species that actually or potentially compete in a local area for the same or similar resources". However, many ecologists do not restrict the species to the same or similar trophical groups, and a community simply includes all species in a specific region or natural environment, which is approximately equivalent to the *metacommunity* Hubbell (2001) defined. The different opinions surrounding the community definitions

spring from the theories of community organizations, or the underlying mechanisms for community to form and evolve with time. The organization directly affects the biodiversity, which consists of two aspects: *species richness* (the number of species in the community), and *relative species abundance*. One of the central themes of community ecology is the relationship between diversity and stability.

There are several theories on community organizations, but two somewhat opposite theories are of particular interests: *niche-assembly hypothesis* and *dispersal-assembly hypothesis* as termed by Hubbell (2001). Niche-assembly hypothesis is the outgrowth of niche theory and evolution biology. Niche requirements determine interspecific functional relationships, which in turn decide which species is admitted to the community of limited membership. It seems that the niche-assembly theory is currently accepted by a majority of ecologists (Kinzig et al. 2002). The collection edited by Kinzig et al (2002) is a state-of-the-art synthesis.

The alternative dispersal-assembly theory assumes that communities are open, non-equilibrium assemblages of species largely brought together by chance, history, and random dispersal. The presence of species is dictated by random dispersal and local extinction. Hubbell (2001) developed a unified dispersal-assembly theory dominantly based on the theory of island biogeography (MacArthur and Wilson 1967), and the inspiration from the neutral evolution theory in population genetics. *Neutrality* is the baseline to describe system behavior and it assumes that all individuals of every species obey exactly the same rules of ecological interactions (Hubbell 2001). Hubbell further assumes that populations and community changes arise only through ecological drift (stochasticity of *demography*, or per-capita birth/death rates), limited stochastic dispersal (species immigration/emigration), and random speciation (new species generations). He further restricts the ecological drift to zero-sum drift, which is a very crucial assumption. This implies that the dynamics of ecological communities are a *zero-sum game*. That is, any increase in one species' number is matched by decreases of other species numbers. With the three assumptions, the community dynamics is simply a stochastic process modeled with Markov Chain. What is particularly interesting for us, is the assumptions of *zero-sum drift game* and *neutrality* assumptions, which seem consistent with the evolutionary dynamics theory we discussed in population level.

5.3. Biodiversity and Stability.

Biodiversity in a community or occasionally in an ecosystem can be characterized by the species richness (number of species), relative species abundance or the synthesis of both. The most well known is the *Shannon Diversity Index*, which is based on Shannon's information theory and essentially measures the *community entropy* by synthesizing both species richness and relative abundance (Kinzig et al. 2002).

Stability is perhaps one of the most ambiguously ecological terms. In a near exhaustive and remarkable survey, Grimm and Wissel (1997) catalogued 163 definitions of 70 different stability concepts. Fortunately they were able to simplify the mess by replacing stability with three of its properties: (1) Constancy--"staying essentially unchanged;" (2) Resilience--"returning to the reference state (or dynamic) after a temporary disturbance;" (3) Persistence--"persistence through time of an ecological system." The difference between constancy and persistency is constancy refers to a certain reference state or dynamics, which may be equilibriums, oscillations or irregular but limited fluctuations. Persistence, on the other hand, does not refer to any particular dynamics, but only to the question whether a system persists as an identifiable entity (Grimm and Wissel (1997)).

Grimm and Wissel (1997) also found that three other terms, which have very close meaning with the three terms described above, also are used frequently. Therefore, they should be accepted to avoid imposing the usage. These three terms are further interpretations of the previous three properties: (1) resistance--"staying essentially unchanged despite the persistence of disturbances", this is a further interpretation of constancy; (2) elasticity--speed of return to the reference state (or dynamic) after a temporary disturbance; and (3) domain of attraction--the whole of states from which the reference state (or dynamic) can be reached again after a temporary disturbance. Elasticity and "domain of attraction" are the further properties of resilience.

These three properties alone or combined cannot solve the ambiguity. One has to ask the question: to what ecological scenario or situation does the statement refer to? It is interesting that the usage of stability in ecology very much mirrors the concept of survivability in survivable network systems (SNS) field of computer science. It also shows that the three aspects of survivability, resistance, resilience and recognition, are indeed precise, except that a separate persistence is not necessary in the case of survivability since the "identifiable" but uncertain state implied by persistence is often not acceptable in the context of survivability.

One central question in community ecology (also the ecosystem research) is the relationship between biodiversity and community (ecosystem) stability. The practical implication of this question is, if diversity does not promote stability, why do we human beings care to preserve nature diversity? One thing for sure is that the relationship is not a simple linear relationship and is very complex, even without the enormous confusions from the "163 definitions of 70 stability concepts" or the ideological or anthropocentric influences. The prevailing theory is that increased diversity tends to stabilize community properties, but tends to destabilize population properties. In addition, species composition or functional group composition (called *guilds*) may be equally important to stability as diversity is (Kinzig et al. 2002).

6. SELF-ORGANIZATION AND EMERGENT BEHAVIOR.

Self-organization refers to a broad range of pattern-formation processes in nature, and the process occurs through system internal interactions without intervention by external directing influences (Camazine et al. 2003). Accordingly, self-organized systems acquire their emergent orders, structure and behaviors via self-organization, rather than imposed on the system by external influences. According to Camazine et al. (2003), self-organization in biological systems can be different from that in physical systems, because individual units in biological systems are affected by genetically controlled properties. Natural selection, therefore, may fine-tune the rules of interactions among the individual units of the system. In addition, some studies have demonstrated that simple local interaction rules may generate very complex emergent system behaviors. This phenomenon has inspired some new computing algorithms such as particle swarm intelligence (Eberhart et al 2001), ant colony optimizations (Bonabeau et al. 1999), stochastic diffusion search (Bishop 1992), etc, and found wide applications in artificial life. Actually, all those three algorithms and some others are termed swarm intelligence in literature, which typically refers to the computation with a population of simple agents interacting locally with each other or through their common environment. Many bio-inspired computing and communication involved self-organization (Ma and Krings 2008e).

Camazine et al. (2003) also discussed the relationship between self-organization and evolution. First, they stressed the argument that self-organization is not an alternative mechanism to evolution. Evolution indeed influences self-organization, or fine-tune self-organization in the words of Camazine et al. (2003). Although both are characterized by the changes over time, the underlying mechanisms are very different. For example, natural selection is often absent from the self-organizing systems. Even if it is present, it is not the primary driving force (Camazine et al. 2003).

Similarly, it might be dangerous to over-extend the computer-simulated self-organizations. Simulation without experiment verifications or lack of sound assumptions in simulation models should not be used to support hypothesis, since the simulation itself is an unverified hypothesis. For example, in computer simulation, a population of particles may simulate migration behavior of birds, and very likely with very minor modifications, one will be able to simulate insects' migration too. The self-organizations, apparently has no way to explain the other differences between birds and insects, except their similarities in migrations flights; there is no way to explain the phylogenetic relationships and the enormous diversity differences between insects and birds.

As indicated by Camazine et al. (2003), positive feedback or self-reinforcing is often responsible for the build-up of patterns, however, antagonizing inhibitory negative

feedback has to stop and shape the build-up process to avoid overgrowth or even the self-destruction. Self-organizing systems are dynamic, and exhibit emergent properties. The emergent property often arises from nonlinear interactions among system components, which are qualitatively new properties and cannot be explained with simple addition of components properties.

Historically, the relationship between self-organization and bio-robustness received relative little attention in traditional biology and ecology. The status has been changing in recent years. One example that shows the obvious trend change is the rediscovery of Turing's (1952) seminar paper on the morphogenesis and pattern formation theory, which is also known as the reaction-diffusion pattern formation model. Turing's paper has spawned extensive research in several subjects including chemistry, physics, biology, and more recently in computer science. Some of the studies were performed from the bio-robustness or fault tolerant perspectives (e.g., Maini et al, 1992, Henry & Langlands 2004). We expect that the ongoing rapid expanding of *system biology* will further accelerate the trend, because both self-organization and bio-robustness exist widely in gene, molecular, cell networks.

Compared with self-organization and bio-robustness, there have been much more studies on the relationship between self-organization and fault tolerance, with the hope to find better engineering designs. Some of these studies also draw inspiration from biology. Certainly, the integration of the three fields: bio-robustness, engineering fault tolerance and self-organization, is highly desirable. A few examples, among many others, in this field include, Greensted's et al. (2004) study on multiprocessor system design inspired by endocrinologic system, Koloskov and Medvedeva's (2001) self-organized multimicrocontrollers, and Zou & Chakrabarty's (2007) distributed self-organization protocol for fault-tolerant wireless sensor networks. Another extensive source of research on this topic is from researchers in evolutionary computing.

7. PERSPECTIVES AND OPEN PROBLEMS

7.1. Perspectives

Perhaps except for medicine, we often take bio-robustness as granted and simply as by-products of adaptive evolution even in biology. The attitude has certainly changed in the last few decades. The most prominent example would be the studies of robustness of *gene control networks*, and the *global climate changes*. Global climate change boils down to the question — how robust the earth biosphere is. In previous sections, we have briefly reviewed bio-robustness from various biological and ecological scales (levels) with the objective to inspire the applications of the bio-robustness mechanisms and principles to enhance the reliability and survivability of computer network systems.

We realize that this is an extremely challenging work, given that the relevant literatures are spread all over several apparently distant subjects, including biology, ecology, mathematics, computer science, and engineering.

We propose to make the analogy between computer networks and biological populations, with network nodes *mapping* to biological individuals and communication links *mapping* to interactions among individuals, both of which can be described by a set of mathematical models, such as graphs or even matrices. Both biological and computer network systems possess adaptability, evolvability, stability, etc, as suggested by numerous research already conducted.

With this framework mapping, we may adapt the concepts, principles and mechanisms from biology/ecology to formulate several thoughts, summarized as follows.

(1) Both populations and computer networks can be abstracted as graph models, with graph vertices representing population individuals or network nodes, and with edges representing individual interactions or network communications paths. By studying the *evolutionary games on graphs*, one can study the *spatial-temporal* dynamics of biological populations or computer networks. The mathematical tools for this research topic would be graph theory (in particular random graphs) and evolutionary game theory. Evolutionary *fitness* in biological population is ideally mapped to network *reliability*; in the broad sense *network performance* is one aspect of reliability.

(2) Selection pressure acts on populations/networks via the *gene mutation*. Mutations can be natural causes, catastrophic events, etc. However, the mutations do not necessarily cause failures (even though it may cause the reduction of fitness or reliability), and the effects depend on the internal network state and the intensity of selection pressure. In computer networks, we can consider the network changes caused by external or internal factors as *perturbations* or *mutation*, which does not necessarily cause failure; instead, most mutations are *neutral* to reliability and survivability. ESS (Evolutionary Stable Strategy) in evolutionary game theory, which is *unbeatable* or resistant to both internal mutations and external perturbations, can be mapped to network survivability. Therefore, survivability is a set of strategies prescribed to organize a survivable network. This notion of survivability may be inconsistent with the existing definition or concept; we adopt the notion as a work definition for practical modeling convenience.

(3) We can borrow the concepts of fitness/adaptive landscape frameworks from evolutionary theory for network reliability and survivability modeling, which acts as a conceptual model for spatial-temporal fitness (reliability) model. High fitness represents high reliability. The *extinction fitness thresholds*, a measure of robustness, represent survivability thresholds.

(4) By treating individuals in a population as playing an evolutionary game, we can model the fitness landscape by using the evolutionary game theory, which has been developed for modeling biological fitness in mathematical biology. The theory of temporal modeling in biology has been established in the last few years; however, the spatial modeling of evolutionary dynamics is barely touched yet.

(5) Evolutionary game theory puts players in the context of populations and emphasizes the dynamic nature of game strategy evolution. The strategies can be inherited and evolved via natural selection that acts as optimization agents. Therefore, there is no rationality assumption required. It unites evolutionary dynamics with ecological dynamics of populations under a common framework. Mapping to network reliability and survivability, evolutionary game theory provides a unified framework for modeling reliability, survivability and *hybrid faults* (from *agreement* algorithms and fault tolerance theory). We will expand this notion in the next subsection—open problems.

(6) The *theoretic morphospace* concept was first proposed by D. M. Raup in 1966 and further expanded by McGhee (2007) to convert adaptive landscape from a conceptual framework to a mathematically rigorous metric space. The difference between theoretic morphospace and adaptive landscape is that the adaptability in adaptive space is replaced by the frequency of the different combinations of the characteristics. Very recently, this concept was introduced to study the geometrics of evolutionary dynamics (McGhee 2007). This new framework may not bring additional advantages to the study of network reliability and survivability, beyond the widely adopted fitness landscape. Nevertheless, we consider it a potentially very useful tool for studying the *intrusion detection patterns* in network security, since it seems an ideal tool for quantifying various intrusions behaviors or characteristics.

(7) *Evolution on graphs* — the graph representation of the population players (or network nodes) and its further integration with landscape can provide a solid paradigm to study the evolutionary dynamics of biological populations or computer networks. Mathematically, deterministic differential equations and stochastic processes have already been applied to this field, and a number of models are already available. The Graph theoretic models, however, bring additional important mathematical theories into the field; notably, Percolation, Interacting Particle Systems (IPS), and Random Graphs, can be used to model spatial dynamics and phase transitions.

More importantly, evolutionary game theory model, adaptive/fitness landscape and hybrid-fault models, can be further integrated, various faults such as symmetrical and asymmetrical in hybrid fault model can simply be treated as the strategies of nodes.

(8) Several metrics can be applied to model network

reliability. The *fitness generating function* (*G*-function) by Vincent and Brown (2005) simply the fitness function in evolutionary game theory are promising. Furthermore, *survivor function* from survival analysis (Ma and Krings 2008a,b,c) can be used as *stochastic fitness function* to build stochastic evolutionary game models. Again, survivability can be prescribed as ESS. As discussed in Ma and Krings (2008a), malicious attacks or catastrophic failures that are hardly predictable can be treated as censoring in survival analysis.

(9) Besides bio-robustness, Darwin's evolutionary theory, evolutionary game theory, and survival analysis, we can also incorporate another important aspect of nonlinear complex system, i.e., self-organization and emergent behaviors. We argue that self-organization is by no means the alternative to evolution. Self-organization itself is subject to natural selection and evolution can fine-tune the self-organization. We consider self-organization and emergent behaviors as the transitions of system behaviors across spatial-temporal boundaries. In the next subsection, we discuss an example of self-organization related application—emulating the *spatial distribution patterns* of insects in *directed diffusion networking* for wireless sensor networks.

(10) We see a potential synergy between biologists who study biological robustness and computer scientists who study reliability and fault tolerance. The influences can be bidirectional.

7.2. Open Problems and Proposed Approaches.

From the above review and perspective, we propose the following four open problems, which we consider of significance in both theory and practice. We also outline our suggested solutions and implementation steps. We further researched them in the context of wireless sensor network. These results will be reported separately. We use the term *open problem* somewhat differently from its usage in mathematics, but similar to how Wagner (2005) proposed his open problems on bio-robustness.

Problem I — Unified Modeling Framework for Network Reliability and Survivability.

Problem description: Survivability can be conceptually defined as the system's capability to endure catastrophic failures, such as a network system under malicious intrusions, while still preserving mission critical functionalities. A survivable system generally has to be reliable, and an unreliable system generally is not survivable. There are no agreed upon modeling frameworks for network survivability (Krings 2008). Survivability modeling should be closely related to reliability modeling. However, the current reliability models do not accommodate survivability, since survivability often involves events such as malicious intrusions that are not predictable.

Proposed approaches: (1) *Deterministic approach*—Formulate survivability as an evolutionary game theory model and use the survival function as fitness function or *G*-function, which is equivalent to reliability. The *survivability* is then prescribed by the ESS. An ESS system is equivalent to Survivable Network Systems (SNS) — resistant to internal mutations and external perturbations or preserve mission critical functionalities under catastrophic failures such as caused by malicious attacks. (2) *Stochastic approach* — Treat unpredictable events that affect reliability and survivability as *censoring*. Censoring means incomplete observation in the failure time data (also known as survival or time-to-event data), and it can be left, right, or random censored or truncated. Survival analysis was advanced to study time-to-event random variables with censoring. Censoring is undesirable but hardly avoidable in reality; for example, the information recorded in the black box of an airplane up to a crash is a typical case of *right censoring* or truncation where the observation is terminated at a fixed time. Censoring is generally assumed unpredictable in survival analysis experiments; otherwise, the experiment design or operation is biased. For instance, in a clinical drug trial an experiment is biased, if individuals are removed (censored) predictably or systematically. To capture unpredictable malicious events in survivability we use the censoring mechanism of survival analysis for network survivability modeling. This proposed approach is further discussed in Ma and Krings (2008 a, b, c).

(3) *Mixed Approach*—This is the integration of the previous deterministic and stochastic approaches. A simple mixed model can be the adoption of the survivor function as the fitness function or *G*-function in the deterministic evolutionary game model (differential equation). A more general formulation can be the adoption of stochastic population theory such as *birth-death process* or *logistic process* (Hallam and Levin 1986, Lande and Engen (2003) as the models for describing evolutionary games. The current evolutionary game theory utilizes differential equations such as Logistic differential equations. Therefore, this extension will lead to significant complication. To some extent, this is the transformation from deterministic to stochastic of an evolutionary game model.

Problem II — Byzantine Generals Play Evolutionary Games.

Problem description: The mathematical theory of consensus in the presence of faults is based on agreement algorithms, which was introduced as the Byzantine general problem by Lamport (1982). The agreement algorithms also form one of the foundations of distributed computing. The resulting hybrid fault models have become essential for fault tolerant design (e.g., Azadmanesh and Kieckhafer 2000, Krings and Ma 2006). However, the hybrid fault models of agreement algorithms are essentially static and discrete. There is a lack of a modeling framework to study a population of sensors in a wireless sensor network, in which each node may fail at different times due to variable failure rates. In other words,

we need a framework that is able to integrate reliability measurement with hybrid faults models in heterogeneous and dynamic environments. This is necessary for studying the reliability and survivability of wireless sensor networks. The integration of hybrid fault models with traditional reliability models is of extreme significance both theoretically and practically. Currently, the two models are connected by simple assumption of constant fail rates or in many cases are disconnected. This makes it very difficult to incorporate hybrid fault model in reliability or survivability.

Proposed approaches: We propose the framework of "*Byzantine generals playing an evolutionary game*". This is essentially an extension of the previous proposed solution for **Problem-I**. In other words, the *generals* are represented as players of the evolutionary games, each general may have its own hazard function $\lambda(t)$, which can be represented as fitness function or G -function in the evolutionary game theory model. Another key extension is that various classes of faults such as symmetric vs. asymmetric, omission vs. transmissive, or benign vs. malicious can be treated as strategies of the players. Of course, the hazard function $\lambda(t)$ and survivor function from survival analysis can be converted from each other. This integration of evolutionary game theory model, hybrid faults model, and survival analysis provides a unified modeling framework to measure network reliability, survivability and fault tolerance with a single model system. For example, whether or not a *Byzantine general* can participate in the next round of vote depends on the general's fitness (or survivor function). In particular, the validity of an agreement algorithm is strongly linked to the assumptions about the thresholds of the number of nodes of specific fault types, i.e., thresholds in the next round of voting depends on the generals' fitness (or survivor function). Furthermore, since the system is continuous and dynamic, this implies that the integrated model system can predict real-time reliability and survivability for various possible faults modes (class of faults).

The practical significance of this extension is obvious. For example, the sensors in a space shuttle or an airplane may be modeled with the proposed scheme. These sensors needing to reach agreement can be treated as generals playing evolutionary games. Each sensor has its own survivor function (failure rate). The system should be able to predict real-time reliability and survivability (in ESS).

To consider topology in the proposed scheme, we can *move* the game onto a graph model — the *evolutionary games on graphs*. Players become the nodes on the graph and the links represent their interactions. This extension is certainly challenging, but the framework is already clear.

Problem III — Spatial Distribution Patterns, Power Law, Directed Diffusion Networks.

Problem description:

In wireless sensor networks, with hundreds of sensor nodes, even ignoring the mobility of the nodes, it is often infeasible to measure distances, and the distance-based design might be hard to validate. Intuitively, nodes' density control in wireless sensor network should be less difficult to implement than the distance-based approach.

Proposed Approaches: The spatial distribution patterns of insects (as briefly introduced in subsection 4.1) is considered as emergent property at the population level from self-organized aggregation or dispersion behaviors. The distribution mechanisms and corresponding mathematical models may offer very useful methodology for addressing the density control issues, since the models for spatial distribution patterns essentially measure the crowding or aggregation degree.

One example to demonstrate this approach is the application to the agent-based directed diffusion networking (Ma and Krings 2008d). Directed diffusion sensor networking was proposed by Intanagonwiwat et al. (2003) as an alternative to the IP-based end-to-end and the hop-by-hop ad-hoc routing architectures. This networking paradigm was apparently inspired by Alan Turing's (1952) seminar paper on the reaction-diffusion pattern formation model. Among numerous follow-up studies to the directed diffusion architecture, Malik and Shakshuki (2007) recently extended it by introducing mobile agents (MA) with the goal of increasing the operation efficiency. The resulting architecture is termed Agent-based Directed Diffusion (AbDD). We suggest two potential improvements to the AbDD: introducing spatial distribution modeling for measure and control sensor density, and optimizing the number of mobile agents (MA) employed based on the spatial distribution model. Both improvements are based on the spatial distribution pattern theory introduced in subsection 4.1 (Ma and Krings 2008d).

Problem IV— Byzantine Faults in DNA Code.

While the predominant focus of this article is to draw inspiration from bio-robustness for research of engineering fault tolerance, we indeed emphasize that the interactions between two fields should be bidirectional. For example, the field of fault tolerance, especially the agreement algorithm and reliability modeling may provide very useful mathematical models for modeling redundancy in molecular biology and system biology.

The current mathematical modeling approaches, such as system dynamics approach, for studying molecular and gene networks in *system biology* seem inadequate because they fail to address a fundamental problem in bio-redundancy (robustness), that is, the distributed synchronization (voting in terms of reaching agreement) among the redundant parts or subsystems. The *Byzantine general* based agreement algorithms (models) should be very promising to fill the current gap.

As a step of our advocacy of introducing fault tolerance theory to bio-robustness and system biology, we present a conjecture about DNA code redundancy based on *Byzantine general problem*. We would like to emphasize that our discussion is a pure conjecture at this stage.

Problem description:

The universal genetic code consists of 64 possible arrangements of the 4 RNA nucleotides, *U, C, A, and G*, in the form of a triplet, termed *codon*. There are *three* codons acting as *stop* codons that terminate the protein synthesis, and they do not map to any amino acids. The remaining 61 codons are mapped to 20 kinds of amino acids from which proteins are synthesized. Since there are only 20 amino acids, there are approximately three times of redundancy in the DNA coding. In other words, the same amino acids may correspond to multiple codons. For detailed description of the genetic code, one can refer to standard molecular biology monographs (e.g., Osawa 1995). As expected, there have been enormous amount of research on the genetic code from perspectives of nearly every scientific disciplines, chemical, physics, biology, and certainly mathematical modeling. Many of the studies indeed focused on the robustness of the genetic code.

Since there are only 20 amino acids and only 4 RNA nucleotides, the minimum codon length should be 3 to encode the 20 amino acid. This explains the triplet nature of genetic code, since doublet codon is not long enough. This also explains the possible number of codons, $4^3=64$. While the simple principle of parsimony (minimum length needed) explains the triplet nature and the 64 possible codons, it does not explain why there are three stop codons. Our questions are: (1) is there an alternative explanation to the parsimony principle, (2) why are there exactly 3 stop codons? We propose the following conjecture to answer the questions.

Conjecture: The universal genetic code follows Byzantine general agreement with *oral messages*.

We first briefly describe the Byzantine General Problem itself and we refer readers to Lamport (1982) for its details. Assume there are n generals who need to reach an agreement by vote (such as simple majority) to determine either attack or retreat (binary decision). Among the n generals, there are m traitors, and the remaining $n-m$ generals are loyal. All loyal generals must reach the agreement (same decision, either *attack* or *retreat*) even if the traitors send conflicting messages to different generals to prevent loyal generals from reaching the consensus. Lamport et al. (1982) proved that, if the generals communicate via *oral messages*, which is the least restrictive form of communication protocols in terms of the possibility that a traitor can induce maximal *confusion* (e.g., telling one general *attack* but *retreat* to another general) to the voting system, then the total number of generals needed to overcome m traitors' sabotage must satisfy, $n \geq 3m+1$. For

rigorous description of Byzantine general problem, one should refer to Lamport et al. (1982).

If we assume that genetic coding is evolved to maximally safe-guide the inheritance of the genes, and further assume that each of the 20 amino acid needs multiple agents to participate a vote and reach an *agreement*, which may simply means the validity of the participants in case some participants are mutated (traitors). To guarantee an agreement is reached, the number of total agents (codons) should be $3m+1=61$, with m possible traitors (mutants). Among the 64 possible codons, we have 3 *extra* agents who are not needed to participate in the voting. It might be that these 3 *redundant* agents are assigned the job of *code terminators* or the *stop codons*. Again, we stress that this is only a conjecture.

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