

Evolution of what? A network approach for the detection of evolutionary forces



Martin Hilbert^{a,*}, Poong Oh^b, Peter Monge^c

^a University of California, Davis, Department of Communication, Kerr Hall 369, Davis, CA 95616, United States

^b University of Pennsylvania, Annenberg School for Communication, 3620 Walnut Street, Philadelphia, PA 19104, United States

^c University of Southern California, Annenberg School of Communication, Watt Way, Los Angeles, CA 90007, United States

ARTICLE INFO

Article history:

Keywords:

Network evolution
Network dynamics
Natural selection
Network partition
Network theory

ABSTRACT

Structures of evolving populations are traditionally derived from traits of its members. An alternative approach uses network metrics to define groups that evolve jointly. This supposes that selection acts not only on who members are (i.e., traits) but also on to whom they are connected (i.e., interdependent relationships). This paper presents a method to meaningfully quantify differences in evolutionary forces over multiple levels of population taxonomies and tests almost 1000 multilevel partitions of 8 empirical networked populations evolving over time. It shows that multilevel network metrics as selection criteria identifies stronger evolutionary natural selection than trait based population taxonomies.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

“Strictly speaking, neither genes, nor cells, nor organisms, nor ideas evolve. Only populations can evolve” (Nowak, 2006, p. 14). The concept of a population implicitly implies a criterion to separate the whole into exclusive and exhaustive parts. In evolutionary theory, these parts are often referred to as *species* or ‘types’. Given the difference in growth rate among different types (i.e., the types’ *fitness*) some increase and others decrease in share, changing the population constitution in relative terms. As a result, the population evolves over time.

Biologists and other taxonomists have long used traits, characteristics, or properties of individuals to define types. For example, Darwin famously used beak length to classify finches. In biology, fields such as phylogenetics, cladistics, and systematics have taken different and sometimes contradictory approaches to the question of what constitutes those shared traits that define a type, including morphological, physiological, molecular, behavioral, ecological, and geographic characteristics. Much more in question are meaningful population definitions in the social sciences. For example, some scholars have suggested that it is important to differentiate among different organizational forms (Hannan and Freeman, 1977; Aldrich and Ruef, 2006), others to generate a taxonomy to classify human routines (Nelson and Winter, 1985),

and still others to classify social dynamics according to cultural norms and institutionalized habits (Boyd and Richerson, 2005). Unlike the beak length of finches, however, the traits of social populations—organizational forms, routines, cultures, etc.—are often not immediately quantifiable. Furthermore, there has been neither agreement nor systematic investigation about which traits should be considered. Indeed, many “official” taxonomies of social populations are rather the result of a political compromise in statistical committees than the consequence of a substantive discussion. For example, the United Nations Statistical Commission reports working on the basis of 870 different national classifications from 154 countries (UNSD, 2014). As a result, the evolving population of the global economy is classified into different co-evolving types not necessarily because of any meaningful argument, but rather because of a compromise among different classification systems.

It is important to note that the interpretation of evolutionary dynamics of a population heavily depends on the choice of traits for defining types, and more generally, on how to partition a population into distinctive parts. To illustrate, consider the evolution of the global export economy, where countries are classified into three types—the United States, BRIC (Brazil, Russia, India, and China), and the rest of the world (Fig. 1). The share of the BRIC countries has grown faster than the other two types, meaning that the BRIC type is fitter than the others (BRIC has tripled, while the other two have grown by a factor of 1.5). This has evolved the constitution of the global export economy. Further, it suggests the outstanding economic growth of the BRIC type.

* Corresponding author.

E-mail addresses: hilbert@ucdavis.edu (M. Hilbert), poong.oh@gmail.com (P. Oh), monge@usc.edu (P. Monge).

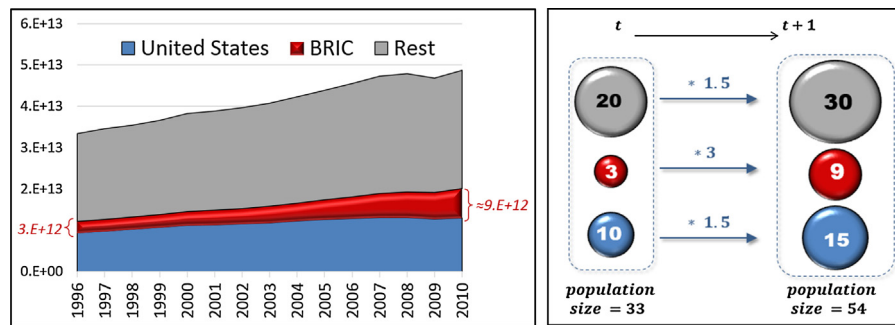


Fig. 1. Schematization of evolutionary selection among three types of the global export economy (a) historical data for U.S., BRIC (Brazil, Russia, India, and China), and Rest of the world (of a total of 118 countries); (b) schematization among three corresponding illustrative types (for more on the data, see Supporting Information).

What if the countries were classified in a different way? An easy answer is that the constitution would have changed differently and suggested a different interpretation, although the overall change of the global total remained the same. In short, the classification criteria that defines the *types* of any social population also defines the kinds of evolutionary dynamics that can be detected and interpreted. As such, the definition of types has traditionally been subject to “context, intellectual goal and subjective bias about what is ultimately meaningful” (Frank, 2012a, p. 230). Then, the question becomes: What classification criterion should be adopted, that is, how should a social population should be grouped in order to detect and analyze the evolutionary dynamics in meaningful ways?

Adding a new perspective to this longstanding debate, Monge et al. (2008) have suggested that it would be beneficial to switch focus from traits of types to their network properties as the basis for defining evolving populations: “Traditionally, evolutionary theorists and researchers have examined organizational populations that comprise organizational communities by focusing on their properties rather than on the networks that link them. However, a full understanding of the evolution of organizational communities requires insight into both organizations and their networks.” (p. 449). Studies have started to explore the evolutionary role of network structures in biology (e.g., Kossinets and Watts, 2006; Palla et al., 2007; Cantor et al., 2015) and in social evolution (e.g., Hausmann et al., 2011; Lee and Monge, 2011). This implies that evolutionary selection does not only favor or disfavor certain population types because of who they are, but also because of who they are with. In terms of Darwin’s finches, some finches, despite having the same beak length as others, could outbreed because of the relationships in their network. Similarly, could it be that some groups of countries achieve higher fitness in the context of global economy, not just because of their traits like the number of inhabitants or income level, but because of how they connect with others? This article asks if there are differences in the strength of evolutionary forces between when a population is classified according to some common trait and according to network metrics.

2. Research question

Increasingly, longitudinal network data have become more available, which has led to different research venues related to dynamics in network analysis (Stokman and Doreian, 1997, 2001; Snijders, 2001). Much attention has been paid to modelling the formation and/or resolution of network ties over time, such as in stochastic actor-oriented models (Snijders, 1996; Snijders et al., 2010), relational event frameworks (Butts, 2008) or economic incentives mechanisms (Jackson and Watts, 2002; Jackson, 2010). A major goal of these approaches is to estimate the likelihood of network ties among nodes, $p(x_{ij} = 1)$, given either the endogenous

or exogenous characteristics of the nodes, or both, and thereby, to identify significant characteristics that contribute to tie formation/resolution.

This study also works with longitudinal networks, but does not ask about tie formation. We explore the structure of networks to create groups of nodes that are defined by network links and then use these groups to define types. We then apply these networked types to the analysis of evolutionary dynamics in terms of changes in population fitness. We compare the network-based classification (i.e., to whom they are connected) with the traditional trait-based classification (i.e., who they are) and contrast differences in the involved evolutionary forces of change. In short, we do not ask how the network ties evolve, but—following the traditional literature of evolutionary dynamics—we ask about the fitness of the population and how different types contribute to it (given a certain network structure or node trait

Ever since the first versions of a “mathematical theory of natural and artificial selection” (Haldane, 1924; Haldane, 1934), the formal evolutionary analysis in biology, ecology, anthropology, economics and other social sciences has defined fitness in terms of the growth factor of the population. Biologists often refer to it as “the number of offsprings” or the “rate of reproduction”, while game theorists refer to it as a “payoff”, and economists as a “return on investment” (e.g., Nowak, 2006, pp. 14, 55). We follow this “growth factor” interpretation of fitness and use \bar{W} to denote the fitness of the entire population. It is defined as the number of offspring at the time $t + 1$ divided by the number of ancestors at time t , $\bar{W} = [\text{units}^{t+1} / \text{units}^t]$. For example, suppose that a population with 8 units at time t grows in size and comes to have 18 offspring units at time $t + 1$ (Fig. 2). Then, the overall fitness \bar{W} is equal to 2.25 (=18/8).

What drives the evolution of the population constitution are differences in type fitness. Types with superior relative fitness gain population share, and will dominate the population in the long run, while types with inferior fitness will be selected against and decline over time. The fitness of each type is denoted by w . For example, the type with the trait ‘white’ in Fig. 2a has a type fitness of 3 (growing from a total value of 4 to 12), while the shaded type has a fitness of 1.5 selection favored white and as a result the new population is two thirds white. That is, the group of white units multiplies by a growth factor of 3 on average, while the group of shaded units multiplies by an average fitness of 1.5. A type with a fitness of $w = 0$ would die out and go extinct.

Based on this common logic, the different versions of Fig. 2 visualize the basic idea behind this article. All four images show the same population, but the population is classified in four different ways. The Figure visualizes that different ways of classifying populations also changes the respective type fitness w . This is what leads to different strengths in the underlying evolutionary selection pressures. For example, the grouping according to ‘shape’ in Fig. 2b does not imply any selection, as it exhibits a uniformly distributed 50% – 50% population both before and after updating. Type

Download English Version:

<https://daneshyari.com/en/article/7538396>

Download Persian Version:

<https://daneshyari.com/article/7538396>

[Daneshyari.com](https://daneshyari.com)