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# Hyperlinked actors in the global knowledge communities and diffusion of innovation tools in nascent industrial field

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## ABSTRACT

Innovation is accomplished through collaborations of thousands of researchers embedded in a growing international knowledge community, where some hyperlinked actors can strongly impact the diffusion of innovation tools within the community. Few extant studies have empirically inspected the following issues which govern the influence of hyperlinked actors: (1) how the heterogeneity in their actor attributes regulates the volume of their influences; (2) how the nature of connectivity of these actors impacts the volume of their influences. Our current study intends to address this gap by examining the diffusion of innovation tools among life scientists around the world in a time span of 16 years, and we find that for hyperlinked scientists: (1) heavy usage and high variety of usage behaviors have stronger relationship with diffusion rate than light usage and low variety of usage; (2) light usage and high variety usage behaviors have stronger relationship with extent of diffusion than heavy usage and low variety usage; (3) international links have stronger relationship with both the rate and extent of diffusion than domestic links. Our work contributes to innovation research by providing a sharper understanding on the social contagion mechanism in innovation diffusion within global knowledge communities.

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## 1. Introduction

In diffusion studies, scholars (Goldenberg et al., 2009; Rogers and Kincaid, 1981; Valente, 1995) have long elucidated how hyperlinked people (i.e., people with a large number of social links with others) can strongly impact the diffusion of innovations (i.e., the rate and extent of the diffusion); and yet, this stream of literature has given little attention to how the heterogeneity in the actor attributes (i.e., the nonstructural features) – such as the different usage behaviors of these people – may govern the amount of such influences. Evidently, personal involvement with the product field, such as high or low usage volume of an existing adopter (Foxall, 1994) may result in different influences in diffusion (Ivengar et al., 2010). However, few extant studies have empirically examined how the heterogeneity in the actor attributes may lead to different impacts on diffusion, in particular in nascent industrial field.

Our current study responds to this call. Specifically, we examine the diffusion of innovation tools within a global knowledge community of life scientists, where some actors are hyperlinked with others in their coauthorship knowledge networks (Newman, 2001a,

2001b; Pandza et al., 2011). In exploring heterogeneity in the actor attributes of these hyperlinked actors, we first use the criteria of usage volumes to distinguish between hyperlinked actors of heavy usage and light usage. Next, we use the criteria of usage diversity to distinguish between hyperlinked actors who have applied an innovation tool in multiple scientific domains and those who apply a tool in only one domain (Shih and Venkatesh, 2004). We expect that the different usage patterns are linked to differences in their impacts on the rate and extent of the diffusion of innovation tools within the network of scientists.

Previous researches (e.g., Chang and Shih, 2005) suggest that network structure (Shin and Park, 2010) can be relevant in examining innovation diffusion. Therefore, in addition to the heterogeneity in the actor attributes, we also examine one important structural feature of the network of scientists—the nature of their connectivity. Specifically, a hyperlinked actor may be connected with other scientists within his or her home country only. Alternatively, this scientist can make wide international connections. Hence, we expect that the unique nature of each type of connectivity (Ganesh et al., 1997; Kumar and Krishnan, 2002) can also lead to different impacts on the rate and extent of the diffusion of innovation tools within the global knowledge communities.

The rest of the article is organized as follows. Section 2 provides a short overview of the research setting and methodology of the study.

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Then Section 3 moves on to give a review of the theoretical background and literatures and formulate the hypotheses put to test through the regressions. Section 4 describes the data, the variables and methodology. Next Section 5 presents the results and discusses the implications. Section 6 conducts additional analysis as robustness checks to our results. Finally Section 7 concludes and proposes future research directions.

## 2. Research setting and methodology

To better understand the nuanced roles of hyperlinked actors in the global knowledge communities during the diffusion of innovation tools, we study the adoption by life scientists of commercial tools to perform site directed mutagenesis technology (SDM), a form of genetic engineering. Since diffusion researchers stress the significance of institutional details for appropriate theoretical inference (e.g., Van den Bulte and Lilien, 2001), we discuss how our research setting and research methodology allows for an informative assessment of the role of hyperlinked actors in the diffusion of the particular innovation tool we examined.

There are two major advantages of this particular research setting. First, SDM technology is among the most important technologies in life science research. So central has SDM technology become to all of biochemistry and molecular biology that its inventor Michael Smith won the Nobel Prize in Chemistry in 1993. However, this technology is not easy to use. Therefore, many companies, such as Agilent Technologies, have started since 1988 providing commercial SDM tools to help scientists in their application of SDM technology. Second, the available data allows us to have full observation of the SDM commercial tools in the most important period of their development from 1988 to 2003. Specifically, 1988 is the year when the first commercial SDM commercial tool appeared, while 2003 is when the tools reached saturation in diffusion, and right censoring of diffusion is not an issue.

There are several possible ways to collect data on how scientists are connected, when they adopt an innovation tool, and how they have used it. The most obvious way is perhaps to ask scientists in the global scientific community to gather such detailed information. However, there are at least two major problems with such an approach. First, human memory is selective; asking people what they can recall about an innovation tool adoption and usage which happens several years ago may eventually lead to inaccurate and biased responses; thus, the collection data can be extremely noise prone and subjective. Second, such data are almost impossible to find, since asking each and every scientist from over 30 countries who have adopted SDM tools is nearly an impossible task, both technically and financially.

To avoid these problems, in this study, we use historical method (Golder, 2000; Tellis and Golder, 1996). Historical analysis involves carefully assembling, critically examining, and summarizing the records of the past and provides a powerful means of understanding innovation diffusion phenomena by recreating high-tech markets as they evolved (Golder, 2000; Golder and Tellis, 1993). The benefits of using the historical method include lower survival and self-report bias, ability to assess causality through longitudinal analysis, and new insights from a fresh reading of history (Golder, 2000; Tellis and Golder, 1996).

Specifically, the scientific papers published by each scientist allow us to have accurate observations on the adoption and usage behaviours (such as heavy vs. light usage; high variety vs. low variety of usage) as well as their co-authorship connections. Each time when a scientist adopts and uses an innovation tool, the

scientist describes the adoption and usage in detail in each paper she or he publishes. Therefore, we use content analysis to analyze these published papers following the guidelines described in Kassarian (1977) and Kolbe and Burnett (1991) to ensure the objectivity and reliability of this research.

The main strengths of using coauthor collaboration to observe social contagion among scientists are two-fold. First, collaborating with other scientists and publishing the results jointly represents a very intensive type of communication (Stokes and Hartley, 1989). Second, such intense interaction is often necessary for transferring mastery of complex research techniques (e.g., Kaiser, 2005) and is an important conduit for social influence about proper procedure (e.g., Latour and Woolgar, 1986). Yet, there is one potential drawback of using coauthor collaboration to describe diffusion of innovation tools. Extremely large research collaborations involving many co-authors may be an exception to this association between co-authorship and intense interaction. Therefore, the assumption that one of co-authors adopts an SDM tool then all other authors are also regarded to adopt and use that SDM tool may not be valid in such large research collaborations. However, this phenomenon is rare in biomedical research (Knorr Cetina, 1999; Newman, 2001a,2001b), and therefore not a concern in our study. Research teams in molecular biology are only of moderate size and nothing like the sometimes massive teams in high energy physics (Knorr Cetina, 1999; Newman, 2001a,2001b). The median number of authors per paper is 4 in our sample, and the 5–95% range is 1–9, so every author is likely to be involved in the decision to use commercial SDM tools or not. Also, even junior researchers like doctoral students and postdocs often have considerable freedom in defining the specific problems they pursue and modalities used in doing so (Knorr Cetina, 1999; Latour and Woolgar, 1986). Admittedly, since current scientific activity is segmented and differentiated even within a single paper, we exclude a small number of scientists specializing in computer modeling, assuming that they will never use an SDM tool for an experiment and so are not part of the “population at risk” for adopting a commercial SDM tool. Otherwise, for the majority of SDM community, they are biochemists and molecular biologists who learn and share new research techniques from each other.

In sum, we employ panel data to address the simultaneity and heterogeneity issues plaguing many social network research (King, 2007). Therefore, results from this study show a compelling causal effect of the hyperlinked actors on innovation diffusion.

## 3. Social networks, extent and rate of diffusion in knowledge communities

### 3.1. Social networks and innovation diffusion

Theories on innovation diffusion have examined the diffusion phenomenon on two important dimensions: the different rate of diffusion and the diverse extent to which the innovation diffuses. Early literatures tend to focus on the issue of rate at which the innovations diffuse (Rogers, 1995). However, the majority of these diffusion models essentially treats the market as homogeneous and largely ignores when and how the structure of social networks can influence the rate of an innovation’s diffusion. For example, the most important thread of diffusion models has been based on the framework developed by Bass (1969). In the Bass model, the social network into which an innovation diffuses is assumed to be fully connected and homogenous (Peres et al., 2010); and yet, the extensive recent research on social networks has revealed that they are neither homogenous nor fully connected (Kossinets and Watts, 2006).

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