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## The light and shade of knowledge recombination: Insights from a general-purpose technology

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### ABSTRACT

This research focuses on a special case of General Purpose Technology: Bioinformatics. It explores whether – and to what extent – Bioinformatics inventions build upon inherently diverse knowledge sources. Precisely, the role of scientific and technological diversity (measured with Shannon-Wiener diversity index) as driver of impactful Bioinformatics inventions (measured at different standard deviations of the forward citations distribution) is investigated. To this purpose, we carried out an analysis of both Non-Patent and Patent references cited into Bioinformatics patented inventions in the period 1976–2014. Results from a series of logistic regression models indicate that different degrees of impact require different degrees of knowledge diversity; at the same time, and importantly for practitioners and scholars, recombining diverse scientific and technological knowledge bases not always lead to impactful inventions. In other terms: the interplay of science and technology is not always the best option to get impactful inventions.

### 1. Introduction

Bioinformatics can be thought of as a special case of important innovation as it comes at the intersection of different General-Purpose Technologies (GPTs) (Foray et al., 2009) mainly generated in the two domains of biological sciences and information and communications technology (ICT) (Majumdar et al., 2009; Lewis et al., 2016). These two domains keep on feeding each other. On one side, ICT, such as computers, networks and robotics, are nowadays playing a central role in transforming the practices of biology (Chicurel, 2002; Pop and Salzberg, 2008); indeed, these advancements are changing what biologists do, how they work, the way they carry out experiments, the universe of objects they deal with, and the kind of knowledge they can generate. They also have reoriented biology towards large-scale investigations through advanced statistical methods and big data. This change marks a break with older kinds of biological work that mainly aimed at identifying and characterizing single and specific entities.

On the other side, having seen new horizons in their research, biologists are increasingly accumulating data from multiple sources (Cook et al., 2016). Therefore, a key challenge for Bioinformatics technologies becomes the creation and maintenance of sophisticated tools and techniques for the storage, analysis, and mapping of this biological information. Therefore, it is reasonable to conceive the

emergence and development of this peculiar type of GPT at the crossroads of science and technology. Such an intersection is made even clearer by referring to the only work (Hallam, 2013) that combines historical developments and ethnographic perspectives on Bioinformatics. Herein, the author depicts a complex relationship between science and technology that contributed - and still shape - the Bioinformatics industry.

However, an important gap remains in the current state of the art: large-scale investigations on the antecedents of the patenting activity in Bioinformatics are almost silent. Pioneering contributions (e.g., Park, 2012; Rasmussen, 2010; Patel, 2003; Saviotti et al., 2000) provide a valuable but still limited view of both the emergence and evolution of the industry, not shedding light on its scientific and technological knowledge recombination and diversity. Therefore, this research focuses on exploring the interplay of scientific and technological diversity in the emergence and developments of the Bioinformatics industry. Precisely, we draw upon GPT and knowledge recombination theory to get insights on whether – and to what extent – scientific and technological diversity contribute to increase the odds for a Bioinformatics invention to have impact and become a platform for other technological developments.

This paper makes a theoretical contribution towards understanding knowledge recombination mechanisms and antecedents for GPTs,

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accounting for the fact that their influence on the generation of impactful inventions is nuanced. Indeed, empirical support reveals that different degrees of impact require different degrees of knowledge diversity. At the same time - and importantly for both practitioners and scholars - recombining diverse scientific and technological knowledge bases not always lead to impactful inventions. Our study may be the first revealing that for GPTs to increase their scope, inventors have to wisely recombine scientific and technological prior art. It is also one of the few studies shedding light on the relationship between diversity and recombination of the antecedents and impact of a special case of GPT.

The remaining of the paper unfolds as follows: the next section discusses relevant theory and motivates the choice of diversity indicators. Then, a discussion about research setting is provided, followed by a methodological section. Finally, results and implications conclude the article.

## 2. Theoretical background and research questions

Since the seminal article on GPTs (Bresnahan and Trajtenberg, 1995), this concept is gaining momentum as it has further evolved (Carlaw and Lipsey, 2011; Bresnahan, 2010; David and Wright, 2006) being applied in knowledge domains such as economic history (e.g., Crafts, 2003), industrial organization (e.g., Lindmark, 2005), economic policy (e.g., Van Zon and Kronenberg, 2007), innovation studies (e.g., Andergassen et al., 2017), and translated into several models (e.g., Schultz and Joutz, 2010; Helpman, 1998). What all these approaches substantially share is the following key point: GPTs stand on technological solutions which, thanks to their high level of technological generality (Gambardella and Giarratana, 2013), may find applications in different markets and knowledge domains (Ardito et al., 2016). They are often considered as impactful innovations that pave the way to a swarm of incremental innovations transversally impacting several industries (Feldman and Yoon, 2012; Coccia, 2017). They are the engine of the economic (endogenous) growth (Ardito et al., 2016; Schaefer et al., 2014) and increased productivity in several contexts (Feldman and Yoon, 2012). Overall, GPTs give birth to technological discontinuities which, for their inherent general scope, bring with them a broad array of applications.

A definition which gathers together these perspectives is provided by Lipsey et al. (2005, p. 96): a GPT “is a single technology, recognizable as such over its whole lifetime that initially has much scope for improvement and eventually comes to be widely used, to have many uses, and to have many spillover effects.” Still Lipsey et al. (2005) distinguish between five classes of GPTs namely, materials, ICT, power sources, transportation equipment, and organizational forms.

But Bioinformatics escapes univocal identifications: it does not seem to fit exactly in one of the five classes only and this is why it is identified as a special case of GPT (Foray et al., 2009). To give the reader an idea of the wide spectrum Bioinformatics opens, it suffices to consider some examples of the ways it aids the experimental approaches: first, for bridging proteins, DNA, and RNA sequences, a number of databases have been built (e.g., NCBI's SNP database,<sup>1</sup> ERGO 2.0 genome browser<sup>2</sup>) for which BLAST<sup>3</sup> (Basic Local Alignment Search Tool) can be used; second, for searching for functional patterns in proteins and nucleic acids, the ExPASy<sup>4</sup> (Expert Protein Analysis Model), or the ENSEMBL<sup>5</sup> tool; finally, GPCRDB<sup>6</sup> is usually used for determining if there are known interactions among proteins. Bioinformatics technologies, applications, and solutions touch the following fields: microbial genome applications, molecular medicine, personalized medicine,

preventative medicine gene therapy, drug development, biotechnology, climate change studies, insect resistance, veterinary science, evolutionary studies.

Notwithstanding its revolutionary role, and although the existence of a rich theoretical literature on GPTs (Feldman and Yoon, 2012), sound empirical investigations on the antecedents of GPTs are scant (Thoma, 2009; Lo and Sutthiphisal, 2010). As recent literature advocates, inventions of such a kind may require a broad search for information and the recombination of different knowledge bases (Kaplan and Vakili, 2015). Recombination mechanisms are increasingly being associated with the accomplishment of impactful inventions (Fleming and Sorenson, 2004; Schilling and Green, 2011; Carnabuci and Operti, 2013; Appio et al., 2017): in fact, recent research shows it is going through a variety of cognitive-search processes (Acar and Van den Ende, 2016) that atypical (Uzzi et al., 2013) or unconventional combinations (Simonton, 1999) make concrete. The fact that there is a link between recombination of diverse knowledge bases and impact is increasingly recognized and empirical studies start to find systematic evidence on it (Keijl et al., 2016). Developing technologies drawing on diverse knowledge areas contribute to the creation of GPTs, since this enhances inventions' technological generality. Accordingly, we take the view of inventions as the outcome of a recombination process over technology and scientific landscapes (Fleming and Sorenson, 2001; Savino et al., 2015, Nakamura et al., 2015). This recombination of diverse knowledge bases, if not their interplay, may play an important role in spanning the boundaries of GPTs (Novelli, 2015). According to Petsas (2003), the inputs of GPTs are basically complementary and it makes relevant looking at whether – and to what extent – diversity is at the basis of the impact of the Bioinformatics industry.

To this purpose, we will have a deep look at the patents' prior art (Trajtenberg et al., 1997; Chen and Hicks, 2004; Callaert et al., 2006) as they reflect the recombined knowledge at the basis of inventions in the field of investigation. Prior art in patents can be distinguished in patent references - PRs, representing the cited technological contributions - and non-patent references - NPRs, representing the cited scientific contributions. Analyzing their inherent diversity may provide us with the opportunity to systematically examine the relationships between scientific and technological contributions at the basis of key inventions in the Bioinformatics industry.

Former contributions (Park, 2012; Rasmussen, 2010; Patel, 2003) focus on patents in Bioinformatics and provide valuable insights when it comes to consider the identification of the main technological classes and subclasses. However, they have two main limitations: first, they do not focus on the characteristics of prior art; second, they do not provide systematic evidence of the link between diversity in the prior art and GPT impact. Following our theorizing, two main research questions emerge:

*What is the link between knowledge recombination and the impact of Bioinformatics inventions? And, to what extent does diversity of scientific and technological knowledge bases matter?*

## 3. Characteristics of bioinformatics

### 3.1. Early days and growth of the industry

The history of Bioinformatics traces back to the late 1970s when Staden, in a series of studies published on *Nucleic Acids Research* (seminal paper published in 1977), outlined the basics for the development of computer programs allowing researchers to analyze DNA sequences. However, they could be used on large mainframe computers and run with non-standard programming languages; these two characteristics made adapting them to small (48 K) microcomputers tile consuming and not even economically affordable. These reasons, along with the need to facilitate dissemination, inspired the work of James M. Pustell (then Ostell) at the Kafatos Laboratory in Harvard's Department

<sup>1</sup> <https://www.ncbi.nlm.nih.gov/SNP/>

<sup>2</sup> <https://www.igenbio.com/>

<sup>3</sup> <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

<sup>4</sup> <http://www.expasy.org/>

<sup>5</sup> <http://www.ensembl.org/index.html>

<sup>6</sup> <http://gpcrdb.org/>

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