Open Platforms Without Software: A Study of Open Source Biology

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Abstract

Over the past decade, the crucial importance of platforms as a precursor to success in the Information and Communications Technologies (ICT) sector has been demonstrated to both researchers and managers of the impacted industries. The construct has also been used to refer to a more general case of two-sided markets, such as help wanted advertising or real estate sales (Armstrong, 2006; Eisenman, Parker & Van Alstyne, 2006), or for families of related products (Meyer, 1997). These platforms can differ dramatically in their degree of firm proprietary control (or converse, openness) by the platform sponsor.

Here I examine the application of platform theory to the life sciences and a cluster of related phenomena, loosely defined as "open source biology." Using interviews and textual data, I identify three categories of communities that produce open platforms, and code these against the prior platform research. From this, I suggest implication for our understanding of openness outside the ICT sector and for platform theory more generally.

Introduction

Innovation scholars have a natural interest in the nature of the technology-based firm. Such firms cooperate with external organizations to obtain, create and commercialize new scientific or technological knowledge to grow revenues and capabilities (Granstrand, 1998; Yli-Renko et al, 2001).

Two of the most economically significant categories of such firms are the biomedical and information-communications technologies (ICT) sectors. These two sectors accounted for $274 billion of the $566 billion of venture capital invested in U.S. companies from 1995-2013 (PricewaterhouseCoopers, 2014). More generally, the U.S. biomedical sector (medical devices, biotechnology- and chemistry-based pharmaceuticals) has more than $200 billion in annual sales (DeVol et al, 2011).

These two sectors have important similarities. Firms are dependent on technological change to create opportunities for new products, firms and industry segments (Mowery & Nelson, 1999). The most radical of innovations often require the innovator (or its partners) to educate the market, create distribution and support infrastructure to bring the technology to market (Teece, 1986, 2006). Innovations are adopted gradually by the market through a process of diffusion to those who seek novelty and have a high risk tolerance (Rogers, 1995). Finally, firms face an imperative to scale quickly, which for new firms requires access to large pools of external risk capital (Gompers & Lerner, 2011).

At the same time, the two sectors have crucial differences. While ICT is engineering based, the biomedical industries (particularly pharmaceuticals) are science-based and thus face greater technical and financial risks (Pisano, 2006). Meanwhile, ICT products are

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often systems products, integrating a variety of components and affected by a wide variety of patents that allow inventing-around complex patent thickets (Prencipe et al 2003, Somaya, 2003). Pharmaceutical (including biological) products are the quintessential point product, where a single patent protects a single compound and provides strong protection against competitors (Dutfield, 2009).

In addition, the ICT systems products are often made possible by building upon product platforms, which for 50 years have played a crucial role in enabling firms to introduce new products and families of products (Bresnahan & Greenstein, 1999). More recently, firms have cautiously leveraged existing and created new open source platforms (Dahlander & Magnusson, 2008; Economides & Katsamakas 2006; West & Gallagher, 2006). More generally, ICT firms that sponsor platforms wrestle with a delicate balance of openness, as they trade off their need to for proprietary control to appropriate profits against sharing control to attract usage and participation (Gabel, 1987; Grove, 1996; Eisenmann, Parker & Van Alstyne, 2009, 2011; West, 2003, 2007).

Until recently, shared platforms were unheard of in the pharmaceutical industry or the broader biomedical sector. The industry is marked by a tension between the norms of open science and the proprietary goals of strong intellectual property protection (Eisenberg & Nelson, 2002). However, more recently firms have created and joined open platforms for knowledge sharing, particularly for pre-competitive pharmaceutical research (Wagner et al, 2010).

This study examines communities and other projects organized around the idea of "open source biology". Among such communities are open biotechnology-related platforms that are modeled — directly or indirectly — on open ICT platforms, specifically those that apply one or more principles of open source software. The study examines the common antecedents of such efforts, their differing interpretations and then contrasts these with the accepted models of open source software platforms.

The paper begins with a review of theories of platforms as they apply to ICT and other contexts, including a discussion of open source software and other open platforms. It then discusses the preliminary findings from a field study of open source biology, and concludes with a discussion of the broader implications for open platforms and open source.

Platforms: ICT and Beyond

While there are differing definitions of platform, all explicitly or implicitly use the platform metaphor to refer to a common technology and/or infrastructure that enables the production of multiple goods or services. The cost of developing these platforms are paid by one or more sponsors (usually firms), who both control the direction of the platform and also many of the returns that accrue to it.

The platform concept is most commonly used in the ICT sector, where inter-organizational platforms facilitate the provision of third-party complements, and where platform sponsors routinely fight for the loyalty of customers and complementors. Originating with IBM in the 1960s, research on such platforms are today builds on three other theoretical constructs: standards competition, business ecosystems and the competitive dynamics of two-sided markets.

However, biomedical platforms can also benefit from others, intra-organizational examples of platforms. These include both incremental product architectures and knowledge management infrastructure, as discussed below.

Origins of ICT Platforms

The genesis of our understanding of ICT platforms came with research on standards architectures.[2] Initial research on standards competition identified the indirect positive network effects model where the value of a standard is mediated by the supply of third party complementary assets: the "hardware-software paradigm" of Katz and Shapiro (1985) posit a virtuous cycle where more hardware buyers bring a greater variety of software and thus more hardware buyers. Meanwhile, these complements create switching costs that make buyers less likely to change between standards (cf. Greenstein, 1993). Heavily influenced by the VCR case, this model tended to focus on a single standard and class of complement.

Subsequent researchers observed that complex ICT systems contained not a single standard, but multiple layers of standards arranged into a product architecture. For proprietary architectures, firms control the value of the architecture by adding or modifying standards layers, and by defining interfaces that enable the supply of various complementary assets and thus the benefits that accrue from such assets (Morris & Ferguson, 1993; West & Dedrick, 2000). During the 1990s, these architectures began to popularly be referred to as computer platforms — particularly in the discussion of competition between the leading personal computing platforms of the day: Wintel, Macintosh and (briefly) PS/2 (e.g. Borrus & Zysman, 1997; Grove, 1996; Wheelwright & Clark, 1992).

However, it came to Bresnahan & Greenstein (1999) to provide a definition of computing platforms. Tracing the three decades of computing platform strategies that began in 1964 with IBM's System/360, they identify computer platforms being created by an architecture of standardized hardware and software interfaces. Both platform sponsors and the creators of complementary components make sizable platform-specific investments in developing and selling related products (cf. Boudreau, 2000; Teece, 1986; Williamson. 1985). At the same time, adoption of a platform and its family of related complements (particularly by firms) typically required buyers to make platform-specific investments, and thus they looked for credible long-term platform commitments from sponsors and complementors (see also Hagiu, 2006).

Since then, researchers have extended studied firm strategies for other forms of computing platforms, notably software-only middleware layers that create new interfaces and complement opportunities (West & Dedrick, 2000). Examples have included Java (Egyedi, 2001), databases (Gawer 2009) and enterprise resource planning software such SAP (Ceccagnoli et al 2012). Overall, much of the flexibility of ICT platforms has come from the malleability of software.

The concept has also been shown to apply to communications equipment, such as local area networks (von Burg & Kenney, 2003), network routers (Gawer & Cusumano, 2002) and cellular telephony standards (Gawer & Cusumano, 2008). Finally, the fusion of computing and communications has brought perhaps the most publicly visible

[2] See Gallagher & West (2009) for a recent review of the standards literature.

platform competition in decades with the global rivalry between the iPhone and Android mobile computing platforms (Pon et al, 2014).

Platforms as a Two-Sided Ecosystem

Since Bresnahan & Greenstein (1999), the platform concept has been made more rich and explanatory by linking it to two related concepts: business ecosystems and two-sided networks.

The reliance of platforms sponsors on third parties to provide complements mean that they have a direct stake in the success of these third parties. The metaphor of the business ecosystem capture this interdependence: the success of the member firms both contribute to and depend on the health of the ecosystem, although (as in environmental ecosystems) these ecosystems are marked by constant competition for overall leadership and dominance of specific niches (Iansiti & Levien, 2004a; Moore, 1993). The success of the ecosystems in jointly creating value through innovation depends not just on the ecosystem leader, but also the efforts of the member firms in overcoming their own technical challenges (Adner & Kapoor, 2010; Iansiti & Levien, 2004b). Thus, firms that sponsor platforms have a strong incentive to maintain a healthy ecosystem by focusing on the success of complementors (Gawer, 2010; Gawer & Cusumano, 2002).

Secondly, the need for the platform sponsor to court both buyers and complementors corresponds to the two-sided network concept of Parker & Van Alstyne (2000), which more recently has been referred to as the multi-sided market (Eisenmann et al, 2006; Evans, Hagiu and Schmalensee, 2006; Rochet & Tirole 2003, 2006).

Intra-organizational Platforms

The platform concept has been used more broadly to refer to concepts beyond the core+complement, multi-sided market described above. At times it seems like the concept has been stretched to its limit (Langlois, 2012). But here we highlight two usages of platform that don't involve external supplier of complements ("software"):

- *Product Families.* Perhaps the oldest definition of the platform concept is as a family of products, in which the manufacturer creates a core product architecture, and then modifies and adds elements around that architecture (Wheelwright & Clark 1992). This conception has been used to explain product strategies in industries of complex assembled goods such as automobiles and construction equipment (Meyer, 1997; Sawhney. 1998).
- *Knowledge Platforms.* The other distinct definition is the idea of internal platforms for knowledge management. Consistent with the knowledge-based view of the firm (Kogut & Zander, 1992), Nonaka and Konno (1998) describe how successful innovators manage internal knowledge as an infrastructure that enables future innovation.

These alternate models can be linked to the more dominant view of platforms in two ways. First, a platform is an architecture for products where some parts stay the same and some change (Baldwin & Woodward, 2009) — although (in the knowledge platform case) those parts may not be tangible artifacts but intangible knowledge. Second, platforms enable the modular division of labor between disparate actors (cf. Baldwin 2008; Langlois, 2012) — in these cases an internal division, while in the aforementioned cases the role of third-party complementors are frontmost.

Degrees of Platform Control and Openness

For a "proprietary" or "closed" platform, a single sponsoring firm controls the platform and its standardized interfaces to assure its own value capture, while sharing enough of the returns from the ecosystem to attract third-party complements (Gawer & Cusumano, 2002; West, 2003). An "open" platform is one where control (including defining the interfaces) is shared across a self-governing community; with the assurance of greater access to the benefits of the ecosystem, such shared control is often more successful in attracting external participation and complement production (West & O'Mahony, 2008; Baldwin & Woodard, 2009). A common example of the latter is created through cooperative standardizations, a pre-competitive collaboration between multiple organizations seeking to enable proprietary offerings (Gabel, 1987; Simcoe, 2012).

However, in the real world, there are a wide range of intermediate points between these two extremes, as measured by the degree to which one or more central firms can control access to use and benefit from platform innovation — which in turn determines the cost paid by customers and complementors to use the platform (West, 2003, 2007). For example, some platforms are tightly controlled by multiple sponsors, with the proprietary benefits accruing to multiple firms (Eisenmann et al 2009).

Open Source Platforms

A distinct and oft-studied category of open platforms is that of platforms associated with the cooperation production of open source software (OSS) through online communities[3]. These communities are similar to standardization efforts in that they involved multi-party cooperation and thus an inherent limitation to proprietary control (cf. Leiponen, 2008; Simcoe, 2012). However, participants in standards communities pool knowledge for the shared production of specifications used by participants to create their own implementations — while open source communities produced a shared implementation (through software source code) that provides a common platform available to all.

What we today call open source software has its origins in the 1980s and 1990s with non-commercial software development efforts, including by an individual hobbyist (Linux), a funded university research project (BSD) and one (GNU) where a university employee sought to appeal to hobbyists (West, 2003). There are two distinct variants, with "free software" used to refer to software that will be free from proprietary control in perpetuity, and the broader "open source" category referring either to software that may have commercial implications or both categories (cf. Stewart & Gosain, 2006; West & Gallagher, 2006).

Such software communities are characterized by (and can vary on) three dimensions: intellectual property, collaborative production and shared governance (West & O'Mahony, 2008). The best known attribute is the IP model, which proscribes a specific form of software license that guarantees that the software and its source code are freely available and distributed to all parties, and that allows the creation of derivative works (Rosen, 2004). Like other nonproprietary information goods, open source software has

[3] For a recent reviews of the OSS literature, see Aksulu and Wade (2010), Crowston et al (2012) and von Krogh et al (2012)

attributes of a pure public good in that possession by one party does not diminish the value held by other parties (Zeitlyn, 2003). This form of openness also means that the implementations tend to be free, with firms generating revenues by offering proprietary software and services that builds on the open platform and firms selectively allocating their efforts between open and proprietary technologies (Dahlander & Magnusson, 2008; Watson, 2008; West & Gallagher, 2006).

A second attribute is a decentralized collaborative production model, likened to a "bazaar", in which a large number of participants donate their labor to create the shared good (Dafermos, 2001; West, 2003; Zeitlyn, 2003?). By crowdsourcing both the production and quality control of this good, there is a belief by open source participants that this produces code quality that is superior to proprietary software (cf. Stewart & Gosain, 2006).[4] Motivating, integrating and organizing such community production is key to the success of this model (Crowston et al 2007 von Krogh et al 2003;)

Finally, OSS communities are associated with a distinctive form of governance, in which the community is independent of any organizational control, is permeable to new contributors and embraces a pluralistic decision process (O'Mahony 2003, 2005; West & O'Mahony, 2008).

Firms have experimented with variants on these OSS models. This has included partly open strategies in which the IP, governance or other attributes are modified by the firm to assure proprietary advantage (Shah, 2006; West, 2003; West & O'Mahony, 2008). When the open source model is used outside information goods, a fourth concern is that of replicability, i.e. the ability of community participants to produce or replicate the goods that are the subject of the community such as a 3D printer or a car (Balka et al 2010).

Research Design

This study explores the use of open source processes related to the biotechnology. It is driven by two related questions. First, what has prompted and enabled the recent application of such processes in such industries? Second, what do the similarities and differences between the ICT and biotechnology models tell us about the generalizability of the open source model and open platforms more generally?

Context

The academic breakthroughs in molecular biology and biotechnology of the 1970s and 1980s were first brought to market through new companies (such as Amgen and Genentech) that produced large-molecule pharmaceuticals (Robbins-Roth, 2000). As with other pharmaceutical companies, the high failure rare and large costs for R&D and clinical trials depended on the temporary monopoly provided by a patent on the therapeutic compound (Pisano, 2006).

On the one hand, these biotech pharmaceutical companies depended heavily on the research created and licensed from university researchers (Macmillan et al, 2000).

[4] The recently discovered security vulnerabilities of the ubiquitous OpenSSL internet security middleware — developed as open source by one full-time employee (Stokel-Walker, 2014) — suggest that the quality effects are driven by the number of participants rather than the open process *per se.*

However, the complete dependence of these companies on proprietary IP business models — and the desire by universities to execute royalty-bearing licenses — has meant that the profit motive has come into direct conflict with the norms of dissemination and openness associated with the academic process of open science (Fabrizio, 2006; Murray et al, 2000; Nelson, 2001). Thus, it was not surprising to discover that much of the impetus for open source biology has come from university researchers interested in creating (or restoring) processes of open science.

Data

Because of the limited research on the nature of the open source biology phenomenon, we chose a qualitative exploratory case study approach; such an approach offers the richness of detail and answers "how and "why" questions. The primary data included 26 interviews with 23 individuals, participant observation in three conferences related to open source biology, and multiple visits to two hackerspaces. It also included written accounts, both primary data (such as published interviews, position papers and other articles written by open source biology participants) and secondary data such as news accounts and web sites.

Unlike open source software after 1998, there is no central definition of open source biology (as in the Open Source Definition), no central nonprofit (such as the Open Source Initiative or the Free Software Foundation), no central repository such as SourceForge. As such we fell back on tried-and-true methods of 21st century exploratory research: searches of the World Wide Web, of published articles and research, and a snowball sample from one informant to the next. For historical trends, we also consulted Lexis-Nexis.

In terms of published articles, the term seemed most often used in *Wired* magazine and the Xconomy online website. The exact phrase "open source biology" appears more than 13,000 times in Google, while other combinations such as "DIY bio" or "biohacking" appeared 10,000s or millions of times.

We were confronted with a welter of efforts seeking to apply the "open source" principles (and mantra) to issues of applied life sciences. After our preliminary research and initial interviews, we decided to focus on those activities that related to biotechnology, consistent with the OECD (2001) definition as "the application of science and technology to living organisms … to alter living or non-living materials for the production of knowledge, goods and services."

Drivers of Open Source Biology

Our research identified different interpretations, motivations and implementation of the open source concept for biomedical products. However, respondents repeatedly identified three key drivers of this trend: a reaction against an increasing emphasis on proprietary IP models (notably biotechnology patents), the exemplar of open source processes in software production, and the rapidly declining costs of biotechnology research and production.

Countering Proprietary IP Policies

When asked about open source biology, many of the respondents emphasized the importance of the efforts as a response to an increasingly proprietary approach to intellectual property.

In their view, biological innovation had strayed from its roots in crop breeding of the 19th and early 20th century. A few made an explicit contrast between earlier and current agricultural research practices, such as biological and contractual restrictions on seed reuse imposed by Monsanto and other companies.

However, every respondent objecting to proprietary IP approaches referenced the current university-industry biotechnology model, in which university research is patented, licensed and sold (often on an exclusive basis) by a for profit-entity. In this telling, the financial success of Cohen-Boyer combined with the Bayh-Dole Act led to a rise of technology transfer offices and university patenting that pushed away previous open norms of science; this interpretation was certainly consistent with academic research summarizing trends of the past three decades in university research, particularly in the life sciences (e.g., Mowery et al, 2001; Nelson, 2001).

In response, promoters of open source biology sought to forestall patent oligopolies to allow greater freedom to innovate by some combination of academic researchers, existing firms, new entrants, or enthusiastic amateurs. Their solutions included a combination of identifying existing IP, weakening or working around those IP rights, and creating new IP unencumbered by proprietary restrictions.

Impact of the Open Source Exemplar

Many of the founders of open source biology efforts were aware of the success of open source software and articulated a desire to explicitly emulate one or more aspects of its success.

In particular, they expressed an interest in two specific attributes of the open source model:

- The crowdsourced community production model
- The IP model that enables open sharing and reuse of designs.

Increasing Democratization of Molecular Biology

The final factor enabling efforts to create open source biology has been the rapidly declining prices of conducting biotechnology research and production.

Among the components of such cost declines:

- the increasing availability of public genomic data such as from the NCBI of the US National Institutes of Health or the Sequence Read Archive hosted by Google;
- aided by Moore's Law, the rapidly declining cost of genomic sequencing, falling from $1+ billion to less than $1,000 in about 15 years (Hayden, 2014);
- from the same declining costs of computing, an increasing shift away from expensive wet labs towards virtual drug discovery (Augen, 2001);
- the tools of synthetic biology (and systems biology) — intentionally modeled on computer engineering — which separate the design of new biological organisms from their production (Endy, 2005; Purnick & Weiss, 2009); and
- new and future methods of production, whether through contract manufacturing, short-run production labs, or desktop printing on new organisms. .

These trends combine to enable for biomedical products the sort of "democratizing innovation" trends observed by von Hippel in information goods and a handful of consumer goods:

> When I say that innovation is being democratized, I mean that users of products and services—both firms and individual consumers—are increasingly able to innovate for themselves (von Hippel, 2005: 1).

> Users' ability to innovate is improving radically and rapidly as a result of the steadily improving quality of computer software and hardware, improved access to easy-to-use tools and components for innovation, and access to a steadily richer innovation commons. Today, user firms and even individual hobbyists have access to sophisticated programming tools for software and sophisticated CAD design tools for hardware and electronics. These information-based tools can be run on a personal computer, and they are rapidly coming down in price. (von Hippel, 2005: 13).

The one difference is that von Hippel emphasizes innovation by users meeting their own needs, whereas (as discussed below) the role of users in open source biology thus far appears limited to providing information to innovators.

Three Archetypes of Communities

From our research, we identified three archetypes of communities (or projects) organized to apply open source principles to biology: an IP commons, patient registry for crowdsourcing patient data and a "hacker" oriented community (Table 2). These communities differed in the nature of their participants, their goals, aspects of open source that they emulate, and their stage in the biomedical value chain (Figure 1). In some ways, these might be considered distinct movements, just as the hackers of free software constituted a distinct movement from firms involved in open source. At the same time, they have overlapping goals of encouraging research and reducing the entry barriers for new therapies.

Based a very preliminary analysis our primary and secondary data, here we discuss these three archetypes, their origins, motives and activities.

IP Commons

The concept of an IP commons is intended to share IP (and create new shared IP) to enable life science research. Its IP models are often modeled on licensing and sharing models developed for open source software, as well as related efforts such as Creative Commons or Science Commons. It is oriented towards the concerns of PhD-holding academic and industry scientists, with an emphasis towards early stage, basic research. Examples of such efforts are given by Table 3.

One of the earliest projects to adapt open source to the life sciences came from Cambia (Center for the Application of Molecular Biology to International Agriculture), an Australian nonprofit founded in 1994 to create public access agricultural biotechnology that was profiled in an early *Wired* article (Goetz 2003) about "open source" in the context of biology.

Lexis-Nexis reports that the earliest occurrences of the phrase "open source biology" refer to an IP commons with a 2001 article on the Molecular Sciences Institute near UC Berkeley:

> [W]ith so much information yet to be uncovered, the two dozen or so scientists at the Molecular Sciences Institute cannot do it alone.
>
> For this reason, along with a belief in the "free distribution of biological information and methods in the service of human kind," the Institute has dedicated itself to practicing what it calls "open source" biology.
>
> "We give away everything," [research fellow Drew] Endy said. "We very much are in support of a socially responsible and open biology going forward."
>
> "I think that's essential," he continued. "Models like this just need to be made available to everyone who's interested in them. We can't afford to go down an alternative path with that one." (Weege 2001)

A third early effort came with the BioBricks Foundation, launched at MIT in 2006, which sought to build a library of synthetic biology components through submissions to its annual International Genetically Engineered Machine (iGEM) conference. In many ways, the BioBricks components were an analog to the software libraries of the Free Software Foundation, formed as an MIT spinoff more than 20 years earlier.

The IP commons demonstrates two of the attributes of open platforms, specifically the open source software. One is the IP openness of open source licenses. The other is the use of a community governance model — similar both to open source software (O'Mahony, 2007) and standardization consortia (Simcoe, 2012). They also feature a shared knowledge platform — in fact, the creation of such a platform is the explicit goal of several of these consortia.

Hackerspace

Other efforts — often termed "DIY bio" or "garage biology" — seek to empower amateur (or beginning) biohackers to conduct low cost experiments in the life sciences (Table 4). In many ways, this is most similar to the early (pre-corporate) days of the free software and open source movements, in which individuals (such as Linus Torvalds) exploited the suddenly availability of desktop computing power to collaboratively develop their own software.

Although inspired by open source communities, in many way the do-it-yourself orientation of these hacker-spaces resemble less the cooperative OSS efforts to build a shared information good (such as the Linux operating system). Instead, they more resemble the earliest do-it-yourself computer hackers 35 years earlier, the amateur inventors of Silicon Valley's Homebrew Computer Club, comparing experiments and discussing their own individual projects.

The DIY bio efforts parallel those of the DIY PC generation in another way, in providing a platform for individual inventors and their entrepreneurial initiatives.[5] Some of the hackerspaces explicitly support entrepreneurial efforts by combining shared lab space with a business incubator, sometimes linked to crowdsourced funding of new firms.

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[5] The Homebrew Computer Club is best known for spawning Silicon Valley's earliest personal computer manufacturers, including Apple Computer, Morrow Design and Osborne Computer Company (Freiberger & Swaine, 1984; Levy, 2001).

When contrasted to the open platforms, they feature IP openness, community governance of open source software. Many of the hackerspaces also seek to create a shared knowledge platform that allows members to develop entrepreneurial projects.

Crowdsourced Patient Data

If the first two communities seek to empower research scientists or would-be entrepreneurs, the third category is organized for (and often by) the nominal beneficiaries of biomedical research: the patients. It seeks to turn their one key asset — control of their own medical data — to catalyze research that will address their medical concerns. These may be organized informally by patients, or through existing patient registries established by disease-specific[6] nonprofit organizations (Table 5).

On the one hand, the desired output of such communities parallels that of the IP commons: compiling large databases that can be freely shared with researchers seeking to develop a cure. On the other hand, the leadership of all but the largest communities — often led by parents of patients with rare inherited disorders — reflect more the amateur ethos of the biohackers than the professional norms and motives of the professional IP commons scientists.

There are two distinct types of patient registries: firm controlled and non-profit controlled. In both cases the sponsoring organization provides the necessary resources, but in the former case it comes from firm profits and in the latter case it comes from donations to the nonprofit to support its mission. They also differ in terms of the access to the knowledge in the registry — whether to benefit one firm (usually with an existing product to diagnose or treat that disease) or a broader range of academic or industry researchers.

These registries demonstrate the two-sided markets seen in ICT platforms. In this case, one class of stakeholder is the patient, and the other is the researcher or health professional (or their respective employers). While there are not complements, there is the mutual dependence found in other forms of business ecosystems: researcher need patients to participate and vice versa.

As with open source, these patient registries also utilize a crowdsourced community production model.

Discussion

This study reviewed the attributes of open platforms and then sought to apply them to an exploratory study of open platforms in the life sciences, specifically those cooperative efforts that fall under the rubric of "open source biology".

It identified three broad classes (or archetypes) of open source biology communities: an IP commons, a hackerspace and a crowdsourced patient registry. These three archetypes were classified using the seven attributes of open platforms identified in the earlier platform literature (Table 6).

In particular:

- Pre-competitive collaboration for knowledge in the IP common resembles the pre-competitive cooperation in standardization (cf. Simcoe, 2012). In fact,

[6] Not all efforts are limited to a single disease, but instead may be grouped to address a category of related conditions (such as muscular dystrophy or heart diseases.)

some of these are directly modeled on standardization consortia (Wagner et al, 2010) and also the industry-funded open source consortia such as Eclipse (cf. West & Gallagher 2006).

- The IP commons and crowdsourced patient data resemble the intra-organizational knowledge platforms of Nonaka and Konno (1998), except that they span organizational boundaries.
- Crowdsource patient registries and hackerspaces resemble the user innovation of early open source (cf. von Krogh et al, 2003). They also have the community production model.

Overall, the communities demonstrated pre-competitive collaboration for shared knowledge (like standardization) but not shared implementations. This is an inherent problem of extending openness for information goods into tangible goods, as noted by Balka and her colleagues (2010).

This study of open source biology did not identify a complements ("software") element to these open platforms. Pharmaceutical products don't have complementary goods in the sense of the Katz & Shapiro (1985) or the hardware-software model (applications, videogames etc.), where the platform sponsor seeks to maximize the number of suppliers of such complements.[7]]. As such, there are not the positive network effects that accrue based on a greater variety of complementary assets. Similarly, the ecosystem model of third-party suppliers was not evident, although the two-sided market of the patient registries demonstrated elements of the ecosystem dynamics.

Finally, consistent with the stated goals, those promoting open source biology embraced many of the same IP policy and ethical positions of open source software. The push for openness by hobbyists (hackers) and academics (university employees) is consistent with the pattern of open source software. Similarly, the limited corporate support for pre-competitive openness in the IP consortia is consistent with the corporate-sponsored open source model by which firms share IP to reduce costs in a model that West & Gallagher (2006) term "pooled R&D."

With the advent of open source software, firms developed strategies for commercializing the open IP. However, for open source biology, the commercializaiton path (if any) is not yet obvious. For corporations sponsoring the IP commons, the lead time for pharmaceutical products in much longer than that for ICT products, so it's possible that these results have not yet been seen. As for the hackerspace, there have yet to be any successes akin to the hacker-founded personal computer startups of the 1970s or the open source startups of the late 1990s.

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[7] Pharmaceutical products have complements such as manufacturing, support and distribution — other complements in the sense of Teece (1986). Some also combine a therapeutic compound with a diagnostic for testing for that condition, or specialized delivery hardware (such as drug-eluding stents).

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Tables and Figures

Research Stream	Key Insight	Examples
Standards	Network effects from the supply of complements	Katz & Shapiro 1985; Teece 1986
	Switching costs	Greenstein 1993
Ecosystems	Interdependence of stakeholders	Iansiti & Levien 2004a,2004b; Ander & Kapoor 2010
Multi-sided markets	Identifying and meeting needs of complementors, buyers or other stakeholders	Parker & Van Alstyne 2000; Rochet & Tirole 2003, 2006
Open source	Guarantee of IP openness	West, 2003; Rosen 2004
	Community production	von Krogh et al 2003; Crowston et al 2007
	Community governance	O'Mahony 2003, 2005; West & O'Mahony 2008
Intra-organizational platforms	Product Families	Wheelwright & Clark 1992; Meyer 1997
	Knowledge Platforms	Nonaka and Konno 1998

Table 1: Theoretical antecedents of open platforms

Archetype	Participants	Main Focus	Desired Outcome	Examples
IP commons	Scientists and other professionals	IP rights	Ability of many players to practice cumulative innovation	Cambia BiOS, SageBase,
Patient Registry	Patients and patient advocates	User empowerment	Leverage self-reported user data to accelerate cures	PatientsLikeMe, Pompe Registry
Hackerspace	Individuals and entrepreneurs	Amateur ("hacker") science	Enable experimentation by individual hackers	Biocurious, DIY Bio,

Table 2: Three archetypes of open source biology collaborations

Founding Date	Organization/ Community	Location	Initial Sponsor	Financial Support	Focus
2006	BioBricks Foundation	Cambridge, Mass	MIT		Synthetic biology building blocks
2006	Biomarkers Consortium	Bethesda, MD		7 major pharma companies and 1 trade association	
1994	Cambia	Canberra†			Agricultural biotech
2009	Coalition Against Major Diseases	Phoenix		9 major pharma companies	
2007	Infectious Disease Research Institute	Seattle		7 major pharma companies	
2009	Innovative Medicines Initiative	Brussels		European trade association and the EU	
1996	Molecular Sciences Institute	Berkeley		US government agencies, corporations, foundations	Synthetic biology
2009	Pistoia Alliance	Boston		9 major pharma companies	
2009	Sage Bionetworks	Seattle†	Merck		Computational biology
2004	Structural Genomics Consortium	Toronto†		4 major pharma companies	

† Also has other locations

Table 3: Efforts to build IP commons in biology

Hacker Space	City	Founding Date
BOSSLab	Boston	
LA Biohackers	Los Angeles	2010
Genspace	New York City	2009
La Pallaise	Paris	
portLAB	Portland	2013
Bio, Tech and Beyond	San Diego	2013
Biocurious	San Francisco Bay Area	2009
Hivebio	Seattle	
Biospace	Vancouver	

Table 4: Examples of biology hacker spaces

Condition	Disease Registry Name	Sponsor	Collaborator	Start Date
Acid Maltase Deficiency	Pompe Registry	Genzyme		2006
Amyotrophic Lateral Sclerosis	National Registry of Veterans With Amyotrophic Lateral Sclerosis	US Department of Veteran Affairs	ALS Association	2003
	PatientsLikeMe	*Started by a patient family*	Numerous academic and industry partners	2004
	Pseudobulbar Affect Registry Series	Avanir Pharmaceuticals		2011
	Amyotrophic Lateral Sclerosis Web Based Patient Care Database	Forbes Norris MDA/ALS Research Center	Muscular Dystrophy Association	2006
Becker's Muscular Dystrophy	Pediatric Cardiomyopathy Registry	National Heart, Lung and Blood Institute		1994
Bethlem Myopathy	Congenital Muscle Disease International Registry (CMDIR)	Many countries		2008
Central Core Disease	Congenital Muscle Disease International Registry (CMDIR)	Many countries		2008
Cystic Fibrosis	Cystic Fibrosis Patient Registry	Cystic Fibrosis Foundation		1970s
Deuchene Muscular Dystrophy	The United Dystrophinopathy Project	University of Utah		
	Deuchene Connect Patient Registry	Deuchene Connect		2007
Myotonic Dystrophy	Myotubular Trust Patient Registry	Myotubular Trust		2013
Spinal and bulbar muscular atrophy	Kennedy's Disease Association	Kennedy's Disease Association		2000

Table 5: Select crowdsourced patient registries

Archetype	Complements	Ecosystems	Two-Sided Market	IP Openness	Community Production	Community Governance	Knowledge Platform
IP commons				X		X	X
Hackerspace					X	X	X
Patient Registry		X	X		X		

Table 6: Platform attributes across the three archetypes

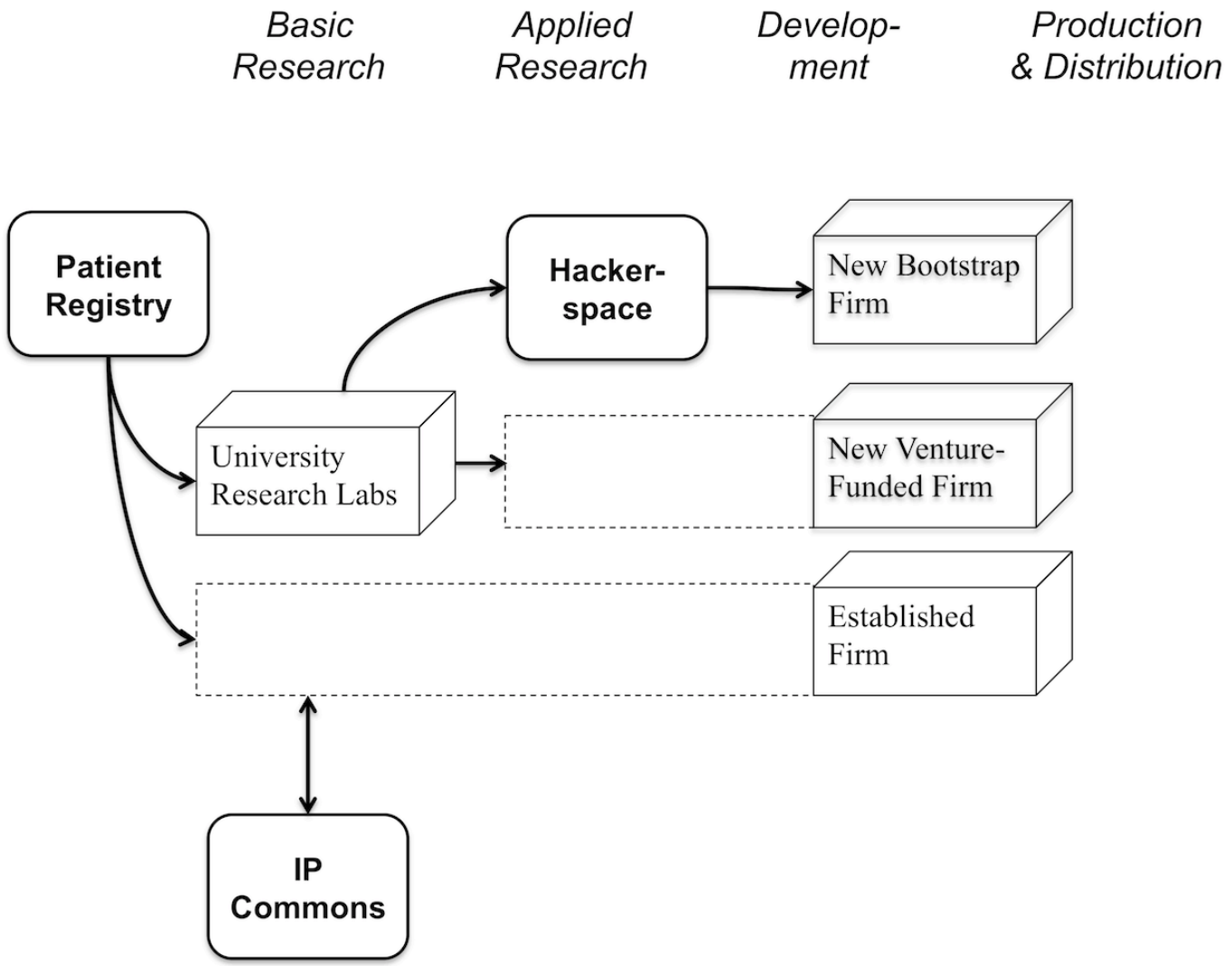

Figure 1: Role of each archetype in industry value chain