Microbial Commons:
Governing Complex Knowledge Assets

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Abstract

The Human Genome Project has advanced the view that biological information operates on multiple hierarchical levels and is processed in complex networks. A new hierarchical framework for biological knowledge is being constructed to understand the relationships between the various levels of biological information. The creation and application of this knowledge occur through cooperative or competitive interactions, often reflecting the perceived value of the knowledge. The public or private value of the knowledge, both for itself and for potential applications, can be determined through an understanding of the classification and characterization of this knowledge.

The transformation of knowledge from a purely public good to a quasi-private good has highlighted the need for balance between incentives for the market provision of scientific and technological knowledge by an innovator and incentives for the market provision of incremental knowledge by a follow-on developer. It has been suggested that a patent system developed for a discrete model of innovation may no longer be optimal for an information-based, cumulative model of innovation. Consequently, it is necessary to reanalyze models of intellectual property protection and knowledge dissemination strategies. Under certain conditions, the biotech commons is an efficient institution that can preserve downstream opportunities for multiple researchers fairly and efficiently.

In this summary paper, I discuss governance issues associated with the biotech commons. Based on this understanding, I extend the discussion to the anticipated governance issues associated with a microbial-specific commons. Of significance is the continued focus on the impact of knowledge structures on governance strategies. Case studies are included to provide a context for analyzing the strategies being used to manage microbial-based data, materials, as well as downstream knowledge assets critical to the development of energy and environment based technologies.

1.0 Introduction: Changing Paradigm and Knowledge Structures

With the completion of the Human Genome Project, systems biology or the information paradigm has emerged. The Human Genome Project has advanced the view that biological information operates on multiple hierarchical levels and is processed in complex networks. A new hierarchical framework for biological knowledge is being constructed to understand the relationships between the various levels of biological information. In the systems paradigm, the focus of intellectual property rights will also gradually shift to the patenting of information (Hood, 2000). This information perspective must incorporate an understanding of the impact of enclosing hierarchical and complementary, basic biological knowledge, on the technological opportunities available for the development of novel products.

Given that an understanding of the interconnections between structures across systems and the interconnections between systems is still forming, actions that result in the enclosing of large research terrains are likely to have significant impact on the technological opportunities available for follow-on developers. Furthermore, research is being conducted to better understand biological systems, the associated pathways, and the central nodes functioning across systems. The greater the applicability, the higher is the likelihood that multiple systems and domains will share the same pool of knowledge. The single structure-single function or system view is problematic as it lacks the biological insight that is required to correctly intervene in a system (Scherer, 2000). This view also distorts the incentives for both a first innovator and follow-on innovator to conduct further research if patent rights are granted on the basis of a single function (Scherer, 2000).

As the biotechnology industry transitions into the current systems paradigm, the nature of biological knowledge, namely the complementary nature of upstream biological knowledge, its complexity in terms of function, and its breadth of application, will encourage the formation of strategic alliances to ensure equitable access to knowledge for future product development. Strong early-mover advantages in downstream product development rest on the ability to rapidly identify, access, and integrate new combinations of knowledge (Antonelli, 2003; Grant and

Baden-Fuller, 2004). Where products require a broad range of different types of knowledge, efficiency of integration is maximized through separate firms specializing in different knowledge areas that are linked by strategic alliances (Grant and Baden-Fuller, 2004). Consequently, many companies are reconsidering their strategies with respect to upstream, pre-competitive, discovery research (Eisenberg, 2000; Cassier, 2002).

Genes, proteins, biological systems, and their associated patents are strategic knowledge-based assets (Blumenthal, 1992; Powell and Owen-Smith, 1998; Arora and Fosfuri, 2003; Jackson, 2003). The importance of these knowledge-based assets, combined with the increased complexity of molecular and systems-based knowledge, is encouraging the view that alliances between firms in this industry should be viewed centrally from a knowledge-based perspective (Hood, 2000; Reid et al., 2001). Although the extent to which critical knowledge assets are protected governs the decision to engage in these alliances, it is interesting to observe, that many biotechnology and pharmaceutical companies also promote and engage in alliances that are committed to open source discovery—through which discoveries are made freely available to researchers.

With this in mind, I begin the discussion on evolving models of innovation in the post-genome era, adopting a knowledge focus and associating the choice of innovation model with knowledge structures. Based on this knowledge perspective, governance issues associated with the biotech commons are discussed including issues for a microbial-specific commons. Case studies provide a context for analyzing the strategies being used to managed microbial-based data, materials, as well as downstream knowledge assets critical to the development of energy and environment based technologies

2.0 Evolving Models of Innovation: A Knowledge Perspective

Chesbrough explains that innovation has become increasingly open through a division of labour. In many industries, the vertically integrated organizational structure where innovation is solely an internal activity is gradually transforming into a more fluid structure tapping into both internal

and external sources of innovation. For example, companies are finding value through the licensing of intellectual property, the development of joint R&D ventures, or other arrangements to exploit technology outside the boundaries of the firm (Chesbrough, 2003; 2007). Giants such as Merck and Pfizer have watched as biotechnology upstarts such as Genentech, Amgen, and Genzyme have exploited external discoveries to become major players in this industry. These companies have used an open business model in which ideas move from discovery to commercialization through at least two different organizations—with different parties involved in the innovation process (Chesbrough 2003).

Rising costs, technological complexities, and shorter life cycles have put pressure on companies and their internal innovation processes. The pharmaceutical industry is facing patent expirations, empty pipelines, increased regulatory complexities, and a shorter life cycle created by brand competitors and generic competitors that quickly enter the market. Chesbrough (2003) discusses that open business models can enable pharmaceutical companies to leverage external resources and human capital to save time and money during the innovation process. The open business model further enables companies to generate revenue through the licensing of technologies that cannot be fully exploited within an organization and through the in-licensing of technologies that are discovered outside the boundaries of the organization (Chesbrough 2003).

From a knowledge perspective, in the closed model, human capital is employed within the boundaries of the organization. Knowledge is generated within and belongs to the originating firm. The organization's profit model revolves around the notion that knowledge is discovered, developed, and then embodied within firm-only products (Chesbrough 2003). Appropriated knowledge is controlled by the originating firm. In the open model, human capital and knowledge are accessed both inside and outside the boundaries of the organization. External knowledge can create significant value for a firm; internal innovation processes are therefore also needed to evaluate and exploit this knowledge. Firms can profit from the embodiment of knowledge within internally developed products as well the embodiment of knowledge in products developed by other firms (Chesbrough, 2003).

2.1 Knowledge-Based Networks: Knowledge-based networks are communities of individuals specifically with the objectives of producing and disseminating knowledge. Norms or rules for knowledge sharing and knowledge appropriation are necessary in networks with varied types of researchers (Ostrom et al., 1994; Liebeskind et al., 1996). Knowledge networks enable multiple researchers to pool assets, know-how, and expertise for the purpose of knowledge generation, knowledge validation, and new wealth creation (Powell et al., 1996; Reid et al., 2001).

Open network structures exist to undertake research and to generate new knowledge in a specific scientific or technological domain (Hacklin et al., 2004). These alliances are only concerned with the generation of new, disembodied knowledge. They are not concerned with the possible application and embodiment of knowledge (Liebeskind et al., 1996; Stokes, 1997). (Figure 1) A formal organizational structure, rules for participation (by invitation or match of qualifications to the theme of the network) as well as norms regarding knowledge dissemination are typical of these types of network structure (Liebeskind et al., 1996). In this type of alliance, members provide a function or resource that is complementary to and synergistic with the contributions of other members of the alliance (Child and Faulkner 1998; Reid et al., 2001). Firms are able to benefit not only from their own knowledge, but also through the recombination of knowledge from other firms (Kogut, 1998).

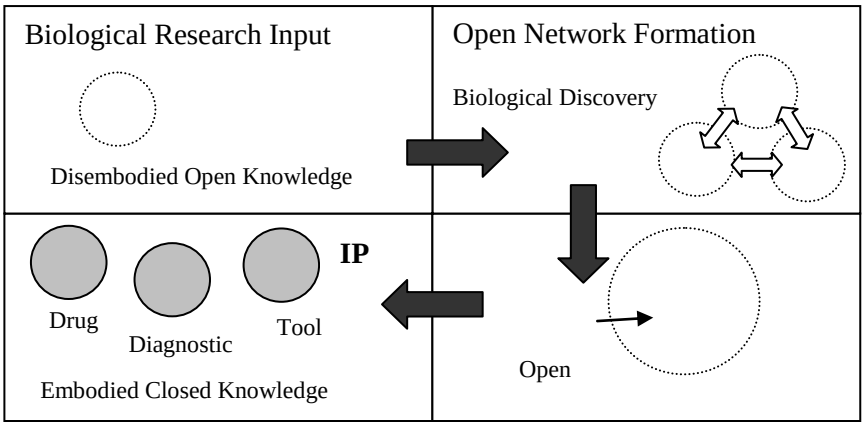
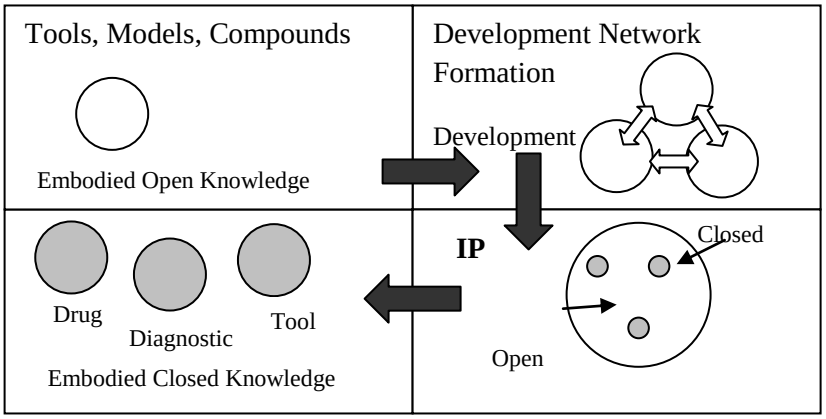


Figure 1: Upstream Knowledge Creation

Dotted, clear circle=Disembodied, open knowledge; Solid, filled circle=Embodied, closed knowledge; IP=Intellectual property rights may be sought downstream

In contrast, development networks exist to create new knowledge and to accelerate the application of the knowledge (Stokes, 1997). A variety of formalized projects may be undertaken in this type of network. Participants are carefully chosen based on reputation and capabilities. These networks are marked by tight forms of governance and hierarchy (Reid et al., 2001). Given the application orientation of these networks, issues relating to the ownership of intellectual property can become important (Oxley, 1999; Das and Teng, 2000). (Figure 2)



Solid, clear circle=Embodied, open knowledge; Solid, filled circle=Embodied, closed knowledge; IP=Intellectual property rights of importance within network

2.11 The Drive toward the Open Source Biological Consortium: Biology knowledge is complex and derives from a variety of scientific and technical disciplines. The molecular level of analysis, the computational nature of discovery research, and the global scale of research, all provide evidence that the product development paradigm has changed dramatically. From a knowledge perspective, biopharmaceutical knowledge production processes, knowledge dissemination processes, and even knowledge appropriation mechanisms are rapidly evolving. To manage the uncertainties in the systems paradigm, a new model of cooperation is emerging— the public-private consortium. The need for diverse skills in systems biology and the complexity of the experimental technologies require the formation of large-scale teams or consortia (Kitano, 2001; Chokshi et al., 2006). In these consortia, the issues of data-sharing and intellectual property are

closely related. As Chokshi, Parker, and Kwiatkowski discuss, consortia must decide in advance what data should be released to the public to ensure equitable downstream access to the data and open opportunities for the development of products; alternatively, in some cases, in may also be necessary to ensure, through the appropriation of data, that downstream incentives for product development are maintained for consortium members. Rules and policies will determine which option should take precedence in a project or consortium.

The International Human Genome Project catalyzed the open-source movement in genomics-based research. Globally dispersed laboratories jointly collaborated to map and sequence the Human Genome (Senker and Sharp, 1997; Larsson et al., 1998; Davies 2001). The resulting data were rapidly deposited into the public domain to ensure an open and level playing field for all researchers (Davies, 2001). Similarly, in October of 2004, Novartis, the Broad Institute of MIT, and Harvard University announced a joint project to decipher the genetic causes of type 2 diabetes. The collaboration reflects the mission of the Broad Institute to bring together researchers to solve complex problems that require multi-disciplinary teams and that are difficult to solve in the traditional (isolated) laboratory setting (Lawler, 2004).

Allarakhia, Kilgour, and Fuller (2009a) recently analyzed 39 open source genomic, proteomic and/or systems-based consortia to better understand how such consortia of public and private sector participants jointly create and manage biological knowledge assets in the post-genome era. Allarakhia, Kilgour, and Fuller (2009a) found that consistently consortia differentiated between disembodied knowledge in the form of raw data and embodied knowledge created by consortium members in the form of tools, biomaterials, and reagents. Although data were mandated in most cases for almost immediate release, tools, biomaterials, and reagents could be appropriated and licensed to consortium members and the public at large. Interestingly, this appropriation was regulated in most cases by the provision of rules regarding licensing terms. Supporting data and materials sharing policies provided by the National Institutes of Health (NIH), the Wellcome Trust, the Creative Commons, the Biological Innovation for Open Society, and even private sector firms such as Open Biosystems enabled for relatively easy access to disembodied and embodied knowledge created within consortia. (See Appendix A) In the section that follows, I

discuss specific details associated with managing data as well as biological materials in the biotech commons as assessed from the above study.

3.0 The Biotech Commons Model: Governance Issues and Lessons Learned

In the commons regime, all researchers have the privilege of using knowledge and resources. In the commons, researchers have one guaranteed right—that of not being excluded from exploiting knowledge or resources. Concerns about the enclosure of genomic resources have led to movements within the industry to preserve the existing "biotech commons" and to reclaim knowledge that has already been privatized.

Under certain conditions, the biotech commons is an efficient institution that can preserve downstream opportunities for multiple researchers fairly and efficiently. Cooperative interactions during discovery research can ensure that knowledge is generated for the purpose of disclosure and deposit into the biotech commons. Foray (2004) proposes five classes of incentives to participate in the commons and freely reveal knowledge:

- Voluntary spillovers are likely to occur when reward systems specifically encourage knowledge diffusion e.g., collegial reputation as a reward for working in open science.
- Voluntary spillovers are likely to occur when researchers or organizations need to create "general reciprocity obligations" in order to access external knowledge from others working in a similar arena.
- Voluntary spillovers are likely to occur when an organization freely reveals an innovation in order to benefit from its increased diffusion e.g., to influence adoption of a technology or technology standard.
- Voluntary spillovers are likely to occur when firms are interested in improvements of the average aggregate performance of an industry e.g., to increase safety and regulation associated within an industry.

- Voluntary spillovers are likely to occur when an organization is attempting to pre-empt rivals from pursuing a particular technological pathway or enclosing a technological arena.

In the management of open source initiatives aimed at the creation of a commons, the research outcomes to be disseminated, the format for dissemination, and the knowledge to be appropriated, should be clearly understood by all the participants. Internal rules or mechanisms to promote cooperative behaviour can include formalizing the requirements to join the knowledge network, ensuring frequent interactions, encouraging communication between participants, and punishing defection. An authority that regulates access to knowledge can ensure that a fair and efficient knowledge governance strategy is used. In sequential interactions, visible signals of cooperation and (binding) cooperative agreements become feasible.

3.1 Participation and Signalling Commitment

The decision to participate in open source initiatives is affected by the degree of accessibility to the associated knowledge. Open access ensures that knowledge is available to all researchers for downstream activities regardless of participation in the initiative. In this case, the possibility of free-riding exists by outside firms who can enjoy the disclosed knowledge at little or no cost (Gintis et al., 2001). Closed access in contrast, ensures that knowledge is only available to those contributing members within the alliance; therefore, the ability for a researcher or firm outside of the alliance to pool internal knowledge with that from the closed pool may not be possible or at a cost that will vary with the market power of the closed group.

The ability to join is further tempered by informal and formal rules of participation. With formality, entrance costs may be used to facilitate research and development activities as well as to signal cooperation and commitment to the consortium (Kollock, 1998; Gintis et al., 2001). The role of such entrance costs or rules for participation is to create trust through a visible signal. For example, committing resources in advance including monetary fees, makes other participants in the consortium, and future researchers who are considering participation, aware of a researcher's

cooperative intentions (Gulati et al., 1994). In terms of participation, consortia may establish rules regarding membership. Offering monetary commitments and/or making formal commitments to the mandate and policies of the initiative serve as signals of cooperation.

Allarakhia, Kilgour, and Fuller (2009a) found that while the majority of consortia allowed members with the requisite research experience to join voluntarily, 18 consortia established rules regarding membership. Of these 18 initiatives, 7 used formal invitations or applications, steering or executive committees, or by-laws to determine membership. Where formal commitments were required, participation by-laws and agreements tended to address both admission policies as well as exit policies.

Ten consortia required a monetary commitment as part of membership; out of this group, 2 required the maintenance of grants and 8 required up-front membership fees. In open access initiatives, large upfront payments were made to support research or membership fees were paid—entitling a member access to beta-version software, experimental instruments, and technology developed by associated research labs and institutions.

3.2 Managing Data

In terms of knowledge dissemination, consortia must have explicit rules and/or procedures described on consortia websites and/or policy statements to ensure knowledge dissemination including the dissemination of data and the sharing of tools, biomaterials, and reagents created by members. Of importance however will be the motivation for participating in such open source initiatives as well as the structure of knowledge to be disseminated. Participant type—public or private—can provide some indication of the underlying motivation for participation including the need to develop a collegial reputation, the need to create general reciprocity obligations, the need to enable the adoption of a technology standard, the improvement of industry performance, and/or the pre-emption of rivals. Knowledge structures including the complementarity, substitutability, and applicability can equally determine the optimal strategy for knowledge management.

Allarakhia, Kilgour, and Fuller (2009a) discovered that in most cases data—high in complementarity, non-substitutable, and high in applicability—were released almost immediately with complete access provided to members and the public at large. Data are maintained within large data repositories with the objectives of standardizing data and enabling linkages between repositories developed within the consortium and between external repositories. For example, 30 consortia use or planned to use databases to provide access to upstream genomic, proteomic, systems, biochemical, or cell biology information. These consortia addressed the open dissemination of data as part of their rules for sharing of information with members and the public at large. In addition, 22 consortia used peer-reviewed publications to provide validated information to the public.

3.3 Managing Materials and Intellectual Property

Tool and/or material development often includes the generation of embodied knowledge that is high in complementarity in terms of downstream development and high in terms of applicability. Biological models, microarrays, software, databases, and/or reagents however, are in most cases, tools that are reproducible by other firms or substitutable by other technologies. Rules can advocate sharing of materials for consortium research, ensuring access to repositories where animal models are housed, or providing for the wide dissemination of materials for the public at large.

If and when knowledge is appropriated through the filing of patents, rules should encourage licensing that provides the greatest collective value to the initiative members and/or the public at large. For example, many of the consortia analyzed by Allarakhia, Kilgour, and Fuller (2009a) advocated the use of royalty-free non-exclusive licenses. Where technology can be substituted through non-infringing work-around solutions, a patent holder will also have an incentive to offer a non-exclusive license, rather than face competition without any possible compensation for his/her initial discovery. Alternatively, in cases where the market for technology is relatively small with technology having zero standalone commercial value, a patent holder may need to

offer a non-exclusive license to ensure that a downstream developer will use the technology in products, thereby enabling the patent holder to reap the rewards of his/her original discovery.

The organization of knowledge production activities will impact not only accessibility to knowledge but also the learning experience for any firm. An awareness of participant type—public or private sector—can enable for a determination of motivation with respect to participation and likely adherence to the open source model. Rules for participation should be understood at the outset as a monetary commitment may be required to join the consortium; in this sense, participation rules can determine which firms can join the consortium as a function of resource availability. Rules regarding knowledge access—ranging from open access for members only, to open access for members and the public at large, to open licensing, will further drive the decision to join the consortium. Depending on the knowledge access policy, a firm may be forced to join the consortium in order to access critical knowledge, a firm may choose to free-ride and access knowledge without any resource commitments to the consortium, and/or choose to access knowledge as a licensee. (Table 1)

Managing the Biological Commons	Participation	Data Management	Materials Management
Governance Mechanisms	Entry/Exit Rules and Management; Commitment Policies including Upfront Payments.	Explicit Rules for Sharing of Information with Members and the Public at Large.	Explicit Rules Regarding Materials Dissemination including Proprietary Materials Management.
Knowledge Dissemination Strategy	Open or Closed Access Based on Structure of Initiative.	Open or Closed Data Repositories, Peer Reviewed Publications.	Transfer of/Pooling of Reagents, Biological Tools, Animal Models, and Cell Lines; Management of Repositories.
Appropriation and Licensing Management		Copy-left Licenses (See Appendix A).	Open Access; Biological Materials Transfer Agreements; Distribution of Materials Through Third Party Services; Non-Exclusive

Managing the Biological Commons	Participation	Data Management	Materials Management
			Licensing; Patent Pools; Geographic-Based Licensing.

Table 1: Governing the Biological Commons

As biotechnology increasingly converges with information and nano-technology to address health issues, food shortages, energy needs and environmental challenges, it will be essential to pay close attention to evolving knowledge structures including the role of knowledge assets in downstream product development. As multiple disciplines increasingly work together to these address these new challenges, stakeholders must further understand the value assigned to various knowledge assets. Each discipline will have its own priorities and conventions regarding knowledge dissemination and knowledge appropriation (Hilgartner, 1996). In the sections that follow, I consider the structure of microbial based knowledge assets and use case studies to highlight the governance issues stakeholders are dealing with as they direct their attention to developing new energy and environment-based technologies.

4.0 The Microbial Commons: Applying the Lessons of the Past

Microbes and their communities make up the foundation of the biosphere and sustain all life on earth. These single-celled organisms can live in almost every environment and can harvest energy in almost any form—from solar radiation to photosynthesis-generated organic chemicals to minerals in the deep subsurface. These unique microbial biochemistries now offer a deep and limitless resource of capabilities that can be applied to national needs, including DOE energy and environmental missions (http://microbialgenomics.energy.gov/).

Before scientists can harness their capabilities, microbes must be understood in far greater detail and in the context of whole living systems—whether as individuals or communities of interacting microbes—rather than as isolated components such as single genes and proteins. Microbes already can be manipulated at the molecular, cellular, and system levels, but understanding and taking advantage of their complexities and surmounting the technical

challenges of whole-systems biology is a daunting prospect (http://microbialgenomics.energy.gov/research.shtml).

In the post genome era, the central task is to integrate and analyze data for the purpose of biological discoveries. Clustering of data based on structure, function, patterns of expression, interactions, and association with biological system has become a key feature of systems biology. The attempt to capture systems-level laws governing cells is in fact a search for the common patterns that apply to complex systems and networks in general. A modular framework for biology will further organize systems into classes that share a common set of characteristics performing a common function.

Therefore, continued data sharing of microbiological information is critical for the quick translation of research results into knowledge and products (Dedeurwaerdere, 2007). Many different initiatives for sharing knowledge through databases exist—gathering knowledge from different fields of microbiology. These include the consortium for Common Access to Biological Resources and Information (CABRI)—connecting world-wide microbiological resources and the ongoing Global Biodiversity Information Facility (GBIF) project (Dedeurwaerdere, 2007).

As has been argued by Reichman (2002) in his work on database policies, the information contained in databases is both the input of the downstream knowledge generation and the output of former knowledge generation activities. Moreover, the use of the information in the microbiological commons often depends either on the possibility of linking databases and downstream user communities (Reichman, 2002). Cost effective access can be guaranteed through governance mechanisms including rules regarding the time of data deposits, access and use to any data deposits, and exemption clauses for non-commercial research (Dedeurwaerdere, 2007). In some instances, the ownership of the data, and any related conditions on the use of the data may remain with the original providers. However, even if information gathering communities do not centrally assert any ownership rights, each data provider will likely transfer some of the management and exclusion rights to the community as specified in any organization memorandums. As Dedeurwaerdere (2007) explains, commercial use of the data is permitted

only when a specific contract that includes restrictions on commercial use and specifies a license fee has been negotiated. Negotiating these ownership licenses could be the task of a collective organization administering the database (Dedeurwaerdere, 2007).

Similarly, the key players providing the infrastructure for the sharing of microbiological information are the organizers of the biobanks and culture collections, who organize the collection, conservation, curation, and exchange of biological resources and related data (Dedeurwaerdere, 2007). These collections—stemming from the pre-genomics ex situ collections of biological materials—have progressively developed into multi-service facilities called biological resource centres (BRCs). BRCs house collections of culturable organisms (e.g. micro-organisms, plant, animal and human cells), replicable parts of these (e.g. genomes, plasmids, viruses, cDNAs), viable but not yet culturable organisms, cells and tissues, as well as databases containing molecular, physiological, and structural information relevant to these collections and related bioinformatics (OECD, 2001). The exchange of these biological materials can be regulated through compulsory clauses in the contractual arrangements, specifying the origin of the resource and/or prior informed consent.

Rai et al. (2008) further discuss a Contractually Constructed Liability Regime in their paper entitled "Pathways Across the Valley of Death: Novel Intellectual Property Strategies for Accelerated Drug Discovery". Rai et al. (2008) advocate a supplementary system of royalties that would govern compensation to any firm that deposits information and/or biological materials into the commons. In essence, firms would be contracting into a subsidiary set of "take and pay rules," or liability rules, rather than relying entirely on exclusive property rights (Calabresi and Melamed; 1972; Merges, 1996). This compensatory liability payment would become available to firms if any of their molecules (the context adopted in this paper) fell within the class of promising "hits" during high-throughput screening for downstream drug development. Firms would therefore benefit not only from any internal downstream value creation activities, but also if they contributed (in the form of structural information on a hit) to upstream work (Rai et. al., 2008, Reichman and Uhlir, 2003).

4.1 The Turning Point: A Knowledge Perspective of Microbial Assets

Returning for a moment back to a knowledge perspective, based on their original study, Allarakhia and Walsh (2009b) define the turning point in discovery research as the moment when researchers come to believe that unilateral gains from private management of knowledge are greater than shared gains from open or shared knowledge. If this turning point occurs too far upstream, holdouts and bargaining failures may preclude downstream development by making knowledge unavailable. Of course, by taking a strong ownership position (capturing a patent for example) a researcher may be giving too little priority to the shadow of the future. Shifts in the turning point are often critical to firms operating in similar research or product domains.

Figure 3 summarizes the impact of knowledge form and knowledge characteristics on the placement of the turning point and the applicable innovation management strategy. The position of the turning point suggests when firms may opt to appropriate knowledge through the filing of patents and pursue licensing or internal development activities. For example, when knowledge assets are high in complementarity and applicability, but non-substitutable (top left quadrant) as is often the case for disembodied, pure knowledge, firms can opt to openly share knowledge (without appropriation) with the public-at-large or within a closed pool, or can pursue a licensing or internal development strategy depending on firm product development goals.

Increasingly, scientists are recognizing that the microbial world is more diverse, more important, and far more interdependent than had previously been imagined. Complex communities of microbes work together to carry out such functions such as digesting food, breaking down waste and capturing solar, or geothermal energy. Consequently, there is now an opportunity and imperative, to develop methods to efficiently characterize these communities. (New Biology, 2009) The sheer volume of data that will be generated by these scientists including the connections between complementary knowledge assets will as a consequence, require the careful management of such assets so as to preserve the downstream technological opportunities not only for multiple stakeholders but now across multiple disciplines.

Culturable organisms, replicable parts, cells and tissues—biological materials or embodied knowledge assets that are high in complementarity and applicability—may found in the top right quadrant. As seen in the case of BRCs, stakeholders can access such materials for a fee and by signing contractual arrangements specifying the origin of the resource and/or prior informed consent (OECD, 2001). Allarakhia, Kilgour, and Fuller (2009a) also found many instances where non-exclusive, royalty-free licenses were used to disseminate biological materials generated by consortia members. For example, a limited use license provided researchers with a limited, non-exclusive, non-transferable right to materials (with no right to resell, repackage, or further sublicense). The purchase of materials distributed through this licensing agreement did not include nor carry any right or license to use, develop, or otherwise exploit products commercially (www.openbiosystems.com, 2007).

We contend that as knowledge complementarity falls, or as it becomes less applicable regardless of substitutability (bottom left and right quadrants) or knowledge form, firms find it more effective to pursue exclusive licensing or internal development activities. This condition is intensified as the size of the market to which knowledge can be applied decreases (for example, in the case of orphan or rare diseases or small markets). Firms then will have to award exclusive licenses or pursue internal product development activities in order for the licensee or firm to unilaterally capture as much of the market available respectively—providing the incentive to pursue expensive downstream product development. Allarakhia, Kilgour, and Fuller (2009a) discovered in one instance that geographic-based licensing permitted exclusive licensing of the consortium's intellectual property where it was necessary to provide a marketing incentive as in the case of technologies for the developing world.

The turning point model provides for many of the realities facing an industry under radical change. The placement of the turning point—upstream or downstream—and the characteristics of knowledge will determine the appropriate innovation management strategy and the resulting transaction costs. The open access initiatives established since the mapping of the human genome are likely all attempts to move the turning point further downstream toward development activities (i.e. further to the right in Figure 3) (Allarakhia et al. 2009).

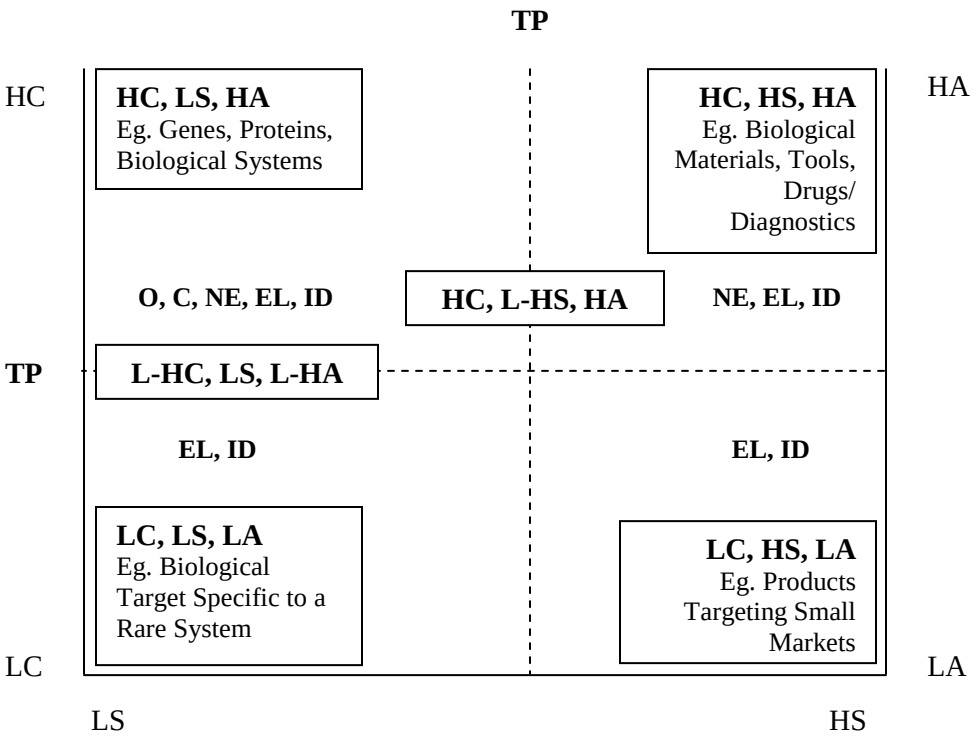


Figure 3: The Turning Point as a Function of Knowledge Form and Knowledge Characteristics

HC=High Complementarity, LC=Low Complementarity; LS=Low Substitutability, HS=High Substitutability; HA=High Applicability, LA=Low Applicability; TP=Turning Point; O=Open Access, C=Closed Pool, NE=Non-Exclusive Licensing, EL=Exclusive Licensing, ID=Internal Development

The turning point model equally provides insight as stakeholders seek to establish the microbial commons. Stakeholders must decide at the outset what knowledge assets belong in the commons—including perhaps both data and key biological materials critical for downstream product development. The case analysis that follows closely looks at the characteristics of the knowledge assets being managed by each open source initiative including those with a focus on the energy and environment sectors. (Table 2)

4.2 The Case Studies

Managing Data: MannDB is a microbial relational database that organizes data resulting from fully automated, high-throughput protein-sequence analyses using open-source tools. MannDB was created to meet a need for rapid, comprehensive automated protein sequence analyses to support the selection of proteins suitable as targets for driving the development of reagents for pathogen or protein toxin detection (Zhou et al., 2006). Specifically, MannDB is a genome-centric database containing comprehensive automated sequence analysis predictions for protein sequences from organisms of interest to the bio-defense research community (Zhou et al. 2006). MannDB provides the user with an interface for comparison of native and non-native sequences and a query tool for conveniently selecting proteins of interest. In addition, the user has access to a web-based browser that compiles comprehensive and extensive reports. Currently 36 open-source tools are run against MannDB protein sequences either on local systems or by means of batch submission to external servers.

The Global Biodiversity Information Facility (GBIF) enables free and open access to biodiversity data online. GBIF is an international government-initiated and funded initiative focused on making biodiversity data freely available. GBIF consists of an information-based infrastructure and a supportive tools infrastructure. The information infrastructure is an Internet-based index of a globally distributed network of interoperable databases that contain primary biodiversity data including information on museum specimens, field observations of plants and animals in nature, and results from experiments; the goal is to enable data holders across the world to access and share these knowledge assets. Community-developed tools, standards, and protocols further allow data providers to format and share their data (www.gbif.org, 2009). In this case, both data (disembodied) and tool based (embodied) knowledge assets are being managed by the Global Diversity Information Facility.

The ownership of the data, and any related conditions on the use of the data, remain with the original providers. This means that GBIF does not assert any intellectual property rights to the data that are made available through its network. Moreover, all the data are made available on

the terms and conditions that data providers have identified in the metadata. However, even if GBIF does not assert any ownership rights, each data provider transfers some of the management and exclusion rights to GBIF as specified in the Memorandum of Understanding established by the organization (Dedeurwaerdere, 2007). The GBIF network therefore handles only biodiversity data. GBIF does not deal with specimen holdings, or with materials that are derived from biodiversity studies or from nature. Thus, GBIF-related Intellectual Property Rights (IPR) and other legal issues are minimized to only those that apply to data. The GBIF itself advocates that GBIF data-sharing services and GBIF-mediated data are global public goods (Dedeurwaerdere, 2007).

Initiatives to share microbial data also have their origins in the private sector. Helicos BioSciences Corporation for example announced in 2008 the launch of the HeliSphere™ Technology Center—an open access web site for sharing Helicos microbial data sets and bioinformatics software tools. The first sample data sets released include whole genome sequences of the microbes Escherichia coli, Staphylococcus aureus, and Rhodobacter sphaeroides. In addition to Helicos data sets, the website is also a gateway to Helicos' open source project, which includes downloadable source code and software documentation and is hosted on the web site. Source code can be licensed through the widely used free software license GPL (general public license) for general use and through a commercial license for corporate partners. While the open source site showcases the capabilities of the Helicos™ Genetic Analysis System this case example is worthwhile to note as a discussion of incentive management. Although the technology is highly substitutable, it is likely that Helicos BioSciences hopes to lock researchers into its technology by developing complementary linkages to knowledge databases and convincing researchers that its technology has very broad applications (Arthur, 1989; www.hcp.com, 2009)

Managing Biological Materials: In the case of culture collections, specimen of bacteria, fungi, microbes, and cell lines can be accessed upon the payment of a handling fee (Cook-Deegan and Dedeurwaerdere, 2006). The Global Biodiversity Information Facility (GBIF) makes information on these resources freely available through a global data portal on the Internet (James, 2002).

Cook-Deegan and Dedeurwaerdere (2006) discuss that the collection of strains by researchers is an important part of the discovery process in microbiology. Researchers deposit their strains in national culture collections. To publish an article on a newly discovered strain two samples have to be deposited in two different culture collections (Cook-Deegan and Dedeurwaerdere, 2006). A similar requirement exists when applying for patent protection. Resources of public collections can be accessed by the scientific community under the conditions of Material Transfer Agreements (MTA). In particular, no express or implied licenses or other rights are provided to use of collection materials or related patents for commercial use; hence recipients have the sole responsibility for obtaining any intellectual property licenses necessary for its use of collection materials.

Europe has a wide variety of resource centres acting as supply and service organizations to the Scientific Community. The Common Access to Biological Resources and Information service (CABRI) offers access to some of these centres. This common interest gateway offers many advantages to both the centres and their user communities. Instead of having to scrutinize a large number of databases, catalogues, and other sources of information, CABRI offers world-wide access to these databases and allows one to simultaneously check on the availability of a particular type of organism or genetic resource and to order the required items once located.

CABRI membership is open to any recognized European Biological Resource Centre, willing and able to work to the CABRI levels of quality. There is no a priori limit on the size or the materials in the collection. The CABRI service has been built around quality and each member resource centre has therefore contributed to defining the set of technical specifications and procedures on how to handle each resource type. These procedures are primarily based upon the centres own procedures but they have been peer reviewed and approved before the catalogue has been mounted online.

The BioBricks Foundation (BBF) is a not-for-profit organization founded by engineers and scientists from MIT, Harvard, and UCSF with significant experience in both non-profit and

commercial biotechnology research. BBF encourages the development and responsible use of technologies based on BioBrick™ standard DNA parts that encode basic biological functions.

Using BioBrick™ standard biological parts, a synthetic biologist or biological engineer can already, to some extent, program living organisms in the same way a computer scientist can program a computer. Interestingly, the DNA sequence information and other characteristics of BioBrick™ standard biological parts are made available to the public free of charge currently via MIT's Registry of Standard Biological Parts. The Registry is a collection of approximately 3200 genetic parts that can be mixed and matched to build synthetic biology devices and systems. The BioBricks Foundation specifically states that its objective is to develop and provide educational and scientific materials to allow the public to use and improve existing BioBrick™ standard biological parts, and contribute new BioBrick™ standard biological parts. Users are free to modify, improve, and use all BioBrick parts, in systems with other BioBricks parts or non-BioBrick genetic material. If users release a product, commercially or otherwise, that contains BioBrick parts or was produced using BioBrick parts, then users must make freely available the information about all BioBrick parts used in the product, or in producing the product, both for pre-existing BioBrick parts and any new or improved BioBrick parts. By using BioBrick parts, users further agree to not encumber the use of BioBrick parts, individually or in combination, by others (http://bbf.openwetware.org, 2009).

Managing Downstream Knowledge Assets: The Eco-Patent Commons represents a new World Business Council for Sustainable Development (WBCSD) project. The mission is to manage a collection of patents pledged for unencumbered use by companies and intellectual property rights holders around the world to make it easier and faster to innovate and implement industrial processes that improve and protect the global environment. Any company or other patent holder can participate as a member in the Commons, as long as the member has one or more approved pledged patents in force, pays the applicable membership fee, and has received approval for membership by the Executive Board. Implementers can make, use, sell, and import infringing machines, manufactures, processes, or compositions of matter under patents on the patent list without payment of any royalty or similar payments to patent pledgers if such infringing items

alone, or when included in a product or service, achieve an environmentally beneficial result. In turn, pledgers guarantee not to assert any of pledged and listed patents against implementers for any infringing machine, manufacture, process, or composition of matter claimed in such listed patent(s) where such infringing item alone (or when included in a product or service) reduces/eliminates natural resource consumption, reduces/eliminates waste generation or pollution, or otherwise provides environmental benefit(s) (Ecopatent Ground Rules). Since the launch of the Eco-Patent Commons in January 2008, almost one hundred eco-friendly patents have been pledged by nine companies representing a variety of industries worldwide: Bosch, DuPont, IBM, Nokia, Pitney Bowes, Ricoh, Sony, Taisei, and Xerox (www.wbcsd.org, 2009).

In parallel, stakeholders are discussing the idea of "green licensing" particularly for developing countries seeking green solutions to their environmental challenges. An alternative to exclusive geographic-based licensing that is currently being proposed is the establishment of an international licensing mechanism focused on green tech and clean tech. This would enable companies and governments in the developing world to use established technologies for a fee, while protecting innovator firms. The goal is to enable economies at different stages of development—such as the US, China, and Bangladesh—to afford to use the same licensed technologies to promote sustainability and cleaner production (Greenwood, 2009).

Finally, AlgOS appears to be an open source initiative seeking the best methods to produce biodiesel from algae. The goal is to aggregate research inputs from a variety of experts in order to arrive at a full-cycle design for biodiesel production from algae. All assets that will be created will be governed by laws similar to those of GNU GPL; this framework should provide the freedom to a multitude of researches to use and modify designs/ideas made by other researchers (www.oilgae.com, 2009).

Managing the Microbial Commons	Data Management	Materials Management	Downstream Assets
Example	MannDB; GBIF; Helicos Microbial Data	Global Biodiversity Information Facility; CABRI (Resource Listing/Access	EcoPatent Commons; AlgOS

Managing the Microbial Commons	Data Management	Materials Management	Downstream Assets
		Service); BioBricks (Standard Biological Parts Repository)	
Knowledge Characteristics	HC, NS, HA	HC, NS-S, HA	HC, NS-S, HA
Knowledge Governance Strategy	Open Access; Use of Supporting Open Access Tools.	Material Transfer Agreements used by BRCs/Licenses Negotiated for Use of Collection Materials; Open Access or Non-Exclusive Royalty Free Licenses for Non-Commercial Use.	Non-Assertion Clauses for Infringement in Downstream Products; Green Licensing Proposed for Developing Countries; GNU-General Public Licenses.

Table 2: Governing the Microbial Commons

5.0 Discussion

The knowledge framework discussed in this paper should enable stakeholders to better understand the underlying structure and state of knowledge. This framework has considerable applicability as the bio-convergence paradigm evolves—where the biological, information, and even devices paradigms intersect. Many of the issues discussed for the information paradigm will have even more serious consequence as these firms seek patents over biological materials that may be placed into synthetic devices, as genomic information is manipulated to develop new organisms, or applied to new domains including the energy and environment domains. Furthermore, as new theories underlying biological processes emerge and researchers re-evaluate their assumptions regarding the value of old knowledge, the strength of patents filed on older knowledge may change. For example, what was once thought of as "junk" DNA may become critical to our understanding of biological processes. Patents that have placed little value on this upstream knowledge may not offer as strong protection over downstream product domains. In other cases, broad patents including claims on such knowledge may now offer new players a stronger seat at the bargaining table. Hence, we contend that researchers and firms should bear in mind that the state of knowledge is constantly changing and as such, this knowledge framework

provides a first glance at the strategies that should be used to evaluate biological knowledge structures and the types of alliances that can be formed to acquire, access, and generate new knowledge.

As new paradigms and knowledge structures emerge, we should also keep in mind that developing markets and new industries will offer once isolated firms the opportunity to develop products. Here, governments including public funding agencies and patent systems, may need to work together in order to ensure an equitable opportunity for these weaker players to enter research arenas. Beyond North-South partnerships and local capacity building, it is necessary that researchers and technology transfer officers take greater caution in the patenting and licensing of technologies that have significant application in developing and under-developed markets. Maintaining and building the public domain with particular attention to knowledge that is of benefit to these economics can enable researchers to quickly and cost-effectively access knowledge. Open licensing, geographic-based licensing, assigning fair-royalties are all options being employed to assist researchers in developing economies access technologies that address for example local health needs and increasingly local energy needs.

Managers of firms in developed and in emerging markets alike should seek out the opportunities presented by open innovation—including participating in open source based innovation. For firms in emerging markets, open source based innovation presents a cost-effective means to learn about a domain and the corresponding product development opportunities. These firms can then use the experience gained from participation in open source based innovation to make an informed decision regarding the investment into downstream product development—particularly in the convergence era.

The practical lessons learned from this paper however, indicate that firms from emerging markets with limited resources will have to carefully evaluate the objectives of an open innovation (including open source) based community and/or network. The objectives can include the creation of pure knowledge or even embodied knowledge in the form of tools and products. Ultimately then, firms hoping to enter an arena will have to analyze where they are located on

the learning curve and what they hope to gain through participation in an open innovation based community. Organizational structures will then determine how firms can participate in any learning and knowledge development processes. Specifically, the distance from knowledge development activities and any supporting organizational structures that seek to minimize this distance, will determine how much learning by doing and using firms will experience. Finally, the mechanisms used to disclose and share knowledge will impact whether firms can indeed move down the value chain. It is therefore anticipated that open innovation based communities with clear rules, leadership, and transparent processes will be more productive—avoiding any surprises for firms with limited resources contemplating participation.

In terms of future research, it is essential to analyze new case studies involving open source innovation targeting the energy and environment sectors. These case studies should seek to observe the evolving models of open innovation as the number and type of participants change, as the objectives with respect to innovation evolve, and as the complexities associated with knowledge structures increase so that knowledge management become paramount. This analysis should further seek to understand any geographic-based issues hampering technological innovation by firms in emerging markets and how to eventually position these firms to meet both global and local product needs through open source innovation. I advocate that a repository of governance strategies including any licensing templates be created, as has been created by BiOS and the Creative Commons so that stakeholders can effectively manage energy or environment based assets from the outset of any collaborative development effort including managing those placed into the microbial commons.

Consortium	Rules or Mechanisms used to Disseminate Data	Rules Regarding Sharing of Tools, Biomaterials, and Reagents
Agilent-Industry Open Microarray Design Program	Based on Consortium Rules	Based on Consortium Rules
Alliance for Cellular Signalling (AfCS)	Database Deposit; Publication	Reagent Sharing for AfCS Research
Beta Cell Biology Consortium (BCBC)		Freely Distributed to Academics for Non-Commercial Use
Biological Innovation for Open Society (BIOS)		Royalty Free, Non-Exclusive Licenses Among Participants
Cancer Vaccine Consortium	Publication	
Cell Migration Consortium	Database Deposit; Publication	Royalty Free, Non-Exclusive Licenses for Non-Commercial Use
Collaborative Cross	Database Development	Repository; Open Subscription to Mouse Repository
Combinatorial Chemistry Consortium	Exclusive Access to Data	Exclusive Access to Licensed Software
Consortium for Functional Glycomics (CFG)	Database Deposit; Publication	Material Sharing for Consortium Research; Royalty Free, Non-Commercial Use
DopaNet	Database Deposit; Publication	
Functional Proteomics Consortium	Exclusive Access to Annotated Data	
HepatoSys	Database Development; Publication	
Human Epigenome Consortium	Database Deposit; Publication	
Human Genome Consortium	Database Deposit; Publication	
International Genomics Consortium	Database Deposit	
International HapMap Project	Database Deposit; Publication	
International Molecular Exchange Consortium	Database Deposit/Management	Creative Commons Copyright Licensing Advocated
International Regulome Consortium	Database Deposit; Publication	
International Rice Functional Genomics Consortium	Database Development	Sharing of Materials
International Rice Genome Sequencing Project	Database Deposit; Publication	
International Sequencing Consortium	Database Deposit	
Knockout Mouse Project	Database Development	Public Repository for Biomaterial; Patent

		Pooling Advocated
MalariaGEN	Data Management Addressed	Restricted Licensing; Geographic Restrictions
MitoCheck Consortium	Database Development	
Mouse Genome Sequencing Consortium (MGSC)	Database Deposit; Publication	
Mouse Models of Human Cancers Consortium (MMHCC)	Database Deposit; Publication	Repository for Biomaterials; Reagent Distribution through Open Biosystems
Nanotechnology Consortium	Exclusive Access to Data	Exclusive Access to Licensed Software
Novartis Institutes for Biomedical Research-Broad Institute Alliance	Database Deposit; Publication	
Osteoarthritis Initiative	Data Repository	Research Tools Wide Available; Limited Materials Priority Distribution
Public Population Project in Genomics	BioBanks-Database; Publication	
Receptor Tyrosine Kinase (RTK) Networks Consortium	Database Deposit; Publication	
Research Collaboratory for Structural BioInformatics (RCSB)	Data Bank; Publication	
RNAi Consortium (TRC)		Distribution through Sigma Aldrich and Open Biosystems
SNP Consortium	Database Deposit; Publication	
Structural Genomics Consortium	Database Deposit; Publication	
SYMBIONIC	Database Development; Publication	
TB Structural Genomics Consortium	Database Deposit; Publication	
The Lipid MAPS Consortium	Database Deposit; Publication	

Appendix A: Analyzing Consortium Rules for the Dissemination of Data and the Sharing of Tools, Biomaterials, and Reagents

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