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Common Genomes:
Open source in biotechnology and the return of common property

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Introduction

This article examines property relations in biotechnology by looking at open source in the sub-disciplines of genomics and bio-informatics within the context established interpretations of common property in international mandates on genetic resources. It is argued that the role of genomics in biotechnology development corresponds to changes in property relations that are increasingly changing analogous to those around opens source in informatics. Moreover these property relations comprise a linkage of open source in biotechnology and genomics to humanitarian objectives. While it is argued that this implies a progressive inaccuracy of argumentations that focus on endorsements of or objections to the relative efficiency of biotechnology patents, it is also argued that the potential to renegotiate and re-design biotechnology development by means of an open source approach needs to be elaborated further in regard of other interpretations of common property.

The examination has as its theoretical background of a number of classical critical studies on the transformation of property relations in the passage from chemical agriculture to biotechnology, emphasising, for instance, multinational concentration, exclusive patent rights and also 'natural patents' like terminator seeds (Mooney 1980, Yoxen 1983, Goodman, Sorj and Wilkenson 1987, Fowler 1988, Goodman and Redclift 1989, Fowler & Mooney 1991). Also genomics, the study of genes and their expression, has more recently been put in the perspective of an on-going 'enclosure of the genome', where gene patents are seen as fragmenting access to the genome and where its status as a common property has been argued as an integral part to modern capitalism, meaning as a strategic site of ownership re-enforcing privatisation (Boyle 2003, Sunder Rajan 2003).

Such 'enclosure' by means of information flows isn't only linked to arguments either in favour of or against biotechnology patents, but has also been linked persuasively to the origin of patented genetic traits in developing countries and their cultivation over centuries by communities that conserve and cultivate biodiversity (Kloppenburg 1988, Dutfield 2001, 2003, Blakeney 2000, Drahos 2000). At a more sociological level this involves studies of how the privatisation of biotechnology is linked to the exclusion of marginalised farmers and indigenous peoples (Ruivenkamp 1989, Pistorius & van Wijk 1999). Ruivenkanp speaks of a progressive 'control at a distance' over crops, food and natural environments.

Critical theorists Hardt & Negri identify these two sides to the property relations of genetic resources as part of a similar process, when they argue that:

'the right or title to property is undercut by the same logic that supports it because the labor that creates property cannot be identified with any individual or even group of individuals. (...) Who, for example, produces the information of genetic code? Or who, alternatively, produces the knowledge of a plant's beneficial uses?' (Hardt & Negri 2004: 187)

This quote catches aspects of the previous sentences when it acknowledges the 'knowledge of plants beneficial uses' and the 'information on the genetic code'. Moreover for Hardt & Negri they illustrate a progressive contradiction within the formal property system.

Such a hypothesis about a strain on property relations also features within a body of studies from information law and economics that perceive open source informatics as the quintessential common property model in the information economy. It conceptualises open source in relation to an 'intellectual commons' perceived as in between the patent system and a free market for information. (Benkler 2002, Hess & Ostrom 2003, Rai & Eisenberg 2003, Reichman et al. 2003, Rose 2003, see also Drahos 1996). Also for biotechnology ideas about open source have almost exclusively been related to sharing information as a common property (see Hughes 2005, Arti Rai 2004, Burk 2002, Boettiger et. al 2004, Opderbeck 2004, and Hope 2006). In addition to such perspectives that emphasise open source's relation to innovation, Negri & Hardt emphasise its political significance by speaking of an 'open source society': a 'society whose source code is revealed so that we can work collaboratively to solve its bugs and create new, better social programs' (Hardt & Negri 2004: 340).

To be able to qualify these ideal typical ideas in relation to property relations in biotechnology, three related questions are examined:

1) How is open source informatics related to common property?

2) How is open source informatics as a common property related to genomics and biotechnology?

3) How is open source in genomics and biotechnology related to the international organisation of genetic resources?

This last question should be seen as an attempt to interpret the relationship of open source and genomics in relation to the wider international organisation of genetic material. This organisation includes the recognition of intellectual property and biotechnology patents, but also acknowledges that genetic resources are sometimes a matter of state sovereignty, while also several notions of common property persist. Although it is beyond the scope of this article to engage in depth with the ownership over 'plant's beneficial uses' or the other mandates at an empirical level, it is possible to interpret them as an international context to the global extension of open source in biotechnology and genomics. Furthermore it is also in this sense that the 'return of common property', which the title announced, should be interpreted; in contrast to the sovereignty and private property perspectives on genetic material.

The design of the article departs from some short observations on the contemporary development of open source in informatics and proposes an understanding of open source as a common property that can examine the property relations of biotechnology. The second question is then answered by means of an empirical survey that is intended to comprise the relationship between open source and biotechnology. For bio-informatics this involves examples ranging from simple programming languages to complex software and hardware closely related to major informatics companies. Within the on-going development of genomics these companies are also discussed in relation to examples like the Human genome project, the 'SNP consortium' and the explicitly open source 'cellular signalling initiative'. Moreover there are also important examples of the networked character of genomics that are less prestigious but important to emphasise in relation to open source. Finally, the extension of open source to biotechnology development is part of the answer to the third question. It involves a number of open source examples in genomics and biotechnology that touch on developmental issues, for instance related to tropical diseases or the release of patented plant biotechnologies.

As already mentioned, such examples are situated within the changing property relations of biotechnology and their potential to renegotiate and redesign biotechnology development should be understood accordingly as well as in relation to some of the more substantive perspectives on genetic resources as a common property.

Some remarks on genetic resources and on open source

Intellectual property was introduced to informatics and biotechnology in the early eighties.[1] For both technological domains this meant that source code and genetic code were to be integrated into market relations organised around intellectual property. However an important difference is that in informatics, the earlier sharing of source code got a second life around open source, while in biotechnology studies it is not unusual to speak of the 'demise of common heritage of mankind'.

This concept of common heritage describes that genetic material, like source code, had in history almost always been shared 'free of private property and sovereignty and available for science' (Brusch 2003, Gepts 2004). By now, there are only a few remaining notions of common heritage in the international organisation of genetic resources, as it has been exchanged for a limited recognition of the contribution of common law systems to biodiversity conservation (see Drahos 2000, Dutfield 2000, 2001). The typical entries in international law are the Food and Agricultural Organisation's (FAO) resolution 5 from 1989 on farmers' rights and article 8J of the Convention on Biodiversity (CBD), which links benefit sharing to the 'knowledge, innovations and practices of indigenous and local communities embodying traditional lifestyles relevant for conservation and sustainable use of biological diversity'. In turn most recognition of indigenous rights is related to ILO convention No. 169.[2] Still, this is of course not the centre stage of the biodiversity approach in international law, which much more explicitly recognizes the sovereign rights of states over their natural resources. Increasingly the international organisation of genetic resources, including these common property models, is about compatibility of the sovereignty approach with the intellectual property approach of the 1992 agreement on Trade Related aspects of Intellectual Property rights (TRIPs) of the World Trade Organisation (WTO) (see Pistorius & van Wijk 1999, Dutfield 2003).

Around the time of the CBD and TRIPS the term 'open source' was proposed to replace the suggestion that there is no money to be made with 'free software'.[3] This term was propagated by the Free Software Foundation (FSF), who described it by the slogan 'free as in free speech, not as in free beer'. Accordingly, sharing source code as a common property, free of intellectual property requirements, is a matter of principle in the deontological approach of the FSF, emphasizing a personal ethic of sharing before additional arguments about a higher efficiency. (see Berry 2004) From the early eighties, the FSF had actively released software with the aim of constructing a free operating system, functionally equivalent to patented software and operating systems. The FSF's criticism was that the intellectual property approach keeps the source code of software inaccessible for its users in order to be able to sell copies, as a consequence Unix systems, like Windows and Macintosh have become unnecessarily incompatible and complex. By releasing source code, the FSF aimed to circumvent the errors, unnecessary complexity and additional features that each new patented Unix version included, for instance to be compatible with older versions and marketable by preventing unauthorized copies. By now Linux is usually perceived as the primary open source system, but it is not unusual to speak of GNU/Linux. GNU is an abbreviation of the FSF for 'GNU's Not Unix', an ironic play of words on the patenting of UNIX. The combination refers to the context wherein Linus Torvald released his kernel in 1990, free software, so that the GNU software project got its missing link to organise the communication between the different components of the operating system.

Also today, for the FSF, GNU/Linux remains 'the key working example, a collective project that has been shared and worked on freely' (Berry 2004: 80). The term 'open source', in contrast to 'free software', is preferred by the open source movement. It argues that: 'code is property owned by an individual who has the right to control and develop it (..), this is strictly associated with the notion of the project itself rather than just the underlying source code' (Berry 2005: 81). Also the response to the typical criticism on open source that it decreases intellectual property incentives is more pragmatic then the FSF approach. It is called 'Linus' law' which says: 'given enough eyeballs, all bugs are shallow' and is attributed to Linus Torvald by Eric Raymond in his essay, the 'Cathedral and the Bazaar'. Raymond distinguishes 'closed source' software development by small groups of programmers from 'open source', which is about free access and adaptability of source code for anyone on the internet (Raymond 1999). As such the open source movement prioritises a focus on where and when exactly a larger quantity of participants makes solutions to

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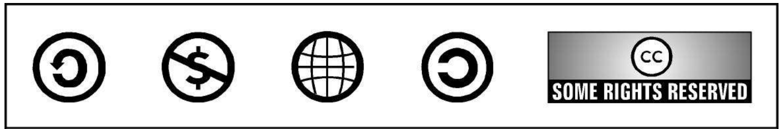
[1] Biotechnology patents are typically traced to the Charbaty patent and the Bayh Dohl act. For software the 1981 case of Diamond v. Diehr is considered the point of reference

[2] On Farmer's rights see ftp://ext-ftp.fao.org/ag/cgrfa/Res/C5-89E.pdfw. See for art. 8 www.biodiv.org/programmes/socio-eco/benefit/default.aspx and for art. 15, www.biodiv.org/convention/articles.asp?lg=0&a=cbd-15 For Convention No. 169 concerning Indigenous and Tribal Peoples in Independent Countries see http://www.unhchr.ch/html/menu3/b/62.htm

[3] Raymond 2001 "Does 'free' mean 'no money charged?' or does it mean' free to be modified by anyone', or something else?"

difficult software 'bugs' more obvious to someone. In other words: the issue becomes whether Linus Law is a law, meaning that open and closed source are different development models that apply to distinct or separate aspects of software development.

Moreover, a similar distinction as between the free software foundation and the open source movement can also be made to the way that the General Public License (GPL). This is the licence that enabled FSF founder Richard Stallman to release software as a common property. The GPL allows for the sharing of source code by stating explicitly that the carrier of the intellectual property renounces some of the exclusive rights with the intention to remove restrictions on copying, redistributing and modifying source code. Although the GPL is still the most widely used license for open source informatics, in informatics 'open licensing' is also increasingly seen as a matter of degree, ranging from the GPL to other licenses where intellectual property holders demand exclusive rights to modifications in exchange for free distribution.[4] In addition to these 'copylefts', there are by now hundreds of copyleft licenses in informatics and also in other domains, for instance music and journalism on the internet.



Share Alike, Non-Proprietary, Development Nations Only, Copyleft and 'Some Rights Reserved'

The most prominent open licences are by now of the creative commons initiative which advocates a 'some rights reserved' approach, meaning that open licensing aims to: 'cultivate a commons in which people can feel free to reuse not only ideas, but also words, images, and music without asking permission - because permission has already been granted to everyone'.[5] Specifically, their copylefts, like the GPL earlier, contain 'non-proprietary' and 'share alike' clauses that require the release of modifications and distribution on the same terms as an original. Also its icons and concepts have wide appeal, demonstrated for instance in the recent elaboration of 'science commons' licenses and 'development nations' clauses by the creative commons and the frequent appearance of the mirror image © and the 'some rights reserved' icons.[6]

There are also some criticisms on the open licensing along the lines of the debate between the free software foundation and the open source movement. A recent example is the 'libre society', which rejects the stretching of the GPL to the many licenses of the creative commons. It argues that common licenses encourage that lawyers 'remain key nodal and obligatory passage points within the creative commons network and thereby constitute blockages in the flow of creativity'. In other words open licensing is about a commons without 'communality', which they advocate at a symbolic level by offering licenses that specify only a moral of common ownership, nothing else, in explicit rejection of state law (Berry & Moss 2005a, 2005b).[7] This point returns in the last section of the article and in the conclusion when open source in biotechnology and genomics is discussed in the context of other notions of common property within mandates of international organisations. However in order to prepare that discussion, the next section deepens the contemporary discourses on free software and open source by looking at some aspects of the theoretical debate on open source as a commons.

Open source and the intellectual commons

The legal adviser and ideologist of the Free Software Foundation, Eben Moglen, explicitly links open source to common property. He argues that the collaborative programming of open source is analogous to the management of 'fisheries, surface water resources, and large numbers of other forms of resource beyond human production'. (Moglen 2003) Instead of emphasising collaboration along the lines of Linus Law, he compares free software to Faraday's law from physics:

> *'Wrap a coil around a magnet; spin the magnet. Electrical current flows in the wire. One does not ask, ``what is the incentive for the electrons to leave home?" It's an inherent, emergent property of the system, we have a name for it: we call it induction. The question we ask is, ``what is the resistance of the wire?" (..), ``What is the resistance of the network?" Moglen's Corollary to Ohlm's Law states that the resistance of the network is directly proportional to the field strength of the intellectual property system. The conclusion is: Resist the resistance. Which is what we do (Moglen 2003).*

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[4] See for instance Microsoft open licensing at http://www.microsoft.com/licensing/programs/open/default.mspx

[5] see http://creativecommons.org/about/legal

[6] For the GPL see www.fsf.org, for copyleft licensing see www.creativecommons.org/ www.sciencecommons.org. For examples of other domains then software see: http://en.wikipedia.org/wiki/ Creative_Commons For the developing nations license see: http://creativecommons.org/licenses/devnations/2.0

[7] See http://www.libresociety.org.

The reach of intellectual property rights over the commons is also part of 'creative commons' protagonist, James Boyle argument in favour of a: 'reinvention of the public domain as a successful commons defined by its restrains or a build in awareness of the limitations into the [IP] grant itself' (Boyle 1996). The commons is for Boyle tied to an historical comparison with the 'enclosure' of the English commons: 'a series of enclosures that started in the fifteenth century and went on, with differing means, ends, and varieties of state involvement, until the nineteenth century'. (Boyle 2003b, Travis 2000). Such concepts correspond to Moglen's notion of the 'resistance of the wire' as Boyle speaks of a 'teleology of intellectual property' and a paradox that forms an 'integral part of the analytic structure of economics', because there is an:

> *'internal tension in the analyses [that] always leaves open the question whether a particular issue is to be classed as a public goods problem for which the remedy is commodification, or a monopoly of information problem for which the remedy is unfettered competition' (Boyle 1996: 36, 40).*

Accordingly for Boyle both free software and the Creative Commons copylefts are mechanisms to resist a 'second enclosure movement' that insist, among other things, on an 'up or down vote on gene patents' and 'black box innovation' (Boyle 2003a).

Also on pragmatic interpretations, common property is being actively advocated. Most prominently Yochai Benkler draws on open source and 'Linus law' as illustrations of the comparative advantage that common property has to patents. This advantage exists because the structural costs of the circulation of information are dropping, resulting in: 'common based peer production'. This term expresses that increasingly networks are emerging that create and distribute goods: 'independent of the more commercially controlled distribution systems, operating from the edges of the network to its edges rather than through a controlled middle' (Benkler 2002: 30).

In table 1, a simplified outline of his argument is displayed. It is an adaptation of two of his tables that relate 'common based peer production' to the 'value of the property system'. In the next sections this model will be followed heuristically to analyse open source in genomics and biotechnology. Firstly, the right side of the model departs at the top from Hardin's tragedy of the commons. The term 'commons' simply refers to the sharing of resources in such a way that 'no single decision-making unit holds exclusive title' (Vogler 2002: 2). It thereby corresponds to Hardin's famous interpretation that common property is about open access. The argument is then that all those that have access to a common resource, will tend to use it as much as they can until they finish the resource. As he said it: 'freedom in a commons brings ruin to all' (Hardin 1968).

Table 1: the intellectual commons and the value of property systems (Variation on Y. Benkler 2002: 34, 35)

	Property system more valuable than transaction costs	**Transaction costs higher than value of the property system**
Market exchange more efficient	**markets**	**Commons**
Organizations more efficient than market exchange	**firms**	**(intellectual) common property regimes**
'Peering' more efficient than organizations or markets	**Proprietary 'open source'**	**Non-proprietary 'peer' production processes**

The tragedy, Hardin argued, is about over-population and the depletion of resources like the atmosphere and oceans. Yet, in contrast to land or biodiversity, here it concerns a different kind of commons, as in involves resources that aren't immediately susceptible to exhaustion, depletion or pollution. The concept of 'intellectual commons' indicates along such lines that Hardin-esk tragedies don't apply to information. For instance Drahos, in line with Boyle's economical paradox, argues that: 'the very protection which encourages production at the same time thwarts the object of the exercise, namely, the diffusion of knowledge' (Drahos 1996: 122). The real tragedy for studies in information law and economics is then about the lack of awareness about the 'synergy of knowledge' in an intellectual commons or on the public responsibilities to 'enlarge and nurture' the conceivable and accessible abstract objects' (Rose 2003, Drahos 1996: 152, 153).

Especially in the context of this article this recalls that the metaphor of the 'tragedy of the anticommons' was about how patents in medical biotechnology fragment the circulation of information, delaying innovation (Heller & Eisenstein 1998, Rai et al. 2003). In relation to Benkler's model, the key concept that was missing in Hardin's metaphor, are the 'transaction costs' that come with his call for public and private institutions to enforce rules about rights and duties. Such costs are of consequence on both sides of the second level of table 1. He explains that transaction costs in economic theory originally explained the efficiency of innovation by firms that have the capability of organising research outside of the free market (Benkler 2002, see also Mandeville 1996). In an ideal typical free market competition takes place with the free circulation of information, without patent incentives. Patents add transaction costs to the free market that can encourage firm formation, not so much as incentives but as obstacles that keep the free market at bay.

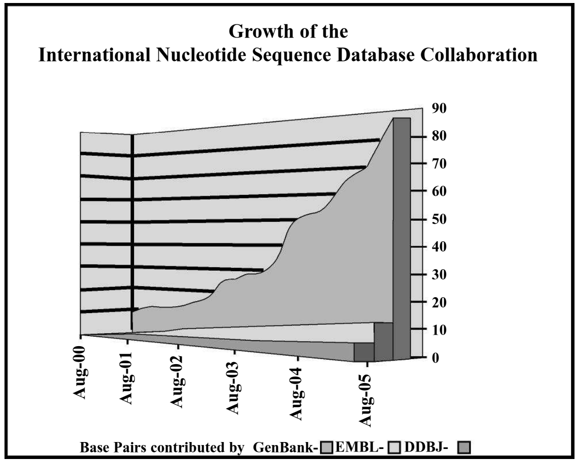
To explain what happens when transaction costs are higher then the value of the property system, Benkler draws on the rehabilitation of common property along the lines of Elinor Ostrom's 'governing the commons'. She has argued that there are also 'common pool resources' that are not about Hardin's open access but are governed by 'common property regimes' that regulate the 'continuous sharing of many physical resources on informal rules and customs that are developed and adapted over long periods of time' (Ostrom 1999, Hess & Ostrom 2003: 3, 4, Drahos 1996: 125). An extended version of this argument for an intellectual commons is the basis for Benkler's extends emphasis on 'peer reviewing' as a common property production model. Its efficiency in comparison to the transactions costs of firms and patent systems could be seen as an 'intellectual' common property regime', but to distinguish it from market based innovation, he calls it: 'common based peer production'. He argues that it constitutes an 'emerging third model of production' that is 'sustainable and productive in the digitally networked environment without reliance either on markets or managerial hierarchy' (Benkler 2002: 14).

For a patent focused sector like biotechnology, such an emphasis on a common-bases to production recalls the objections of the anticommons in medical biotechnology. Along such lines the next paragraph traces the changing role of patents in genomics and bio-informatics. Its purpose is to prepare an examination of the potential of open source in bio-informatics, genomics and biotechnology. Subsequently, the criticism that open projects and open licenses can also constitute 'new gatekeepers' will be part of the discussion of open source approaches to common property over genetic resources. In the following three sections, open source in genomics and biotechnology is interpreted along the lines of 'common-based peer production' from table 1.

Biotechnology patents in genomics and bio-informatics

In 1977 the first organism was mapped, a 'phage', a small virus of 11 genes that affects bacteria. More recently it has been succeeded by the first free living organism, Haemophilus Influenzae in 1995, a plant sequence, Arabidopsis, in 2000 and also the human genome project and the first higher plant organism, rice. In other words, the mapping process, also called sequencing, has changed considerably and now involves 'high throughput determination'.

For instance the human genome project involved 3.12 billion base pairs and there are around 60 million sequences of over 130.000 organisms in GenBank, the primary public database for genome research. Other numbers to indicate that gene sequencing is a matter of quantity come from the count of the database GOLD that for April 2006 reports 373 genomes that have been published, 2024 projects that have been completed and 1605 that are in progress. Then there is still the discovery from the human genome project that over 20.000 genes don't correspond to an equal amount of proteins, as was expected, but to at least ten times more. Therefore sequencing isn't quite finished, also because, as Oldham mentions, there are an estimated 14 million species that have not been sequenced at all (Oldham 2004).[8]



Source: http://www.ncbi.nlm.nih.gov/Genbank/

The science behind these genome maps is genomics, which studies the functions of these genes and base pairs.[9] To interpret the information from the databases, 100 giga-bases for GOLD alone, it relies on the sub-discipline of bio-informatics that has as its objective the construction of databases and models of sequences and base pairs. These maps, models and databases are intended to help in the study of 'genetic similarity', meaning the overlap between and within 'genotypes' which display very diverse 'phenotypes', for example for

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[8] http://www.genomesonline.org. Oldham 2004: in September 2003, there were 803 projects, in September 2004, 1182. http://en.wikipedia.org/wiki/Proteomics also http://www.hupo.org/ the human proteome organisation. Moreover www.ncbi.nlm.nih.gov/Genbank reports that there are 59,750,386,305 bases in 54,584,635 sequence records in the traditional GenBank divisions and 63,183,065,091 bases in 12,465,546 sequence records in the WGS division as of February 2006.

[9] See the press release of august 2005 at www.nlm.nih.gov/news/press_releases/dna_rna_100_gig.html

71% Arabidopsis and rice overlap, while 85% of human genetic variation can be found in any human population.[10] Moreover the map of the 'Fugu Puffer' fish helped to identify close to 1000 human genes (OECD 2002: 33).

The most obvious question would then seem to be: 'should these genes be patented?' A recent political issues that touch on genetic similarity is the withdrawal of Syngenta of its 'mega-patents' on the flowering process for 34 crops based on its rice sequence. One of these got branded the 'daisy cutter' patent by the NGO, ETC group. (ETC Group 2005, Trippe 2005) Another such theme is about the small biotech company 'Sangamo bio-sciences' who acquired a complete monopoly on 'zinc finger', important to gene-therapy, while Genetic Technologies Limited has developed usages for non-coding DNA in the detection of alleles and its claim extends over all 'junk DNA patent' (Scott 2005, Nottenburg 2004). Moreover these cases are not easily isolated because also more generally speaking 'whole genome patents' on sequenced viruses and cells have already been granted (O'Malley et. al. 2005).

Indeed, a general steep rise in gene patents in the United State, Japan and Europe is widely acknowledged, for instance the OECD says this means that patent databases have to be organised in line with the increasing role of information technologies and speaks of a rise from thousands to ten thousands of DNA patents that include the term 'nucleic acid' (OECD 2002: 8, 33 - 38). However Oldham disputes such numbers because he estimates that the pressure on patent systems as much greater, because between 2000 and 2003 the main biotechnology subclass in patent databases has gone from below 200.000 to above 300.000 patent publications. He reports that the United States patent office indicated that in 2000 it had around three and a half million patents pending on a total of seven million (Oldham 2004: 30, 31).[11]

Consequently there is some evidence that suggests that the transaction costs of the patent system are rising with the development of genomics. Another closely related theme from the tragedy of the anticommons is the fragmentation of information. It has, for instance, been estimated that 20%, or about 4000 thousand, of the human genes are already disclosed or claimed.

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[10] See the 'international rice genome sequencing project' (IRGSP) at http://rgp.dna.affrc.go.jp/IRGSP/nature436_793-800/nature05.html. The rice genome sequence contains 37,544 genes 'many of which are represented by 2 or more copies. About 71% of these genes are similar to genes found in Arabidopsis', a model experimental dicot plant which has been completely sequenced in 2000. A total of 2,859 rice genes however could not be found in Arabidopsis and may represent genes which differentiate the two major groups of flowering plants, monocot and dicot'. On the Human genome diversity project see GenEthics News issue 10: 4 at http://www.hgalert.org/topics/personalInfo/hgdp.htm (last checked april 2006)

[11] A comparison of OECD 2002: 8 with Oldham who looks at the sub-class, C12n sub-class of the WIPO database and speaks of 3433022 patents pending in 2000.

This includes more than half the known cancer genes and a minority carrying multiple patents, up to 20, for different usages. These are claimed by more than a thousand assignees of which nine out of ten are from the United States and about half are from private companies with the biggest, Incyte pharmaceuticals, with claims over two thousand claims on human genes, mainly for micro arrays (Jensen & Murray 2005).[12]

These micro-arrays, or gene chips, are perhaps the most illustrative departure point for a focus on the tension between genomics and patenting. The instrument consists of a series of ordered small glass slides with thousands of DNA sequences and markers that allows for the identification of gene expressions. More specifically this instrument provides input needed to construct databases and quantitative models. These models run on algorithms and allow statistical interpretations that 'normalize' the data. Eventually it is hoped that these algorithms and numeral coordinates can describe a higher dimensional space that constitute a model for the expression of genes, proteins and enzymes.

Economically speaking, this promises to replace much of the experimentation on chemical traits, which is getting particularly expensive. However, another way of looking at micro-arrays is that its aim of normalisation relies on the same statistical techniques as elsewhere. For instance it concerns serial and interval analyses, surveys, clusters, slopes, density maps and regression techniques. Accordingly the patterns revealed do not necessarily correspond to a fundamental biological principle but are determined by comparisons and experimentation on gene expression levels and vectors (Quackenbusch 2001). This is significant because such statistical aims have an uneasy relationship with biotechnology patents. There is evidence of patenting by key institutions of 'lower levels of the biological information hierarchy', meaning that gene patents apply also to the levels of proteins, metabolism and a range of phenotypes (Allarakhia and Wensley 2005: 1486). The objectives of 'system biology' are to understand system interaction and hierarchy, for instance between genes, proteins and metabolisms. It has been argued that system biology relies on bioinformatics to achieve the: 'ultimate integration of biological databases [which] will be a computer representation of living cells and organisms, whereby any aspect of biology can be examined computationally (Kanisha 2003).

Such system biology 'idealism' has little in common with the objectives of the patent system for biotechnology. Moreover there are, at the moment at

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[12] Jensen and Murray also say that the most highly patented genes were BMP7 an osteogeneic factor and CDKN2A a tumor suppressing gene. Of 23.688 genes in the database, 20% or 4382 are patented

least, only relatively few software patents in bio-informatics that have been claimed, are pending or are operational. (Welch 2002). Of course software patents were further extended in the 1990s by major patent offices to comprise the organisation of information in databases according to algorithms or as business models.[13] However the 'method and system' claims of such patents are particularly difficult and costly, either to enforce or to challenge. Consequently, in comparison to either biotechnology patents or software patents, it would seem therefore that 'system biology' takes place at a considerable distance from patent systems and the related 'anticommons' problems that were discussed previously.

Finally, the status of biotechnology as being the most patent-dependent sector can be limited further by emphasising that the few patents in bio-informatics coincide with a profitable market. While estimates are not always reliable, it can still be said that popular expectation of the market for bio-informatics tools and services runs on estimates in tens of billions, while the hardware market for the life sciences alone is estimated in single digit billions (see DiCarlo 2000, Welch 2002, Ricella 2001).[14] This absence of patenting from such markets takes the discussion of open source in biotechnology a step further then debates on the significance of the anti-commons metaphor. Of course, while the property relations of the informatics sector have been developing themselves around open source for some time and at a considerable distance from the relative efficiency of patents, they do apply to biotechnology instantaneously. As a first step, the linkage of property relations in informatics to developments in biotechnology is explored further around the transition from the initial 'high throughput determination' of early genomics to a deeper understanding of biological hierarchies.

With this aim in mind, the next section traces the commercial linkage of open source to bio-informatics and genomics and subsequently discussed the empirical evidence for speaking of open source in genomics in relation to common-based peer production.

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[13] In addition to the Charbaty patent, the Bayh Dohl act and Diamond v. Diehr of the early 80s (see footnote 1), here the major case is 'State street bank vs. Signature financial group' from 1998. The latter party had a patent on a "Hub and Spoke" method of running mutual funds. The Federal Circuit rejected the arguments of State Street Bank, and upheld the patent by explicitly stating that business methods can form patentable subject matter. See http://en.wikipedia.org/wiki/Software_patent (last checked April 2006)

[14] Welch estimates 40 billion in 2001 following Licking et al. 2000. Di Carlo (2000) says that IBM estimated conservatively 9,5 billion in hardware in 2003. International Data corporation estimates $38 billion prize by 2006 (Hall 2002).

Open source in bio-informatics

Already there are many straightforward examples of open source bio-informatics, like bio-java and bio-perl. These are 'bio' versions of existing programming languages that, like their counterparts in open source informatics, rely on their own voluntary support communities. There is an 'open bioinformatics foundation' and an 'open biology foundation', amongst many others, and there are software tools for the analyses of DNA functions, like Bio-bricks, and search engines for the comparison of genomic sequences, for instance Blast.[15] Therefore open source bio-informatics has objectives that are very similar to other open source informatics projects like the coordination, modification and the integration of improvements. They also periodically release upgraded versions under copyleft licenses.

Some have argued that also the human genome project is to be considered an 'excellent example' of open source in biotechnology, mainly because the project involved a lot of different institutes that had to decide on flexible research standards (Opderbeck 2004: 21). Indeed open source software was developed to support the effective participation of the laboratories in using different methodologies and precision standards. However open source was also explicitly decided as being too controversial for the human genome project's public objectives. In the end its sequences and annotation tools were released into the public domain without non-proprietary or share-alike clauses (Cukier 2003). If anything, the choice emphasises that commercial intentions are an integral part of sharing information in genomics; its results being an open source project might conflict with the emphasis on biotechnology patents.

Nevertheless open source has subsequently been emphasised by some of the institutes behind the human genome project. Firstly the specialised public genomics centres like the Welcome Trust Sanger institute and The Institute for

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[15] bioinformatics.org is an open source repository dedicated strictly to bioinformatics projects (over 150 projects). www.r-project.org is an open source language for data, statistics and graphics that is useful in a wide variety of areas including bioinformatics. www.mgb.pitt.edu/moleculartoolbox.htm is a list of "Useful Molecular Biology Bookmarks" that includes lists of recommended free software and web-based tools. See also www.sourgeforge.net with over 75,000 projects some of which are biology oriented. See also http://bioinf.kvl.dk/biolinux/, www.dnalinux.com, The best known biology tool is 'Blast' see www.ncbi.nlm.nih.gov/Education/BLASTinfo/information3.html There are also bio-informatics meta search engines and portals like 'Entrez' also of the National Center for biotechnology information (NCBI), part of the National library of medicine and part of the NIH. Another search engine is the bio-informatics Harverster see http://harvester.embl.de/ of the European Molecular Biology Laboratory. There is also STING (Sequence to and withIN Graphics), a free Web-based suite on protein sequence, structure, function, and stability, there are open source scripting languages such as Emboss (http://emboss.sourceforge.net), Bioconductor (http://www.bioconductor.org, BioPerl (http://www.bioperl.org/wiki/Main_Page), BioPhyton (http://biopython.org), BioJava (http://biojava.org/wiki/Main_Page) and Bioruby (http://bioruby.org/) For a more comprehensive explanation see http://en.wikipedia.org/wiki/Bioinformatics

Genomic Research (TIGR) have continued to support the open development of the management of genetic data. The Sanger institute has an open source project that aims to develop an open source automated sequencing browser and TIGR is integrating complementary research tools for researchers into a single operating system.[16] Other such examples are the 'science commons license' that has recently come online and that is being used by the most comprehensive protein database, called a 'neurocommons'.[17] Moreover there are also a few bio-informatics counterparts to Red Hat, the service provider to users of open source users that has listed stocks. For instance Electric genetics, a South African corporation offers validation of open source bioperl.[18]

To argue that open source in bio-informatics follows the commercial line of Red Hat would be to underestimate that it is still exceptional within the informatics market; not because it is open source, but because it is 'only' open source. In bio-informatics the obvious departure point is Compaq's role in the human genome project. The informatics company was contracted to provide the computing resources of Craig Venter's Celera and also for a number of institutes of the international consortium, for instance the Massachusetts Institute of Technology and the Sanger institute. This shows that it wouldn't make a difference for the commercial relation with the informatics market, whether it was the private or the public sector that first completed the draft map in the human genome race. Regardless whether the aim was to claim biotechnology patents, create a subscription database or to release the data, there was enormously expensive hardware involved (Einstein 2000, Cukier 2003). There is no reason why this would be different for Cereon's sequencing of Arabidopsis and Monsanto's and Syngenta's episodes on the rice genome (see Niller 2000).

By now Compaq, which merged with Hewlett Packard (HP) in 2002, seems to be loosing terrain as the market leader to Sun and IBM, a notable late comer considering it has a reputation in hardware. Compaq was still working with Celara's before its merger and has close relations to Oracle, who, in turn, supplies another big genomics company, Myriad that works with Celara on the sequencing of the human proteome (Herper 2001). Nevertheless by 2002 IBM got the contract with Celara, although HP announced a new collaboration with the Sanger institute at about the same time. (Vance 2002) The comeback of IBM has its main profile from Blue Gene, a successor to 'Deep Blue', the chess champion-beating computer that runs 'peta-bytes' and can do 1 quadrillion floating point operations per second, outrunning the predecessors of nuclear physics as the fastest computer in the world (Port 2005, Ricadela 2001, Herper 2001, Laird 2002).[19] It offers sophisticated management tools for supercomputers that can handle a higher complexity of operations, while Sun, HP-Compaq and Oracle organise parallel computing that can break down and reconnect operations; in principle even into hundreds of thousands independent systems.

For both approaches this denotes engagement with genomics ranging from open source methods and communities that develop the software up until IBM's hardware that comes with fully integrated management tools that run on Linux.[20] Moreover the competition over the contracts with major genomics companies is only one element among a range of domains within biotechnology development. IBM works with bio-informatics, software tools, gene chips, drug discovery and academic medical research centres. For instance it works with Lion bioscience in receptor drug discovery, with Nutec sciences on algorithms in parallel computing, MDS proteomics on mass spectrometry (protein behaviour in chemicals), Phase Forward on clinical trials and with Mayo clinic Duke University and the University of California (Hall 2002b &). Therefore the engagement of the informatics companies takes place across bio-informatics, software tool development and genomics but doesn't seem to feature biotechnology multinationals.

In the terms proposed in table 1, the previous discussion can be interpreted as related to 'proprietary open source', supporting the related thesis that projects that 'peer' shared information are becoming more efficient. The suggestion of Benkler of common-based production as a third production model is further supported by the observation that informatics companies are as supportive of such a market as they are ambivalent to the portrait of genomics as a race between private companies and public institutes. This places genomics as a market for informatics companies and raises a question about the relationship of open source to biotechnology multinationals and patenting. As a 'pragmatic' answer, it is important to keep in mind that, despite the mutual excite-

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[16] See http://www.ensembl.org/info/about/index.html on the ensemble genome browser and 'TIGR' for the CHADO project

[17] see http://sciencecommons.org/weblog/archive/2006/02/09/worlds-largest-protein-db-now-under-cc-license. see also http://sciencecommons.org/data/neurocommons and http://sciencecommons.org/licensing/scmta

[18] the South-African corporation Electric genetics offers services for bioperl users and SRS bioscience AG from Germany commercialises open source software developed by the European molecular biology laboratory. Red hat is the most famous company dedicated to open source that is listed in the Nasdaq 100. It started on services for users of Linux and from the revenues of subscriptions to its software modules.

[19] See Port (2005) for a listing of supercomputers, also it mentions that Blue gene has gone up from 187 to 367 tetraflops.

[20] see http://oss.oracle.com. For comment from the open source community see: http://www.oreilly.com/catalog/oracleopen/chapter/ch01.html on HP see: http://opensource.hp.com/index.php, http://h10018.www1.hp.com/wwsolutions/linux/index.html In 2002 Compaq led all vendors with 37% IBM 29% HP and SUN 10% and Silicon graphics had 7% (See Liard 2002, Herper, 2001)

ment between informatics and genomics, the bio-informatics market has so far been discussed mainly in relation to how statistics on genetic information get linked to software problems. These are notably large but are still about databases and software tools, for instance it involves the usual computing tasks of restarting operations after interruptions, absorbing new priorities in cues and assigning disk space.

Therefore the next section focuses on the notion of peer-production by further elaborating the linkage of the informatics and biotechnology sectors. In addition to the argument that bio-informatics is an important patent-less business, it is argued that 'common based peer production', as discussed in relation to table 1, is becoming integral to the contemporary science of the on-going gene research of genomics networks. Examples of sharing of information and peer production involve the SNP consortium and the more explicitly open source 'cellular signalling initiative' but also less commercial networks on yeast and 'Receptor Tyrosine Kinase'. Finally also the non-proprietary side to peer production is related to the Tropical Disease Initiative and the Brazilian ONSA network.

Open Source in Genomics

The typical example of sharing information in genomics is the SNPs consortium. It is a project of some of the major institutes in genomics and corporations in biotechnology that has the objective to encourage the sharing of information on DNA sequence variation. The members of SNPs consortium have agreed not to patent their sequence maps.[21] This is also the case in another prestigious project, the 'Cellular Signalling' initiative of Alfred Gilman, a winner of the Nobel Prize for medicine, which explicitly self-identifies as a 'commons' and as open source. Similar to the SNPs consortium it has its background in the institutional and financial backing from prestigious stakeholders and researchers like the National Institutes of Health (NIH), Eli Lilly, Merck, Aventis, Johnson and Johnson, Novartis and also the scientific journal Nature. However a relevant difference with the SNPs consortium is that Gillman's project not only uses a copyleft license to convince researchers to release their data into a commons but, in addition, also models quantitative virtual cells by interactive peer reviews of genetic information outside of journals or patent offices.[22]

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[21] for the SNP consortium see http://snp.cshl.org/

[22] see www.gmm.gu.se/YSBN, www.signaling-gateway.org.

Of course a straightforward observation should be that, in both cases, the stakeholders contribute to the commons because they rely on a few patented and, more importantly, marketable products. In other words they have little interest in an extension of patenting to sequence variations, especially if the patents aren't exclusively theirs. It already appeared from the previous section that the business of bio-informatics is being organised along open source lines. Consequently a formation of scientific networks that share and peer review data should also be seen as a projection of the informatics market. However there are also examples of open source networks in genomics that are less explicitly tied to commercial interests of either the informatics or the biotechnology corporations.

The Yeast Systems Biology and the Receptor Tyrosine Kinase networks are examples of scientific attempts to pool the necessity of researchers and to share their research around flexible global standards and dynamic protocols. In comparison to the SNP consortium or Gilman's network, these networks involve hardly any external backing and take a more gradual and global approach to the management and integration of the different information flows. (Ewan 2004, Kitano 2005) In addition there is the 'Tropical Disease Initiative (TDI) that is similarly about a non-proprietary approach to interactive and quantitative modelling, but also tries to motivate scientists through a humanitarian objective. For instance it aims to address the failure to develop drugs for purposes that don't support the sale of patented products by proposing research on diseases like Chagas and Malaria that mainly affect the poor and are therefore without a lucrative market.

TDI's take on open source is similarly about the construction of a global network that is internet based and involves shared annotation and cross referencing by researchers. Also here the idea is that the scientists will analyse public genetic information and contribute it to a common database where it can be peer reviewed and oriented to the identification of interesting candidate genes for further research. The organisers argue that in: 'the same way that programmers find bugs and write patches, biologists look for proteins ("targets") and select chemicals ("drug candidates") that bind to them and affect their behaviour in desirable ways'. In line with the prevalence of open over closed source, also here the 'research consists of finding and fixing tiny problems hidden in an ocean of code'.[23]

However, in contrast to the other genomics networks, the motivation of participators isn't only purely scientific, but is tied to the project by its aim of

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[23] http://www.tropicaldisease.org/about

organizing early phase drug discovery so that it reduces the cost of developing and manufacturing cures for tropical diseases. In the end the suggestion is that a 'virtual pipeline' of drug development oriented at tropical diseases will fill with potential candidates and targets, so that governments and charities can sponsor contrasts for drug development, much the same as they already do, but without intellectual property. Thereby publicly financed contracts on tropical diseases can be more focused in terms of research and therefore also financially, while later the production of drugs will not depend on royalties and only depend on manufacturing costs and market competition (Maurer et al. 2004).

Although TDI is hardly operational and its take on open source is not oriented at the value of the formal property system, it is still an illustrative addition to a line of arguments that emphasises the opportunities of genomics for developing countries (Thorsteinsdóttir et al. 2003 and Masiga et al. 2004). Such arguments encourage the further participation of public institutes from developing countries like China, Brazil, India and Thailand in the public consortia of the human and rice genome projects and support frameworks wherein regional genomics research and biotechnology industries could flourish. Indeed the typical examples of the importance of genomics in relation to the national interests of developing countries are the two rice genome projects. One of these involved a variety called japonica Nipponbare, which is mainly grown in Japan, South Korea and the US, while China released its own draft of the 'indica' variety, which is also the most cultivated rice in the world (Niller 2000, National Science Foundation 2000). There are also projects at a more regional level like the ONSA network from the Brazilian state of Sao Paolo, the first public scientists to sequence a genotype.[24]

As one of its researchers argues, the Brazilians follow a different model then a 'purpose built and professionally staffed genome centre like TIGR', because it isn't necessary anymore to have a lengthy process of organisation to set up a dedicated genomics centre. Instead they follow the shotgun method of the private sequencing projects and apply it to bacterial genomes that are of interest in the Brazilian context. While for instance the TIGR centre follows the commercialisation of hardware with integrated open source software, the Brazilians linked a small number of traditional resource labs in an extensive network by the internet. Of course what motives the researchers is its low costs but also its additional benefits because such integration of researchers with different expertise around a sequence means that 'specialist knowledge in many unsuspected facets (..) [came] to light, immediately leading to new research avenues' (Simpson 2001: 989).[25]

As might be expected the research relies on public sponsorship and is being oriented towards commercial applications and even has a small sector of venture capital spin offs in Sao Paolo (Ferrer et al. 2005, Greco 2003, Kumar 2004). The public funding and market orientation of ONSA and also TDI, can be differentiated on the latter's explicit denunciation of patenting. It has linked its idea of a public good, tropical medicine, to a non-proprietary common based peer production process, while ONSA, the SNP consortium and Gilman's network are attempts to link the sharing of information and the networked character of genomics to firm efficiency in the patent based innovation process. While TDI also aims to release its results into the market, it is much closer to an open source service company. In this sense it is like Red Hat, but with a focus on public sponsors and mission. This also recalls the distinction between the proprietary and non-proprietary sides of table 1. The latter can then be related to TDI and networks like those on Yeast, Receptor Tyrosine Kinase because of their appeal to voluntarism in science, sometimes based on humanitarian aims, to increase the availability and accessibility of interactively peer reviewed information. On a more commercial note, a stakeholder framework is the point of departure for certain genomics projects that can thereby draw on a pre-defined community of scientists that share information of interest to distinct public and private investors.

Although there are differences between these networks, the examples also deepen the claim that property relations in biotechnology are changing. The relative value of the property system from Benkler's model could be traced for both sides to common-based peer production. This also means that none of them directly engages with patent offices and in the case of Gilman's network even seems to replace scientific publishing. A difference with previous paragraphs on bio-informatics that the commercial side to these networks not only involved the informatics multinationals but this time also biotechnology multinationals that perceive the sharing of information on the genetic code in relation to biotechnology patents.

Finally, TDI takes the heuristic focus on 'common based peer production' in genomics to an international level. On the one hand it demonstrates that genomics might also be oriented at the social and humanitarian objections to biotechnology patents. On the other hand, the project's engagement with

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[24] First ONSA sequenced Wylella fastidiosas, a bacterium that attacks citrus fruits. Later they also sequenced organisms that are of interest in relation with sugar cane, grapevine strains and finally for cancer, tuberculosis and Chagas.

[25] Simpson 2001: 981. The Brazilian network comprised more than a hundred scientists and twenty-five laboratories

biotechnology patents is also strictly limited to tropical diseases. The next paragraph briefly reflects on more principled grounds behind an emphasis on the accessibility and free release of information within the international organisation of genetic resources along open source lines, mainly by comparing a substantive notion of common property, analogues to the Free Software Foundation, to the existing mandate on genetic resources as a common property.

Open source and common property politics

Open source has already been argued as an alternative common property model for the current international organisation of genetic resources; both by persuasive argumentation and by manifestos directed at the World Intellectual Property Organisation of the United Nations (WIPO) (Drahos 2005, Boyle 2004, Oldham 2004).[26]

The WIPO was assigned a section of the mandate that its successor on intellectual property the WTO got at the revision of TRIPS in the 2001 Doha trade round. They received the task to 'foster respect for intellectual property in regard of traditional forms of ownership'. The WIPO relates compensation for traditional knowledge (TK) to patents on plants and medicines but describes TK as something holistic, meaning that it is: 'inseparable from their very ways of life and their cultural values' as well as important to sustainable development (WIPO no date). Currently there are on-going negotiations on the agreement on 'access to genetic resources and benefit sharing, traditional knowledge and folklore'. Moreover open source models are also associated with the explicit attempts to strike a balance between sovereignty and intellectual property. The FAO has recently devised a compensation scheme in the International Treaty on Plant Genetic Resources for Food and Agriculture. (Graff & Zilbermann 2001, Grain 2004) It means that the recipients of certain genetic resources agree to pay into an international fund (Global Crop Diversity Trust) an equitable share of benefits arising from the commercialization of the included 100 crops and forages, including rice, banana and potato but excluding commercial crops like tomato and soybeans.

Both of these international agreements revolve around an idea that was launched in the eighties after patents had been introduced to biotechnology, the right to compensation for the developing countries that were supplying the basic material (Kloppenburg 1988). This argument refers to the Vavilov centres of biodiversity, the areas where most species can be found, located by and large in developing countries.[27] Subsequently there have been series of attempts to make the recognition of sovereignty over genetic resources of the CBD and the emphasis on patents of TRIPS compatible by calling for compensation for developing countries. Of these the FAO and WIPO are two of the latest. (Seiler & Dutfield 2002, Dutfield 2001, 2003 Blakeney 2000, Drahos 2000).

These mandates engage with common property but its interpretation is also secondary to the stagnated attempt to achieve compatibility between the principles of sovereignty and private property. This stagnation can be seen in the negotiations over the Cartagena Protocol on bio-safety, especially around article 18 on the labelling of genetic modified organisms, which either attributes jurisdiction to southern countries receiving GMOs or with the northern countries producing them (Dutfield 2003, Bereano et.al 2004). Moreover, at a wider reach, the latest trade rounds tend to fail because developing countries have refused to discuss intellectual property without concessions on conventional agriculture. The question to consider here is then: 'how is open source in genomics and biotechnology related to the international organisation of genetic resources?' On the one hand the release of genetic information in open source projects seems to resonate with the FAO approach to common property, extending a common property of crops with the explicit release of genetic information without patents. On the other hand, the genomics networks, at least at the moment, don't engage explicitly with the common property politics around the traditional knowledge mandate of the WIPO.

Firstly, it is perhaps the ONSA network that comes closest to the traditional knowledge field of interest because it has branched into the Amazon, becoming the first genomics institute located inside a biodiversity centre. This isn't meant in the contentious way that the Human Genome Diversity Project (HGDP) maintained that samples of DNA needed to be collected as quickly as possible before small native population disappear. The peoples in question, rightfully, considered this an insult, because the project regarded their DNA but not their rights to self-determination and their continued survival. Instead ONSA is an illustration along the lines of the International HapMap which came afterwards. This project only involved 269 individuals from four different populations, because thereby it seems that it avoids much of the controversies of the HGDP. Recently, the Hapmap released the preliminary results of the sam-

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[26] The Geneva Declaration on the future of WIPO (2004: 1) At:
http://www.cptech.org/ip/wipo/futureofwipodeclaration.pdf

[27] For different maps on the Vavilov centres and also on 'biomes', see
http://oregonstate.edu/instruct/css/330/two

ples of human sequence variations it collected and if further aims to find haplotypes with frequencies above 5 % (Wade 2006, Bakalar 2005).[28]

The point, to emphasise it again, is that projects like ONSA and the Hapmap, even in the middle of a zone as symbolic as the Amazon, could sidestep the community approach to biodiversity reflected in the entries on farmer's rights, indigenous rights and traditional knowledge. At its widest extension this seems to mean that by sequencing and releasing genetic similarity into the public domain, both the patent and the public regulation frameworks can be left in place. Therefore it would seem that open source, being closely related to the networked character of genomics, is only about economic efficiency, scientific necessity and doesn't yet extend its potential to a renegotiation of the demise of common heritage and the peripheral standing of the common property approach in global governance.

However, in second place, the FAO approach to common property does resonate with a re-interpretation of open source: the 'Biological Innovation for Open Society (BIOS) initiative of the Center for the Application of Molecular Biology to International Agriculture (CAMBIA). Its principle protagonist is Richard Jefferson, amongst other things, the inventor of the renowned glucuronidase (GUS) reporter-gene system.[29] His take on open source is that he wants to 'free the tools of genetics', currently locked up in patents, so that there might be 'cropping systems suited to their environment their societies and their economies' (O'Neill 2003). Therefore, not only genetic information or crops would be released into an intellectual commons but also plant biotechnologies.

Specifically BIOS offers a technology package that includes an alternative method for transferring genes to plants for Monsanto's agrobacterium patent (the agrobacterium-independent TransBacter™ plant transformation system) and an activity colour test that visualizes where genes are and what they do (the GUS-PLUS). In the future the package will involve more gene transfer tools, as well as selective markers, promoters, gene silencing and perhaps, a nicely named proposal of Jefferson: 'minor HART surgery (homologous allelic recombination/replacement technologies)', which involves 'subtle, in situ surgery on the plant's own genes changing the performance of crops. (Cambia 2003)

In addition BIOS' follows the copyleft 'share alike' principle, meaning that it encourages researchers to draw freely on its collection but it also requires

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[28] See also GenEthics News issue 10 at http://www.hgalert.org/topics/personalInfo/hgdp.htm (last checked april 2006) Included in the hapmap 90 people from Ibadan, Nigeria; 90 Americans from Utah; 45 Han Chinese from Beijing; and 44 Japanese residents of Tokyo. See www.hapmap.org/abouthapmap.html

[29] Gus concerns a blue-staining enzyme that when co-expressed with a chosen gene, highlights the gene's expression pattern in plant tissues. The invention is one of the most widely used in plant molecular biology.

that modifications of research tools are added to the common pool. Its aim is to make its entire technology package available for downstream research. This already resonates much more with the aim of the FSF to construct an operating system that is an equivalent to those that are patented then the other examples of open source in bio-informatics or genomics. Moreover it also has a 'patent lens' project that runs parallel to the complicated public databases of national patent offices and especially to the commercial patent services. It aims for an open source database of intellectual property that reviews the obscure licensing practices of different biotechnologies (Nottenburg et al. 2002, Nature Publishing Group 2006, see also Graff & Zilberman 2001). In this regard open source biotechnology also enters the line of work of companies like Thompson, a major scientific publishing house that is also big in valuing intellectual property by concentrating intellectual property management services.

Although BIOS has argued that open source corresponds with the genotype approach, like TDI and other networked approaches to genomics, it is still very much involved with more conventional aspects of biotechnology development. Their technologies have already been used in corporate and public research on plant biotechnology, for instance in cell lines developed in China and landraces in India. In addition they are also explicitly supported by the public research institutions from the United States of the Public Intellectual Property Resource for Agriculture (PIPRA); a coalition of universities that are interested in biotechnological development of specialty crops along similar lines as during the Green Revolution.

At that time conventional specialty crops with higher yields were developed and introduced to developing countries in the late seventies, mainly involving public institutions.[30]

PIPRA argues that this approach can't be extended to biotechnology development because the introduction of intellectual property has led to a fragmentation of the ownership of genetic information. Accordingly there is an anticommons tragedy that supposedly obstructs more effective modifications meaning that while working with a particular technology no single public institution can be sure about their Freedom To Operate (FTO). On condition of FTO, PIPRA argues that biotechnology could be extended to a next Green Revolution, especially considering that the more important crop biotechnologies have been developed by the public sector, like the transfer of genes into plant cells, unique patters of gene expression and the identification of many

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[30] See also http://www.pipra.org/

genes that confer important traits (Binenbaum et al. 2003). PIPRA's association with BIOS involves a contribution to the technology package by the reorganisation in a patent pool of public sector patents which still number substantially more then those owned by any single company. Moreover a shared collective management regime aims to become an equivalent to an international 'patent clearing house', a governmentally organised patent pool, by developing open source tools and mechanisms that could make the patent landscape more transparent and that can focus public biotechnology development on the construction of FTO (Atkinson et al. 2003). Recently also the International Rice Research Institute, part of the Consultative Group on International Agricultural Research, announced a joint venture with the BIOS initiative.[31]

However, the typical criticisms on the Green Revolution would then also apply to modern biotechnology along open source lines. Firstly the monocropping systems of many developing countries are already organised exactly along the lines set out by the Green Revolution. This suggests that open source in biotechnology and genomics would further compromise sustainability at the community level along the lines that Broerse & Bunders have described by calling for a 'contextualisation' of biotechnology within the regional 'social-ecological' systems because otherwise: 'ag-biotech is likely to threaten the stability and social cohesiveness of the developing world by jeopardizing food security and reducing the viability of small scale farming' (Broerse & Bunders 2005). Therefore, Ruivenkamp calls for a 're-connection to endogenous developments' of biotechnology tools. In the context of open source in genomics such a perspective would not emphasise the transfer of patents or the release of biotechnologies but mechanisms that allow for sustainable ownership of 'tailor made' biotechnologies. An example of such a mechanism is Ruivenkamp's discussion on alternative techniques to genetic modification, for instance how Apomixes can let plants reproduce without seed, thereby possibly reversing the exclusion of farmers from the propagation of seeds by natural patenting like hybridization and terminator technologies (Ruivenkamp 2005).

It is also in terms of such mechanisms that an open source approach to the polemic discourses on 'piracy' should be seen. This term has two interpretations, 'patent piracy' and 'bio-piracy', meaning on the one hand, that patent royalties get lost in the black markets of developing countries or, on the other hand, that corporations receive patent royalties for genetic traits that are part of traditional knowledge (see May 2000, Sell 1998, also see Bonalume 2001, Zi, 2005). While open source seems to remove much of the sting from the questions of recognizing patents and traditional ownership, replacing it by FTO for genome scientists, it is questionable whether this should be welcomed as good news. The Hapmap, ONSA, and also Ruivenkamp's example have illustrated that such a straightforward interpretation of open source would leave the community approach to biodiversity without a linkage to the introduction of biotechnology. By extension a turn towards open source would runs contrary to the persistent optimism about compensation and benefits from bioprospecting, which is more difficult to maintain if communities are less strategically important. (see Pires de Carvalho 2005, Sheridan 2005, Svarstad 2002).

Finally then the discourse of the FSF has been interpreted within the context of biotechnology development. Its principled interpretation doesn't yet seem to have much points of reference in the international politics of common property over genetic resources. Despite the higher number of pragmatic examples, this doesn't mean that such an approach can ignore its relationship to a 'Freedom To Operate, the wider intellectual property system, juridical compensation schemes or state policies over safety policies. Only a distinctive open source philosophy of 'commonality' for genetic resources would address such themes and be able to engage with the marginal position of common property in the international system in general. At a philosophical level the distinction between the two interpretations follow Hardt & Negri who differentiate the 'commons' and the 'common'. It means that there is an historical commons that in a distant past was a 'part of pre-capitalist shared space from before the advent of private property', and there are common resources that are related to the recognition of: 'cultural singularities, not as anachronistic survivals of the past but as equal participants in our common present' (Hardt & Negri 2004: 126). This, in turn, means the social potential of open source in biotechnology should have as its political context the relation of genetic material to the lack recognition of individuals, communities and peoples that do not have clear national or international legal personalities (see Kingsbury 1998, Meijknecht 2001).

Conclusion

At various levels the principled and the pragmatic interpretations of open source as a common property, could be demonstrated as being closely related to biotechnology development.

Firstly, along the lines of the pragmatic approach to common property the practices of open source in genomics can be said to correspond to a growing

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[31] See http://www.bios.net/daisy/bios/1374/version/live/part/4/data

and diversifying market for hardware systems and software programs for informatics companies. It can be expected that many of the scientific objectives in genomics, as an articulation of informatics, are unsuitable and sometimes even unsusceptible to biotechnology patents. Its implication is, following Yochai Benkler's 'common based peer production', that there seem to be less chance for start-ups in open source biotechnology to strategically develop a single or a few commercial patents. In exchange it would emphasise start-ups in genomics that draw on information along open source lines, earning their money by delivering services to the biotechnology multinationals that control downstream patents and develop products.

Secondly, a more principled interpretation of common property can be emphasised analogues to the FSF. Such an explanation of open source would find it objectionable to be part of the construction of an 'intellectual common pool' that delivers patentable products for biotechnology multinationals but can't be patented by others. In such a context there is little relevance about how projects engage with open source principles in the public release, sharing and interpretation of genetic information, as long as it takes place within the given context of how informatics and biotechnology companies relate to market value. Instead a strict FSF analogy would follow the idea of the 'kernel' that in informatics is associated with Linux was as the missing link to the objective of a free operating system. In a similar sense, a kernel in system biology refers to the 'higher dimensional feature space' where vector distances that demonstrate or obscure features can be rotated and measured by mathematical functions (Quackenbush 2001). Consequently the ideal of a free kernel for genomics would at least revolve around a comprehensive integration of biological databases in computer representations, and could perhaps be connected to the sort of active engagement to release biotechnologies of BIOS.

However this strict comparative design, FSF informatics - biotechnology, might also distort its extension to biotechnology development when interpret within a wider context. While in informatics open source succeeded the principled approach to common property, in biotechnology, the most far reaching ambition is still only about a 'freedom to operate' for scientists. These scientists might do very important work on development issues, perhaps even be in developing countries, but doesn't take the open source idea about a free commons towards its full conclusion. Perhaps, the over-emphasis on the difference between the intellectual commons in genomics and intellectual property has gone at the expense of orienting open source towards its physical commons. Paradoxically, a re-organisation along open source lines seems to 'return' common property, as the title has announced, to scientists that are involved in biotechnology development. It isn't necessarily engaged with the original purpose of common property approaches: supporting the conservation and cultivation of biodiversity as common properties when it emphasises curing tropical diseases and constructing 'freedom to operate' biotechnologies.

While the concept stretch might not matter much in relation to open source code, within the wider political context of genetic resources, it is insufficient to interpret open source biotechnology as a 'new commons' for scientists when the parallel with an 'old commons' runs along a conceptual line that is void of communality. To that end, the principled approach of Free Software should also for open source biotechnology be thought through: 'in terms of participation, value sensitive design and transparency' (Berry 2004: 83). At a more systematic level it should then also engage further with the wider discourses on democracy and the democratization of technology in contemporary critical theory around interactive processes, sub-politics and the re-appropriation of the design of technologies (See Habermas 1991, Beck & Giddens 1994, Feenberg 1999).

In this sense the ideas behind free software and also open licensing initiatives are powerful departure points for a re-interpretation of open source that emphasises a common property approach against the frameworks of TRIPS and CBD. In this regard research/advocacy organisations like BIOS would be the most suitable candidates to explore copyleft licenses that attribute the ownership over genome research to communities and explore commonality with the genomics networks and gain a more recognizable identity in regard of the current humanitarian mainline on biotechnology in the process. Open source should be a mechanism to insist that common property is not about genome scientists or access to biotech in developing countries, but about finally prioritising a common ownership that is specific to genetic resources.

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