Genomic information and the public–private imbalance

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This paper investigates the extent to which public–private relationships produce unbalancing effects in the case of the generation and use of genomic/genetic information. To this end, it focuses on two interconnected issues. The first is the purported importance of genomic information, which is used to justify public spending on its production. The second is the problem of ownership and accessibility. By examining the 'balance' rhetoric together with the information/molecule separation, the patentability of DNA, university–industry–government relations and the role of extended public networks for proprietary genetic products and technologies, it suggests that the supposed balance between private interests and public benefits is in fact an unbalancing act in favour of private interests under the capitalist social formation.

Introduction

The 'genome race' between the Human Genome Project (HGP) of the publicly-funded International Human Genome Sequencing Consortium and the privately-funded Celera Genomics Corporation, the latter founded and led by Craig Venter, had a happy ending.[1] There was an official joint announcement of the completion of the first survey of the human genome at the White House in June 2000.[2] What was initially thought of as 'a clash of ideologies and sequencing strategies, academia against big business,

public ownership versus private entrepreneurship' (Davies, 2002: xi) was, in the end, presented as 'a marriage between public funding and private entrepreneurship' (Jasny & Kennedy, 2001). The accomplishment of the mapping and sequencing of the human genome was represented as a celebrated success story for public–private cooperation. This view of the competition–cooperation oscillation is predicated on the notion of there being two firmly separated public and private planes. The pitting of the two spheres against each other is based on competing and conflicting connotations such as public/national interests, solidarity, distributive justice, openness, inefficiency and slowness on the public side; and individual interests, injustice, enclosure, freedom, entrepreneurial qualities, efficiency, productivity and speed on the private side. What follows from this, then, is the suggestion that the success of the genome undertaking lies in the reconciliation of the distinct qualities embedded in the public and private spheres: Celera's sequencing method was very fast, but the time-consuming sequencing method of the HGP made the research outcome more reliable; the speed of Celera, which declared the job complete in three years, pushed the HGP (launched with a fifteen-year plan in 1990) to speed up and become more efficient by obtaining more public funding in order to catch up with its rival. Equally, the HGP provided us with unrestricted, open access to the produced genomic data, undermining the company's selfish attempts at profit-making from the data (Dennis & Gallagher, 2001: 32; Jasny & Kennedy, 2001; Davies, 2002: xiv).

So we are told that the two research efforts to sequence the human genome not only contributed to each other's work in technical terms, but that the end product was an indication of a political balance between private interests and public benefits for the common good. This idea was reinforced by Prime Minister Tony Blair, who announced via satellite at the White House: 'We, all of us, share a duty to ensure that the common property of the human genome is used freely for the common good of the whole human race' (Blair, 2000). In a similar vein, it is generally agreed that the justification for the existence of intellectual property rights (IPRs) over genetic information and materials is based on the idea of the public–private balance. This constitutes rewards and incentives for inventions and innovations (private interests) on the one hand, and the diffusion of knowledge and technology (public benefits) on the other.

Through balancing mechanisms, it seems as if everyone is better off.

However, in this article I revisit the public–private divide to show that the supposed balance is in fact an unbalancing act in favour of private interests under the capitalist social formation. To this end, I shall raise two interrelated points. The first concerns the importance of this information in providing the justification for public spending on its production. The second concerns the problem of ownership and accessibility. If genomic information is so important that taxpayers' money is spent in order to produce it, how can proprietary rights bound to limit its accessibility be explained? I shall not attempt to contribute to long-established, well-developed theoretical discussions about the formal separation between public and private spheres, the political and the economic, the state and civil society, and sovereignty and property rights. Rather, I will investigate the extent to which the public–private relationship produces unbalancing effects in the case of the generation and use of genomic/genetic information.

From genome to public benefits: An easy path?

The media usually draws a mathematical equation between genome sequencing and public benefits. Following the publication of draft sequences of two subspecies of rice, a British newspaper recently reported that 'Rice DNA finding will transform how the world is fed' (quoted in Cyranoski, 2003: 796), as if hunger were a genomic problem. Similarly, the importance of human genome sequencing has always been based on high expectations on the political front. President Bill Clinton hailed this scientific breakthrough as 'the language in which God created life'. He suggested that 'with this profound new knowledge, humankind is on the verge of gaining immense, new power to heal' human diseases (White House, 2000). This emphasis on the public benefits of genomic information is not merely confined to popular and political jargon. In scientific literature, too, it is described as 'the most precious collection of information imaginable' on the grounds that, since we can now read the instructions for making human beings, human genome sequence information is at the pinnacle of the realisation of self-understanding of humanity on the one hand, and a technical achievement promising disease diagnosis, therapy and prevention on the other (Dennis & Gallagher, 2001: 7–8). From the very

inception of the HGP, the scientific value of human genomic information was repeatedly constructed on the basis of these two benefits (Keller, 1992: 294).

In fact, the formal objectives of the project were the sequencing and mapping of three billion DNA bases in the human genome, and the development of the methods and technology with which to do this. Human genomic research was conceived in the US Department of Energy (DOE) in the mid-1980s in order to understand the mutagenic effects of exposure to radioactive and other toxic waste. DOE involvement in microbial genomic research was encouraged by the possibilities of genetically engineering certain bacteria for the purposes of waste control and environmental clean-up. As the DOE's research initiative with the involvement of the US National Institutes of Health (NIH) became a publicly-funded mega-project to sequence the whole human genome, its public benefits were also expanded from being 'a cleaner environment' to 'unravelling the mysteries of life', 'knowing ourselves', 'revolutionising genetics' and 'thwarting diseases' (Human Genome Program, 1996: 2–6). Establishing a direct link between the HGP and genetic therapy on scientific and political fronts would justify its use of public funding. According to James Watson, the first director of the HGP, 'Congress actually seemed to like the human genome program because it promised to find out something about disease'. The logic behind the justification of the publicly-funded HGP as presented by Watson is simple: since many diseases, including Alzheimer's, manic depression and even alcoholism have a genetic cause, and since the HGP comprises genetic research helping to discover the genes involved in genetic diseases, public funding through the NIH, whose objective is 'to improve American health', is being properly used for the public good (Watson, 1992: 165–7).

This logic is problematic at every point. First, bald claims about the genetic causes of diseases resonate with gene reductionism. In biology, a gene is a stretch of DNA that consists of adenine, guanine, cytosine and thymine bases, represented by the letters A, G, C, and T respectively. The reading of the order of the four letters gives the 'genetic code'. When it is claimed, in a reductionist fashion, that the genetic code contains the instructions by which a human being is made, the HGP becomes an attempt 'to explain people our physical and our social presence, by going back to the seed, the moment of zygotic zero, when sperm joins egg' (Rothman,

2001: 19). Since some of us are alcoholics, there must be a gene for it, since it is the genetic code that makes us individuals. However, even if an 'alcoholism gene' were identified, its effects would be different in different people embodied in different time–space contexts. Even when the gene associated with a single-gene disease is identified, the cause–effect relationship is not straightforward. Consider the 'cystic fibrosis gene', which has been located and sequenced. Although the disease is said to be caused by a mutation to a gene on chromosome seven, there are actually more than 850 identified mutations, deletions and insertions leading to the altered function of the protein[3] responsible for the disease. The gene becomes active in some individuals but is recessive in many others, who show no adverse symptoms. And yet research has shown that its symptoms are also related to socioeconomic status, diet and exposure to infectious bacteria (Nossal & Coppel, 2002: 90; Bowring, 2003: 153–4; Ho, 1999: 227). In this way, the reductionist understanding of the static sequence of the genome fails to see the complexity of the multifaceted and dynamic relationships between genes, organism and environment (natural and social).[4]

This brings us to the second flaw in the view equating the HGP with public health. The HGP has provided us with the map showing the location of genes on chromosomes and with their sequence information. Some disease-associated genes can be identified and placed on the chromosome by using the genomic data. However, as John Sulston, one of the scientists involved in the HGP, points out, too little is known about how genes actually work. Having the inventory of genes to hand, 'each gene has now to be painstakingly examined to identify its role. The gene list will be constantly scrutinized by people who are looking at systems in the body' (Sulston & Ferry, 2002: 249). Just as gene expressions for good or bad (diseases) are dependent on physiological, cellular and environmental contexts, so too interactions between genes, the role of regulatory regions that turn genes on and off, cellular instructions and the responses of the organism to external stimuli and environmental changes are all important factors in supposedly genetic diseases. Genetic variations within the human population are indicative of these complex relationships manifesting themselves over the course of the developmental process. Single-nucleotide polymorphisms (SNPs) indicate sequence variations within the human genome. SNP is a difference in a single base—a single-letter difference

between my genome and anyone else's, which could be associated with variants of a particular disease from which I suffer. It is estimated that each individual genome differs from all others at about 3 million SNPs within the 3 billion bases of human DNA (Melton, 2003: 917). Even from a genetic-reductionist perspective, without personal SNP genotypes, susceptibility to genetic diseases due to disorders in gene sequences cannot be determined through the standard sequence of the human genome. Furthermore, if there were a causal link between gene sequences and diseases independently of physiological and environmental contexts, the genomic data of the HGP would only be the first humble step towards 'thwarting diseases'. This is because the biomedical steps of diagnosis, therapy and prevention include gene/target identification, target validation, drug/technique identification, clinical trials and marketing. However helpful genomic data may be in discovering and correcting genetic disorders, therapy is based on techniques, methods and reactions to drugs rather than on the sequence 'language in which God created life'. Another aspect of treatment is the gap between possibility and actuality, as with the case of sickle cell anaemia. Theoretically speaking, it seems possible to restore the defect in the haemoglobin gene associated with this diagnosable disease; but there has been no cure for it so far. Even if there had been, since the gene is also associated with resistance to the malaria parasite in carriers of only one mutant-haemoglobin gene instead of two, any treatment would have counterproductive implications (see Bowring, 2003: 151; Nossal & Coppel, 2002: 85–90; Lewontin, 2000: 156–7) for those who live in malarial environments, for genetic diversity and for future generations.

The third flaw in the argument justifying the HGP concerns the beneficiaries of the outcome of the HGP. As we have seen, there is no linear, cause–effect link between the genomic information provided by the HGP and the healing of diseases. This information does not necessarily result in any therapeutic power to improve 'American health'. One might put an emphasis on the second, purportedly public benefit of the HGP, which is 'to know ourselves', as it is put in a DOE publication (Human Genome Program, 1996). It is true that genomic data and research may well serve to help us understand our genetic structure, but the genome is only one component among many others that make up the whole. When 'to know ourselves' is predicated on knowing the genomic

sequence that, as claimed, makes us human, 'deciphering the code' conceals more than it unravels, not least because the social component of our human condition is completely missing from the sequence of As, Cs, Gs and Ts. For example, President Clinton's claim that all humans are equal stems from the sameness of 99.9 per cent of our three billion nucleotide bases, identified thanks to the HGP and Celera (White House, 2000)—as if inequalities in the social world were not socially structured, but rather endured due to the lack of an understanding of genomic sameness. Thus the public is not the immediate beneficiary of the publicly funded project in terms of its two celebrated benefits.

The real beneficiary of the project is, however, the 'private sector'. Biotechnological and pharmaceutical corporations that develop and sell diagnostic and therapeutic products for gene-related diseases, and bioinformatics corporations that store, process and sell genomic databases with computer-related techniques and programmes, are largely dependent on the sequence information and genomic maps as the 'infrastructure' or 'raw materials' of the process of developing marketable end products. At first sight, it seems contradictory to argue on the one hand that the beneficiary of the HGP is not the public in health terms, and to suggest on the other that corporations reap the benefits as they use genomic information to develop new drugs and diagnostic procedures. However, there is no contradiction. For one thing, to criticise the rhetoric implying that sequence information has an intrinsic therapeutic power in itself is not to assert that genome knowledge has no use in developing therapeutic tools at all. It is one thing to see the HGP as being about saving children's lives, as Francis Collins, director of the US arm of the HGP, put it in the HGP's earlier stages (Roberts, 2001: 1188)—as if the reading of sequences put an end to diseases. But it is quite another to talk about the production of infrastructural information, as Collins and his colleagues did following its completion. While refuting the former rhetoric, my argument finds the significance of the latter view within an understanding of capital accumulation. In their paper sketching out the multi-stepped future challenges facing researchers, Collins and his colleagues emphasised the foundational importance of genomic information with the following example: the identification of disease-associated genes, 'once a Herculean task requiring large research teams, many years of hard work, and an uncertain outcome, can

now be routinely accomplished in a few weeks by a single graduate student' (Collins, Green, Guttmacher & Guyer, 2003: 835). The genomic data produced by the HGP has not only enormously speeded up and cut the cost of the search for new genes, but the HGP itself has also identified many more (Nossal & Coppel, 2002: 184). New genes are new profit opportunities for corporations, either through the development of expensive drugs and diagnostic techniques, or through working on new genes or discovering patentable genes. Thereby, the outcome of the HGP facilitates 'gene hunting'. I shall elaborate on the question of gene patenting in the following section.

Craig Venter's business enterprises are a good example of how the benefits of the HGP can be reaped. Celera Genomics, set up by Venter in 1998 to sequence the human genome, directly and indirectly benefited from the HGP. Celera's ambitious project was based on an automated sequencing machine called ABI Prism 3700, which speeded up the sequence process by a factor of eight. The machine was the product of the Perkin-Elmer Corporation, which also owned 80 per cent of Celera. Emphasising its speedy process, Celera turned genome research into a race, driving the public initiative to buy high-speed machines at a price of $300,000 each from Celera's sister company (Marshall, 1999: 1906–7; Sulston & Ferry, 2002: 196; Davies, 2002: 145–8). Venter's 'non-profit-making' Institute for Genomic Research was recently reported to have a plan to sell the personalised sequence of an individual's genome on CD to anyone ready to pay around $710,000 now, and possibly as little as $1,000 in the future (Burkeman, 2002). In order to accomplish this plan, the J. Craig Venter Science Foundation is ready to pay 'a $10 million prize for anyone who can get the cost of sequencing an individual's genome down to $1,000' (Jones, 2006: 28). Obviously, the HGP's foundational sequence information as well as Celera's database would be used to produce these CDs.

Rather than representing public–private cooperation for the common good, the genome case suggests that the public sector fostered the process of capital accumulation in the biotechnology sector. As discussed above, the publicly-funded HGP produced the foundational genomic information. It was the public that bore the $3bn cost of this foundational information, while it was corporations that translated DNA sequences into profits through intellectual property rights,[5]

(IPRs), as the case of Celera illustrates. All of the sequence data produced by the intellectual labour of hundreds of publicly-funded researchers was deposited into public databases within twenty-four hours of its generation. It was freely available, through the internet, to the scientific community as well as to commercial database corporations. As Venter acknowledged, Celera used the publicly accessible sequence data of the HGP in its sequence assembly (Venter, 2001: 1305). Celera did not, however, provide unrestricted public access, but safeguarded its IPRs over its database. Between 1999 and 2001, the company made about thirty subscription deals with pharmaceutical companies, universities and research institutes, which had to pay from $7,500 to $15 million a year, depending on the access contract (*Science*, 2001: 1203). As Wickelgren (2002: 245) emphasises, 'drug industry users such as Amgen, Pharmacia & Upjohn, Novartis, and Pfizer paid millions of dollars per year to subscribe and, in some cases, agreed to share future revenue on any drugs derived from the use of Celera's data and software tools'. So the publicly-funded sequence data incorporated into Celera's database became part of a lucrative business. The reasons why subscribers were ready to pay in spite of the fact that they might freely access similar data produced by the HGP are various, and include factors such as the need for timely access to the sequence data integrated with data from other genomes, e.g. the rat genome; the pressure to stay competitive in the market; and the data's provision in a user-friendly form. It should be noted, however, that the rat genome research obtained $20 million of public funding, and that the NIH's National Cancer Institute, which was not involved in competitive business activities and therefore did not actually need timely access, was among the subscribers (Davies, 2002: 261–2). In other words, the public sector, either in the form of funding or subscription fees, nurtured the process of capital accumulation. (I shall discuss in the next sections some other aspects of the articulation of the public sector within the regime of capital accumulation.) Although some pharmaceutical companies did subscribe to Celera's database, they and many others also accessed and examined the public sequence data for potential clues to patentable products and profitable drugs. Using the foundational information of the HGP, pharmaceutical companies try to develop genetic testing techniques, gene therapy and drugs (Gottweis, 2005: 185). When successful, they sell these products and make monopoly

profits without having to share their revenues by paying Celera for a licence, since they have accessed the data from the HGP with no restriction.

We have seen that the justification for the public funding of the HGP has been based on unfounded arguments about its public benefits. This rhetorical justification appears to have been effective if one considers that the translation of genomic information written in a four-letter DNA alphabet to public benefits was politically highly functional for the scientists involved, who were trying to get public funding; for the politicians allocating the money; and for the governmental institutions housing the project. There is, however, a disguised practice in the imbalance between the public and private benefits of the HGP—between the purported public and actual private beneficiaries—which is masked by the rhetorical justification. In addition, the unfounded argument paves the way for continued justification for the use of public funds and the exploitation of the publicly funded sequence information (through creating exclusive proprietary rights) by biotechnology corporations, which can repeat the claim that they are solving the enigma of genetic diseases. Furthermore, the sequence databases and disease-associated gene catalogues marketed by biotechnology corporations gain an additional market value, irrespective of their use value, when an imaginary therapeutic power is assigned to DNA sequences and genes. The tremendous increase in the market value of Celera's stocks, from $20 to $258 in two years (Bowring, 2003: 149; Davies, 2002: 168; Sulston & Ferry, 2002: 218), is indicative of the financial benefits of this therapeutic power assignment.

With regard to the disease sufferers, since the supposed value of the 'therapeutic power' is embedded in the database subscription fees and licence fees for access to gene catalogues paid by those using gene sequences as raw materials in their activities, the net result of the sequence–therapy equation is that patients will eventually pay all the factual and fictitious costs of these allegedly life-saving end products. Patients will have to bear these costs themselves, either directly or indirectly through their insurance schemes or the public health system (see the case of breast-cancer testing tools, discussed below). Neither does the free availability of the public sequence data generate any substantial benefit to patients, the elderly or the poor. While companies can make money now—for example, as a result of rising share prices based on the hope of the

future benefits of genome knowledge—the possible public health benefits are long-term, and dependent on more research and the tackling of the environmental and social issues (pollution, poverty, bad housing, malnutrition, etc.) associated with diseases. In the long term, too, the genome sequence is helpful to companies, which can make monopoly profits by obtaining patents on the novel diagnostic and therapeutic methods and medicines developed through using this free foundational data. Patents worsen public accessibility to medical care. Because of the spread of patent rights all over the world, the provision of generic drugs and cheaper treatments is becoming more difficult. It is estimated that 2 billion people do not have regular access to most medicines, and it is argued that 'as a result of continuously increasing prices, fewer and fewer people can afford the newest medicines' (Timmermans, 2006: 41, 48). Since large sections of the public will not be able to afford outrageously expensive, patented diagnostic techniques and drugs even if the equation view were true, the from-HGP-to-therapy argument leads to a false expectation of accessible/affordable therapy. Overall, the justificatory rhetoric becomes an ideological tool for obscuring the imbalanced characteristic of its benefits, rather than providing a proper justification for the public funding of the HGP.

IPRs as a relationship of imbalance

If the above discussion has merit, it might lead one to suggest that public institutions should retreat from funding genome research, given that it works in favour of private interests rather than public benefits. This suggestion assumes that public money is always allocated in order to produce the common good or public benefits. The analysis so far has not implied this. It has connected the involvement of public institutions in producing the infrastructural information with the process of capitalist accumulation in the biotechnology sector, rather than having used the public benefit argument for or against public funding. This involvement, however, leads us to raise the question of public access to genomic/genetic information. Put otherwise, is it possible to balance private interests against public benefits through the mechanisms of patent law? The patent system gives rise to many controversies. Amongst the targets of patents are units of life (such as cells, plants and animals), genes, DNA sequences, and diagnostic and

therapeutic methods and processes based on gene expression and manipulation (Drahos with Braithwaite, 2002: 155). The commodification and ownership of the components of living entities through patents raises ethical and legal issues. Patents on genes and sequences discourage end-product development because of high royalty costs, while patents on genetic methods and processes add to health expenditures. Patents also impose restrictions on further research on genes because of possible infringement penalties (Basu, 2002: 346). I shall elaborate on these issues, in terms of public–private benefits, below.

To begin with, we can wrestle with the question of balance by investigating the problem of the sequence information–molecule relationship. Rebecca Eisenberg's view can be considered here. Eisenberg suggests that 'DNA sequences are both molecules and information', and that it is necessary to distinguish between the two in order to resolve the issue of the patentability of DNA. She employs an 'intangible–tangible' distinction by claming that the value of intangible DNA sequence information can generally be separated from the commercial value of a functional DNA molecule. Some DNA sequences contain the information needed to form a protein. She argues that in the case of DNA sequences that encode a protein, the sequence information, once discovered, becomes a useful, industrially-applicable invention, since we know what the sequences in a gene do. Thus the information about these coding sequences has tangible value. It can, for instance, be used in drug development, which leads to public benefits. According to Eisenberg, the tangible/useful sequence information embedded within the molecular form of DNA is and should be patentable because 'patent claims to DNA sequences in molecular form have been and will probably continue to be crucially important in motivating costly and risky investments in the commercial development of new therapeutic proteins' (Eisenberg, 2000: 800). She emphasises, however, that most of the DNA sequences identified do not encode therapeutic proteins, or we do not yet have the knowledge of their functions, as in the case of 'junk DNA' or partial DNA sequences of human genes (called 'expressed sequence tags' or ESTs), which have no known functions. These uncovered sequences are intangible information in the sense that the sequence information is not a practical/useful invention because we do not know what to do with it. Their importance resides in their value as an information resource

for future research. In this case, she holds the view that the sequence information as such is and should be unpatentable. Establishing proprietary rights over these sequences will have detrimental effects on their potential to be worked on, either in order to understand their function or to develop novel diagnostics and therapeutics, thereby damaging public interests. In her view, allowing patents on sequences with tangible value while prohibiting the patenting of sequences with intangible value is consistent with long-standing patent practice.

In addition to the tangible-intangible distinction, a second safety valve Eisenberg finds in the patent system is that DNA sequences in naturally occurring forms are unpatentable. Reproducing the logic of patent practice, she maintains that only if the intervention of human technology is involved are sequences patentable. As she puts it, 'patents issue on isolated and purified DNA sequences that are separate from the chromosomes in which they reside in Nature or on DNA sequences that have been created by splicing with recombinant vectors or introduction by other recombinant means' (Eisenberg, 2002: 195). This again generates a private-public balance, because the patentee is rewarded for her/his money and time spent in the processes of isolation and purification, while society gets the benefits of a novel and industrially applicable human intervention. The third aspect of her argument is the disclosure requirement in patent law. Once patents are issued, the information about the invention is disclosed and becomes freely available to the public. Since the disclosure requirement permits access to information about the invention as distinguished from the tangible invention itself, it balances public (free access to information for future research) and private interests (the recouping of the investment through proprietary rights over the tangible invention). Overall, Eisenberg (2000; 2002) sees the patent system as being the embodiment of a balance between private and public interests.

But however reasonable it may sound, the 'balance' view as such has a number of shortcomings, for several reasons. The 'separation' assertion can be questioned both in theory and in practice. In theory, Francis Crick's 'sequence hypothesis' indicates that the informational content of DNA determines protein molecules. Crick wrote in 1957 that 'the specificity of a piece of nucleic acid is expressed solely by the sequence of its bases … this sequence is a (simple) code for

the amino acid sequence of a particular protein' (cited in Davies, 2002: 27; and Keller, 2000: 52). In other words, the 'sequence hypothesis' suggests that the sequence of bases in DNA dictates the sequence of amino acids in the protein molecule (Griffiths et al., 1996: 320; Ho, 1999: 110). Crick's view has faced significant criticism on several counts: for its seeing a mathematical correspondence between genes and their expressed functions as proteins, for ignoring regulatory mechanisms, for reducing the physicality of a molecule to the genetic code contained in DNA, and for its genetic determinism, etc. (Lewontin, 2001: 17-18; Keller, 2000: 54-72; Ho, 1999: 111-35). However, since it is not the job of patent offices to discuss the criticisms levelled against the sequence hypothesis, it might yet be possible to make a patent claim over sequence information in order to reap the benefits arising from the claimant's sequencing efforts, since s/he can claim that it is this information that ultimately encodes a particular protein. 'All that is required', as Sandra Braman notes ironically, 'is convincing a patent office that information supplied by the inventor sufficiently alters the nature of the genotype to be distinguishable as something new' (Braman, 2004: 108).

In practice, a large number of gene sequences are claimed as intellectual property. Biotechnology firms have obtained patents on databases of sequence information provided, stored or analysed in computer-readable media by applying genomic information to software-related products, while some firms such as Celera have established IPRs over sequences under copyright law and contract law (Rimmer, 2003). The US Patent and Trademark Office issued patents over non-protein coding sequences (Basu, 2002: 342). Although there is no research on the extent of the rapidly growing IP protection over non-protein coding units of the human genome, according to a recent survey of protein-encoding sequences nearly a fifth of human genome sequences have already been patented in the USA (Jensen & Murray, 2005: 239). In the USA and in Europe, patents on DNA sequences have been granted in cases such as the so-called 'breast cancer genes' (BRCA1 and BRCA2), DNA sequences coding for the human protein relaxin, and DNA sequences encoding erythropoietin protein (Bostyn, 2003: 76; Demaine & Fellmeth, 2002: 358–60).

Patent protection for DNA sequences requires that these sequences should be 'isolated and purified', since manifestations of nature are unpatentable in patent law. The

problem here is that the DNA sequences of BRCA1 and BRCA2, or erythropoietin, *are* products of nature since they occur naturally in the body, even though it is claimed that they are 'isolated and purified'. Criticising the European Biotechnology Directive for accepting that sequences and partial sequences of a gene are eligible for a 'composition of matter' patent when the gene is replicated outside the organism or copied in bacteria, Sulston and Ferry (2002: 269) state that 'the essence of a gene is the information—the sequence—and copying it into another format makes no difference'. In other words, it is rather difficult to distinguish between unpatentable discoveries of sequences as manifestations of nature and patentable inventions of sequences as purportedly human interventions in nature through isolation and purification. A case in point is the unpatentable chemical elements of the periodic table. These elements 'while unique, non-obvious when first isolated, and very useful, were nonetheless not considered patentable, as they were discoveries of nature' (Rifkin, 1998: 45). And yet, 'isolated and purified' DNA sequences are regarded as meeting the patentability criteria of novelty, inventive step and utility. Thus, discoveries of 'isolated and purified' but in reality naturally occurring genes gain the status of patentable inventions. The supposedly patentable commercial value of the 'tangible' molecule is in fact based on the value of 'intangible' information itself. The deciphered DNA sequence information, which is in fact embedded in the material molecule and should indeed be considered a natural manifestation, is accorded the status of invention when DNA molecules are regarded as patentable.

So if the 'sequence hypothesis' is true, one cannot separate information from its function (encoded protein molecule). In this case, Eisenberg's argument suggesting a separation between intangible sequence information and tangible molecule is unable to prevent sequence information from being patented. But if the critiques of the hypothesis are right, the sequence of DNA is a piece of articulated genomic information. In turn, many processes need to take place in the cell and organism in order for it to fulfil its function. As Ho (1999: 111) puts it, 'the first reductionist fallacy in the patenting of genes is that DNA by itself can specify anything at all, as DNA depends for its replication on the entire cell'. The code carried by the gene is not only read, but also interpreted by the cell. So it is not that the gene is wholly

responsible for specifying the next step, but rather that the next step is open to the interpretation of the cell. It is also open to the effects of environmental variations as well as those of molecular interactions within the cell. In this case, even if one were able to patent only tangible DNA molecules, the separation argument, just like the 'sequence hypothesis', fails to appropriately consider that there are interactions between genes, the organism and the environment.

The rationale for the patenting of the physical DNA molecule externalises the molecule from these multi-dimensional and complex interrelations. This externalisation, in effect, means the externalisation of nature's handiwork from the 'human-made', 'invented' material. The presumed externalisation, thereby, serves to establish patent claims since it is claimed that by its being externalised, the DNA molecule or sequence information in question is not a manifestation of nature but a product of human ingenuity. Following a reductionist molecular approach, the justification for patentable DNA through externalisation focuses on the so-called 'essential power' of the DNA molecule. The patent system, indeed, ignores cellular and intercellular interactions as it ascribes an independent meaning and commercial value to DNA itself either in an informational or molecular form. Thus justification for patenting DNA is based on an ideological belief in the causal, determining power of DNA as information bearer and master molecule, regarded as a self-referential, fixed, static 'thing-in-itself'. DNA or a gene as a particular stretch of DNA, thereby, becomes a fetish 'when it seems to be itself the source of value' (Haraway, 1997: 143), irrespective of other complex interactions.

Furthermore, when commercial value is assigned to DNA molecules, it implies that that value should be captured through patents while the yet-unknown commercial value of sequence information, as in the cases of 'junk DNA' and sequenced genes with no clearly-defined functions, should be left in the public domain. This would in turn mean submission to the logic of the market. For my purposes here, the real issue does not concern the logic itself but its implications for the public–private balance. When the public has free access to something which in commercial terms is useless, but has no access to something that is considered to be commercially valuable, which is how the logic works, the situation by definition does not suggest a public–private balance but quite the contrary: an imbalance. A price has to

be paid by the public to obtain access to what has been made commercially valuable as a result of monopoly patent rights. Take the example of the BRCA1 patent. Any hospital or lab using the gene to carry out breast cancer screening and testing for diagnostic or therapeutic purposes may have to pay a significant fee to Myriad Genetics, because it holds the patent to the sequences and testing. Non-compliance with the patent would result in legal suits, thereby undermining clinicians' ability to provide medical services. Equally, compliance with it would give rise to high additional costs to health services, thereby imposing restrictions on access to screening and testing medical services (Williams-Jones, 2002: 139). In defiance of the EU patent, many European labs have developed and conducted their own methods of diagnostic testing instead of sending samples, as required by the patentee, to Myriad's labs in the USA for analysis at a fee of over $2,600. Recently, after consideration of the material filed in opposition, the European Patent Office announced that it has amended the patent, which 'now relates to a gene probe of a defined composition for the detection of a specific mutation in the breast- and ovarian-cancer susceptibility gene and no longer includes claims for diagnostic methods' (EPO, 2005). Myriad is entitled to contest this decision (Wallace, 2005). As reported recently, a US company, DNA Direct, offers BRCA1 and BRCA2 genetic susceptibility Myriad test kits for sale directly to individuals for up to $3,312, depending on the complexity of mutation screening selected (Harding, 2005: 617; Brice, 2005). For those who either cannot afford or are unable to access the test, medical care becomes a derivative of income injustices, which in turn has consequences for social welfare and public morals. It is important, therefore, to protect the public against the commercialisation of so-called 'breast cancer genes', and against royalties and licence fees for what has been regarded as commercially valuable in a market economy.

It should also be emphasised, however, that the commercial value of a test kit purportedly flowing from its diagnostic value seems controversial in medical terms. Spending a lot of money on breast cancer testing might not necessarily bring about very significant health benefits for several reasons. Apart from BRCA1 and BRCA2, there are many other genes and hundreds of gene mutations identified and associated with breast cancer, as a recent study shows (Sjöblom, 2006). The current test can only detect a small percentage. The patient

also has to state whether or not her relatives have a familial trait for breast cancer. If the result of the test is negative, this does not necessarily mean that the patient will not get breast cancer, because 'a negative test would not usefully distinguish between whether the mutation was not present (that she has not inherited it) or whether it had simply not been identified due to the limitations of current techniques' (Lucassen, 2005: 12). And if a result is positive, it does not mean that the patient *will* develop cancer, because the test merely shows a susceptibility to the disease. An inherited mutation is not the disease's cause per se, since some women with the mutation develop cancer and some do not. The interactions between gene, organism and environment as discussed in the previous section come into play in the development of breast cancer. A patient with a positive result is advised either to consider an operation to remove her breasts, which does not completely eliminate the risk of cancer, or to take regular mammogram tests, which do not pick up all cancers. Or, alternatively, she is advised to change her lifestyle and diet (Lucassen, 2005: 23–4). In the latter case, the patient is, ironically, expected to take into consideration the socio-environmental components of her possible breast cancer, which has been predicted through screening a so-called 'cancer-causing gene' from a genetic-reductionist perspective.

A second, related issue in terms of the public–private balance is whether rewards in the form of patents or IPRs in general stimulate research. It is argued that IP protection is necessary to encourage creativity and innovation. IPRs are seen as incentives for investment in genetic research, the successful outcomes of which are new diagnostic and therapeutic products and methods brought into the market. While the inventor gets a return on the costs of research efforts through IPRs, the public gets health benefits from the products (Gilbert & Walter, 2001: 52; Ramirez, 2004: 362). The equation is simple: IPRs as incentives for research = useful/marketable products = public benefits. Since misapprehensions about the second part of the equation have already been discussed in the previous section, the discussion will now expand on the question of IP protection as a research incentive. This presumes that the researcher is involved in genomic knowledge production processes simply because of a market-revenue incentive, as if there were no other incentives at all for scientists and researchers to study DNA, and as if no inventions in history could have occurred before the

enforcement of IPR law. In this way, the incentives for knowledge production and innovation are reduced to a single, material incentive (patent, royalty, copyright, licence fee) leading to the ownership of research outcomes. However, in direct contrast to this, the HGP is an example in which many of the researchers involved wanted genomic information to be publicly accessible, and finished the job without any market incentive. According to one study, the relatively open-access regime of the EU in comparison with the USA's is not seen by interviewees from pharmaceutical companies as an impediment to the development of bioinformatics research (Brown & Rappert, 2000: 448). In contrast with open-access regimes, IPR regimes create obstacles to the development of research. It has been noted, for instance, that 'Myriad's patents on BRCA1 prohibited research groups from being reimbursed for performing BRCA1 testing, and several research protocols have been halted because of this limitation' (Marks & Steinberg, 2002: 211). It has also been suggested that because of the threat of patent infringement, researchers will have fewer incentives to work on this gene in order to make new discoveries or develop better, quicker and more efficient tests and treatments (Sulston & Ferry, 2002: 143; Williams-Jones, 2002: 139). Other detrimental effects of IPRs are the encouraging of a patent race, which helps engender a profit-oriented science rather than stimulating collective research efforts; the suppression of innovative ideas and research for the sake of seeking IPRs; the creation of costly IP protection systems; and time- and money-consuming patent suits and litigation battles, which waste the potentially productive energies of investors and researchers (Perelman, 2003: 309-10; Boldrin & Levine, 2002).

Moreover, technically speaking, each inventor is not protected by patent systems, but only the first-comer is given priority (Cornish, 1999: 129). This means that 'a later-in-time independent inventor obtains no rights', i.e. there is no 'incentive' for him or her (Picciotto & Campbell, 2004: 293). At the very beginning of the invention process, a researcher has to make sure that he or she will be the first-comer if he or she is seeking proprietary rights. Since this restricts the researcher in deciding what to study, expected rewards through IP protection turn out to limit inventive activities. Even for the first-comer, the IP incentive argument for the 'balance' thesis looks contentious. Since IP protection follows the completion of innovative activities but not their inception,

IP regarded as a research incentive, if ever, appears to be an *ex post*, incidental stimulus. No researcher or investor can be sure at the outset that the process of innovative activity will successfully result in distinct, patentable end-products considering the nature of scientific research and the limitations of IP law. It must also be added that if IP protection ever gives incentives, it does so for the investor and not for the researcher. This is because it is usually the case, in the modern biotechnology sector, that the investor and the researcher are not one and the same person. Although it is not the investor but rather the researcher who creates the value that IPRs ostensibly attempt to protect and reward, it is the former who holds the IPRs as a result of contract law and IP law (see Çoban, 2004: 741-42). Once again, researchers have to find other incentive and reward schemes. All this shows that IP protection puts additional costs on medical care, increases the costs of research investments, and constrains research efforts. Therefore the justification for IPRs as incentives for inventive research is untenable, and does not support the public–private balance argument.

The third aspect of the balance debate is the disclosure requirement. It is argued that a full disclosure of the information describing the patented invention enables both the industry and researchers to find out about new developments in the field, and to use this information for making further improvements. While useful information becomes publicly available (public benefit) thanks to this requirement, commercial users of the tangible invention itself have to pay royalties to the patentee in return for the investment of effort and money required during the invention process (private interests), and hence there is a public–private balance (Gilbert & Walter, 2001: 49; Eisenberg, 2002: 200-201). It is true that the public enjoys a benefit from the disclosure of information, since this disclosure contributes to the accumulation of knowledge. However, it is a long jump from this to the conclusion that there is a balance for at least two reasons. First, it is paradoxical by definition to balance proprietary rights over genomic information and genetic materials against public access rights. The establishment of IPRs is intended to limit accessibility, because IP protection secures the monopoly rights of the owner in the first place. The 'balance' between the right of the owner and the right of the user comes into play *ex post* through an 'external' intervention of the state, which sets limitations and conditions. However, since it is an *ex post*

balance, the former outweighs the latter. As Picciotto and Campbell (2004: 287) state, 'this ex post balancing inevitably prioritises the former' as 'the owner's right is that of dominion and the rights of the others are regarded as an intrusion'.

Secondly and in relation to this, in many genetic advances it is difficult to protect the access rights of the user to disclosed information without infringing the rights of the patent owner over the material substance, because of the difficulty of separating the tangible material from the sequence information, as already discussed. A gene as material substance and its sequence as genetic code embedded within it are the very same thing in the sense that a gene has to have DNA sequences. Consider an IP claim made over sequences of an 'isolated and purified' gene. The claim is that what the gene in question performs as its function depends on the sequence of its bases. When the applicant obtains IPRs over DNA sequences as his or her novel, useful invention, anyone who uses and works on these sequences has to recognise the monopoly rights of the right-holder. No matter how properly the sequence information is disclosed as a result of the disclosure requirement, this does not necessarily guarantee the access rights of the user. On the contrary, disclosure and enclosure are in effect bound together in this case, since the disclosed information including the DNA sequences is nothing but 'invention' itself (i.e. the DNA sequences) under IP protection. In a similar way, when an applicant obtains IPRs over an 'isolated and purified' gene as material substance, the disclosure requirement does not help resolve the access issue either. How the disclosed sequence information is used by researchers will depend on access to the very material substance. However, this physical gene within which the genetic code expresses itself is inaccessible due to IP protection. For instance, disclosing genomic information without providing access to the physical gene does not allow drug research to flourish. It has been noted that the process of drug discovery starts with the searching of sequence databases to find specific drug targets; but without using the physical gene or encoded protein, one can neither create specific drugs to target the protein, nor determine and reduce its side effects (Marks, 2002: 205-206). Another example is the case of the clone-based landmarks used in genome mapping. For those seeking to test a DNA sample for the presence of these landmarks, access to this kind of mapping landmark data does not create practical use unless they also

have access to the clone into which the DNA fragments have been inserted, because each landmark is an assemblage of inscription and biological material (Hilgartner, 1998: 208). These cases suggest that the disclosure requirement does not guarantee that the disclosed information can be made use of. If it is not to be used without accessing the genetic material involved, disclosure seems to have no effective difference from enclosure. Thus the disclosure requirement is not indicative of the public–private balance argument, but rather of a flawed justification for exclusive rights over genomic information/genetic materials.[6]

Uneven cooperation

The balance argument defends public–private cooperation, within which private interests are balanced by public benefits. It is suggested that:

> For the most part, the relationship between the public and private spheres of biotechnology, although at times antagonistic, is cooperative and even symbiotic. Indeed, maintaining the health of this relationship benefits both spheres: the publicly funded sector gains from having privately funded outlets for vitality, imagination, and rapid growth; the private sector builds upon the base of knowledge, talent, and competitive-but-cooperative spirit that the publicly funded sector supplies. It should come as no surprise that a balanced patent law is critical to the maintenance of a healthy relationship between the public and private spheres. (Golden, 2001: 131)

It is true that the relationship between the two spheres in the field of genomics is symbiotic. However, as I explored in the first section, it is the private sphere that benefits from this symbiosis. The cooperative-but-uneven public–private relationship, as such, is not coincidental but structural in capitalism in the sense that it cannot readily be balanced through patent law. Since I have already set out the ways in which the patent system itself is bound to produce an imbalance rather than a balance, in this section I shall further discuss the imbalanced structure of cooperation between the public and private spheres by focusing on the 'triple helix of university–industry–government relations' (Etzkowitz & Leydesdorff, 1997). This investigation will further help us to

understand the extent to which both spheres are structurally articulated within the regime of capitalist accumulation.

If an important criterion for the public–private divide is accessibility as opposed to exclusion (Weintraub, 1997: 5), one would expect to find that the outcomes of publicly-funded research conducted in public institutions were not subject to property relations bringing about exclusive rights—an expectation made all the more significant considering the supposed equation of genomic research with public health. This, however, is not the case. Of the DNA-based patents issued between 1980 and 1999 in the USA, almost half 'are owned by "public" organizations such as universities, nonprofit research centres, and government' (Cook-Deegan, 2003: 92). A counterpoint might be that public institutions seek patents 'to prevent private entrepreneurs, and especially foreign capital, from controlling what has been created with American public funding', as Bernadine Healy, then director of the NIH, suggested (Lewontin, 2000: 164). This could explain the NIH's attempts to obtain ownership rights. Similarly, the idea behind the filing of a UK patent on the BRCA2 gene was to prevent Myriad from having exclusive control (Williams-Jones, 2002: 132).

This 'control idea', however, fails to see that public-sector organisations are caught by capitalism's law of motion (a law that they ostensibly, in this case, oppose), which is the creation of exclusivity in the form of property rights. One might point to the possibility that royalties demanded by public organisations may be lower in comparison with those that would be necessary if patents were privately held. This would serve the control purpose. Yet even in this case, once exclusive patent rights are established, no matter who holds them, accessibility becomes problematic, because it can only be functional as a result of either royalties when charged, or the consent/goodwill of the patentee. Patents held by public institutions actually convert accessibility into something attached to a protected territory. In fact, Healy's actual purpose is profit-making. According to Healy, government-funded researchers 'had a duty to forsake scientific ideals of "free information" in order to secure for their nations the profits at stake' (Dreger, 2000: 176). In a similar vein, James Watson remarked before a congressional subcommittee in 1989 that 'it would be against America's national interests to essentially work out the human genome and then pass it free to the rest of the world' (Dreger, 2000: 179). Since the late-

1970s, the biotechnology sector has been presented as the answer to the economic downturn (Gottweis, 1998: 107-8; Loeppky, 2005: 268; Perelman: 2003: 307; Sell, 1999: 175); and so 'national interests' manifest themselves as exclusive rights in order to pursue competitive advantage in the global market. In effect, publicly funded exploration becomes associated not with open access, but with exclusive rights. The difference between public and private patents, therefore, is only the difference between competing exclusivities.[7]

It should be emphasised that competing exclusivities do not produce a balance in favour of the public. Not only did the US state allow public organisations to establish exclusive rights over outcomes of publicly funded genetic research, it also encouraged the transfer of knowledge and technology from public research to companies through regulations such as the Bayh-Dole Act of 1980, and the Federal Technology Transfer Act of 1986 (Loeppky, 2005: 276; Audretsch et al., 2002: 185). By allowing universities to patent innovations and licence new technologies to the industry, it has fostered 'the privatisation of university research by removing any claims on behalf of the public regarding ownership of government-funded research' (Kenney, 1998: 134). Tax-supported intellectual labour within the public sector is thereby dragged into capital's logic. The state's refusal to make its outputs available to all converts intellectual labour into private property (Perelman, 2003: 309). Research conducted in the private sector is also financially supported by funding from government agencies. For example, the NIH provided researchers at Myriad with more than $5 million specifically to look for BRCA1 (Williams-Jones, 2002: 131). The company then translated the discovery of the gene into a means of commercial exploitation through IPRs, as did the private entrepreneurs in the case of the funded genome research. Thus public funding of genetic research becomes the funding of would-be patented discoveries/inventions by the industry and universities, and in turn, the accommodation of capital accumulation through public funding. Considering that the government fund pool is limited, the allocation of money to those who are also given rights to patents lessens the chances of the available money being used for advancing freely accessible knowledge that is truly devoted to public benefits. Additionally, these monopoly rights arising from funded research are protected against infringements by the judicial system in order to secure capital accumulation in the form of

monopoly profits. This legal protection, too, is maintained through taxpayer's money which could otherwise be allocated to, say, the improvement of public health.

We can see other uneven effects of public–private relationships within the functions of 'extended networks'. Michel Callon (1994: 412) suggests that a scientific network is an interaction of various elements such as articles and books that present and circulate constitutive statements; skills embodied in human beings; tools, machines and technology which are the practical results of scientific knowledge; and the institutions, such as government agencies, universities and laboratories, that support and develop it. Today, each network mingles with other networks and in this way is extended. It has already been shown in the first and second sections of this article how public institutions, as elements of networks, prepare some of the necessary conditions for the transformation of genomic knowledge into a commodity. Public investment in university education and Ph.D. programmes are also necessary to improve skills in understanding scientific statements and carrying out research. According to one study, 'the percentage of bioinformaticians in major pharmaceutical companies who had received public sector training was typically in the region of 90-100%' (Brown & Rappert, 2000: 447). While the costs of training young researchers at public institutions are socialised, positive externalities subsequently arising from this training are captured by private entrepreneurs when employing these graduates.

An important role of extended networks regarding private appropriation lies in the establishment of standards and the verification of findings. Extended networks circulate statements, scientific results and research materials, thereby helping to create a shared terminology, stabilise results and standardise the use of research materials. This is related to the obvious collective characteristic of knowledge production. Following Callon's analysis, Cambrosio and Keating (1998) have clearly shown that the commercially widespread application of the hybridoma technology used to produce monoclonal antibodies was dependent on extended networks for their circulation, stabilisation and standardisation in different settings. Circulation and stabilisation on the basis of the shared terminology and standards are also critical for the elaboration and validation of potentially commercial techno-scientific advances. The reason for Merck's

sponsorship of DNA sequencing that was to be placed in the public domain makes sense in this regard. According to Merck, 'the majority of genetic information will not yield products for commercial development until further research is done' (Marks & Steinberg, 2002: 211). Inter-firm networks serve to encourage elaboration and validation, as well as the identification of targets, the testing of internal expertise and the enhancement of learning capabilities (Powell, Koput & Smith-Doerr, 1996; Groenewegen & Wouters, 2004; Cooke, 2004: 164-5). While inter-firm networks are managed by means of subcontracting, sponsoring or any other financial mechanism, the job is carried out in extended public networks free of charge. A case in point is that of the CCR5 gene. Human Genome Sciences sequenced the gene, encoding a receptor on the cell surface. The gene was thought to be responsible for inflammatory diseases such as arthritis. In its application for the patent on the sequence of CCR5, the company could not specify the function of the gene. While the patent was pending, publicly funded researchers at the Aaron Diamond AIDS Centre in New York and at the NIH discovered that some people with defects in CCR5 developed resistance to the AIDS virus, i.e. the virus uses CCR5 as a gateway to infect cells. Once its function had been validated through extended networks, the company, Human Genome Sciences, was able to obtain the patent. The company's stock price increased substantially as a result (Bowring, 2003: 95: Sulston & Ferry, 2002: 268). This operational role of extended networks in facilitating the development of privately owned, marketable genetic products and technologies does not suggest a flaw emerging from within the patterns of extended networks. Rather, it is symptomatic of the contradiction between the social characteristic of the knowledge production process and the private appropriation of its products—a contradiction embedded in the regime of capitalist accumulation.

Conclusion

This paper has investigated the ways in which the public–private imbalance is structured to meet the requirements of capitalist accumulation in the field of genomics. Instead of seeking a balance in the public–private relationship, it has questioned the main assumptions of the balance argument. It has shown that the involvement of the public sector in the process of genomic knowledge production does not

necessarily produce immediate public health benefits as claimed. The justificatory rhetoric based on the assumption of the sequence–therapy equation blurs a proper understanding of the imbalanced structure of the public and private benefits of genomic knowledge production. An elaboration of the difficulties arising from the separation that is made between sequence information and the physical molecule, and of the tensions between accessibility and ownership, has shown that the regime of IPRs itself is a mechanism of an imbalance rather than a balance. We have seen throughout this paper that the public–private relationship—which has emerged in ways such as the production of infrastructural genomic information through the HGP, the research funding policy, legal encouragement of the commercial exploitation of innovations through IPRs, and the operations of extended networks—produces unevenly formed public and private consequences when they are considered through the lens of capitalist accumulation.

These mechanisms serve private entrepreneurs, since they have a function in capitalist accumulation. As discussed in this paper, some provide the conditions for the collective process of knowledge production, while others provide the conditions for the private appropriation of the products that would not be produced without the existence of the collective process. This would suggest that an IPR system is not the right instrument by which to undo the Gordian knot emerging from the contradiction between the collective characteristic of the knowledge production process and the private ownership of its products. Researchers themselves are now looking to reform the IPR system because they are encountering barriers to research. But it is unlikely to help. The IPR system itself is, in the first place, designed to protect the rights of the appropriator against the rights of the user involved in the collective process. Without resolving the main contradiction, any attempt to establish a well-balanced IPR system is bound to fall gravely short of the desired results. Resistance to the establishment of IPRs over genomic material with its physical and abstract components would be a more useful approach to righting the current imbalance and tilting it in the public's favour, combined with new system of legal protection based on the rights of the user. It must be noted, however, that it would be hard to put it into practice without changing the structure of the regime of capitalist accumulation, fed through and feeding on the private appropriation of things.

Notes

1. An earlier version of this paper was presented at the Technonatures III interim conference at the 37th world congress of the International Institute of Sociology, Stockholm, Sweden, 6-9 July 2005. I would like to thank the two anonymous referees and Ian Fitzgerald for their useful suggestions.
2. The HGP's and Celera's working drafts of the human genome were respectively published in *Nature*, vol. 409, 15 February 2001, pp. 860–921, and *Science*, vol. 291, 16 February 2001, pp. 1304–51. The working drafts were incomplete and still needed much more work in order to resolve ambiguities. They were like Yellow Pages containing all the numbers, but not divided into actual telephone numbers. The successful completion of the HGP was officially announced on 14 February 2003—see press release at <http://www.ornl.gov>.

   It should be noted that DNA sequences are not entirely identical from one person to the next. Because of significant sequence variations in human genomes, the notion of a generic 'human genome' has been critiqued (Bowring, 2003: 149). Given this sequence variation between individual genomes, the completed human genomic sequence is a reference sequence or composite sequence of several anonymous donors (Sulston, 2002: 67). For background information about genomes, chromosomes, genes and DNA, see Gribbin, 2002; Nossal & Coppel, 2002; Ho, 1999; Gould, 1981; Hubbard & Wald, 1999; Lewontin, 1993; Lewontin, Rose & Kamin, 1985.
3. The sequence information in a gene contains the code to make a protein. Proteins are molecules that perform most of the structural and functional work of cells. Proteins are like the workhorses of the cell: 'they carry messages within and between cells, enable the chemical reactions essential for life, and form many of the structural components of living things' (Gribbin, 2002: 68). For example, the protein keratin makes up hair, and antibodies protect us against infections.
4. Although some of the revised versions of genetic determinism now acknowledge the links between gene and environment, they still give genes the causative role. The UK Biobank (Revill, 2003) and many geneticists can see the relative importance of the environment in

explaining variations in trait while they still maintain that one has to look at genetic effects on these traits (see Kaplan, 2000: 9–13 for the tensions and links between varieties of genetic determinism). According to Craig Venter, the geneticist and businessman who ostensibly 'does not believe in genetic determinism', a personal genomic sequence 'might even give you the information you need to ensure your kids reach their full potential' (Jones, 2006: 28).

5. 'Intellectual property' includes patents, copyright and trademarks. Patents give around twenty years' protection to technological inventions and improvements, while copyrights establish proprietary rights in literary, artistic and musical creations. Trademarks are protected symbols used on products.
6. Some companies might inappropriately exclude important information about the invention from a patent application because of commercial fears. In this case, the disclosed information does not necessarily help anyone else to work on it, because the key information has been left out. Similarly, if information is classified as 'commercially confidential', it will not be released. As Rimmer notes (2003: 43), some companies might be reluctant to patent their technologies and products because they do not want to disclose any useful bits of information. This leads a number of companies to keep their intellectual property a trade secret—a lawfully protected item of information.
7. For the last two decades, neoliberal politicians and free-market enthusiasts have been using the concept of the public good/interest/benefit, but they have ascribed a different meaning to it. In this redefinition, the meaning relates to economic efficiency, privatisation, competitive advantage, global market share, profits, etc., while its 'old-style' meaning relates to accessibility, affordability, distributional equity, social justice, etc. For instance, in its old meaning, the proprietary/exclusive rights of public institutions and private investors over knowledge would not be defended in the name of the public good/interest/benefit. Conversely, within the new meaning of 'public good' it is difficult to argue the case for human genome data being made free and available, since it clashes with the economic imperative to carry out confidential research for the development of commercial products in the pursuit of substantial profit opportunities.

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