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# Too Much Ownership: Bio-prospecting in the Age of Synthetic Biology

**Alain Pottage**
Reader in Law, London School of Economics, Houghton Street, London WC2A 2AE, UK
E-mail: r.a.pottage@lse.ac.uk

**Abstract**
*Taking the example of Craig Venter's marine bio-prospecting expedition, this article explores the effects that bioinformatics and sequencing technologies have had upon the process of bio-prospecting. What kind of an aggregate is a collection that spans evolutionary ecologies, database logics and programmable synthetic organisms? And by means of what displacements, translations and topologies are genetic collections 'made up' in the age of bioinformatics and synthetic biology?*

**Keywords** Bio-contracting, Bio-prospecting, Convention on Biological Diversity, Ownership, Synthetic biology, Venter

In August 2003 the molecular biologist Craig Venter embarked on his widely publicized expedition to sample the genomic diversity of marine micro-organisms. A press release marked the moment by rhetorically inscribing the enterprise in the lineage of two of the great scientific explorations of the nineteenth century, the voyage of Darwin's *Beagle* and that of the British oceanographic vessel *HMS Challenger*.[1] According to Venter, Halifax, Nova Scotia, was chosen as the port of departure because of its symbolic significance. Halifax was one of the first provisioning ports for the *Challenger*, which arrived there in May 1873, six months into its extensive survey of the topographic and ecological characteristics of the deep seas.[2] The symbolism of pioneering science was sustained throughout the projected course of Venter's yacht, the *Sorcerer II*, which took in all the cardinal points of the classical scientific itinerary of the eighteenth and nineteenth centuries: the Galápagos Islands, Australia and Madagascar. The declared objective of the expedition, which was to collect marine genomic diversity into what Venter called 'the mother of all gene databases' (Shreeve, 2004: 8), merged traditional topologies of biological collecting into informatic sequencing technologies (more precisely, the shotgun sequencing technique developed by Venter in the course of his controversial career with the US National Institutes of Health (NIH), the Institute of Genomic Research (TIGR), and as the leader of the Celera corporation during the celebrated 'race' to sequence the human genome). Venter's earlier

**Alain Pottage** is currently Visiting Professor at Cornell Law School. At the London School of Economics he teaches courses in intellectual property law, anthropology and social theory.

1 See the press release at URL (accessed March 2006): www.venterinstitute.org/press/news/news_2004_03_04.php

2 Samples taken from Halifax harbour revealed some interesting bacteria and micro-organisms, perhaps because Halifax is the only large North American city to release raw sewage directly into the sea.

career excited controversy because he consistently seemed to promote 'private' science over 'public' knowledge. By announcing the construction of 'a freely shared, global environmental genomics database that can be used by scientists around the world'[3] the *Sorcerer II* project advertised a renewed commitment to 'basic science' at the same time as it enhanced Venter's reputation as a 'maverick' scientist (Rabinow and Dan-Cohen, 2005: ch. 1).

The *Challenger* expedition worked with the instruments of 'heavy' nineteenth-century science. Manoeuvring the cables, weights, dredges, trawls and water samplers that were used to record measurements and take samples, and then lodging these forms of data in a paraphernalia of preserving jars, tin boxes and paper catalogues for periodic shipment back to Britain, was a laborious, time-consuming, and not especially exciting process. By contrast, the tasks undertaken by the crew of the *Sorcerer II* seem lighter in every sense. The yacht stops every 200 miles or so to take samples of seawater from a depth of 5 feet. Each batch of water is sieved through a set of progressively finer meshes to produce paper-bound samples of marine micro-organisms, which are then frozen and airlifted back to Venter's Institute for Biological Energy Alternatives (IBEA) in Rockville, Maryland. In the laboratories of the IBEA, DNA from the genomes entangled in each sample is extracted, fragmented, amplified and then recomposed into a set of plausible genomes by means of the bioinformatic technologies developed by the Celera corporation. Because it links classical prospecting itineraries, informatic simulations of evolutionary mutations and the 'circuitry' of programmable organisms, the *Sorcerer II* expedition offers an especially rich illustration of contemporary modes of bio-prospecting.

The enterprise of 'combinatorial genomics'[4] extended sequencing programmes across new geopolitical planes and into new corporate and governmental networks. When Venter left Celera in 2002, he set up a number non-profit research foundations, one of which was designated the Institute for Biological Energy Alternatives (IBEA). Almost immediately after it was established, the IBEA received funding of $1m per year (later increased to $4m per year) for its Global Ocean Sampling Expedition (the *Sorcerer II* project, in other words) under the auspices of the US Department of Energy's 'Genomes to Life' (GTL) programme (DOE, 2004a). Of the four 'scientific and technical milestones' of the GTL programme (see, generally, DOE, 2004b), two coincided very closely with Venter's project, namely the goal of understanding the 'functional potential' of microbiological organisms and that of gaining a predictive knowledge of 'complex biological systems'. And these goals linked the GTL programme to the Bush administration's 'Clear Skies and Global Climate Change' initiative of 2002,[5] which proposed a technological solution to the problem of global warming. From this perspective, the attraction of marine micro-organisms was their potential value as an alternative source of energy (deep-sea micro-organisms that live and reproduce without sunlight are especially promising candidates in the search for new 'biofuels') and their supposed capacity to metabolize industrial carbon dioxides. Venter's explanation of his Institute's role in this global warming strategy was as follows: 'This is a basic science project, but it's driven

3 See the press release at URL (accessed March 2006): www.venterinstitute.org/press/news/news_2004_03_04.php

4 'It's one of my better ideas if it works. In fact, it's one of my better ideas if it doesn't work' (Venter, cited in Shreeve, 2004: 8).

5 Announced by the White House on 14 February 2002.

by an attempt to fix a fundamental problem: We're pumping way too much carbon into our atmosphere' (cited in Jaffe, 2004: 26).

Genetic resources are no more natural than any other 'natural' resource, and any productive engagement with the question of bioprospecting has to address the multiplicity of processes and regimes in which 'natural' materials precipitate from social interactions. These processes of fabrication have largely been explored as aspects of the production of scientific and technological knowledge. One persistent theme in these analyses is a critique of 'linearity' and, more especially, of the 'developmental sequences'[6] and topological forms that have configured 'life' for centuries, and which are represented in conventional evolutionary and geographical understandings of biodiversity. The critique adopts an idiom of 'kinetics', centred on the theoretical figures of velocity, transformation and acceleration. For example, Helmreich's study (2003) of marine bioinformatics explores the effects that certain kinds of lateral movements (notably genetic 'transfer' in archaea and bacteria) have on the rooting and ramification of 'arborescent' genealogies. Mackenzie (2003) tracks similar kinds of lateral effect in the context of bioinformatics databases. Modes of acceleration are unfolded in Bronwyn Parry's account of digitized bio-information, which argues that technologies of the sort exemplified by Venter's project allow collectors 'to *speed up* the social and spatial dynamics of biological collecting whence power and profit derive ... by making it easier for a select few to collect, concentrate, control, and recirculate valuable biological resources to strategic or personal advantage' (2004: 43). And, switching to 'deceleration', technologies that suspend ontogenic or metabolic process make a given state of bio-potentiality available over longer time-spans, so allowing additional value(s) to be extracted from bioactive materials (see Hayden, 2003a; Parry, 2004).

One might see the *Sorcerer II* expedition as emblematic of these modes of 'lateral' process, and as an ideal index to the configurations of economic, scientific and political interest that are generated by lateral movements. But Venter's project is interesting not because it illustrates the eclipse of linearity, but because it suggests that bio-prospecting consists in a mode of action that cannot be reduced either to 'lateral' or 'linear' forms. The intense political and legal controversy generated by Venter's appropriation of what many people regarded as sovereign or proprietary resources revealed the centrality of ownership—and hence notions of origin, derivation and definition—to practices of bioprospecting. What if, instead of enfolding ownership in lateral processes, one were (provisionally) to reverse the critical achievement represented by Foucault's absorption of law into biopower, and use law to model the biopolitics of contemporary prospecting? Might this be a productive way of developing Bruno Latour's (2002: 278) suggestive observation that there is more 'society' in law than there is 'law' in the sociological concepts that are so often used to 'explain' law?

The point is not to rediscover the old economic ordering of life; rather, it is to get at what 'kinetic' analyses of biosociality might 'really' be after. Figures of 'laterality' point beyond themselves towards a notion of potentiality. For example, the lateral movements observed in marine bioinformatics elicit a mode of 'bare life' (Helmreich, 2003); compensation strategies reveal the unacknowledged potentiality of normative instruments to create objects and entitlements (Hayden, 2003b, 2003c); and, as 'bio-information', life is

6 To borrow a phrase from Maurer (1999: 673).

(re-)potentialized by liquid modes of conservation, transfer and replication (Parry, 2004). Precisely because they imagine laterality as movement, and as a mode of articulation rather than a quality inherent in particular concepts or techniques, these analyses suggest that bio-social potential emerges from the way that (lateral or linear) forms are mobilized. And, ironically, the linear form of ownership is a good way of getting at this process of mobilization. Because ownership claims to genetic resources presuppose radically different narratives of entitlement, with radically different constructions of subjects and objects of ownership, the proliferation of these claims multiplies (incommensurable) linear forms to the point at which linearity becomes a figure of contingency and complexity. Two interesting observations follow if bio-prospecting is modelled in terms of ownership and legality. First, it is easier to see how even the most archaic 'linear' forms can be mobilized by complex social processes. Second, it becomes clear that no dimension of society is inherently 'linear' or 'lateral'; rather, these qualities are ascribed to the world by particular regimes or discourses, and the potentiality of life emerges from the productive tensions between these different perspectives. The story of the *Sorcerer II*, precisely because it spans the diverse fields of evolutionary biology, bioinformatics, synthetic biology and bio-contracting, is the perfect index to this kind of multiplicity.

## Digital genes

> Darwin was limited by what he could see with only his eyes ... we want to use the minimal unit of the gene to look at evolution. (Venter, cited in Shreeve, 2004: 8)

'Combinatorial genomics' was presented by Venter as ('public') biological science carried to an order of resolution at which genes are apprehended without reference to phylogenetic 'structures' or ecological matrices: 'One of the things about shotgun sequencing is that it gives you the complete genetic repertoire of what's there, without knowing the structure a priori' (Venter, cited in Russell, 2004: 9). There is an instructive similarity between Venter's mode of biological collecting and the techniques practised by Diversa, one of the world's leading bio-prospecting corporations. Even before Venter began a trial prospecting run in the Sargasso Sea, Diversa had already negotiated a prospecting agreement with Venter's Bermudan collaborators, and had patented the first technology produced under that agreement.

> Diversa bypasses the traditional step of culturing out micro-organisms from samples and jumps right to the DNA. It runs samples of soil, seawater or tissue through its DNA sequencing technologies to get the DNA fragments of all the micro-organisms present in the sample. It then takes this mess of DNA, chops it up into gene fragments and genetically engineers them into easy-to-culture micro-organisms that express the proteins encoded by the genes and screens for promising enzymes (GRAIN, 2005).

What kind of shift in the grid of biological observation is signalled by this mode of bio-collecting? From one perspective, 'gene-centric' biology involves only a change in the direction of analysis: 'It's the reverse of traditional biology, where we spot a new creature

and then analyse its DNA. Now we get the DNA first, then find out what made it' (Marine biologist Ed DeLong, cited in Helmreich, 2003: 351). But Venter and Diversa are not interested in returning to organisms as the frames within which evolutionary and ecological processes become visible and tractable.[7] And this points to a decisive transformation in the bioeconomic 'diagram'[8] that conditions biological knowledge, from a Darwinian economy of selection to an economy of bioengineering.

The role that the practical expertise of breeders played in shaping Darwin's theory of natural selection is well known. According to Darwin, the essential technique of artificial selection was to actualize potentialities that nature had already set in motion: '[M]an does not cause variability and cannot even prevent it, [but] he can select, preserve, and accumulate the variations given to him by the hand of nature almost in any way he chooses' (1998 [1868], vol. 1: 3–4). Breeders worked with a natural faculty of variability, or with what might be called 'evolution's values' (Swanson, 1995). So the special art of breeder was to draw latent or potential characters into visibility: 'The importance of the great principle of Selection mainly lies in the power of selecting scarcely appreciable differences, which nevertheless are found to be transmissible, and which can be accumulated until the result is made manifest to the eyes of every beholder' (Darwin 1998 [1868], vol. 2: 177). But the insight or intuition of the breeder often went before the eye of the beholder; the good breeder had 'an almost prophetic vision into futurity' (1998 [1868], vol. 2: 179), so that the desired character almost seemed to exist already. This bioeconomy of 'accumulation' worked with and within the logic of genealogical time. In this primordial form of developmental sequence, the new is always a continuous accretion to what exists already; all the more so when the contingencies of selection are recapitulated in the mode of what Ernst Mayr called 'teleonomy'[9] or rationalized from the perspective that Susan Oyama describes as 'evolution's eye'.[10] And evolutionary genealogies are genealogies in spatial extension. Mutational distances—and hence evolutionary 'variability' as a whole—are legible in the geographical distribution of phenotypic variations, and the purpose of many classical explorations was to collect these phenotypes into a map of biological-taxonomic order. In practice, biocollecting meant travelling, relocating or bringing organisms together in novel places or configurations, and all of this was done by reference (implicitly or explicitly) to evolutionary genealogies.

This bioeconomic paradigm informs the characterization of biodiversity in the 1992 Convention on Biological Diversity (CBD) as 'diversity within species, between species and of ecosystems'.[11] Of course, there is no single or non-contingent principle of accounting

7 'Organisms themselves embody genetics, development, morphology, physiology and behaviour, and they are the fundamental components of populations, communities and ecosystems' (Greene, 2005: 24).

8 In the sense of Michel Foucault's use of the term to describe a historically specific condition of social actuality, or a (paradoxically) historical a priori (see generally Deleuze, 1986).

9 Namely, a concept of emergent finality—things are what they will turn out to have been: 'Individual development and behaviour manifest the same qualities of responsiveness as 'the actions of a computer that has been programmed to respond appropriately to various inputs' (Mayr, 1961: 1501).

10 'Evolution, or natural selection, with which evolution is too often identified, is frequently depicted as an agent that continually scrutinizes organisms in order to identify those best suited to life.... Evolution's eye in this sense is a critical eye, measuring, comparing, and evaluating' (Oyama, 2000: 10).

11 In classically Darwinian terms, article 2 of the CBD defines 'biological diversity' as 'the variability among living organisms from all sources'.

for diversity. For example, species are increasingly understood as 'information units in a genealogical hierarchy', with the implication that one should conserve ancestor species, these being 'the minimum dataset which is needed in order to preserve biodiversity' (Bowker, 2000: 671). To some extent, this approach abstracts genetic potential from 'ecology' in a similar manner to Venter's and Diversa's mode of bio-collecting, but the point about conserving potential in the form of a 'minimum dataset' is precisely that it can then be unfolded or 'reflated' by means of an ecological genealogy, within the spatio-temporal frames of evolutionary biology. This is precisely what Venter's project of combinatorial genomics does not seek to do. Evolution and ecology do return at a certain point, but only in the form of software-generated hypotheses about mutational distances and their meaning. And this is where attention to 'lateral' topologies or kinetics is particularly rewarding.

Venter's mode of bio-collecting is premised on informatic sequence similarity technologies. First, in order to count species, the IBEA laboratory uses a version of 'shotgun sequencing' to (re-)assign entangled gene fragments to their original genomes. The technique of shotgun sequencing that Celera used in the sequencing of the human genome involved shearing genomic DNA into short nucleotide strands, cloning these strands to create a DNA library, and then using massive computing power to recompose the entire human genome by identifying and marrying overlapping sequences. In the case of the *Sorcerer II* project, the task is not (just) to match overlapping sequences from multiple copies of a single known genome, but to assign sequences to genomes by reading and comparing them to ensure that apparently 'overlapping' sequences actually belong to the same genome. Second, the identification of interesting gene functions begins with a comparison of each candidate sequence, with sequences deposited and annotated in bioinformatics databases. The only way of telling whether a given sequence is likely to be (say) a photoreceptor is to compare sequence homologies. Homology is more than a matter of molecular structure. The degree of 'similarity' between structural forms is a variable whose (qualitative) value is given by statistical hypotheses or calculations about rates of mutation or about the 'conservation' of particular structural motifs throughout the process of evolutionary differentiation. Once calculated by algorithms which, for example, extrapolate a rate of mutation observed in 'closely related' motifs to more 'distantly related' motifs, these homology values are configured by visualization software technologies—'graphical user interfaces'—which present sequences (and, more especially, protein sequences) in familiar semantic, geometric or aesthetic forms: alignments, phylogenetic trees, 2D or 3D structures, or structure predictions. Evolutionary ecologies return in the peculiar form of these phylogenetic trees, which express algorithmically modelled hypotheses and which are represented on computer screens as algorithmically modulated light intensities.

The starting point for algorithmic calculations of homology is the basic device of the edit distance—'the number of single character edit operations [that] would be needed to transform a given sequence file into another given sequence file' (Mackenzie, 2003: 323). Of course, these distances are as much qualitative as quantitative, but what is significant is the topological plane of the calculative process; leaving aside the modalities of access to sequence databases, or the mode of visualization of sequence information, one might say that informatically archived sequences exist entirely contemporaneously, so that movement

'between' them does not run up or down the vertical axes of a ramified evolutionary tree, but 'across' trees in a movement of lateral comparison:

> The real issue concerns how to move between different sequences, or how to establish relations between them. Different sequences potentially lie on one or many branches or leaves of the phylogenetic tree. As graduated evolutionary descent flattens out into continuous transformation and recomposition of sub-segments of living things, and the vision of moving freely between branches of genetic trees supplants an irreversible river of historical time, the question of how to steer lateral movement arises. (Mackenzie, 2003: 321, referencing Sarah Franklin's notion of 'axial transposition')

In its role of discovery and accumulation, the *Sorcerer II* crosses the conventionalized space of the map and the spatio-temporal distributions of evolutionary ecology; but, to the extent that this role has already been programmed by the logics of the databases into which its discoveries are to be (re-)collected, the yacht also traverses the virtual topologies of the bioinformatics database. The samples collected by the yacht acquire their meaning and value from movements of comparison within the medium of the database. But this mode of iteration is interesting precisely because it shows how the 'lateral' is always linked to the 'linear' as a term in more extensive configurations. In bioprospecting mode, the *Sorcerer II* necessarily follows the grain of evolutionary processes (which is precisely why Venter's expedition was so politically controversial); and on the 'other side' of the database, 'lateral' algorithmic processes are visualized and interpreted through modes of representation based on familiar (linear) cognitive geometries—graphs, wave flows, maps, texts and diagrams. These representations are then sent from one research institute to another, across networks that are themselves complex articulations of computer hardware, embodied technical knowledge, and economic or normative interests. So what is interesting about the *Sorcerer II* expedition is the sense in which it holds open relations between analogue and digital, material and immaterial, or linear and 'lateral'.

## Synthetic biology

> Breeding and selection can take you only so far. Look at what's going on with this planet—we need to do some accelerated evolution. (Venter, cited in Reiss, 2005)

Within the *Sorcerer II* project, bioinformatic sequence analysis is just the first stage in a project of bioengineering that seeks to convert living processes or organisms into programmable digital media. In November 2003, a team led by Venter assembled a replica of the complete genome of the φX174 virus. A set of commercially produced oligonucleotide strands was composed into a genome, first by using computerized sequencing technologies to match the 'ends' of sequence fragments, and then splicing this genome into a host bacterium.[12] This programme of bioengineering is presented as complementary

12 See *The Economist* (14 Nov. 2003), available online (URL accessed March 2006): http://www.economist.com/displaystory.cfm?story_id=E1_NNNQDDR

to the *Sorcerer II* expedition, not only because it extends Venter's commitment to 'basic science',[13] but more specifically because it provides the means by which genes collected by the *Sorcerer II* are to be exploited. The objective is to splice functional sequences into what Venter calls a 'cellular context'.[14] An IBEA press release announcing the sequencing of the φX174 genome described the project as the first step towards producing 'cassettes of particular genes or pathways that could be inserted into host organisms to conduct many types of functions'. The first objective is not to industrialize determinate functions, but to assay candidate genes randomly:

> If you want to find the role of 100,000 genes, Venter says, the trick is to find a way of doing 100,000 experiments at once. All you would need that's not already available is a synthetic genome, a sort of all-purpose template onto which you could attach any gene you wished, like inserting a blade onto a handle. You could then test the resulting concoction to see if it performed a specific vital task, such as metabolizing sugar or transporting energy. Using existing robotic technologies, you could do thousands of such experiments at once, in much the same way that a combinatorial chemist tests thousands of chemical compounds simultaneously to see if they have the desired effect on a target molecule. (Shreeve, 2004: 8)

The success of the φX174 venture, set in the context of the broader activities of the IBEA, prompted Venter to set up a venture capital firm, Synthetic Genomics, which seeks to 'design, synthesize and assemble specifically engineered cell level bio-factories'.[15]

The programme of 'combinatorial genomics' gives a new instrumental edge to digital biology. In bioinformatics databases, life is a medium of lateral action in which there is, as yet, no acknowledged criterion for validating alternative methods and hypotheses about sequence homology and mutational distances. Synthetic biology, by contrast, seeks to engineer a (linear) order into digitized genes. Were the ambitions of synthetic biology to be realized, projects such as Venter's would not only 'accelerate' evolution, they would also open up a kind of 'life' or 'biology' that is quite unlike 'life' as it is construed by existing biotechnologies.

The programme of synthetic biology may not seem especially novel. Biotechnologies have already made the break with Darwinian genealogies by suspending the potentialities set in motion by evolution and making them available as the unmotivated elements of a rewritable molecular text. Unlike techniques of artificial selection, biotechnologies have the power to 'invent' biological reality:

> What is new about molecular biological writing is that we have now gained access to the texture—and hence the calculation, instruction, and legislation—of the human individual's organic existence—that is, to a script that until now it has been the privilege of evolution to write, rewrite and alter. What Darwin called 'methodical'

13 Of the synthetic biology dimension of the enterprise, Venter suggests (again) that: 'This is true basic science. Even though we've found all those genes in the human genome, we can't understand the most basic cell yet. That is what's driving this' (cited in Davidson, 2002).

14 Venter, cited in Shreeve, (2004: 9).

15 From the presentation of the corporation at http://syntheticgenomics.com

> or 'artificial selection' has barely scratched the surface of this script in the last 10,000 years. For, in a sense, artificial selection itself was still nothing more than a specific human mode of natural evolution. This has now gone; and with its disappearance, natural evolution has come to an end. Molecular biology will come to invent biological reality. (Rheinberger, 1995: 252)

From this perspective, computer-directed technologies of bio-molecular synthesis are just the latest realization of the two basic strategies that have motivated biotechnological interventions since their inception, namely the reduction of genes to functions and the instrumentalization of organisms and metabolic processes as living 'production systems' for the (commercial) performance of these functions (see Knorr-Cetina, 1999: ch. 6). These interlinked strategies are illustrated and enacted in a range of established technologies: in, for example, the identification of function by 'knocking out' targeted genes, recombinant DNA technology, the statistical and laboratory knowledges that organize positional cloning, or technologies of 'biolistic' bombardment.

Conceptually, bioinformatics incorporates the dual strategy of fabricating molecular scripts and media of inscription into a new narrative of technological mastery. The use of computational tools not only as instruments of biological analysis but also as epistemic models for cellular or metabolic processes has recast the distinction between 'production systems' and 'genes' as a distinction between 'machine' and 'programme', or 'circuitry' and 'code':

> Since the mid-1970s it has been possible to isolate a fragment of the genetic programme (in physical terms, a DNA fragment) and insert it into the programme of the chosen host (directly into a chromosome, or in the form of an artificial chromosome, in a replication unit such as a plasmid or virus). The descendants of that host then behave as if they had been reprogrammed to take into account the programme fragment which has been added (or which has inactivated a fragment originally present in the host). The formal separation is effective, because although scientists initially perform these operations on paper, they subsequently put them into practice physically, in the organism to be modified.... In this situation, the separation between the machine (a certain type of cell) and the programme (the modified DNA) can actually be seen to be a reality. (Danchin, 2003: 233–4)[16]

The old 'ecological' articulation of genome/organism/environment and the newer biotechnological figure of gene/expression vector are both eclipsed by this informatic configuration of machine/programme/data—or, more crudely, by the distinction between hardware and software. What are the implications of this apparently simple re-description? There is—again—nothing novel in seeing organisms as bearers of interesting traits: consider Darwin's appreciative observation that it had taken a particular pigeon-breeder 15 years to move a white head from one breed of pigeon and attach it to another (1998 [1868], vol 2: 179). Nor is there anything new in using cellular metabolism to instrumentalize a

16 The cell is defined as 'a machine that puts the genetic programme into operation according to the data provided by its environment'; and '[the] same programme can produce different outcomes, demonstrating that the external environment is an intrinsic part of the way the program is expressed, because it contains the data that determine the outcome' (Danchin, 2003: 270).

specific gene function: expression vectors have been in routine use for decades. Rather, the distinction between code and circuitry (re-)configures life's potentiality by profoundly reconstituting the materiality and mode of organization of biological molecules. What is significant about synthetic biology is not (just) that it suspends evolutionary genealogies, but that it collects biological elements into digital media and modes of organization. Synthetic biology aims to generate what could once have been made only by 'Nature'. The adage that 'biologists don't make DNA, organisms do' (Landecker, cited in Franklin and Lock, 2003: ) holds true as long as bioengineering is conceived in terms of recombinant DNA technologies, but it might seem less apt if or when 'programmed synthesis' is routinely practised.

A European Union survey of synthetic biology describes a broad project of 'bringing the engineering paradigm to biology' (European Commission, 2005: 10). 'Engineering' involves dismantling biological processes and reassembling them by means of programmable synthetic circuits, switches, and interfaces:

> The introduction of design principles such as modularity of parts, standardization of parts and devices according to internationally-recognized criteria, and the (reciprocal) adaptation of available abstract design procedures to biological systems, coupled to novel technological breakthroughs (such as cheap mass synthesis of DNA segments) that allow the decoupling of design and fabrication will fundamentally change our current concepts of how to manipulate biological systems. In this sense, synthetic biology is not primarily a 'discovery science' (that is, concerned with investigating how nature works, but is ultimately a new way of making things. (2005: 10)

Leaving aside what might (following Bruno Latour) be called the extreme ideological 'purification' of complexity expressed in this paradigm of 'engineering', one should notice the extent to which synthetic biology is premised on informatic technologies: indeed, synthetic biology is apparently 'the design counterpart of systems biology' (2005: 11). So it is no surprise to find that most of the projects that are gathered together as proto-examples of synthetic biology are essentially computer science projects: protein design algorithms, cellular logic gates and cellular switches, synthetic gene circuits, microfluidics and 'virtual cells' (2005: 22–33). Ultimately, bioengineering seems to be an exercise in circuit design, or the 'rational construction and redesign of biological circuitry' (2005: 5).

Incautious presentations of synthetic biology dismiss recombinant DNA technology as crude 'DNA bashing', and herald the emergence of true bioengineering, which involves 'specifying every bit of DNA that goes into an organism to determine its form and function in a controlled, predictable way, like etching a microprocessor or building a bridge' (Morton, 2005). The text of a US patent recently granted to Egea Biosciences of San Diego emphasizes the novelty of its claimed technique of computer-directed synthesis—which would, it claims, enable 'the creation of novel DNA molecules in a single step without requiring the use of any existing recombinant or naturally-occurring DNA'—by observing that recombinant DNA technology 'does not permit the creation of entirely artificial molecules, genes, genomes or organisms, but only modifications of naturally-occurring organisms'.[17] Eventually, according to the patent text, the patented mode of high-throughput synthesis might 'be employed to create entire genomes for introduction into host cells for the creation of

entirely artificial designer living organisms'. Patent specifications should be taken for what they are—as optimistic or opportunistic claims to the potential applications of an invention—but the language of the Egea Biosciences patent echoes other rhetorical formulations of synthetic biology. For example, the European Union's report, observing that biotechnologies have thus far been based on 'tinkering rather than rational engineering' (European Commission, 2005: 11), goes on to identify one of the reasons; biotechnology addresses life as a system each part of which is 'a unique—messy—result of millions of years of evolution and frequently is subject to a large amount of cross-regulation from functionally rather distant elements of cellular function' (2005: 24). Engineering makes biological systems less messy—not necessarily less complex—by replacing 'evolutionarily-designed' articulations, connections and switches with quasi-informatic devices: synthesized cellular switches or circuits.

In some sense, synthetic biology is a technology of 'interfaces'—a science of creative assembly. The notion of 'modularity of parts' offers a good illustration. To the extent that the 'messiness' of biological systems is a result of their dependence on chemical specificity (a given molecule will complement or interact with only a limited set of other molecules) or spatial separation (different functions are carried out in different cellular components) to differentiate the elements or phases of metabolic process, the objective of synthetic biology is to replace biological articulations with synthetic operators. Theoretical bioinformatics has already achieved 'conceptual' modularization by imagining cellular metabolism as programmed circuitry.[18] Synthetic biology seeks to 'realize' this conceptual schema by integrating the components of metabolism 'into circuits that implement more complex functions' (McDaniel and Weiss, 2005: 476). Starting from the premise that cellular metabolism is a form of digital information-processing system, so-called 'natural computing' technologies recruit the regulatory components (interfaces) of cellular metabolisms in order to 'implement digital logic functions' (Weiss *et al.*, 2003: 4). For example, the expression of a given protein might be used as an element in the construction of a logic gate by treating a high concentration of the protein as (in binary notation) 1, and a lower concentration as 0 (Klarreich, 2003). This difference sets up a kind of metabolic 'switch', the most basic element of a synthetic gene circuit. In theory—the practice is more difficult—these elements can be linked together to create a circuit programmed to perform 'functionalities that do not exist in nature' (European Commission, 2005: 10). So the natural—and 'messy'—reactions and complementarities that organize cellular processes are broken down into components that are neither mechanical nor biological, and which take their value and instrumentality from the configurations into which they are assembled. As an illustration from the theory of computing suggests, this process of digitizing and re-assembling bio-molecules thoroughly transforms their materiality:

> A combination lock is a finite automaton, but it is not ordinarily decomposable into a base set of elementary-type components that can be reconfigured to simulate an arbitrary physical system. As a consequence it is not structurally programmable.

17 See US patent 6,521,427, Method for the complete chemical synthesis and assembly of genes and genomes, issued 18 Feb. 2003.

18 See for example Bentolila (2003: vi): 'the programme is not coded in A,T,G,C but in sequences of biochemical bindings between molecules'.

> [A] digital computer used to simulate a combination lock is structurally programmable since the behaviour is achieved by synthesising it from a canonical set of primitive switching components. (Conrad, 1988: 289)

Whereas recombinant DNA technology works within biological media of inscription, splicing living process into living process and inflecting innate molecular complementarities, this mode of digitization is not so much a practice of 're-writing' as it is a practice of 'over-writing'. The object is not so much to reorganize metabolic materialities and competences by recomposing 'natural' affinities and specificities, as though one were recomposing molecular 'type', but rather to re-inscribe 'analogue' molecular script as programmable digital notation.[19]

Unlike the programme of biotechnological instruction, which is premised on recombinant DNA technologies, and which has to work with or around the specificities of DNA molecules, synthetic biology invents its own building-blocks. And this difference between 'DNA bashing' and synthetic biology is crucial to any reflection on the bioeconomic potentiality of life. But the more immediate question is whether, if Venter's 'combinatorial genomics' is really the endgame of the *Sorcerer II* project, the form of multiplicity that I ascribe to the practice of bio-prospecting is about to be enclosed, ordered and simplified by digital engineering. In addressing that question, Katherine Hayles' argument for 'intermediation' is instructive. Hayles resists the common argument that the computer is 'the ultimate solvent that is dissolving all other media into itself', precisely because that approach risks 'flattening complex interactions back into linear causal chains' (2005: 31). 'Intermediation' describes the various ways in which digital code presupposes and engages with analogue media, notably texts, bodies and consciousnesses. The point is that the world is not entirely digital, it consists in the difference between the digital and analogue, and is animated by the 'complex feedback loops [that] connect humans and machines, old technologies and new, language and code, analogue processes and digital fragmentations' (2005: 31).

The core example of this co-variation of digital and analogue media is Hayles' example of TTL (Transistor to Transistor Logic) chips, which generate a sustainable digital signal by smoothing out the inevitable fluctuations in 'real world' analogue voltages. The chip represents 0 by zero volts and 1 by five volts: 'If a voltage fluctuation creates a signal of .5 volts, it is relatively easy to correct this voltage to zero, since .5 is much closer to zero than five' (2005: 43). So digital processes remain closely –and problematically—coupled to the 'noise' of the material world: 'For code, the assumption that the sign is arbitrary must be qualified by material constraints that limit the ranges within which signs can operate meaningfully and acquire significance' (2005: 43). Hayles sees the distinction between analogue and digital as consisting in the difference between continuous processes and discrete states. The sociological version of this difference identifies the digital with cognition (or constructive observation) through binary distinctions (see, generally, Luhmann, 1995). In this latter sense, the term 'digital' describes the selective 'order' that communicative systems produce from the 'noise' of the analogue world. In systems theory, the 'analogue' (meaning the environment) is constructed by the 'digital' process (the system) that treats it as environment: 'Environments

19 Though the logic seems less alien if one imagines metabolism as a parallel mode of digital information-processing.

do not pre-exist systems but are called into being, through exclusion, by the systems they thereby help define' (Rasch, 2000: 87). In other words, the 'environment' is an effect of the (digital) schemata through which it is observed, so there are as many environments as there are systems.

More important, digital systems are reflexive: not only do they observe their environment, they also observe themselves observing their environment. So observations are subject to correction by later, 'second-order' observations. But 'correction' does not mean that these second-order observations have achieved a closer or more direct correspondence with the 'real' environment. Digital systems are still bound to the cognitive frames that they use to pattern the 'noise' of the environment, so they can still see only what those frames apprehend as the 'world', but subsequent observations can test the consistency and viability of first-order observations within the operations of the system. It is precisely this mode of reflexivity, or this kind of self-referential 'feedback loop', that is encrypted in TTL chips. The algorithmic 'smoothing out' of voltage differences is a mechanism by which a digital medium configures its own susceptibility to 'its' analogue environment. Of course, the contingency and complexity of this openness to analogue 'noise' is reduced or 'managed' by the algorithmic procedure encrypted in the chip. But, in other contexts, and depending on the complexity of its analogue medium,[20] the algorithm that articulates intermediation may have to embody enhanced 'learning' capacities.

Returning to the theme of potentiality, Hayles' 'degree zero' example of the 'intermediation' of analogue and digital very nicely expresses the sense in which potentiality does not 'inhere' in any term of the distinction but arises from the inter-articulation of the two. It also expresses the idea that this articulation—whose effects might be extended into broad networks of 'intermediation'—is not ontologically inscribed in the world.[21] If the 'analogue' is always correlative to a particular 'digital' process, so that the difference between them is a function of perspective, then there is no such thing as the Analogue or the Digital. In other words, these are not real dimensions of the world so much as the instruments and effects of particular cognitive and practical strategies. One might say, then, that there are many processes of 'intermediation', each referable to a particular strategy or perspective, none of which enjoys any kind of epistemic or ontological privilege. And this mode of diffraction articulates the principle of 'collection' that animates contemporary bio-collecting. Far from being the ultimate medium of collection, the digital is just one fold in an unfinished multiplicity. Interestingly, and somewhat ironically, this formula for multiplicity emerges just as strikingly if we return to the undeniably 'linear' dimension of the *Sorcerer II* expedition, namely, the dimension in which ownership of collected resources is at stake. Here the distinction between material and immaterial, which is often used as though it were interchangeable with the distinction between analogue and digital, illustrates how even the most traditional conceptual forms can take on interesting kinetic attributes.

20 And in the case of DNA computing, where protein concentrations are even more unruly than voltages, the function of TTL chips is taken on by switching between simulated genetic circuits and actual genetic circuits (see generally Klarreich, 2003).

21 Alain Badiou's critique of the hidden ontology in Deleuze's celebration of rhizomatic 'middles' is also pertinent here (1998: ch. 4).

## Too much ownership

> The irony is just too great. I'm getting attacked for putting data in the public domain. (Venter, cited in Shreeve, 2004: 5)

Before its 'official' departure in August 2003, the *Sorcerer II* undertook a trial run in the Sargasso Sea in collaboration with the University of Southern California and the Bermuda Biological Station for Research (BBSR), a non-profit marine research station established in 1903 by scientists from Harvard and New York University. The BBSR had just established its own bio-prospecting initiative in the form of a Marine Genome Bank holding genomic data from the Sargasso Sea. Two kinds of 'dividend' were anticipated: the scientific insights or advances that might be elicited by the publication of genomic data, and the more bankable profits that were to come from royalties paid by licensees of genomic data (BBSR, 2002). Venter's technique of combinatorial genomics turned out to be essential to the identification of diversity because it disclosed a previously invisible number of 'new' species. According to an article subsequently published in *Science*, the search discovered more than 1.2 million 'unknown genes' and some 1,800 new species—or rather 'data estimated to derive from at least 1800 genomic species' (Venter, 2004). Consistent with the ostensibly public mission of the *Sorcerer II*, these sequences were immediately posted in the public access database GenBank. The prospecting permit granted to Venter by the BBSR masked a complex and unresolved articulation of state jurisdiction, public interest, commercial science and international obligation. An article in *Nature* reported that officials in the Bermuda Ministry of the Environment were unhappy about the BBSR's exercise of its delegated authority over Bermudan waters: 'Something that held value has been placed in the public domain and made valueless for the people of Bermuda' (Dalton, 2004). This same point was pressed more forcefully when the *Sorcerer II* visited the Galápagos Islands. Ecuadorean environmental organizations and international pressure groups claimed that Venter had failed to obtain all the necessary permissions for prospecting and that micro-organisms from Ecuadorean waters had been improperly obtained. Venter's response was to emphasize the integrity of his pursuit of 'basic science'; counsel for the IBEA wrote to affirm that 'no patents or other intellectual property rights will be sought by IBEA on these genomic sequence data' (ETC Group, 2004: 26). But, according to his critics, this completely missed the point: Ecuadorean microbes were not Venter's to gift to the world (and depositing them in a public database offered no guarantee against the patenting of derivative inventions).

These legal difficulties were apparently unexpected:

> It was a big surprise to me that there's very little international waters left. I thought I was out sailing free in the ocean and somebody's claimed it all. (Venter in Russell, 2004: 21)

The force of Venter's appeal to the ensign of Science lay in the way that it conjoined the two media that in conventional symbolism (or mythology) have come to represent the quintessence of the 'public' or the 'common': basic science and the 'open' sea.[22]

22 In the language of the classical legal treatises the 'essential destination' of the sea was to be an open medium of communication.

What could be less objectionable than basic science pursued on the open seas?[23] But when the Convention on Biological Diversity (CBD) came into force in 1992, genetic materials ceased to be the 'common heritage of mankind', and instead became 'genetic resources', subject to the sovereignty of the states from whose jurisdiction they were taken. The central mission of the CBD is to promote the sustainable use of biodiversity by providing for 'the fair and equitable sharing of benefits arising out of the utilization of genetic resources'.[24] Because the CBD is a 'framework convention', the detail of its normative programme emerges from an ongoing succession of meetings of the Conference of Parties,[25] which are themselves coupled to a process of transnational law-making[26] which joins heterogeneous actors in associations that transect—or 'lateralize'—the old hierarchies of international or supranational law. One might say that the CBD establishes 'a common domain for producers and users of genetic resources to negotiate interests and balance interests' (Brush, 1997: 546), but precisely because this transnational process has no centre or apex, and no other warrant of commonality, this 'public' or 'common' domain is diffracted into a multiplicity of actor-perspectives, each of which makes the distinction between public and private in its own way. From one perspective, for example, no 'private' intellectual property rights arise until a compound has been synthesized by techniques recognizable in Euro-American patent law; from another, material sovereign resources already embody intangible rights arising from cultural 'authorship'. The effects of this process of multiplication resonate in Venter's complaint that he always seemed to be on the wrong side of a shifting normative line: 'We're now getting criticized for making our data public. I can't seem to get on the right side of this equation' (Venter, cited in McDonough, 2005).

As a result, ownership narratives continue to proliferate around genetic resources. Two conventionalized narratives of provenance and derivation form the basis of these narratives. First, there is the common idea that genetic resources travel through the world much like rare (tangible) commodities; they have to be 'prospected' in remote locations and physically transported (or smuggled) across borders. Topologically, this image of displacement across juridically configured territories, or of trading across 'ecological divides', develops the classical theme of property and territoriality, which is exemplified in the Roman law category of *accessio*, and specifically *alluvio* (see generally Madera, 2004). Second, there is the legal-economic representation of the axis of natural products innovation, which imagines the progressive reduction of natural structures to properties, and properties to industrial functions.[27]

The persistent assumption that 'objects of property come first; their movements, second'[28] is nicely unravelled in Cori Hayden's account of bio-prospecting in Mexico. Hayden

23 Most complaints related to territorial waters; for a discussion of bio-prospecting on the high seas, see Lawson and Downing (2002).

24 CBD, Article 1. For a critical perspective on the assumed value of genetic resources, see Firn (2003).

25 And the most significant dimension of this is 'document production', see, generally, Riles (2000).

26 'Lawmaking in this arena is emergent, iterative, and performative: it reproduces like a multisectoral virus as model legislation, contracting practices, database models, protocols and declarations are spread across the internet and adapted, adopted, and proclaimed in local communities, regional networks, national government agencies, and legislatures' (Coombe, 2003: 276–7). For a stricter theoretical account of 'emergent, iterative, and performative' transnational law-making, see Teubner (1997).

27 Bensaude-Vincent (1998) superbly deconstructs this representation.

describes how researchers from the National Autonomous University of Mexico (UNAM) fulfilled their obligations under a multipartite bio-prospecting contract by buying plant samples from vendors in a number of urban market places. There were some obvious advantages to this method. The presentation of plants on a market stall forms a ready conspectus of ethnobotanical knowledge. Each pile or bundle of flowers, leaves, stems or roots manifests the classificatory principles by which therapeutic properties are attributed to the parts of plants: 'when you buy plants in markets, you also buy information—about how the plant is prepared, where it is collected, and, with luck, how to locate the collectors' (Hayden, 2003b: 126; see also Hayden, 2003c: 363–4). And although by recording each market transaction the UNAM researchers created a version of the administrative trace required by emerging norms of access and benefit-sharing, they did not use that trace to identify an absolute 'origin'.

> [The researchers'] view of market-mediated relations between resources collected and interlocutors enrolled does not rest with the absence or evasion of benefit-recipients. Rather, it is the market that enables [the researchers] to identify and enrol a range of benefit-recipients outside the logics of authorship and ownership that benefit-sharing agreements implicitly and explicitly require. (Hayden, 2003b: 137)

Market-mediated prospecting allowed the researchers to reinvent the conventions of access and benefit-sharing in such a way as to allocate compensation to (more) appropriate recipients. The example is well chosen—it emphasizes that the persons and objects collected in a benefit-sharing agreement cannot simply be 'read off' from a singular biography of an object or its 'authorship'. As Hayden puts it: 'prospecting agreements do not merely *direct* the traffic in resources but rather help *generate* their constituent subjects and objects' (Hayden, 2003b: 127).

If the UNAM researchers' practice created what Hayden calls 'a vivid breach in the bioprospecting imaginary' (Hayden, 2003c: 360), it did so by exposing a central problem with access and benefit-sharing: 'in what idiom—territoriality, nationalism, cosmopolitanism, authorship—will biological collections be attached to social relations, interests, and claims?' (2003c: 368). That complication was already evident in the minor furore surrounding Venter's accord with the Bermuda Biological Station for Research. Officials might have been anxious about a loss of 'value' because the Diversa corporation had just patented a fluorescing protein extracted from coral collected under its agreement with the BBSR (which provided for the BBSR to receive a 1 percent royalty on any profits of the patent). The question was how to resolve 'sovereignty' over genetic resources into determinate regulatory and proprietary rights. What does sovereignty (in both its domestic and external dimensions) mean in a transnational process that transects legal hierarchies? And this question arose in a specific context. The director of the BBSR, writing to refute the allegations aired in *Nature*, observed that 'seawater moves quite fast off Bermuda', and that as a result the collected samples were likely to contain bacteria 'from many Exclusive Economic Zones of many countries in the world', making ownership 'a difficult and complicated issue'.[29] It is not just that the entitlements inscribed in objects shift and multiply as they move across diffracted legal topologies, but also that the movement of

28 See the critique in Maurer (1999).

these objects has the effect of sharpening and multiplying the diffractions of these legal regimes.

The fact is that a state's interest in genetic resources—or any other actor's interest—arises only when a resource is actually or anticipatorily set in motion. And the dynamic or directionality of this movement is a function of the perspective from which it is observed and from which it is 'interrupted'. Processes of material displacement and/or intangible enhancement can be retraced from a number of (interested) perspectives, each of which will map the flow of value and the genealogy of entitlement-generating contributions in its specific manner. So there is, one might say, 'too much' ownership in the Convention. And there is no 'legal-sociological' counterpart to Maxwell's demon, a lightning-quick observer who could stand outside social-historical mixing and distinguish contributions or accretions.[30] Indeed, sociologically speaking, the trouble is that there are just too many interested demons. The difficulty is not that of distinguishing entities that were once ontologically distinct; rather, it is that of reconciling different constructions of this original 'ontological' distribution of subjects and objects.

In law, the form that keeps genetic resources in motion is a particular form of contract. The contractual frameworks which structure bio-prospecting agreements are often presented as extended material transfer agreements (MTAs) (see Gollin, 2002). To the extent that complexity or heterogeneity are quantifiable attributes, one might say that bio-prospecting agreements are considerably more heterogeneous than MTAs in biomedical research: 'the rights of the provider of the material go beyond simple property rights and include issues raised under the CBD, such as sovereign rights, prior informed consent, access to land and resources, ''fair and equitable'' benefit sharing, conservation, and environmental permitting' (Gollin, 2002: 310). But the parallel remains instructive. Typically, MTAs are used to regulate the terms on which biological materials are transferred from one research laboratory to another. Transferors usually seek to retain certain rights—or more or less opportunistic 'proprietary positions'—in respect of any innovations subsequently developed from their research materials, and agreements will often contain stipulations as to, for example, the permitted uses of the materials, the timing of any resulting scientific publications, or the provision of grant-back or reach-through rights in relation to derivative inventions. Typically, material transfer agreements construct transactions in what the NIH (1999: 72092) describes as 'unique research resources'. Biomedical research tools—cell lines, enzymes, plasmids, clones, gene probes, etc.—have to be acquired in material form because, although recombinant DNA technologies can recruit bioactivity, they cannot (yet) replicate it artificially (bioactivity in this case consisting in the ability to bind or hybridize rather than to reproduce). Some biomedical artefacts resemble bio-prospected resources in that their uniqueness is attributed to source-specificity. For example, the enzyme that powers the most famous (and the most litigated) of all biomedical research tools, polymerase chain reaction, was synthesized from

29 Letter to the *Royal Gazette*, Bermuda. URL (accessed March 2006): www.gene.ch/genet/2004/Jul/msg00080.html

30 Referring to Maxwell's observation that 'the 2nd law of thermodynamics has the same degree of truth as the statement that if you throw a tumblerful of water into the sea you cannot get the same tumblerful of water out again', Bruce Clarke observes that the demon 'could just as easily part the waters and reassemble the contexts of the tumbler from the jumble of the sea' (Clarke, 2002: 24).

*Thermus aquaticus*, a thermophilic bacterium originally discovered in the springs of Yellowstone Park.[31]

Obviously, the (biological) materiality of research tools is central: 'control over physical access provides an easy mechanism for identifying users and imposing restrictions on the dissemination and use of proprietary materials and data' (NIH, 1998: 8). Suppliers of bioactive materials deploy them strategically as instruments of speculation, which suggests an alternative meaning for the term 'bio-prospecting': the use of biological research materials as a means of staking a claim to future profits or inventive opportunities. Again, there is 'too much' ownership here; too many plausible stories of origin and transmission, and too many perspectives on 'value'. To begin with, there is a distinction between producers and users: 'What a user sees as a research tool, a provider may see as a valuable end product for sale to customers' (1998: 10). And as between themselves, providers of research tools or the 'inventors' of metabolic 'mechanisms of action' will have conflicting senses of the (potential) significance of their proprietary technologies in the emergence of valuable innovations. From the perspective of the supplier, the continuity of the contract is premised on the idea that subsequent enhancements should be seen as variations on the original invention, so that material or bioactive continuity becomes an index to *intellectual* or *intangible* enhancements. What the producer or supplier sees as a derivative invention will be presented by the user-inventor as an original invention, though this will typically be a 'novel' iteration of a known bioactive object. Either way, the 'property' in question is neither tangible nor intangible; it consists in rights to extract value from the process of research into bioactivity.

In legal and economic critiques, multiplicity is a negative attribute. Specifically, the multiplication of ownership claims gives rise to what Michael Heller and Rebecca Eisenberg call 'the tragedy of the anticommons':

> Anticommons property can best be understood as the mirror image of commons property. A resource is prone to overuse in a tragedy of the commons when too many owners each have a privilege to use a given resource and no one has a right to exclude another. By contrast, a resource is prone to underuse in a 'tragedy of the anticommons' when multiple owners each have a right to exclude others from a scarce resource and no one has an effective privilege of use. (1998: 698)

Because researchers now value profit as much as, if not more than, publication,[32] the linear flow of basic science is captured in eddies of private interest, with each contributor to an inchoate project overvaluing their own stake in the process. The progressive commodification of science is presented as the most malign influence here because it gives rise to a situation in which 'intellectual property rights in upstream biomedical research belong to a large, diverse group of owners in the public and private sectors with divergent institutional

31 The bacterium itself, *Thermus aquaticus* (*Taq*), was discovered in 1966 and deposited in the American Type Culture Collection, from which it was taken—free of charge—by the Cetus corporation which used it to produce the enzyme (Taq polymerase) that is stable at the high temperatures needed for the PCR reaction. The website of Yellowstone Park tersely notes that 'none of these revenues has benefited Yellowstone National Park and its resources' (see www.nps.gov/yell/index.htm).

32 On the difference between these two economies, see Biagioli (1998).

agendas' (1998: 700). In other words, as Eisenberg puts it, 'what you have is a heterogeneous set of owners—too many people with rights to exclude' (cited in Coale, 1998: ).

To what extent should 'heterogeneity' be seen as a deficit of unity? There are various reasons for being sceptical about arguments premised on the metaphorical distinction between 'up-stream' and 'down-stream' research,[33] and to these one might add the very heterogeneity that is revealed by the notion of an anticommons. There is of course a trivial and incontrovertible sense in which innovation is linear. By definition, attributions of originality or authorship depend on distinctions between past and present. But the point is that these attributions of origin are now traced from numerous perspectives, and the complexity of bioactive process gives no necessary warrant for privileging one over another. So the engaging insight of the 'anticommons' argument is that we actually have too much linearity, too many trajectories of innovation, and that insight resonates very closely with more general theoretical observations about the 'disembedding' of temporal schemata in contemporary society. In such circumstances, academic evocations of a lost linearity merely add a further fold to heterogeneity. By contrast with the 'anticommons' argument, the technique of biocontracting is interesting because it acknowledges—performatively—that biomedical research is articulated by an economy of 'unfinished' and non-linear invention. Increasingly, research tools and pieces of cellular machinery are understood as inventions whose value and identity will be revealed and reconstructed only in the uses that others make of them. Although MTAs construct transactions in finished products, many of which are patented inventions, they negotiate a relation to a future that remains—pending the realization of synthetic biology—open-ended.

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Modes of bioprospecting have been profoundly transformed by the emergence of sequencing technologies, bioinformatics and synthetic biology. These technologies have their effects on the 'materiality' of collections and the media into which they are collected. Bio-collecting was once ordered by the logic of Linnaean nomenclature (see especially Müller-Wille, 2003) or Darwinian genealogies, but in the era of 'bio-information' (Parry, 2004) collections are articulated in a number of media, topologies and 'kinetic' modes. 'Information' acquires multiple meanings and values as it is switched across these media, so much so that, as in bioinformatics, 'information' is better imagined as a verb rather than a noun:

> The information contained in genes and in the relationships between them is what 'informs' the organism, expressed in the *action of giving the organism its form*, not just in the [abstract sense] of a 'formative principle or vital quality', but in the very concrete sense of shaping its body. (Danchin, 2003: 178–9)[34]

33 'While most who study systems of innovation have long since abandoned the "pipeline" model in which research dollars are pumped in and commercial products flow out, Heller and Eisenberg's repeated allusions to "upstream" and "downstream" suggest that the general metaphor still pervades policy analysis. A river has many tributaries and is a pipeline open to the sky, but it still flows in only one direction. But producing new knowledge and developing new technology depends on bidirectional flow' (Cook-Deegan, 1998).

34 So 'information' means to *in*-form in the positive sense of bestowing form on a previously uncharacterized element. On this usage, see von Baeyer (2003: ch. 3).

This is what the 'intermediation' of digital/analogue already suggests; there too, (informatic) materialities are an effect of a specific 'in-forming' event. So, for example, one might say that the 'speed-up' of bio-information is less an effect of shifting from one term of a distinction to another, from materiality to immateriality,[35] and more an effect of the intermediation of these terms. Bioactivity—or bio-information—is neither tangible nor intangible, neither material nor informational; even within digital media, information is already diffracted into the intermediating elements of code, circuitry, graphic representations, cognitive interpretations, etc., and then multiplied again when it is grafted, replicated and cultured by means of some combination of breeding, recombinant DNA technology and bioinformatic simulations.[36] 'Information' is the same and yet always different. And this mode of 'multiplying intermediation' is precisely what the practice of bio-contracting illustrates and articulates. On the basis of nothing more than the old (legal and linear) distinction between tangible and intangible, MTAs allow idioms and entitlements to be multiplied into a particular kind of unfinished object. The *Sorcerer II* is such an opportune conceptual device because it figuratively and performatively expresses the way in which idioms of political interest and legal entitlement index and articulate the multiple intermediations that inform the technological construction of bio-collections.

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35 'What begins as a thick, messy whole organism—something unquestionably corporeal in form—becomes, through this process, progressively decorporealised, existing in the final analysis as what could only be described as a body of information, an archive of stored data or images' (Parry, 2004: 68).

36 On the role of bioinformatics in agricultural innovation see Mazur (1999: 9).

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