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Configurations 11.1 (2003) 47-79

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What Is Biomedia?

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Virtual bodies, cyberbodies, cyborgs, avatars, hypertext bodies, and a host of other "incurably informed" corporealities continue to populate the ongoing discourses surrounding cyberculture and new media (which, as Friedrich Kittler reminds us, are not so new). [1] At the core of these and other formulations is a concern for the ways in which a medium associated with immateriality and disembodiment will affect our views of having bodies and being bodies (and becoming bodies . . .) . In this almost mythic encounter, an assumedly preinformatic body confronts a set of techniques and technologies whose central aim is to render everything as information—not only can everything be understood as information, but information is everything, in that every thing has a "source code." While some perspectives see this as an emancipatory promise of the posthuman, other, more critical perspectives have questioned the hidden theology masked by the technical speak of pattern, emergence, and code. **[End Page 47]**

A number of media theories do highlight the "materiality of informatics," or the ways in which information technologies articulate themselves as technologies of immateriality, but there has been relatively little exploration of the ways in which an informatic paradigm pervades the biological notion of the body and biological materiality itself. [2] The aim of this essay is to outline some concepts for doing so, and, hopefully, to point to directions in need of further consideration. As we will see, the position taken here goes against many of the current discussions surrounding cyberculture and virtual bodies. Instead of pointing to the pervasive "informatization" of the body, my aim will be to ask two questions: First, in what ways is the notion of biological materiality already informatic? And second, in

what ways does information (biologically) "matter"?

In particular, the wide range of techniques and technologies that are grouped under the rubric of "biotechnology" (or just "biotech") will be considered. The historical trajectory of biotech as a science, as an industry, and as a cultural force has been recounted by others, and will not be repeated here. Instead, the focus will be on biotech as a set of practices in which the body is a medium. Put another way, biotech will be considered here, not simply as a technological instrumentalization of the (natural, biological) body, but as a unique domain in which biology is a technology (in fact, a better technology than any we can build). It is not just that the medium is the message, but that biology is the new medium: the medium is a message, and that message is a molecule. This is the crux of the concept of "biomedia," which will be explained further on.

In its current state, we can describe biotech not as an exclusively "biological" field, but as an intersection between bioscience and computer science, an intersection that is replicated specifically in the relationships between genetic "codes" and computer "codes." Areas **[End Page 48]** of specialization in biotech, such as genomics, proteomics, or pharmacogenomics, are each unthinkable without an integrated relationship to computer technologies. [3] Increasingly, a large number of the tools that researchers use are not only computer-based, but also Web-based, running from servers housed at universities, companies, or research institutes. As industry publications have noted, the traditional "wet lab" of molecular biology is being extended, augmented, and even replaced by the dry lab of "point-and-click biology" in bioinformatics and computational biology. [4]

What Can a Body Do?

This intersection between genetic and computer "codes" is more than merely technical. It involves the intermingling of two disciplines—computer science and molecular biology—which have traditionally held radically different views on the body. To begin with, let us take two techniques, from two related fields, both of which make use of DNA.

The first technique is protein prediction, often referred to as "homology modeling." [5] The field is proteomics, or the study of how DNA sequences produce amino acid sequences, and how those amino acid sequences fold into the complex structures we know as proteins. [6] One way to do this is to make use of a number of computational **[End Page 49]** tools that are part of a growing field known as "bioinformatics." One such tool is a Web-based application that lets you input a DNA sequence you are studying, and that then searches several genome databases (online) for candidates for a likely match. The results might contain several DNA sequences, or even genes, that are close to your sequence. You can then use another tool (also online) which will take your DNA sequence, and its potential matches from the genome databases, and will create a profile of the amino acids the sequence is likely to produce. These will be sequence data, and

so you will have your original DNA sequence, plus close matches from a genome, and amino acid sequence data (or the raw "protein code"). We have sequences, but no structure yet. We can then take the protein code (the 1-D sequence of amino acids) and put it through another tool (yes, online) which will, based on existing databases of known proteins, draw up predictions for how different parts of that protein (known as "domains") will fold into different three-dimensional structures (known as "motifs"). A final tool (online, but you also have to install a plug-in for viewing 3-D molecular models . . .) will collate all those predictions to test for their compatibility as one whole protein structure. If you are lucky, you will get a close match, a 3-D file of the molecular model, and data on the reference model in a database such as the Protein Data Bank. You then have some idea (and a lot of data) about the relationship between your candidate DNA sequence that you started with, and the possible proteins or protein domains it may code for.

The second technique is biological computing, or biocomputing (computing using biomolecules). [7] Also called DNA computing, this technique was developed in the mid-1990s as a proof-of-concept experiment. The concept is that the combinatorial possibilities inherent in DNA (not one, but two sets of binary pairings in parallel, A-T, C-G) could be utilized to solve very specific types of calculations. One famous type is the so-called "traveling salesman" problem (also more formally called "directed Hamiltonian path" problems): You are a salesman, and you have to go through five cities. You can visit each only once and cannot retrace your steps. What is the most efficient way to visit all five cities? In mathematical terms, the types of calculations are called "NP complete" problems, or "nonlinear polynomial" problems, because they involve a large search field which gets exponentially larger as the number of variables increases (five **[End Page 50]** cities, each with five possible routes). For silicon-based computers, calculating all of the possibilities of such problems can be computationally taxing. However, for a molecule such as DNA, the well-understood principle of "base-pair complementarity" (that A always binds to T, C always binds to G) makes for something like a parallel-processing computer, except that it functions not through microelectrical circuits but through enzymatic annealing of single strands of DNA. You can "mark" a segment of any single-stranded DNA for each city (using gene markers or fluorescent dye), make enough copies to cover all the possibilities (using your PCR thermal cycler, a DNA xerox machine), and then mix them in a test tube. The DNA will mix and match all the cities into a lot of linear sequences, and, quite possibly, one of those sequences will represent your most efficient solution to the "traveling salesman" problem.

The reason for briefly introducing these two techniques is that they are exemplary of the ways in which biology becomes a medium. They both use DNA, and they both perform "computational" work in relation to DNA, but there are important differences as well. In a sense, one technique is the inverse of the other: in the first example of bioinformatics, the DNA is fully digital, and the entire process takes place on and between computers; in the second example of biocomputing, the DNA is fully biological, and the entire process of computation takes place in the test tube. While the digital DNA of bioinformatics makes use of computer

technology to "model" biology (simulations of "molecular dynamics" in protein folding), the biological DNA of biocomputing is repurposed as a computer in its own right ("base-pair complementarity" as two binary sets). The output of bioinformatics is always biological: its point of reference is always the world of the biological cell, the DNA molecule, and various proteins in the body. By contrast, the output of biocomputing is not biological (despite its medium), but rather computational; a "computer" can, theoretically, be made of any material, as long as certain principles (e.g., a storage device, a read-program, a write-program) are fulfilled.

With these two techniques—gene and protein prediction in bioinformatics, and NP complete calculations in biocomputing—we have a twofold dynamic, in which the relationship between biology and technology is significantly reconfigured. On the one hand there is the premise that biology is computational: that the essence of DNA as a code makes it fully amenable to the digital domain, for archiving, searching, editing, pattern-matching, and other computational procedures. It could be said that the success of emerging fields such as bioinformatics largely depends on the viability of this **[End Page 51]** premise, that we are not simply "representing" DNA but, in some important way, actually working with DNA as code. On the other hand, there is the premise that computation is biological. Here the emphasis is not so much on computer technology utilized in biological research, but on biology utilized in computer science research. The suggestion here is that the characteristics of a "universal computing machine" (in Turing's terms) are such that a variety of material substrates may fulfill a single function. [8]

These two premises—computational biology and biological computing—are informed by a single assumption: that there exists some fundamental equivalency between genetic "codes" and computer "codes," or between the biological and informatic domains, such that they can be rendered interchangeable in terms of materials and functions. Whether it be the use of biological data in protein prediction (bioinformatics or computational biology), or the use of biological function for nonbiological purposes (biocomputing or biological computing), the emphasis is less on "technology" as a tool, and more on the technical reconditioning of the "biological."

It is this assumption that characterizes the concept of "biomedia." Put briefly, "biomedia" is an instance in which biological components and processes are informatically recontextualized for purposes that may be either biological or nonbiological. Biomedia are novel configurations of biologies and technologies that take us beyond the familiar tropes of technology-as-tool, the cyborg, or the human-computer interface. "Biomedia" describes an ambivalence that is not reducible to either technophilia (the rhetoric of enabling technology) or technophobia (the ideologies of technological determinism). Biomedia are particular mediations of the body, optimizations of the biological in which "technology" appears to disappear altogether. With biomedia, the biological body is not hybridized with the machine, as it is in the use of mechanical prosthetics or artificial organs. Nor is it supplanted by the machine, as it is in the many

science-fictional fantasies of "uploading" the mind into the disembodied space of the computer. In fact, we can say that *biomedia has* **[End Page 52]** *no body-anxiety*, if by this we mean the will to transcend the base contingencies of "the meat" in favor of virtual spaces. [9]

By contrast, what we find with biomedia is a constant, consistent, and methodical inquiry into the technical-philosophical question of "what a body can do." The apparent paradox of biomedia is that *it proceeds via a dual investment in biological materiality, as well as the informatic capacity to enhance biological materiality*. In some instances, we can refer to this as a "lateral transcendence," or the recontextualization of a "body more than a body." To refer to the examples with which we started: the investment in bioinformatics is not purely digital or computational, but a dual investment in the ways in which the informatic essence of DNA affords new techniques for optimizing DNA through novel software, which in turn makes possible the development of techniques for enhancing the biological body via new compounds (pharmacogenomics), new therapies (stem cell therapy), or new diagnostics (patient-specific disease profiling). Biomedia is only an interest in digitization inasmuch as the digital transforms what is understood as biological. In short, the body you get back is not the body with which you began, but you can still touch it. The "goal" of biomedia is not simply the use of computer technology in the service of biology, but rather an emphasis on the ways in which an intersection between genetic and computer "codes" can facilitate a qualitatively different notion of the biological body—one that is technically articulated, and yet still fully "biological."

Though the concept of biomedia presented here is, certainly, open to several interpretations, and more than one application, it is crucial, for a critical understanding of biotechnology, that biomedia not be confused with "technologization" generally. *Biomedia is not the computerization of biology*. Biomedia is not the "digitization" of the material world. Such techno-determinist narratives have been a part of the discourse of cyberculture for some time, and, despite the integration of computer technology with biotechnology, biomedia establishes more complex, more ambivalent relations than those enframed by technological determinist views. A key component to the questioning of biotechnology is the attention paid to the ways in which biomedia consistently recombine the medium of biomolecular **[End Page 53]** systems with the materiality of digital technology. The biological and the digital domains are no longer rendered ontologically distinct, but instead are seen to inhere in each other; the biological "informs" the digital, just as the digital "corporealizes" the biological.

New Media, New Bodies?

These characteristics also point to a significant question: is the juxtaposition of "bio" and "media" (or "bio" and "tech") not in itself a redundancy? In other words, is the "body" itself not already a medium? To answer this we can look to two contemporary formulations in the context of "new media."

In *The Language of New Media,* Lev Manovich puts forth a series of characteristics of new media which distinguish them from earlier media such as film or television—namely, the principles of "numerical representation," "modularity," "automation," "variability," and "transcoding." [10] Among these it is the concept of transcoding that elaborates the most on the ways in which new media may transform certain visual, haptic, auditory, and corporeal habits specified by earlier media such as film. Technically, transcoding involves all types of file-conversion procedures that translate between any two media objects (from still .GIF images to a QuickTime movie, for example). Culturally, this implies that there is a certain universality among heterogeneous media objects, that a universal code underlies different media and thus makes possible a horizontally multimediated space. As Manovich states:

> New media in general can be thought of as consisting of two distinct layers—the "cultural layer" and the "computer layer." . . . Because new media is created on computers, distributed via computers, and stored and archived on computers, **[End Page 54]** the logic of a computer can be expected to significantly influence the traditional cultural logic of media; that is, we may expect that the computer layer will affect the cultural layer. [11]

Similarly, in *Remediation*, Jay Bolter and Richard Grusin discuss how "media" and "mediation" have been theorized in ways that have been intimately tied to particular technologies and their broader cultural and experiential impact. "Remediation" is a concept that describes the ways in which any historically situated medium always re-mediates prior media, and thus also re-mediates prior social and cultural modes of communication. For Bolter and Grusin, the concept of remediation involves a complex dynamic between two technological processes: "immediacy" and "hypermediacy." The former involves the use of new media to the extent that the media themselves—the "window"—disappear, bringing forth a kind of direct experience where technology is transparent and unnoticed by the subject. By contrast the latter process—hypermediacy—involves the overcoding, heterogeneity, and saturation of the subject by different media, the empowerment of multiplying media tools in the hands of the subject.

For Bolter and Grusin, a level of transcoding is implied in the very act of remediating; thus, remediating print or film in a new digital medium such as the Web suggests a transcoding, such that both a print object and a film object can be re-presented in a digital medium. Likewise, one of the things that Manovich's characteristics of new media make possible is an unprecedented ability to remediate, permutate, and recombine media elements due to the technical code-conversion properties of digitization generally. In other words, the concept of "remediation" provides us with one meaning in the "cultural layer" of transcoding. For both Bolter and Grusin, as well as Manovich, the characteristic common to new media is this technical capacity to encode, digitize, and transcode various "things" from the real world (including other media objects).

If this is the case—that is, if it is possible to transcode and remediate various objects from the physical world—what effect would this have on the body of the human subject, as an object? Can the body be "transcoded"? Is the body a type of "remediation"?

Bolter and Grusin suggest that the body remediates various cultural and social meanings, while it is also subject to remediation. We may additionally cite phenomena such as fashion, modern primitivism (piercing, tattooing), body play, cosmetic surgery, transgenderism, body building, cyborg performance, and other areas of culture **[End Page 55]** as examples of the body both as a medium (a means of communication) and as mediated (the object of communication). As the authors state:

> In its character as a medium, the body both remediates and is remediated. The contemporary, technologically constructed body recalls and rivals earlier cultural versions of the body as a medium. The body as enhanced or distorted by medical and cosmetic technologies remediates the ostensibly less mediated bodies of earlier periods in Western culture. [12]

Bolter and Grusin suggest that any "techniques of the body" situate the body both as a medium and as mediated. [13] Following this, it would seem that cultural attitudes toward the body are the same as those toward media: our culture wants to render the body immediate, while also multiplying our capacity to technically control the body.

However, for Bolter and Grusin—and for many of the theorists they mention—this remediation of the body reveals an assumption regarding the ways in which "body" and "technology" are ontologically distinct entities. In such a case, one applies techniques and/or technologies to the body—in cosmetic surgery, for instance—in a way that transforms that body into both a medium (communicating ideas of appearance and aesthetics) and a mediation (a sculpted object of beauty). In other words, in considering the remediated body, something is done to the body in the first place; the body's techniques do not arise from within itself, it gains its remediation externally. One puts on clothing, inserts a piercing, injects ink into the skin, cuts and tucks a section of flesh, attaches prosthetics, utilizes "extensions of the body" such as mobile phones or PDAs in the performance of the everyday.

As a way of diversifying Bolter and Grusin's discussion of the body as remediated, we might ask: What would it mean to approach **[End Page 56]** the body as a medium in itself? We can begin by considering those instances in which selected properties of the body are geared toward extraorganismic ends. In other words, if we want to inquire into the body as a medium, the first step is to consider the components of the body as networks of relations, along with their range of uses (that is, the relationships between components—components indistinguishable

from relations—that constitute the body's range of activity).

That being said, scientific practices such as biotechnology have, for some time, focused precisely on this question of the body-as-medium. The basic question that biotech research asks is: How can selected properties and processes in the biological body (in "nature") be geared toward novel medical, industrial, and economic ends? Specialized research fields in regenerative medicine, genetic diagnostics, and genomics all have this general goal of a nonorganismic technical utilization of the body's biology. While most utilities are for bioscience research and medical application, others are used in computer science research (DNA computing), drug development (rational drug design), or the materials industries (biomimicry). [14]

As an extension to media studies' discussion of the body, we can add that a consideration of the body as a medium means that those techniques and technologies are not external to or qualitatively different from the body. Whereas the examples raised by Bolter and Grusin—fashion, body building, cosmetic surgery—rely on both this externalization and this qualitative separation, the body as seen in biotech research generates its technicity from within; its quality of being a medium comes first and foremost from its internal organization and functioning. In earlier techniques such as animal breeding or fermentation, the literal meaning of the term "biotechnology" is indeed this technical utilization of biological processes toward a range of novel ends. [15] The key to the general logic of biotech is that it is not a "technology" in the colloquial sense of the term; that is, it is not directly concerned with developing external technologies which then operate on, control, or transform the "natural/biological" world. But this absence of an identifiable instrument does not mean **[End Page 57]** that instrumentality as such has also disappeared. While its overall intentions may be congruous with ideologies of technology, from industrialism to the so-called computer revolution, biotech is specifically interested in the ways that the material components and biological organization of the body can in effect be rematerialized, renormalized, even redesigned. Informatics, as both an immaterial and material worldview, plays a central role in this process, and it is to the role of informatics in biomedia that we can now turn.

Bio-logics

In a way, the preliminary definition of biomedia—as the informatic recontextualization of biological components and processes—is broad enough that it can cover a wide range of practices, from the selective breeding of animals and plants, to the everyday use of vitamin supplements or over-the-counter drugs. However, while biomedia may be a labile concept, there are important reasons to argue against such a broad application.

The specific locale of biomedia is an interdisciplinary one, in which biological and medical approaches to understanding the body become increasingly indissociable from the engineering and design approaches inherent in computer

science, software design, microelectrical and computer engineering, and other related fields. The "body" in biomedia is thus always understood in two ways: first, as a biological body, a biomolecular body, a species body, a patient body; and second, as a body that is "compiled" through modes of information processing, modeling, data extraction, and *in silico* simulation. [16] It is this interdisciplinary cross-pollination (biological computing, computational biology) that is one defining characteristic of biomedia.

That being said, biomedia does not approach technology along the lines of the familiar tropes of the tool, the supplement, or the replacement to the human. In the first case, formulated most thoroughly by Martin Heidegger, technology is taken as a tool for the human user, meaning that it is distinct from the body, and comes from the outside to be used by the body, so that it forms a complex of "enframing." [17] This trope is extended in the second trope, where the **[End Page 58]** tool becomes an extension of the body of the user, a supplement that adds new functionalities to the body not inherent in it. This twofold moment of extension and supplementing may also lead to a third trope, where the processes of automation and control lead to technologies that displace or replace the body of the user. [18]

By contrast, biomedia do not so much configure technology along the lines of instrumentality (tool, supplement, replacement)—although an instrumentalization of the biological body is implicit in the practices of biotechnology. Rather, technology for biomedia is generative, establishing new technical configurations in which the biological can constantly surpass itself. Along these lines, biomedia is also not about the relationship between the body and technology as a bilinear, one-to-one dichotomy. The body-technology relation in biomedia is not based on the substances or composition of the components involved (where carbon-based organisms are opposed to silicon-based computers). Likewise, it is not based solely on functionality (e.g., the artificial organ that functions analogously to the biological body). Finally, it is not based on the technical metaphor of the "interface," in which parts identified according to substance are combined into some hybrid form (the design engineering principle of "human-machine interface"). Technology is not a "fit" with the body, or vice versa—be this in terms of identifications, functions, or interfaces.

How does biomedia conceive of the body-technology relationship? In part, it doesn't, and that is perhaps its unique feature. *In biomedia the biological body never stops being biological; it is precisely for that reason that the biological body is inextricably "technological."* This does not, of course, mean that there are no technological objects involved, and no techniques or specific practices. Quite the contrary. But it is the way those techniques and technologies are articulated in **[End Page 59]** these biotechnological practices that makes this a unique situation. In biomedia, the "media" employed, and the "technologies" applied, are organized in a way that prioritizes the biological domain as a set of components in interaction with each other via various biomolecular, biochemical, and cellular processes. [19] The media in biomedia create novel contexts, and establish novel

conditions for biological components and processes. This may involve "technologies" or "media" in the usual sense of the term (from PCR machines to pipettes and petri dishes), and it may involve the techniques that have been standard fare in molecular biology for some time (such as gel electrophoresis, recombinant DNA, or cell culturing). [20] What is different in the case of biomedia is that the use of such technologies, media, and techniques is specifically geared toward enabling the biological domain to technically operate in novel contexts.

We could say that this is a principles-based approach to the design of the biological domain. For instance, a biological principle such as " base-pair complementarity" is recontextualized in a wide range of practices. [21] It is found, certainly, in laboratory analysis techniques **[End Page 60]** such as PCR. It is also found in genetic engineering, in the use of enzymes (DNA ligases, restriction endonucleases) that act on DNA; and in the use of DNA chips or "microarrays," in which single-stranded DNA is used for medico-genetic diagnostics. Finally, base-pair complementarity is found in areas outside the biosciences, such as the field of DNA computing (cited above), which is more about computer science than it is about molecular biology. The same basic biological principle concerning the double-helical nature of DNA is "ported" across different domains, from biology research, to clinical diagnostics, to instrument design, to computer science.

BmTP: Biomolecular Transport Protocol

Biomedia vary with each particular constellation of biological and technical elements. However, biomedia can also be said to have several characteristics in common. One way of approaching these common characteristics is through the technical principle of "protocols." [22] In computer networking terminology, a "protocol" is a set of rules for establishing how a network operates in a range of contexts. "IP" or "Internet Protocol" is perhaps the most common type of protocol; others that may be familiar to Internet users include "FTP" or "File Transfer Protocol" and "HTTP" or "Hyper-Text Transport Protocol." Protocols dictate such things as how a network is operationally configured (do all nodes have direct access to each other?), the relationships between "host" and "client" computers (for instance, in uploading files or downloading email), and the ways in which data are transmitted from computer A at one point on the network to computer B. One of the interesting things about network protocols is that they often employ a flexible set of rules that can adapt to different circumstances. For instance, when viewing a web page, the HTML files with text, images, and any other media are delivered from a host or server computer to a client or the user's computer. However, those files are not delivered en masse; rather, the HTTP **[End Page 61]** protocol slices them up into small chunks, giving each chunk a unique identifier, and each of them is then sent along many different possible routes along the Internet. These chunks of data (not full files, but parts of files) are referred to as "packets." Ideally, they all take the shortest route between two points. However, when Internet traffic is heavy, or when a bottleneck occurs in one of the network connections, the shortest route is often not possible; therefore, each packet takes

one of many alternate routes along the network, sometimes taking detours which may, geographically speaking, span a wide area. This is the reason why, when viewing web pages, sometimes all of a page will load except for one little image, icon, or banner: the Web browser is waiting for the missing packet to literally complete the picture. When all the packets arrive, their unique identifiers tell the browser in which order they are to be reassembled.

If we switch our attention from "new media" to biomedia, we can see a similar protocol at work, but with very different effects and consequences. In short, biomedia can be said to operate according to an informatic protocol in which the principles for managing data are the means by which biomedia recontextualize the biological domain. This informatic protocol proceeds by a three-step process of "encoding," "recoding," and finally "decoding."

Encoding

Encoding is a boundary-crossing process. When, in speaking of media technology, we say that we are "encoding" (be it scanning digital images, capturing digital video, or coding a text file in HTML), we imply a transition from one medium to another, a shift in material substrates. Note that the process of encoding is not identical with dematerialization, as it is often taken to be with digital media. The most abstracted, most virtual medium still operates through some material substrate, as all software operates through hardware. [23] Therefore, although encoding—or its special case, "digitization"—may be commonly understood as a move from the world of materiality to the world of information, it is important to underscore the complicity of materiality with information.

Encoding, then, is akin to a process of data-translation, from one format to another, from one material substrate to another. The key to encoding is, of course, the "difference" between **[End Page 62]** material substrates. It goes without saying that if there were no difference between material substrates, then there would be no reason for a translation in the first place. Translating data from one format to another—from a photograph to a digital image, from VHS to QuickTime, from .doc to .html—implies a difference that encoding aims to ameliorate. The way in which it does so is through an informatic approach in which "data" are seen to inhere in any organization of matter, any relationship of matter and form. Whereas a more traditional philosophical definition situated matter as formless, and form as realizing matter, the process of encoding adds another dimension, which is that of data. [24] As cybernetics and information theory have suggested, data may not only inhere in matter and form (modeling air, light, or water in computer graphics; 3-D modeling based on simple forms), but may also be transported across different media. Classical information theory explicitly states—in language and in mathematics—that data may be transmitted from point A to point B, irrespective of the "content" of the data. [25] What makes data different from matter and form? We might say a quantifiable iteration, a persistence in spatialized rhythm, a pattern of relationships: anything consistently peculiar within the matter-form complex that is

amenable to quantification (bits, bytes, and data as objects). For the process of encoding, "data" becomes a third term, a trajectory across complexes of matter and form.

What is of interest in the process of encoding is that, on the one hand, it implies a significant difference constituted in part by the materialization of data—literally, a "difference that matters" between, say, a photographic print and a digital image on a computer screen. On the other hand, encoding's main reason-for-being is to overcome this difference (and, arguably, its "matter"), and in the process to facilitate a separation between essential data and material substrate. On a philosophical and technical level, encoding raises the question: when a pattern of relationships is transferred from one material substrate to another, does that pattern remain the same? [26] **[End Page 63]**

An example within biotech research is the broad category of "biochips." Research in this field incorporates approaches from mechanical engineering, electrical engineering, computer science, and molecular biology. The hybrid objects produced as part of this research are a paradigmatic example of biomedia. One class of biochip is the "microarray," or the DNA chip. As its name implies, this is a tiny silicon chip on which single strands of "sticky" DNA are attached using photolithographic processes. These strands of DNA—thousands are "spotted" on a single chip—stand on their ends like tiny hairs in an aqueous solution. Because they are single-stranded, or sticky, they will "naturally" bind with their complementary base when it is present in solution. Therefore, a sample solution of fragmented DNA of unknown sequence can be washed over the DNA chip, and the right base pairs of DNA will automatically attach themselves to their corresponding strands (A and T binding; C and G binding). [27]

Researchers can perform analytical and diagnostic tests on the genetic mechanisms in conditions such as breast cancer or Alzheimer's disease by using biochips. If you have a known genetic sequence, such as one from the *p53* tumor-supressor gene, you can spot it onto a DNA chip, and give each strand an extra genetic "marker." This marker is really part of a dyed gene which, when bonded with its complementary pair, will cause a fluorescent glow to occur. You can then pass an unknown DNA sample over the DNA chip and see if there are any "hits." If there are, certain spots will glow. This can be organized as a grid, with glowing and nonglowing regions. A specialized computer system can "read" the microarray pattern of activity caused by the process of binding single-stranded DNA. Analytical software can perform pattern matching on this microarray output against a microarray database to assess whether this particular DNA test sequence has a close match to any known sequence. The results for this procedure are of two kinds: if there are a significant number of hits on the DNA chip, there is a high likelihood that the test sample is related to your control sample; and, if the test sample **[End Page 64]** returns a match with a microarray database, then there is a high likelihood that the sequence is already known and has been studied. That information can then be utilized to tell you something about your test sample.

This procedure contains many levels of mediation, to be sure. The one we can focus on, however, is the one related to the process of encoding. What is encoded in this use of the DNA chip? In the common sense of the term, nothing is really encoded, and there are no proprietary technologies used in the process: basic tools of molecular biology (generating cDNA libraries; adding gene markers) and basic computer technologies (digital scanning; database queries) are both employed. What we would normally call "digitization" does occur, when the computer scans the microarray pattern as a grid of spots of different colors—but this is basic digital imaging, and it would be a stretch to say that the actual DNA is "encoded" in this process.

But what in fact is encoded? It seems that what is encoded is not just an image, but an index, which points to an enframed technical context in which biological processes do or do not occur. Recall that the main principle of the DNA chip is the "natural" process of base-pair complementarity. This process occurs, for instance, during protein synthesis, when the tightly woven DNA double strand uncoils and "denatures" itself, so that a single-stranded RNA molecule may be "transcribed." [28] This denaturing and annealing (DNA restitching itself) is recontextualized in the DNA chip, not for protein synthesis, but for gene-expression analysis. So what we see being encoded is not just an image of a microarray, but patterns of relationships: base-pair binding in DNA, which enables DNA diagnostics and which triggers the gene markers (the fluorescent glow), which reiterate the microarray as a grid, which can be digitized by a computer, parsed **[End Page 65]** into quantifiable data, and compared against several databases for further analysis.

Recoding

It is at this step of analysis in the computer that the transition from encoding to recoding becomes evident. Not only have certain patterns of relationships been "translated" across material substrates (from the laboratory-prepared test sample, and the DNA-silicon hybrid of the biochip, to the computer system), but this pattern of relationships is preserved in the new medium. That is, the data that are encoded into the computer are more than just an image. That image is analyzed as a grid, and each grid is a known DNA sequence. Therefore, any "hits" on the grid denote a complementary DNA sequence (you know one side, you know the other). The computer can write those sequences and assemble them into a model sequence of DNA. The model sequence from this original test sequence can then be analyzed using bioinformatics software tools.

This brings us to the second process that defines biomedia, which is "recoding." We are now no longer in the "wet lab" but in a "dry lab," doing "biology *in silico*." And, we have moved from the field of biochips to the field of bioinformatics. If the encoding process carried patterns of relationships across material substrates, then the recoding process will extend the functionality of those encoded or translated data in ways that are specific to the medium.

Like "encoding," the term "recoding" also has its common connotations. A major one of these is that recoding constitutes a form of programming—or better, of reprogramming. For example, in an open-source environment, where a number of people will contribute to a common database of program code (adding code, modulating code, distributing code), the practice of recoding itself constitutes what is meant by "open source." [29] Recoding raises issues pertaining to the malleability of data, in which data can be positioned along any of the axes that a particular material substrate enables. In the case of open-source initiatives, code can be widely distributed, authored **[End Page 66]** by several programmers, and customized according to very specific activities.

Recoding can be generally thought of as working with data within a context defined by a material substrate (that is, without moving those data to another material substrate). An example within the field of bioinformatics is genetic analysis performed using software tools. If we continue our previous example, we see how the DNA chip enabled an encoding of particular processes (gene expression via base-pair binding). Now that these patterns of relationships have been transported to another material substrate (now that they have been digitized), the same genetic test sequence can be worked with in that new medium.

A common technique employed in genetic analysis is "pairwise sequence alignment," one of many methods used to identify an unknown genetic sequence by comparing it to databases with known sequences, [30] with the overall goal of developing a full "profile" for the test sequence—from characteristics of its sequence, to its role in intracellular processes such as protein synthesis or gene expression. With these techniques, the test sequence (now in digital form) is arranged in a line, and paired against similar sequences from genome databases. A "scoring matrix" is generated for each sequence comparison, which may be as specific or as general as the research dictates. A genetic analysis of this kind actually combines two types of recoding practices: sequence alignment, and sequence queries. The latter is often the precondition for the former, in that most sequence alignment analyses depend on being able to use the test sequence to search a genome database. For instance, our *p53* test sequence may be compared to several human genome databases using any software tool that manipulates strings of data (such as FASTA), and that accesses a database and looks for similar sequences (using tools such as BLAST). [31] Analyses can be based on exact identity, sequence similarity (using quantitative methods), or sequence homology (which may combine statistical with evolutionary data on a sequence). The data resulting from a number of pairwise sequence alignments can then be given hierarchical values according to which alignment returned the best results.

The test DNA sequence can be analyzed not only as a sequence (that is, from the computer's perspective, as strings), but also according **[End Page 67]** to its potential role in the processes of transcription, translation, and protein synthesis

generally. Once a high-scoring alignment is achieved, the test sequence can then be further analyzed by automatically translating it into an amino acid sequence. Another, different set of software tools (such as those at ExPASy) perform such operations as "translation" (from DNA sequence to amino acid code) and "backtranslation" (from amino acid code into DNA sequence). [32] Because the genetic code is "degenerative" (that is, more than one DNA triplet or "codon" codes for a single amino acid), the user can specify the relations that will constrain the translation process. Once an amino acid sequence (a linear, 1-D protein code) is derived from the test DNA sequence (also 1-D), a range of "structural data" can be generated with these two sequences (DNA and protein). This is, broadly speaking, the interest of the fields known as "structural genomics" and "proteomics": how characteristics of DNA play a part in the structural formation of a 3-D protein. Like the test DNA sequence, the 1-D protein code can now be put through various sequence-alignment procedures. However, for the protein code, the data generated will be quite different: instead of looking for expressed regions in the sequence (as we would with DNA), we are now looking for correspondences between protein sequence and protein structures. Protein structures can be secondary (basic folding classes such as "alpha-helix" or "beta-sheet"), tertiary (combinations of secondary structures together in side-chain formations), or quarternary (the entire assemblage of the protein). Using the data generated from the DNA pairwise sequence alignment, and the protein sequence alignment, aspects of the 3-D protein structure can be predicted. This "protein prediction" is the same technique with which this essay began—matching relevant data against known sequence and structural data in databases. With a full profile of a test sample (DNA or protein), a researcher can either identify an unknown molecule (gene or protein region), perform further diagnostic studies on already-identified molecules, or, in the case of medical genetics and pharmacogenomics, isolate candidate "targets" for the development of specific molecular genetics-based therapies.

As is evident from this brief description of bioinformatics techniques, there is a minimal amount of molecular biology work going on, and a great degree of computation. However, despite the thorough use of software tools in this genetic analysis, it would be a mistake to conclude that biology has simply become programming. **[End Page 68]** What is important to note is that the bioinformatics tools such as those employing sequence alignments (FASTA), database queries (BLAST), or structure prediction (SWISS-PROT) are all developed around biological components and processes. We could be more accurate still, and suggest that the aforementioned bioinformatics tools are an example of computer programming creating a context in which certain biological components and processes may function as they do "naturally" in vivo or in vitro. Note that although the material substrate is radically changed (from carbon-based systems to silicon-based ones; from the biological to the digital), what remains the same across this difference are the foregrounded patterns of relationships: transcription (DNA to RNA), translation (DNA to protein), and folding (protein synthesis). Bioinformatics tools provide a context in which these patterns of relationships are "recoded" as computational integers, algorithms, and sets of rules. It is not

enough, in the case of biomedia generally, to say that bioinformatics tools "simulate" the biological body or the cell, for there are no ontological claims being made in these practices of recoding. [33] Rather, the bioinformatics tools, as recoding practices, assume the coexistence of multiple material substrates, and they also assume the capacity for inherent data (patterns of relationships) to be mobilized across those media. In this sense "recoding" is equivalent to, but not identical with, "wet lab" work with the same patterns of relationships in test tubes, petri dishes, or bacterial plasmids.

The reason this warrants consideration is that bioinformatics, as a recoding practice, bears within itself a tension generated by this character of working with the "essential data" of the biological domain.The very fact that such software tools have been developed for molecular genetics research, and are used on a daily basis, implies that there is much more going on here than a secondary simulation of an originary object. The application of the data generated by bioinformatics tools directly and indirectly "touch" the wet lab (genome sequencing) and the biological body (DNA profiling in medicine, gene therapy clinical trials, drug development). However, when the philosophical question is raised, as it is in the techniques and application of such tools, the implicit assumption is that the digital DNA sequence in the computer points to a corresponding "real" DNA in the laboratory. **[End Page 69]**

Thus with the recoding practices of bioinformatics, we see a variable shift in the ontological status of that which is recoded. This is characteristic of biomedia; the ability to continuously modulate the relationships between objects, and the status of individual objects, means that something called "DNA" can be split along the lines of instrumentality (digital DNA and bioinformatics as tools for working on real DNA), and simultaneously be fully integrated along the lines of code-work (the essential patterns of relationships in both digital and real DNA, dry and wet bodies). In the same way that encoding provides a context for the mediation of patterns of relationships across platforms (cross-platform DNA), the practices of recoding extend, modulate, and diversify those patterns in ways that are specific to the medium. The "bio-logic" of DNA is never abandoned—in fact, that is what is preserved as the essential data, the patterns of relationships. But if the bio-logic of DNA is never abandoned, then it is also true that the question "what can a body do" is answered in ways that are specific to the material substrate (in this case, the digital domain). The "biological" principles of protein synthesis, base-pair complementarity, and DNA transcription are still protein synthesis, base-pair binding, and transcription—only now, those patterns of relationships are recoded into medium-specific permutations, enabling "backtranslation," pairwise sequence alignment, and online protein-folding predictions. From the molecular biological perspective, these are processes that, though based on the same biological principles of DNA, do not occur "naturally" in the living cell. In practices of recoding we perhaps find one of the central tensions in biomedia: a body that is biological, but a body that is more than biological.

Decoding

As I have stated, the practices of recoding do not exist for biomedia as ends in themselves. The hallmark of biomedia is that the so-called computerization of biology is only completed by a third procedure, that of "decoding," in which practices of recoding afford new approaches to biological materiality itself. The form here is less a loop, and more a spiral. In many specific instances—such as "rational drug design," gene therapy based on sequence-insertion, and programmable stem-cell differentiation—an originary wet biological sample is encoded, then recoded, and finally decoded, so that either that sample may be transformed (using the principles established by genetic engineering), or new contexts may be developed (using the principles from more recent fields, such as "regenerative medicine"). [34] **[End Page 70]**

If encoding elicits associations with digitization (but is really a transport of data across media), and if recoding elicits associations with programming (but is really an extension of data specific to a medium), then decoding would appear to elicit associations that have to do with cryptography (encryption, decryption, code-breaking, code-translating). At the basis of cryptography and practices of decoding one finds the productive process of making-sense—that is, making "information" from "noise." [35] Decoding does not make sense from nothing, but rather works with prior material in a combinatory, even stochastic, method, in order to generate sense from the combinations of parts (literary uses of anagrams are the "poetic" equivalent to this technical approach). However, decoding, as a making-sense from prior material (in-formation from noise), has specific connotations when we consider it in relation to biomedia.

What would it mean, given our discussion thus far, to "decode" the body? Aside from the popular notions of a "genetic code" and efforts to "crack the code," both of which self-consciously reference cybernetics, the decoded body in this case is also a rematerialized, "rebodied" body. In many ways, decoding can be regarded as the converse of encoding. Both employ a common technique, which is the isolation of certain types of essential data (patterns of relationships) and the mobilization of those data across media (material substrates). In the case of encoding, we saw how this was specified as a move from the wet lab to the dry lab. In the case of decoding, this relationship is reversed: the essential data from a dry-lab context (the particular medium of the computer) are mobilized to a wet-lab context (the particular medium of an engineered bacterial plasmid, or cells in culture). Notice that this is not simply a move "back" to the wet lab from the dry lab, for two reasons: The first is that decoding does not necessarily select the same essential data that encoding does; what is considered "essential" about the data may be in principle the same (e.g., preserving protein synthesis of a particular molecule), but in the process of recoding, what constitutes that particular principle may be different (e.g., specific gene-expression patterns that cannot be "naturally" observed). This leads to the second reason **[End Page 71]** why we do not simply go "back" to the wet lab, which is that recoding has redistributed the types of medium-specific relationships that may occur, such that a design approach to molecular biology can afford novel products (e.g., protein

inhibitors) from familiar processes (e.g., repression of gene expression).

Furthermore, not only do we not go "back" to a starting point, but decoding is also not simply a direct "materializing" of what was once immaterial. If we accept that encoding is not a dematerializing (even in cases of "digitization") but a rematerializing, then the same would hold for decoding practices as well. There is no originary object in biomedia, no originary moment in which materiality was forever lost by sampling; but this does not mean that materializing procedures do not play an important role as mediating functions. Put another way, we can say that *biomedia is the continued, material reprocessing of biological information*—indeed, the processing *is* the biological information, for information never just exists; it always acts. In fact, if we were to condense our description of biomedia, we could describe it as biotechnical contexts in which the biomolecular body is materialized as a mediation: materialization is the medium.

An example, within biotech research, is the broad area defined as "pharmacogenomics." Also known as "rational drug design," this field is identical with in-house research in pharmaceutical corporations whose primary aim is to mine the data from genomes and proteomes to develop novel "drug targets" for possible testing, clinical trials, and, if lucky, actual product development (including patents and approval by governmental regulatory organizations). As with any pharmaceuticals field, rational drug design involves coming up with novel compounds that in themselves do not exist in nature, though their components may. And, as with a great deal of biotech research, rational drug design depends on computer technology to enable the efficient, "intelligent," and reliable discovery of potential drug targets. Rational drug design can proceed along a number of lines, but its general premise is that, in the long run, synthetically produced drugs in the laboratory should be replaced by novel genes and proteins in the body which can produce such compounds on their own. [36]

This involves a combination of traditional drug design (analysis of compounds, and synthesis of "responses" to those compounds) **[End Page 72]** with genome and proteome analysis. The protein prediction techniques alluded to earlier are here utilized in a combinatorial fashion, to test the viability of different compounds. For instance, in the testing of a novel drug therapy that involves a protein inhibitor which will bind to a specific antigen, a number of biochemical and biophysical considerations are computed by a software program, to check for potential nonviable atomic-force repulsions. The program will then further analyze the compound by performing "molecular docking" tests to assure the correct three-dimensional "fit" between antibody and antigen. If a likely candidate is developed, it can be cross-checked against a protein database for similar structures, which will in turn lead to a search against a genome database for potential genes or gene sequences that play a role in the production of a particular protein. These candidate genes can then be analyzed, and, potentially, modified in a way that may produce the desired novel protein.

If a bio-logical connection can be established between a candidate gene and a

designed compound, then the main goal of rational drug design becomes one of creating the right types of contexts in which that connection may be functionally (that is, biologically) established. In the recent past, gene therapies have been used in this way, inserted into the human patient's genome to either supplement or inhibit certain biochemical processes. [37] However, because a great number of processes that occur in the cell are not unilinear or even remotely centralized processes, gene therapy has had a great deal of trouble—and tragedy—in clinical trials. [38] Another end application, aside from gene therapy, has been the production of "custom-tailored drugs": when combined with same-day genetic profiling of patients, rational drug design has been hoping to use practices of decoding to design and administer drug therapies specific to the genome of each individual patient.

In these techniques there are (at least) two decoding processes occurring. The first is that between the computer-modeled novel protein and its potential extension in the wet lab: patterns of relationships **[End Page 73]** that exist in the digital domain (which are themselves encoded from molecular dynamics studies in the biological domain) are "extended" from the molecular docking software to the wet-lab bioreactor in which the protein may be synthesized. A second process is nearly the reverse of the first: the extension of particular candidate sequences from a genome database into the wet lab, in order to establish a bio-logical connection between novel compound and candidate gene sequence. Again, it is not simply the sequence itself which is extended from the digital to the biological domain; in this process of decoding, it is the capacity for a candidate sequence to function as a gene which enables its decoding across media, across platforms. Of course, not all patterns of relationships are viable across media, and only those that are will fulfill the aim of biomedia, which is to enable a cross-platform compatibility for selected patterns of relationships. When a novel compound is synthesized in the wet lab, made possible by analyses using computer and bioinformatics tools, themselves using data that are encoded from prior wet-lab analyses, then the process of decoding signals a final turn in the spiral of biomedia.

Rational drug design proceeds by step-by-step analysis, testing in "wet-dry cycles," and modulation of drug candidates. It is, by and large, dependent on the data, and on the general premise of the genome—that DNA sequences of variable length called "genes" play the central role in the production of proteins, which in turn play a key role in the composition of cells, tissues, and organs. The identification of a "source code" here opens the biomolecular body to the principles of design. "Design" in this context implies the configuration of an open-ended set of approaches and principles whose aim is to lead to the most optimal integration between form and function, sequence and structure, decoding and the capacity to be upgraded. "Design" in this context is also not to be immediately taken as a term with automatic moral designations when applied to living beings; that is, it should not be immediately interpreted here as "dehumanizing." It may be said that, in biomedia's technical recontextualization of the biological domain, design often comes to play the role of the "tonality" of the

recontextualizing process. Increasingly, living systems are no longer viewed in biotech research through the mechanist lens of engineering, but are approached from the perspective of design, and design as both a set of principles and an approach, an attitude, rather than an application of sets of discrete techniques.

To summarize, in our discussion of this "informatic protocol" that constitutes biomedia, we can note a twofold tendency, which is a **[End Page 74]** product of the intersection between bioscience and computer science. The first tendency is that of establishing a cross-platform compatibility, by selecting certain types of essential data or patterns of relationships in a given context (e.g., DNA translation into protein). The implication here is that the medium does not matter, since that same pattern of relationships can be implemented in a variety of media (e.g., protein synthesis in a petri dish, in a bioinformatic application, or in drug design). In this sense "data" are not specific to the digital domain, but are something that inheres in any material substrate. However, this also leads to the second tendency, which is that the medium does in fact matter. A given pattern of relationships will taken on significantly different characteristics given a different material substrate or technical context (e.g., "natural" protein synthesis replicated in a petri dish vs. multiple "impossible" pairwise sequence alignments in a computer). Biomedia is defined by this twofold approach to the body, by this investment in the capacity of information to materialize, and in the capacity of biological materiality to be understood as already being informatic. Biomedia affirms data into flesh, as much as it confirms flesh into data.

Not Bioports but Porting Biology

Given these characteristics of biomedia, we can now ask about the kinds of bodies generated through such practices of encoding, recoding, and decoding. They are not "bodies" in the sense of anatomical or even anthropomorphic bodies (a traditional biological standpoint, with an emphasis on the composition of parts in relation to a whole), and they are also not "bodies" in any mechanistic sense (be it a "clockwork machine" or a cyborgic, human-machine "interface").

One of the characteristics is that the notion of enabling a cross-platform compatibility runs parallel with the enabling of "passages" between genetic "codes" and computer "codes." This passage between codes is the foundation that informs much of molecular genetics, though it has been transformed significantly between the postwar era and the new millennium. The establishing of such a passage is based on the assumption that some essence or essential data pervades biomolecular bodies such as DNA or proteins that enables them to be compositionally and functionally transported from one medium to another, or that, at the very least, enables them to be technically enframed as units that operate according to an informatic logic. The genetic "code" is not just a trope, it is also a database, a search engine, and a CPU (central processing unit), and the passage between computer and genetic codes is not only a back-and-forth mobility, but also one in which code comes to account for the **[End Page 75]** body (e.g., genetic profiling), just as the body is biotechnically enabled through code

practices (e.g., genetic drug therapy).

This total passage across platforms is not, it should be reiterated, a pure investment in the supposed dematerialized domain of the digital. Such claims have characterized research associated with "posthumanism," or "extropianism," in which the liberatory promises of new technologies (such as AI, robotics, nanotech, and smart drugs) lead the way to a kind of utopian perfection of "the human" through life-extension, intelligence augmentation, and the science-fictional concept of "uploading" (or replicating one's mind into software systems). [39]

In this way, the perspective of biomedia is to be distinguished from the liberal-humanist visions of posthumanism, in authors such as Ray Kurzweil and Hans Moravec. While the extropian paradigm of uploading the mind into a computer bears witness to the body-anxiety that runs through posthumanist thinking, the examples of biomedia state something different: in biotech, the body is not to be avoided, but is a constant site of biological investment. While the posthumanist position embraces digital media as an answer to the limitations and contingencies of biology, biomedia incorporates an informatic worldview as an answer to the problem of how to optimize, enhance, and renormalize what counts as biological.

But biomedia is also distinct from the more critical views on posthumanism expressed by Katherine Hayles and others. [40] Hayles rightly critiques the position of Moravec and other posthuman- ist thinkers as a one-sided emphasis on the immaterial and the disembodied, showing how posthumanism privileges the pattern/randomness dyad over the traditional presence/absence dyad. While, in Hayles's view, what gets left out in such cases is the materiality of informatics and the embodied features of digital media, this is not the case with biomedia. To reiterate, in biomedia there is no body-anxiety, but rather an approach in which the body is revered, precisely because it is both material and immaterial, both biological and **[End Page 76]** informatic. While Hayles extensively analyzes the influence of informatics on the body and subjectivity (particularly Claude Shannon's information theory and Norbert Wiener's cybernetics), she says little about the influence of molecular biology on informatics, or, indeed, the ways in which molecular biology's understanding of the body is inseparable from informatics. In a sense, biomedia already enacts the materiality of informatics that Hayles points to—though in a noncritical manner, and with a very different agenda. We see this in fields such as genomics, genetic drug development, and bioinformatics: the point is not just to digitize the biological, but to technically articulate the biological as informatic, in such a way that the biological can be improved, enhanced, or analyzed in further detail. In a sense—though not in the sense intended by Hayles, or by phenomenology—biotech fields are embodied practices, a unique type of embodiment that is cellular, enzymatic, and genetic.

There are several consequences of this. One is that the body is accounted for through data, and that access to the body, access to "knowledge of the body," is

provided for by the context of biomedia. Not only does this affect individual instances such as genetic disease profiling in the clinic, but it also affects research broadly—for instance, in the ways in which a universalized "human genome" as well as various population and ethnic genomes come to account for the biomolecular body of the informatic patient of medical genetics.

The accountability for the body through information also means that the context of biomedia (its informatic framework) facilitates certain approaches, techniques, and research questions at the expense of other approaches and modes of critical inquiry. Medicine—at least in the form envisioned by the biotech research community and industry—will move a long way from the prior models of Galenic bedside medicine or early twentieth-century holistic medicine, and, in its emphasis on the mediations between genetic and computer codes, will emphasize a biomolecular body that is open to biological optimization.

In this sense, the viewpoint of bioinformatics gives us a radically different notion of biological normativity and health. Modern molecular biology can, in some ways, be read as a refrain of the question **[End Page 77]** "what is life?" [41] Different researchers, at different periods, working within different disciplinary contexts, will answer this question in their specific ways. But one common trend is that biological "life" has some essential relationship to the notion of information, be it purely metaphoric or immanently technical. Increasingly, the field of molecular genetics research is demanding that the biologist also be a computer scientist. This is borne out by the increase in job positions and industry productivity in the field of bioinformatics; a number of subfields are almost unimaginable without computer science (structural genetics, high-throughput genomics, proteomics, comparative genomics). We might say that, from the perspective of biomedia, biological life is largely becoming a science of informatics, but an informatics whose existence, practices, and worldview are predicated on both the materiality and the mobility across platforms.

Conclusion

While biomedia do take into account the role of material substrates, those substrates exist, as we have seen, in the background, as support for "what the body can do" (or, more accurately, what patterns of relationships can do). Again, biomedia generally and biotechnology specifically are not dematerializing technologies, at least in some posthumanist or extropian sense of the term. Biomedia is constantly working toward the body, always coming around via a spiral, and enframing this movement as a return to the body, a body-to-come. The difference within this spiral movement, the difference that makes it a spiral and not a loop, is the tension between abstract essential data (patterns of relationships) and the media (material substrate) in which those data inhere. However, as we have seen in the examples of bioinformatics, biocomputing, microarrays, protein prediction, and rational drug design, the materiality of the medium literally matters, a "difference that makes a difference." Biomedia is not only predicated on the ability to separate patterns of relationships from material substrates, but, in

never completely doing away with the material order, it implicitly suggests the inseparability of materiality and informatics in our modern understanding of the biological, genetic body.

To return to our definition: Biomedia is neither a technological instrument, nor an essence of technology, but a situation in which a technical, informatic recontextualization of biological components and processes enables the body to demonstrate itself, in applications that may be biological or nonbiological, medical or militaristic, cultural or economic. In its informatic protocol of encoding, recoding, **[End Page 78]** and decoding, biomedia bears within itself a fundamental tension. On the one hand there is the ability to isolate and abstract certain types of essential data, or patterns of relationships, which are independent of and mobile across varying media, or material substrates. On the other hand, there is implicitly something added through these varying media, such that the essential data never remain completely untouched, but themselves becoming infused and in-formed by the integration with the medium. This is further complicated by the fact that, with biomedia, the aim or application is not to move beyond the material substrate, but to constantly appear to return to it, in a self-fulfilling, technical optimization of the biological, such that the biological will never stop being biological, a body that is at the same time more than a body.

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Footnotes

1. On virtual bodies and cyberculture, see Anne Balsamo, *Technologies of the Gendered Body* (Durham, N.C.: Duke University Press, 1997); Mark Dery, ed., *Flame Wars* (Durham, N.C.: Duke University Press, 1994); Mike Featherstone and Roger Burrows, eds., *Cyberspace / Cyberbodies / Cyberpunk* (London: Sage, 1995); Arthur and Marilouise Kroker, *Hacking the Future* (New York: St. Martin's, 1996); Allucquère Rosanne Stone, *The War of Desire and Technology at the Close of the Mechanical Age* (Cambridge, Mass.: MIT Press, 1996). On the questionable "newness" of new media, see Friedrich Kittler, "What's New about the New Media?" in *Mutations*, ed. Rem Koolaas et al. (New York: Actar Editorial, 2001), pp. 58-69.

2. Of note is N. Katherine Hayles's study, *How We Became Posthuman* (Chicago: University of Chicago Press, 1999). Historical and theoretical studies that have investigated the informatics of biology include Richard Doyle, *On Beyond Living: Rhetorical Transformations of the Life Sciences* (Stanford: Stanford University

Press, 1997); Lily Kay, *Who Wrote the Book of Life?* (Stanford: Stanford University Press, 2000); Evelyn Fox Keller, *Refiguring Life: Metaphors of Twentieth-Century Biology* (New York: Columbia University Press, 1995); Hans-Jörg Rheinberger, *Toward a History of Epistemic Things* (Stanford: Stanford University Press, 1997). While Kay's work provides the most in-depth engagement with the sciences of cybernetics and information theory, all these studies highlight the linguistic, conceptual, and metaphoric exchanges between cybernetics and molecular biology. The point in this essay is to acknowledge this important work, but to also move beyond the preoccupation with rhetoric and ask how contemporary biotech transforms the trope of a genetic "code" in a range of processes (wet-dry cycles in pharmacogenomics) and artifacts (genome databases, DNA chips, lab-grown tissues).

3. Briefly, *genomics* is the study of entire genomes. Some branches of genomics specialize in a single species, such as the yeast, fruit fly, mouse, or human genomes. Other approaches compare similar genomes (say, mouse and human) in order to seek common bases for disease (hence the wide use of mice in cancer genetics research). *Proteomics* is the study of the proteins produced by a genome. Many suggest that proteomics is impossible without genomics, implying that genomics provides the foundation upon which proteomics works. Proteomics has the immense challenge of articulating how the genome dictates the production of specific proteins, and what those proteins do. There are several initiatives under way for a "human proteome project," although, given the number of possible proteins in the human body (there is no definite count, but it is exponentially greater than the number of genes), this is a daunting endeavor. Both genomics and proteomics intersect with industry in *pharmacogenomics*, which is the application of genomic and proteomic knowledge toward drug design. This is the primary reason for "big pharma" or large pharmaceutical company interest in genomics and proteomics, as possible techniques for "targeting" key disease genes.

4. Ken Howard, "The Bioinformatics Gold Rush," *Scientific American,* July 2000, pp. 58-63; Aris Persidis, "Bioinformatics," *Nature Biotechnology* 17 (1999): 828-830.

5. The basic bioinformatics techniques of homology modeling are described in some detail in Andreas Baxevanis et al., *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (New York: Wiley-Liss, 2001).

6. Fields such as these have been central to current methods in genomic and proteomic drug design. See Jeffrey Augen, "Bioinformatics and Information Technology: Reshaping the Drug Discovery Process," *Drug Discovery Today* 7:11 (2002): S39-40.

7. For descriptions of DNA computing, see Alan Dove, "From Bits to Bases," *Nature Biotechnology* 16 (1998): 830-832; Antonio Regalado, "DNA Computing," *MIT Technology Review* (May/June 2000):

http://www.techreview.com/articles/may00/regalado.htm.

8. Alan Turing's famous paper describing his hypothetical "universal machine" is often cited as a key text in the history of computer science, for, at an early stage in the development of mainframe digital computers, it articulated the limits of computing. The universal machine was an imaginary construct, a computer that could be fed the instructions of another machine and that would then run just like that machine (analogous to emulators in modern PCs); however, when this universal machine was fed its own instructions, it would be unable to get outside itself in order to compute, caught in a positive feedback loop (unable to emulate itself because it already is itself). See Alan Turing, "On Computable Numbers with an Application to the *Entscheidungsproblem*," *Proceedings of the London Mathematical Society* 2:42 (1936): 230-267.

9. The theme of the technologically enabled "brain in a vat" is one that runs through much science fiction. It signals the privileging of "mind" (often conflated in SF with the brain) and intelligence over the limitations and contingencies of the "flesh," or what Cyberpunk SF authors often called the "meat." Its most recent manifestation is in cyberspace, what William Gibson referred to as the "nonspace of the mind." See William Gibson, *Neuromancer* (New York: Ace, 1984).

10. The first four of the characteristics are immanently technical, with broader cultural impact. "Numerical representation" begins as a descriptive notion, that new media objects exist in digital format as numbers; and is extended into a proscriptive notion, that anything which can be digitally encoded is amenable to the manipulations of new media. "Modularity" describes the ability of new media elements to be combined and recombined in a variety of ways: QuickTime movies in Flash files in Netscape browsers on Mac OSX platforms. "Automation," as its name implies, points to the continued interest in software development and new media generally to "black box" much of what happens behind the scenes; for example, a series of laborious steps in rendering a 3-D object can be automated using a single menu option in a graphical interface. "Variability" describes the metamorphic nature of new media objects: Web pages are not static, but can be updated, redesigned, relocated, downloaded, and viewed in a variety of ways. While these characteristics are implicit in the discussion of biomedia here, the primary focus is on Manovich's fifth characteristic of "transcoding." For more on these characteristics, see Lev Manovich, *The Language of New Media* (Cambridge, Mass.: MIT Press, 2001), pp. 27-48.

11. Ibid., p. 46.

12. Jay David Bolter and Richard Grusin, *Remediation* (Cambridge, Mass.: MIT Press, 1999), p. 238.

13. The term "techniques of the body" refers to an essay of the same name by Marcel Mauss. Mauss's anthropological perspective analyzes the ways in which everyday actions such as walking, running, sleeping, swimming, playing, climbing, etc. are not abstract but contextualized in social settings, where the

biological, the psychological, and the social intersect. Modes of walking, for instance, are contextualized one way in dense urban settings, and another in country settings. Mauss states: "I call 'technique' an action that is effective and traditional." The role of training, education, and "tradition" (normal vs. abnormal) are key elements in Mauss's view of how the body becomes a set of learned "techniques." See Marcel Mauss, "Techniques of the Body," in *Zone 6: Incorporations,* ed. Jonathan Crary and Sanford Kwinter (New York: Zone, 1992), pp. 454-477, quotation on p. 461.

14. We can refine this further by distinguishing the uses of bioscience for medical ends, such as regenerative medicine (the use of the body's own cellular regenerative capacities to develop novel therapies); those for diagnostic ends, such as biochips (DNA on chips used for genetic analysis); those for computational ends, such as DNA computing (described above); and those for engineering, such as biomimicry, or the application of biological principles toward industrial and mechanical engineering.

15. Robert Bud, *The Uses of Life: A History of Biotechnology* (Cambridge: Cambridge University Press, 1993).

16. In computer programming terms, "compiling" is the process in which a program is translated from human-readable form (e.g., a higher-level programming language such as Java or C++) into a "machine-readable" form of ones and zeros.

17. Though this point is arguable, Heidegger's overall approach of eliciting the "essence" of technology as an activity begins from the premise of the ontological differentiation between human subject/body and technical object/activity. Whether it is in the premodern mode of "revealing" or "bringing forth," or in the modern, instrumentalized mode of "setting upon," Heidegger's questioning of technology centers on the point of contact between hand and tool, whose essence is a particular mode of activity in relation to the material ("natural") world. See Martin Heidegger, "The Question Concerning Technology," in idem, *The Question Concerning Technology and Other Essays* (New York: Harper, 1977), pp. 4-12.

18. The best examples of the latter two technological tropes—that of the prosthetic and that of displacement—come not from theory but from science fiction. Cyborg narratives, such as Frederik Pohl's *Man Plus* (London: Gollancz, 1972), explore how prosthetic technologies not only augment the human subject, but in the process also transform human subjectivity as well. SF films such as *Robocop* replay this theme. Similarly, intelligent-machine narratives such as Brian Aldiss's *Supertoys Last All Summer Long* (New York: Griffin, 2001) pose the familiar question of the point at which machines begin to compete with the human—a theme played out famously in the film 2001 *: A Space Odyssey*.

19. Again, Heidegger's notion of "enframing" is useful here, in the sense that it highlights the way in which "technology" is a particular mode of relating to the world. However, in his distinction between premodern crafts and modern

industrialism, Heidegger tends to evoke a kind of romanticism for one relating (based on a more anthropomorphic relation, mediated by the "hand" of the craftsperson) over another (based on an empty application of rational principles to the resourcing of the natural world). A critical reading working from Heidegger's text would need, in addition, to "question" the role of nature and the biological as well as the artificial means for relating, and in doing so, to address the tendency to equate mediation with alienation. See Heidegger, "Question Concerning Technology" (above, n. 17), pp. 19-23.

20. PCR stands for Polymerase Chain Reaction, and is a standard laboratory technology for rapidly replicating desired sequences of DNA. PCR machines take in a sample and put it through cycles of cooling and heating, which causes the DNA to denature into single strands and then replicate into duplicate strands. Gel electrophoresis—an earlier form of gene sequencing—is another standard laboratory technique which involves passing a DNA sample through a gel-like medium using electrical charges; a researcher can sequence the DNA based on the combination of fragment length and its comparison to a known sequence. Recombinant DNA is a basic technique in genetic engineering, which utilizes special "cutting" molecules known as restriction endonucleases to snip a DNA sequence at a desired spot, so that a new sequence can be inserted into the DNA.

21. Base-pair complementarity, also known as "Watson-Crick complementarity," is the principle that complementary base pairs in DNA and RNA will, under normal conditions, always bind to each other: Adenine (A) always binds with Thymine (T), Guanine (G) always binds with Cytosine (C). This principle, articulated by Watson and Crick in the 1950s, is one of the most commonly used processes in biomedia. See James Watson and Francis Crick, "General Implications of the Structure of Deoxyribonucleic Acid," *Nature* 171 (1953): 964-967.

22. The contextualization of biomedia as a "protocol" of encoding, recoding, and decoding was presented at a Crossroads in Cultural Studies conference (Birmingham University, 21-25 June 2000), as part of a panel on posthumanism. There the specific example referred to was tissue engineering, and the ways in which cellular regeneration was recontextualized as biological optimization. It has also, more recently, greatly benefited from the work of Alex Galloway, who has elaborated how computer networking forms a materialization of "how control exists after decentralization." See Eugene Thacker, "Data Made Flesh: Biotechnology and the Discourse of the Posthuman," *Cultural Critique* 53 (Winter 2003): 72-98; Alex Galloway, "Protocol, or, How Control Exists after Decentralization," *Rethinking Marxism* 13:3/4 (2001): 81-88. For a reasonably easy read on network protocols, see Craig Hunt, *TCP/IP Network Administration* (Cambridge: O'Reilly, 1992).

23. As Hayles states, "information in fact derives its efficacy from the material infrastructures it appears to obscure" (Hayles, *How We Became Posthuman* [above, n. 2], p. 28).

24. The best-known of such formulations is in Aristotle's notion of "entelechy," where formless matter exists in a teleological framework so as to be realized in form: see Aristotle, *De Anima* (New York: Penguin, 1986), book 2, chaps. 1-3.

25. See Claude Shannon and Warren Weaver, *The Mathematical Theory of Communication* (Urbana: University of Illinois Press, 1964).

26. Such a question, which at first seems abstract, is implicit in current debates over intellectual property, the patenting of biological materials, the privatization of genome databases, and the state of open-source movements in the biotech software industry. In particular, the current trend of gene patenting has raised the question of the relationship between information, property, and biological "life." Interestingly enough, some landmark rulings in biotech, such as the 1980 *Diamond v. Chakrabarty* case (where a patent was granted to a living microbe), occur right alongside similar cases to do with computer algorithms and software. The role of "information" is key here, because it almost leads to the equivalence between "life" and intellectual property, the point at which biological "life" becomes a concept (and that concept becomes property). See Richard Gold, *Body Parts: Property Rights and the Ownership of Human Biological Materials* (Washington, D.C.: Georgetown University Press, 1996).

27. On microarrays, see Andrew Marshall and John Hodgson, "DNA chips: An Array of Possibilities," *Nature Biotechnology* 16 (January 1998): 27-31; Robert Service, "Microchip Arrays Put DNA on the Spot," *Science* 282 (October 16, 1998): 396-401.

28. It is significant that, in molecular biology, the terms "transcription" and "translation" have been used for some time to describe the process by which DNA is "read" onto RNA, and the process by which RNA "writes" an amino acid chain that becomes a protein. It can be argued, however, that a textual view of the genome is quite different from an informatic view. The prevalence of textual tropes ("book of life" and so forth) implies that DNA has a grammar, and that, as a language, it signifies and generates meanings through its linguistic mechanisms, its use, and its context. This is very different from the informatic understanding (which Kay traces in *Who Wrote the Book of Life?* [above, n. 2]). In the informatic understanding, DNA has no grammar, it does not signify, and there are no words. DNA is pure combinatorics, not unlike the binary operations in computing machines. This view has been taken quite literally in biocomputing. However, as several cultural critics have noted, the application of such tropes often problematizes, rather than clarifies, the situation; see, for example, Keller, *Refiguring Life* (above, n. 2), pp. 79-118. The lesson to be taken from this distinction (textual vs. informatic views of DNA) is that, in the informatic view, which is the hegemonic view today, DNA does not say anything: it only calculates, operates, and parses.

29. "Open source" generally refers to any instance in which the source code for a software program, operating system, or other type of computer-based media

object, is made available to the public. Most often communities of developers organize around a particular project, in a collaborative environment. The open-source movement has often been lauded as the latest instance of utopianism on the Internet, with the Linux operating system being the most famous example. However, while software code may be free, it has also spawned an industry surrounding it, including technical support services, book publishing, and cloned for-sale applications. See Adrian MacKenzie, "Open Source Software: When Is It a Tool? What Is a Commodity?" *Science as Culture* 10:4 (2001): 541-552.

30. For more on this technique, see Cynthia Gibas and Per Gambeck, *Developing Bioinformatics Computer Skills* (Cambridge: O'Reilly, 2000).

31. Both tools are freely accessible through the National Center for Biotechnology Information's website, at *http://www.ncbi.nlm.nih.gov*.

32. The ExPASy (Expert Protein Analysis System) set of tools are freely available through the Swiss Bioinformatics Institute, at *http://www.expasy.ch*.

33. While Jean Baudrillard suggests that the very notion of a genetic "code" shows how informatics is an exemplary case of simulation, it is also manifested in techniques such as human cloning, which Baudrillard refers to as an ontological "forgetting of death." What he overlooks, however, is the way in which fields like bioinformatics constitute modes of technically impelling biological life to be even more "biological." See Jean Baudrillard, *The Vital Illusion* (New York: Columbia University Press, 2000).

34. "Regenerative medicine" is a broad name for research fields including tissue engineering, gene therapy techniques, and stem cell research. The term has been promoted by William Haseltine, CEO of Human Genome Sciences, as the application of biotechnology to enable more long-term, robust therapies of genetically based disorders that affect cell and tissue function. In popular terms, this hints at improved immune systems and "lab-grown organs," though the feasibility of these has yet to be shown.

35. The connection between the genetic code and cryptography has been made several times. Among the earliest instances was the initial "cracking of the genetic code" by Heinrich Matthai and Marshall Nirenberg in the early 1960s: see Lily Kay, *Who Wrote the Book of Life?* (above, n. 2), pp. 246-256.

36. For more on pharmacogenomics and rational drug design, see D. Duckworth, D. Malcolm, and Philippe Sanseau, "*In silico* Identification of Novel Therapeutic Targets," *Drug Discovery Today* 7:11 (2002): S64-69; W. E. Evans and M. V. Relling, "Pharmacogenomics: Translating Functional Genomics into Rational Therapeutics," *Science* 286 (October 15, 1999): 487-491.

37. This "silver bullet" approach was pioneered by French Anderson, who treated a young girl with a rare single gene mutation disorder (ADA) with this type of gene

therapy. See French Anderson, "The ADA Human Gene Therapy Clinical Protocol," *Human Gene Therapy* 1 (1990): 327-362.

38. One example is the 1999 death of a teenage boy undergoing a gene therapy clinical trial, due to side effects resulting from the novel genes in other, nonrelated organ systems in his body. The death not only raised issues of human subject research in gene therapy, but also marked, perhaps permanently, the cultural connotations of gene therapy.

39. See Ray Kurzweil, *The Age of Spiritual Machines* (New York: Penguin, 1999); Hans Moravec, *Robot: Mere Machine to Transcendent Mind* (New York: Oxford University Press, 1999); Max More, "The Extropian Principles: A Transhumanist Declaration," *Extropy.org* (1999): *http://www.extropy.org*. These and other accounts tend to be more uncritical, technophilic narratives of progress. However, authors differ on how the story ends: some, like Kurzweil, see humans exponentially evolving and merging with computers in a kind of socialist data haven; others, like Moravec, see human beings becoming geriatric, retiring as machines take over the day-to-day jobs of running society.

40. See Hayles, *How We Became Posthuman* (above, n. 2). For a perspective from philosophy, see Keith Ansell Pearson, *Viroid Life: Perspectives on Nietzsche and the Transhuman Condition* (New York: Routledge, 1997). Also see the special issue of *Cultural Critique* (#53, Winter 2003) on posthumanism.

41. There is a specific discourse within molecular biology that extrapolates from the specifics of the genetic code, to its general meanings for teleology, determinism, and reductionism. This can be seen through popular books by scientists with either the title "What Is Life?" or a title that is some comment on this question. See, for instance, Erwin Schrodinger, *What Is Life?* (Cambridge: Cambridge University Press, 1967); Francis Crick, *Life Itself: Its Origin and Nature* (New York: Simon and Schuster, 1981); François Jacob, *The Logic of Life* (New York: Pantheon, 1974).

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