STEFAN HELMREICH
Massachusetts Institute of Technology

Trees and seas of information:

Alien kinship and the biopolitics of gene transfer in marine biology and biotechnology

ABSTRACT
Examining discussions of "lateral gene transfer" in marine biology and biotechnology, I maintain that "natural" bonds between genealogy and classification in biology may be dissolving. I argue that marine microbial biology is good to think about with the rise of new kinships and biopolitics organized less around practices of "sex" than politics of "transfer." I draw on fieldwork among academic and industry marine biologists to explore implications of rhizomatic, informatic, watery articulations of "bare life." *[biopolitics, kinship, gene transfer, anthropology of science, maritime anthropology, biotechnology]*

In Western scientific culture, at least since Charles Darwin, the family tree has been an algorithm for thinking about evolutionary genealogy, origins, and identity. The object that trees have been asked to trace has been heredity, famously figured in the symbol of blood or bloodlines, though more lately rendered in the idiom of genetics. But genes have been enlisted to do something blood was never asked to do, and that is provide the substance that gathers together *all* living organisms on earth, through the ramifying lineages of animals, plants, fungi, protists, and bacteria, and across prokaryotes and eukaryotes. As this list illustrates, the fivefold division of life into kingdoms has coexisted with a twofold distinction based on the absence or presence of a nuclear membrane; the partitions have not been strictly commensurate, but they have been compatible. And both have found their anchors in genealogy, which Darwin named the ideal principle from which to generate "natural classification" (1859:411–434). Such genealogical classification, as Marilyn Strathern (1992a) has argued, derived for Darwin from Victorian social practices of family record keeping.[1] Reading such kinship customs onto the organic world, Darwin effectively naturalized and universalized them, suggesting through a now commonplace epistemological reversal that such practices were themselves emanations of a natural logic organizing all relatedness.

Such a tale provides one origin story for David Schneider's famous claim that "in American cultural conception, kinship is defined as biogenetic. This definition says that kinship is whatever the biogenetic relationship is. If science discovers new facts about biogenetic relationship, then this is what kinship is and was all along" (1968:23). One expectation of Schneider's pronouncement was that as the disciplines of biology got a firmer fix on genes, Euro-American folk notions of genealogy might find tighter confirmation. As anthropologists studying reproductive and genetic technologies in the context of kinship studies have found, however, "new facts about biogenetic relationship" do not always have such straightforward or consolidating meanings for kinship imaginaries (see Franklin 2001; Franklin and McKinnon 2000).[2] In her introduction to *Cultures of Relatedness*, Janet Carsten argues that, in the age of in vitro fertilization, cloning, and the laboratory transfer of genes across species—when cultural practice must be mobilized to guide "biology" toward social goals—the notion that nature grounds social relations "appears

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to have been destabilized" (2000:3). In this article, I point to an unexpected arena in which "new facts about biogenetic relationship" may disturb one facet of biogenetics' founding function for cultural classification, and indeed, for Darwin's "natural classification." It is an extreme case, the case of *lateral gene transfer* in microbes, and it may uproot the very base of what biologists call the "tree of life," that structure linking together all life on earth in a great biogenetic genealogical branching (Doolittle 2000; Pennisi 1999; Woese 2000). The new facts of gene transfer may unfasten links between genealogy and classification, between trees and the organisms they purport to organize. I argue that there are implications extending beyond the concerns of microbial molecular taxonomy; new kinship and biopolitical imaginaries may be in the making.

My story begins in the deep sea, in the microbial ecologies around hydrothermal vents, undersea locations where tectonic plates meet and molten rock emerges from the earth's crust, dosing the ambient water with superheated minerals. These are sites where dwell microbes capable of living without light, creatures that engage in chemosynthesis, the production of organic compounds using energy from chemical reactions, like the oxidation of hydrogen sulfide, endemic to vents. Hydrothermal vents captured my attention when I discovered marine biological accounts of how these ecologies might stretch scientific understandings of the conditions that could support life. Having previously studied amplifications of the definition of life in the field of "Artificial Life," a hybrid of computer science and theoretical biology devoted to modeling organisms as information-processing systems (Helmreich 2000), I found my attention riveted by the strange habits and materialities of these deep-sea chemosynthetic creatures. I found out, through reading popular and scholarly texts, that vent microbes were considered potential links to the earliest earthly life, having traits in common with *both* prokaryotes and eukaryotes, and that some biologists had wondered whether such creatures might suggest the outlines of life on lightless alien worlds (Bock and Goode 1996). I learned that accommodating such creatures into existing taxonomy was pressing for a deeper rooting of the tree of life. As I began to interview scientists working with these creatures, however, the picture turned out to be considerably less clear. It had become evident that these microbes shuffled genetic information back and forth with their contemporaries, moving genes laterally (within generations), not just vertically ("down" generations), an activity mixing up their own and others' genealogies, making it difficult to arrive at a root for the tree of life.

In this article, I argue that the taxonomic untidiness such microbes have introduced through their lateral gene transfer reaches beyond issues in phylogeny and molecular systematics into arenas adjacent to kinship concerns and biopolitics. The scrambling of the biogenetic phylogenetic signal that these creatures enact has implications for the integrity of Darwin's link between genealogy and taxonomy—as well as, perhaps, for the biogenetic kinship imaginary outlined by Schneider. More interesting, however, may be the entailments of gene transfer for biopolitics—those relations of power organized around the management of biological systems, including those of which humans are a part (Foucault 1978). In *Homo Sacer: Sovereign Power and Bare Life,* philosopher Giorgio Agamben (following Hannah Arendt and rephrasing Foucault) argues that biological life as such—what he calls "bare life"—has come "to occupy the very center of the political scene of modernity" (1998:3). He notes that tracking changes in what counts as bare life—once, functional anatomy; later, with Darwin, the principle of heredity; today, genetic codes—requires scrutinizing the scientific practices that make this substance available to the calculations of biopolitics. I maintain here that we are seeing the rise of an informatically inflected bare life that is increasingly agenealogical, and I argue that tracking the ramifications of this bare life in the circuits of marine microbial biology and biotechnology can provide an instructive view into the limits and possibilities of this fluid substance. As I hope to demonstrate, marine microbes are good to think with about kinship and changing relations between "society" and "biology"—that is, biopolitics.[3]

Foucault argued that in the 19th century new conceptualizations of the relation of individuals to populations—articulated in part by nascent evolutionary theory—focused state attention on the sexual behavior and reproductive health of national citizenries, something that changed how governmentality worked and, in its extreme expression, led to eugenics. The biopolitics of our contemporary world, however, are different; genomics and transgenics are not eugenics, and they enable different biopolitical constellations, ones not so neatly organized around genealogy and birth. When genes become information and are made legible through gene sequencing and bioinformatics (the use of computers to organize and analyze biological data), the biopolitics that result may well be new; they may be transspecific and translocal.[4] When the genes in question belong to waterborne creatures like marine microbes—variously scripted as creatures that can offer views into the origin of life (Corliss et al. 1980), resources for pharmaceutically and industrially useful biotechnological products (Robb 2000), and tokens for rethinking the nature of property in fluid, often ambiguously territorialized zones like the so-called high seas or ocean commons—such biopolitics may fasten together genes, ecologies, global biogeochemical processes, and legal and political economies at national and transnational scales.

In *French DNA,* Paul Rabinow writes,

> we now have a more problematized understanding of the *bios* in biopower. That the new genomic knowledges will form assemblages with social and political networks

> is clear; precisely how changes in *bios* will interact with old and new forms of power relations is open to question, and the evolution must be observed and analyzed. [1999:15]

In this article, I seek to contribute to the analysis of such evolution, asking how a genomically shuffled bios might be inserted into new biopolitics. I argue that if "sex" was the pivot point of classical biopolitics, tying together both individuals and populations as well as subjects and states, "transfer" will be the logic and practice through which genomic assemblages will be networked to social and political formations. Exactly what kinds of assemblages will be webbed together by transfer is of course very much under construction. I consider here a few possibilities, elaborating on fieldwork I have done among marine microbiologists and biotechnologists.

Detailed connections are drawn from ethnography I conducted at the following locations: the Monterey Bay Aquarium Research Institute in Moss Landing, California, in summer 2000; at a symposium on microbial biotechnology at the Center of Marine Biotechnology in Baltimore, Maryland, in July 2001; and at the Fourth Asia–Pacific Marine Biotechnology Conference, held at the University of Hawai'i in Honolulu in April 2002. This fieldwork included interviews and participation in scientific lectures and symposia; I also read extensively on recent marine microbiology. I was inspired to do this work by earlier attendance at a Public Ocean Fair held in Monterey, in coordination with the United States' First National Ocean Conference in June 1998, where I happened upon persistent enunciations of the maxim that the "sea is life" (see the *Californian* 1998). While finishing up my project about Artificial Life scientists, who often claimed that information processing was life, I was struck by the resuscitation of the maxim that "water is life." I came to wonder if a new bare life might be in the making or, indeed, whether "information as life" and "water as life" might not be recombining in the age of marine genomics and biotechnology. Certainly, microbial gene transfer and genetic engineering are not unique to marine biology; however, I think this context brings into special relief the biopolitical networks within which new bare life might materialize. Let me begin with a story about category-confounding microbes.

Trees of information: Lateral gene transfer and the reticulations of alien kinship

This is a story of scientific—and ethnographic—inquiry, beginning for me with a July 2000 discussion with microbial biologist Ed DeLong at the Monterey Bay Aquarium Research Institute (MBARI), the research-oriented sibling of the Monterey Bay Aquarium. DeLong has been a pioneer in using genomic techniques to investigate the doings of marine microbes. After hearing DeLong speak at MBARI's summer open house, where he discussed the role of microbes in searching for the origin of life, in shaping the chemistry of the sea and atmosphere (DeLong called these creatures "stewards of our planet"), and in biotechnological enterprise, I approached him to ask about the vent creatures I had read so much about. We set up an interview. I walked into DeLong's office prepared to ask about vent microbes and their evolutionary and ecological relationships. I had read of the discovery of these microbes on the undersea Galapagos Ridge in 1977 and 1979, by scientists diving in the research submersible *Alvin.* I had also read that in 1990, microbiologist Carl Woese, along with a couple of colleagues, had argued that microbes at these vents were "members of a class that seemed to have undergone less evolutionary change than any other living species on the planet, implying that their ancestors were perhaps the original forms of life" (Broad 1997:112; see Woese et al. 1990, also Woese and Fox 1977). I had learned too that these hyperthermophilic—very-hot-temperature-loving—microbes, along with their recently discovered cold- and salt-loving, methane-metabolizing similars (all called "extremophiles," or "loving extremes"; see DeLong 1998), had been gathered into a newly created taxonomic category above the kingdom level: the domain. In an article entitled "Towards a Natural System of Organisms"—an explicit nod to Darwin, who wrote in *Origin,* "I believe [the] element of *descent* is the hidden bond of connexion which naturalists have sought under the term of the Natural System" (1859:433, emphasis added)—Woese et al. (1990) argued that genealogies guided by molecular genetics led the way toward a view of life on earth as divided into three domains: Bacteria, Eucarya, and the new microbial group Archaea, meaning "ancient ones."[5] This nomenclatural move, widely though not universally accepted by the mid-1990s, amplified the framework of Linnaean taxonomy by creating a new level, a step taken in part because of Archaea's apparent genetic uniqueness, a property that in turn rendered them candidates for the most conserved life on earth, a direct line to the planet's vital history. Woese, along with common biological wisdom (see Zuckerkandl and Pauling 1965), held that following this line—filling in family trees, or phylogenies, along the way—could be done by chasing genes back to ancestral origins. Molecular phylogeny would confirm and extend large-scale organismic phylogeny. Students of descent theory in kinship studies will not find this view surprising.

As DeLong told me, finding genes that lead cleanly back to ancestral destinations requires looking for particular kinds of genes, genes that accumulate random mutations at a constant rate, that are sheltered from the vicissitudes of natural selection, and that can therefore act as molecular clocks. Woese had argued that small-subunit ribosomal RNA—genetic material from ribosomes (cellular organelles where protein is synthesized)—was a good candidate for such a chronometer because it is present in all genomes and, since its function is so fundamental (see Doolittle 1996:8797), it is not likely to change much over time. More importantly, Woese considered ribosomal RNA the center of what he termed the cell's "information processing systems" (2000:8393)—a complex of genes coding for replication, transcription, and translation; in other words, the part coding for coding itself. As one researcher has ventriloquized this view, "Transcription and translation genes are central to the 'essence of the organism.' They encode the hardware that reads the exchangeable genes for the cellular software" (Doolittle 1999:2127). Family trees planted in the ground of this "essence" produced Archaea as quite distinct from Bacteria and Eukaryotes. The traits Archaea shared with prokaryotes and eukaryotes looked very early on to be explained by the possibility that Archaea could be ancestral to both.[6]

Such an idea was reinforced by descriptions of hyperthermophilic Archaea as inhabiting the kinds of extreme environments that may have characterized early earth. Some scientists argued that amino acids could only have originated in chemically rich water where temperatures soared above boiling and where high pressure prevented these temperatures from denaturing such complex configurations (Corliss et al. 1980). It looked like the family tree for life on earth would turn out to be rooted, as many had suspected, underwater. As I spoke with DeLong, I mused that the information provided by genes looked to be leading the way to the origin of life. Genetic information, as a sort of kinship substance, looked to be constitutionally thicker than the watery worlds inside and outside the organism through which it had to be transmitted.

At this juncture in our discussion, DeLong paused to say that in the late 1990s, a number of microbial biologists began to point out that assumptions about linear genealogy might be all wrong for these organisms. When researchers tried to corroborate ribosomal RNA phylogenies of Archaea, Bacteria, and Eucarya by choosing genes *other* than those related to "information processing systems," the trees that resulted were quite contradictory. Crafting phylogenies, as I had learned from talking with DeLong's colleagues at MBARI, depends on a complex set of bioinformatic tools: DNA sequence databases, techniques for comparing sequences or whole genomes, and computer software for using these comparisons to generate possible relationships between genomes or organisms, including tree relationships (see Mackenzie 2001; Thacker 2000).[7] Similarities in sequences—known as homologies—can be examined to ascertain whether they are the result of common ancestry. Software packages like PHYLIP and MacClade—popular among my interlocutors—aid in the making of family trees and do so by allowing researchers to play around with different assumptions about parsimony, generation lengths, or molecular clock rates, to take a few examples.[8]

In 1996, molecular biologist Kim Borges, signaling the prospect of classificatory systems that might embrace polyglot categories—much like that other Borges, whose heterogeneous "Chinese Encyclopedia" was memorialized in the preface to Foucault's *The Order of Things* (1970)—wrote, "It is possible to support four possible rooted universal tree topologies, depending on the protein encoding genes chosen" (Borges et al. 1996). A variety of theory-driven decisions must be made on the bioinformatic path to a tree, and these choices take on a life of their own, once plugged into programmed procedures.[9] Rooting a tree requires grounding one's logic in better or worse assumptions, as one team of molecular biologists concerned with Archaea noted in an article I discovered after my conversation with DeLong:

> There is in fact in principle no way . . . to root . . . a universal tree based only on a collection of homologous sequences. We can root any sequence-based tree relating a restricted group of organisms (all animals, say) by determining which point on it is closest to an "outgroup" (plants, for example). But there can be no such organismal outgroup for a tree relating all organisms, and the designation of an outgroup for any less-embracing tree involves an assumption, justifiable only by other unrelated data or argument. [Doolittle and Brown 1994:6724]

As Geoffrey Bowker (2000) puts it in a discussion of biodiversity databases, the problem here is that the data are radically "singular"; that is, they cannot be compared with anything else until that something else is specified, which turns out to involve specifying the initial object of inquiry, in this case "all organisms" and their relationships.

Given the logical tangles endemic to building family trees, it may be no surprise that consensus phylogenies have been elusive. After all, as Adrian Mackenzie has argued, "Bioinformatics, when it works on comparing sequences, cuts across genealogical descent and historical unidirectionality" (2001:11). However, DeLong continued, some researchers were beginning to believe that there may be something other than methodological heterogeneity at work. They believe that the genetic "information" contained in microbes like the Archaea—and the Bacteria, too, by the way—may itself not be behaving in a predictable generation-to-generation way. It may be difficult to build trees not only because of the tools we use but also because the "information" genes carry may be smeared laterally across generations, in addition to cascading vertically "down" generations.[10]

Discerning that I was unusually interested in this scrambling of the genealogical logic underwriting evolutionary notions of relatedness, DeLong handed me a photocopy of a 1999 article from *Science* by a man he called an "ex-Carl Woese kind of guy," microbiologist W. Ford Doolittle, entitled "Phylogenetic Classification and the Universal Tree." As I sat in a Mexican restaurant–bar outside Monterey just after the interview, I read through the article, in which Doolittle argued that molecular phylogenetics may, in fact, reveal that one cannot do phylogeny for very early microbes, for the first earthly life. The relationships of early organisms may not be treelike in character or nature. As Doolittle phrased it, the tree of life would turn out to be a net:

> If . . . different genes give different trees, and there is no fair way to suppress this disagreement, then a species (or phylum) can "belong" to many genera (or kingdoms) at the same time: *There really can be no universal phylogenetic tree of organisms based on such a reduction to genes.* [1999:2128, emphasis added][11]

A later article I found on the web, written by John Paul, a professor in the Department of Marine Sciences at the University of South Florida, put it this way:

> The sequencing of complete genomes of archaea, bacteria, and eukaryotes has clearly "shaken the tree of life"; [it] has shown that microbes are mosaics of acquired genes. In fact, the rooting of the universal tree is highly problematic because of multiple transfer events between the kingdoms. [Paul 1999; and see Pennisi 1998][12]

(See Figures 1 and 2, reproduced from Doolittle 1999, for a representation of what the tree of life looks like before and after taking lateral gene transfer into account.) Deleuzian discussions about rhizomes as alternatives to trees find a scientific analog here. So much for the genealogical origin of species.

Doolittle was challenging the logic at the heart of ribosomal RNA reasoning, the idea that transcription and translation genes were central to the "essence of the organism." Doolittle pointed out that "cells do not actually know what is fundamental to them, which of their genes encode hardware rather than software" (1999:2127). The language of computation that formats this discussion—and that is indicted by Doolittle—points us toward many molecular geneticists' commitments to an abstract understanding of "information"—as a formal, quantifiable property of a message or program—that turns out not always to be consistent with the particular materialities of so-called genetic information. That is, the meaning of information as an instruction set or program only partially overlaps with biochemical specificities instantiated in DNA (and see Kay 2000).

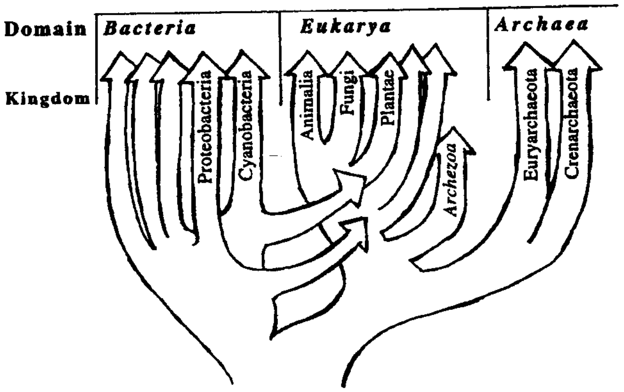

Figure 1. "The current consensus or standard model" of the "universal tree of life" (Doolittle 1999:2125, figure 2).

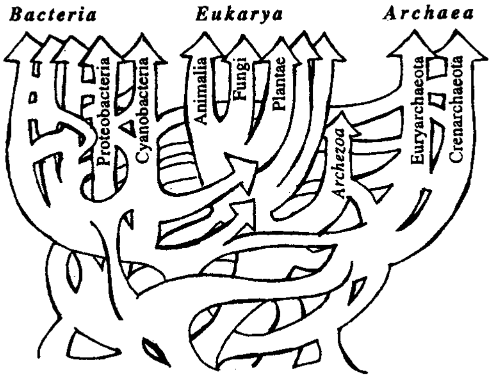

Figure 2. "A reticulated tree, or net, which might more appropriately represent life's history" (Doolittle 1999:2127, figure 3).

It occurred to me that what was happening here was that a biogenetic understanding of relatedness had pressed researchers into phylogenies based on genes, had grafted a genetic logic onto the arborescent image of the family tree (see Malkki 1992). On this view, relations of species could be discerned by following genes through the naturalized biopolitical objects—individuals and populations—of Darwinian theory. Rather than pointing toward a common ancestor, however, this focus fragmented the very object of inquiry. "Natural classification"—translated into the information processing systems of genealogy—turned back on itself to take apart its own constitution as naturally classificatory. Readers might not find this surprising, since the particulate, discrete, informatic logic that has inflected biology since the rise of genetic codes has long been at work disaggregating the genealogical ontologies of such items as races and species—as Stephen Jay Gould (1977), Sarah Franklin (2001), Paul Gilroy (2000), Donna Haraway (1997), Lily Kay (2000), Paul Rabinow (1992), and many others have argued. As Harriet Ritvo maintains in *The Platypus and the Mermaid* (1997), taxonomic systems have long embedded philosophical commitments containing the seeds of their own deconstruction (and see Bowker and Star 2000). After all, as John Paul—and this time I mean the Second; that is, I *do* mean the Pope—writes in his introduction to a Vatican volume on evolution, although evolutionary theory "complies with the need for consistency with observed data," it also "borrows certain notions from natural philosophy" (1998:4). Such notions can bend back to take apart their own premises.

As Doolittle was urging, scientists' traditional adherence to the tree image was in part the result of treating genetic information as an abstract entity: As he maintained, there is no part of the genome—no self-evident information-processing backbone—sitting outside the material circumstances of organisms. In many ways, this is a very contemporary anthropological observation. As Strathern (1992b) has argued, when biotechnological practice seeks to make explicit exactly what kind of "nature" is meant to ground culture, this reveals that nature to be culturally constituted. In this case, commitments to the notion that genes are information explicitly dissolve when they run up against the material circumstances of lateral gene transfer—which in many hyperthermophilic Archaea takes place in superheated, high-pressure water.

It seemed to me that understanding the movement of genes across organisms entailed considering the physical conditions under which this could happen. I was curious if attention to lateral gene transfer would swing emphasis back to genetic *material*, and I wondered whether it might turn out that for many of the organisms that trade genes—like marine microbes—the particular properties of the water they inhabit will turn out to be important for such transfer. I had read in an article by Paul that "terrestrially-derived models of gene transfer may have no validity in marine or other environments" (1999). But given that water is present in all organisms, there seems nothing necessarily unique about marine environments. And given that gene transfer is an outcome, not a mechanism, Paul's contention might be overdrawn. But might it be that information is *not* always thicker than water? Might water sometimes act as a solvent to break "information" down and facilitate its flow across boundaries? Was there something particular about water that impinged on this lateral gene transfer? At the risk of putting the question too poetically, was water as life dissolving information as life? I decided I had to ask Dr. Doolittle.

In summer 2001, I contacted Doolittle by email and after an exchange or two, I sent him an early version of this argument, which he kindly read. Afterward we set up a phone interview. He argued that Archaea (and Bacteria) were undoing the tree metaphor for microbial life and complained that "people have deep paradigmatic commitments to trees; they are wedded to genes and trees." Dr. Doolittle—like his fictional near-namesake, drawing our attention to menageries of creatures that confound species boundaries—reiterated his argument that genes could not stabilize trees for these creatures because "as few as five percent of the genes may be faithful to one another," a phrasing that both retains and refuses the link between relatedness and heredity. (In one article, Doolittle suggests that lateral gene transfer may lead to dynamics "akin to adoption in their confusing effects" [1997:12751].) But Doolittle was suspicious of my curiosity about water—"What are you, a Pisces?" he asked. He did not see that water as such had shown "genetic information" to be a metaphysical conceit, directing attention to the material circumstances in which genes actually exist, and he said, "It's not so much that recent work on extremophilic microbes and lateral gene transfer has *materialized* the genome. We [microbial biologists] knew genes were material all along," but that "bioinformatics has *dematerialized* the genome." I later recalled a passage from Adrian Mackenzie, who has written, "bioinformatics software systems currently coming to bear on biotechnical research and innovation materially fortify the metaphor of life as information system" (2001:2), and I saw Doolittle's point. It seemed to me, too, that another dynamic was in place here, one that might contradict Mackenzie's contention; bioinformatics seemed to be *allowing* lateral gene transfer to become visible. It was not water, but, ironically, information—computationally rendered and instantiated—that was being used to denature abstract notions of genetic information.

Not in every instance, of course. "Information" continues to be used in ways solidifying traditional associations of genetic information with genealogy. A marine biologist at Penn State, who works on hydrothermal vents put the phylogenetic issue to me in terms directly borrowed from information theory: The "signal" of origin may not be easily audible through the "noise" of gene transfer.[13]

Although the image of a scrambled communication from a remote source may destabilize any originary character of Archaea, it does not entirely displace an early figure used in connection with Archaea: the alien.[14] Early stories about hyperthermophilic Archaea as the Earth's most autochthonous residents often featured descriptions of these creatures as nearly extraterrestrial. Researchers have viewed hydrothermal ecosystems as "models for sites where life might have originated on this planet and where extraterrestrial life is speculated to exist on Mars and Europa" (Van Dover 1996:back cover). Science journalists have often described populations of hydrothermal life forms with colonial science fiction tropes: "an alien horde that thrive[s] in total darkness" (Broad 1997:109). As archaeal origins have been obscured, the alien rhetoric has attenuated these days. No longer do researchers consider these microbes alien invaders that may have seeded the planet in its infancy (once a favorite speculation of people in the field of astrobiology). Now, along with their bacterial and viral cohorts, the Archaea have become agents of lateral gene transfer, installing alienness at many sites around the root of the tree of life.

It seemed that Doolittle and I were in agreement that genetic information must be understood as materially instantiated. What N. Katherine Hayles (1999) has called "the materiality of informatics" takes shape with respect to genetic information in the context of particular cellular, organismic, and evolutionary circumstances. Bioinformaticians who take genetic data and build phylogenies based on treating information as an abstract entity risk floating free of the contingencies of the physical world (Doyle 1997; Kay 2000; Oyama 2000).

There has been intriguing fallout of this sort of forgetting where the Archaea have been concerned, too. According to the life science editor for *Science*, Elizabeth Pennisi, some microbiologists have

> suspected that the placement of the hyperthermophiles, microbes that live at extremely high temperatures, toward the bottom of the tree might be an artifact resulting from assumptions about how fast these microbes evolve and on their initial discovery in extreme environments reminiscent of what early life might have experienced. [1999]

Archaea's placement near the bottom of the tree of life

> was based in part on the finding that the DNA in the ribosomal genes of the organisms has lots of guanine and cytosine bases, an indication that their genomes had been around long enough for certain bases to become over-represented. [Pennisi 1999]

But it turns out that these bases tend to dominate in the genomes of organisms living in extreme environments, as they help stabilize DNA (Pennisi 1999; see also Galtier et al. 1999; Vogel 1999). Creatures with higher guanine and cytosine content might be erroneously brought closer to the root of the tree of life because the thermal stresses to which their genomes are subject may slow down their molecular clock; assuming their clock to tick at the same rate as other creatures' would then place them too far back in time. In other words, commitment to the idea that Archaea were "ancient ones" living at the bottom of the sea came together with a treatment of "genetic information" as abstracted from its local substantiation in particular organisms in particular circumstances, such as variously hot or cold, differently pressured, and diversely salty water. Such idealized genetic information was conflated with—but, to use Andrew Pickering's (1993) language, finally mangled, undone by—the abstractions of bioinformatics.[15] The systematic conflation of metaphysical "information" with genetic "information" looks to have been denatured by the gene-shuffling properties of microbes.

So, where does this leave bare life? What emerges from this tale of lateral gene transfer is the possibility that genetic information, ironically enough through bioinformatics, might be reacquiring the materiality that was muted when it was first theorized as "information." When speaking about the transfer of genetic information demands talking about temperatures, the chemical properties of water, and so forth, it becomes difficult to treat information as a metaphysical principle (see Oyama 2000). When I spoke with Doolittle about this, he pointed to colleagues who had become too attached to the computers on which they generated trees; he did not see that genetic material had become newly visible because of fissures in the information metaphor, though he graciously added, "I suppose you could argue that I'm a part of some Hegelian dialectic that I don't understand—which might be fair enough, but I don't see the shift in quite this way." The difficulty, he said, was methodological, even disciplinary; proper biologists never lost sight of materiality, were never blinded by analogies between genes and information.

Whichever is the case, the "bare life" at the root of the tree of life looks to be becoming agenealogical. Links between life, genealogy, and classification have been destabilized. It would be easy to say this upends one of Darwin's dearest premises, if one imagines he wanted the "hidden bond of connexion" of descent to lead to a unitary ancestor. But, even if Darwin was probably answering polygenists who believed in multiple origins (especially for humans) in the final sentence of *Origin*, his statement still reads as open to the multiplicity of bare life: "There is grandeur in this view of life, with its several powers, having been originally breathed into a *few forms* or into one" (1859:490, emphasis added). The frame of "a few forms" offers a path into imagining multiple organismic relationships, patterns of biogenetic relatedness at once unitary and multiple, at once familiar and alien.

Seas of information: Marine biotechnology and transspecific biopolitics

What might this resubstantialization, recorporealization of genetic information mean for biopolitics? What kinds of networks, new socialities, might this new bare life, this genomically scrambled bios—of heterogeneously materialized and rhizomatically dispersed genetic information—be written into? I suggested in my introduction that "transfer" would be the logic and practice conjoining new genomic assemblages. I look now at the politics of gene transfer in the practice of marine biotechnology.

Even if Doolittle had disabused me of the idea that there was anything particular about water or seawater at issue in microbial gene transfer, I was struck by how much of the tree of life discussion seemed sited in the sea. More, I was impressed by the fact that, even though microbes themselves make no hard distinction between land and sea ecologies, scientists working in biotechnology were beginning to organize their endeavors around a specifically *marine* microbial biotechnology—looking to marine creatures for genetic materials useful in pharmaceuticals and industrial products. Several institutions dedicated to marine biotechnology have been launched in the past few years. The Center of Marine Biotechnology at the University of Maryland and the Marine Bioproducts Engineering Center at the University of Hawai'i are just a couple. I decided to take a closer look.

Thinking back to DeLong's open house talk at MBARI, in which he mentioned biotechnological applications of Archaea, I began to learn more about the biotechnologies to which archaeal hyperthermophiles might be useful. I was curious, too, to know whether lateral gene transfer had any implications for biotech and for the biopolitical frames into which such technologies might be inserted. And what did the sea have to do with all of this, either as an empirical or rhetorical site for biotechnology?

I did some reading. I learned that the extreme temperatures at which vent microbes thrive are of interest in the process of gene amplification, because enzymes from these creatures—extremozymes—can be used to make biochemical reactions run hotter and faster. DNA polymerase derived from hyperthermophiles well withstands the temperature fluctuations required in the polymerase chain reaction, the process used to make copies of DNA (see Rabinow 1999). In William Broad's *The Universe Below,* I read that

> from a hot spring more than a mile deep in the Gulf of California, amid dense thickets of tube worms thriving in otherworldly darkness, Holger W. Jannasch, a microbiologist at Woods Hole, in 1988 isolated an Archaeal hyperthermophile of the *Pyrococcus* genus. The microbe was obviously special. It grew at temperatures of up to 104 degrees Celsius and could withstand much higher heats for short periods of time. New England Biolabs, Inc., of Beverly, Massachusetts, took the microbe, isolated its DNA polymerase, cloned it, and then sold the enzyme, beginning in December 1991. It was the first time a deep-sea microbe had been brought to market. Appropriately enough, the trade name of the DNA polymerase was Deep Vent. "Thermostability, Fidelity & Versatility from the Ocean Depths" read one of the company's ads. [1997:280]

The transfer events here—a microbe from the Gulf of California transported to Beverly, Massachusetts; a gene from an archaeon copied into another creature's genome (in this case *E. coli*); a polymerase moved from lab to market—place the bare life of Archaea at the center of assemblages of deep-sea submersibles, biotech labs, and corporations. These Archaea were hyperlinked not just to other organisms through gene transfer but also to new kinds of biotechnological science and capital. Many marine biotechnology centers, I discovered, worked in partnership with industrial concerns.

To learn more, I signed up for a workshop on extremophiles at the Center of Marine Biotechnology (COMB) in Maryland. Arriving in waterfront Baltimore one morning in July 2001, I walked through a scattering of whimsical sculptures of fish (a public art project called "Fish Out of Water"), past the city's Hard Rock Café—brashly announcing itself with "Save the Planet" emblazoned across its logo—and came upon COMB, housed in a glass-windowed office building covered by an undulating roof suggesting the mantle of a mollusk. I arrived early, before the doors to the conference were open, and wandered around a public area on the ground floor. I read on one colorful poster aimed at children—nearby small furniture suggested day care and fieldtrips—that

> scientists work to improve the future using cutting-edge biotech tools to investigate the oceans—earth's last frontier. They strive to develop products to improve our lives—new food sources; cures for cancer, AIDS, Alzheimer's; and clean up the planet, from the bay outside to marine ecosystems worldwide.

I walked up a flight of stairs and saw painted on the wall the legend "Give a man a fish, he eats for a day; teach a man to fish and he eats for a lifetime—ancient Chinese proverb." The biotechnological sea, it seemed, was to be a space of bounty—fitting, perhaps, in an age when fish populations are famously dwindling. COMB scientists do work on biotech for aquaculture, and the quotation brought to mind the biblical miracle of loaves and fishes, finally realized through the high-tech promise of fish cloning.

Or gene cloning. I'd come here to learn about the promises of multiplying, through genetic engineering, the useful adaptations of cloned Archaea. In the workshop's first presentation, microbiologist Michael Madigan announced that "extremophiles represent valuable genetic resources for solutions to unique biological problems" (2001). Shortly thereafter, in a talk entitled "Archaeal Molecular Biology," another scientist opined that "the hyperthermophiles are gold mines for biotechnologically important products that demonstrate enhanced biological activity and stability at high temperatures." Extremophiles like Archaea had many applications aside from their use in gene amplification. Many Archaea thrive on hydrogen sulfide, a toxic waste of the mining and power industries. Several talks discussed Archaea's ability to break down this poisonous compound, a capacity that made them of interest in bioremediation, in cleaning up the biosphere. I recalled that the COMB website had announced work on biotech "tools with which to process and degrade a wide variety of natural and man-made substances."[16] This is a technological fix to a social problem and gathers force from its phrasing as a "natural" solution. Ecologically minded scientists, with the aid of industry, are giving Archaea the opportunity to bend their adaptations toward remediating deleterious effects of human activity. We might see this as a kind of microbiological instantiation of imperialist nostalgia (Rosaldo 1989), where humans turn to a form of life imagined as primitive and in tune with nature to renounce and redeem their own depredations. The biological resources of the planet are called on to help the planet heal itself. The transfer events here added another element to the assemblage linking genes to capital: the "environment." Punning on Rabinow's "biosociality"—that biopolitics that constitutes individuals not so much in relation to populations but in relation to nongenealogical networks organized around shared genetic polymorphisms, transgenes, and the like (and see Heath 1997; Rapp 1999; Taussig et al. in press)—it seemed as though here I was looking at "gaiasociality": Genes would tie together not just people but also microorganisms, metabolisms, people, and the planet. In gaiasociality, the globe, understood as a cybernetic whole (see Haraway 1995), is enlisted as an important node in and context for relations among humans and nonhumans.

If such earth-healing secrets were locked up in extremophiles, how did scientists go about finding them? Bioinformatics. Identifying interesting properties of Archaea depended on comparing gene sequences across creatures for signs of useful proteins. Using data from Archaea, scientists at COMB were looking to rationally design macromolecules, using comparative genomic analysis to infer, reconstruct, and modulate such properties as protein thermostability (see Robb 2000). I learned from a talk at the symposium that researchers often go online to acquire sequences for creatures, using computational tools like Cross BLAST (Basic Local Alignment Search Tool; version for Archaea available at http://comb5-156.umbi.umd.edu/genemate/) to compare genomes point by point. In this technique one genome sequence is put along a horizontal axis, and a second is placed along the vertical axis; similarities are noted by marking spots of coincidence. The more exactly diagonal the line, the better match. A schematic example:

G	X			
C		X		
T				X
T				X
	G	C	A	T

Where genomes match up, scientists call these homologies. Searching for homologies, of course, might be aided by having a sense of which creatures are most closely related, on having to hand a family tree. Given that family trees looked to be in trouble, however, I wondered how much this could help. Homologies *could* be due to gene transfer. Did that matter? When I asked one researcher during a coffee break how he located organisms with promising properties, he said, "Well, I wouldn't want to be relying on phylogeny these days!" and suggested that finding genes proceeded much more opportunistically.

What other implications did lateral gene transfer have for biotechnology? Shortly after this brief exchange, I heard a talk that posited lateral gene transfer as holding a lesson for scientists. A speaker interpreted it as akin to human biotechnological enterprise, arguing that "natural genetic engineering is very common." The nature at the heart of this biotechnology does not seem to be one of biological constraints. I thought back to an argument of Rabinow's—that, in the culture of late modernity, "nature will be modeled on culture understood as practice. Nature will be known and remade through technique and . . . become artificial, just as culture becomes natural" (1992:241). The "natural genetic engineering" of Archaea gives an organic heritage to a future in which biology becomes technology. Bare life becomes an informational vector of relentless connectivity, which in turn comes to be seen as the nature of nature itself. As scientists know from experience, however, genetic engineering, even if it has "natural" instantiations, is more often than not mediated by constellations of institutional, market, and other forces. The social ecologies in which the lateral gene transfer of genetic engineering takes place are shot through with politics and economics.

How? Almost a year later, at a meeting on the tree of life at the American Museum of Natural History in New York City, I ran into W. Ford Doolittle, and we had a conversation about how microbial gene trading might lead to a proliferation of phylogenies and of taxonomies. He remarked that he had overheard someone at the meeting say, "If you own a patent on an organism's genome and a taxonomist changes its name, you can lose your patent!" He said he had no idea whether this was true but mused that if it was, scientists could threaten other people's intellectual property by saying, "Look out—I'm a licensed taxonomist!"

The remark resonated. I had just come back a few weeks earlier from the Fourth Asia–Pacific Marine Biotechnology Conference, held in Honolulu at the Marine Bioproducts Engineering Center. One of the plenary talks perfectly embodied the anxieties condensed in Doolittle's joke about taxonomy. In a talk entitled "Tapping into Nature's Diversity for Novel Biomolecules Discovery," delivered by a scientist at Diversa, a private biotech concern in San Diego, the speaker—after offering that "the tree of life contains a broad array of metabolisms" and that his company was "cultivating organisms from all over the tree" for recombinant natural products—showed us a microbial species the company had patented, *Stryptomyces diversa,* which perfectly embodies in its name what Donna Haraway (1997) has called a shift in biological nomenclature from "kind" to "brand." It is possible, owing to lateral gene transfer, that someone might find another name for this creature, embedding it in a different set of relations. Indeed, one person asked, at the end of the talk, "How do you define a species in microbes when they're shifting their genes all around? If you have something that differs by one base from another creature? Is that a different species?" The speaker said no, "a similarity of 70 percent or more at the DNA level makes a microbial species, but that's artificial and conventional." Artifice and convention, of course, are precisely what hold in place patent rights.

Some people in the audience at this meeting were disturbed. I spoke with a scientist from Chulalongkorn University in Thailand who complained that the Diversa scientist was "changing evolution." She saw the proper use of marine biotechnology in the domain of aquaculture (for example, in biocontrol, trying to keep shrimp from being infected in aquaculture ponds). She felt that engineering new creatures would lead to runaway competition between microorganisms and people that could have deleterious effects. As she put it, "If we fill the world with all these aliens, they will attack us and we will all die in 50 years." She saw keen differences in how U.S. biotech and Southeast Asia biotech operated. She said that U.S. scientists seemed to take for granted that they could change nature.

Even if the Diversa speaker might brush off the complaint that he was transforming nature, he was at pains to speak carefully about the political dimensions of how Diversa obtained rights to genes and metabolisms. He detailed the benefit-sharing plans Diversa had with concerns in foreign nation-states. As he put it, "Gone are the days when you can just send your scientists on vacation to collect samples. Now, you must have rights from governments to look for and commercialize biodiversity." He said that listeners could rest assured that Diversa had 100 percent legal rights to all genes and pathways, but that they kept firmly in view the need for sustainable use and equitable benefit-sharing (and that some revenue should go for conservation ["exploration of biodiversity should be contrasted with biopiracy; we should protect, not pillage"]). The speaker was talking here of course of bioprospecting—the activity of looking for biological resources useful in biotechnological enterprise and of securing access and rights to these resources through contacts drawn up between host nation-states (or NGOs) and corporations or university research groups. There is a growing literature in anthropology investigating the political economy of genetic material; much examines what happens when local knowledge about plants or animals is transformed into intellectual property that can be patented (Brush 1999; Hayden 2000; Moran et al. 2001; Orlove and Brush 1996). Here there exist transfer events of many kinds. To date, there is relatively little social analysis of marine bioprospecting (though see Aalbersberg et al. n.d. and Qanungo 2002 for short takes), particularly in areas of jurisdictional ambiguity, like the so-called high seas. As the Diversa speaker said, the open ocean is "fair game."

As it turns out, many interesting vent Archaea reside in just such legally ambiguous areas, being "primarily found in the deep sea in areas beyond national jurisdiction, typically occurring in conjunction with volcanically active undersea mountains in water 3,000–4,000m deep" (Glowka 1996:158). During an interview I conducted at Penn State, a biologist showed me a map of these mountainous ridges, pointing out that many fall outside exclusive economic zones—those areas extending 200 nautical miles off the shores of terrestrial nations. Once "alien" in a fanciful sense, such Archaea are "alien" as citizen creatures, which makes accessing their biodiversity a complex prospect. Their extraterritoriality has been particularly potent for a Lockean liberal bioprospecting imagination, which sees spaces outside national jurisdiction as ripe for first-come, first-served appropriation (see Brush 1999). According to legal officer Lyle Glowka of the Environmental Law Center, "The potential market for industrial uses of hyperthermophilic bacteria has been estimated at $3 billion per year" (1996:160). But if plans for accessing extraterritorial biodiversity have, until recently, depended on a Lockean gold rush attitude—with U.S. governmental agencies, universities, and companies leading the way toward "mining" new unclaimed biotic wealth (with the aid of declassified military technology [see Mukerji 1989])—this approach has started to come under scrutiny.

As I listened to the Diversa speaker, I recalled meeting a scientist at Monterey who pointed me to the InterRidge group, an international consortium of marine scientists who informally convened a few years ago to figure out the ethics of using genetic resources collected outside national jurisdiction, in what they term "the Area." In a piece of gray literature entitled "Management and Conservation of Hydrothermal Vent Ecosystems," the InterRidge group expresses concern about ecological effects of bioprospecting in these jurisdictional gray areas, charging that nations that are contracting parties to the United Nations Convention on the Law of the Sea and the Convention on Biological Diversity (CBD) should be obliged to protect and preserve marine biodiversity and ecological sustainability (Dando and Juniper 2001:1). A key issue at these sites remains "resolving and avoiding conflict between different types of field investigations. . . . As vent sites become the focus of intensive, long-term investigation, oversight organization will need to introduce mitigative measures to avoid significant loss of habitat or over sampling of populations" (Dando and Juniper 2001:2). Noting that "vent organisms may prove to have a large biotechnological potential, in terms of both enzymes and specialised compounds," and reporting on a case in which "an Australian-led expedition to the Bismarck Sea north of Papua New Guinea dredged seafloor vents, prospecting for minerals and micro-organisms of potential economic value," the InterRidge scientists argue that the biodiversity that supplies this potential must be protected "for evolution and for maintaining life-sustaining systems in the biosphere" (Dando and Juniper 2001:3–4).[17] Realizing that key players such as the United States do not recognize the convention, they also argue for more informal mechanisms among scientists themselves.[18] Their report suggests zoning hydrothermal vents for different uses, including mining and biological sampling; in their formulation, mining would happen on the periphery of vents and bioprospecting somewhat closer to the center, leaving the absolute center untouched—a literalization of a Lakotosian view of science that keeps pure nature–science at the core.[19] Noting that "at this time, there is no agency with a mandate to oversee marine scientific research activities of biological resources on the seabed," InterRidge proposes that it act as a "research reserve system regulated entirely by consensus" (Glowka 2001:17). In a kind of Mertonian revivalist spirit, the InterRidge report argues for informal mechanisms among scientists themselves—a "code of conduct" (Dando and Juniper 2001:25) that my Monterey contact, himself a former participant in InterRidge, described to me as a "gentleman's agreement." Given the heterogeneity of the scientists involved and the corporate partnerships in which many may participate, this appears ambitious. There are various other plans in formulation to deal with this oceanic commons, coming from the UN and from indigenous groups in the South Pacific.[20] The transfers entailed here summon alternative assemblages that might link vent organisms to projects of rethinking property, equity, and the commons in a contested seascape.

These are assemblages that might be seen profitably through the lens of maritime anthropology. Drawing on early work in the traditions of economic anthropology and cognitive anthropology (Barth 1966; Frake 1985), maritime anthropology has explored how fishers think about the nature of property in ocean resources. Contrary to liberal economists who hold that the seas are a common resource inviting overexploitation owing to an assumed "natural" selfishness driving human action (see Hardin 1968 on the "tragedy of the commons"), maritime anthropologists have argued, using case studies, that people understand ownership in relation to ocean resources in ways more to do with local systems of cultural meaning and with such global processes as colonialism and capitalism (Befu 1980; Boxburger 1989; Durrenberger and Pálsson 1987; McCay 1992; McCay and Acheson 1987; Olson 1997; Pálsson 1991; Walley 1999). Scholars in this tradition have demonstrated that the idea of the oceans as a commons is a recent, and European, one: "The idea of freedom of the seas was a precursor to the social relations of both colonialism and capitalism in an era in which transformations and communication still occurred primarily across water" (Walley 1999:282). Western constructions of the "nature" of the sea as "fluid" and "protean" (Raban 1993) or as "another world . . . without human culture" (Davis 1997:100) in contrast to the grounded "culture" of the land are hardly universal. What we see in debates about the status of extraterritorial biodiversity is a contest over how the transfer of biowealth will be accomplished and what sorts of property imaginaries will be deployed.

So, what *are* the biopolitics of the new gene-swapping "bare life" made legible by bioinformatics? And is the equation of the sea with life at all relevant? Why is there a field of *marine* biotechnology? Is this simply a rhetorical frame to trade on associations of the sea with health? During a coffee break at the Hawaii meeting, I picked up the 1999 inaugural issue of the journal *Marine Biotechnology,* which editorialized that "In the next millennium, the world's aquatic systems will be the new frontier for intensive biological investigation, resource development and management, and industrial application."[21] Was this just hype? Most scientists I spoke with said yes. One researcher opined that while the big selling point of the ocean is that it contains vast, untapped biodiversity, creatures like Archaea exist in a wide range of environments, including not only vents, but also geysers and cow's stomachs. More may be picked up at vents by deep-diving submersibles like *Alvin* simply because this approach is romantic. If marine biotechnology *initially* attracts money, this often backfires because it is too expensive to do for long. Universities and research institutes in wealthy countries have an advantage because many of them are able to capitalize on technology initially developed by the military to get access to new seabed resources. For scientists with whom I spoke, these were the realities behind what they read as cynical attempts to use the sea's association with health to sell this brand of biotech. And this introduces a formulation in tension with the alienness of Archaea; the sea is scripted in many venues as familiar, even familial, motherly. When I summarized my research project to a doctor during a check-up, he was able to rattle off an imitation of the rhetoric instantly: "Since time immemorial, mankind has known the healing power of the sea. Now, our biotech company brings it to you in a pill." This link between the symbolics of the sea and the political economy of the wealthy exactly points out the ideology at work. It is rich countries that will look for unique boutique compounds in the deep, not poorer nations, for which marine biotechnology is often associated with more low-tech aquaculture.

Because vent microorganisms are so cosmopolitan, some of the discussion of the political status of genetic resources on the seabed grasps at a problem of territoriality that may not exist. A more immediate site where gene transfer may have meanings for transspecific biopolitics is in new work about marine microbes that shows them to be everywhere in the water column and, moreover, hyperlinked to the earth's biogeochemical processes, like the carbon cycle (DeLong 1992). Consortiums of gene-trading microbes constitute communities whose metabolic processes may have large-scale effects on climate (see Béja et al. 2000:1905). Ed DeLong is at the center of this work. During my interview with him, he said to me,

> It's difficult for people to get a visceral sense of microbes. You start teaching them with stories about *E. coli* at Jack in the Box, but then tell them that that is a very small piece of the puzzle. Microbes are by far the most numerous and biodiverse organisms on the planet. We're only beginning to understand how they mediate biogeochemical processes.

At Monterey, DeLong has been at the forefront of marine "environmental genomics," and his research has received attention in the mainstream press:

> At his lab in Monterey, Calif., DeLong runs mud from 3,000 feet below sea level through centrifuges, then filters, and treats it with chemicals that dissolve the microbes embedded within. Their DNA floats free, a cocktail of genetic essences. Using the latest tools of biotechnology, he and his co-workers separate the genes and compare their DNA sequences to genes of known microbial classes. Later, they put fluorescent tags on the more distinct DNA and put it back in the mud, where it sticks to members of parent species and makes them light up. "It's the reverse of traditional biology, where we spot a new creature and then analyze its DNA," says DeLong. "Now we get the DNA first, then find what made it." Every time, he adds, "we find something new." [Petit and Tangley 2001]

Identifying microbial communities by sequencing large quantities of seawater—to "see who's there," as DeLong put it to me—and assessing how these communities might be linked to human practice is a political question. They are alien and kin at the same time. As a PBS series on microbes has it, such creatures are "intimate strangers" (Oregon Public Broadcasting and PBS Online 1999). The sea and its currents stand for the transfers they allow.[22]

Gene transfer, hyperactive kinship, and biopolitics

In meditating on the changed notion of bios at stake in contemporary biopower, Rabinow argues that the ancient Greek distinction between *zoe* and *bios* may be useful: *Zoe* refers "to the simple fact of being alive," whereas *bios* "indicate[s] the appropriate form given to a way of life of an individual or group" (1999:15). Rabinow maintains that

> the biopolitical articulation of *zoe* and *bios* that emerged after World War II—which centered on the "dignity" of "the human person" in response to programs to strengthen the race (or population)—is today being disaggregated . . . "Life" is problematic today because new understandings and new technologies that are involved in giving it a form are producing results that escape the philosophical self-understanding provided by both the classical world and the Christian tradition. [1999:16]

What is "life"? Or, to be more precise what is bios in the age of a zoe made of marine mangles of heterogeneously materialized genetic information?

Declarations from 1998's Year of the Ocean offer one way into the question. Carl Safina, director of the Living Oceans Program at the National Audubon Society offers the following: "It is said that where there's life there's hope, and so no place can inspire us with more hopefulness than the great life-making sea" (1997:440). In an age in which genes have been touted as the essence of life, the maxim that water is life is being resurrected. And this water is often depicted as a salty substance mooring humans to their planetary home. Safina: "We are, in a sense, soft vessels of seawater. Seventy percent of our bodies is water, the same percentage that covers Earth's surface. We are wrapped around an ocean within" (1997:435).[23] The bios here leans on an ethic of stewardship based on a kinship of reflection–resemblance that links individual humans to the planet in ways that both call on and bypass evolutionary history—offering a kind of one-step program of communion with the planet. Bios, "the appropriate form given to a way of life," is channeled through a rhetoric not of biosociality but of gaiasociality. But "genes" are not absent in this revival of the "water is life" narrative; they appear as an infotechnique linking microbes to people to politics to planet. This is not just about the return of "water as life" in the age of information. Water has been informaticized because information as biology, as genetic, has been materialized.

In previous work on theoretical biology, computer modeling, and transgenics, I explored the possibility that we may be witnessing an ascendant formation of "kinship in hypertext," as genes become "information" and begin to conjoin organisms and objects usually kept far apart by the rhetoric of genealogy (Helmreich 2001; see also Franklin 2001; Haraway 1997). Hints of this mode of hypertext kinship were apparent in the Human Genome Project's shortcuts to the human genome through sequencing related genes in mice, yeast, and other creatures (see Rabinow 1992), though this has often been seen as a sign of boundary crossing and category confusion rather than as a practice attentive to the shared but not neatly nested characteristics of different species in the first place. Transgenics has been popularly figured as enabled by artifice rather than by "nature." Now, however, microbial marine geneticists are locating in lateral gene transfer a hypertextual logic tethered explicitly to "nature," to how these things really work. The tree of life was always a net. Nature was always a genetic engineer. Such declarations find further support in recent discussions of mobile elements in the human genome, like transposons, retrotransposons, and human endogenous retroviruses that have likely origins in retroviral material incorporated into early eukaryotic and mammalian lines (Prak and Kazazian 2000), suggesting that lateral gene transfer might have shaped nonmicrobial life forms as well.[24] Lynn Margulis (Margulis and Sagan 2002) suggests that many animal traits might owe their origin to acquired genomes.

Following Schneider, one might say that this naturalizes transgenics as an operative logic of kinship. But one could also ask why this rhizomatic genetic connectivity should be called "kinship" at all![25] Why be so literal minded as to insist on following genes into all the networks they connect? One reason: Because the stories that conjoin zoe and bios—like COMB's rhetorics about using genetic engineering to do the good work of saving the environment—link genes and appropriate social forms, what Schneider called "substance" and "code for conduct," in ways that still sit—uneasily and deconstructively, to be sure—at the boundary between nature and culture. Kinship, as Marilyn Strathern reminds us, "connects the two domains" (1992b:17). Kinship is, as Donna Haraway notes, "a technology for producing the material and semiotic effect of natural relationship, of shared kind" (1997:53).[26] The "nature" that can produce these special effects is changing. Another reason to call it "kinship" is that the term draws attention to social, political, and economic inequalities that operate through substance often considered to speak for itself. I join Haraway here in partially advocating that the "new facts of biogenetic relationship" be seen as kinship facts—because seeing them in this way allows us to deploy other kinship tropes of shared risk.[27]

But let me be clear. I do not want to claim that bare life has meaning in itself. It does not essentially entail particular conjunctures between zoe and bios. Claming this would be to fall into the same trap Franz Boas (1940) did, seeing "biology" as speaking for itself to demolish "race," or, indeed, Paul Gilroy (2000), who similarly claims that the latest bare life, genomics, cannot support racism. Biology cannot mean anything in itself, and so particular biopolitics do not follow from given articulations of bare life. Indeed, my use of the word *transfer* to name a new biopolitical mechanism might properly be placed alongside words like *translation, transposition,* and *transformation* to highlight the densely social webs within which new kinds of bare life come to matter. More, it remains to be seen whether and how the bare life I have identified issuing from bioinformatically enabled microbial marine biology and biotechnology will materialize in other domains of biological practice and politics.

What I am describing as a new, agenealogical, watery bare life is impressionistically condensed in Carl Safina's "70 percent of our bodies is water" kinship. But the notion that the ocean is within us is also gathering a scientific warrant. In geobiologists Mark and Dianna McMenamin's theory of "hypersea," life on land is sustained through a rhizomatic, interior ocean: "In a way, the land biota has had to find ways to carry the sea within it and, moreover, to construct watery conduits from 'node' to 'node' " (McMenamin and McMenamin 1994:5). This redefinition of "life" as a network of salty fluid provides a trope for connecting local organisms to global systems—a trope that may be increasingly prevalent in discussions of what kinds of "biology" texture contemporary shape-shifting, gene-swapping biopolitics. It also suggests that we think of the metaphorics of "fluid" alongside those of "networks"—something that Marianne de Laet and Annemarie Mol (2000) have suggested can accent the mutability of objects—like genes—that move through what are only in retrospect legible as networks. "Genes," after all, are not quite the same thing wherever they are transited—and especially when they get hot, wet, or patented. If, as Foucault suggested at the conclusion of *The Order of Things,* "man" may someday "be erased, like a face drawn in sand at the edge of the sea" (1970:387)—if the "human" is a fleeting construction of science and politics—it might be worth asking whether the ocean, as it becomes a site in which links between genealogy and evolution are denatured, could become a solvent aiding a near-future gaiasocial liquefaction of the human, *anthropos.* An anthropology of science that follows the saturation of "bare life" by the hyperactive politics and unexpected kinships of seawater should be attuned to this possibility and attentive to the specificity of the networks of property, law, governmentality, and capital that will connect genes to Gaia through some channels and not others. Thinking about the alien kin networks scrambling up the domain of Archaea may help us track the recombinations of the domains of Nature and Culture in the transspecific biopolitics of gaiasociality.

Notes

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1. For deeper history of family trees, see Klapisch-Zuber 1991 and Pálsson 2002.
2. Indeed, Schneider himself wrote

> it does not follow that every fact of nature as established by science will automatically and unquestioningly be accepted or assimilated as part of the nature of nature. People may simply deny that a finding of science is true and therefore not accept it as a part of what kinship "is." By the same token, some items in some people's inventories of the real, true, objective facts of nature may be those which scientific authority has long ago shown to be false or untrue but which these Americans nevertheless insist are true. [1968:24, note 3]

Franklin writes, however, that Schneider "ignored the extent to which biology, even its traditional form, is about change. Biotechnology today is the matrix of unprecedented life-forms that have as little to do with the nature biology once depicted as they do with the biology portrayed by Schneider" (2001:320).

3. For another recent anthropological use of marine creatures to rethink history and time, see Maurer 2000.
4. The term *transspecific* is taken from the title of the panel for which the paper giving rise to this article was developed: "Transspecific Biopolitics: Animals as Models and as Collaborators," organized

by Deborah Heath and Michael Silverstein and held at the 2001 meeting of the Society for Cultural Anthropology.

5.

> Molecular structures and sequences are generally more revealing of evolutionary relationships than are classical phenotypes (particularly so among microorganisms). Consequently, the basis for the definition of taxa has progressively shifted from the organismal to the cellular to the molecular level. Molecular comparisons show that life on this planet divides into three primary groupings, commonly known as the eubacteria, the archaebacteria, and the eukaryotes. The three are very dissimilar, the differences that separate them being of a more profound nature than the differences that separate typical kingdoms, such as animals and plants. Unfortunately, neither of the conventionally accepted views of the natural relationships among living systems—i.e., the five-kingdom taxonomy or the eukaryote–prokaryote dichotomy—reflects this primary tripartite division of the living world. To remedy this situation we propose that a formal system of organisms be established in which above the level of kingdom there exists a new taxon called a "domain." Life on this planet would then be seen as comprising three domains, the Bacteria, the Archaea, and the Eucarya, each containing two or more kingdoms. [Woese et al. 1990:4576–4579]

6. Though, according to Doolittle and Brown (1994:6724), there were three ways of reading the tree, including the possibility that bacteria branched off first, the possibility that researchers have come to favor.

7. Doing phylogeny requires gene sequences that can be compared. Gene sequences are the much-celebrated products of the various genome projects. These genomes might be accessed from a variety of databases, and, as Donna Haraway notes, databases are not always or only digital or computer based. Genome databases can also have a carbon-based instantiation, as with "yeast artificial chromosomes or bacterial plasmids, which can hold and transfer cloned genes" (Haraway 1994:351). Here "the entire genome of an organism might be held in a library of such artifactual biochemical information structures" (Haraway 1994:351).

Organisms' genomes can also be held in DNA microarrays, also known as genome chips, gene chips, or DNA chips or probes. DNA microarrays are arrangements of DNA samples (on microplates or standard blotting membranes) that allow for matching known to unknown DNA sequences based on the principles of nucleotide base pairing. A DNA microarray or gene chip can be constructed for a set of characteristics of interest and then used to investigate whether a particular individual organism has those characteristics; probe will match target if sequences match. There are issues of categorization and slippage (false positives and negatives) too dense to go into here.

8. An excerpt from a footnote in a marine biology article illustrates the extent to which such tweaking is important to report:

> The 16S ribosomal neighbor-joining tree was constructed on the basis of 1256 homologous positions by the 'neighbor' program of the PHYLIP package. . . . The numbers at forks indicate the percent of bootstrap replications in which the branching was observed. The least-square method (the Kitch program of PHYLIP) and the maximum likelihood method (the Puzzle program) produced trees with essentially identical topologies, whereas the protein parsimony method (the Protpars program of PHYLIP) placed proteorhodopsin within the sensory rhodopsin cluster. [Béja et al. 2000:1905, n. 16]

9. As Geoffrey Bowker writes in "Biodiversity Datadiversity," "The world that is explored scientifically becomes more and more closely tied to the world that can be represented by one's theories and in one's databases: and this world is ever more readily recognized as 'the real world' " (2000:659). A similar view is forwarded by Michael N. Liebman, a bioinformatics researcher quoted in *Scientific American*: "How we store data becomes critical in the types of questions we can ask" (Howard 2000).

10. Moreover, such "information" can be lost as it proceeds forward in historical time. As Bowker points out, "When producing computer models, it is assumed that time is unidirectional—species cannot lose characteristics once acquired. And yet we know some species do just that" (2002).

11. See also Doolittle's "Uprooting the Tree of Life" (2000). In an earlier article, Doolittle asked, "To what extent is our desire to look at early evolution in terms of cellular lineages preventing us from seeing that it is about genes and their promiscuous spread across taxonomic boundaries, which then have no permanent significance?" (1997:12753).

An interesting critique of this position is that it must assume the very vertical model it seeks to explode. This Derridian reading is offered in Gupta and Soltys's (1999) response to Doolittle in the same issue of *Science*.

12. Also:

> Archaea are now recognized as having mixed heritage. The genes for replication, transcription, and translation are all eukaryote-like in complexity (Doolittle and Logsdon, 1998). However, the genes of intermediary metabolism are purely bacterial. The Archaeal genome sequencing papers indicate that the genes for replication, transcription, and transduction form an enduring cellular hardware, whereas the other genes for biochemical functions are a type of software, and prone to change. [Paul 1999]

And:

> A major mechanism for acquisition of genes by eukaryotes may have been grazing on prokaryotes and/or eukaryotes ("you are what you eat"; Doolittle, 1998). That is, over time, there has been a tendency to replace true eukaryotic or archaeal genes in eukaryotes with those coming in from the food source. Although such transfer may be infrequent, there is a constant influx of genes, and once a eukaryotic gene is lost, it is lost for good. The replacement of archaeal genes in eukaryotes was thought to occur quite early in the evolution of eukaryotes, and that archaeal genes are found at all is surprising. [Paul 1999]

In other words, appeals to the fact that groups of organisms have many genes in common can no longer unequivocally ground an argument that these creatures are related. Woese writes: "This assertion is based on numerology, not phylogenetic analysis" (2000:8393). And Doolittle, writing against the argument from numbers as well as the centrality of ribosomal RNA (rRNA):

> the "majority-rule" and "core function" approaches both seem arbitrary, and tinged by the same sort of essentialism that colors our thinking about "eukaryotes" and "prokaryotes." We want to believe that organismal and species lineages do have discrete and definable histories that we can discover and not that we are choosing, arbitrarily, genes whose phylogeny we will equate with that history. [1996:8799]

13. Note that gene transfer is only "noise," however, if it is seen as undesirable. If it is constitutive in the production of organisms, then figure and ground shift and gene transfer becomes the signal.

14. We might note that Lovecraft's "ancient ones," the hideous Arctic progenitors of humanity in his "At the Mountains of Madness" (1971), were extraterrestrials!

15. From the vantage point of my previous work on Artificial Life (the attempt to simulate and synthesize living things in the virtual universe of the computer), in which I documented how coding metaphors from computer science were mapped onto biology and then folded back into computational theories of biology, this denaturing of computational and biological information is refreshing. Also noteworthy is that bioinformatics is beginning to be called "biology *in silico*" (see Howard 2000), a phrase I often heard in connection with Artificial Life. In Artificial Life, however, it was meant to suggest creation of "biological" objects in cyberspace. For bioinformatics, the "biology" at stake is disciplinary practice.

16. Electronic document, www.umbi.umd.edu/~comb/programs/biorem/bioreme.html, accessed March 4, 2003.

17.

> Adaptations to high temperature are a continuing focus for research, as are adaptations to other extreme conditions. In an example of the latter, some vent organisms are known to survive under highly radioactive conditions, resulting from the presence of radionuclides in polymetallic sulphide deposits. The study of such organisms may lead to the discovery of new DNA repair mechanisms that could be of use in medicine. Similarly, the tolerance of vent organisms to high heavy metal concentrations may find beneficial applications in bio-remediation, allowing the recovery of badly polluted sites. [Dando and Juniper 2001:4]

18. They argue that

> beyond the limits of national jurisdiction, the CBD's provisions on genetic resources access and benefit sharing are not applicable. Nevertheless, the CBD Conference of the Parties to the Convention on Biological Diversity (COP) has called upon the CBD Secretariat to study the conservation and sustainable use of deep seabed genetic resources in relation to bioprospecting. [Dando and Juniper 2001:20]

19.

> The true extent of marine bioprospecting at hydrothermal vent sites within and beyond areas of national jurisdiction is unknown. However, these activities probably do not pose an immediate threat to biological communities associated with hydrothermal vents, with the possible exception of the risk of redistribution of endemic micro-organisms between vent sites. At present, there is no scientific basis to suggest that endemic microbial populations exist at any hydrothermal vent site. Sustainability may need to be considered where bioprospectors need large quantities of a macro-organism to obtain useful quantities of a secondary metabolite produced by, for example, a mutualistic micro-organism. If the secondary metabolite is not readily synthesizable and the micro-organism is not culturable, then harvesting the macro-organism at unsustainable levels could threaten both the micro-organism, as well as the particular ecosystem. [Dando and Juniper 2001:19]

20. More reading directed me to the UN's response to extraterritorial marine biodiversity, which has asked whether deep-sea creatures—microbes included—might not need international representation. International debates over access to deep-sea biodiversity extend from early contests over rights to mine the ocean's minerals. In 1967, the Maltese ambassador Arvid Pardo famously addressed members of the UN General Assembly, urging them "to declare the deep ocean floor the 'common heritage of mankind' and to see that its mineral wealth was distributed preferentially to the poorer countries of the global community" (Jacobson and Rieser 1998:103). Adherents of free-market ideology did not much take to this notion, most notably the delegation from the United States, which continued to mine the deep seabed, a project that eventually turned out to be so cost-intensive as to be unprofitable. But the deep sea became newly interesting in the age of biodiversity. *New York Times* science writer William Broad summarizes: "It is no small irony that the greatest excitement to date in undersea mining centers not on deep minerals" but on "the mining of life. . . . By weight, . . . single cell organisms are worth far more than gold. The mining of deep life was never anticipated in all the international hubbub over the divvying up of the sea's mineral wealth" (1997:276).

In 1995, the UN commissioned an independent study of the state of the oceans. Following Pardo, the Independent World Commission on the Ocean contested the notion that the ecologies of the deep seabed were up for grabs for the first nation or company able to exploit them. Commission members took ocean space as a blank slate on which to rethink the distribution of resources, writing in their report, "Contrary to what occurs with terrestrial resources, which can be individually possessed and appropriated in forms developed and consecrated over the centuries, marine resources are by their own *nature* common, and are generally considered as such" (Soares et al. 1998:10, emphasis added). For the commission, marine resources had a watery life of their own resistant to incorporation by national politics, state territorial claims, and the free market. The commission turned to deep-sea vents as sites from which to revive Pardo's vision of the ocean floor as "the common heritage of mankind," proposing a project for the redistribution of genetic wealth to poor nations, which they called "Hydrothermal Ocean Processes and Ecosystems," or HOPE.

In another, contemporaneous formulation, however, critical Pacific studies scholar Epeli Hau'ofa (1994) of the University of the South Pacific in Fiji argued that treating the sea as a kind of blank space between nations (a place by its "nature" common) ignores indigenous sovereignty in what Europeans have called "the Pacific Islands" and local people are coming to call "the sea of islands." Questions of how to access the archaeal diversity of the mid-Pacific rise must engage with these politics. Transspecific biopolitics must take place in the "trading zone" (to borrow a term from Peter Galison [1997]) of trans-Pacific bioprospecting. And genes, as heterogeneously realized information (materialized in labs, patent offices, the UN, etc.), are the biopolitical substance that will be the currency in these unequal trading zones.

21. Electronic document, http://link.springer.de/link/service/journals/10126/papers/1n1p1/sec00.html, accessed May 1, 2002.

22. Another site where gene transfer might have direct effects on humans is in the exchange of genes among waterborne viruses (see Rayl 2001).

23. This comparison, of course, makes little except a loose symbolic sense, since Safina is comparing volume to surface area! The power of this remark comes not from its accuracy but from its sentimental and numinous appeal. Safina is not alone in using such microcosm/macrocosm reasoning. Hillary Clinton, speaking at the United States' first National Ocean Conference in 1998, pronounced that "Seventy-one percent of our planet is ocean, and seventy-one percent of our body is salt water. . . . There is this extraordinary connection between who we are as human beings and what happens in this magnificent body of water" (quoted in U.S. Department of Commerce 1999:6). This mystical 70 percent similarity serves a rhetorical function akin to the oft-cited 98 percent

genetic similarity between humans and chimps—also a percentage that does not capture more compelling evolutionary or behavioral connections since it conflates organisms with only one of their dimensions and then without regard for the scale or context of the comparison (see Marks 2002).

24. See Ansell Pearson 1997 for a Deleuzian discussion of the rhizomatic dynamics of this kind of "viroid life."

25. We might also ask how we can think about this as *transspecific biopolitics* any longer when the very concept of species is put at risk!

26. Also, in a passage that speaks to the imbrication of bioinformatics, genomics, and theories of lateral gene transfer: "The action in technoscience mixes up all the actors; miscegenation between and among humans and nonhumans is the norm. The family is a mess" (Haraway 1997:121).

27. Lest I be accused of fetishizing the gene as the only vehicle for rethinking biological connection in a lateral mode, I might point to important work by Kath Weston (2001) on blood transfusion and the constitution and instabilities of genealogically figured "race." More generally, Marilyn Strathern's study of Melanesian relationality in *The Gender of the Gift* (1988) attends to how personhood can be constructed through lateral exchange of disposition.

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Stefan Helmreich
Anthropology Program
Massachusetts Institute of Technology
77 Massachusetts Avenue
Cambridge MA 02139-4307