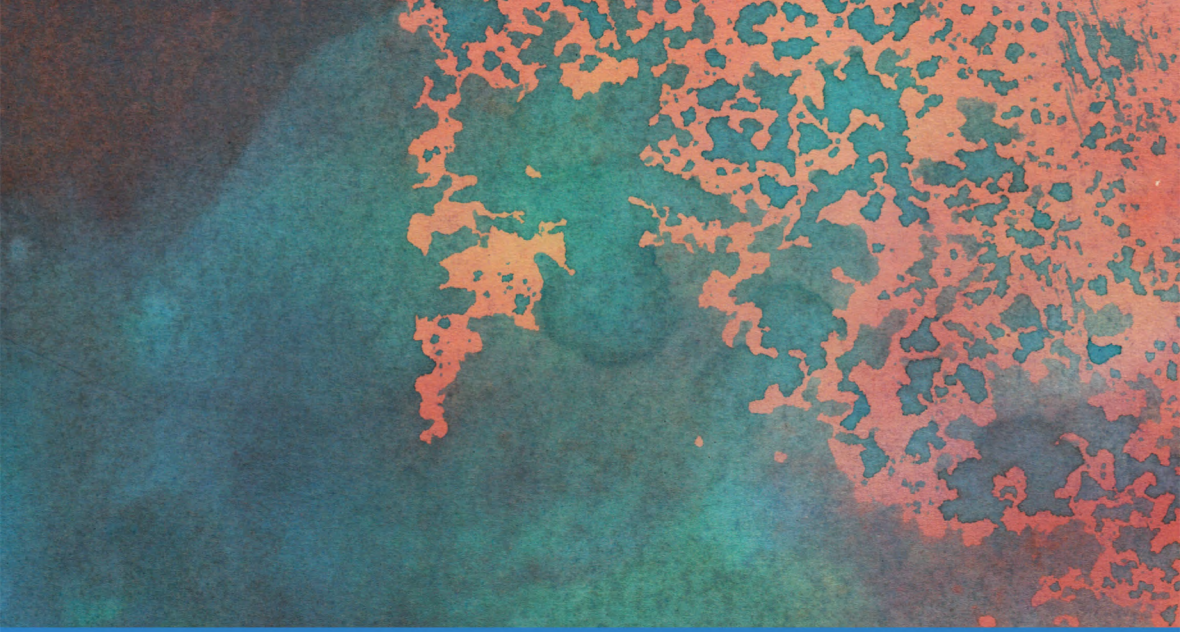

Routledge Studies in Anthropology

BIOINFORMATION WORLDS AND FUTURES

Edited by
EJ Gonzalez-Polledo and Silvia Posocco

Bioinformation Worlds and Futures

This book sets out to define and consolidate the field of bioinformation studies in its transnational and global dimensions, drawing on debates in science and technology studies, anthropology and sociology. It provides situated analyses of bioinformation journeys across domains and spheres of interpretation. As unprecedented amounts of data relating to biological processes and lives are collected, aggregated, traded and exchanged, infrastructural systems and machine learners produce real consequences as they turn indeterminate data into actionable decisions for states, companies, scientific researchers and consumers. Bioinformation accrues multiple values as it transverses multiple registers and domains, and as it is transformed from bodies to becoming a subject of analysis tied to particular social relations, promises, desires and futures. The volume harnesses the anthropological sensibility for situated, fine-grained, ethnographically grounded analysis to develop an interdisciplinary dialogue on the conceptual, political, social and ethical dimensions posed by bioinformation.

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The friction and flow of bioinformation at the Smithsonian

Adrian Van Allen

Museum genomics is merely the most recent iteration of viewing the natural world as a data set to be collected and analyzed. Framing natural science collections as databanks reconfigures the collections as valuable to expanded audiences, transforming them into resources—and potential solutions—for contemporary crises both social and biological. This chapter examines the negotiation and creation for a data standard for "genome-quality" frozen tissue collections at the Smithsonian National Museum of Natural History in Washington, D.C. – a practice the museum scientists termed "capturing genomes." My ethnographic study of biodiversity biobanking in the museum focus on the material practices of making and remaking life in an era of increasing biotechnical capacity as well as increasing biodiversity loss. Standards make data accessible, but they also draw invisible lines between what is kept and what is discarded, naturalizing the remaining data, practices, specimens, and interests and obscuring the labor required to make and maintain them. That is, biobanking practices orient museum sociologies, biologies and ecologies—engaging them in ongoing processes of re-inscribing and removing the boundaries of nature and culture. In turn, these nature-culture assemblages have the potential to expand the multiple possibilities for thinking about interspecies relationships as we move into uncertain futures.

Introduction

On a cold morning in March 2015, I stood in the Smithsonian Institution's Biorepository holding an insulated box as my colleague swiped his badge to open the door. Within the box I held were stacks of smaller boxes holding tissue tubes, samples from species around the world that were being collected and collated into a genomic archive of life, now being sorted and placed in liquid nitrogen filled tanks to preserve them in perpetuity. In this vast off-site facility in rural Virginia, the frozen spaces were clustered together—the Biorepository next to freezers full of cancer-riddled kittens, part of a long-term study for the National Institute of Health, adjacent to the film vaults for the National Museum of American History, stacked full of reels of flammable silver nitrate film. These various frozen materials were being kept cold for perpetuity, frozen for the future while at the brink of dissolving into something else, decay kept at bay.

Setting down our tissue sample box at a workstation, we opened it and removed the two tubes that were to play a vital role in determining the data standard for what would be included or excluded in this ever-growing genomic archive—slivers of muscle tissue from a White perch (*Morone americanus*) and a Chesapeake blue crab (*Callinectes sapidus*) in two slim plastic cryotubes, a barcode label affixed to their sides [Figure 1]. Logging into a computer at the workstation we scanned the barcodes of our fish and crab, noting what their location would be within the rows of massive stainless-steel tanks behind us. Together, the tanks had a capacity

to hold up to 5 million tissue tubes suspended above a pool of liquid nitrogen to keep the samples frozen at -190˚C. Donning lab coats, face shields and large blue padded gloves we climbed up the steps on the side of the tank, opening the lid to withdraw a rack that held the frozen tubes in place [Figure 2]. Brushing aside the frost on the rack to read the numbers, we slide our tray of fish and crab into its allotted space, resealing the tank lid as quickly as possible to maintain the internal temperature and keep the tissue tubes in their state of suspended animation [Figure 3].

I begin at the end for this story, with the placement of these two tissue tubes into their final resting place within the Smithsonian's Biorepository. This moment was but one link in a long chain of events in the life history of two animals that became specimens—specimens that would mark the genome-quality standard for amassing one of the largest tissue collections in the world, currently being built to put "all life on ice" for uncertain ecological futures. This chapter examines the negotiations and practices of transforming life into data at the Smithsonian National Museum of Natural History in Washington D.C., focused on the Global Genome Initiative (GGI). The GGI's self-described project is to create a "genome-quality" frozen archive of half of all taxonomic families of all life for an uncertain ecological future within the next six years, collaborating with a global coalition of over 100 other museums, herbariums, biorepositories and DNA banks. What constitutes a "genome-quality" tissue sample is at the center of this project, entangled with the layers of infrastructure and politics of integrating genomics into the museum context.

The site of this ethnographic inquiry is within these two tubes, as I seek to unravel how much meaning is condensed into such a small object, these simple 2ml vials of plastic that can contain multiple imagined futures bound up within the tissue samples they contain. The material practice of creating these two unassuming tissue tubes is one of "rendering flesh into data" (Radin 2012, 310), following the biologies of these creatures as they are fractioned into new kinds of museum objects that are capable of both carrying and reproducing certain kinds of information, including negotiating certain kinds of (genomic) futures. Attending to how these tissue tubes came into being, I examine how the material properties of their original animals – a fish and a crab – then become a standard for measuring the relative quality of other tissue tubes taken from other animals collected across the globe in a mass salvation effort. This chapter will focus on these processes, or series of transformations from animal to specimen, from specimen to data, and finally into a data standard for future specimens. In doing so, I

want to suggest that engaging first-hand with the material practices of museum genomics is essential – that is, the site of this ethnographic research combines views gleaned from the work bench and in the lab meetings where genomic tissue standards are negotiated. The standardization processes of making a variety of specimens fit into a single data schema are based not only on making data standards uniform across disciplines, but are also, I argue, profoundly shaped by the material practices from which those data standards arise.

Based on three ethnographic episodes at the Smithsonian Institution in Washington, D.C., I argue that the material practices preceding the movements of data fundamentally shape and inform the paths which a specimen can take. Save the entire fish and you have a traditional voucher, but preserve it in formalin before you take a tissue sample, and you won't be able to get DNA from it. In short, biodiversity conservation through genomic collecting orients museum sociologies, biologies, and ecologies—continually engaging them in ongoing processes of remaking, re-inscribing, or perhaps removing (if indeed they ever existed) the boundaries between nature and culture. Engaging the material practices of how archives are made, I examine how these negotiations for knowledge standards are made manifest through the biomaterials of the specimens themselves, as they are unraveled from wholes and into parts. I suggest that it is within this fragile network of negotiations that different forms of power are rendered visible. Further, it is the importance of the biomaterials themselves in making the data standards that comes to the fore in these encounters—what "behaves" or "misbehaves," that is, what to do with specimens and their data that don't fit into pre-existing categories, where life continues to overfill the preset frames of reference. It is these moments of alignment and misalignment, of multiply layered frames of reference that bind these specimens and their samples together, but not always in unison, where we can see the friction and flow of bioinformation in and through the genomic museum.

I began in the Biorepository, sorting the tissue tubes into their identified slots, each tube serving as the voucher for the genetic information that was extracted from them—the physical anchors in the chain of information binding a physical specimen in a museum cabinet, drawer, or liquid nitrogen tank to the abstracted genetic data that lives on servers and circulates beyond the specimen it originated from. These frozen tubes in their numbered rack were the ending point of the specimens after they had been collected, processed, sectioned into parts and pieces, and portioned into various tissues tubes. One of these tubes went to the Biorepository, another to the Laboratories of Analytical Biology at the Smithsonian National Museum of Natural

History, to be consumed as the DNA was extracted and measured. This is my second encounter at the lab bench extracting DNA and assessing its viability for being used as standard for "capturing genomes" by global partners at other museums. Finally, my third encounter is in a lab meeting to discuss the results, and ultimately defining the Global Genome Initiative's genome-quality data standard.

Bringing into question the contemporary standardization of biodiversity to make it knowable, computable and sharable, I examine the Smithsonian's Global Genome Initiative (GGI) creation of a "genome-quality" tissue standard. Through exploring the reassessment of natural history collections as biological libraries of "life's code" and as the setting for the standardization of biodiversity data, the drive to create an entire corpus of human knowledge of life through, as one of the Smithsonian scientists phrased it, "putting all life on ice." This urge to archive all life connects issues of care for biodiversity, as well as its potential loss—as taken from one specific and culturally situated perspective, a perspective that fundamentally orients collection strategies. Within this context, I consider the way that the biodiversity biobank-as-archive holds together particular ideas about future orderings of nature and culture, and facilitates new collaborations around the unraveling biological objects in its care.

To begin to answer these questions I turn to longer histories of specimens-as-data within the museum. Tracing back to seventeenth-century cabinets of curiosity, I examine how every age has been one of "data deluge," faced with the challenge of incorporating new categories of life into existing classification systems. Following these histories of standardizing biodiversity in museum work, I connect ongoing debates on creating a "genome-quality" tissue standard to the friction of and flow of biodiversity as specimens move into the Smithsonian National Museum of Natural History collections—points in a trajectory towards organizing biological life into an abstracted open-source data project.

The Material Practices of Constructing Genomic Archives

Scholarship on the creation of archives has looked to the forms of power created in the hierarchies of knowledge (Bowker and Star 1999; Daston 2004; Durkheim and Mauss 1963; Ellen 1993; Lampland and Star 2009; Needham 1979). Instead I focus on the material practices that bring these forms of data into being, moving back along the trajectory of the specimen to the inflection point when it is transformed by the labor and thought of specimen preparators and lab technicians, moving from meat to meaning, from matter to immateriality. Further, I

want to place these material practices of museum genomics in their historical context, where the generation of new types of objects and their associated data has always been a problem for collections, dating back to early cabinets of curiosities (Strasser 2012).

Previously, I've examined the shifting value of natural history collections and their articulation as untapped resources (Van Allen 2018; 2019), looking at the conceptual framing of collections as "biological libraries," that is, as sites to extract data relevant for fields such as agriculture, national security, disease control and as storehouses of knowledge for biodiversity conservation. One aspect of conservation is preservation, which I argue can be understood as a return to eighteenth-century encyclopedic collecting now utilizing contemporary genomic tools. Frictions between these two orientations—to conserve for future use or to preserve in perpetuity—are brought into focus through the daily practices of crafting data standards for making "genome-quality" tissue collections, or what the scientists at the Smithsonian called "capturing genomes" (Droege et al. 2016; Mulcahy et al. 2016).

As making collective meaning through classification continues across cultures (Bleichmar and Mancall 2011; Levi-Strauss 1966), it also changes in materials, forms, and the details of how a classification system is "anchored" over time. This includes, in my particular context of the contemporary natural history museum, the "anchors" of physical specimens tied to the genetic data derived from them. For taxonomy, the value of biological specimens and the natural order(s) they are taken to represent are upheld by meticulously observed chains of connections vitally linking the specimen to information, to nature, and back again. These connections are built from data—data that is derived from the biomaterials of the specimens themselves, from what is preserved versus what is discarded. Each discipline values and discards different pieces, as seen in one of the parasitologists I worked with defining her "field site" as the intestines of birds, a site where she could extract worms with the tips of two needles, utilizing a part of the specimen that would have been thrown away by the ornithologists at her museum.

While the classification of nature has been acknowledged as a central human activity (Foucault 1966; Levi-Strauss 1966), and one shaped by hopes for its protection on the one hand and exploitation on the other (Hayden 2003; Lowe 2006; Tsing 2005), taxonomy as an endeavor continues to be perceived as a rarified and esoteric set of knowledge-generating practices. However, one consequence of the signing by over 150 nations of the Convention on Biological Diversity (CBD) in 1992 was an unprecedented focus of global attention upon the significance of taxonomic knowledge as an underpinning prerequisite for the protection of an ever-

dwindling global biodiversity. The United States, it should be noted, was not one of the signatories of the CBD, though the "best practices" of the collecting and curation of the Smithsonian's natural history collections, I was assured by Smithsonian staff that "it's not only the legal thing to do, even if we aren't a signatory, it's the right thing to do," and the museum follows the Convention on Biological Diversity and the Nagoya Protocol. Biodiversity, then, is shifting from being defined simply as a network of all living things to being defined as a (continually emerging) network of interests negotiated between nations, institutions, and individuals. Museum collectors and their ever-growing genomic archives are but one stakeholder in this web.

Extending the Collections: Capturing Genomes

January 2015. Another snowy morning, now a year after the Smithsonian's Global Genome Initiative was launched as a new project to collect and centralize all the tissue samples from across the various museum departments. I sat in the long white conference room in the Laboratories of Analytical Biology (LAB) at the Smithsonian National Museum of Natural History. Six of us were at the table, all heads turned towards the monitor at the end of the room that displayed two DNA gels [Figure 4]. The DNA gel images are two dark gray rectangles, filled with pale smudges in ordered rows, each row marking the progress of extracted DNA through the thick gel under a low current. The brighter the small square smudges, the higher the molecular weight of your DNA, and therefore the higher the quality of your samples. It is, I come to learn, a matter of contrast.

The goal of this meeting was to finalize a scientific paper titled "Capturing Genomes," which when published will serve as a protocol for how to measure the quality of the DNA in one's collections—be they collections in the NMNH Biorepository or one of the (at last count) 34 collaborating institutions worldwide that are part of the Global Genome Biodiversity Network (GGBN). The Capturing Genomes paper had been through many iterations, and was a core piece of the puzzle for the GGI to move forward with its goals—a standard was needed to determine the quality of the collections being made in the GGI's name, and across the other collecting activities of the GGBN. Since the GGI's stated purpose is "Preserving and Understanding the Genomic Biodiversity of Life on Earth," it was key that what was being collected and preserved was in fact "genome quality." Precisely what determined "genome quality" was under scrutiny as well, and went through a number of iterations, but the "working

answer," as one curator put it, was to "settle on a DNA fragment length of 9kb (kilobase pairs), for the time being," since "things change so quickly."

The meeting today was to go over the remaining issues about the paper. These included looking at the gel images that had been run by the GGI lab tech of a fish and a crab, the two test cases for the paper, who we have already encountered at the beginning of this story, as they were sorted into the frozen time of the Biorepository. And then there was the issue of vouchers—the specimens that would go into the collections as the reference for the tissues of the fish and the crab—ideally a whole identifiable organism that would become part of the Departments of Ichthyology for the fish and the Department of Invertebrate Zoology for the crab. For now, we collectively stared at the screen, looking at the smudges of black and gray on the DNA gel. The gel images were not as hoped, and there were many concerned expressions and the occasional frustrated sigh. The paper was overdue, but the results from assessing the amount of DNA in the samples didn't seem viable.

As we examined the gels on the screen in front of us, the fish and the crab were pale smudges compared to the "ladders," or controls that ran along on either side—the reference so one could gauge that the test worked. Beyond the paleness of the smudges, and far more problematically, they were inconsistently pale. The trouble with the fish and the crab was their variability—the same sample "run" on two gels, mixed and cast at the same time, returned wildly different results. The general consensus (after a careful recounting of the process to make sure an error hadn't been made) was that the results were unusable.

"We're making a standard for everyone in the GGBN [Global Genome Biodiversity Network] to use, it has to be rock solid. And this isn't it," stated an Invertebrate Zoology curator. The protocol being put forth in the paper was going to be integrated into the collecting practices of the full network of collaborators, over 100 global collaborating institutions each with varying degrees of funding and access to advanced tools. Questionable data were not acceptable. Debate ensued, going over the details of the numbers, re-doing the calculations, asking what the best way was to standardize against the opacity of the gel, how to equalize the contrast in the image, visiting the possibility of re-doing it all from scratch. Time, funds, labor and accessibility of specimens were all factors against re-doing all of it from the beginning. Not to mention, as one curator pointed out, the need to get the protocol tested and out into the GGBN community so they could begin adding to the genomic archive as quickly as possible in the face of mass biodiversity loss. Conversation lulled into silence.

"What's the standard deviation for the TapeStation?" the Invertebrate Zoology curator asked into the silence. Heads popped up from behind sheets of paper and laptops. More debate ensued, but with a renewed pitch of excitement. This might be a way through. To ensure that genomic DNA is of the quality required, the group agreed, each sample needed to be screened to determine its suitability before committing the time, money and resources to preserving it in a biorepository, and taking up space in the collections for its voucher. Assessing genomic DNA is usually performed by agarose slab gel. However, this is a slow, labor-intensive, and manual process that can take several hours. In contrast the largely automated workflow of the TapeStation uses a credit-card-sized device made of three separate polymer layers that separate biomolecules through a gel matrix in separated channels. Genomic DNA is mixed with buffer, and then placed in the TapeStation for automated analysis. A "plug-and-play way to get your DNA's molecular weight" as a lab tech interjected into the conversation.

In this narrative the traditional agarose slab gel is considered outmoded, slow, and ultimately somewhat unreliable given its handmade quality. However, the very cheapness of the handmade slab gel is precisely what makes it appealing for a global collaboration such as the Global Genome Biodiversity Network (GGBN), stretching across institutions in many third world countries located in biodiversity hotspots that were desirable for the genomic archive, but these institutions had varying amounts of labor, funding and equipment available. Microwaves to heat up buffer and melt agarose gel, UV lights, and electricity to run a traditional agarose gel were usually accessible to those with even limited means. TapeStations were not. A quick scramble as heads bent back to their laptops, clicking away as the variability rates for the TapeStation were looked up from previous projects. "The variability of the results of the fish and crab aren't really different than the TapeStation," another lab tech offered up. "I think we're OK." The mood in the room swung in a sea change, it was almost jubilant. The details of where and how to word the protocol were nailed down; the process of collating edits and comments into one document organized. Another lull in the discussion, and someone asked, "What about the vouchers?" More silence as various gazes locked across the room.

The original specimens had been collected off the coast of Panama, at the Smithsonian Tropical Research Institute (STRI).[1] This was an efficient way to collect specimens, I was told,

[1] The Smithsonian Tropical Research Institute (STRI) is a bureau of the Smithsonian located on Barro Colorado Island in the Panama Canal Zone "dedicated to understanding biological diversity" (STRI 2016). Begun in 1923 as a small field station, the current institute's research activities extend across the tropics. These include STRI's Center for Tropical Forest Science that uses labeled forest plots to monitor tree demography in

with a minimum of permits and paperwork as the research station and collections made within its boundaries are considered a priori part of the Smithsonian. "Were they collected before October 14, 2014?" a GGI staff member asked one of the lab techs. He checked the paperwork and nods. "Good, before Nagoya," a reference to the Nagoya Protocol, a piece of international legislature that came into effect during my fieldwork at the museum, a refinement of the Convention on Biological Diversity from 1993. In defining the biowealth sovereign nations and their control over their flora and fauna, it also fundamentally changed the political topography of moving specimens across international borders.

According to scientists I interviewed across the Smithsonian, specimens were getting much more difficult to get, to move, and to keep. The crab and the fish, however, predated the entanglement. Not much of them was left, however. Apparently, the fish were collected as "little fish fillets" into a jar of ethanol, according to one of the lab techs, and the only remains of the crab was the left claw. "We need a phylogenetically valid voucher somewhere," one of the GGI staff says, "at least two tubes in the biorepository, if nothing else. If there's a claw in a jar in IZ [Invertebrate Zoology], fine, but we need to have these live on GGBN before [the paper] gets published." Heads nod. "Voucherless tissues?" someone asks. The carefully connected links in the chain between the original whole fish and crab, their tissue samples, and their extracted and abstracted DNA data were starting to come apart. A pause in the conversation as various minds imagined that chain and how to rebuild it. "The vouchers are the tissues," one of the curators replies, and pauses before adding "for now." The possibility of getting a substitute voucher for the fish tissue is discussed briefly—what's referred to as an allotype, one of the same species (usually verified through DNA barcoding[define], as well as being a visual, morphological match), but not the specific individual that the tissue sample came from.

Population sampling is a common practice in various Divisions and Departments across the Smithsonian, as it is in many other natural history museums. For example, Invertebrate Zoology collectors often sample various marine creatures in a colony, such as a coral polyp colony living in a reef, where many are samples, but one is picked to serve as a voucher. Similarly, collectors for the Botany Department take samples from fields of the same plant and then press one full individual as their voucher specimen. The relationship of one-to-many in

fourteen countries located in Africa, Asia and the Americas, and STRI marine scientists conducting a global survey of levels of genetic isolation in coral reef organisms as well as providing fish and crab specimens for the GGI (STRI 2016).

the collections made in these disciplines runs counter to the one-to-one relationship in other disciplines, such as Vertebrate Zoology. For the Division of Birds, a part of Vertebrate Zoology, where many of the first genomic collections were made 20 years ago, the ideal relationship remains as a whole, stuffed bird skin in a drawer, with tissue tubes sampled from the heart, muscle and liver stored in the Biorepository, extracted and replicated DNA from those tissues used in the biolab and then sent to join their tissues in the Biorepository, and all the associated genomic data filed into several online databases. Various extraneous pieces can unravel from these specimens—the parasites in the intestines are of interest to the invertebrate zoologists for their National Parasite Collection—but the essential links in the chain of whole specimen to tissue to DNA to data remain unbroken. The fish's replacement voucher specimen would just be a bit out of sequence—tissue first and allovoucher second (at some point in the future). Someone suggested putting the jar of "little fish fillets" preserved in ethanol in the Division of Fishes as the voucher. One of the curators grimaces, shaking his head, this solution seems to offend his sensibility of what belongs in a collection. One of the lab techs agrees. "It just looks like meat," he says with a dismissive note, "why would it go into the Ichthyology collections? Just put it in a tube in the Biorepository—that's where it belongs. Meat in a tube" [Figure 6]. That seems to resolve the issue. Notebooks and laptops are closed, and we shuffle out, turning off the monitor with its fading glow of DNA gels. They, too, have been sorted into their appropriate category of unexpected results, which though at first considered too variable, were then rendered into results that were no more variable than other practices already in place.

Standards were kept, boundaries of acceptability negotiated and maintained, vouchers found, or a future slot positioned for them. The fish and the crab were misbehaving, or more precisely the "read" on the molecular weight of their DNA was misbehaving (and certainly their vouchers were misbehaving). However, they were not misbehaving substantially more than the TapeStation or other vouchering methods. Therefore, it was an acceptable amount of misbehavior and could be accommodated. Despite their resistance, standards were being crafted to accommodate their idiosyncrasies and make them do the work necessary—that is, provide a method for "capturing genomes" for the Global Genome Initiative and its partners.

From Meat to Meaning: (Frozen) Cabinets of Curiosity

We now return to the Biorepository, carrying our precious tubes of fish and crab, ready to be sorted into the trays afloat above liquid nitrogen. Through following their journey from meat

to meaning we can see them transform in front of us. A tiny frost-covered cryovial becomes link in chain binding together its data on the servers, to the data set associated with the "Capturing Genomes" paper, to the small pieces deposited in the Departments of Invertebrate Zoology (but not Ichthyology). A crab claw, it seems, is worthy of space on a museum shelf, but a tiny scrap of fish flesh in a jar is not. These kinds of sortings of matter and meaning have a long history, of new kinds of objects emerging and being categorized.

Data within the museum has always been a central concern, and I began to think about both natural history and the larger histories of nature in the context of genomic collecting, its data and expanding networks of tissue tubes. What began as studies of local flora and fauna in sixteenth-century Europe was soon complicated and broadened by objects, specimens, and even living humans brought back to Europe from explorations to the New World and traders returning from expeditions (Daston and Park 1998; Findlen 2002; Greenblatt 1992; Impey and MacGregor 1985; Olmi et al. 2001; Pomian 1990). Collecting provided a means not only to assemble the newly discovered, but to make sense of it and exert control over its natural resources—a cabinet of curiosity built in 1648 demonstrates a complete cosmos in miniature, combining coral and shells from expeditions with a clock, biblical scenes carved into semi-precious stones from around the world, and a hidden pharmacy with jars carved from African ivory. The world remade from the material evidence of colonial domination, imprinting Western scales of time, Christianity and medicine on those representative fragments of coral, gems, and ivory. These collections within these early modern cabinets of curiosity formed the basis for many contemporary museums (cite), and in perhaps some deep-seated and unexpected ways, they have also formed the basis for how the miraculous and the mundane are standardized to fit within a particular ontological schema. The freezer in the Laboratory of Analytical Biology, where our fish and crab tissues were stored while their DNA was being sampled and extracted, features an array of global diversity condensed into a new form of curiosity cabinet, one full of spiders from Costa Rica, fish from Timor, mammals from Brazil, snakes and lizards from Myanmar.

In addition, newly emerging technologies in the seventeenth century facilitated the preservation, circulation, and documentation of collections in new ways—such as specimens preserved in alcohol, and an outpouring of books that cataloged, categorized, inventoried and illustrated the collections in printed catalogs that could circulate far further than the stuffed, pinned, and pickled specimens they represented (Findlen 1994; Zorach et al. 2005). Massive

collections spanning fields of knowledge and new areas of the world were amassed, organized, displayed, and circulated. Laying a claim to the value(s) of biological specimens thus raises a whole range of questions concerning what a specimen can ultimately stand for and forces us to imagine what it might mean to scale-up from a specimen in a mahogany drawer in the sixteenth century or in a liquid nitrogen tank in the twenty-first century to an appreciation of (potentially multiply constituted) "life itself" (Rose 2009).

Objects are made meaningful according to how they are placed within relations of significance. These relationships, in turn, depend on who is determining what counts as significant. Objects are therefore likely to be spoken, rather than to speak (Haraway 1997). This is not to say that all meanings are of equal value, of the same power, or of the same validity. We see this in the shifting interpretation of a crab broken into its biomaterials, as it is unraveled into different parts and pieces with each transformed to carry different weights of meaning with them—be it a claw in a jar, a tissue sample frozen in a tube, extracted DNA expanded across a gel, or its DNA barcode uploaded to a database.

Conclusion: The Friction and Flow of Bioinformation

The move towards a stable (taxonomic) ontology of biodata and the corresponding claims towards the "data deluge" of contemporary science obscures a much longer history of biological collections as data sources. In other words, current museum genomics does not take into consideration the long history of museum collections as sites for data extraction—museums have always been "data banks," and each era is one of "data deluge" (Strasser 2012). As the life sciences increasingly become the biggest of Big Data projects (Leonelli 2013; 2014; Page et al. 2015), it is crucial to contextualize them in a longer genealogy of museum collecting.

The entangled histories of natural history museums and bioscience research can be followed through the divestment and reintegration of lab science in the museum in the early twentieth century to the present, a timeline that also corresponds to the emergence of anthropology as a discipline. However, in this chapter I have looked further back to the origins of the natural history museum, examining the shifting assemblages of specimen-as-data and the global networks of living (and formerly living) things in the first natural history collections in early modern European cabinets of curiosity. In contrasting these with contemporary genomic collecting, I have begun to think through the continuities and ruptures in the material practices of nature-making in museums.

Museum genomics is merely the most recent iteration of viewing the natural world as a data set to be collected and analyzed. Framing natural science collections as databanks reconfigures the collections as valuable to expanded audiences, transforming them into resources—and potential solutions—for contemporary crises, both social and biological. These include more obvious projects such as biodiversity conservation in the face of mass species extinction, as well as less obvious projects such as agriculture negotiating the influx of invasive species, national security dealing with invasive-species-as-potential-bioweapons (Dudley and Woodford 2002), disease control by charting contagion vectors from historic specimens (Suarez and Tsutsui 2004), and even the improbable de-extinctioning of species such as passenger pigeons (Revive and Restore 2013) and mammoths (Church and Regis 2012; Poinar et al. 2006; Shapiro 2015; Zimov 2005). However, it is also worth considering what kinds of labor and interests are involved in reconfiguring collections as data resources, and as we have seen, the handcrafted standards that shape these collections.

Different forms of life, including biodiversity, have been increasingly defined by molecular biology (Bowker 2000; Keller 2009; Sunder Rajan 2006)—where the metaphor of DNA as a code (Kay 2000) or a text (Ridley 2000) to be written or rewritten replaces the sticky materiality of the thing itself (Tsing 2005). Attending to the gap between "genetic 'information' and biological meaning" (Keller 2009, 7–8) is one productive way to think through how specimens become data. The details of an organism's genome, its parts and interrelated functions increasingly define what it means to be "alive" in the contemporary moment, as determined by human biomedical and biodiversity genomics and then dispersed and "naturalized" into larger cultural domains (Genome 10K Project 2016; Kowal, Radin and Reardon 2013; Parry 2004).

Species, in this conceptual framework, become their genomes in one sense—the protein sequences extracted from frozen samples, "read" and sorted into the "book of life" (Canguilhem 2008; Kay 2000; Ridley 2000), ready to be read again or rewritten as needed with emerging technologies such as genome engineering (CRISPR/Cas9 Guide 2016). From this standpoint "capturing genomes" and collecting "all life on ice" become plausible endeavors, based on a view that life is reducible to a 2ml cryovial, the tissue inside it, and the genomic data that can be extracted from it. The diversity of biodiversity is in the process of being transformed into stable, standardized categories to enable its collection, preservation, analysis and use within an existing ethos of "natural order"—an ethos that privileges the rarity of the species, the high molecular weight of the sample, the analytical chain of permits and vouchers, and the accessibility and

visibility of the genomic data to institutional infrastructures or partner networks (such as the Global Genome Biodiversity Network)—all pointed towards preservation for an uncertain future.

To return to the shifting value of biomaterial as it is transformed into bioinformation, I want to highlight the creation of a "genome-quality" tissue standard as a way of thinking through things (Henare, Holbraad, and Wastell 2007; Ingold 2010). The ways these standards and the objects they organize come-into-being (Gosden and Marshall 1999; Moutu 2006) shifts the focus to new conceptual linkages between the lives—and afterlives—of organisms, both human and nonhuman, as they circulate. My ethnographic engagement with biodiversity collecting in the museum and the complicated webs of interaction that define it—socially, biologically and ecologically—relate to Helmreich's work on collecting the scientists who collect aquatic microbial life (2009). His concern with the microscopic, molecular, and genomic explorations of the open ocean and deep-sea point to an expansion of the concept of bios, of life in the alien ocean as other life. While his focus centers on engaging the scientists on their own particular spaces and their own particular terms—an orientation to ethnographic practice I find compelling—his collection of scientists offers up a somewhat homogenous narrative of biodiversity salvation. In contrast, the creators and collectors of museum genomics in my own research offered a variety of narratives based on their own disciplines' distinct histories of collecting and preserving, which they struggled to fit into a standardized schema.

From this perspective, the scientists I worked with are in the process of transitioning from being stewards of life's diversity in distinct disciplinary ways to becoming the conduits for increasingly standardized versions of life as they integrate genomic collecting practices, such as the protocol detailed for capturing genomes of a specifically high molecular weight. Standards make data accessible, but they also draw invisible lines between what is kept and what is discarded, naturalizing the remaining data, practices, specimens and interests and obscuring the labor required to make and maintain them. In other words, biodiversity conservation through genomic collecting orients museum sociologies, biologies and ecologies—continually engaging them in ongoing processes of remaking, re-inscribing or removing the boundaries of nature and culture. In turn, these nature-culture assemblages have the potential to expand the multiple possibilities for thinking about human and nonhuman relationships as we move into ever-uncertain futures.

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