Reading *meat*phors in DNA (and RNA): A bio-rhetorical view of genetic text metaphors

Erika Szymanski, Department of English, Colorado State University

Abstract: The ongoing digitization of biological life rests in part on the idea of genetic information being contained in genetic texts written in the four-letter language of DNA. Genetic text metaphors have been criticized for being inaccurate, misleading, and outdated. They are also inescapable, malleable, and remarkably generative for engineering biology. Yet problematic understandings of genetic texts as containing information do not inhere in the metaphor but rather depend on particular ways of understanding how texts work—in particular, texts as containing information as shaped by cybernetic redefinitions of information. The concept of *meat*phor, analogizing biomolecular relations to discursive relations described through metaphor, enables rethinking those metaphors through a bio-rhetorical approach. Doing so foregrounds how nucleic acids make meaningful relationships in context over how they contain deterministic or controlling information. That approach distinguishes between how human readers have tended make meanings with genetic texts and how molecules that interact with or "read" texts do so, opening up underexplored ways to think about those metaphors. Through this lens, *meat*phor becomes one strategy to attend to how diverse meanings may be made with genetic text metaphors themselves, with consequences for bioengineering and societal practices.

Keywords: synthetic biology, biotechnology, genetic engineering, rhetoric of biology, RNA

Introduction

The digital metaverse and its fleshy meatverse counterpart are imploding into each other, and have been for some time. Even as immersive virtual reality platforms fail to take off as anticipated by their backers, distinctions continue to blur between real and virtual, digital and fleshy, meta and meat. Twenty-first century humans are constantly co-constituted as data-objects through the mundane computational scaffolding that translates physical, biochemical operations into binary logic to be registered by FitBits, communicated across videocalls, or registered as a request for takeout. This is an ongoing project, of expressing the recursive systems that comprise living-as-fleshy-life as mathematical expressions about deviations from randomness to collapse big, endlessly varied material interactions into tidy, uniform, easily exchanged sets of numbers. And while genetic information is not (yet) ubiquitously associated with our always-online selves, the very idea of genetic *information* makes imagining it trivial to express in the same terms.

But there's a problem with that translation, beyond thoroughly justified concerns associated with privacy, social justice, ethical behavior, and corporate greed—a simultaneously biotechnical and semiotic problem. Genetic information ceased being good science even before it became widely commodified. Genetic information suggests that DNA instructs and describes biological entities. Yet the history of molecular genetics is a story of scientists progressively finding more complexity in that equation, in how bits of DNA come together with whole troupes of other molecules to participate in biological functions and characteristics of life.

In that context, engineering biology encompasses a funny peculiar tension: a computer-engineering mindset to designing and building with nucleic acids continues to conceptually and materially reproduce the reductionist idea of 'a gene for X.' This tension is evident in the tinkering necessary to make algorithmically designed genetic assemblies work in complex biological contexts, but also in wider societal applications of biotechnologies. Nonspecialists can simultaneously recognize the error of treating genomes as deterministic blueprints (Condit et al., 2001) while also employing direct-to-consumer genome sequencing to, at some level, reveal who—according to the biocentric views endorsed by the companies that sell that service—they really are.

Donna Haraway discusses the reductionist half of this situation as the fetishization of the genetic map, mistaking pictures of genes for dynamic living processes that cannot be captured in a snapshot at all (Haraway and Goodeve, 2018). The possibility of that error is enabled by an even more fundamental confusion between genetic information and genetic meaning-making, grounded—though, as I will argue, not inherent—in the genetic text metaphors that liken nucleic acids to language and that ubiquitously underpin molecular biology and its biotechnical offspring. While "genetic texts" could, in a much more general sense, describe scientific articles and other human-language texts written about genetics, I use this term exclusively in the specific technical sense employed widely across biology, to describe stretches of DNA or RNA sequences written in the "language" of DNA and RNA.

DNA (and RNA) are ubiquitously analogized to text, written in strings of A, T (or U, for RNA), C, and G. But bits of DNA (and RNA) are, of course, also physical molecules that interact with other physical molecules. The question is: how can entrenched genetic text metaphors account for and work with that fundamentally material, contextual complexity—and is that even possible? Inspired by the term *meat*verse to describe the physical, fleshy world now contrasted with its online, digital metaverse counterpart, I use *meat*phor to describe the fleshy, molecular counterpart to the metaphor. In doing so, I point to the possibility of rethinking genetic text metaphors through rhetorical concepts—a bio-rhetorical perspective—to account for dynamic meaning-making in context.

This argument stems from a feminist and posthumanist reading of reading. A central tenet of posthumanism is that a human is always more-than-human through their interdependence with diverse human and other-than-human, living and other-than-living others. This redescription necessitates rethinking human actions, such as reading and writing, as more-than-human actions. Donna Haraway (1991), Katie King (2010), and other feminist science studies theorists also characterize writing as a biotechnology through which discursive practices participate in worldbuilding, enacting phenomena as fundamentally relational. As I use it here, describing molecules interacting with genetic texts as 'molecular reading' is simultaneously a metaphor to human reading, a description of a biotechnical practice through which living things are written, and a gesture of respect to the arbitrariness of taking the conventionally bounded 'individual human' as the agential unit which reads.

I begin by reviewing how conventional interpretations of genetic text metaphors mark the influence of cybernetics in early molecular biology. I then explain how and why I am suggesting *meat*phor as a neologism and concept, and how my argument about the need to and possibility of reinterpreting genetic text metaphors through a bio-rhetorical lens builds on prior critiques of genetic text metaphors. I then introduce how a posthumanist rhetorical perspective reasserts the difference between information content and meaning-making in context that has become muddied in conventional uses of 'genetic information.' I exemplify how that difference matters for the particular case of trying to build an RNA chromosome, and how *meat*phor suggests an alternative approach to understanding that biotechnical problem, before briefly addressing how my suggestion of biorhetoric differs from biosemiotics. I conclude by contextualizing this particular case in the wider rationale for why attention to metaphor matters in bio-socio-technical context.

Analytical perspectives on genetic text metaphors

Cybernetic influences

Exploring how biological systems embed analogical reasoning is hardly new. Norbert Weiner initiated cybernetics by equating the problem of how organismal behavior is controlled with the problem of controlling machines. In doing so, he also laid groundwork for wide-ranging theories about how systems of all kinds can be productively conceptualized as information and communication (Kay, 2000; Klein, 2015). One of the freewheeling interdisciplinarians who built on that foundation, Gregory Bateson, characterized metaphors broadly as a recognition of similarity across difference, without constraining or specifying the medium in which such a relationship might play out (Bateson and Donaldson, 1991). Through that lens, the whole planet could be seen as a semiotic system held together by metaphor, or to use an alternative metaphor, an organism held together by recursive circuitry—a concept that gained traction in the form of James Lovelock's Gaia hypothesis. (As Zoe Todd (2016) points out, conceptualizing the whole planet as a living, breathing thing was not Lovelock's innovation and has a long history in Inuit and other Indigenous philosophies, though without the peculiarly computational inflection that it took in cybernetic discourses.)

While Gaia has remained a niche approach, another idea influenced by cybernetic thinking has become inseparable from the fabric (or textile, or *textus*) of molecular biology: the idea that nucleic acid messages carry biological information. The ubiquity of representing nucleic acid polymers as strings of letters, corresponding to proteins via a genetic code, has made thinking about DNA and RNA *without* thinking of them as texts virtually impossible. DNA and RNA texts became understood as information-containing molecules through the cybernetic redefinition of information as a quantifiable property of a message.

Lily Kay's (2000) *Who Wrote the Book of Life?* extensively traces the origins and early development of those metaphors, with particular attention to cybernetics and information theory as they developed in the early twentieth century. Cybernetics began with macro-scale analogies between computing systems and men, exemplified through cyborg military technologies such as missile targeting systems comprised of machines and the man who operated them. These new ways of thinking were easy to align with existing analogies of cells to factories, reconfiguring cells as command-and-control systems guided by a series of feedback loops. From the 1950s onward, information and communication language permeated molecular genetics discourse even as direct applications of information theory to 'cracking the genetic code' repeatedly failed (Kay, 2000). Genetic text and information metaphors nevertheless persisted and expanded, but became increasingly distant from their technical cybernetic definitions (Kay, 2000; see also Brandt, 2005; Keller, 2002).

Kay's historical analysis emphasizes genetic code metaphors' inaccuracy and even absurdity. As she frequently reminds, relationships between DNA, RNA, and protein are more precisely described as tables of correlations and are not technically codes at all. And, the path to those metaphors' ubiquity is lined with people calling them a bad idea. With similar derision, she outlines how genetic text metaphors are inaccurate because DNA and RNA lack many features of human languages. Her critique is excellent history, but from at least one possible rhetorical perspective, it misses the point about how metaphors function. Metaphors are never about accuracy or complete and perfect alignments between the domains they connect. They are always imperfect, incomplete, and imprecise—generative precisely in their imprecision and ambiguity, such that they can *carry* multiple interpretations (Haraway and Goodeve, 2018). The relevant question, at least with respect to whether a metaphor is a good metaphor, is whether the conceptual links that it constitutes are useful for doing things.

Just because genetic text metaphors are popular does not necessarily mean that they do good work. However, as these metaphors have proliferated, they have in their myriad forms underwritten an impressive array of developments in molecular biology and biotechnology. Molecular biologists routinely work with DNA and RNA principally as strings of letters, from DNA sequencing machines to so-called gene-editing techniques such as CRISPR. For many, we could say that the genetic code has ceased to be a metaphor altogether in the sense that it now embeds ontological reasoning rather than analogical reasoning. DNA and RNA are understood to veritably *be* codes rather than to be *like* codes.[i] Indeed, the Oxford English Dictionary catalogues the genetic code as one of the primary meanings of the word 'code.' Genes and genomes are read and written and edited, decoded and recoded, refactored and debugged. Correct or useful or not, those metaphors are tightly woven into the fabrics of biotechnology.

Interpretive flexibility

Genetic text metaphors are unquestionably generative, productive, and tenacious. Yet at least in part because of their cybernetic roots, genetic text metaphors have embedded particular ideas about texts that facilitate unhelpful and damaging societal applications, in addition to technical hiccups in employing them in molecular genetics. Many scholars have described how the idea that genetic texts *contain* information has underpinned technically unsupportable and socially problematic ideas about genetic determinism, including the explicit or tacit assumption that genes determine identity—a biologically insupportable view that has been mobilized to uphold White Nationalism (Panofsky and

Donovan, 2019) and other forms of extreme prejudice (e.g. Anaya-Muñoz, García-Deister, and Edna Súarez-Díaz, 2017; Tallbear, 2013). Associating bits of genetic text with functions or individual characteristics also participates in the commodification of personal data across the metaverse, wherein textual descriptors of embodied characteristics are extracted from their wider context, bought and sold, and then taken to represent an individual—fetishizing the person as a biotechnical picture compiled from digital snapshots of contextually responsive living processes.

Even as digital information continues to accumulate social significance, the deep legacy of hierarchical command-and-control frames in molecular biology is slowly being unwound and rethought. Systems biology is indicating how populations of molecules participate in multidirectional networks. Epigenetics is revising the former dogma that DNA transfers information to RNA and RNA to protein with no looking back in the other direction. Investigations into the non-coding DNA formerly known as 'junk' are challenging the established belief that only differences in protein-encoding genes matter to an organism's behavior or evolution. These are just a few among many examples of how conceptualizing DNA in terms of information-containing genes that *determine* anything is wildly outdated in molecular biology. Yet genetic text metaphors, understood through cybernetic framing, have nevertheless contributed to stabilizing that operating principle in both disciplinary and popular imaginations.

Rhetorical perspectives

Cybernetics and information theory, however, are far from the only way to make sense of texts. From a contemporary rhetorical perspective—concerned with strategic communication, or what texts *do* rather than with their structure as such—texts do not contain information, and information is not a property of a message or molecule or any other thing. That principle is easily demonstrated with polysemic phrases such as 'the bat flew out the window' (has an airborne mammal left the room, or did someone have a baseball-related accident?), 'hit me' (do I want you to strike me with your fist, call me about a future get-together, or deal me another card?), and 'I'd love to come' (am I pleading for an invitation, enthusiastically accepting one, politely acquiescing to something I feel obliged to do, or softening the blow of ‘but I can’t’?). Rather, texts participate in meaning-making through reader-text relationships in particular contexts, through which readers are informed by those texts, and through which texts as living documents are informed or shaped by readers (Fish 1990). Indeed, the roles of text and reader are themselves constituted in their interaction; their material configuration, coming together in a particular moment through environmental constraints on what relative shapes are possible or probable, constitutes the reading (see, e.g., King, 2010).

In that light, determinism is not inherent in genetic text metaphors but is a function of a particular way of employing those metaphors. This distinction is essential. Reversing or replacing genetic text metaphors is both improbable and unproductive. Reinterpreting, extending, or building on them to do new things is a different matter, as demonstrated by repeated shifts in what ‘code’ has been taken to signify.

Keller, Nerlich, Oyama, and others have also suggested alternative metaphors or frameworks to foreground complexity and function. None has ushered in a new era of biological paradigms, nor, I am certain, is any suggestion I might make. In advocating for a bio-rhetorical perspective on genetic texts, I aim to follow the example that Evelyn Fox Keller set in advocating that the fraught noun ‘gene’ might be productively reclaimed as a verb ‘to develop a lexicon more suited to the dynamic interactivity of living systems to which current research in systems biology introduces us’ (2017a, 373). Responding to criticism that a new paradigm might yield a biology irreconcilable with the established form of molecular biology, Keller replied that her goal was not to replace or subsume ‘old agendas,’ but to ‘encourage the development of new agendas,’ particularly because ‘multiple agendas have always coexisted in biology (as in many other fields)’ (2017b, 418). To the extent that genetic text metaphors remain ubiquitous, multiple strategies for interpreting them might similarly enable conceptual innovation.

I suggest *meat*phors, and bio-rhetoric more broadly, as tools to encourage a perspective on ‘writing’ or ‘editing’ genetic texts oriented to how DNA and RNA are meaningful in a relational sense, rather than containing information—instructions or blueprints for cells—in a discrete sense. To make that distinction, I need to briefly review how information took on a new set of meanings in information theory.

Information content versus informative relationships

Information, prior to the early twentieth century and excepting a few highly specialized legal usages, indicated a relationship between someone or something who had knowledge and someone or something to whom or to which that knowledge was imparted. Vilem Flusser (2011) (a journalist, philosopher, and media scholar) links the idea of imparting knowledge through imparting form—of in-forming—to early inscription technologies through which texts were in-scribed into hard rock or soft wet clay. Messages were in-formed by their authors and information was inseparable from physical form (see also Hayles, 1999). But in the first few decades of the twentieth century, information theorists began using 'information' in a categorically different way—to indicate a property of a thing 'divorced from any concept of news or meaning,' not the property of a relationship (OED).

This usage was apt for solving such problems as constructing efficient telephone networks that preserved intelligibility while maximizing the volume of signal they could carry (Klein, 2015; Nerlich, 2020). As Claude Shannon and Norbert Wiener famously defined it for such purposes, information became a mathematical quantity related to entropy that indicates how unlikely a message is to occur by random chance, completely independent of what (if anything) the information means to a sender or receiver. Information was a signal to be distinguished from noise. Wiener and Shannon disagreed on precisely how information related to entropy. Nevertheless, between their individually impressive dissemination efforts, their generally shared concept became widely known and wildly popular for devising new approaches to diverse problems that would not previously have been imagined as 'information' problems—molecular genetics among them.

When Watson and Crick's seminal 1953 publication on the double-helix structure of DNA established what portions of the molecule were important to its protein-encoding function, it did so in informational terms: ‘the precise sequence of the bases is the code that carries the genetical information’ (737). Genetic messages, they suggested, depended on the variable nucleobase portion of ribonucleic acids, represented as A(denine), T(hymine, or U for uracil in RNA), C(ytosine), and G(uanine); the relatively invariant sugar-phosphate portion of the molecule appeared to merely hold the bases together. Left unanswered was how that four-letter alphabet specified a corresponding sequence of amino acids. Deciphering the genetic code—a phrase which does not appear in Watson and Crick’s publication but which was emerging among the relevant community of scientists at the time—became the pressing biological problem of the rest of the 1950s (Kay, 2000).

According to Kay (2000), Michael Morange (2020), and other historians of biology, scientists attempted to ‘crack the code’ in two broadly distinct ways. Information theorists saw it as a math problem and went about calculating how an adequate quantity of non-randomness—to unambiguously but economically specify all twenty standard amino acids—could be contained in a four-letter alphabet. They then tried to solve the corresponding logic problem, eventually applying the day’s most advanced computer-aided cryptographic analyses to deciphering the handful of known sequences. Meanwhile, biochemists saw the code as an empirical problem to be resolved by experimenting with nucleic acids in the lab.

The information theorists generated plenty of mathematically plausible combinations, but none that were problem-free or empirically supported. Decoding algorithms arrived at no solutions when handed amino acid sequences. But in 1961, J. Heinrich Matthaei and Marshall Nirenberg, biologists using an experimental system developed by the Harvard biochemist Paul Zamecnik, identified that an RNA molecule consisting entirely of U(racil) led to the production of a peptide consisting entirely of the amino acid phenylalanine (Morange, 2020). Experimenting with other repeating nucleic acid sequences eventually enabled matching the remaining 19 common amino acids to their three-base-pair codons, completing a table that has been part of biology’s canon ever since.

Information theorists could calculate the information *content* of a DNA molecule, but that quantity was unhelpful for understanding biological function. As has now been very thoroughly demonstrated, the degree to which a string of As, Ts, Cs, and Gs statistically deviates from randomness is irrelevant to the shape or function of the protein it encodes. And as Kay (2000), Keller (2002), and others detail, that demonstration did nothing to interrupt the application of information discourse in biology. Instead, the idea of biological information became increasingly untethered and distant from information as a technical cybernetic concept. It nevertheless retained some elements of its cybernetic framing, at least in part by way of structural linguistic perspectives on cybernetic text metaphors.

Structural linguistics was itself informed by cybernetic conceptualizations of communication as hierarchical, linear processes of information transmission, as Roman Jakobsen's participation in conversations about genetics in cybernetically informed linguistic terms underlines (Brandt, 2005; Nerlich, 2020). Since then, David B. Searls and others have applied structural linguistic methods to genetics to develop what Searls calls 'nucleic acid linguistics,' including applying Chomsky's formal hierarchical grammar to predict physical nucleic acid structures through 'a grammar of genes' (Searls, 1992, 1997, 2002). Even if nucleic acid linguistics sounds niche, these ways of thinking have become embedded in how molecular genetics gets done, in how algorithms are applied to parsing DNA and RNA sequences and in searching for grammar-like 'features' by lining up bits of genetic text and asking what they have in common (e.g. Cai et al, 2009; Collado-Vides, 1991; Hie et al, 2021). Algorithms built for parsing language are routinely used to parse nucleic acid polymers. Quantitative semantics, for example, has been applied to identify 'mutations that will change the semantics of [a] virus while maintaining its grammaticality so that the virus will remain infectious but escape the immune system' (Kim and Przytycka, 2021, 233).

Biology as an information science and an in-forming science

Biology is now routinely described as an information science, its information-theory framing taken for granted. The chapter on 'DNA and chromosomes' in my copy of the canonical textbook

Molecular Biology of the Cell, for example, begins: ‘Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism…These instructions are stored within every living cell as its genes, the information-containing elements that determine the characteristics of a species as a whole and of the individuals within it’ (Alberts et al, 2002, 191; see also Hester, 2020).

Yet two characterizations of information, one cybernetic and one relational, continue to characterize the field, underpinning ambiguities about DNA function with consequences for contemporary genetics as technical practice and social phenomenon. The knowledge my biology textbook relates has been built experimentally, through investigating how molecules bump into other molecules—how, in Flusser’s terms, they *in-form* one another. Simultaneously, even as systems approaches indicate that biological phenomena come about through bumping, in-formational, multidirectional interactions among populations of molecules or cells, much of the knowledge that results from those experiments is described in terms of one molecule (or other biological entity) controlling or determining another (Davies, 2014; Keller, 2005).

An analogous tension troubles synthetic biology, where genes and other segments of DNA are routinely manipulated as though they ‘have’ functions. The computational tools widely employed for DNA design associate genetic parts or ‘words’ with a discrete function, independent of how they interact with their surrounds, operationalizing a tacit assumption that words contain information (Szymanski and Scher, 2019). As biologists ask how and why context matters, they are finding that whether and how a bit of DNA is expressed—transcribed into an RNA molecule that might then be translated into a protein—is a function of its genetic ‘neighborhood’ (Brooks et al, 2022) and its larger physical landscape (Johnstone and Galloway, 2022). In practice, achieving a functional genetic assembly—one that reliably performs its theoretically predicted function in a living cell or other biological context—requires making context-sensitive adjustments beyond the predictions of context-insensitive algorithmic tools. Such slow tinkering has become a major bottleneck for a set of technologies to which many promises involving acceleration have been attached.

The challenges of rewriting RNA texts

I have come to think about the challenges of genetic text metaphors as a social scientist involved in the nascent field of RNA synthetic biology, wherein my collaborators aim to construct novel RNA chromosomes for yeast and bacteria. This aim presents myriad methodological challenges. Scientists must build RNA through DNA as an intermediate, because synthetic biology tools are built for DNA, and because yeast and bacteria (like all creatures other than a subset of viruses) have DNA-based genomes. But DNA cannot simply be translated into equivalent RNA, because RNA forms shapes that DNA does not.

The genetic text metaphors that enable DNA-based synthetic biology are very likely inadequate for RNA-based synthetic biology, and so I was enrolled in this project as a science and technology studies researcher who studies metaphors. My analysis of what other metaphors we might imagine is informed by having interviewed students and post-doctoral researchers, participated in team meetings, read about varied RNA biotechnologies, and analyzed metaphors in relevant peer-reviewed publications. I also draw on my prior studies of DNA-based synthetic biology.

In contrast to philosophical and historical attention to the inaccuracies of genetic text metaphors (e.g. Hedgecoe, 1999; Kay, 2000), my analysis build on scholarly attention to these metaphors as practical tools (e.g. Brandt, 2005). In particular, it shares some common ground with Susan Oyama's (2000) suggestion that the "information gene" be replaced by 'constructivist interactionism,' and Evelyn Fox Keller's call for replacing the 'gene' with concepts that describe how biological development and function rely on multidirectional molecular networks (Keller 2000, 2014, 2020). Oyama and Keller chiefly investigated developmental and evolutionary biology, addressing inconsistencies in the nature/nurture debate and what counts as a biological explanation, toward offering improved paradigms. My goals are smaller—in line with Keller's (2020) suggestion that making more nuanced sense of biology calls for multiple ways of thinking that nevertheless cohere. My argument is also oriented toward future efforts to construct biological systems more than past efforts to describe them, and arises in a different historical moment.

Twenty or so years after Oyama's and Keller's seminal contributions were published, molecular genetics has expanded along the more complexly networked paths they heralded. Simultaneously, engineering-modeled biotechnologies have embedded more linearly deterministic ideas about genetics that recall an era of linking individual genes to individual phenotypes, associating discrete bits of DNA with discrete functions. Those operating assumptions have enabled substantial achievements in constructing customized cells to produce valuable molecules or exhibit other useful behaviors. They are also increasingly inadequate for increasingly ambitious projects, in which assembling bits of DNA like Lego bricks, equating modular structures to modular functions, no longer brings scientists close enough to their bio-design goals that they can tinker the rest of their way to a successful genetic construct (Frow and Calvert, 2013).

Reading *meat*phors in genetic texts

Metaphor is the recognition of similarity across difference (Ricoeur, 1997; Bateson and Donaldson, 1991). Analogizing molecular interactions to discursive interactions—that is, using metaphor as a metaphor—a *meat*phor is the recognition of similarly but differently shaped biological molecules, whose interactions on the basis of that similarity-across-difference participate in processes that constitute life. As a unit of analysis, *meat*phor points to how the meaning of molecules for biological processes is constituted in interaction—an analytical term for an empirical phenomenon.

*Meat*phor *could* be employed to discuss 'the meat of metaphor' (Haraway and Goodeve, 2018), the physical embodiment of conceptual analogies, through which metaphors participate in the iterative reconstruction of material relations. That is not the usage I want to develop here. Instead of metaphors *becoming* meat, I want to analogize material or *meat*erial interactions—not just among biomolecules, but among biomolecules as they participate in life-as-process—to the semiotic interactions described as metaphor. In particular, I want to emphasize how a cybernetic interpretation of genetic texts (stretches of DNA or RNA sequences) has supported one dominant way of reading those texts among a wider set of possibilities. Ultimately, the confusion between information and meaning embedded in that dominant reading has technical consequences for manipulating nucleic acids as well as societal consequences for manipulating metaversical information associated with humans and other biotechnical things.

My point in introducing *meat*phor is two-fold. I am making a serious joke about entrenched interpretations of genetic text metaphors for the sake of revitalizing those 'dead' metaphors and opening them back up for doing differently, to expand on what they can carry. The other is to exemplify one mode of rethinking them—a bio-rhetorical approach—as a suggestion that may be useful in conjunction with other alternatives for working with DNA (and RNA) in more multiple and resilient terms. For ease of readers' meaning-making in *this* context, I partially italicize *meat*phor, not to emphasize *meat*, but to emphasize that *meat*phor is not an inadvertent misspelling of its familiar cousin.

A bio-rhetorical approach to understanding RNA texts

Structural linguistics has been a prominent part of the conceptual history of nucleic acids. But texts can be understood in other ways. Keller (2014) has argued that molecular biology has—for decades now—needed to shift its focus to what genetic texts *do*, rather than what they *are*. So has Brigitte Nerlich (2020), who writes that 'as a consequence of side-lining the more complex, processual and dynamic aspects of cybernetics as a source for metaphors, scientists and lay people are trapped in a set of metaphors, and thus ways of thinking, which highlight the description of what DNA, genes or genomes *are*, or are supposed to be (a code, a book, a machine) rather than what they *do*' (312). Nerlich's critique also often applies to social scientific and humanistic analyses.

I suggest a bio-rhetorical approach as a strategy for attending to genetic *doing* because rhetoric reframes genetic texts as fundamentally relational, significant not because of what they *are* but because of how they in-form one another. The foundations of rhetoric, as the study and practice of strategic language use, are in how texts do things in context. Metaphor, a fundamental rhetorical device (even *the* fundamental rhetorical device, in Bateson's analysis; Bateson and Donaldson 1991), describes how discursive links constitute the meaning of things through their relation as alike, but still different. Thinking of nucleic acid polymers in bio-rhetorical terms therefore has consequences for how DNA and RNA are understood, investigated, and constructed, all grounded in the difference between theorizing texts as containing information versus texts as in-forming—making meaning through relationships.

'Meaning' has become a dirty word in some biology conversations. The idea that biological entities—genetic texts, cells, organisms—have meaning has become associated with a flavor of teleological reasoning to the effect that biological phenomena were designed (by something, someone, or some One) for specific purposes. The troublesome word, for my purposes, is 'have," as for post-structuralist rhetoricians, texts do not have or contain meaning; discursive meaning is always relational and often context-dependent.

Molecular biological meaning is likewise fundamentally relational because what a molecule does is a function of how it interacts with other molecules. We could say that an RNA-dependent RNA polymerase *reads* an RNA molecule, and that the meaning or function of that RNA molecule is made between the RNA text and its polymerase reader, in the context of an environment (temperature, pH, the presence of other molecules, and so on) that encourages those molecules to make particular similar-but-different shapes. Thinking rhetorically about the meaning of genetic texts makes it possible to distinguish information, as a description of a molecule's structural characteristics, from meaning, as a description of a molecule's function, and to characterize the latter in terms of the context in which messages are read and who or what is doing the reading. Thinking about genetic texts rhetorically brings context back, explicitly, into the textual picture.

If DNA and RNA are understood to contain information, then understanding how they work requires looking for patterns in nucleic acid-polymer texts. If DNA and RNA make meaning in context, with their readers, then understanding how they work requires looking for patterns in how one molecule interacts with another molecule. For protein-coding DNA, these two approaches may be very similar in many instances; not only is DNA is typically found in only one broad context in a given cell (as that cell's genome), but protein-coding DNA is 'read' in the same relatively stable set of ways by the same relatively limited spectrum of molecules. The same is less true for so-called non-coding DNA that does not directly encode proteins but may participate in regulatory functions with an array of molecular partners. It is not true at all for RNA, a category of molecule that occupies diverse roles around the cell related to its sequence, higher-order structure, or both.

Building RNA chromosomes and appreciating the readers' perspective

Trying to build an RNA chromosome for *S. cerevisiae*, as my collaborators aimed to do as part of developing tools for RNA synthetic biology, provides an example of how informational versus relational approaches may differ. The most expedient way to make an RNA yeast chromosome is first to replicate a gene from yeast's ordinary DNA genome as an RNA molecule with an equivalent sequence, then insert that bit of RNA into the genome of an RNA-based virus. Helpfully, two RNA-based viruses routinely infect *S. cerevisiae* with, as far as anyone knows, no detrimental effects on the yeast. Even better, those viral genomes encode only one gene, the RNA-dependent RNA polymerase responsible for copying themselves.

Being so small and uncrowded, converting those viral genomes into a mini yeast chromosome by adding a yeast gene should be simple. In practice, that hasn't been the case. Pasting the new coding sequence into any of the promising locations on either side of the polymerase gene changes the RNA molecule's three-dimensional structure in ways that disrupt how it interacts with the polymerase enzyme. The resulting shape change prevents the polymerase from copying the augmented genome, and thus obviates the whole point of the exercise. Scientists have no trouble designing an RNA molecule with the appropriate sequence information to replace the role of a DNA gene in encoding a particular protein, but lots of trouble with sustaining a functional relationship to the polymerase while doing so, even though they know which part of the genome initially binds the polymerase. Changing the surrounding context for the polymerase recognition sequence changes its shape and therefore how it relates to its reader.

RNA sequence and RNA shape are not simply equivalent. Viruses with RNA genomes—including these benign yeast viruses and the SARS CoV-2 coronavirus at the center of the COVID-19 pandemic—demonstrate how varied sequences may sustain the same kind of functional, three-dimensional relationship. These viruses mutate easily (Domingo et al, 2021). While not every mutated genome is functional, a viral genome sequence can vary in many respects without disrupting the ability of the enzyme responsible for copying the genome to recognize (that is, appropriately interact with) and catalyze its replication.

We could say that these viruses try out answers to the question 'does this shape work for sustaining replication?' across a large design space. As synthetic biologists now ask similar questions in designing RNA molecules for specific purposes, they are finding that they cannot predict from RNA sequence alone which features of the molecule are essential for its function, or whether or not a redesigned molecule will be functional. Sequence variability complicates text-focused searches for patterns that can be definitively associated with functional replication. Scientists need tools about how RNA molecules form *relationships* that do not yet exist.

I am not suggesting that the problem is simply that scientists are not thinking about RNA shape (they are), but that the available tools for understanding, documenting, and manipulating nucleic acids—including metaphors and tools built on and through metaphors—have not *prioritized* shape. Structural molecular relationships are notoriously difficult to visualize and predict. AlphaFold2, a neural network-based method developed by Google's Deep Mind team and published in 2021, became a landmark breakthrough—not just in protein-folding, but in machine learning broadly—for its success in confidently predicting the three-dimensional structure of about sixty percent of proteins in the human proteome from sequence information (Tunyasuvunakool et al, 2021). Significantly, while a massive improvement over previous tools, AlphaFold2 can still only provide *a* structure for a protein with a given amino acid sequence; it cannot predict how proteins take on different shapes in the presence of other molecules. It also fails to predict structures for ‘intrinsically disordered’ proteins that only take on defined shapes when they interact with other molecules, which may describe a third or more of human proteins (Eisenstein, 2021).

AlphaFold2 was developed on the back of a large training set of proteins whose three-dimensional structures have been determined experimentally, and an even larger set of proteins whose structures have been confidently inferred on the basis of similarities to those empirically determined proteins. Protein structures have warranted that laborious experimental treatment—and the labor of devising algorithms to make those experiments less necessary—because three-dimensional structure is understood as the key to understanding their function. DNA and RNA, like all other biological molecules, also function through three-dimensional interactions with other molecules. RNA, however, has long understood primarily as messenger for DNA, an intermediate and less durable kind of text.

RNA is now recognized to carry out an impressive variety of enzymatic and regulatory functions around the cell, so that RNA molecules are like DNA in some ways and like proteins in others. However, humans primarily read RNA through scientific tools, grounded in the messenger analogy, that rely on unfolding molecules so that they can be read as straight lines of letters. On the basis of calculating minimum free energies for those strings of nucleotides, RNA structural prediction tools can suggest how those strings form two-dimensional structures. But scientists lack reliable tools for using sequences to predict the three-dimensional structures that RNA molecules form in cells, and on which their interactions with other molecules and therefore their functions depend.

Resolving individual RNA structures remains incredibly laborious and uncertain (Kappel et al, 2020). Consequently, researchers who need to identify those structures—to identify whether disrupting genome folding might be helpful in therapies against COVID-19, for example (Huston et al, 2021), or to avoid disrupting genome folding while trying to engineer a synthetic chromosome—face two challenges. One: a lack of technological infrastructure for imagining RNA molecules in three dimensions. Two: a lack of conceptual infrastructure for imagining RNA structures as essential to biological function (Keeley, 2020).

Understanding a text requires understanding how its readers will understand it. So, while a bio-rhetorical approach begins with a shift from information-content to meaning-making in context, it ends with a second shift, from humans as audiences to molecules as audiences for genetic texts. Tools for making sense of DNA and RNA are largely predicated on humans as readers, instead of the molecules that interact with or "read" them in the cell. For both DNA and RNA, one-dimensional sequence is described as 'primary' and three-dimensional structure as 'secondary' (and, for larger, multipart molecules 'tertiary' or 'quaternary') structure. The priority given to sequence reflects how *humans* have learned to read nucleic acid polymers. Other molecules read the same polymers as shapes, such that structure is primary and sequence is secondary. In other words, what matters to genetic texts' biological function, or meaning in context, is not what a molecule is, but how a molecule participates in a *meat*phor—a meaning-making connection between two molecules. Thinking bio-rhetorically foregrounds how human and molecular audiences read differently.

Meat*phors*

*Meat*phors have become my response to the twin frustrations of genetic text metaphors for engineering biology and for building equitable societies, extending the work that metaphors do in human languages to suggest a rhetorical approach to the metaphorical language of nucleic acids. Metaphors, as rhetorical meaning-making devices, embed and reproduce context; they carry bits of context with them. Employing a metaphor does not locate something on one discursive point; it maps discursive entities with respect to each other. Metaphors constitute respective conceptual locations, connecting things that are related but separate when seen from a particular vantage, and so creating webs of meaning.[ii] Metaphors thus act bidirectionally, not only constituting the target domain in terms of its likeness to the source domain, but also influencing how the source domain is understood through its association with the target. They are also about the shape of the relation in ways that exceed and are not entirely described by the two things being connected, so that they are more than the sum of their parts—important, given the parts-based orientation of synthetic biology and molecular biology in general (Keller, 2005).

*Meat*phors, metaphorically, map biological entities—a bit of DNA or RNA, protein, cell, creature, community of creatures—by identifying what they do with respect to one another, generating biological webs of interaction. A *meat*phor, constituted in the relation between one biological thing and another—such as the functional shape made between an RNA chromosome and its polymerase—is a description of meaning-making in a context that is itself part of the relation.

Thinking about genetic texts in rhetorical, *meat*phorical terms constructs a different vision of a biological system, and a different approach to engineering them, than does thinking about them in terms of formal grammars. Formal grammars suggest that skillfully learning to compose DNA and RNA requires learning how to read the language of biological texts; *meat*phors suggest that composing DNA and RNA requires learning to recognize and intervene in the shape of interactions in particular contexts. The former has oriented scientific investigation around sequencing nucleic acid polymers, lining them up, and making sense of them on the basis of patterns in those sequences. The latter might instead focus attention on learning to see congruence across webs of connection. For RNA, that might begin with building tools to identify how three-dimensional structures shape up in the presence of partnering molecules. For DNA, the difference becomes more relevant as genomes are 'experimentally reappraised' as complexly organized physical objects in a post-genome sequencing era (Meloni, 2018; see also Barnes and Dupré, 2009)—as bioengineers both move DNA into new contexts and realize that their ordinary biological contexts were perhaps not always so uniform as had previously been imagined.

Thinking about texts as making meaning through relationships in context, rather than as containing information, also leads to different ways of thinking about how and why DNA and RNA matter *outside* of cells. A bio-rhetorical view suggests that genetic texts do not, on their own, contain information about human individuals or other living things. Beyond genetic determinism, for example, bio-rhetoric suggests that the possession of a string of letters that represents a hazardous virus is not itself dangerous, but rather the *meat*phor in which that sequence may participate—between the string of letters, a human reader who knows what to do with it, and the biological and technical infrastructure that enables making dangerous meaning with it (Hester, 2020). This view also suggests that genetic text-based biotechnology is about learning to work strategically with those texts in context, with attention to the audiences that matter most, not achieving mastery and control over them.

Earlier, I quoted Brigitte Nerlich about how molecular geneticists have elided ways of thinking that might foreground processes and relationships. That quote continues:

> As a consequence of side-lining the more complex, processual and dynamic aspects of cybernetics as a source for metaphors, scientists and lay people are trapped in a set of metaphors, and thus ways of thinking, which highlight the description of what DNA, genes or genomes *are*, or are supposed to be (a code, a book, a machine) rather than what they *do*. These metaphors also pervade speculations about what scientists, having achieved mastery over genes or genomes, are supposed to be able to do with genes and genomes (to code, to read, to edit, to write, to engineer). This overemphasizes the influence of genes on what makes us human and the supposed control that scientists have over genes. (Nerlich, 2020, 312-13; see also Balmer and Herreman, 2009)

Genetic code and text metaphors have often been criticized for producing the impression that scientists know more about and have more control over DNA, genes, and life than they really do. As they have typically been employed, they also facilitate commodifying genetic information (Calvert, 2007, 2008) and feed metaverse-enabled regimes of disaggregating consumers or citizens into bits of institutionally relevant data to regulate and manipulate behavior. If information is understood to be contained in molecules, the scientific question is how to design a good molecule that contains the right information, before fitting it into a system comprised of similarly designed unit parts. If molecules make meaning through relationships, the cognate question is how to design a good relationship within a system comprised of many relationships—a question that extends far beyond the membrane encompassing a cell.

In *Ghost Stories for Darwin*, Banu Subramanian (2014) traces how contemporary genetics is rooted in eugenics, with eugenics' reprehensible values embedded in now-unseen ways in how fundamental concepts such as diversity are employed. One response to that history has to be to keep talking about it, acknowledging where the field has come from. Another has to be doing things differently, including rethinking established epistemic tools so that using them does not continue reproducing the same unconscionable dynamics. Language choices—and they are choices, even if materially and societally constrained ones—embed values, and coproduce scientific knowledge and political relations.

Why bio-rhetoric is not biosemiotics

Finally, I need to distinguish between what I am calling bio-rhetoric and the established, if small domain of biosemiotics. Early proponents of what would become biosemiotic ideas, particularly Charles Saunders Pierce and Jakob von Uexküll, are still read and cited for their expansive constitution of sign systems. But the core biosemiotic proposition, that semiosis is an emergent property and the central organizing principle of all living systems, has failed to gain traction save among a small and insular group of adherents. That is no doubt at least in part because (unlike some other analogies of biology to language) it has not been especially useful for scaffolding biology experiments.

Among other things, a trouble with biosemiotics is that it aims at building a universalizing science of absolutes largely on the basis of abductive reasoning or inference to the best explanation. By relying on apparent similarities rather than experimental or direct observational evidence for support, abductive biosemiotics tends to confuse hypotheses about what *may* be true with propositions about what *is* true. Biosemiotics has been out to make big statements about what things are, and to set up semiotics as the ultimate underlying explanatory structure for the natural world. In suggesting the utility of a bio-rhetoric, I am instead out to explore how things can be understood and to make little statements about the potential utility of thinking in particular ways about the infrastructure that scientists have built for studying DNA and RNA and the societal infrastructures built around genetic information—without suggesting that DNA and RNA are themselves languages, at least in any conventional human sense.

I need to make this distinction because the biosemiotician Wendy Wheeler (2010) argues for the application of metaphors to biological systems on the basis of the 'fundamental reality of metaphor,' observing that an organism responding to its environment interprets or 'carries over' the meaning of signs from its outer world/environment to its inner world/physiology. In Wheeler's (2010) words, 'what humans describe as "metaphor" (and believe is something which only pertains to human speech and mind and, in essence, is "not real") is, in fact, fundamental to all semiotic and biosemiotics sign processes in all living things' (277). Where Wheeler argues that metaphor is a unifying principle of a fundamentally semiotic world, I suggest drawing on metaphor as an exploratory tool.

I am also very much not trying to suggest that DNA and RNA are like human languages in every way but, rather, that the analogy is useful for specific purposes—and is, in any case, inescapably embedded in scientific tools. All the same, bio-rhetoric is inclined to kick up at least one other objection related to how the analogy does not hold, about authorship. The classic rhetorical triangle, stemming from Aristotle and introduced to many North American university students in their first-year composition course, has author, audience, and text (or speaker, audience, and message) at its vertices. From a human-centric perspective, nucleic acid messages have no authors and suggesting otherwise is intensely problematic (Kay, 2000). The thing is that when seen simultaneously as texts and as molecules read by other molecules, genetic messages *do* have authors. Those authors are not merely DNA or RNA polymerases but—seen from a systems perspective—a whole network of interacting molecules. Moreover, authorship is a tool for explaining how texts are produced. We do not need that explanation to make sense of how genetic texts function, and the same metaphors may not be apt for both tasks. The value of a metaphor, after all, is in how the domains being analogized are alike in some ways but different in others.

The title of Kay's (2000) book, *Who Wrote the Book of Life?*, addresses a question about DNA authorship, albeit in terms of collections of whole genomes or 'the book of life.' She compares three possible responses: 'objectivist, constructivist, and deconstructivist' (xvii). The objectivist response is that 'Nature' is the author. The constructivist response is that 'scientists themselves' construct DNA as 'molecular writing' in studying it as such. The deconstructivist response she provides is that complex heterogenous networks construct DNA as writing, not merely scientists acting with an individual agency that humans alone possess, such that as elements of that pattern accrete over time. 'it is the writing itself that writes' (xviii). These are useful responses to filling out the rhetorical triangle in which scientists or other humans sit at the vertex labeled 'audience.' They also emphasize just how distant the human and molecular reading contexts can be, particularly with respect to expressions such as 'book of life' that are useful as narrative imagery more than as practical tools for doing biology.

Conclusion

The prevailing interpretation of genetic text metaphors are grounded in cybernetics and its redefinition of information as a property of a thing, rather than a property of a relationship as had previously been common. That former interpretation continues to prevail even as ongoing technical and social developments indicate a need for a very different kind of systems (and political) thinking, emphasizing context and networks over one biological bit of information merely determining anything—within cells and across society. But ethical and epistemic problematics attached to particular ways of interpreting and employing genetic text metaphors do not inhere in the metaphor any more than information inheres in texts. Metaphors are built to carry flexible loads; they are constructed and reconstructed in practice, not fixed entities. Genetic text metaphors in particular invite carrying over the myriad conceptual resources brought to bear on human-language (and other) texts to the worldbuilding exercises of designing and building with nucleic acids.

The answer to the question, 'how can entrenched genetic text metaphors account for and work with that fundamentally material, contextual complexity—is that even possible?' should explore diverse ways of understanding texts upon which molecular biology has not typically drawn. Genetic text metaphors are far too tightly woven into biology to be replaced, but they can and should be reinterpreted as the work their users need them to do changes. Thinking through contemporary rhetoric of science theory, seeing metaphors as a reinterpretable resource, part of scientific toolkits and not either incidental or inevitable, invites experimenting with what else they can carry. Here, I have suggested one experiment, building on prior STS attention to molecular biology that yielded calls for new metaphors and approaches that make room for context and relationality—against now-outdated (but often invisible) discursive tools that essentialize bits of biology.

The bio-rhetorical approach, drawing on poststructuralist rhetorical and feminist STS scholarship as well as my observations in RNA synthetic biology, suggest that the biological relevance of genetic texts lies in how they participate in meaning-making relations among their readers and contexts. Through this lens, analogizing biology to language by employing metaphor as a metaphor, biological systems can be understood as held together by *meat*phors—recognitions of similarity across difference among biological molecules that build meaning-making webs of biological relationships.

Fundamentally, my point is a common one in STS: that the problem is not the tool, nor that the tool is subject to both beneficial (within science) and nefarious (popular press) purposes, but rather how the tool is used. Metaphors are tools through which humans make sense of and iteratively reconstruct the world. Choices about how to use them embed values about what kinds of work we should be doing or want to be doing—in this case, about what engineering biology should be and about what kinds of relationships bioengineers should construct with biological systems. Rather than demonizing the tool or arguing that it should be replaced or rejected, as has sometimes been advocated in historical and philosophical studies, science studies researchers should work with bioengineers to explore how genetic metaphors may be rethought to do additional kinds of work: first, to make choices about how to use them visible *as choices*, where the status quo might otherwise be seen as inevitable; and second, to try out strategies that might be more apt for the work that people are presently trying to do in and around bioengineering.

Acknowledgements

I am grateful to the members of the 'Rules of Life with an RNA Genome' project for discussing their work with me, to the other RNA biologists and synthetic biologists who have spoken with me about their work, and to cookie egret and Marie Turner for their help in exploring metaphors applied to RNA. This work was supported by the National Science Foundation (awards #1935361 and #2042475).

---

[i] Lakoff and Johnson's characterization of metaphor relies on a distinction between what a word "actually" means and applications of that word outside its "real" meaning. This is a practical limitation. Because the "actual" meaning of a word shifts across time and discourse communities so that a usage may be metaphorical in one location and literal in another, analyzing metaphor through Lakoff and Johnson's lens in interdisciplinary context, or in other situations in which discourse communities meet and mix, requires ad hoc decisions about which "actual" meanings to prioritize. An alternative view characterizes all language as metaphorical such that metaphor analysis is about what kind of connection is being made or what kind of link is being carried by a term in a particular setting, not whether or not a term is "actually" a metaphor. This perspective also clarifies that whether a metaphor is accurate or not is the wrong question.

[ii] Ricoeur speaks of grids when he characterizes what metaphors do, but I would rather speak of webs to acknowledge that relational threads aren't tidily equidistant at ninety-degree angles.

References

Alberts, B, Johnson, A., Lewis, J., Raff, M., Roberts, K. and Walter, P. (2002) *Molecular Biology of the Cell*, 4th ed. (New York: Garland Science).

Anaya-Muñoz, V. H., García-Deister, V. and Suárez-Díaz, E. (2017) Flattening and unpacking human genetic variation in Mexico, postwar to present, *Science in Context*, 30(1), pp. 89–112.

Balmer, A. and Herreman, C. (2009) Craig Venter and the re-programming of life: How metaphors shape and perform ethical discourses in the media presentation of synthetic biology. In: R. Elliot and B. Nerlich (Eds.) Communicating Biological Sciences: Ethical and Metaphorical Dimensions. (London: Ashgate), pp. 219-234.

Barnes, B., and Dupré, J. (2009) *Genomes and What to Make of Them*. (Chicago: University of Chicago Press).

Bateson, G, and Donaldson R. E. (1991) *Sacred Unity : Further Steps to an Ecology of Mind*, 1st ed. (New York: HarperCollins).

Brandt, C. (2005) Genetic code, text, and scripture: Metaphors and narration in German molecular biology, S*cience in Context*, 18(4), pp. 629–648.

Brooks, A. N. Hughes, A. L., Clauder-Münster, S., Mitchell, L. A., Boeke, J. D. and Steinmetz, L. M. (2022) Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. *Science*, 375(6584), pp. 1000–1005.

Cai, Y. Lux, M. W., Adam, L. and Peccoud, J. (2009) Modeling structure-function relationships in synthetic DNA sequences using attribute grammars. *PLOS Computational Biology*, 5(10), pp. e1000529.

Calvert, J. (2007) Patenting genomic objects: Genes, genomes, function and information. *Science as Culture*, 16(2), pp. 207-223.

Calvert, J. (2008) The commodification of emergence: systems biology, synthetic biology and intellectual property, *BioSocieties* 3(4), pp. 383–398.

Collado-Vides, J. (1991) The search for a grammatical theory of gene regulation is formally justified by showing the inadequacy of context-free grammars, *Bioinformatics* 7(3), pp. 321–326.

Condit, C.M., Ferguson, A., Kassel, R., Thadhani, C., Gooding, H.C., and Parrott, R. An exploratory study of the impact of news headlines on genetic determinism. *Science Communication* 22(4), pp. 379-95.

Davies, J. (2014) The feedback loop is a better symbol of life than the helix, Aeon Essays, Aeon. https://aeon.co/essays/the-feedback-loop-is-a-better-symbol-of-life-than-the-helix, accessed 16 July 2022.

Domingo, E. García-Crespo, C., Lobo-Vega, R. and Perales, C. (2021) Mutation rates, mutation frequencies, and proofreading-repair activities in RNA virus genetics, *Viruses* 13(9), p 1882.

Eisenstein, M. (2021) Artificial intelligence powers protein-folding predictions, *Nature*, 599(7886), pp. 706–708.

Fish, S. (1990) *Is There a Text in This Class?: The Authority of Interpretive Communities*. (Cambridge Mass: Harvard University Press).

Frow, E. and Calvert, J. (2013) “Can simple biological systems be built from standardized interchangeable parts?” Negotiating biology and engineering in a synthetic biology competition, *Engineering Studies* 5(1), pp. 42–58.

Flusser, V. (2011) *Does Writing Have a Future?* 1st ed. Translated by N.A. Roth. (Minneapolis: Univ Of Minnesota Press).

Haraway, D., and Goodeve, T. (2018). *Modest_Witness@Second_Millennium.FemaleMan-_Meets_OncoMouse.* 2nd ed. (New York: Routledge).

Haraway, Donna Jeanne. 1991. *Simians, Cyborgs, and Women : The Reinvention of Nature*. New York : Routledge.

Hayles, N. K. (1999) *How We Became Posthuman: Virtual Bodies in Cybernetics, Literature, and Informatics*. 1st ed. (Chicago, Ill: University of Chicago Press).

Hedgecoe, A. M. (1999) Transforming genes: Metaphors of information and language in modern genetics, *Science as Culture*, 8(2), pp. 209-229.

Hester, R. J. (2020) Bioveillance: A techno-security infrastructure to preempt the dangers of informationalised biology, *Science as Culture*, 29(1), pp. 153-176.

Hie, B. Zhong, E. D., Berger, B. and Bryson, B. (2021) Learning the language of viral evolution and escape, *Science,* 371(6526), pp. 284–288.

"information, n.". OED Online. June 2022. Oxford University Press. (accessed July 7, 2022).

Johnstone, C. P. and Galloway, K. E. (2022) Supercoiling-mediated feedback rapidly couples and tunes transcription, bioRxiv, 2022.04.20.488937. Available at: https://doi.org/10.1101/2022.04.20.488937.

Kappel, K., Zhang, K., Su, Z., Watkins, A. M., Kladwang, W., Li, S., Pintilie, G., Topkar, V. V., Rangan, R., Zheludev, I. N., Yesselman, J. D., Chiu, W. and Das, R. (2020) Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures, *Nature Methods,* 17(7), pp. 699–707.

Kay, L. E. (2000) *Who Wrote the Book of Life?: A History of the Genetic Code*. (Stanford: Stanford University Press.)

Keeley, J. (2020) *Mapping the 3-D Geometry of SARS-CoV-2's Genome*, *HHMI*. Available at: https://www.hhmi.org/news/mapping-the-3-d-geometry-of-sars-cov-2s-genome, Accessed: 26 July 2022.

Keller, E. F. (2000) *The Century of the Gene*. (Cambridge, MA: Harvard University Press).

Keller, E. F. (2002) *Making Sense of Life*. (Cambridge, MA: Harvard University Press).

Keller, E. F. (2005). Ecosystems, organisms, and machines. *BioScience*, 55(12), pp. 1069-1074.

Keller, E. F. (2014) From gene action to reactive genomes, *The Journal of Physiology*, 592(11), pp. 2423–2429.

Keller, E. F. (2017a) Globalization, Scientific Lexicons, and the Future of Biology, *East Asian Science, Technology and Society*, 11(3), pp. 373–382.

Keller, E. F. (2017b) Response to Comments on "Globalization, Scientific Lexicons, and the Future of Biology", *East Asian Science, Technology and Society*, 11(3), pp. 417–419.

Keller, E. F. (2020) Cognitive functions of metaphor in the natural sciences, *Interdisciplinary Science Reviews*, 45(3), pp. 249–267.

King, K. (2010). Pastpresents: Playing cat's cradle with Donna Haraway. Available at: https://playingcatscradle.blogspot.com/. Accessed: 23 January 2024.

Kim, Y. -A. and Przytycka, T. M. (2021) The language of a virus, *Science*, 371(6526), pp. 233–34.

Kline, R. R. (2015) *The Cybernetics Moment: Or Why We Call Our Age the Information Age*. (Baltimore: Johns Hopkins University Press).

Haraway, D. (2004). *Crystals, Fabrics, and Fields: Metaphors that Shape Embryos*.

Lakoff, G., and Johnson, M. (2003) *Metaphors We Live By*. 1st ed. (Chicago: University of Chicago Press).

Lovelock, J. (2000) *Gaia: A New Look at Life on Earth*. 3rd ed. (Oxford: Oxford University Press).

Morange, M. (2020) *The Black Box of Biology: A History of the Molecular Revolution*. Translated by Matthew Cobb. (Cambridge: Harvard University Press).

Nerlich, B. (2020) Encounters between life and language: Codes, books, machines and cybernetics, *Nottingham French Studies*, 59(3), pp. 311–32.

Oyama, S. (2000) *The Ontogeny of Information: Developmental Systems and Evolution*. 2nd ed. (Durham: Duke University Press).

Panofsky, A and Donovan, J. (2019) Genetic ancestry testing among white nationalists: from identity repair to citizen science, *Social Studies of Science*, 49(5), pp. 653–81.

Ricoeur, P. (1977). *The Rule of Metaphor: Multidisciplinary Studies of the Creation of Meaning in Language*. 1st ed. Translated by Robert Czerny. (Toronto: University of Toronto Press).

Searls, D. B. (1992) The linguistics of DNA, *American Scientist*, 80(6), pp. 579–91.

Searls, D. B. (1997) Linguistic approaches to biological sequences, *Computer Applications in the Biosciences: CABIOS,* 13 (4), pp. 333–44.

Searls, D. B. (2002) The language of genes, *Nature,* 420(6912), pp. 211-217.

Subramaniam, B. (2014) *Ghost Stories for Darwin: The Science of Variation and the Politics of Diversity*. 1st ed. (Urbana: University of Illinois Press).

Szymanski, E. and Scher, E. (2019) Models for DNA design tools: The trouble with metaphors is that they don't go away, *ACS Synthetic Biology*, 8(12), pp. 2635-2641.

Szymanski, E. (2023). Conversations with other-than-human creatures: Unpacking the ambiguity of "with" for multispecies rhetorics. *Rhetoric Society Quarterly*, 53(2), pp. 138-152.

TallBear, K. (2013) *Native American DNA: Tribal Belonging and the False Promise of Genetic Science*. 1st ed. (Minneapolis: University Of Minnesota Press).

Todd, Z. (2016) An indigenous feminist's take on the ontological turn: 'Ontology' is just another word for colonialism, *Journal of Historical Sociology*, 29(1), pp. 4–22.

Tunyasuvunakool, K., Adler, J., Wu, Z., Green, T., Zielinski, M., Žídek, A., Bridgland, A., Cowie, A., Meyer, C., Laydon, A., Velankar, S., Kleywegt, G. J., Bateman, A., Evans, R., Pritzel, A., Figurnov, M., Ronneberger, O., Bates, R., Kohl, S. A. A. … and Hassabis, D. (2021) Highly accurate protein structure prediction for the human proteome, *Nature*, 596(7873), pp. 590–96.

Watson, J. and Crick, F. (1953) A structure for deoxyribose nucleic acid, *Nature*, 4356, pp. 737-8.

Wheeler, W. (2010) Delectable creatures and the fundamental reality of metaphor: Biosemiotics and animal mind, *Biosemiotics*, 3(3), pp. 277–87.