In “What Was Life?,” Stefan Helmreich explains how recent developments in biotechnology have reignited a series of debates on the ontology of life by uprooting it from any explicitly biological or even natural roots. More than a century after the development of biology as a unified discipline, he argues, biology’s theoretical object of knowledge—life—has become indistinguishable from science’s modes of representation, leading life to be systematically displaced by specific instances or mechanisms of life (e.g., genes, cells, evolutionary systems, etc.).

This phenomenon, however, is not limited to the field of biology. Many scholars in the humanities investigate the displacement of life by its mediation as both a concept and an object. Wendy Hui Kyong Chun, for instance, frames the reduction of life to programmable code as a misleading analogy between biological systems and computational media. Kaushik Sunder Rajan, for his part, links the constitution of genes as self-contained informational units to the conflation of a partial, materialist perspective on biology with an ontology of life. Finally, Joanna Zylinska and Sarah Kember situate current conceptualizations of life as mediation in the context of the mobilization of new media within a larger biopolitical framework. In all these cases, the reformulation of life by new media is conceived as a privileged object of study for media studies, implying that some original, pre-mediated form of life can be excavated from life’s current, mediated manifestations.
It is in this context that Helmreich’s investigation of how limit biologies capture life as an object of knowledge becomes interesting to consider—not because these fields convey the potential to restore a stable ontology of life before, after, or despite media, but rather because they destabilize the edges that life’s mediated manifestations posit as constitutive of life. This line of inquiry thus seems to carry the possibility of transforming biological discourses and key debates in media studies alike by engaging with the way forms of life and life forms mediate each other.

While Helmreich focuses on artificial life, marine biology, and astrobiology—fields which respectively emphasize the abstraction, porosity, and schematization of life—this paper explores a fourth limit biology: epigenetics. By inquiring into the influence of environmental factors on phenotypic expression, epigenetics offers a privileged perspective on the zone of indistinction where information contained in the environment intervenes upon the medium of molecular biology. In that context, this survey examines the tension between epigenetics as a new semiotics of life linking genetic material and environmental conditions together and epigenetics as a privileged framework through which norms about life are defined and established. To do so, this paper first highlights how the major manifestations of epigenetics blur the edges between categories that are often assumed to be constitutive of life (e.g., organism vs. environment, individual vs. population, etc.). Then, it investigates how these edges are also reinforced by neuroscience’s reformulation of epigenetics as a form of regulation of life. Epigenetics will thereby be framed here as both mediating the type of edges imposed upon life and hinting at forms of mediation prefiguring media altogether.

Epigenetics broadly refers to the effects of external information including milieu, habit, experience, and environment on the targeted activation of genetic material. In that sense, it encompasses phenomena ranging from the silencing of flowering-related genes when plants from the Arabidopsis genus experience cold weather to variations in the expression of the genes regulating the mouse’s coat color based on the animal’s diet. As a field, epigenetics thus studies variations in observable traits, developmental processes, and physiological properties—i.e., variations in phenotypic expression—that are not the product of changes in the DNA itself. Under specific circumstances, environmental cues can cause the methylation or demethylation of DNA segments, which respectively prevents or activates the phenotypic expression of these genes.
One of the significant manifestations of epigenetics—germline and early embryonic reprogramming—illustrates the fundamental role that semiotics plays in biology. Epigenetic reprogramming refers to the methylation or demethylation of specific genes depending on the environment in which an embryo or germline develops. Breaking away from the clear division in traditional genetics between information contained in DNA and information situated in the environment, epigenetic reprogramming highlights the close intertwining of the two as they together inform phenotypic expression. This closed feedback loop between organisms and their environment resonates with Eduardo Kohn’s argument that life is inherently semiotic. Across realms, living beings produce and interpret signs to navigate their environment, Kohn emphasizes, and this phenomenon “is one example of the ways in which representation exists in the world beyond human minds.”

Epigenetics, however, takes Kohn’s argument ever further. While Kohn refers to multispecies relations to frame such exchanges of signs in terms of communication, epigenetics reframes semiotics as what both enables and interrupts communication by the way signs shape yet disappear behind the medium of molecular biology. Epigenetic variations in phenotypic expression are themselves signs of entanglement between genetic and environmental information—signs that manifest only when genetic and environmental information fail to coincide and lead to the activation or deactivation of genes. Through epigenetics, signs are then framed not only as “relational processes,” as Kohn argues, but also evolutionary ones regulating the entanglement between organisms and their environment.

Another manifestation of epigenetics—transgenerational epigenetics—offers a privileged perspective on the relationship between form and life in biology. This phenomenon refers to the transmission across generations of epigenetic traits acquired during an organism’s lifetime. Generally, current biological practices such as synthetic or marine biology tend to highlight the modularity of life: a life that can be endlessly recombined to create new forms of life. However, as Veena Das explains, such materialist views of life are “not able to convey the mutual absorption of the natural and the social,” and they therefore “emphasiz[e] form but not life.” In contrast to these views, transgenerational epigenetics emphasizes the richness of life in relation to form by accentuating how genes contain a wide range of forms of life that can be transmitted across generations without each of these forms being expressed.
Epigenetics thus embodies the “revelatory” nature of life. Forms of life exist as potential life forms inscribed in genetic material, and their actualization is dictated by the way meaning and matter, the natural and the social, come together both within individuals and across generations. In her work on developmental systems, Susan Oyama argues that any form of life “exists before the interactions in which it appears.” Similarly, epigenetic forms precede the interactions that give rise to specific phenotypic traits, as they first exist as disembodied, potential forms of life within genes. Yet transgenerational epigenetics also nuances Oyama’s account: since epigenetic forms are both embodied through phenotypic expression and disembodied when passed along to subsequent generations as epigenetic marks, developmental systems appear first and foremost as mediating entities.

The way epigenetic forms of life inform subsequent life forms through the transmission of information from genes and the environment alike then emphasizes how no form is biologically or semiotically meaningful until it mediates phenotypic expression. In that sense, forms indeed exist before the interactions in which they emerge but also shape the way these interactions are made meaningful to subsequent generations. Potential forms of life are then contained in life forms, while life forms are in return informed by the forms of life that are given primacy through epigenetic variations.

Helmreich notes, however, that “the form in a life form is a sign of one’s methodological and theoretical approach,” emphasizing the key role of mediation in framing how life is conceptualized at its edges. In Helmreich’s case studies, there seems to be an implicit tension between limit biologies’ capacity to destabilize traditional readings of life and how these alternative accounts are also formalized by these fields’ tools and methods.

Artificial life, for instance, relies on technics such as evolutionary algorithms and game engines to develop artificial agents capable of adapting to their environment. Through these technologies, life is captured in terms of iterative processes outside any material substrate, offering a “processual” perspective on life. Marine biology, for its part, has been directly shaped by breakthroughs in DNA sequencing and bioinformatics, which together articulate a “relational” account of life. With DNA sequencing pointing out the connectivist nature of lateral gene transfer and bioinformatics offering the formalist backdrop upon which these connections are mapped, life is captured as a privileged site of recombinant practices. Astrobiology, finally,
conceives life in terms of the necessary conditions for the development of living organisms and relies on sensors to identify such indirect traces of life on other planets, illuminating an “indexical” notion of life.\textsuperscript{14}

Epigenetics, in contrast, does not rely on such advanced computational media. Analyzing epigenetic marks such as allelic expression and methylation indeed requires technics like DNA sequencing and bioinformatics, but these phenomena cannot be linked back to epigenetics through these tools alone. When studied at the level of individuals, epigenetic variations can also be often explained by bacterial effects, cytoplasmic inheritance, and other understudied genetic mechanisms. Consequently, the only way to link some variation back to epigenetic marks is through the statistical analysis of phenotypic expression in populations across generations, linking the way life is conceptualized statistically to how individuals are themselves conceived as populations.\textsuperscript{15}

Figure 1: Normal distribution, which has the greatest frequency concentrated at the center. In 1925, Ronald Fisher popularized the use of probability theory to construct normal distributions representing the expression of phenotypic traits within populations.\textsuperscript{16}
Statistics then appears as a privileged tool through which epigenetic variations are not only registered but also closely linked to a determinism that was previously associated with genetics. Many of the statistical methods that are used in contemporary epigenetics were in fact first popularized by early twentieth-century geneticists such as Ronald Fisher.\textsuperscript{17} For him, probability theory could be used to map the distribution of phenotypic traits in large populations,\textsuperscript{18} while differential calculus could provide new ways to measure genetic variation as determined by mutation and selection.\textsuperscript{19} Mirroring Lorraine Daston and Peter Galison’s account of the rise of “mechanical objectivity” and the adoption of self-registering scientific instruments around that period, these methods were first adopted to allow scientists to outsource the conclusions of their analysis to external devices.\textsuperscript{20} Now used to measure the influence of environmental conditions on phenotypic expression, statistical methods endow epigenetics with similar ontological assumptions regarding the possibility of “objectively” mapping the ideal conditions in which life can grow and develop.

Such a formalist approach to statistics, however, overlooks the intervention of researchers in selecting the data that are analyzed and the correlations put forward. Through statistics, life is captured in terms of the impact of environmental cues on the otherwise “normal” distribution of phenotypic traits in populations whereas gene expression is endowed with the formalism of linear regressions, reframing epigenetics as an “inferential” science of life. Life, from that perspective, is divided into sets of phenotypic expressions which are individually investigated to measure their prevalence in relation to environmental cues. Through statistical analysis, environmental cues (e.g., temperature, atmospheric pressure, or sunlight in the case of plants) and experience (e.g., access to food, stress, or fitness in the case of animals) are thus isolated in order to infer their positive or negative influence on populations as a whole.

It is in such terms that the moral metaphor at the heart of statistics becomes relevant to consider. As noted by Georges Canguilhem, statistics plays a key role in defining normality—and therefore abnormality—in medicine and biology alike.\textsuperscript{21} Contemporary epigenetics and its statistical framework tend to emphasize a materialist, almost deterministic reading of the influence of environmental cues, overlooking the position of epigenetics at the edge of both life and semiotics. Das problematizes such deterministic accounts of forms of life by suggesting a distinction between “the ethnological or horizontal sense of form of life and its vertical or ‘biological’ sense”:\textsuperscript{22} while
the former encompasses institutions and social structures, the latter refers to the distinctions between “so-called ‘lower’ or ‘higher’ forms of life.” The vertical sense, she emphasizes, is especially unstable, and evolves in relation to epistemological shifts.

It is in that context that statistics, just like language or ontology, can become the object of a “grammatical investigation,” understood here in the Wittgensteinian sense as the study of the conditions through which a statement, process, or method is endowed with meaning. Through concepts such as average, distribution, and correlation, statistics establishes the norms in relation to which forms of life are classified and the edges delimiting them enforced. Statistics, however, cannot cover all possible forms of life that epigenetics instantiates, highlighting how, as Das affirms, “there is always a gap between the rule and its execution.” In that sense, while epigenetic forms leave no gap between signs and gene expression or between meaning and matter, statistical representation translates biological norms into social ones while overlooking their mutual irreducibility. It is in that context that the vertical sense of epigenetic forms of life is redefined via statistics as norms of life—norms that establish the distinction not so much between forms of life, but rather between what a form of life should and shouldn’t be, between good and bad environmental conditions, between what lies within and beyond the edges of life.
The point of investigating life at its edges, i.e., the conditions through which forms of life are differentiated and classified, is to shed light not so much on these edges per se as on the tools and discourses, media and mediations that produce the norms within which life is expected to be contained. In that sense, the displacement of forms of life by norms of life as the vertical, biological sense of epigenetics seems more closely linked to the recent reformulation of epigenetics as a science concerned with the regulation of life than any fundamental principle underpinning epigenetic mechanisms.

As noted by Loren Graham, the current renewed interest in epigenetics has been directly fueled by its mobilization within the field of neuroscience.\textsuperscript{26}
From neuroscientist Michael Meaney’s work on the epigenetic regulation of neurological receptors in offspring whose parents suffered from childhood abuse and other forms of trauma\textsuperscript{27} to psychiatrists Brian Dias and Kerry Ressler’s research on the reduced sensory sensitivity inherited from parents experiencing PTSD,\textsuperscript{28} epigenetics tends to be increasingly linked to the transmission of predispositions for specific forms of mental illness and negative life outcomes across generations. The mobilization of epigenetics within neuroscientific research then hints towards the ongoing hybridization of epigenetics with current trends related to how mental illness and risk are managed. As illustrated by the aforementioned studies, today’s use of epigenetics mirrors the general tendency of neoliberal societies to address medical predispositions, risk, and mental illness as problems situated within individuals rather than the products of systemic conditions. Combined with the field’s reliance on statistical inference as its main methodological framework, the current applications of epigenetics accentuate the way modern institutions and media are organized to respond proactively to the risk that specific people represent.

The resurgence of epigenetics in neuroscientific research then appears to reinstate a form of determinism that was first popularized by genetics. Traditional genetics’ reduction of genes to linear, executable code may no longer predominate, but the current applications of epigenetics reproduce a similar logic by situating the influence of environmental conditions on life outcomes not at the social level, but at an embodied, biological one. When conceived as a set of biological processes, epigenetics refers to the mediation of genetic and environmental information. When conceived as a discipline, however, it mediates the broader intellectual landscape surrounding developmental psychology, mental healthcare, and the management of risk. What emerges at the intersection of both accounts of epigenetics is thus a semiotics of life which defines and mediates the conditions and norms through which organisms and their environments interact with and influence one another. In this regard, epigenetics appears to support a co-constitutive theory of life and media: by emphasizing how the logic of media always seems to be prefigured by mediations that were already perceived as constitutive of life, epigenetics highlights how new media tend to materialize edges that were first imposed upon life as norms.

To conclude this brief survey, it is tempting to go back to Helmreich’s initial question: \textit{What was life?} To ask this question in the past tense is to assume that life has been altered beyond recognition by its encounter with old and
new media. One might attempt to reconstitute some pre-mediated form of life by investigating life at its edges, i.e., the mediated manifestations through which new forms of life are produced and sustained. Yet doing so also threatens to naturalize the edges that are discursively and materially produced by the media behind these manifestations. To ask *What was life?* thus necessarily involves asking *What is media?* as the former implies that life has been mediated in ways that now makes it irreducible to some idealized, pre-mediated state.

Epigenetics, however, complicates this assumption. This field has taken many forms throughout the last decades yet systematically reflects a more flexible vision of life: by emphasizing the transversal influence of the environment on all levels of the Aristotelian pyramid of life, it also mediates how these different levels interact with one another. That way, epigenetics not only destabilizes the type of edges—interior vs. exterior, individual vs. population, organism vs. environment, etc.—that are often assumed and, arguably, produced by contemporary media, but also posits mediation as one of life’s defining features. From that perspective, the question that unites biology and media studies together is thus not so much how to reconstitute life before media, but rather how mediation was already present in life long before the emergence of media as we know it.

**Notes**

12 Ibid., 679–83.
13 Ibid., 686.
14 Ibid., 690–91.
23 Ibid., 180.
24 Ibid., 179.
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