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Toward a biosemiotics framework for AI: Folding and the dynamics of meaning

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Abstract: This paper is dedicated to the intersections between folding and semiotics, serving as a meta-commentary on Howard Pattee's "Symbol grounding precedes interpretation" (2021), a response to Terrence Deacon's work, that was further elaborated in 2023. Framed within a context of recursive self-reflection, the paper scrutinizes folding as a fundamental semiotic activity and elementary semiotic modelling, drawing connections to Pattee's proposition regarding protein folding as a precursor to semiosis and interpretation. Central to this discourse is the assertion that folding serves not only as a foundational prerequisite for semiosis but also as a potent modelling system. Through a multidisciplinary lens, the paper elucidates how folding manifests as a modelling mechanism across diverse domains from biology to syntax. Notably, the paper proposes an application of folding principles in AI. By navigating the framework of folding as semiotic modelling, this paper contributes to a deeper understanding of the foundational mechanisms of signification and interpretation in semiotic systems.

Keywords: folding; protein folding; semiotic modelling; artificial intelligence; symbol grounding; syntax

1. Introduction

This paper[2] is a commentary on Howard Pattee's paper entitled "Symbol grounding precedes interpretation" (2021) that is a commentary on Terrence Deacon's work. It is thus a meta-paper, a self-reflection, a recursive paper on the phenomenon of folding understood as a basic semiotic activity. The paper by Pattee is about protein folding as the very precondition for semiosis and inter-

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pretation, and has recently been re-elaborated and published under the title "Symbol grounding by folding: The primary biosemiosis" (Pattee 2023). While I proposed a very similar idea already in my PhD dissertation (Lacková 2018), there are some points of disagreement between my proposal and Pattee's vision about the role of folding in his semiotic model. In this paper, I will explain my agreements and disagreements with Pattee. The main aim of this paper is to present folding as a minimal precondition for semiosis, but also as a modelling system. The very modelling capacity of folding has been applied to AI, and a model of protein folding for AI has been proposed (Romanini, Lacková 2023; see also a recording of our talk given at the conference Gatherings in Biosemiotics in 2022[3]). Folding as modelling will be explained with examples from (1) protein folding; (2) artificial intelligence; (3) syntax in languages; and (4) to conclude, I present the overall model of folding as semiotic modelling.

2. Protein folding

Proteins, known as the fundamental functional components of living organisms, are intricate organic macromolecules that might have originated at the very beginning of life on Earth. Of course, the very origin of life is still an unsolved question. Many alternative hypotheses are prevalent in the scientific discussion: there are, to mention some of them, metabolism-first models or RNA-first models (the so-called "RNA world") – for a general overview, see Markoš, Švorcova 2019: 10–19. Yet in many traditions, the inquiry into how life began and the development of the genetic code is closely tied to the emergence of proteins (Crick 1968). The existence of the genetic code is fundamentally linked to the necessity of synthesizing proteins, as it encodes the instructions for producing specific proteins. In essence, the process of life hinges on the synthesis of proteins, which serve as the core building materials for cells and are crucial for executing metabolic activities. Despite their complexity, proteins are formed from simple linear arrangements of molecules, but upon folding they transform into a compact, functional three-dimensional structure that orchestrates various biological activities. The role of proteins has been a captivating subject for philosophical exploration since the early days of molecular biology and genetics (Jacob 1970; Monod 1972; Deleuze, Guattari 1987). The journey from a straight peptide chain to a well-defined protein structure has inspired significant philosophical discussions. However, the mechanism of protein folding remains largely elusive, with

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[3] The video "Gatherings in Biosemiotics 2022 Day 2" is accessible at: https://www.youtube.com/watch?v=EWYdDZzZ-jM&t=30342s The presentation starts at 1.47.00.

the underlying principles still to be uncovered. A comprehensive understanding of the chemical and physical attributes of peptide chains does not sufficiently clarify why proteins adopt particular folding patterns (Holm, Sanders 1997). While chemistry and physics contribute to the understanding, they do not provide the complete explanation. The terms 'protein code', 'protein grammar', and 'protein syntax' have emerged from the search for alternative explanations beyond the purely chemical ones (Ji 1999).

Protein structures are evolutionary habits, final interpretants of protein synthesis. The unsolved problem in current research in protein studies is the process of transition from the unfolded sequence into a unique three-dimensional conformation. One single amino acid sequence (peptide chain) may form different structures in different proteins. The question about the relationship between sequence and structure warrants research into thermodynamic explanations. A possible thermodynamic explanation would be that all possible constructions are tested to find the energetically most favourable one. Still, the number of all possible constructions of one peptide chain is so large that understanding how evolution came up with stabilized protein structures remains a mystery. Cyrus Levinthal (1969) calculated that a random search for protein structure would take up to 5×10^{34} seconds, or 1.6×10^{27} years. The enormous difference between the calculated and actual folding times is called Levinthal's paradox. Finding the native form of a protein by using a random search among all possible structures would take an unimaginably long time. Yet proteins fold in seconds; this is indeed a biological example of saving and minimizing energy: only a limited number of folds occur in nature.

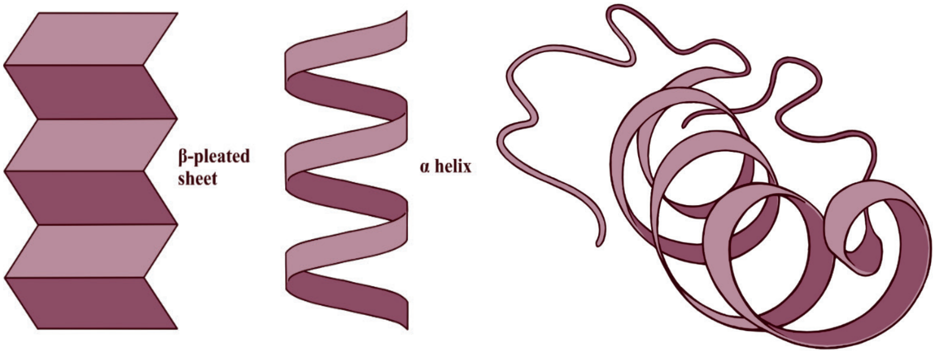

Figure 1. Folded protein structures.

Protein folding has been of interest to some philosophers and thinkers representing structural semiology, such as Gilles Deleuze. Deleuze was fascinated by the notion of the fold in general, dedicating to this the essay *The Fold: Leibniz and the Baroque* (1988). Deleuze (1988: 6) contends that the fold, not the point, is the smallest element of matter:

> The unit of matter, the smallest element of the labyrinth, is the fold, not the point, which is never a part, but a simple extremity of the line. That is why parts of matter are masses or aggregates, as a correlate to elastic compressive force. Unfolding is thus not the contrary of folding, but follows the fold up to the following fold.

When it comes to protein folding, Deleuze also commented on the very notion of the fold in proteins. In the chapter "Geology of morals" from *A Thousand Plateaus* (Deleuze, Guattari 1988), the authors present a very interesting insight into the molecular biology of the DNA molecule and the very process of protein synthesis.

3. Artificial Intelligence

One of the most pressing questions for today's society is the question of AI agency, interpretive potential, and the symbol-grounding problem. Within the biosemiotic context, I see intelligence as not human-specific, and to study intelligence, one has to start at the evolutionary lower levels of what we call 'intelligence'. A biosemiotic approach to AI can help to shed a different kind of light on the very definition of intelligence. Concepts such as 'biosemiotic agency' seem to be promising in this regard. I would like to see the notions of agency and intelligence as co-extensive.

While the current AI systems are based on different types of data (e.g. computer vision), for the purposes of this paper I wish to focus on large language models (LLMs) based on linguistic data. In the context of the overall boom with bot systems such as Claude or ChatGPT, there is a schism between LLM and natural intelligence. In the context of biosemiotics, it has been proven that the organismal agency (intelligence) works on a basis quite different from that of large-scale data processing. In nature, to make sense of their environments, organisms normally need only very little data input to reach semiosis, to come to making sense of the world. In nature, more data can lead to more confusion, and organisms try to avoid confusion. In other words, nature tends to save and minimize energy to achieve big goals (for more on this topic, see Romanini, Lacková 2023). In Peirce's theory, this economization principle can be called the pragmatic maxim: "I do reason not for the sake of my delight in reasoning, but solely to avoid disappointment and surprise. Consequently, I ought to plan out my reasoning so that I shall evidently avoid those surprises" (CP 2.173).

The current AI is trying to imitate the brain and neuronal activity with neural networks, but maybe the current trend in LLMs is not the best possible way to achieve the optimal results. To avoid the problem of stochastic parrots (Bender *et al*. 2021), and in order to start developing less energetically and environmentally demanding AI, we should start taking steps to understand how intelligence works in nature, but not on models of the brain, but on the models of the smallest intelligent agents: proteins.

Taking proteins as the models for minimal intelligence is not a new idea. It could be stated that already Peirce proposed a similar hypothesis with his protein–phaneron analogy. To proceed, let me first briefly explain the notion of the 'phaneron'. 'Phaneron' is defined by Peirce as "the collective total that is present to the mind":

> By the phaneron, I mean the collective total of all that is in any way or any sense present to the mind, quite regardless of whether it corresponds to any real thing or not. If you ask present when, and to whose mind, I reply that I leave these questions unanswered, never having entertained a doubt that those features of the phaneron that I have found in my mind are present at all times and to all minds. So far as I have developed this science of phaneroscopy, it is occupied with the formal elements of the phaneron. (Peirce 1905: MS 1334)

With the vocabulary of the current science, we can "translate" 'phaneron' as 'collective mind', 'intelligence', or 'cognition'. Peirce (1905 MS 1334, 1907 MS 293: 1) extends the notion of the 'phaneron' further to biology, concretely to the proteins:

> [...] but whatever I may conjecture as to those vast super-molecules (proteids[4]), some containing fifteen thousand molecules, whether it seems probable on chemical grounds, or not, that they contain groups of opposite polarity from the residues outside those groups, and whether or not similar polar submolecules appear within the complex inorganic acids, it is certainly too early to take those into account in helping the exposition of the constitution of the phaneron.

Thus, in the very first decade of the twentieth century Peirce proposed an analogy between protein structures and the structure of the human mind. As limited as the knowledge of proteins was at that epoch, we can see that Peirce had an idea about the complexity of the protein structure's being similar to the intelligence structure. This gives us even more courage to develop this analogy and to apply it to artificial intelligence, especially in the context of the biosemiotic project.

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[4] Inserted by the author of the article.

Code duality is considered the central, or perhaps even the founding, principle of biosemiotics, though its significance extends into general semiotics as well. Jesper Hoffmeyer and Claus Emmeche (1991) note that life depends on a semiotic interplay between the analogue and digital versions of the message, in other words, on code duality. The self, in this view, can only be understood as the unity of these two aspects. In biosemiotics, the digital code typically refers to DNA, while the analogue code pertains to its active interpretation within living systems. It is this interplay between the digital code and its analogue interpretation that generates morphological plurality and biological variation. Importantly, code duality involves not only the presence of two distinct codes, but also their mutual compatibility, while remaining untranslatable. In this way, code duality confronts the enduring Cartesian divide between information and substance, a divide that echoes, but is not reducible to, the traditional dualism of mind and body. As Hoffmeyer and Emmeche (1991: 121) write:

> […] this dualism, is it not just a new disguise for the old dualism of mind and body, which since the time of Descartes has tended to envelope the kinds of knowledge obtainable in western science? To answer this question one should note, that the relation between information and substance is quite different from the relation between mind and body. While information and substance are separable concepts in our descriptions the two are inseparable in the 'real' world. They are different aspects of the same world. Information does not exist except as carried by (immanent in) matter and energy.

Thus, code duality can be understood as a semiotic challenge to the analytic and reductionist 'either–or' logic. It gestures toward a third way, toward what some have called a participative opposition (Lacková 2022; see also Anderson *et al.* 1984).

Protein folding can be understood as analogue coding to complement or complete the digital nature to the genetic script. I argue in many of my papers that the proteins are minimal semiotic agents (see, e.g. Lacková 2020) because they are directly involved in performing biological functions, metabolism, or other biological functions. So, with a presupposition that intelligence is originally a biological or natural phenomenon, we can take proteins as models for artificial intelligence.

To relate the above to the question of artificial intelligence, the book by Brian Smith called *The Promise of Artificial Intelligence* (2019) can be referred to. In this book, the limits of the current state of artificial intelligence research are described, mostly dealing with the limits of digital computing. Similarly to language or the linguistic metaphor of life, the computation metaphor will not suffice for intelligence.[5] The computational metaphor is not enough, and we are seeking something else. Natural intelligence, differently from artificial intelligence, is related to life, including subjective involvement, personal interests, and intentions, etc. This is why proteins can be introduced as models for AI. Because proteins bear minimal potential intelligent agency, protein folding is the minimal model for intelligent design. Because protein folding is about bringing together distant and unrelated parts of a sequence of the linear peptide chain, AI can now do this. Protein folding is about creating a shape from a pure linear string, and it is done by simply connecting – connecting adjacent parts of the string. And this is what we can call a minimal syntax or a minimal model for genuine intelligence. After a semiotic study of protein folding, we will see that it reveals code duality: the digital code alone is not sufficient to explain the activity of protein folding. Biology aids general semiotics by showing the basic status of code duality, where the digital is represented by the genetic code and the analogue is represented by interpretations for the very reading of the genetic script.

4. Syntax: recursion as folding

So far, we have seen folding as modelling for protein synthesis and more natural Artificial Intelligence, applied to the case of LLMs. Another area where we can apply folding as modelling is the syntax of natural languages. Syntax was probably the first scholarly area where folding was indeed applied as modelling. From linguistics to biology, 'folding' is just one more terminology borrowing, at least in the Czech language. In Czech, the term 'folding', that is, '*skladba*' or '*skládání*', is used both for syntax ('*větná skladba*') and protein folding ('*skládání proteinů*').

An entire range of linguistic terminology pervades biology, e.g. translation, transcription of DNA, reading and interpreting of the DNA script, the notion of 'code' itself, etc. In recent studies on protein folding, the folding process is explained by analogy with syntax in natural language. The syntactic analogy (Chomskian syntax is mostly used) has appeared in numerous scientific papers on protein studies in recent years (Gimona 2006; Loose *et al.* 2006; Kister 2015; Lacková 2019a). It is quite easy to understand what led biologists to using a syntactic metaphor. Folding of proteins is a process involving connecting smaller units into larger and more complex units. In syntax, clauses or sentences (complex units) are described as complexes of words (smaller units). Yet syntax is not a mere building mechanism involving connecting smaller units into larger units. A sentence must be meaningful; within a sentence, smaller units are related in a

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[5] On the computation metaphor see also Bolshoy, Lacková 2021.

certain way to constitute a coherent and meaningful whole. The packing of the complex meaning into small units lined up together is, however, an extremely complicated process that grammarians and linguists are trying to understand. The great question of grammar is to resolve the relationship between sound and meaning, between linear sound and non-linear meaning.

The linear order imposed by modern linguistics goes as follows: phonemes (expression) bind sequentially and form words (content), words bind sequentially and "fold" by flexion-syntactic (expression) and form sentences (content). Analogically, in the classic language metaphor of life, DNA molecules bind sequentially and by combinatory rules form RNA molecules, RNA molecules bind sequentially and form peptide chains from amino acids, protein chain folds and form proteins. This is related to the concept of double articulation by French linguist André Martinet (1957, 1967): the first articulation divides a sound chain (phonemes) into units of meaning (words or morphemes), the second articulation concerns further subdivision of single meaning units into meaningless elements (phonemes). The result of the first articulation is an open set of elements; the result of the second articulation is, on the other hand, a closed set of discrete units, digits.

As we can observe, Martinet's double articulation moves in the direction from content (meaning) to expression (sound) and not *vice versa*: thus, contrary to the direction imposed by the central dogma of molecular biology, and contrary to the classic language metaphor for life, in which the smaller discrete digits compose bigger units, creating meaning. In Martinet's order, meaning comes first. In language acquisition, and probably also in language evolution, meaning comes first. Discrete units appear in later phases: in the case of language acquisition, children first learn words and their meanings, only later, at school age, do they learn letters (consequently, they learn the very notion of phoneme, or the discrete unit as they learn to read – they do not need to learn to distinguish phonemes to understand words' meanings). In the case of language evolution as proposed by the very first theories on language evolution (De Condillac 2001[1746]; Rousseau 2012[1781]) people needed language, no matter whether it was gestures or unarticulated sounds, to communicate meanings, not to sequence meanings into discrete units. Thus, in the context of language evolution, the distinction between discrete units (phonemes) probably arrived together with the invention of alphabets, that is, very late in the course of language evolution. Applying this logic to DNA and proteins, and finally to AI, can help us understand all these phenomena more holistically. Whether and how a phoneme exists is a very important ontological question (Vachek 1976), and in the same way, it is legitimate to ask whether a nucleobase exists in nature in the form of a discrete unit (Markoš, Faltýnek 2011).

This paper was introduced as a recursive paper, recursively folded not only in content but also in its form. Talking about syntax, we cannot omit the notion of recursion as a syntactic operation. Noam Chomsky defined 'recursion' as the elementary computation mechanism for human syntax and also a unique computational pattern in human cognitive apparatus (Hauser *et al.* 2002). Chomsky argued that recursive grammar is at the point of origin for all human languages (Berwick, Chomsky, 2016), and thus language evolution would originate from recursion. The famous disagreement between Chomsky and Everett brought along some alternative proposals about the evolution of language: not from recursion, but from symbols (Everett 2017, see also Barham, Everett 2021). Everett based his theory on a case study of the Pirahã language, which he defined as lacking recursion. While Everett's study is extremely relevant and important for language evolution inquiries, his argument about the lack of recursion in the Pirahã language was not fully accepted for the major reason that we do not have accurate knowledge about this language. As Mikhail Ilyin (2023: 60) has noted, "it is difficult to reliably judge this based on Everett's publications alone […] Perhaps some markers or communication customs were simply not noticed. In any case, logonomic constructions were not taken into account."

While Ilyn's observation concerned the inaccuracy in Everett's analysis, there are many other arguments to contradict Chomsky's universal recursion theory. We can refer to numerous other studies – for example, most of the known ancient manuscripts written in Hittite, Akkadian, or biblical Hebrew prove to be very repetitive, using syntactic structures lacking any formal use of recursion, such as subordination: "The reason is that the mechanisms of subordination were less developed in these languages, so the coherence of their narrative relied to a much greater extent on a simple type of 'and . . . and . . .' concatenation" (Deutscher 2010: 120).

Terrence Deacon (2003: 126) explored the linguistics recursion from a critical perspective, replacing universal recursion with universal semiotic constraints, arguing against the innate biological recursive processing:

> An evolved innate neurally based recursive processing faculty is both unnecessary and unsupported by the evidence. The absence of anything quite like a generative grammar outside human language is consistent with the absence of symbolic reference in these forms and does not call for any special evolutionary explanation. The implicit affordance for recursion that symbolic reference provides is a semiotic universal that can be expected in any symbolic system, no matter what device implements it, whether a socially embedded human brain or a mind rendered in silico. How it is neurally processed and how the symbolic medium is structured may, however, make a difference to the extent and form of its use, and

> so it need not be invariably expressed any given language feature nor even severely reduced in a given language (e.g. in a pidgin or a proto-language form).

Deacon observes that recursion appears to be more of an epiphenomenon than a linguistic universal. What is universal in all languages, instead, is the symbolic threshold and semiotic constraints. For this reason, I prefer to use the notion of 'folding', rather than 'recursion'. It is a recursive circular autopoietic movement of the fold and can be observed in language as well as in protein synthesis.

5. Folding as modelling

To conclude this paper, let us have a closer look at what the notion of modelling means and how we can differentiate it from other semiotic or biological terminology. Here, a recent paper by Tyler Bennett (2023)[6] can serve as a source of inspiration. Bennett distinguishes between modelling capacity and informational capacity, inspired by Soviet cybernetics (Zaliznjak *et al.* 1962) and the cybersemiotic theory by Søren Brier (2008). According to Brier, more information does not equal more meaning, and as Bennett (2023) suggests, more modelling capacity entails less information. This is to say that the notion of information is not useful in semiotics, or better, that the notion of meaning is more important. Sometimes more information leads to less meaning, and this, for sure, applies to what has been said before about the stochastic parrots and the LLMs compared to biological intelligence. Instead of feeding the language models with endlessly long sequences of language data, it can prove more meaningful to try to model the sequences, to fold them. Folding as modelling has the specific feature of spatiality, dimensionality that is typical in general for graphs and diagrams (what I have in mind here is Peirce's Existential Graphs in particular). Bennett (2023) uses examples of maps and dioramas as prototypical spatial modelling systems. Only spatial models can capture the excluded middle, that is, they do not pre-require discrete digits defined in terms of binary relations 'either–or'. Peirce explains this kind of modelling, the modelling of a continuum, mathematically, as a dispute of the famous Dedekind cut:

> I agree with James, against Dedekind's view, and hold that there would be no existent points in an existent continuum, and that if a point were placed in a continuum, it would constitute a breach of the continuity. Of course, there is a

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[6] See also the video from the presentation at Nitra University, Slovakia: https://www.youtube.com/watch?v=ZrUtFktANqg.

> possible, or potential, point-place wherever a point might be placed; but that which only may be is necessarily thereby indefinite, and as such, and in so far, and in those Thought experiment respects, as it is such, it is not subject to the principle of contradiction, just as the negation of a may-be, which is of course a must-be, (I mean that if "S may be P" is untrue, then "S must be non-P" is true), in those respects in which it is such, is not subject to the principle of excluded middle. (CP 6.182)

If we imagine a continuum as a continuous line, Dedekind's comprehension of cutting a line consists in the fact that the cutting point, the border between parts in relations to each other (two parts of a line), must always be assigned to only one of the two parts to be able to be always reduced to a determined individual entity. For Peirce, the cutting point does not belong to either of the two parts, or rather, it belongs to both of them (Paolucci 2004: 125); therefore, it creates a logical paradox of the violation of the law of the excluded middle.

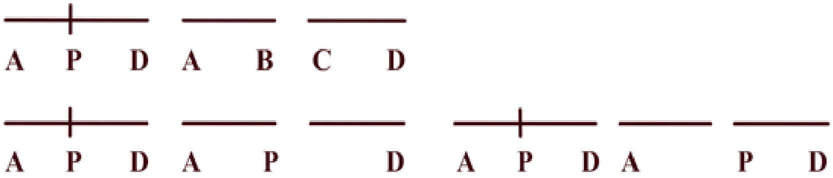

Figure 4. Cutting a line by Peirce and by Dedekind. The Peircean cut is represented by the upper line (AB, CD), and Dedekind's cut is represented by the lower line (AP, D or A, PD). See also Ketner, Putnam 1992: 39–41.

If we imagine the continuum as a continuous surface, then, according to Dedekind, the individual points belonging to the borderline (cutting line) must always be assigned to only one of the two parts in the relationship (A or B). On the contrary, for Peirce, the division of a continuous surface into two parts leads not only to two distinguished parts, but also to a third part considered to belong to both parts – in other words, the third part is undecided and exists in the conditional mode, as possibly either A or B or both of them.

Paolucci explains how the coexistence of continuity and discontinuity is possible, and how binary oppositions are possible even within the Peircean theory of continuity. The idea of folding a continuum means that when the continuum is folded, it never breaks its continuity; it is just folded. "From continuum and in continuum, without ever interrupting continuity, it is possible to create discontinuity effects that give rise to opposition relations,"[7] as Paolucci (2004: 135) writes.

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[7] In the original: "*Dal continuum e nel continuum, senza mai interrompere la continuitá, é possibile creare degli effetti di discontinuitá che danno origine a relazioni di opposizione*."

Folding as semiotic modelling can also be compared to the already proposed model of bet structure by Mayer-Foulkes, with a specific focus on differentiating between subjective folding (spiralling) and objective folding (cycling): "I shall refer to cycling on the side of the object and spirallic on the side of the subject. Living beings construct their experience of cycling spiralically" (Mayer-Foulkes 2023: 52). Folding as modelling can be the modelling of the future, allowing the co-existence of exclusive terms, which results in extreme usefulness in today's realities we live in, which are virtual, extended, and digital, but still analogue.

6. Discussion

In Pattee 2021, protein folding is proposed as a particular model for symbol grounding preceding interpretation. By this, Pattee is linking machine semiosis and molecular semiosis, with the only exception that he does not want to call this process 'semiosis'. The symbol-grounding problem is solved, according to Pattee, by the action of the fold. Pattee wants both the molecular and the technological levels to be clearly defined as non-semiotic realms, that is, as he calls this, 'interpretation'. Of course, these two phenomena are localized at the very thresholds of semiosis – lower and higher thresholds (in other words, they would be proto-signs and tardo-signs, see Bennett 2021: 191–204; see also Lacková, Faltýnek 2021), and it is good to distinguish them from fully-fledged semiosis. Yet we would still like to disagree with Pattee as to his standpoint towards interpretation, and the very notion of interpretant being of no use in biosemiotics and in general not helping explain any biological phenomena. First of all, if we exclude the interpretant and interpretation from semiosis, it is hard to talk about semiosis.[8] We see many similarities between the argumentation by Pattee and that by Barbieri: both authors are making almost identical claims about the uselessness of the notion of interpretant and the Peircean theory in general, presenting some kind of non-scientific interpretation of Peirce's theory. This claim might seem a little paradoxical, especially because Peirce made his career first and foremost in natural science, especially in chemistry, mathematics, and logic. He also elaborated a very important evolutionary theory (Peirce 1998; see also Švorcová *et al.* 2023). Peirce's semiotic theory is nothing but an elaboration of his logic, the iconic logic he proposed in the form of Existential Graphs. In his paper from 2023, Pattee (2023: 107) states that "protein folding is the primeval case where the symbolic information constrains physical laws directly. There is no interpreter." The notion of the 'interpreter' is not made part of the sign model

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[8] For an overall theory of interpretants in Peirce see Fomin 2023.

by Peirce, and I agree that there is no interpreter. This does not imply, within the framework of Peirce's sign model, that there is no interpretant (see also the notion of Non-Self-Conscious Interpretant by Ketner in Ketner 2025).

First of all, let me comment on the notion of the proto- and tardo-signs as established by Bennett (2021a). As you can see in Fig. 5, the quasi-signs (both proto- and tardo-signs) are visualized in the upper part of the diagram, and they are characterized by lacking one of the sign components. In case of the tardo-sign, the lacking object is the interpretant, and this is to be understood in contiguity with the notion of simulacra. While the proto-sign theory already has some tradition in biosemiotics and biology, the tardo-sign theory is a new invention by Bennett (2021), further elaborated by Fomin (2024), and it has been designed for ideology critique. In the case of proto-sign, the lacking element is the object, and this is partially derived from the protosemiosis theory by Sharov and Vehkavaara (2015), where 'protosemiosis' is defined as agency with reduced representation capacity. Thus, given the representational character of the object in a sign relation, in protosemiosis the object is missing: the only parts entering into a sign relation are representamen and interpretant.[9] Fomin (2024: 429) defines the concept of 'quasi-sign' as "a typology of dyadic semiotic entities in which the triad of vehicle-interpretant-object has not yet emerged (proto-signs) or has degenerated (tardo-signs)".

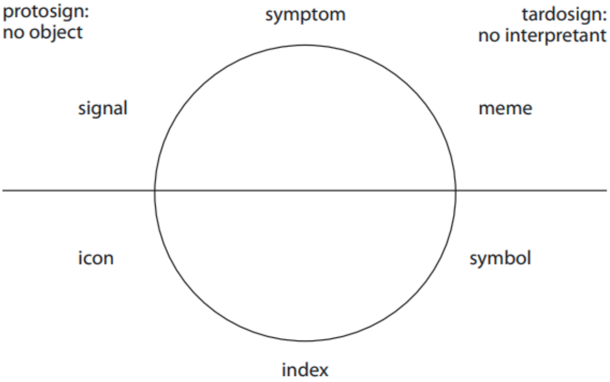

Figure 5. Proto-signs and tardo-signs (adapted from Bennett 2021: 193).

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[9] This definition of the proto-sign of course depends on the interpretation of Peirce's theory as detached from the naive realism that some authors are pushing. In this interpretation of Peirce, the object (dynamic and immediate) is an object of the semiosis, defined in terms of representation, and not an object in the "objective reality".

It is important to emphasize that reduced representational capacity alone does not suffice for protosemiosis. Stereochemical relationships, while potentially foundational, are not semiotic in themselves, semiosis inherently requires mediatedness. This mediatedness may take the form of iconic, indexical, or symbolic relations, or more commonly, a combination of these. In other words, even if the object is absent in protosemiosis, the interpretant is not. It is the interpretant that ensures the mediated nature of the sign. Kalevi Kull explores the significance of mediatedness in this context (see Kull 2020, 2023). For a more detailed discussion on mediatedness and the role of the interpretant in protosemiosis, see also Ketner 2025 and Lacková 2020, Lacková 2021.

Italian biologist Giorgio Prodi was the first to introduce the notion of protosemiosis. He defined protosemiosis as choice-making. The discussion between Umberto Eco and Prodi about semiosis at the cellular level became a famous academic discussion and culminated on the occasion of the NATO Advanced Research Workshop on the Semiotics of Cellular Communication in the Immune System held at Ciocco, Lucca, Italy in 1986. Papers by Eco, Prodi, and other semioticians and immunologists are available in the proceedings from this conference (Sercarz *et al.* 1988). Eco disagreed with the attribution of semiosis to lower forms of life, but finally immunologists persuaded him to accept that one can speak, on a cellular level, of a kind of elementary semiosis. Eco (1987: 228) placed elementary semiosis in the lower threshold of semiotics, yet doubted that cells could have interpretive options, refusing to assign Space C (Space of interpretation options) to them and arguing that the way cells communicate and interact with the environment works according to the stimulus–response scheme and not according to choice making. Prodi's vision was a little different, and he proposed Space C, that is, choice making, for example, in the interaction between an enzyme and its substrate (Fig. 6).

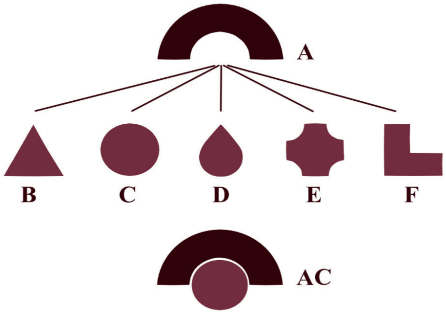

Figure 6. Interaction of an enzyme (A, subject) with its substrate (B, object) as a model for proto-semiosis (inspired by Cimatti 2000: 52).

To conclude, Pattee defines protein folding as the lawful process without interpretation. We have seen in this paper that protein folding is a very complicated mechanism, impossible to explain with pure physics or chemistry (see, for instance, Levinthal's paradox). It appears lawful because of the evolutionary habit. Protein structures are products of evolution. Exactly in the same way, meanings attached to the words appear lawful because of the evolution of language, which has made a strong habit that can behave as a law, and these laws are even written: just open any dictionary. For Peirce, laws are born from habits, as dyads are born from triads. Some of the natural processes can be qualified both as genuine anancasms or degenerate agapasms. Peirce also established the notion of the 'final interpretant', where it is hard to make a clear distinction between the final interpretant and law. I believe that this is also the case with protein folding. By critically engaging with Pattee's interpretation of folding, this paper has shed light on both points of convergence and divergence with the existing literature, including prior work by the author of this article. Through diverse examples spanning from protein folding to linguistic syntax and beyond, the significance of folding as not only a minimal precondition for semiosis but also a potent modelling system has been underscored. Furthermore, the application of folding principles in artificial intelligence highlights its relevance in contemporary interdisciplinary research. By integrating insights from multiple disciplines and culminating in an examination of Ilyin's and Paolucci's comprehensive models of folding and recursion types, this study hopes to contribute to a richer understanding of the intricate interplay between folding and semiotic modelling, prompting further inquiry into the profound implications of folding as a fundamental process underlying the construction and interpretation of meaning across diverse domains.

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Vers un cadre biosémiotique pour l'IA : le pli et la dynamique du sens

Cet article se consacre aux intersections entre repliement et sémiotique, servant de méta-commentaire au discours de Howard Pattee en réponse à l'ouvrage de Terrence Deacon intitulé « Symbol Grounding Precedes Interpretation » (2021), approfondi en 2023. S'inscrivant dans un contexte d'autoréflexion récursive, l'article examine le repliement comme activité sémiotique fondamentale et modélisation sémiotique élémentaire, établissant des liens avec la proposition de Pattee concernant le repliement des protéines comme précurseur de la sémiose et de l'interprétation. Au cœur de ce discours se trouve l'affirmation selon laquelle le repliement constitue non seulement un prérequis fondamental à la sémiose, mais aussi un puissant système de modélisation. À travers une perspective multidisciplinaire, l'article explique comment le repliement se manifeste comme mécanisme de modélisation dans divers domaines, de la biologie à la syntaxe. Il propose notamment une application des principes du repliement à l'IA. En naviguant dans le cadre du repliement en tant que modélisation sémiotique, cet article contribue à une compréhension plus approfondie des mécanismes fondamentaux de la signification et de l'interprétation dans les systèmes sémiotiques.

Tehisaru biosemiootilise raamistamise poole: voltimine ja tähendusdünaamika

Artikkel on pühendatud voltimise ja semiootika lõikumiskohtadele, olles metakommentaariks Howard Pattee artiklile “Sümboli aluspõhistamine eelneb tõlgendamisele” (2021), mis on vastus Terrence Deaconi töödele ja leidis edasist täiendamist 2023. aastal. Rekursiivse enesepeegelduse kontekstis raamistatud artikkel uurib voltimist kui fundamentaalset semiootilist tegevust ning elementaarset semiootilist modelleerimist, leides kokkupuutepunkte Pattee oletusega, mis peab valkude voltimist semioosi ja tõlgendamise eelkäijaks. Selles diskursuses on keskne väide, et voltimine toimib mitte üksnes semioosi algatamistingimusena, vaid ka võimsa modelleeriva süsteemina. Läbi multidistsiplinaarse prisma valgustab artikkel seda, kuidas voltimine ilmneb modelleeriva mehhanismina mitmekesistes valdkondades alates bioloogiast kuni süntaksini. Eriti osutab artikkel voltimispõhimõtete võimalikule rakendamisele tehisarus. Käsitades voltimisraamistust semiootilise modelleerimisena annab artikkel panuse tähistamise ja tõlgendamise aluseks olevate mehhanismide sügavamale mõistmisele semiootilistes süsteemides.