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Categorical Abstractions for Representing Temporal Organizations of Type Mechanisms

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【Abstract】 Craver's diagram, comprising symbols such as X (entity), S (mechanism), ϕ (activity), and ψ (phenomenon), is widely used to represent biological mechanisms in the New Mechanism. However, this paper demonstrates that Craver's framework lacks the formal capacity to adequately capture the organizational structures and functional dynamics essential for mechanistic explanations, particularly the temporal interplay among entities and activities or the relational nature of enzymatic state transitions. To address these limitations, this paper proposes a supplementary framework based on category theory, enabling the abstraction of mechanisms as temporally organized structures of state transitions. By integrating key features such as order, frequency, and duration, categorical diagrams provide a cohesive representation of type mechanisms, supporting the deficiencies of token-centric approaches. Using protein synthesis as a case study, the paper illustrates how categorical abstractions enhance the formal representation of biological mechanisms while emphasizing the philosophical importance of organizational dimensions.

【Key Words】 Craver's Diagram, Biological Mechanisms, Organizations, Representation, Category Theory

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1 Introduction

Biological objects in living systems are composed of their own components and participate in mechanisms that produce regular phenomena. The New Mechanism is a contemporary philosophical framework for understanding biological practice to explain the phenomena. Within this framework, Craver (2007) introduces a symbolic diagram to represent entities (X_i), activities (ϕ_i), mechanisms (S), and its phenomena (ψ). According to Glennan (2017: p. 22), Craver's diagram is a two dimensional representation of biological mechanisms. The horizontal dimension depicts temporal and causal interactions of token events (X_i's ϕ_i-ing) within a mechanism, while the vertical dimension illustrates hierarchical relations between a mechanism (S) as a whole and its individual components (X_i or ϕ_i). Craver's diagram is widely adopted by proponents of the New Mechanism to address various debates, including the metaphysical controversy over constitutive relevance (Baumgartner & Gebharter (2016), Baumgartner & Casini (2017)), the nature of interlevel experiments (Krickel (2018); Craver, Glennan & Povich (2021)), methodological inquries for discovering mechanistic components (Kästner (2021), Kästner and Haueis (2021)).

Although Craver's symbolic diagram has been widely used to represent mechanisms in various philosophical discussions, it is necessary to assess whether it adequately captures the essence of the New Mechanism. Most proponents of the New Mechanism emphasizes that mechanisms consist of two interdependent components, entities and activities, which *must* be spatially and temporally organized to produce phenomena (Machamer, Darden & Craver (2000), Bechtel & Abrahamsen (2005), Illari & Williamson (2012)). Distinct from

mere aggregates of components, mechanisms derive their explanatory power from the cooperative interactions and organizational features of their components. The explanandum phenomenon, understood as the behavior of the mechanism, emerges from a continuous and temporally coherent association of entities and activities without gaps. Recently, philosophers such as Kästner (2017: ch. 8) and Zednik (2019: pp. 41-46) have underscored the significance of organizational aspects in the New Mechanism, arguing that component-centered representations like Craver's diagram fail to sufficiently address the explanatory role of spatio-temporally organized structures.

Despite Kästner and Zednik's emphasis on the explanatory power of organizational aspects, how to formally represent the organizational structures of mechanisms remains largely unexplored. This paper proposes a mathematical approach to representing these structures, moving beyond Craver's component-centric approach to mechanistic explanation, by introducing category theory. Specifically, this work focuses on the temporal structures of biological mechanisms — characterized by order, rate, and duration — while acknowledging the importance of spatially organizational aspects.[1)]

It is important to clarify that I do *not* argue Craver's diagram is useless or inherently problematic. I recognize its utility in depicting highly linear sequences of events in the world. Furthermore, I ac-

[1)] Spatial organization is pivotal for inferring an entity's pre- or post-activities through its interrelationship between structure and function. Gim (2023a) highlights the significance of this interrelationship in molecular biology and identifies several key types of spatial organization in biological entities, including compositional hierarchy, orientation, shape, and related features. A separate article will address the hierarchical structure of entities represented by spatially organized graphs through category theory in the explanatory context of constitutive relevance. However, due to space constraints, this paper focuses on temporal organizations rather than spatial organizations.

knowledge that Craver's component-centric approach to mechanistic explanation remains vital for identifying the constitutively relevant components of the explanandum phenomenon through experimental strategies. Rather than undermining Craver's diagram or dismissing his focus on components in mechanistic explanation, my aim is to build upon the established contributions of the New Mechanism by seeking to highlight the importance of representing the organizational structures of mechanisms. I believe this work will enhance and extend the foundational achievements of the New Mechanism, fostering a more comprehensive understanding of mechanistic explanations.

The paper is structured as follows: Sec. 2 examines the core principles of the New Mechanism in relation to Craver's symbolic diagram, emphasizing the ontological distinction between *type* mechanisms and their *token* instantiations. It also focuses on the limitations of Craver's diagram in representing spatio-temporal organizational structures and advocates for a more robust framework to capture these organizational dimensions, which are essential to mechanistic explanations. Sec. 3 introduces category theory as a formal tool for representing the temporal structures of type mechanisms. It outlines key categorical concepts, including monoidal categories, and demonstrates their utility in abstracting temporal characteristics such as order, frequency, and duration. Sec. 4 applies category theory to the biological mechanism of protein synthesis, illustrating how processes such as DNA replication, RNA transcription, and protein translation can be formally represented as temporally organized structures of enzymatic state transitions. It will emphasize on the philosophical implications of categorical abstractions for advancing mechanistic explanations, particularly in capturing the dynamical interplay between

states and activities in biological mechanisms.

2 Examining Craver's Diagram

2.1 Type Mechanism and Token Causal Chain

Craver introduces symbolic notations to illustrate mechanisms, as shown in Fig. 1. At the phenomenal level, a phenomenon (ψ-ing) represents the behavior of a mechanism (S), while its components, $X_1, X_2, ..., X_n$ and $\phi_1, \phi_2, ..., \phi_n$, denote entities and activities contributing to S's ψ-ing at the mechanistic level. Entities encompass objects at various ontological levels, such as ionic types (e.g., sodium ions), molecular types (e.g., nitrogenous bases like adenine), macromolecular types (e.g., DNA, RNA), cellular types (e.g., neurons), etc.[2)] According to Machamer, Darden, & Craver (2000, p. 14), activities can be classified into four types: (i) geometrico-mechanical (e.g., opening, closing, rotating, bending, fitting), (ii) electro-chemical (e.g., attracting, repelling, bonding, breaking), (iii) energetic (e.g., diffusing), and (iv) electro-magnetic (e.g., electrically conducting). Craver (2007, p. 7) states that entities are represented by *circles*, while activities are depicted as *arrows* connecting one entity to another. Subcomponents of an entity X_i are organized at a lower level, forming hierarchical interlevel relations: (i) components (X_i's ϕ_i-ing) and a mechanism (S), and (ii) sub-parts (P_i's ρ_i-ing) and a component (X_i).

Craver's symbolic notations are widely used to discuss mechanisms

[2)] The first distinction between levels in mechanistic explanation involves separating the explanandum phenomenon from the underlying mechanism that explains it. The second distinction pertains to classifying objects based on criteria such as size or compositionality. While there are ongoing philosophical debates regarding the nature of mechanistic levels (Eronen (2013), Craver (2015)), this paper does not engage with those discussions.

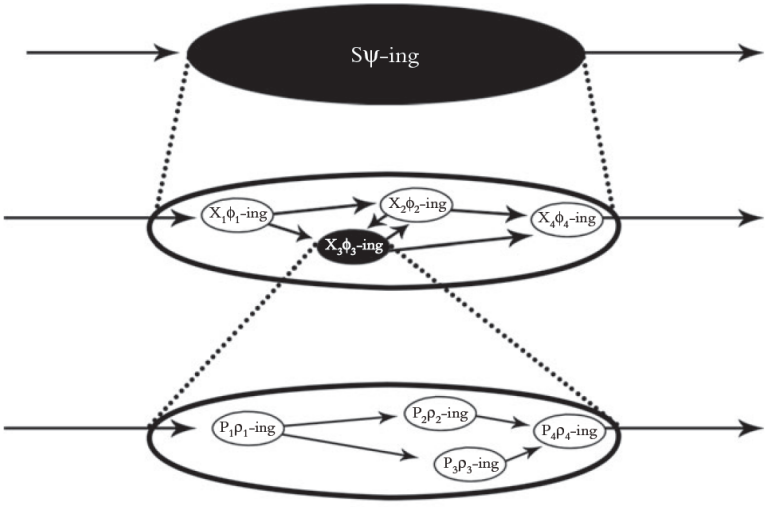

Figure 1: Craver's symbolic diagram (Craver (2007, p. 189))

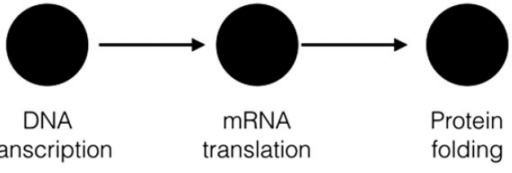

Figure 2: Protein synthesis as a causal chain (Kästner & Andersen (2018, p. 2))

in the philosophy of science. When focusing solely on intra-level interactions among components, without considering hierarchical structures, an explanandum phenomenon (S's ψ-ing) can be represented as a temporal sequence of chain of type entities and type activities (X_i's ϕ_i-ing). For instance, the mechanism of protein synthesis can be expressed as a simple temporal arrangement, DNA $\rightarrow$ mRNA $\rightarrow$ Proteins, by considering only entities (Craver and Darden 2013, p. 32). Kästner and Andersen (2018) provide a more detailed representation, describing the mechanism of protein synthesis as a causal chain of components (see Fig. 2), with activities such as transcription, translation, and folding associated with each entity. Assuming a type mechanism (S's ψ-ing) consists of three type entities and their corresponding type activities (X_i's ϕ_i-ing, where $n = 3$), Kästner and Andersen's diagram represents a token mechanism, instantiated as the specific case of protein synthesis.

Craver's diagram reveals several key principles in the New Mechanism. First, the symbolic notations represent dual ontologies: objects (a mechanism S or entities X_i) and their activities (a phenomenon ψ-ing or activities ϕ_i-ing). Second, Craver's framework maps entities to activities in a one-to-one manner, as illustrated by the protein synthesis: DNA (X_1) is transcribed (ϕ_1), mRNA (X_2) is translated (ϕ_2), and so on. Third, the symbolic notations refer to types rather than tokens. For instance, when concrete macromolecules such as DNA, mRNA, and proteins are assigned to a temporal chain of type entities and type activities (X_i's ϕ_i-ing) as shown in Fig. 2, a type mechanism's phenomenon (S's ψ-ing) can be instantiated by a token mechanism in the case of protein synthesis. As Craver explains: "a token instance of the property ψ is, in part, constituted by an instance of the property ϕ" (Craver (2007, p. 153)).

Craver's diagram is fundamentally rooted in notations representing types that can be instantiated by specific objects and their corresponding activities. These instantiated entities and their activities are typically regarded as *events* that causally produce the explanandum phenomenon. While Craver's notation ostensibly emphasizes types, it is ultimately associated with token events involving concrete objects and their activities within causal chains to mechanistically explain the targeted phenomenon (see Overton (2011), for a similar perspective). This ontological emphasis on token-level causal interactions is evident in discussions such as Craver, Glennan & Povich (2021, p. 8826) refinement of how token events instantiate constitutive relevance. By grounding mechanistic explanation in the causal chain of token events, Craver's framework transitions from abstract type-level representations to the concrete process of causal sequences that underpin mechanistic phenomena.

2.2 The Explanatory Significance of Organizations

Craver's diagram, while widely recognized for its utility in representing causal chains among token events of instantiated mechanisms, has faced significant criticism for its lack of a formal framework to represent organizational aspects. As Wimsatt (1997) argues, a mere collection of components is never equivalent to a mechanism. Regardless of how accurately we identify the relevant components of an explanandum phenomenon, the mechanistic explanation remains incomplete if we fail to comprehend how these constitutively relevant components are *organized* spatio-temporally. Craver (2007, p. 153) acknowledges this, emphasizing that mechanistic explanations require more than identifying entities and activities—they must also describe how these components are organized to produce phenomena

(Craver (2006, p. 373), Craver (2007, p. 138)).

Despite this acknowledgment, Craver does not provide a formal framework for representing organizations. Instead, he just introduces dual notations for entities (X_i) and activities (ϕ_i) and vaguely references organizational features as "ϕ #," described as the property of being a given combination of components and organization (Craver (2007, p. 212)). Temporal organization is implied to emerge from activities (ϕ_i), while spatial organization is linked to the arrangement of entities (X_i). Consequently, "#" functions as a limited symbol for partially representing organization depending upon type components. However, Craver's diagram lacks explicit tools to capture organizational features among type entities and type activities simultaneously essential for mechanistic explanations.

Given the symbolic limitations in representing organizational structures, Craver's diagram appears to adopt an *object-centered* view, emphasizing the intrinsic properties of individual entities and their activities. This approach has prompted debates regarding its adequacy in capturing the organizational dimensions of mechanisms. Kästner (2017, pp. 122–123) argues that Craver's diagram focuses excessively on localized interactions among individual components, neglecting the organizational structures essential for explaining complex phenomena. The explanatory power of a mechanism often hinges not only on identifying its parts but also on understanding how these parts are spatially and temporally organized. Kästner highlights that targeting organizational structures, rather than individual components, often yields more insightful explanations, particularly in cases involving global patterns or systemic behaviors within neuroscience.

Zednik (2019, pp. 43–44) extends this critique by contrasting Craver's component-centered approach with the organization-centric practices

prevalent in network neuroscience. He observes that models in network neuroscience prioritize organizational properties—such as connectivity patterns and topological features—over the intrinsic properties of individual components. Zednik critiques Craver's account of constitutive relevance, particularly his *mutual manipulability* criteria, for failing to accommodate these organization-centric models.[3)] He argues that models representing organizational features are essential for understanding distributed neural activity and emergent phenomena in brain networks, suggesting that mechanistic explanations should shift toward dynamic and relational representations aligned with contemporary scientific practices.

Both Kästner and Zednik converge on the view that Craver's diagram, while useful for detailing component-level interactions, inadequately addresses the organizational structures crucial to many mechanistic explanations. However, neither offers concrete methods for formally representing spatio-temporal organization or developing type-level formalizations of mechanistic explanations. To address this, advancing an organization-based framework requires developing an abstract, type-level formalism to better capture the explanatory relevance of organizational features in mechanistic explanations.

In sum, the absence of formal constraints for representing spatio-temporal organization in Craver's diagram limits its capacity to fully capture the explanatory relevance of underlying mechanisms. While effective in depicting entities and their activities, the symbolic framework overlooks the organizational structures that integrate these components into cohesive mechanisms. Addressing this deficiency is cru-

[3)] Craver (2007) introduced the concept of mutual manipulability to account for the nature of constitutive relevance in mechanistic explanations. According to this concept, X is considered as a part of the whole S if and only if an ideal intervention that alters X's ϕ-ing also changes S's ψ-ing, and vice versa.

cial for enhancing the explanatory power of mechanistic models, particularly in fields where spatio-temporal dynamics play a central role in explaining biological phenomena. The next section will examine methods for representing organizational aspects, with a focus on the temporally organized structures of mechanisms.

3 Representing Temporal Structures

3.1 The Necessity of Abstraction

As previously discussed, Craver introduces straightforward symbolic notations to represent key concepts in the New Mechanism, such as X_i, its ϕ-ing, S, and its ψ-ing. While Craver's symbolic diagram is both intuitive and widely adopted, it raises a critical question: how can the essential organizational feature, particularly the *temporal structure* among components at a specific level, be formally represented? As illustrated in Fig. 2, the only means of linking an individual entity's activity (X_i's ϕ_i-ing) involves arrows within Craver's diagram, which are used to depict the organization of entities and activities.

Biological mechanisms, however, are far more complex than a linear causal chain of token events. This complexity can be classified into four key features: (i) the intricacy of initial and final states, (ii) branching and convergence in intermediate steps, (iii) multi-entity interactions within a single activity, and (iv) the recurrent usage of a single entity. Concrete examples illustrating each of these features are provided below.

First, most biological phenomena begin with an input state and culminate in an output state, both of which are inherently complex. In protein synthesis, the initial state includes DNA as the primary en-

tity along with essential transcriptional components like RNA polymerase, nucleotides, and promoter regions. The final state involves the synthesized protein and critical conditions for folding, such as molecular chaperones and an optimal cellular environment.

Second, many processes involve branching, convergence, or both. In protein synthesis, branching occurs when multiple RNA polymerases simultaneously transcribe different DNA segments, while convergence is seen during translation as ribosomes process multiple mRNA transcripts to produce identical proteins. These pathways enhance robustness and efficiency, reflecting intricate interdependencies.

Third, activities within intermediate stages often rely on interactions among multiple entities. During DNA transcription, RNA polymerase collaborates with promoter regions, transcription factors, and helicase enzymes to elongate RNA strands. Similarly, in mRNA translation, ribosomes work with tRNA, aminoacyl-tRNA synthetases, and elongation factors to assemble polypeptides. These interactions exemplify the cooperative dynamics essential for biological functions.

Finally, a single entity can participate repeatedly across stages. Ribosomes, for instance, sequentially translate multiple mRNA transcripts, producing numerous polypeptides. This repeated involvement underscores their versatility and centrality within the mechanism of protein synthesis. (See Gim (2023b) for more details on this case study.)

Biological mechanisms, as discussed above, are far too complex to be adequately represented by a linear causal chain of discrete events. Representing all activities and organizational features within a single, comprehensive type mechanism is fundamentally unfeasible. However, this complexity does not preclude the possibility of

formalizing the temporal structure of mechanisms as a type. While it may be impractical to capture every possible token instantiation within a unified organizational type, identifying and abstracting specific core characteristics of temporal organization into a formalized type is achievable. This endeavor requires a deliberate epistemic focus on *abstraction*, a critical methodological strategy for deriving generalized schemas with varying degrees of detail from the intricate dynamics of biological mechanisms. The subsequent discussion will address which characteristics of temporal organization are pivotal for abstracting biological mechanisms and how these characteristics can be formally represented as type-level temporal structures to enhance the explanatory power of mechanistic explanation.

3.2 Abstracting Temporal Structures of Type Mechanisms

Some proponents of the New Mechanism have identified three key features of temporally organized structures in mechanisms: order, frequency, and duration (Darden (2006), Craver (2007), Craver & Darden (2013)). These elements are not merely descriptive but serve as essential foundations for understanding how the temporal organization of type mechanisms contributes to the explanandum phenomena they produce. Building on these foundational insights, I propose an approach for abstracting complex token instantiations of mechanisms into generalized temporal structures of type mechanisms at the molecular level and formalizing their temporal organization. This proposal seeks to address previously unexplored limitations in Craver's diagram within the New Mechanism, offering a formal framework for conceptualizing the intricate temporal dynamics of biological reactions.

The first step in formalizing the temporal structure of type mecha-

nisms is to focus on the sequential *order* of stages within a biological process. For instance, protein synthesis can be represented by the sequence: DNA $\rightarrow$ mRNA $\rightarrow$ Proteins, which encapsulates the flow of genetic information culminating in the synthesis of amino acids. This sequence underscores the informational transformation inherent in the process, with each stage serving as a critical foundation for the next. By prioritizing the order of events, this framework captures the directional nature of temporal organization, a defining characteristic of many biological mechanisms.

While *order* provides a foundational framework, the integration of *frequency* and *duration* is crucial for fully representing the temporal structures of type mechanisms. Enzymatic reactions form the cornerstone of this abstraction, mediating transitions between biochemical states. Enzymes act as *functions* that facilitate state transitions, where a preceding state (S_{pre}) transforms into a subsequent state (S_{post}) within a temporally ordered framework: $f : S_{\text{pre}} \rightarrow S_{\text{post}}$. For example, in DNA replication, the frequency of helicase activity at the replication fork directly determines the rate of strand unwinding. Concurrently, the polymerization activity of DNA polymerase governs the duration required for nucleotide incorporation. Similarly, during mRNA translation, the elongation cycles facilitated by ribosomes reflect both the frequency of peptide bond formation and the duration of polypeptide elongation.

This enzyme-centered abstraction highlights that state transitions are driven by enzymatic functions, which temporally organize reactions while preserving the ordered progression of states. Moreover, this approach facilitates the consideration of ordered entities as discrete states within enzymatic reactions. Most biological mechanisms primarily involve chemical reactions mediated by enzymes, making

this enzyme-centered approach a suitable method for abstracting the temporal structures of type mechanisms.[4)]

This proposed abstraction significantly diverges from token-level representations, such as Craver's diagram, which primarily focus on individual components and their activities. Instead, it emphasizes a generalized understanding of temporal structures, integrating order, frequency, and duration into a unified and abstract framework. By moving beyond token-specific details, this approach accommodates the inherent complexity of biological mechanisms while maintaining

4) The *frequency* and *duration* of enzymatic reactions, as described above, can be effectively modeled using the Michaelis-Menten equation:

$$v = \frac{V_{\max}[S]}{K_m + [S]},$$

where v is the reaction rate, $V_{\max}$ is the maximum rate, $[S]$ is the substrate concentration, and K_m is the Michaelis constant. This equation illustrates how substrate concentration influences reaction *rates*, directly correlating with enzymatic activity *frequency*. For example, RNA polymerase activity during transcription exhibits a saturation point at which the reaction rate plateaus, reflecting the temporal limits of enzymatic efficiency. Additionally, the *duration* of enzymatic activity can be inferred from the turnover number (k_{cat}), which measures the number of catalytic cycles per unit time:

$$k_{\text{cat}} = \frac{V_{\max}}{[E]},$$

where $[E]$ is the enzyme concentration. Incorporating Michaelis-Menten kinetics into the abstraction of temporal structures strengthens the connection between biochemical principles and the broader framework of type mechanisms. This approach captures the interplay between *order*, *frequency*, and *duration*, offering a cohesive framework for representing temporal dynamics in biological mechanisms.

conceptual clarity.[5] [6]

3.3 Category Theory for Representing Type Mechanisms

Category theory, often described as "the language of arrows in mathematics", provides a powerful framework for abstracting the temporal structures of type mechanisms. Unlike set theory, which emphasizes individual objects and their properties, category theory prioritizes relationships (morphisms) between objects, capturing the structural and dynamic characteristics of systems. This shift from object-centric to structure-centric representation is particularly well-suited for modeling the temporal organization of biological mechanisms,

[5] One reviewer highlighted the need for further logical and mathematical investigation into whether Craver's diagram at the token level and my categorical abstraction at the type level can formally coexist. To address this, the reviewer proposed two possible approaches: (i) extending event-centered diagrams to the type level and subsequently integrating the extended model with category theory, or (ii) directly establishing a formal connection between the diagram and category theory. Of these, the reviewer considered the second approach to be theoretically more promising. I sincerely appreciate this insightful suggestion and fully concur with its significance. In particular, the relationship between Craver's token-level diagram and categorical abstraction at the type level is not only closely tied to the challenge of representing mechanisms but also has profound implications for the methodology of mechanistic explanation. I plan to explore this issue in greater detail in future research.

[6] This reviewer also suggested a novel possibility for representing temporal organization by integrating category theory with probabilistic approaches. Specifically, He (or she) proposed that incorporating Markov chains into categorical frameworks could lead to a more plausible methodology for studying biological processes, which inherently involve uncertainty. This is a highly intriguing suggestion, as it closely relates to existing research on representing mechanisms using Bayesian network theory (see Gebharter 2014 etc.) and raises the question of how such approaches can be effectively integrated with category theory. Furthermore, this topic is deeply connected to the broader challenge of constructing a more general formal theory of mechanisms, making it a promising avenue for future exploration. I am sincerely grateful to the reviewer for this innovative and valuable suggestion.

where interactions and transformations are fundamental. Category theory offers a formal framework for representing enzyme-centered abstractions of type mechanisms.

First, let me define a category: A *category* $\mathscr{C}$ consists of the following elements:

1. A collection of *objects* (e.g., A, B, C).
2. A collection of *morphisms* $f : A \to B$, representing relationships or transformations between objects.
3. *Composition* of morphisms $g \circ f : A \to C$, satisfying associativity.
4. *Identity morphisms* $1_A : A \to A$, ensuring each object has a self-loop that preserves its structure.

Second, a *monoidal category* $\mathbb{C}$ is a basic mathematical structure in order to abstract temporal structures of type mechanisms by introducing a *tensor product*, $\otimes$, which combines objects and morphisms to represent interactions or parallel processes. Formally, a monoidal category includes:

1. A *tensor product functor* $\otimes : \mathbb{C} \times \mathbb{C} \to \mathbb{C}$.
2. A *unit object* I, representing an identity element for the tensor product.
3. *Natural isomorphisms*, including (Fig. 3):
    - The *associator*: $(A \otimes B) \otimes C \xrightarrow{\alpha_{A,B,C}} A \otimes (B \otimes C)$,
    - The *left unitor*: $I \otimes A \xrightarrow{\lambda_A} A$,
    - The *right unitor*: $A \otimes I \xrightarrow{\rho_A} A$.

Third, *graphical calculus* provides an intuitive way to visualize monoidal categories:

1. Objects (e.g., A, B) are represented as lines.
2. Morphisms (e.g., $f : A \to B$) are depicted as boxes with input and output lines.
3. Tensor products (e.g., $A \otimes B$) are represented as parallel lines or combined paths.
4. Identity morphisms and natural isomorphisms (e.g., associators, unitors) are explicitly represented, preserving structural consistency.

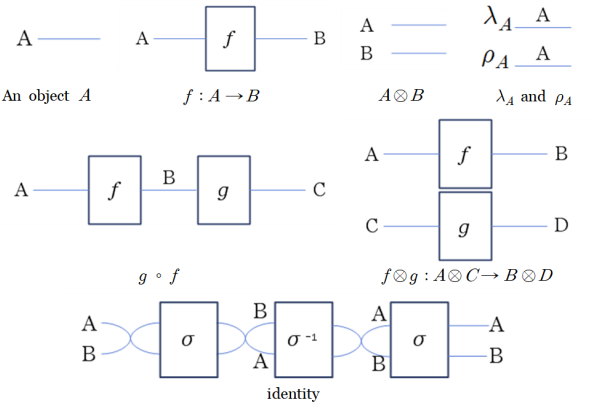

Figure 3: Graphical calculus

To formally represent biological mechanisms as temporally organized structures using monoidal categories, it is essential to establish certain rules (Fong and Spivak 2019), with a formal interpretation of the enzyme-centered abstractions of type mechanisms. Assume that

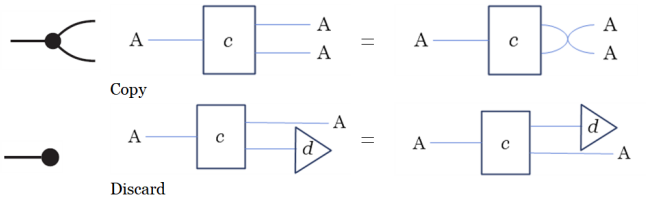

Figure 4: Comonoids

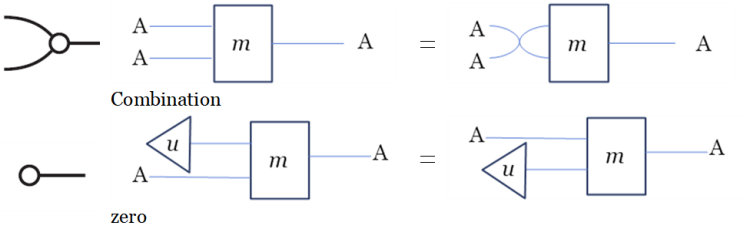

Figure 5: Monoids

the primary structures of biological macromolecules, such as DNA, RNA, and proteins, exhibit a preordered structure.[7)]

Using the definition of monoidal categories, the basic components for graphical representations are (Fig. 3):

- **Objects**: Represented as lines (e.g., A), where the identity morphism $id_A : A \to A$ is implied.
- **Morphisms**: Represented by boxes, with inputs on the left and outputs on the right (e.g., $f : A \to B$).
- **Composition**: Connecting outputs and inputs of sequential morphisms (e.g., $f : A \to B$ and $g : B \to C$ produce $g \circ f : A \to C$).
- **Tensor Product**: Represented by parallel lines (e.g., $A \otimes B$) or combined morphisms (e.g., $f \otimes g : A \otimes C \to B \otimes D$).
- **Symmetry**: Over-crossing and under-crossing morphisms (e.g., $\sigma_{A,B} : A \otimes B \to B \otimes A$) are equivalent in symmetric monoidal categories.

This graphical calculus can be classified into two fundamental structures: monoids and comonoids.

- **Comonoids** (Fig. 4): Include operations like *copy* ($c : A \to A \otimes A$) and *discard* ($d : A \to I$). These satisfy rules ensuring consistency, such as $\rho_A \circ (id_A \otimes d) \circ c = id_A$.
- **Monoids** (Fig. 5): The dual category of comonoids, involving operations like *combination* ($m : A \otimes A \to A$) and *unit addition* ($u : I \to A$).

7) A preorder relation on a set X defines a structure denoted by $\leq$, where X consists of objects, and relationships are preserved through monotone morphisms, which are structure-preserving maps. For instance, a monotone morphism $f : X \to Y$ connects each element $x \in X$ to a corresponding element $y \in Y$, maintaining the preorder relationship.

Monoidal categories, combined with graphical calculus, offer type-level frameworks that effectively abstract the intricate temporally organized structures of type mechanisms, including branching, convergence, and enzymatic mediation of state transitions. For example:

- **Branching and Convergence**: The tensor product $\otimes$ represents the parallel composition of processes, while morphisms capture their interactions. Additionally, comonoids and monoids are particularly useful for representing branching (diverging) and converging pathways, respectively.
- **State Transitions**: Enzymes can be modeled as morphisms facilitating state transitions: $f : S_{\text{pre}} \to S_{\text{post}}$, where S_{pre} represents an input state, and S_{post} represents an output state. In graphical calculus, enzymes can be represented by boxes, while states are depicted as lines. Examples include:
  - In *DNA replication*, helicase unwinds the DNA helix, and DNA polymerase incorporates nucleotides, both of which can be represented as sequential morphisms.
  - During *DNA transcription*, RNA polymerase transitions genetic information from DNA's double-helical state to mRNA's single-stranded state.
  - During *mRNA translation*, ribosomes catalyze elongation cycles, with each cycle corresponding to a morphism that transforms the biochemical state of the growing polypeptide.

Using monoidal categories, biological mechanisms can be represented as temporally organized structures of state transitions me-

diated by enzymatic activities. This approach abstracts the temporal structures of type mechanisms by emphasizing sequential order, branching and converging pathways, and enzymatic functions that transform input states into output states. Unlike Craver's token-focused diagrams, monoidal categories provide a formal framework that integrates order, frequency, and duration, enabling the cohesive representation of temporal complexity. By modeling mechanisms as processes from an initial to a terminal state, with enzymes facilitating regular and enduring state transitions, this framework offers a robust mathematical foundation for advancing mechanistic explanations in molecular biology. The essential temporal structures of protein synthesis, demonstrating these principles, will be explored in the following section.

4 A Case Study: Protein Synthesis

4.1 Overview from DNA to Proteins

Protein synthesis transforms genetic information encoded in DNA into functional proteins through three sequential and enzyme-mediated processes: replication, transcription, and translation. Each molecular structure—DNA, RNA, and protein—can be interpreted as a distinct state of genetic information, with transitions between these states driven by enzymatic activities that govern the temporal organization of the entire mechanism

Replication initiates the transformation of genetic information by duplicating the double-stranded DNA into two identical copies. Helicase unwinds the double helix, converting the DNA from a stable double-stranded state into two single-stranded templates. Single-stranded binding (SSB) proteins stabilize these strands, while DNA

polymerase catalyzes the synthesis of complementary daughter strands. This enzymatic activity proceeds in the $5'$-$3'$ direction, creating the leading strand continuously and the lagging strand discontinuously through Okazaki fragments. DNA ligase completes the process by joining fragments, ensuring the newly synthesized DNA returns to its double-stranded state. Each step represents a precise enzymatic state transition, maintaining the integrity of genetic information.

In transcription, genetic information is transcribed from DNA into messenger RNA (mRNA), transitioning from the stable double-helical state of DNA to the single-stranded state of RNA. RNA polymerase binds to specific promoter sequences on DNA, unwinds the double helix locally, and catalyzes the synthesis of mRNA in the $5'$-$3'$ direction. Unlike DNA replication, transcription does not require a primer and is driven forward by the hydrolysis of pyrophosphate. Once synthesized, the mRNA represents a new state of genetic information, ready to guide protein synthesis.

Translation converts the genetic state encoded in mRNA into a functional protein. Ribosomes, transfer RNA (tRNA), and associated enzymes coordinate this process. During initiation, the ribosome assembles at the start codon (AUG), and tRNA delivers the corresponding amino acid (methionine). In elongation, peptidyl transferase catalyzes the formation of peptide bonds as the ribosome moves along the mRNA in the $5'$-$3'$ direction, sequentially linking amino acids into a growing polypeptide chain. Termination occurs when the ribosome encounters a stop codon (UAA, UGA, or UAG), releasing the completed polypeptide. The enzymatic activities at each step represent state transitions that progressively transform the genetic information into a functional protein structure.

In sum, protein synthesis integrates the replication of DNA, the

transcription of RNA, and the translation of mRNA into proteins as a series of temporally organized, enzyme-mediated state transitions. This framework highlights the role of molecular structures as states of genetic information and the importance of enzymatic processes in driving these transitions. These cases provide the foundation for the categorical abstraction of temporal structures in protein synthesis, explored in the next subsection.

4.2 A Categorical Abstraction of Temporal Structures from DNA to Protein

In the mechanism of DNA replication (Fig. 6), helicase unwinds (h) the double strands ($S_1 \otimes S_2$) into two individual strands (S_1, S_2). DNA polymerase (and DNA ligase) then copies each strand. The copied strands (S_1' and S_2') are rewound with their respective templates, forming $S_1 \otimes S_1'$ and $S_2 \otimes S_2'$. Although parental DNA is copied twice, only one generation is shown in this scheme.

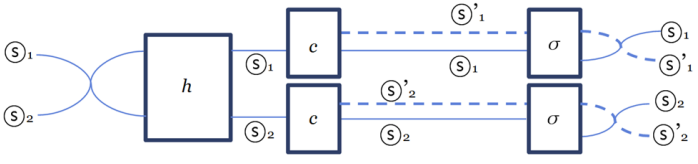

Figure 6: A Scheme of the Mechanism of Replication

In the transcription mechanism (Fig. 7), RNA polymerase performs both unwinding (h) and copying (c) functions. A messenger RNA (mRNA, m) strand is synthesized on a single-strand template (S_1). After transcription, the original strands (S_1, S_2) are rewound ($S_1 \otimes S_2$).

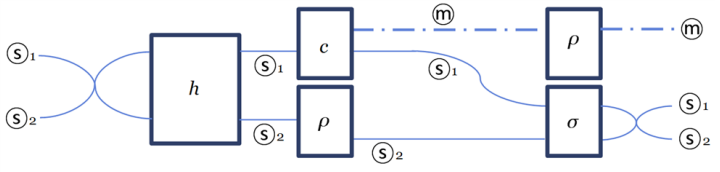

Figure 7: A Scheme of the Mechanism of Transcription

Figure 8: A Scheme of the Mechanism of Translation

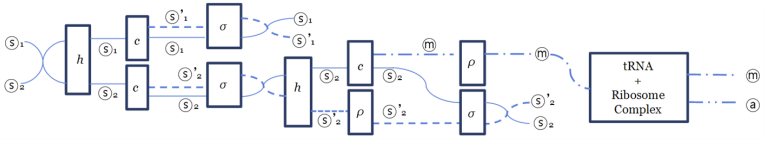

Figure 9: The Complete Process of Protein Synthesis from DNA to Proteins

In the translation mechanism (Fig. 8), transfer RNAs (tRNAs) partition the mRNA sequence into codons (three-nucleotide units), forming a poset. For example, the mRNA sequence A-U-C-G-C-C-A-G-A-U-A-C can be partitioned as [A-U-C], [G-C-C], [A-G-A], [U-A-C]. Each codon corresponds to a specific tRNA carrying an amino acid. Ribosomes synthesize these amino acids into a linear polypeptide chain, such as [Ile]-[Ala]-[Ser]-[Tyr].

Table 1: Functional interpretations of mechanism of protein synthesis

	enzyme	input	output
REPLICATION	helicase	$S_1 \otimes S_2$	S_1, S_2
REPLICATION	DNA polymerase	S_1, S_2	$S_1 \otimes S_2$, $S_1' \otimes S_2'$
TRANSCRIPTION	RNA polymerase	$S_1 \otimes S_2$	S_1, S_2
TRANSCRIPTION	RNA polymerase	S_1, S_2	$S_1 \otimes S_2$ or m
TRANSLATION	tRNA	codon	anti-codon
TRANSLATION	ribosome	amino acids	a chain of AAs

The complete temporal structure of protein synthesis is depicted in Fig. 9, which links the mechanisms of replication, transcription, and translation into a cohesive input-output system. This diagram illustrates how genetic information flows from DNA to RNA and finally to proteins. Unlike Craver's diagram, this categorical graph in Fig. 9 successfully represent temporal structures of type mechanism of protein synthesis. It also represents branching, convergences, and enzymatic functions mediating state transitions (Table. 1). For example, a helicase divides double helical strands into individual strands, and RNA polymerase transcribes genetic information into mRNA.

The categorical abstraction of protein synthesis not only formalizes the temporal structures of enzymatic processes but also provides a

conceptual perspectives for understanding the dynamic interplay between states and activities. By representing type mechanisms as temporally organized structures, category theory emphasizes the relational nature of biological processes over isolated components. This abstraction supports traditional token-centric models by illustrating how type-level patterns of chemical reactions contribute to the emergent properties of mechanisms. Philosophically, this approach underscores the importance of recognizing mechanisms as dynamic systems, where organizational features and state transitions are integral to explanatory practices in the biological sciences.

5 Conclusions

This paper has explored a novel approach to interpreting and formalizing the key characteristics of biological mechanisms, particularly their temporal organizations, through a categorical framework. While Craver's symbolic diagram has been widely influential in the New Mechanism, it demonstrates significant limitations in capturing the temporal structures that are crucial for a comprehensive mechanistic explanation. By addressing these gaps, this paper provides supplementary demonstrations for advancing not only token instantiations but also their type mechanisms.

First, temporal organizations, characterized by order, frequency, and duration, require a shift from Craver's token-centric perspective to a type-level framework that emphasizes state transitions mediated by enzymatic activities. This enzyme-centered abstraction highlights how mechanisms dynamically progress through biochemical states, with enzymes facilitating transitions that define the temporal structure of replication, transcription, and translation. By integrating tem-

poral characteristics into a cohesive framework, this approach offers a more robust representation of the dynamical processes inherent to biological mechanisms.

Second, the paper distinguishes between passive entities, which represent biochemical states, and active entities like enzymes, which perform state transformations. Unlike Craver's approach, which treats entities and activities without differentiation, this work underscores the need for a formal system that clearly represents both types of entities and their roles within mechanisms. Such distinctions are crucial for defining mechanisms as dynamical structures, where state transformations are explicitly mediated by enzymatic functions.

To operationalize these conceptual advances, I propose categorical graphs as a formal framework for representing type mechanisms. Category theory offers a systematic method for abstracting the temporal structures of mechanisms. Through the use of monoidal categories, this approach captures essential features such as branching, convergence, and enzymatic state transitions, providing a mathematically grounded representation of biological complexity.

In sum, this paper advocates for a categorical abstraction of type mechanisms that transcends token-level interactions and linear causal chains. By formally integrating the temporal and spatial dimensions of mechanisms, this framework not only enriches the New Mechanism but also offers practical tools for advancing explanatory models in molecular biology. Future research should further explore the application of categorical frameworks to other domains of biology, particularly those involving complex spatio-temporal dynamics, to fully realize their potential in mechanistic explanations.

References

Baumgartner, M., & Gebharter, A. (2016), "Constitutive relevance, mutual manipulability, and fat-handedness", *The British Journal for the Philosophy of Science*, 67(3), pp. 731–756.

Baumgartner, M., & Casini, L. (2017), "An abductive theory of constitution", *Philosophy of Science*, 84(5), pp. 1–22.

Bechtel, W., & Abrahamsen, A. (2005), "Explanation: A mechanist alternative", *Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences*, 36(2), pp. 421–441.

Craver, C. F. (2007), *Explaining the Brain: Mechanisms and the Mosaic Unity of Neuroscience*, Oxford University Press.

Craver, C. F. (2015), "Levels, mechanisms, and the explanatory power of description", in A. Grüne-Yanoff and S. R. H. Eronen (eds.), *Explanation Beyond Causation: Philosophical Perspectives on Non-Causal Explanations*, Oxford University Press.

Fong, B., & Spivak, D. I. (2019), *An Invitation to Applied Category Theory: Seven Sketches in Compositionality*, Cambridge University Press.

Gebharter, A. (2014), "A Formal Framework for Representing Mechanisms?", *Philosophy of Science*, 81(1), pp. 138–153.

Gim, J. (2023a), "Categorical Abstractions of Molecular Structures of Biological Objects: A Case Study of Nucleic Acids", *Global Philosophy*, 33, No. 43.

Gim, J. (2023b), "The Ontic-Epistemic Debates of Explanation Revisited: The Three-Dimensional Approach", *Philosophical Problems in Science (Zagadnienia Filozoficzne w Nauce)*, 74, pp. 99–169.

Glennan, S. (2017), *The New Mechanical Philosophy*, Oxford University Press.

Illari, P. M., & Williamson, J. (2012), "What is a mechanism? Think-

ing about mechanisms across the sciences", *European Journal for Philosophy of Science*, 2(1), pp. 119–135.

Kästner, L. (2017), *Mechanistic Explanations in Physics and Beyond*, Cambridge University Press.

Kästner, L., & Haueis, P. (2021), "Componential mechanistic explanation meets the integrated hypothesis", *Synthese*, 199(1–2), pp. 3489–3513.

Krickel, B. (2018), *The Mechanical World: The Metaphysical Commitments of the New Mechanistic Philosophy*, Springer.

Machamer, P., Darden, L., & Craver, C. F. (2000), "Thinking about mechanisms", *Philosophy of Science*, 67(1), pp. 1–25.

Stryer, L., Tymoczko, J. L., & Berg, J. M. (2015), *Biochemistry*. W. H. Freeman and Company.

Zednik, C. (2019), "Mechanistic explanations, computational models, and top-down causation in neural networks", *Philosophy of Science*, 86(1), pp. 41–59.

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유형 메커니즘의 시간적 구조를 표상하기 위한 범주적 추상화

김 진 영

크레이버(C. Craver)의 다이어그램은 X (개체), S (메커니즘), ϕ (활동), ψ (현상)과 같은 기호들로 구성되어 있으며, 새로운 메커니즘(New Mechanism) 철학에서 생물학적 메커니즘을 표현하는 데 널리 사용된다. 그러나 본 논문에서는 크레이버의 다이어그램이 메커니즘적 설명에 필수적인 조직 구조 및 기능적 역학, 특히 개체와 활동 간의 시간적 상호작용이나 효소 매개 상태 전환의 관계적 본질을 충분히 포착할 형식적 능력을 결여하고 있음을 보여준다. 이러한 한계를 극복하기 위해 본 논문은 카테고리 이론(category theory)을 기반으로 한 보완적 틀을 새롭게 제안하며, 이를 통해 메커니즘을 상태 전환의 시간적으로 조직된 구조로 추상화하는 방식을 제시한다. 순서(order), 빈도(frequency), 지속 시간(duration)과 같은 시간적 구조의 핵심 요소를 통합함으로써 카테고리 이론은 유형(type) 메커니즘을 응집력 있게 표현하며, 기존의 개별 사건 중심 접근(token-centric approach)의 한계를 보완한다. 단백질 합성을 사례 연구로 활용하여 범주적 추상이 생물학적 메커니즘의 형식적 표현을 어떻게 향상시키는지 보여주며, 메커니즘 연구에서 조직적 차원을 강조하는 철학적 중요성 또한 논의한다.

주요어: 크레이버 다이어그램, 생물학적 메커니즘, 조직 구조, 표상, 카테고리 이론