

Derived Hamiltonians as Cohomological Translators:

A Unified Framework for Physics, Biology, and Computation

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December 30, 2024

Abstract

This paper explores the role of cohomological projections and derived functors as tools to unify disparate domains of physics, biology, and computer science. We introduce the concept of the *derived Hamiltonian* as a fundamental abstraction that translates between classical and quantum systems, encoding hidden symmetries and higher-dimensional topologies. By integrating derived categories, spectral sequences, topos theory, and motivic cohomology, we reveal universal principles underlying natural and computational systems. This framework provides insights into unifying physical theories, modeling biological complexity, and optimizing computational architectures.

1 Introduction

The quest to unify the fundamental forces of nature, describe biological complexity, and improve computational frameworks has driven researchers to explore higher-dimensional and topological structures. Traditional approaches often fail to reconcile the apparent differences between classical and quantum systems, biological evolution, and distributed computation.

Cohomological projections and functorial physics offer an alternative by representing these domains as shadows or projections of a higher-dimensional mathematical reality. This paper proposes that **derived Hamiltonians**—generalizations of classical Hamiltonians—serve as the unifying bridge between these domains by embedding higher-order symmetries, topologies, and invariants.

2 Derived Functors and Cohomological Projections

Derived functors measure the failure of exactness in mappings between mathematical objects, revealing hidden topological and algebraic features. In the context of physics and biology, they map local phenomena (e.g., quantum fields, genetic mutations) to global structures (e.g., spacetime, evolutionary trees).

$$R^i F(A) = H^i(F(I^\bullet))$$

where I^\bullet is an injective resolution of A .

$$H^i(X, \mathcal{F}) = R^i \Gamma(X, \mathcal{F})$$

3 Derived Hamiltonians as Translators Across Domains

The classical Hamiltonian $H(p, q)$ describes the dynamics of particles and fields through phase space. Extending this to a derived setting introduces higher-order corrections that account for topological features, gauge anomalies, and emergent symmetries.

A **derived Hamiltonian** takes the form:

$$\hat{H} = \sum_i R^i H(p, q) + \int_{\Sigma} \mathcal{F} \wedge dA$$

where Σ represents a cohomological surface, and \mathcal{F} encodes topological forms.

This structure applies across domains:

- **Physics:** Higher-order quantum corrections and gravitational anomalies.
- **Biology:** Evolutionary dynamics and protein folding.
- **Computer Science:** Neural network optimization landscapes and algorithmic phase transitions.

4 Motivic Cohomology and Physical Invariants

Motivic cohomology serves as a bridge between algebraic geometry and topological invariants, providing deep structural insight into the fabric of space, matter, and computation. Motivic cohomology links algebraic cycles with higher-dimensional forms, generalizing traditional cohomology theories.

The motivic cohomology of a space X is denoted by:

$$H_M^i(X, \mathbb{Z}(j))$$

where j represents a filtration by codimension, and i measures the degree of cohomological information.

4.1 Physical Interpretation of Motivic Cohomology

In physics, motivic cohomology explains:

- **Gauge Theory:** Classifying gauge bundles through algebraic cycles.
- **String Compactification:** Encoding hidden symmetries in Calabi-Yau manifolds.
- **Black Hole Entropy:** Counting microstates as algebraic cycles.

$$H_M^3(X, \mathbb{Z}(2)) \implies \text{Gauge Anomaly Classes}$$

5 Applications in Biology and Computer Science

5.1 Protein Folding and Evolutionary Pathways

Proteins fold into complex three-dimensional shapes, driven by evolutionary pressures and energy minimization. This folding process can be modeled using derived categories, where each resolution represents an intermediate folding state.

$$H^i(\text{Protein Complex}, \mathcal{F}) = \text{Stable Folding Configuration}$$

5.2 Neural Networks and Topology

Neural networks evolve as high-dimensional manifolds, with each layer acting as a projection of abstract cohomological spaces. The activations across layers can be interpreted as sections of a sheaf, evolving through spectral sequences.

$$E_2^{p,q}(\text{Network}) \implies H^{p+q}(\text{Output Layer})$$

5.3 Persistent Homology in Data Science

Persistent homology tracks the evolution of topological features in data, revealing stable clusters and transient noise. Spectral sequences facilitate efficient computation of persistent homology by iteratively approximating the data's cohomology.

$$\pi^* : H^i(\text{Data Set}) \rightarrow H^i(\text{Filtered Complex})$$

6 Acknowledgments

This research was conducted under the auspices of Magnetron Labs, a research lab dedicated to the intersection of quantum physics, algebraic geometry, and advanced computation.

7 References

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