

Topological decoding of biomolecular fold complexity Scalvini, B.

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Stellingen Behorende bij het proefschrift TOPOLOGICAL DECODING OF BIOMOLECULAR FOLD COMPLEXITY

- 1. The development of biophysical modelling techniques which can integrate biological complexity is critical for the applicability of such methods to biomedical questions.
- 2. While artificial intelligence allows us unprecedented predictive power for protein structure, it has the great limitation of providing little explanation about its decision-making process.
- 3. Topology can be used to extract design principles for drug engineering, development of new materials and technologies with biomimetic properties (Chapter 1).
- 4. In the future, the development of automated topology-based data analysis software will prove fundamental for the screening and diagnosis of malignant mutations in genome sequence.
- 5. Single molecule techniques such as force spectroscopy are uniquely suited to probe the cellular environment because of the insight they allow into transient molecular interactions (Chapter 4).
- 6. While purely geometric approaches provide too much detail and are computationally expensive, an ideal topological tool in the field of biopolymers should retain some geometric information to yield optimal qualitative and quantitative information (Chapter 2).
- 7. The development of a robust theoretical framework can have far-reaching impact, enabling the application of concepts and methods in fields that may appear vastly dissimilar from the framework's original domain (Chapter 6).
- 8. Obtaining a PhD requires both academic dedication and relentless stubbornness, often in equal measure.
- 9. Innovation happens at the intersection between different fields.

Barbara Scalvini Leiden, 5 juli 2023