

# Exploring Persistent Homology: from foundations to protein applications

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Persistent homology is a powerful tool in topological data analysis, offering insights into the shape of data across multiple scales. In this talk, we will start with a theoretical introduction to persistent homology, covering the essential concepts and computational methods, aimed at an audience with a background in graduate-level mathematics. We will then shift focus to an exciting real-world application: the use of persistent homology to study lasso proteins, a newly studied class of proteins [1]. Unlike classical methods based on minimal surfaces, our approach leverages topological features to recognize and classify the distinctive shapes of these proteins, opening new pathways for research in computational biology.

## References

- [1] W. Niemyska, P. Dabrowski-Tumanski, M. Kadlof, E. Haglund, P. Sulkowski and J. Sulowska, *Complex lasso: New entangled motifs in proteins*, Scientific Reports, 2016.