P1: Statistical Inference on Graph Isomorphism

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Abstract. Two graphs are said to be isomorphic if there exists a bijection between their vertex sets that preserves adjacency. Graph isomorphism plays a fundamental role in graph matching, alignment, and representation learning, and is widely used in machine learning to compare network-structured data. However, exact isomorphism is rarely observed in real-world networks, particularly in biological and social systems, where noise, heterogeneity, and measurement variability break strict structural equivalence.

Rather than treating non-isomorphism as a failure of graph matching, we view it as an informative signal. In many applications, networks arise from populations that share a common underlying generative mechanism but differ through noise, perturbations, or disease-related effects. Within a homogeneous group, such as healthy controls, networks are therefore expected to remain closer to a common isomorphism class, whereas between heterogeneous groups, such as clinical populations, systematic deviations from this class may emerge. This perspective motivates quantifying the *degree of deviation from isomorphism* as a statistical descriptor of population-level network organization.

In this work, we propose a principled framework for measuring divergence from graph isomorphism and demonstrate how this measure can be used to statistically characterize within-group consistency and between-group differences in network data. By reframing isomorphism from a binary property into a continuous, quantifiable notion, our approach enables population-level inference on network structure without requiring exact graph matching, providing a robust tool for statistical analysis of complex networks.