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12:00-1:00 pm

**Biotechnology Center Auditorium
or via Zoom**

<https://uwmadison.zoom.us/j/97615509019>

Aligning Asynchronous Network Data through Persistent Homology

Abstract: We introduce a novel topological data analysis (TDA) approach for aligning asynchronous dynamic networks over time. Our method leverages persistent homology, which decomposes 0D topological features (connected components) and 1D topological features (loops) orthogonally. This decomposition enables the exact computation of the Wasserstein distance, a probabilistic version of optimal transport, into a squared Euclidean distance form with $O(n \log n)$ run time. Our scalable approach allows for localized matching of networks at the edge level, facilitating precise inference and learning. This method can reduce statistical variability by up to 500 times, enabling the detection of signals previously undetectable. We demonstrate the application of this method in aligning asynchronous human functional brain networks obtained from resting-state functional magnetic resonance imaging (rs-fMRI). Human brain activity at rest does not synchronize across subjects, making direct comparisons nearly impossible and posing a significant challenge to the clinical relevance of rs-fMRI. Our approach addresses this challenge by providing a workable solution that performs topological registration of time-varying networks. This talk is partially based on arXiv:2012.00675 (Annals of Applied Statistics) and arXiv:2201.00087 (PLOS Computational Biology).



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