

Compressive Data Fusion and Persistent Homology

Written by Marinka

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My talk at the Summer School on Computational Topology in Ljubljana, Slovenia was about coupling a compressive data fusion methods with algebraic topology, in particular persistent homology. There, I discussed how the latent data space obtained by fusion of heterogeneous biological data sets can be explored with topological methods.

In a case study from molecular biology, which included nearly two dozen data sets, we studied persistence (lifetime) of various topological features, e.g. connected components, loops, voids, tunnels, etc. We showed that significant topological features, i.e. features with long lifetime, also carry biologically relevant information. For example, gene modules with significant topology were enriched for cellular functions and biological processes, and, similarly, persistent drug modules captured the structural similarity between drugs.

The slides of the talk are available.