

Parenclitic hypergraphs and their applications to personalized medicine

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Understanding the differences between individual instances of the same complex system remains a central challenge, particularly in biological contexts. Parenclitic networks offer a means to detect deviations in correlations with respect to reference populations. I will discuss parenclitic hypergraphs, a general framework for identifying anomalies in higher-order correlations across arbitrary interaction orders. After validating the method on synthetic datasets and benchmark ones, I will show how to apply it to patient-derived cancer organoids, capturing temporal changes in gene expression between healthy and cancerous tissues as the disease progresses.