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## On the power and limits of structure-based exon-exon interaction prediction

To perform important cellular functions, Proteins physically interact with each other through protein-protein interactions (PPIs). However, PPIs are not constant but change with varying cellular conditions, e.g., those induced by infections or other diseases. These changes in PPI can be caused by alternative splicing (AS), a biological process, by which a single gene gives rise to multiple proteins. Our goal is to predict PPIs that occur in the event of AS. We explore whether we can exploit existing computational PPI interface prediction methods, based on geometric and convolutional neural networks, to create a network of exon-exon interactions (EEIs). A main task is to evaluate how effectively such an EEI network can be used to predict PPI rewiring caused by AS.

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### Keywords

Protein-protein interaction  
Alternative splicing  
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### TentID

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