# Exploring **possibility** of reusing LIGR-seq datasets for **biological data supported** RNA secondary structure prediction

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LIGR-seq and PARIS are methods for studying RNA-RNA interactions *in vivo* based on reversible crosslinking of double-stranded RNA mediated by a psolaren derivative AMT. Albeit names the methods are very different, the methods themselves are very similar, briefly: crosslinking of double-stranded RNA *in vivo*, digestion of single-stranded RNA, proximity ligation, decrosslinking and sequencing. Apart from the primary objective of detecting intermolecular RNA-RNA interactions, the data from PARIS method were also used to detect intramolecular interactions, thus providing evidence of based paired regions from single RNA molecule. These can be used for directed secondary structure prediction with IRIS method which was developed for PARIS data. Here we explore if there are sequencing reads supporting intramolecular interactions present in *Bacillus subtilis*  LIGR-seq dataset and the possibility to use the IRIS method for the secondary structure prediction.