**STAR3D (Ping Ge and Shaojie Zhang)**

1. The approach does not take into account the self-complementarity in RNA sequences. The base pairs being considered are only for RNA-A with RNA-B. Infact a lot of lncRNAs (rRNAs, miRNAs, snRNAs) show self-complementarity, and the realization of a model for 3D structural alignment of RNAs seems incomplete without taking self-binding into account.
2. Similarly, pseudoknots are prevalent in many ncRNAs – and it has been noted elsewhere that many structure prediction algorithms ignore pseudoknots due to computational costs. However, one possible expansion that is evident from STAR3D is to identify homologous RNA 3D structures. I wonder if the complete exclusion of pseudoknots will give more false positives in homology searching from this method? If that is the case, then one of the major applications of the proposed algorithm will be rendered worthless, so it seems.
3. Silly how the authors only provide some accuracy stats at the very end of the paper, and do not comment on the MCC scores and/or false positive rate from any of the methods. I think this should have formed a necessary output of their comparative analysis, but they did not include it.

**RNABindRPlus**

1. Given the reliance of HomPRIP on the existence of >1 homolog to a query protein’s RNA binding site, cannot the physicochemical features of the residues corresponding to the putative homologous sequences be used for sequence matching to protein binding RNAs? If a sequence of residues binds to a protein site, it does so due to complementarity in residue charge and/or other inherent physicochemical traits. So it seems to me that an easy workaround for excluding any proteins that don’t have experimentally validated RNA homologs would be to use putative homologs based on these properties (A blossom62 matrix can be used, or the alphabet reduction approach discussed earlier in the class).
2. Since the HomPRIP method relies on existence of homologous sequences in the Protein Databank, it appears that it cannot be used to predict new protein-RNA interaction spaces. But what would happen if the SVMOpt output (predicting the binding residues in the query protein) can be used to generate possible homologous RNA sequences as binding candidates. Would this approach still rely on our pre-existing knowledge of protein-RNA interactions, or can it be modified to learn what ‘sequence neighbourhood features’ facilitate strong protein-RNA sites, and thus provide potential new protein-RNA candidates for experimental validation?

Consider

* complexity of algorithm, why it’s faster
* reference databases you use (use ones normally used in the field, along with any additional ones you want)