miRBind: a Deep Learning method for miRNA binding classification

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**Abstract**

The binding of microRNAs (miRNAs) to their target sites is a complex process, mediated by the Argonaute (Ago) family of proteins. Prediction of miRNA:target site binding is an important first step for any miRNA target prediction algorithm. To date, the potential for miRNA:target site binding is evaluated either using co-folding free energy measures, or heuristic approaches based on the identification of binding ‘seeds’, i.e. continuous stretches of binding corresponding to specific parts of the miRNA. The limitations of both these families of methods have produced generations of miRNA target prediction algorithms exclusively focused on ‘canonical’ seed targets, even though unbiased experimental methods have shown that only approximately half of in vivo miRNA targets are ‘canonical’. Here we present miRBind, a deep learning method and web-server that can be used to accurately predict the potential of miRNA:target site binding. We train our method on seed-agnostic experimental data, and show that our method outperforms both seed-based approaches and co-fold free energy approaches. The full code for development of miRBind is freely available at <https://github.com/ML-Bioinfo-CEITEC/miRBind>, and a free web-server is available at <https://ml-bioinfo-ceitec.github.io/miRBind/>