# Modelling small RNA binding using Convolutional Neural Networks

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MOTIVATION

- gene expression regulation by small RNAs is a very important process, it's dysfunction plays a role in many diseases (Alzheimer's disease or cancer)
- experimental identification of small RNA - mRNA interactions is slow and very costly
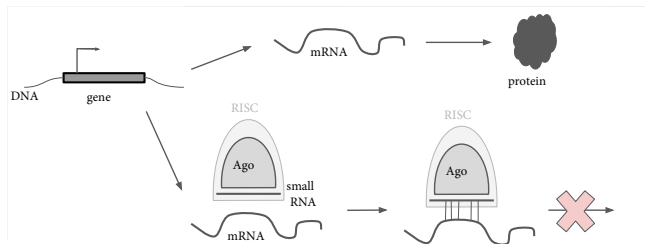
STATE OF THE ART

- predicting small RNA - mRNA interactions using computational predictions such as 'seed' region binding or cofolding
- almost all prediction tools are tuned on seed-biased datasets

Cofold
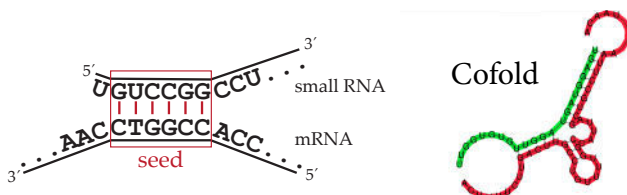
GOALS

- build a method for the prediction of Ago loaded small RNA – mRNA binding
- based on seed unbiased dataset
- compare with state of the art tools
- open the method to biological society

METHODS

- training based on datasets from unbiased CLASH experiments
- working with more small RNA types (miRNA, tRNA, YRNA)
- custom negative dataset to simulate real sequencing experiments
- input sequences encoded to matrix based on Watson-Crick binding
- for predicting small RNA - mRNA pairs trained Convolutional Neural Network (CNN)
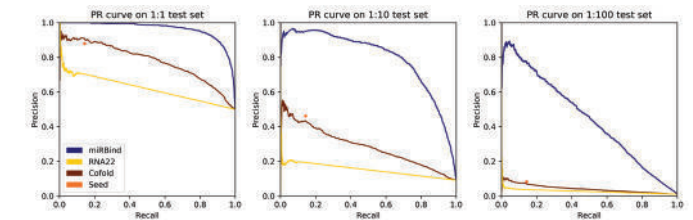- experimenting with different CNN parameters and positive:negative dataset ratios
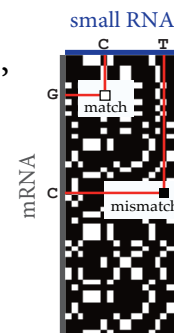
RESULTS

- created CNN for prediction of potential Ago loaded small RNA - mRNA binding
- our method (miRBind) outperforms state of the art approaches (seed, cofold and RNA22)

- for biologists created simple and easy to use web server
- our method can be used for example to allocate miRNAs to CLIP-Seq peaks or as a part of a target prediction program
- part of the thesis presented on conference and two manuscripts are in preparation [1], [2]

[1] E. KLIMENTOVÁ, J. KRČMÁŘ, V. HEJRET, K. GREŠOVÁ, I-C GIASSA a P. ALEXIOU. miRBind: a Deep Learning method for miRNA binding classification. 2022. (in preparation)
[2] V. HEJRET, N. M. VARADARAJAN, E. KLIMENTOVÁ, I-C GIASSA, Š. VAŇÁČOVÁ a P. ALEXIOU. Ago2-CLASH reveals a wide repertoire of small RNA mediated regulation. 2022. (in preparation)