Work Report: Evolutional couplings RNA

TC

2019-08-28

Background

- Goal: Automatic tool for RNA evolutional coupling

- Procedure

  1. Query RNA

  2. Build RNA profile from homologs

     - RFAM
     - **Not belong to existing RFAM**

  3. Evolutional coupling analysis

Pipelines

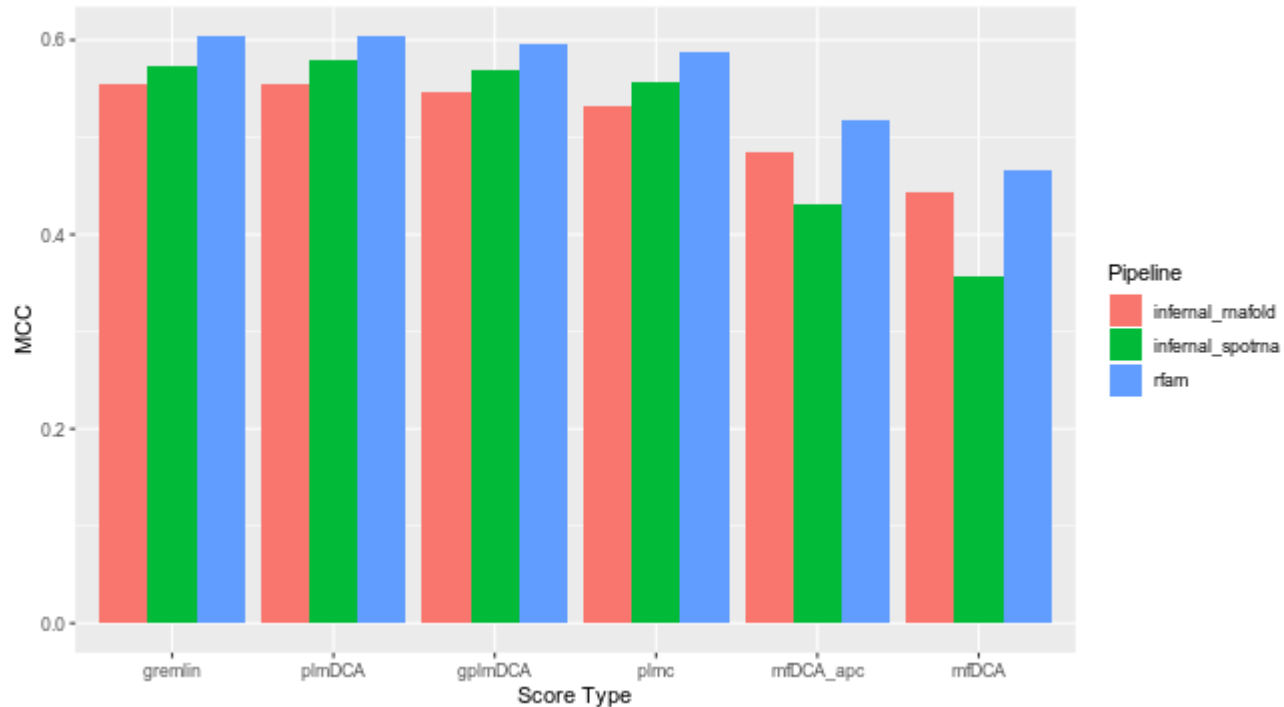**blastn+ infernal pipeline**

1. input RNA sequence
2. Blastn + nt database
3. Predicted Secondary structure(SS)
   1. **SPOT-RNA**
   2. **RNAfold**
4. cmbuild
5. cmsearch
6. DCA

RFAM pipeline

1. input RNA sequence
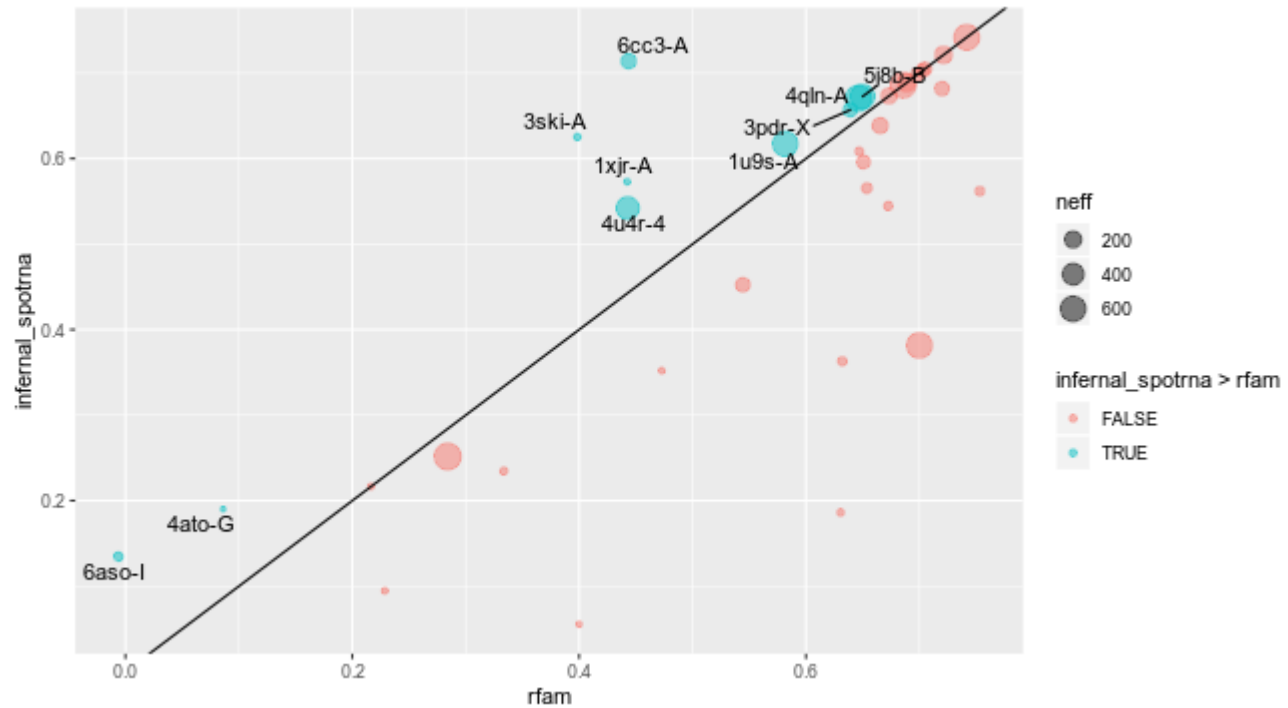
2. cm

3. CMalign with RFAM family sequence

4. DCA

Results

Comparison of the 3 pipelies

- RFAM > infernal
- GREMLIN > Others
- Ongoing: Need to fine tuning DCA parameters

By Case

Comparison of SS prediction (DCA: TOP L/4) and spot-RNA and RNAfold

type	mcc	f1	precision	sensitivity
spotrna	0.74	0.73	0.90	0.61
rnafold	0.59	0.58	0.71	0.48
DCA_plmDCA	0.58	0.56	0.77	0.44
DCA_gremlin_cpp	0.57	0.55	0.76	0.43
DCA_gplmDCA	0.57	0.55	0.76	0.43
DCA_dca_plmc	0.56	0.54	0.74	0.42
DCA_mfDCA_apc	0.43	0.42	0.57	0.33
DCA_mfDCA	0.36	0.35	0.48	0.27

SS prediction: SPOT-RNA predicts more basepairs

All 1460 basepairs from RF35, predicted by gremlin(Top L/4) and SPOTRNA
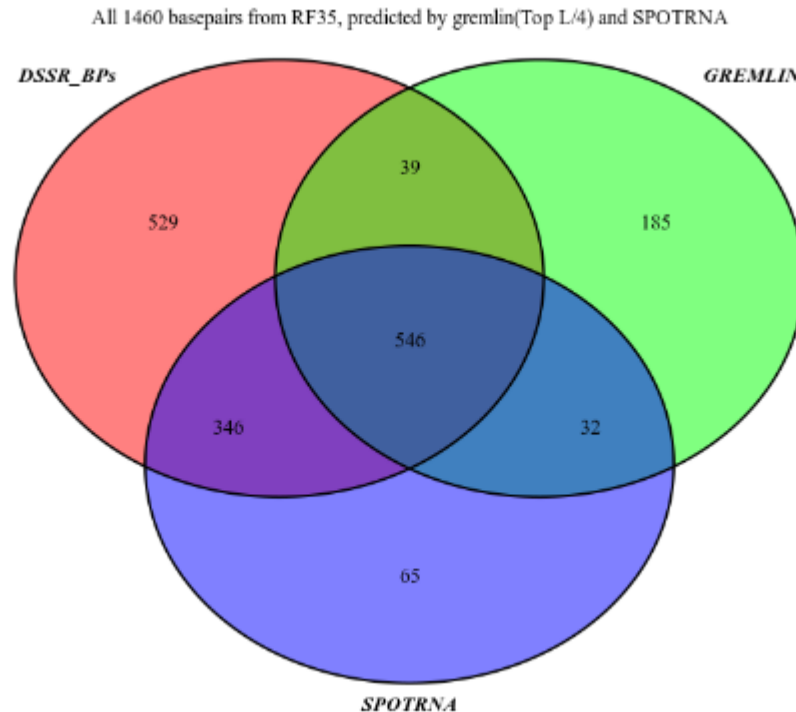
By Case: basepair prediction of SPOT-RNA and GREMLIN(top L/4)