Reviewer’s report

Title: nRC: non-coding RNA Classifier based on structural features

Version: 0 Date: 23 May 2017

Reviewer: Emanuel Weitschek

Reviewer's report:

Fiannaca et al. propose a novel pipeline for classifying non-coding RNA (ncRNA) sequences. Their method starts from the RNA fasta sequences, continues with the secondary structure prediction by using the IPknot tool, then the MoSS algorithm for molecular sub-structures (sub-graphs) detection is applied, and finally a supervised machine learning algorithm based on a deep learning Convolutional Neural Network for classification of the ncRNA sequences is adopted. The method is tested on RNA sequences extracted from the Rfam database and compared with other supervised classifiers and the state of the art RNAcon tool for ncRNA prediction.

The work is interesting, the method is sound, the obtained results are promising and the comparison with other state of the art methods confirms the validity of the approach.

Prior publication the authors have to perform following minor revisions.

Abstract
- page 2 line 30 change "Proposed method outperforms…" with "The proposed method outperforms…"

Background
- The authors write a very good introduction and a comprehensive state of the art about RNA and RNA classifiers;
- page 2 line 51 when writing about "regulation of gene expression" cite also:


Methods
- The proposed approach is valid and well presented;
- The authors should better justify the use of the IPknot tool for predicting the secondary structures of ncRNA and explain why they did not use the widespread Vienna Package suite (https://www.tbi.univie.ac.at/RNA/);
- Regarding RNA structure prediction, the following papers have to be considered:
  "G. Fiscon, et al.: A perspective on the algorithms predicting and evaluating the RNA secondary structure,. Journal of Genetics and Genome Research, 3, 2016" and
  where the authors propose a review on the RNA structure prediction tools and an example of application.

Results
- The design of the experimentation flawless and the presented results are promising;
- If possible I would like to see a comment about computational times of the proposed method, of the different classifiers, and of the RNAcon tool.

Discussion, Implementation details, and Conclusion
- The covered topics are well presented and the statements are correctly argued;
- My only suggestion is to move the subsection "Implementation details" at the end of section "Methods".

Finally, the paper is well written, the English language is correct, and the structure is adequate.

Level of interest
Please indicate how interesting you found the manuscript:

An article of importance in its field

Quality of written English
Please indicate the quality of language in the manuscript:
Acceptable

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