Review of: "Prediction of potential prognostic biomarkers in metastatic prostate cancer based on a circular RNA-mediated competing endogenous RNA regulatory network"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

The authors mainly designed the open framework B4PPI as a benchmark for comparing different predictive PPI models, and chose two models based on functional genomic information and only based on amino acid sequence for comparison, indicating the different usage scenarios of the two models. Validated on both human and yeast datasets, it was found that models based on functional genomic information were more suitable for PPI prediction across species. There are several major problems:

(1) Only two methods based on functional genomic information and only based on amino acid sequence are compared and compared, will other PPI prediction methods be compared later?

(2) Only human and yeast datasets were analyzed, why only these two datasets were chosen? Will other datasets be compared later? Only these two datasets show that models based on functional genomic information are more suitable for predicting PPI across species, and feel less reliable.

(3) What are the advantages of B4PPI compared with some existing benchmarks?

(4) Is there no protein-level overlap in test set T2?

(5) The quality of functional genomic annotation will affect the result of annotation, is there any way to improve the quality of functional genomic annotation now?

(6) In the evaluation section of methods, long short-term memory network (LSTM) and convolutional neural network (CNN) are mentioned. Why use these two networks to compare with GRU? Need to explain why.

(7) Among them, functional genomic (FG) is written in the INTRODUCTION section, and other parts of the article that involve functional genomic suggestions are also represented by FG.