Mathematical Biosciences and Engineering

Correction

Correction to "IMC-MDA: Prediction of miRNA-disease association based on induction matrix completion" [*Mathematical Biosciences and Engineering* 20(6) (2023) 10659–10674]

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A correction on

"IMC-MDA: Prediction of miRNA-disease association based on induction matrix completion" [*Mathematical Biosciences and Engineering* 20(6) (2023) 10659–10674]
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Upon careful review of the published manuscript [1], we have unfortunately discovered some issues with the citations. We understand the seriousness of this situation and the importance of maintaining the integrity of scientific literature.

To rectify these issues and ensure the accuracy of our published work, we have prepared a detailed report outlining the necessary corrections, which includes the following key points:

➤ Removal of 20 inappropriately cited references;
➤ Addition of 18 more relevant references;
➤ Nine specific modifications in the original manuscript.

The report presents a thorough breakdown of these changes, including specific locations and updated text. Below is the detailed revision report.

1. On page 1, references 4 and 6 have been removed from the original manuscript, and the first sentence of the introduction has been modified from "... a unique and irreplaceable manner [1–6]." to "... a unique and irreplaceable manner [1–4]."

2. On page 2, references 8 and 10 have been removed from the original manuscript. Additionally, the first line has been modified from "... of human illnesses, including cancer [7–10]." to "... of human illnesses, including cancer [5,6]."

3. On page 2, three relevant papers were incorporated, and the third line was revised from "long non-coding RNAs [11], and interactions between miRNA and environmental factors" to "long non-coding RNAs [7,8], and interactions between miRNA and environmental factors [9,10]."

The newly added papers are as follows:
[8] L. Zhuo, S. Pan, J. Li, X. Fu, Predicting miRNA-lncRNA interactions on plant datasets based on bipartite network embedding method, *Methods*, **207** (2022), 97−102. https://doi.org/10.1016/j.ymeth.2022.09.002
[9] L. Peng, Y. Tu, L. Huang, Y. Li, X. Fu, X. Chen, DAESTB: inferring associations of small molecule–miRNA via a scalable tree boosting model based on deep autoencoder, *Brief. Bioinformatics*, **23** (2022), bbac478. https://doi.org/10.1093/bib/bbac478
[10] J. Wei, L. Zhuo, Z. Zhou, X. Lian, X. Fu, X. Yao, GCFMCL: predicting miRNA-drug sensitivity using graph collaborative filtering and multi-view contrastive learning, *Brief. Bioinformatics*, **24** (2023), bbad247. https://doi.org/10.1093/bib/bbad247

4. On page 2, references 18 and 19 have been removed from the original manuscript, and the second line of the second paragraph has been revised from "… that are related with disease [15–19]" to "… that are related with disease [14–16]."

5. On page 2, paragraph 2, we added three related papers and changed the fourth line of the paragraph from "large-scale predictions of new human miRNA-illness relationships [20]." to "large-scale predictions of new human miRNA-illness relationships [17–20]." The newly added papers are as follows:

[18] Y. Chen, X. Fu, Z. Li, L. Peng, L. Zhuo, Prediction of lncRNA–protein interactions via the multiple information integration, *Front. Bioeng. Biotechnol.*, **9** (2021), 647113. https://doi.org/10.3389/fbioe.2021.647113
[19] J. Wei, L. Zhuo, S. Pan, X. Lian, X. Yao, X. Fu, Headtailtransfer: an efficient sampling method to improve the performance of graph neural network method in predicting sparse ncRNA–protein interactions, *Comput. Biol. Med.*, **157** (2023), 106783. https://doi.org/10.1016/j.compbiomed.2023.106783
[20] L. Zhuo, B. Song, Y. Liu, Z. Li, X. Fu, Predicting ncRNA–protein interactions based on dual graph convolutional network and pairwise learning, *Brief. Bioinformatics*, **23** (2022), bbac339. https://doi.org/10.1093/bib/bbac339

6. In the third paragraph on page 2, references 23–28 have been removed from the original manuscript, and 8 new references have been added. The initial four lines of this paragraph were modified from:
"Among them, machine learning algorithms and models have been triumphantly utilized in numerous fields, such as economics, the Internet, and medicine, which helps to increase the forecast performance and classification precision [23–28]. For the purpose of predicting new disease-miRNA associations, some researchers have suggested methods based on machine learning."
to:
"Among them, machine learning algorithms have gained widespread adoption in the field of bioinformatics. For instance, they are utilized in biological sequence prediction [23–25], circRNA-disease interaction prediction [26,27], and ncRNA-protein interaction prediction [28,29]. These applications have significantly advanced the study of disease-miRNA association prediction [30-31]."

The newly added literature includes:

[23] L. Cai, X. Ren, X. Fu, L. Peng, M. Gao, X. Zeng, iEnhancer-XG: interpretable sequence-based enhancers and their strength predictor, *Bioinformatics*, **37** (2021), 1060–1067. https://doi.org/10.1093/bioinformatics/btaa914

[24] X. Fu, L. Cai, X. Zeng, Q. Zou, StackCPPred: a stacking and pairwise energy content-based prediction of cell-penetrating peptides and their uptake efficiency, *Bioinformatics*, **36** (2020), 3028–3034. https://doi.org/10.1093/bioinformatics/btaa131

[25] X. Fu, L. Ke, L. Cai, X. Chen, X. Ren, M. Gao, Improved prediction of cell-penetrating peptides via effective orchestrating amino acid composition feature representation, *IEEE Access*, **7** (2019), 163547–163555. https://doi.org/10.1109/ACCESS.2019.2952738

[26] W. Liu, T. Tang, X. Lu, X. Fu, Y. Yang, L. Peng, MPCLCDA: predicting circRNA–disease associations by using automatically selected meta-path and contrastive learning, *Brief. Bioinformatics*, **24** (2023), bbad227. https://doi.org/10.1093/bib/bbad227

[27] L. Peng, C. Yang, Y. Chen, W. Liu, Predicting CircRNA-disease associations via feature convolution learning with heterogeneous graph attention network, *IEEE J. Biomed. Health. Inform.*, **27** (2023), 3072–3082. https://doi.org/10.1109/JBHI.2023.3260863

[28] T. Wang, W. Wang, X. Jiang, J. Mao, L. Zhuo, M. Liu, et al., ML-NPI: predicting interactions between noncoding RNA and protein based on meta-learning in a large-scale dynamic graph, *J. Chem. Inf. Model.*, **64** (2023), 2912–2920. https://doi.org/10.1021/acs.jcim.3c01238

[29] Z. Zhou, Z. Du, J. Wei, L. Zhuo, S. Pan, X. Fu, et al., MHAM-NPI: Predicting ncRNA-protein interactions based on multi-head attention mechanism, *Comput. Biol. Med.*, **163** (2023), 107143. https://doi.org/10.1016/j.compbiomed.2023.107143

[30] Q. Liao, X. Fu, L. Zhuo, H. Chen, An efficient model for predicting human diseases through miRNA based on multiple-types of contrastive learning, *Front. Microbiol.*, **14** (2023), 1325001. https://doi.org/10.3389/fmicb.2023.1325001

[31] W. Liu, H. Lin, L. Huang, L. Peng, T. Tang, Q. Zhao, et al., Identification of miRNA–disease associations via deep forest ensemble learning based on autoencoder, *Brief. Bioinformatics*, **23** (2022), bbac104. https://doi.org/10.1093/bib/bbac104

7. In the fourth paragraph on page 2, three additional papers were incorporated. The first line of this paragraph was revised to read: "At present, more researchers are beginning to predict the relationship between disease and miRNA by utilizing a web-based approach [38–41]." This modification reflects

the updated reference numbering and the emphasis on prediction.

The newly included literature comprises the following:

[39] Q. Qu, X. Chen, B. Ning, X. Zhang, H. Nie, L. Zeng, et al., Prediction of miRNA-disease associations by neural network-based deep matrix factorization, *Methods*, **212** (2023), 1–9. https://doi.org/10.1016/j.ymeth.2023.02.003

[40] W. Liu, Y. Yang, X. Lu, X. Fu, R. Sun, L. Yang, et al., NSRGRN: a network structure refinement method for gene regulatory network inference, *Brief. Bioinformatics*, **24** (2023), bbad129. https://doi.org/10.1093/bib/bbad129

[41] L. Peng, C. Yang, L. Huang, X. Chen, X. Fu, W. Liu, RNMFLP: predicting circRNA–disease associations based on robust nonnegative matrix factorization and label propagation, *Brief. Bioinformatics*, **23** (2022), bbac155. https://doi.org/10.1093/bib/bbac155

8. References 36–41 have been removed from the original manuscript. Additionally, the sentence located in the third line of the fourth paragraph on page 2 has been deleted. The sentence originally stated: "Such algorithms are similar to the link prediction issue of binary networks and are widely used in a variety of other areas such as social tags, journalism, and movies [36–41]."

9. The original manuscript's citations 50–52 have been removed. Additionally, the fourth line of the second paragraph on the third page has been revised from "Lastly, despite the fact that some approaches, like NetCBI, are able to forecast separated diseases, their cross-validation performance is subpar [49–52]." to "Lastly, despite the fact that some approaches, like NetCBI, are able to forecast separated diseases, their cross-validation performance is subpar [49]."

References

1. Z. Li, Y. Zhang, Y. Bai, X. Xie, L. Zeng, IMC-MDA: Prediction of miRNA-disease association based on induction matrix completion, *Math. Biosci. Eng.*, **20** (2023), 10659–10674. https://doi.org/10.3934/mbe.2023471