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Corrigendum

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DDR: efficient computational method to predict drug–target interactions using graph mining and machine learning approaches

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In our study (Olayan *et al.*, 2018), we performed 96 computational experiments, including six that are related to the COSINE method (Lim *et al.*, 2016). Re-evaluating all numerical results we reported, we found that out of the six tests (5 cross-validation tests and 1 hold-out test) we performed for the COSINE method, the performance of COSINE in two of these tests, both related to the DrugBank_FDA dataset, should be corrected. This implied a few corrections in the article. The repeated analysis confirms that the original qualitative conclusions regarding the newly introduced DDR method stands unaltered.

All necessary changes are implemented in the article and associated Supplementary material. The article has also now been updated online.

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Conflict of Interest: none declared.

Supplementary information: Supplementary data are available at *Bioinformatics* online.

References

Lim,H., *et al.* (2016) Improved genome-scale multi-target virtual screening via a novel collaborative filtering approach to cold-start problem. *Sci Rep*;**6**:38860.

Olayan,R.S., Ashoor,H. and Bajic,V.B. (2018) DDR: efficient computational method to predict drug-target interactions using graph mining and machine learning approaches. *Bioinformatics*;**34**(7):1164–1173.