Corrigendum

Corrigendum to article "DriverML: a machine learning algorithm for identifying driver genes in cancer sequencing studies"

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In our original article published in *Nucleic Acids Research* (1), we developed a machine learning algorithm for identifying driver genes (i.e., DriverML), and benchmarked it with 20 other existing tools (including ExInAtor) in 31 TCGA exome mutation datasets. It was brought to our attention by Dr. Rory Johnson, the developer of ExInAtor (University of Bern, Switzerland), that the use of whole-genome sequencing data is critical for the ExInAtor as mutations in intronic and intergenic regions are required to estimate background mutation rates. In our article, the exome mutation data were used for ExInAtor analysis, which resulted in a significant underestimation of background mutation rates. The results of ExinAtor analysis presented in our article didn't represent its optimal performance. The requirement to use only whole-genome SNVs has now been clarified in the ExInAtor Github page (https://github.com/alanzos/ExInAtor/). The corrections do not affect the conclusions of the article. We deeply regret this oversight and any confusions over this issue.

REFERENCES

1. Han,Y., Yang,J., Qian,X., Cheng,W.C., Liu,S.H., Hua,X., Zhou,L., Yang,Y., Wu,Q., Liu,P. *et al.* (2019) DriverML: a machine learning algorithm for identifying driver genes in cancer sequencing studies. *Nucleic Acids Res.*, **47**, e45. doi: 10.1093/nar/gkz096.

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