

CORRECTION

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Correction to: binomialRF: interpretable combinatoric efficiency of random forests to identify biomarker interactions

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The original article can be found online at <https://doi.org/10.1186/s12859-020-03718-9>.

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Following publication of the original article [1], errors were identified in the References of the Discussion section.

The updated discussion is given below and the changes have been highlighted in **bold typeface**.

Discussion

Using trees to identify interactions dates back to [37] and partial dependence plots to examine candidate feature interactions. Some algorithms identify sets of conditional or sequential splits, while other strategies (i.e., [37]) measure their effect in prediction error. More recently, works such as [25, 58] look at the frequency of sequence of splits or "decision paths" as a way to determine whether two features interact in the tree-splitting process. For example, iterative random forests (iRF) [58] identify decision paths along random forests and captures their prevalence, therefore benefitting from a combinatoric feature space reduction in the interaction search. Similarly, BART conducts interaction screening by looking at inclusion frequencies of pairs of predictors [25].

58. Basu, Sumanta, Karl Kumbier, James B. Brown, and Bin Yu. Iterative random forests to discover predictive and stable high-order interactions. *Proceedings of the National Academy of Sciences* 115, no. 8 (2018): 1943–1948.

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