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Publisher Correction: A sequence-based evolutionary distance method for Phylogenetic analysis of highly divergent proteins

Wei Cao, Lu-Yun Wu, Xia-Yu Xia, Xiang Chen, Zhi-Xin Wang & Xian-Ming Pan

Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-023-47496-9>, published online 20 November 2023

The original version of this Article contained an error in Figure 3, panel b, where the labels are not displayed.

The incorrect Figure 3 and the accompanying legend appear below.

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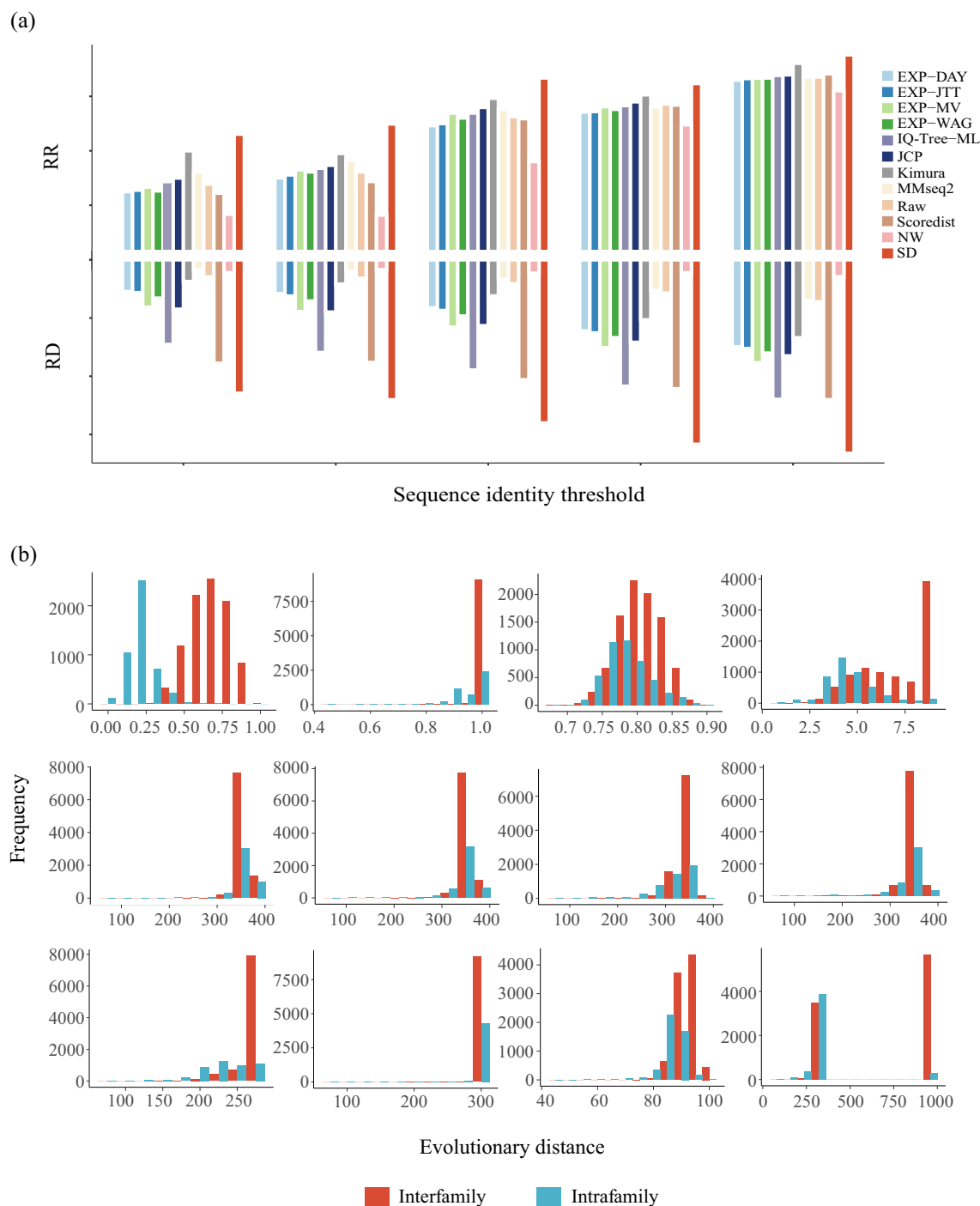


Figure 3. The SD algorithm can effectively distinguish evolutionary relationships at superfamily level. (a) Performance of evolutionary distance methods under different homology thresholds. SD outperformed other sequence-based evolutionary distance methods at each threshold, and this superiority remained even under low sequence identity. (b) Distribution of distinguished evolutionary relationships by SD distance and other evolutionary distances in the Homeodomain-like superfamily based on PSA (MMseq2 distance, NW distance), complex amino acid substitution matrix (IQ-Tree distance), simple amino acid substitution matrix (EXP-Dayhoff, EXP-WAG, EXP-JTT, EXP-MV), mathematical correction model (Raw distance, JCP distance, Kimura distance, Scoredist distance) methods.

The original Article has been corrected.



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