

*Supplementary material for:*

## **Incorporating information on predicted solvent accessibility to the co-evolution-based study of protein interactions**

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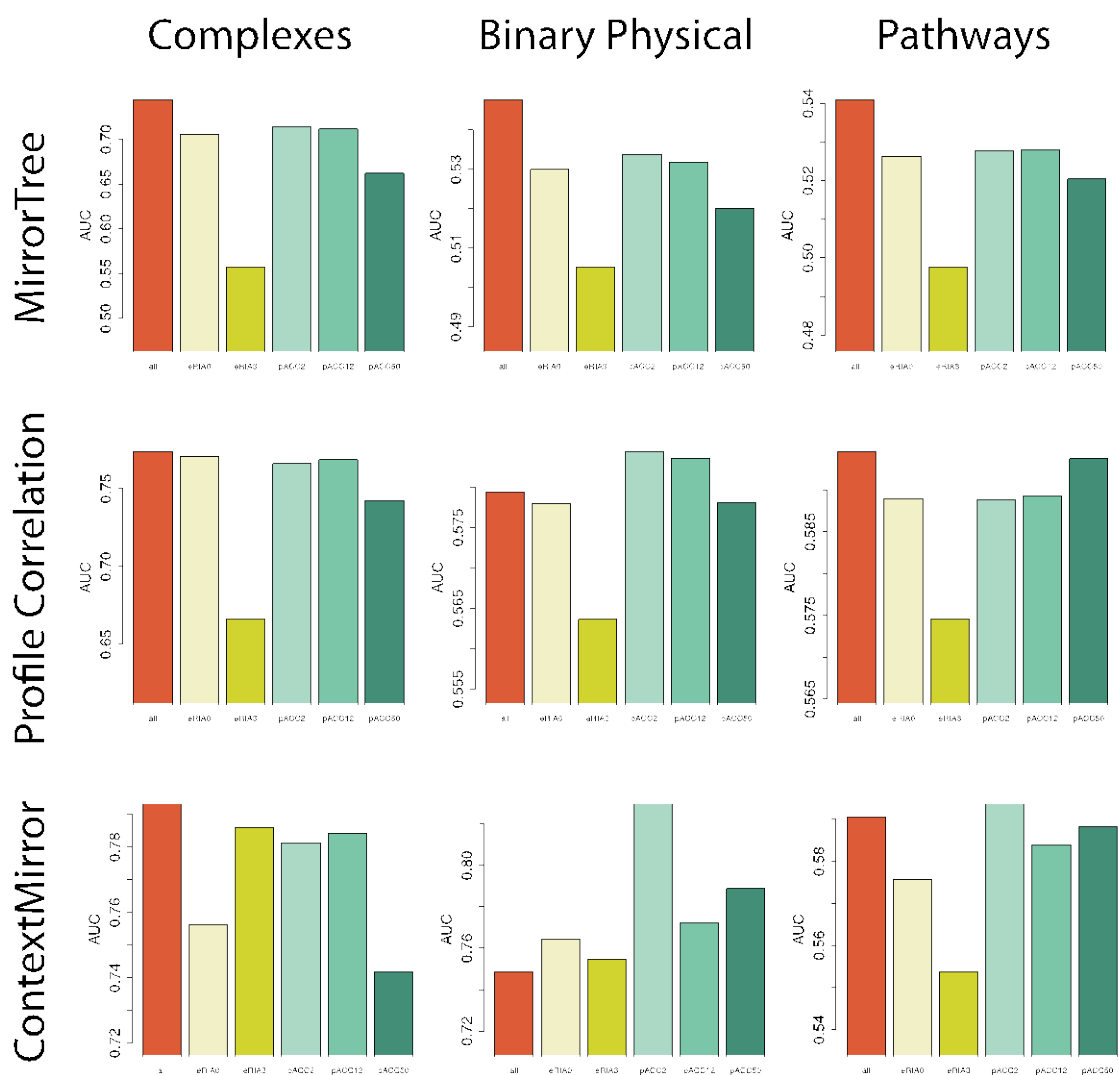
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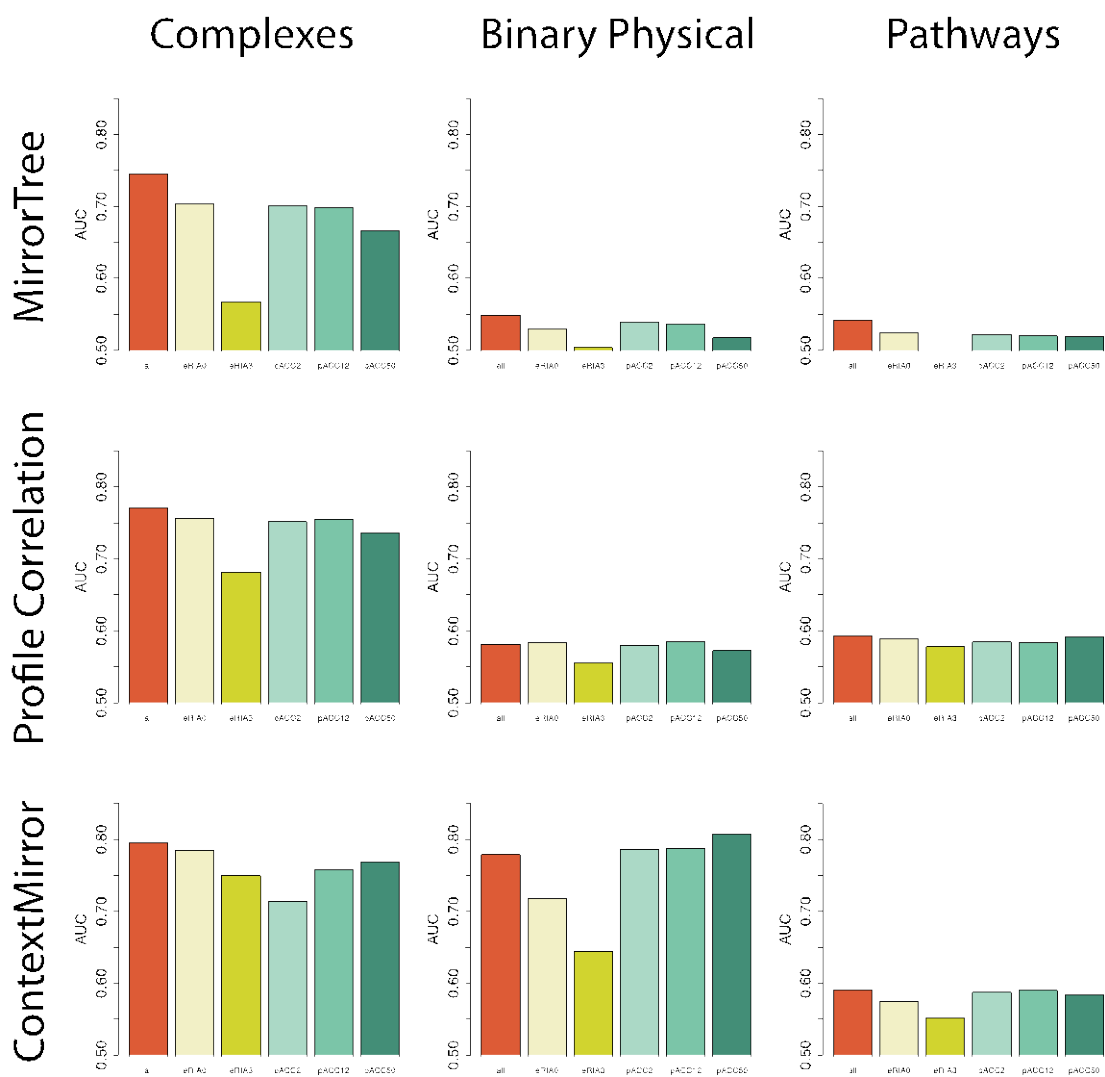
[pazos@cnb.csic.es](mailto:pazos@cnb.csic.es)

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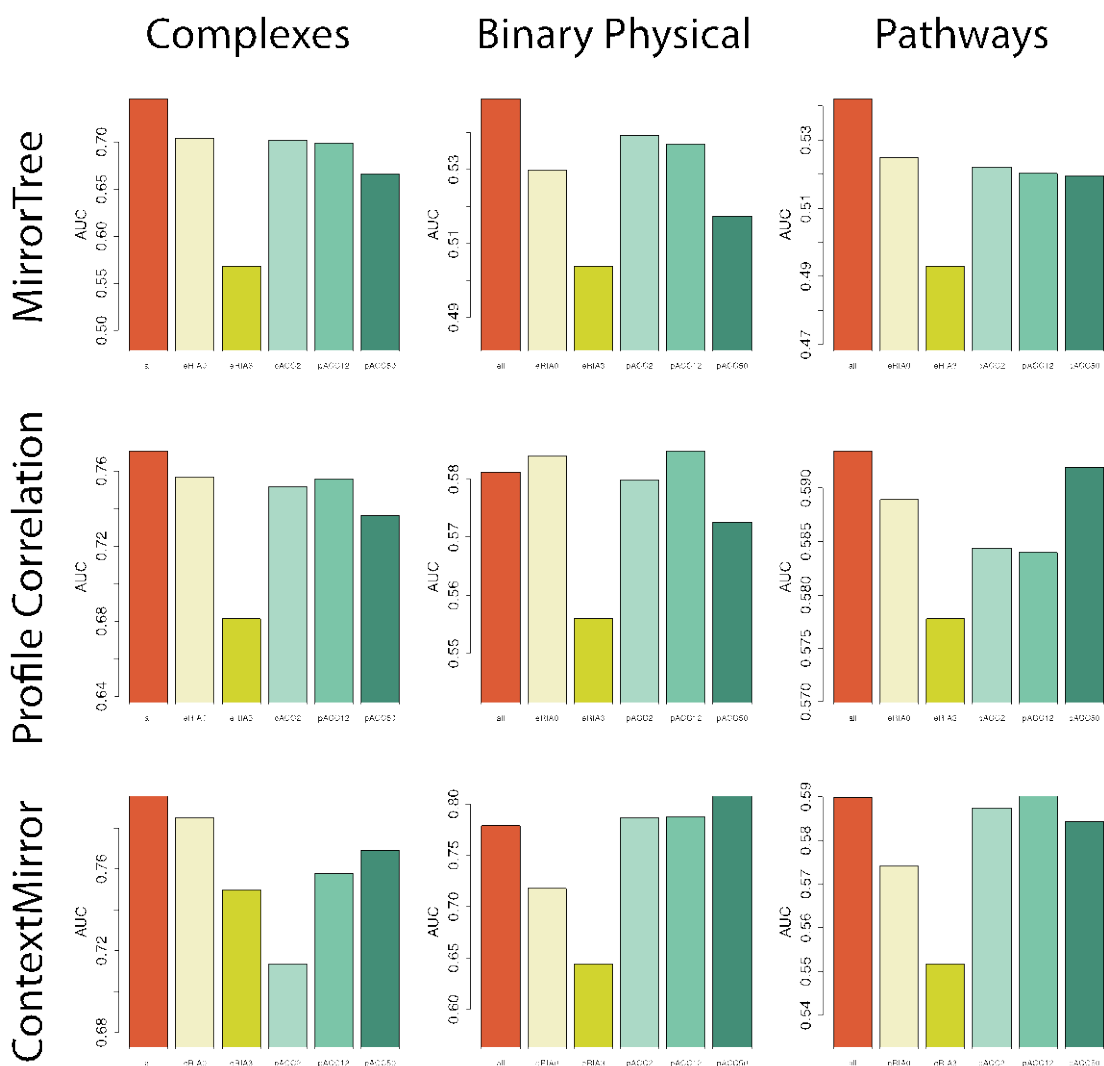
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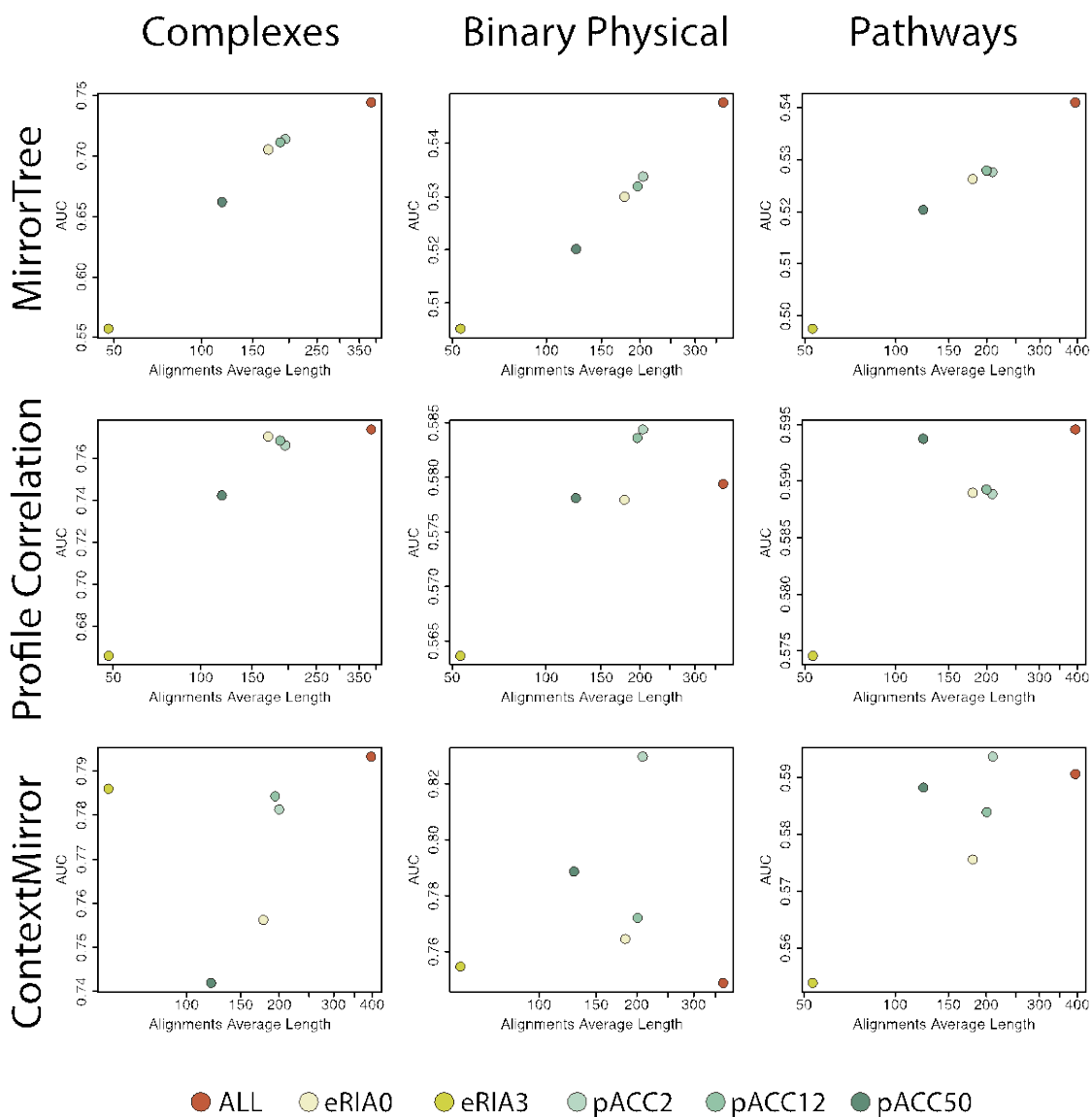
**Fig. S1 Performances for different combinations of: phylogenetic tree comparative methods, interaction evidence and predicted accessibility filter.** Performance is evaluated as the “Area Under the [ROC] Curve” (AUC). In order to show up the differences, the scales were adjusted independently for each case.



**Fig. S2** Performances of the different methods predicting different types of interactions using trees derived from positions with different predicted accessibility features. The performance is evaluated as the “Area Under the [ROC] Curve” (AUC) using predicted accessibility derived from MSAs of orthologs.



**Fig. S3 Performances of the different methods predicting different types of interactions using trees derived from positions with different predicted accessibility features.** The performance is evaluated as the “Area Under the [ROC] Curve” (AUC) using predicted accessibility derived from MSAs of orthologs. In order to show up the differences, the scales were adjusted independently for each case.



**Fig. S4 Relationship between the performances of the different methods and the lengths of the virtual alignments for the different datasets.** The length of the virtual alignment is the number of positions (fulfilling a given predicted accessibility criteria – colors-) used for deriving the trees.