



Conservation of Divergent Transcript in Fungi



Philip R. Kensche, Martin Oti, Bas E. Dutilh, Martijn A. Huynen

Center for Molecular and Biomolecular Informatics / Nijmegen Center for Molecular Life Sciences, Radboud University Medical Center. PO Box 9101, 6500 HB, Nijmegen, The Netherlands.

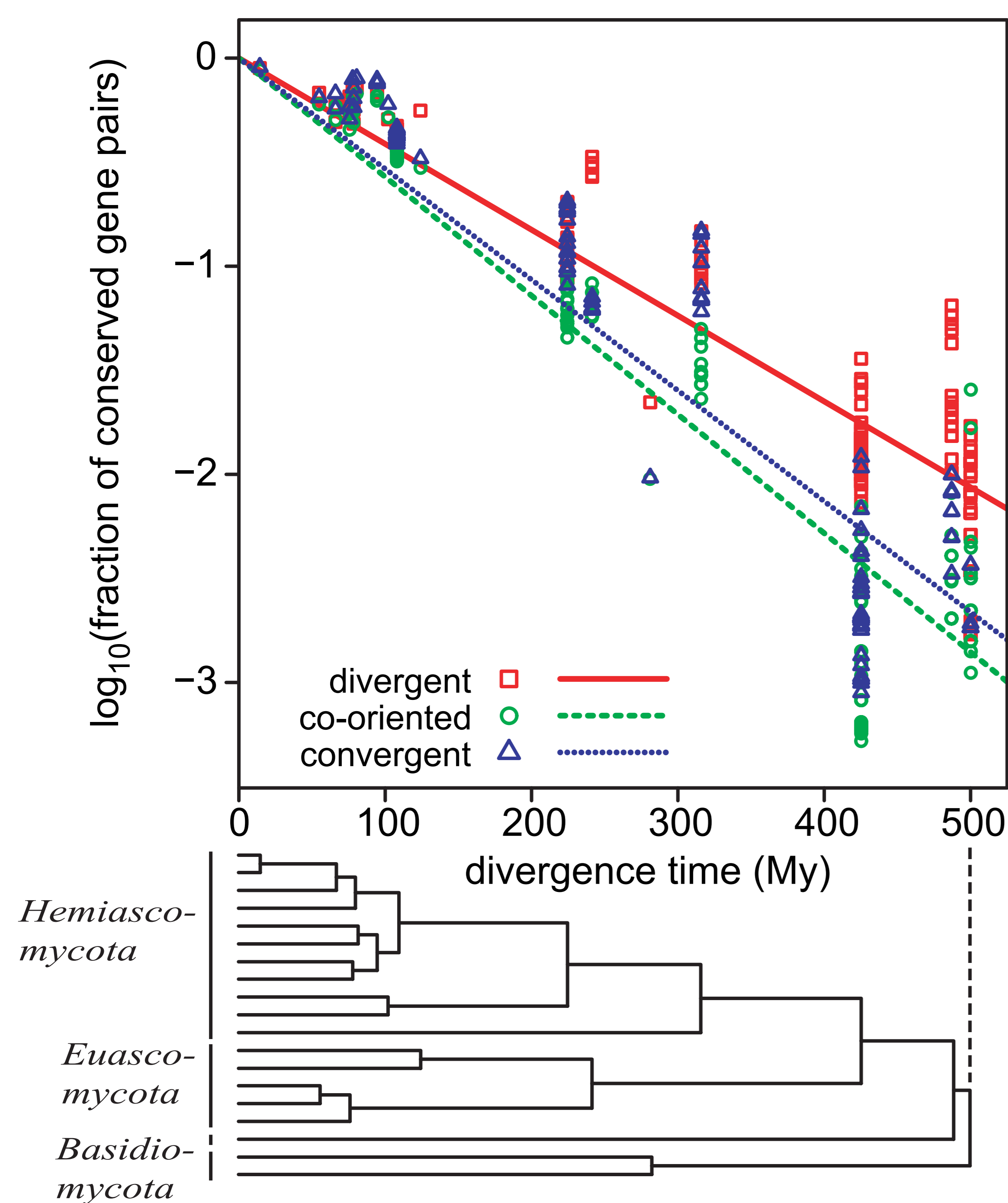
PMID 18375009, email: pkensche@cmbi.ru.nl



Introduction

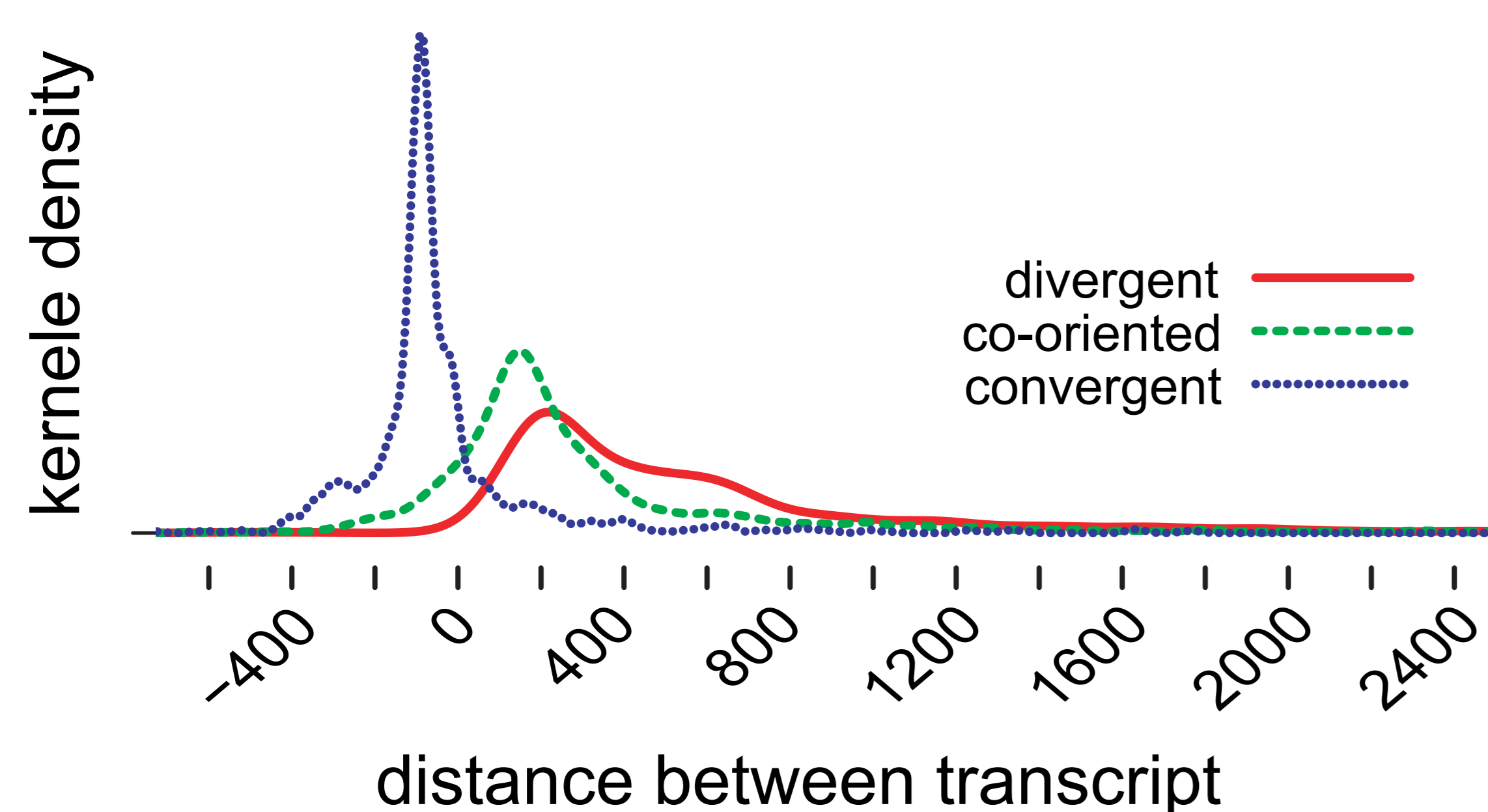
We quantified the conservation of divergent ($\leftarrow\rightarrow$), co-oriented ($\rightarrow\rightarrow$) and convergent ($\rightarrow\leftarrow$) genes in the genomes of 19 asco- and basidiomyceteous fungi. Divergent gene orientation is most conserved, which suggests an abundance of bidirectional promoters.

Divergent gene pairs are more conserved in orientation ...



... although they have longer intergenic spacers.

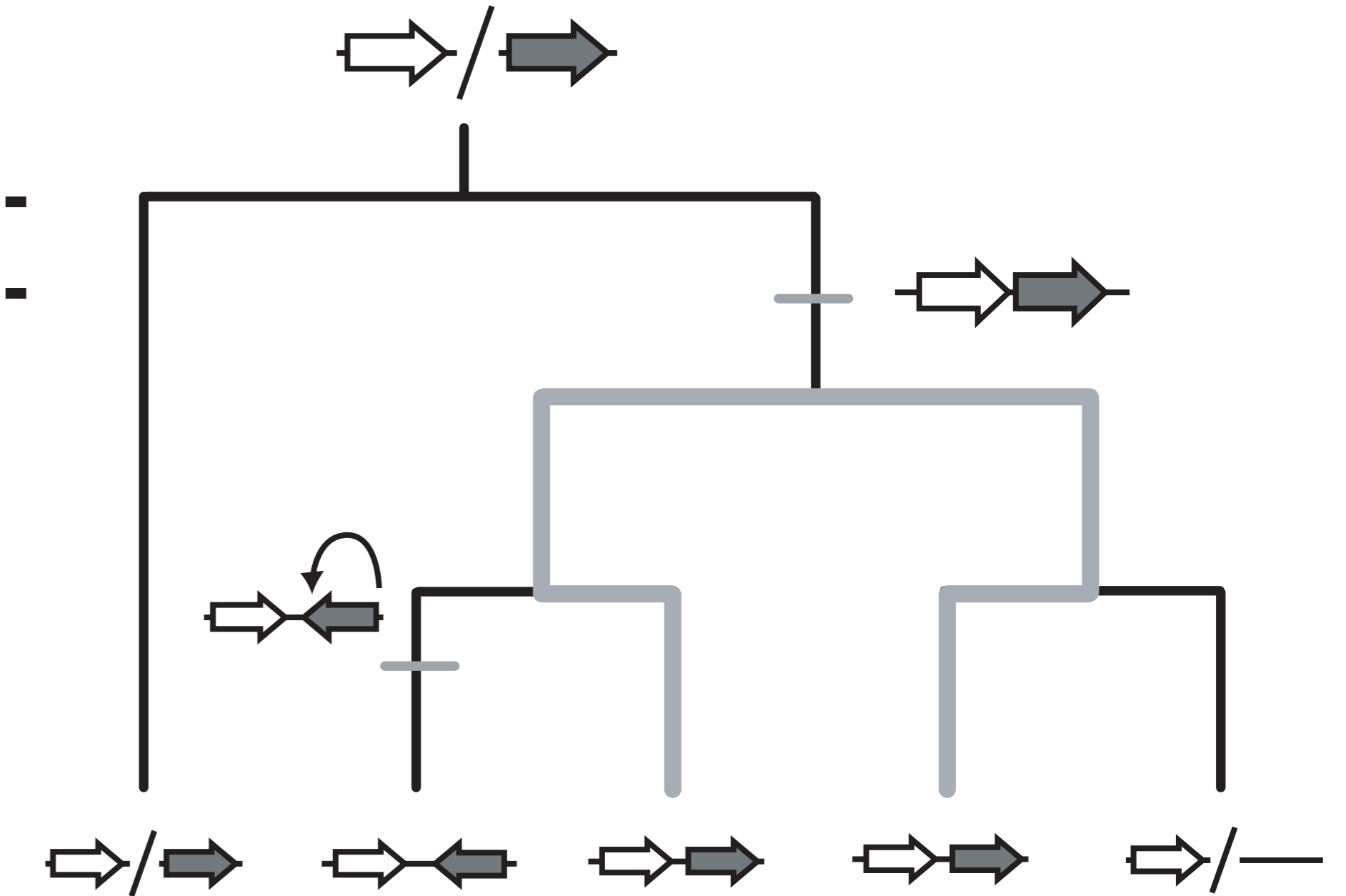
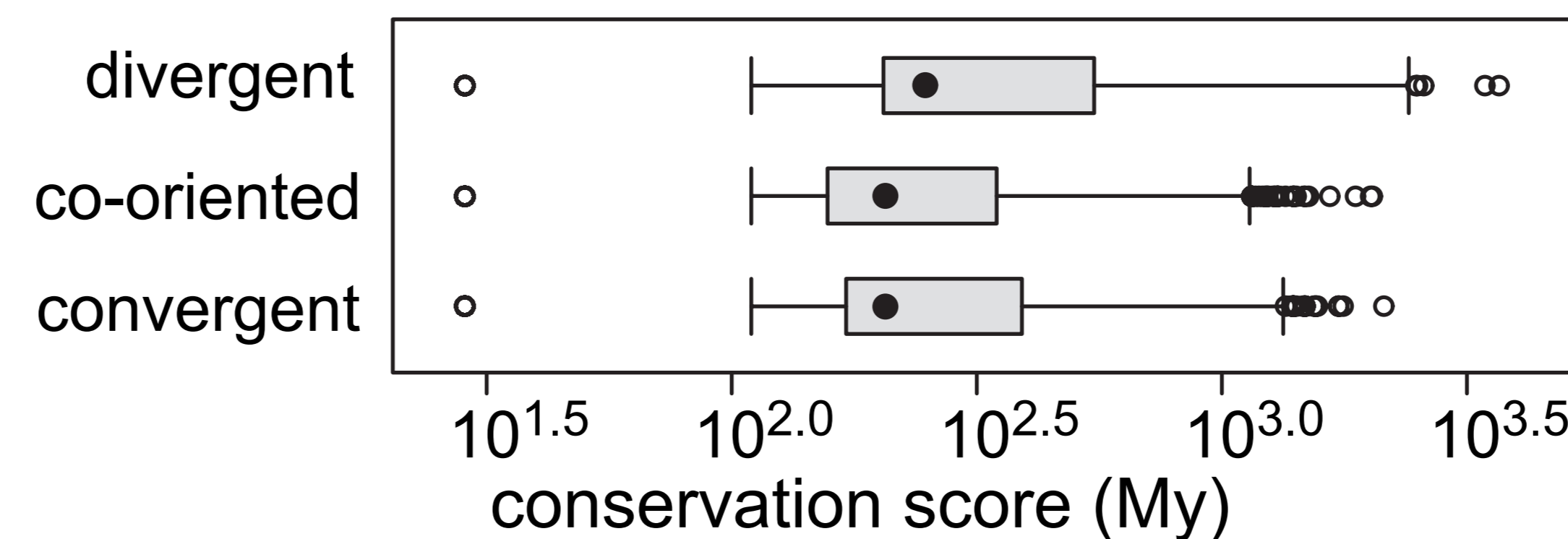
If separation of genes was only dependent on intergenic distance (neutral model), then the more conserved divergent gene pairs should have shorter intergenic spacers.



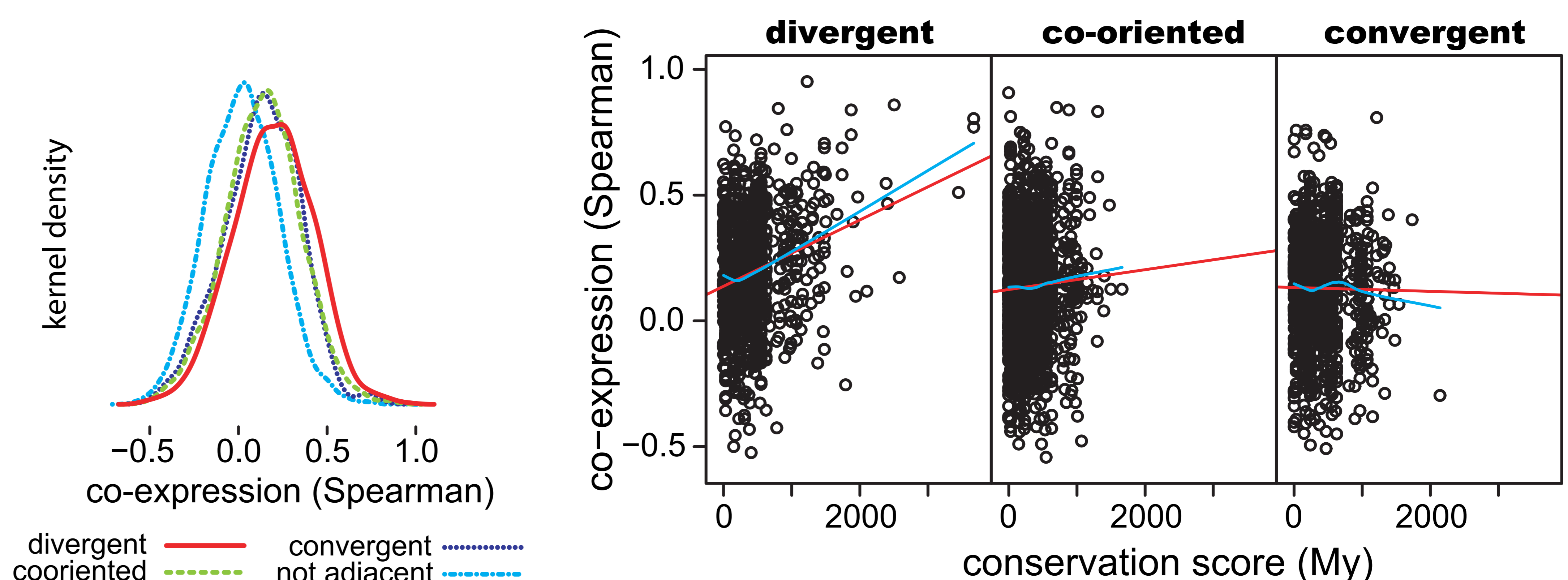
Quantify the conservation of individual gene pairs

Gene pairs were scored by how long their orientation was maintained during fungal evolution.

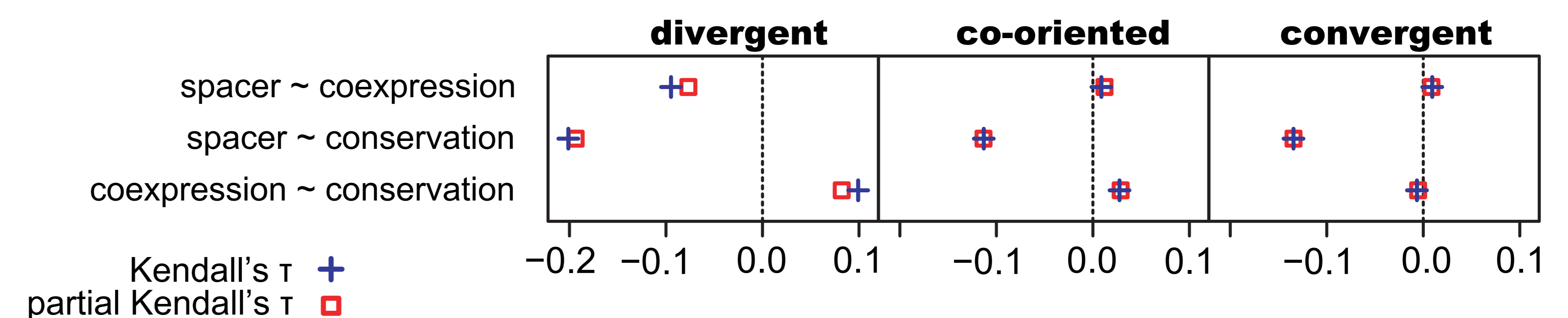
We assumed that a gene pair gained its orientation exactly once during this time (Dollo parsimony).



Conservation of orientation correlates with co-expression ...



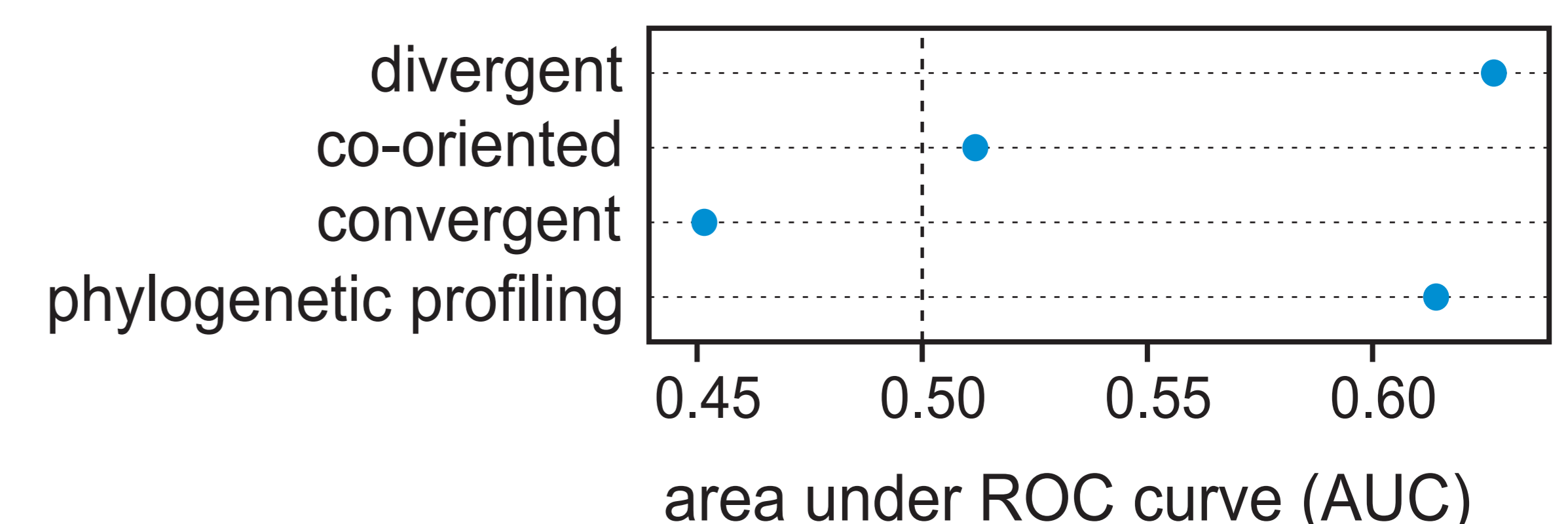
... independent of spacer length.



Conserved divergent gene pairs are functionally related!

Interactions from KEGG, MIPS, and Yeast GRID.

Higher conservation of functionally related gene pairs only for divergent gene pairs (one-sided U-test, $p=1.65 \times 10^{-2}$).



Acknowledgements This work was funded by the Netherlands Bioinformatics Centre (NBIC), which is supported by the Netherlands Genomics Initiative (NGI) and by the European Union's Sixth Framework Programme EPSTEM (CT-2005-019067).