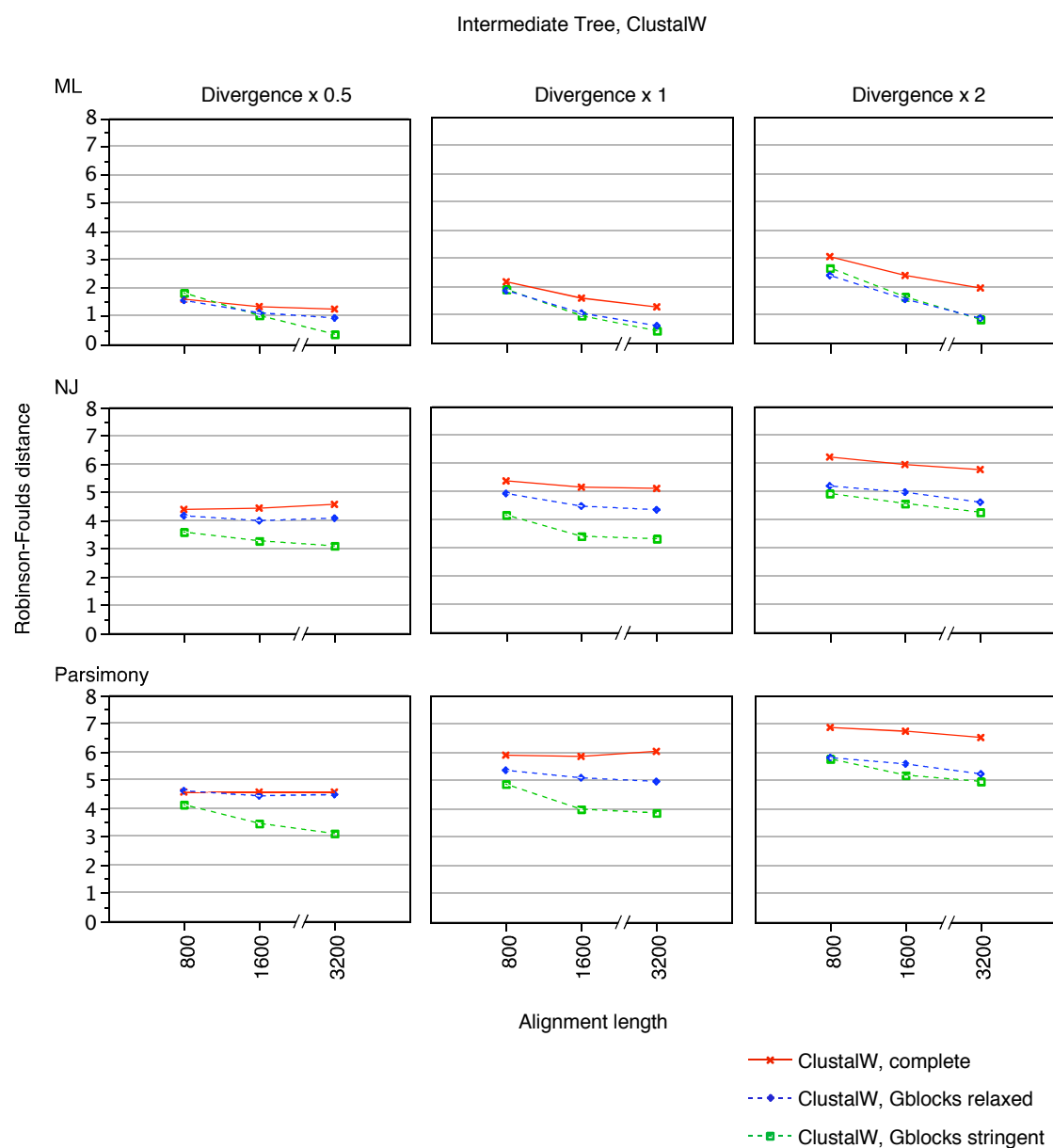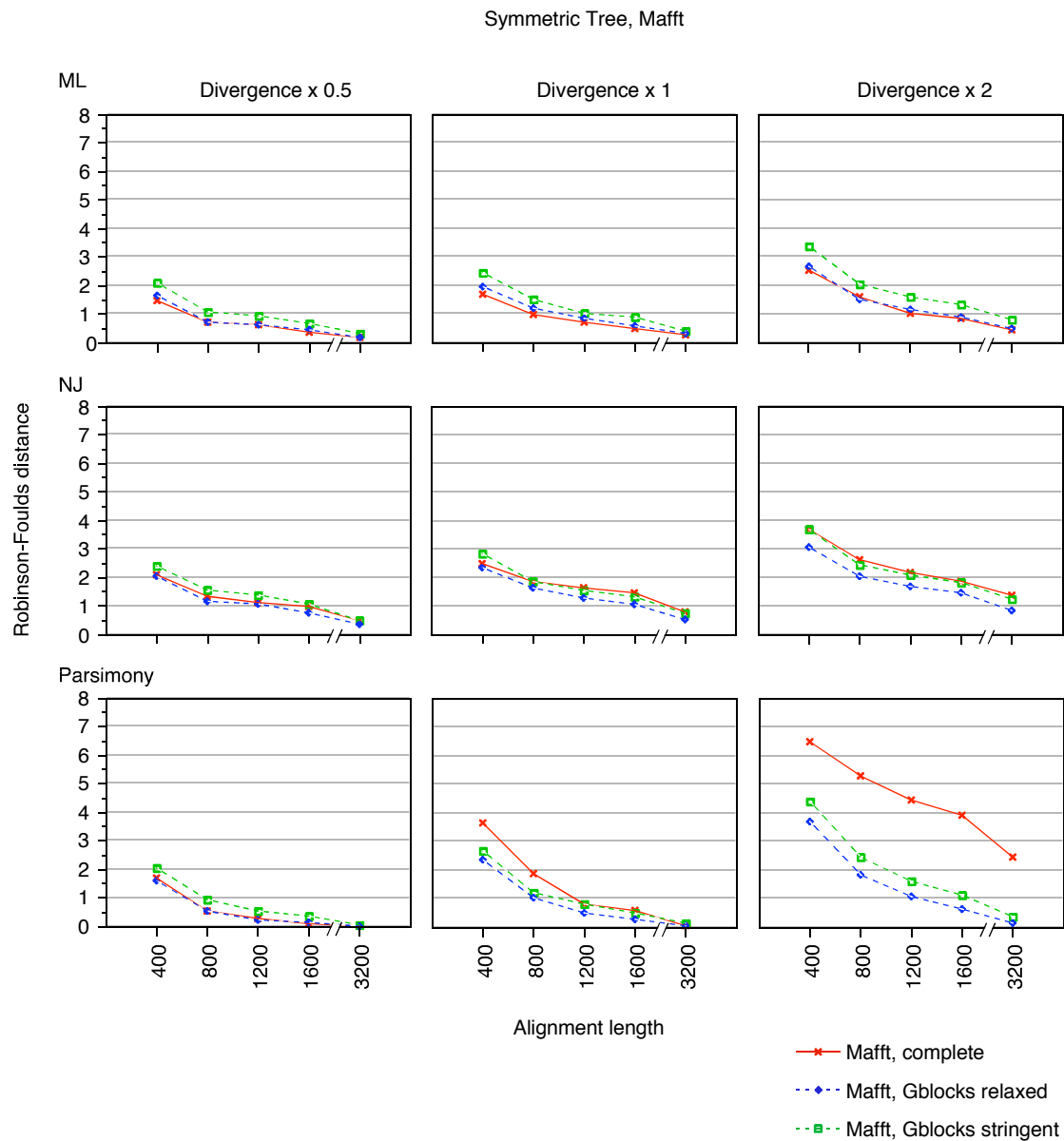**Online Appendix - Figure 1**. Average Robinson-Foulds distances to the real tree from the tree calculated with ClustalW alignments (solid, red line), and the same alignments after treatment with Gblocks relaxed (dotted, blue line with diamonds) and stringent (dotted, green line with square symbols) conditions. The symmetric tree with three different divergence levels was used for the simulations. Trees were reconstructed by ML, NJ and parsimony.
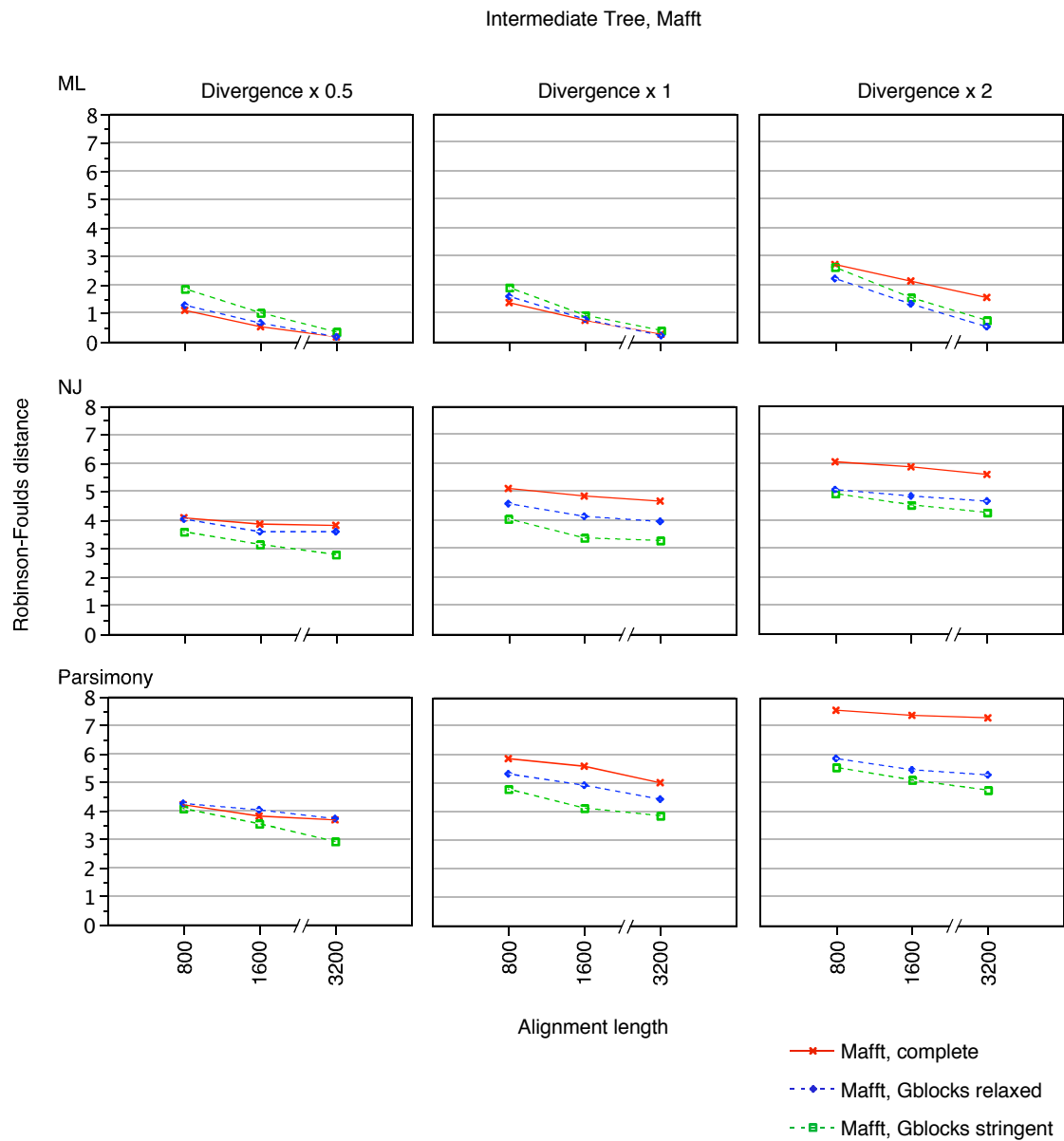
Intermediate Tree, ClustalW

Online Appendix - Figure 2. Average Robinson-Foulds distances to the real tree from the tree calculated with ClustalW alignments (solid, red line), and the same alignments after treatment with Gblocks relaxed (dotted, blue line with diamonds) and stringent (dotted, green line with square symbols) conditions. The intermediate tree with three different divergence levels was used for the simulations. Not all alignment lengths were simulated. Trees were reconstructed by ML, NJ and parsimony.

Online Appendix - Figure 3. Average Robinson-Foulds distances to the real tree from the tree calculated with Mafft alignments (solid, red line), and the same alignments after treatment with Gblocks relaxed (dotted, blue line with diamonds) and stringent (dotted, green line with square symbols) conditions. The symmetric tree with three different divergence levels was used for the simulations. Trees were reconstructed by ML, NJ and parsimony.
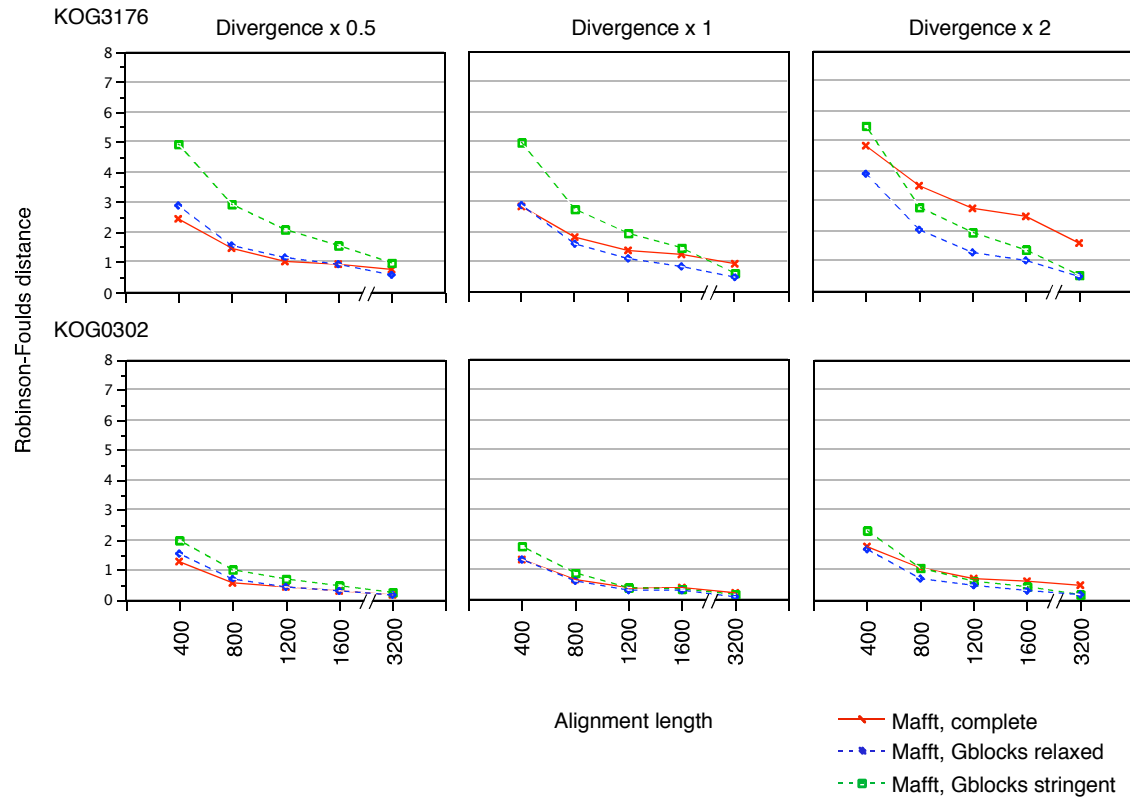
Online Appendix - Figure 4. Average Robinson-Foulds distances to the real tree from the tree calculated with Mafft alignments (solid, red line), and the same alignments after treatment with Gblocks relaxed (dotted, blue line with diamonds) and stringent (dotted, green line with square symbols) conditions. The intermediate tree with three different divergence levels was used for the simulations. Not all alignment lengths were simulated. Trees were reconstructed by ML, NJ and parsimony.
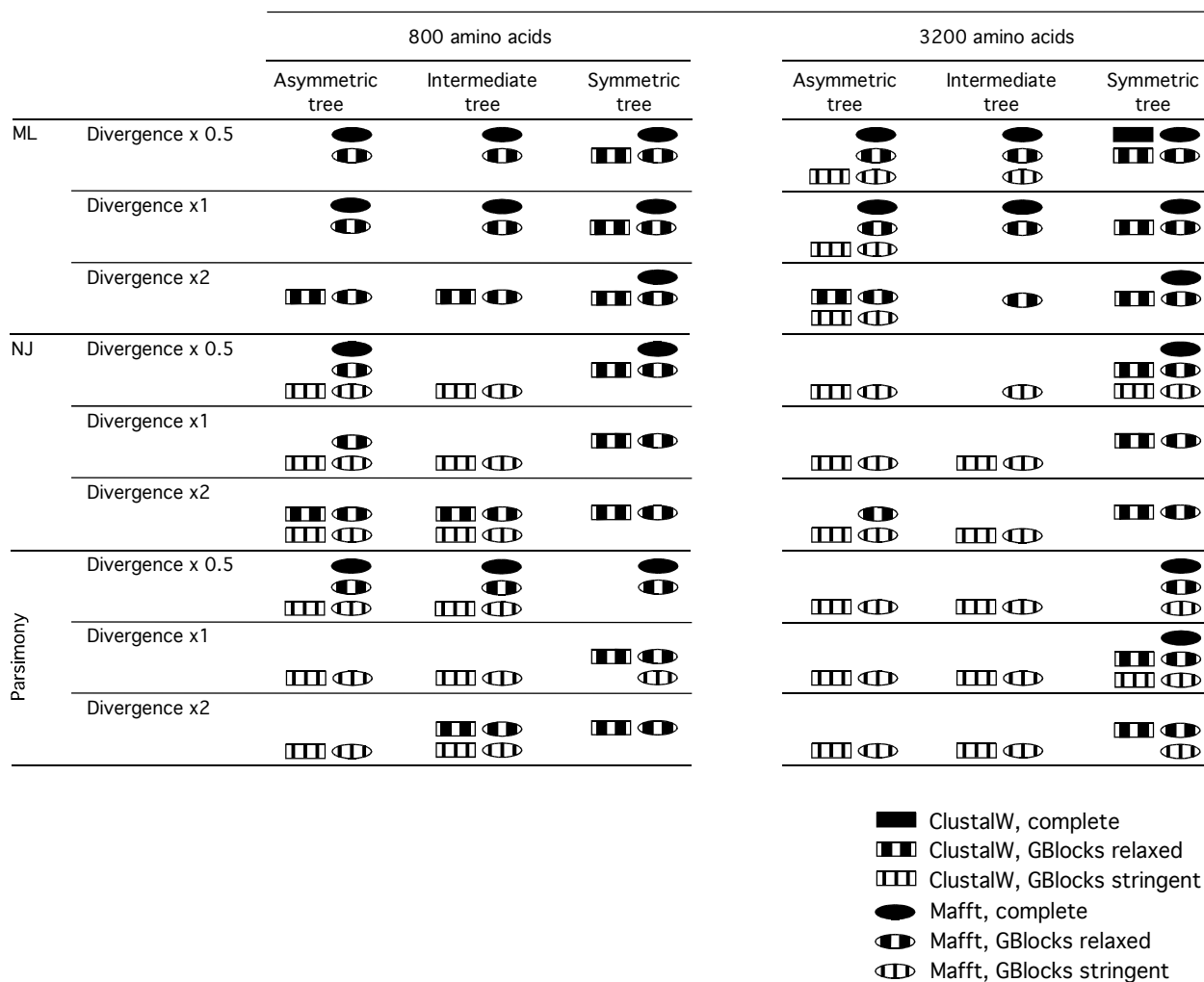
Online Appendix - Figure 5. Average Robinson-Foulds distances to the real tree from the ML tree calculated with Mafft complete alignments (solid, red line), and the same alignments after treatment with Gblocks relaxed (dotted, blue line with diamonds) and stringent (dotted, green line with squared symbols) conditions. The asymmetric tree with three different divergence levels was used for the simulations. Profiles of rate heterogeneity derived from two different proteins, KOG3176 and KOG0302, were used.

|		800 amino acids			3200 amino acids		
		Asymmetric tree	Intermediate tree	Symmetric tree	Asymmetric tree	Intermediate tree	Symmetric tree
ML	Divergence x 0.5						
	Divergence x1						
	Divergence x2						
NJ	Divergence x 0.5						
	Divergence x1						
	Divergence x2						
Parsimony	Divergence x 0.5						
	Divergence x1						
	Divergence x2						

Legend:

- ClustalW, complete
- ClustalW, GBlocks relaxed
- ClustalW, GBlocks stringent
- Mafft, complete
- Mafft, GBlocks relaxed
- Mafft, GBlocks stringent

Online Appendix - Figure 6. Overall alignment strategies that give rise to the statistically best topologies. The complete alignment is represented by a black rectangle (ClustalW) or oval (Mafft), and the two different Gblocks strategies by rectangles or ovals with stripes that represent the stringency of the selection.

Bootstrap analysis

Symmetric Tree - NJ
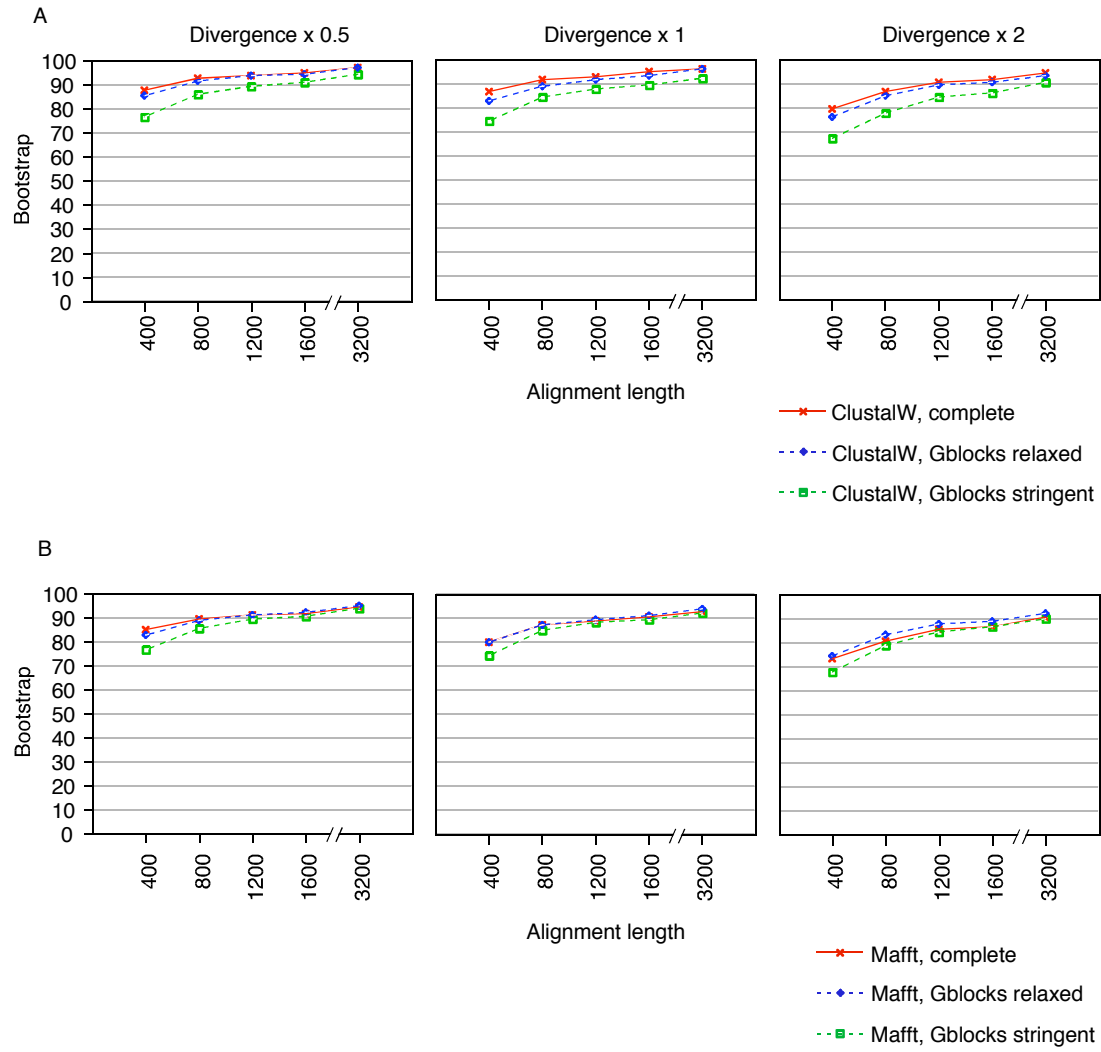
Online Appendix - Figure 7. Average bootstrap values of NJ trees obtained from ClustalW (A) and Mafft (B) alignments simulated from the symmetric tree with three different divergence levels. Complete (solid, red line), Gblocks relaxed (dotted, blue line with diamonds) and Gblocks stringent (dotted, green line with squared symbols) alignments are shown.

Bootstrap analysis
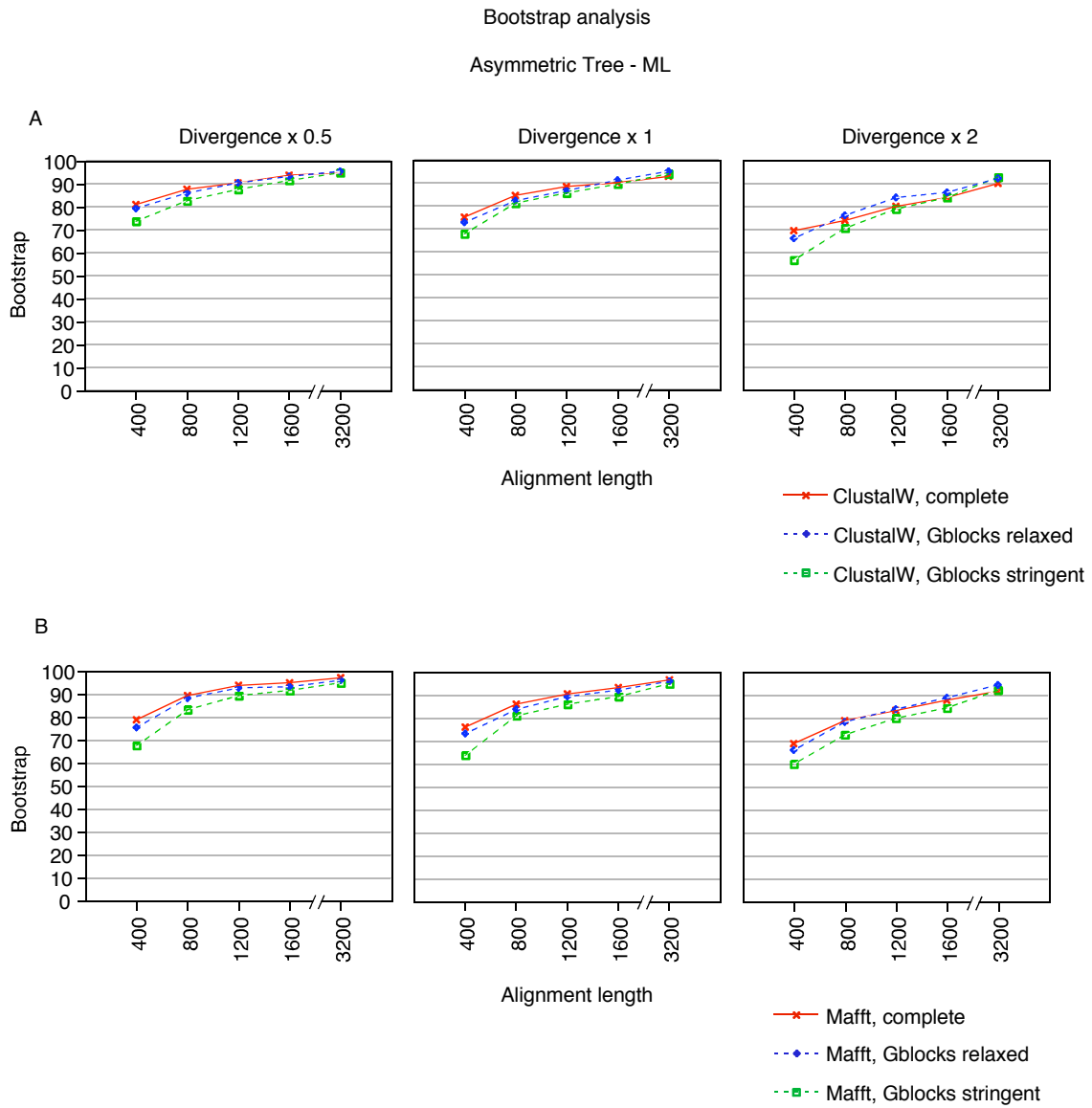
Asymmetric Tree - ML

Online Appendix - Figure 8. Average bootstrap values of ML trees obtained from ClustalW (A) and Mafft (B) alignments simulated from the asymmetric tree with three different divergence levels. Complete (solid, red line), Gblocks relaxed (dotted, blue line with diamonds) and Gblocks stringent (dotted, green line with squared symbols) alignments are shown.