

Table 4. The model effectively infers characteristic network parameters describing a pre-duplication network and its post-duplication dynamics

	P_{si}	P_i	P_+	P_-
Network Parameters	28.%	0.22%	0.070%	59.%
Inferred Parameters	26.%	0.23%	0.071%	57%
Difference*	7.8%	2.8%	1.5%	2.6%

* This simulated network had 900 genes equivalent to the 450 ohnolog pairs in Kellis *et al.* [Kellis M, Birren BW, Lander ES (2004) "Proof and evolutionary analysis of ancient genome duplication in the yeast *Saccharomyces cerevisiae*," *Nature* 428:617-624]. Using network motifs our model extracted the defining parameters of the network with > 90% accuracy.