Supporting information for
Modeling gene expression evolution with an extended Ornstein-Uhlenbeck process

Supporting tables

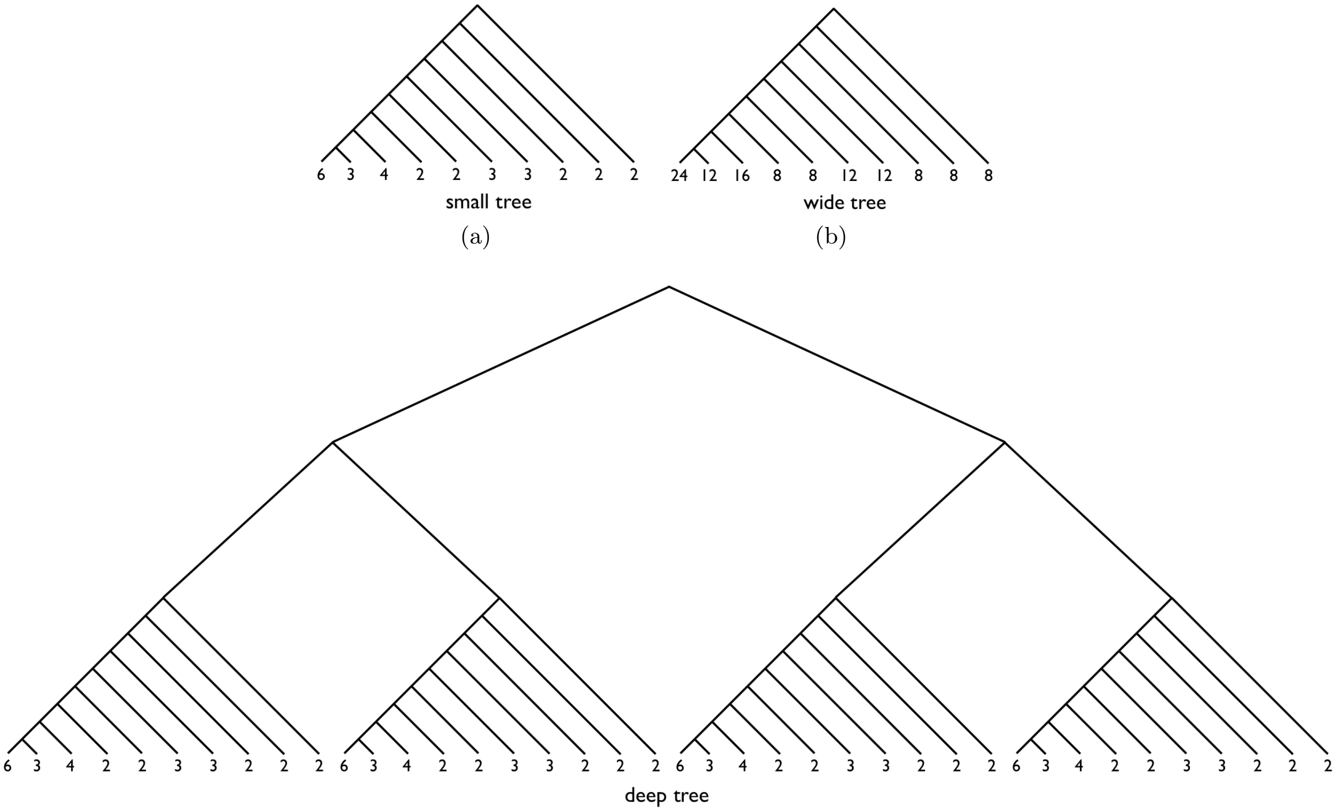
	small tree	deep tree	wide tree
species mean	13.0	9.29	9.41
species variance	2.89	6.31e-8	3.59

Table S 1: Simulation-determined drift v. stabilization critical values to obtain a null hypothesis false positive rate of 0.05 when $\tau^2 = 5$ and $\sigma^2 = 25$.

	small tree	deep tree	wide tree
non-evolutionary v. drift	0.99	0.98	0.98
drift v. stabilization	0.00	0.06	0.01
stabilization v. shift	0.67	0.98	0.95

Table S 2: Positive rates of model comparison tests for data simulated under expression shift with $\Delta\theta = 10$.

Supporting figures



(a) (b)

(c)

Figure S 1: Schematics of phylogenies used in analysis with the number of individuals per leaf node for (a) small tree, (b) wide tree, (c) deep tree

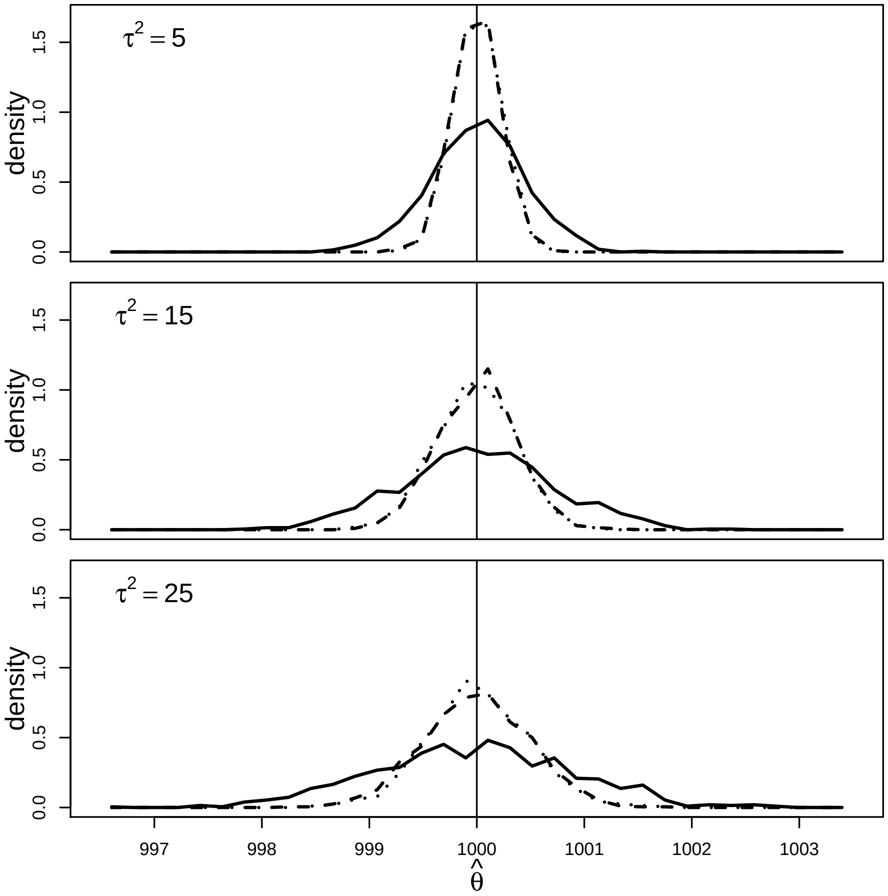


Figure S 2: Maximum likelihood θ estimates ($\hat{\theta}$) for data simulated under non-evolution and various true τ^2 values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree)

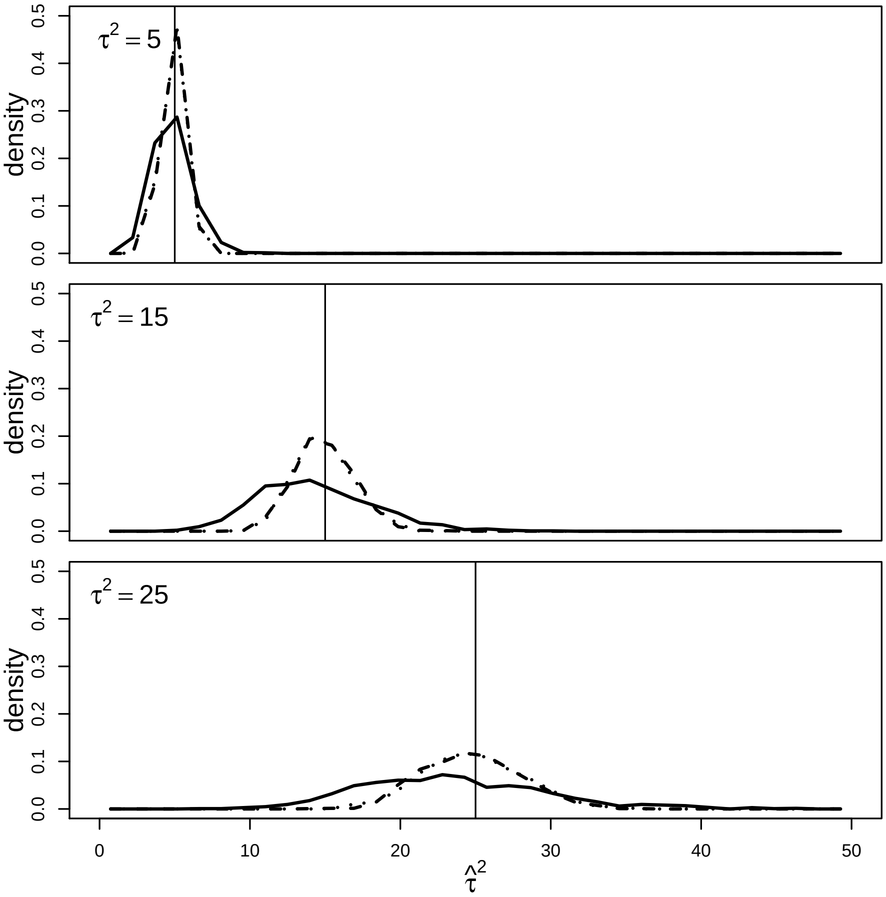


Figure S 3: Maximum likelihood τ^2 estimates ($\hat{\tau^2}$) for data simulated under non-evolution and various true τ^2 values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree)

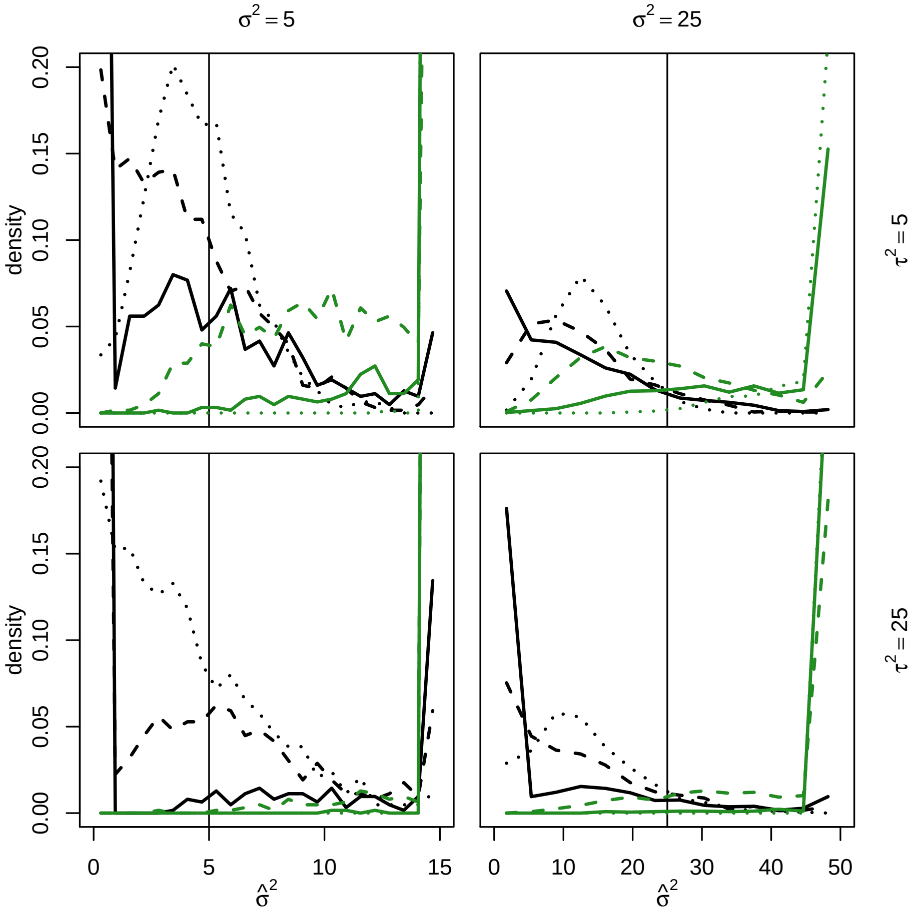


Figure S 4: Maximum likelihood σ^2 estimates ($\hat{\sigma}^2$) for data simulated under drift with various true τ^2 and σ^2 values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree), and both the species variance (black) and species mean models (green). Note that parameter values greater than 15 are represented in the right-most bin.

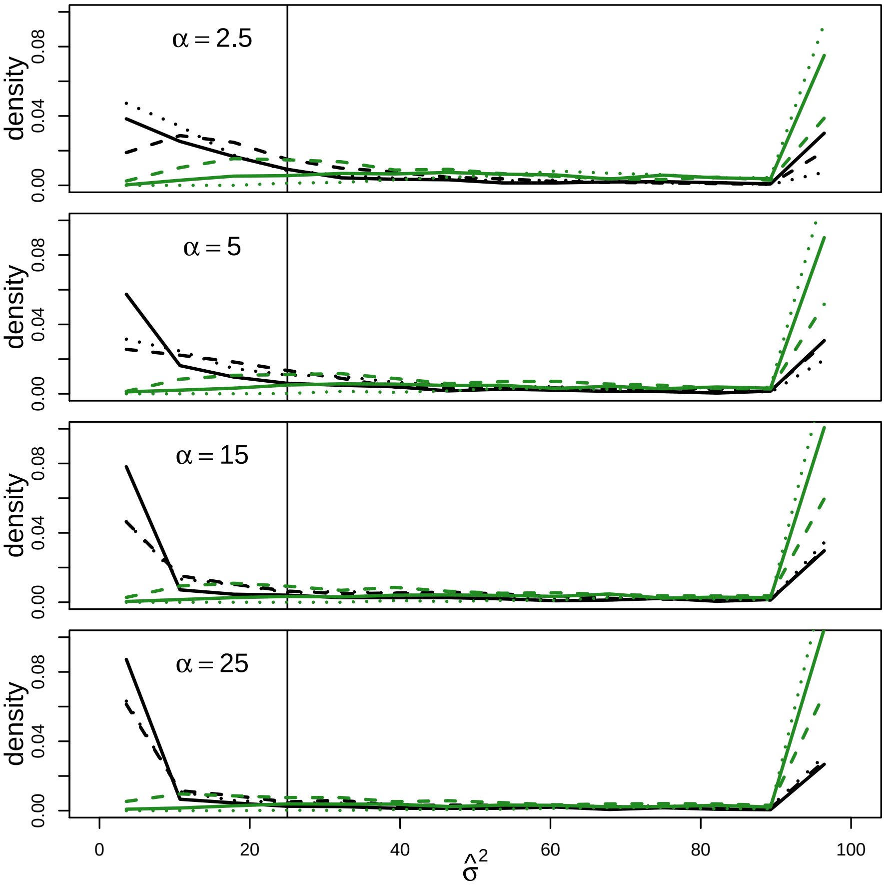


Figure S 5: Maximum likelihood σ^2 estimates ($\hat{\sigma}^2$) for data simulated under stabilizing selection with various true α values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree), and both the species variance (black) and species mean models (green). Note that parameter values greater than 100 are represented in the right-most bin.

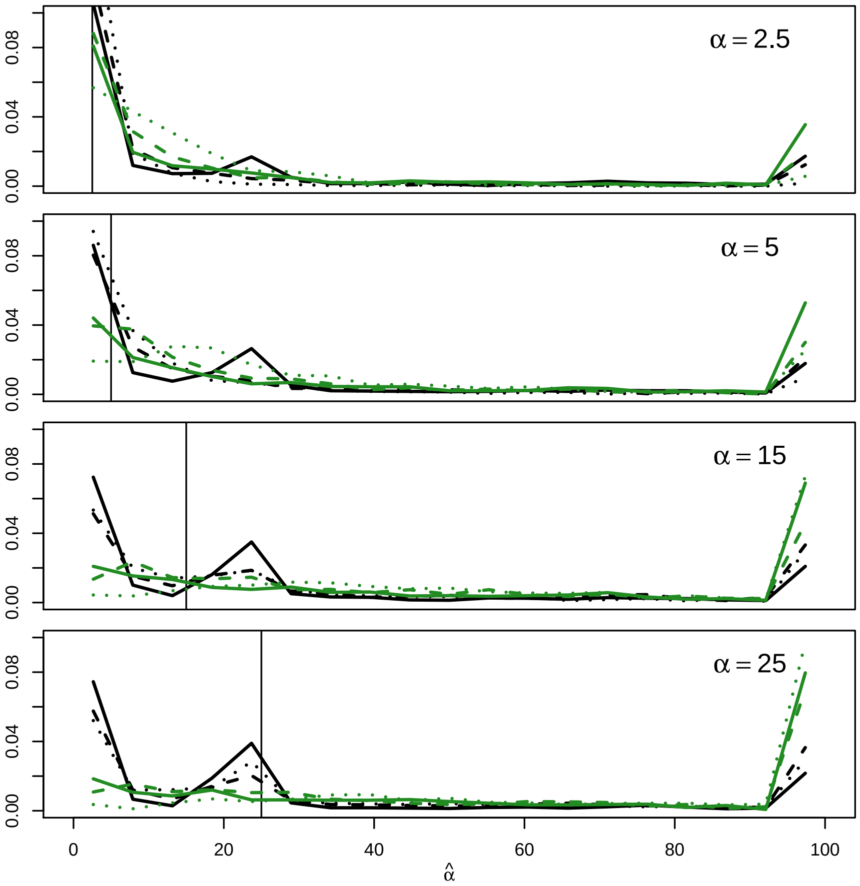


Figure S 6: Maximum likelihood α estimates ($\hat{\alpha}$) for data simulated under stabilizing selection with various true α values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree), and both the species variance (black) and species mean models (green). Note that parameter values greater than 100 are represented in the right-most bin.

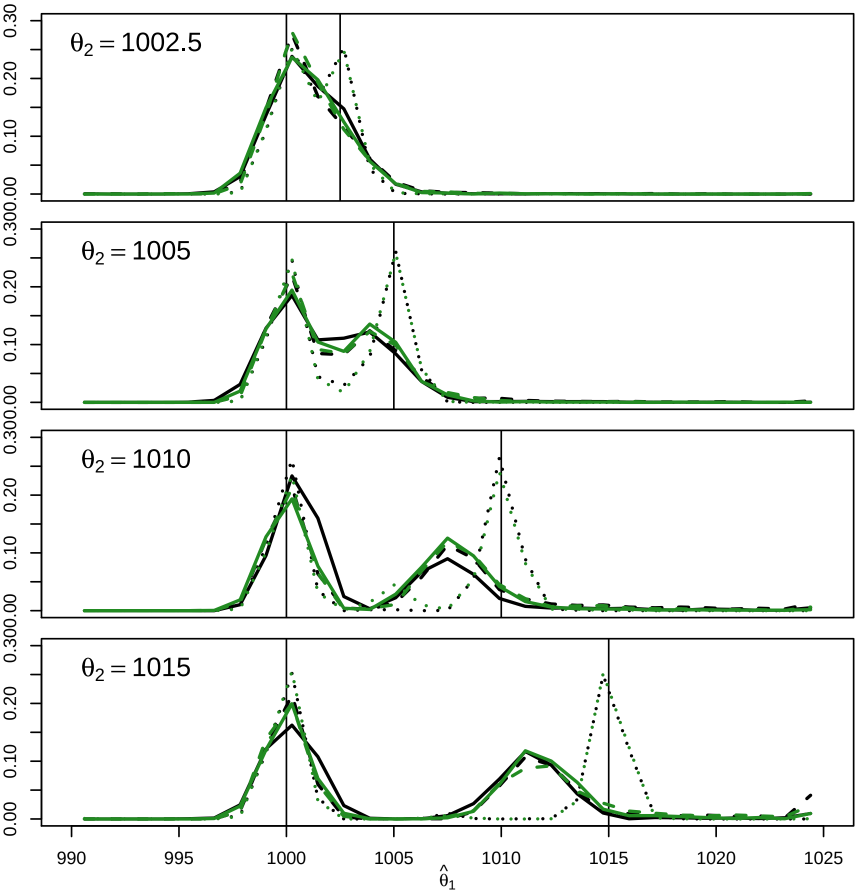


Figure S 7: Maximum likelihood θ_1 and θ_2 estimates ($\hat{\theta}_1$ and $\hat{\theta}_2$) for data simulated under expression shift with various true θ_2 values and different phylogenetic structures (solid: small tree, dashed: wide tree, dotted: deep tree), and both the species variation (black) and species mean models (green).