

MCMC Convergence Report

Condition 001

Simulation Parameters:

T=500 | A1=-9 | A2=9 | Cop=Gaussian | Tau=0.4

VAR Coefficients: $\phi_{11}=0.50$, $\phi_{12}=0.30$, $\phi_{21}=0.30$, $\phi_{22}=0.50$

Interpretation Guide:

- * Divergences: Should be 0 (numerical issues if present)
 - * E-FMI: Should be > 0.3 for efficient sampling
- * R-hat: Should be < 1.05 for reliable chain convergence
 - * N_eff: Should be > 400 for key parameters
- * Accept Stat: Should be near adapt_delta (often 0.99)

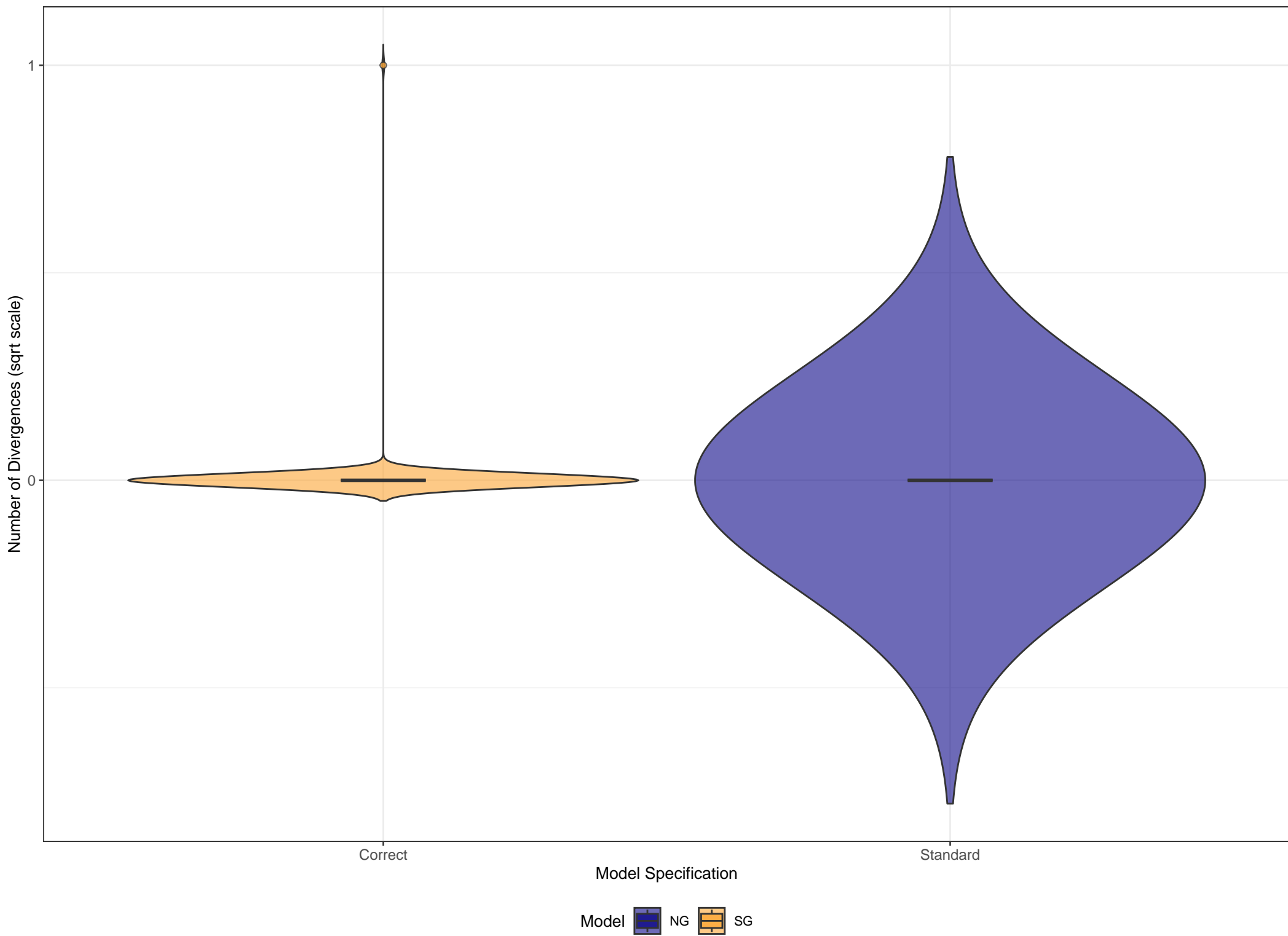
Convergence Summary & Parameter Diagnostics

	Model	Divergences	% with Divergences	E-FMI	Min E-FMI	Avg R-hat	Max R-hat	Median N_eff	Accept Stat
1	NG (Standard)	N/A	0.0% [GOOD]	0.500 [GOOD]	0.488 [GOOD]	1.000 [GOOD]	1.005 [GOOD]	4338	0.989 [GOOD]
2	SG (Correct)	1 [WARNING]	0.4% [WARNING]	0.499 [GOOD]	0.484 [GOOD]	1.000 [GOOD]	1.036 [WARNING]	5138	0.988 [GOOD]

	Parameter Group	Model	Avg R-hat	% R-hat > 1.05	Median N_eff	Min N_eff
1	Copula Params	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6094	4187
2	Copula Params	SG (Correct)	1.000 [GOOD]	0.0% [GOOD]	6920	4882
3	Intercepts	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6074	4710
4	Intercepts	SG (Correct)	1.000 [GOOD]	0.0% [GOOD]	5299	3584
5	Other	NG (Standard)	1.001 [GOOD]	0.0% [GOOD]	3917	2605
6	Other	SG (Correct)	1.000 [GOOD]	0.0% [GOOD]	4994	528
7	Residual Params	NG (Standard)	1.000 [GOOD]	0.0% [GOOD]	6392	4869
8	Residual Params	SG (Correct)	1.000 [GOOD]	0.0% [GOOD]	5085	88
9	VAR Coeffs	NG (Standard)	1.001 [GOOD]	0.0% [GOOD]	4042	2610
10	VAR Coeffs	SG (Correct)	1.000 [GOOD]	0.0% [GOOD]	5134	2933

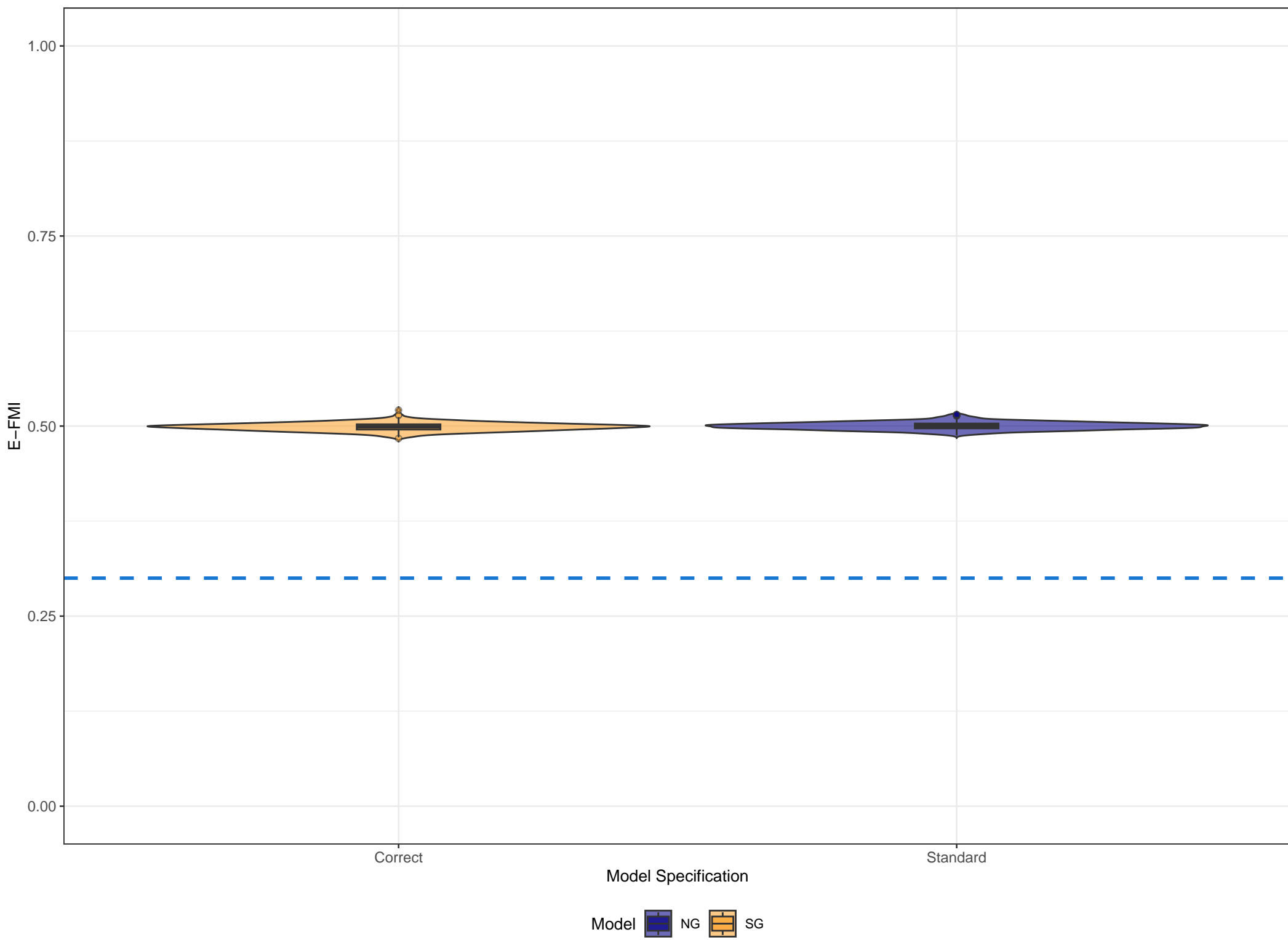
Divergent Transitions by Model Type

Lower is better (ideally zero). Distribution across replications (violin).



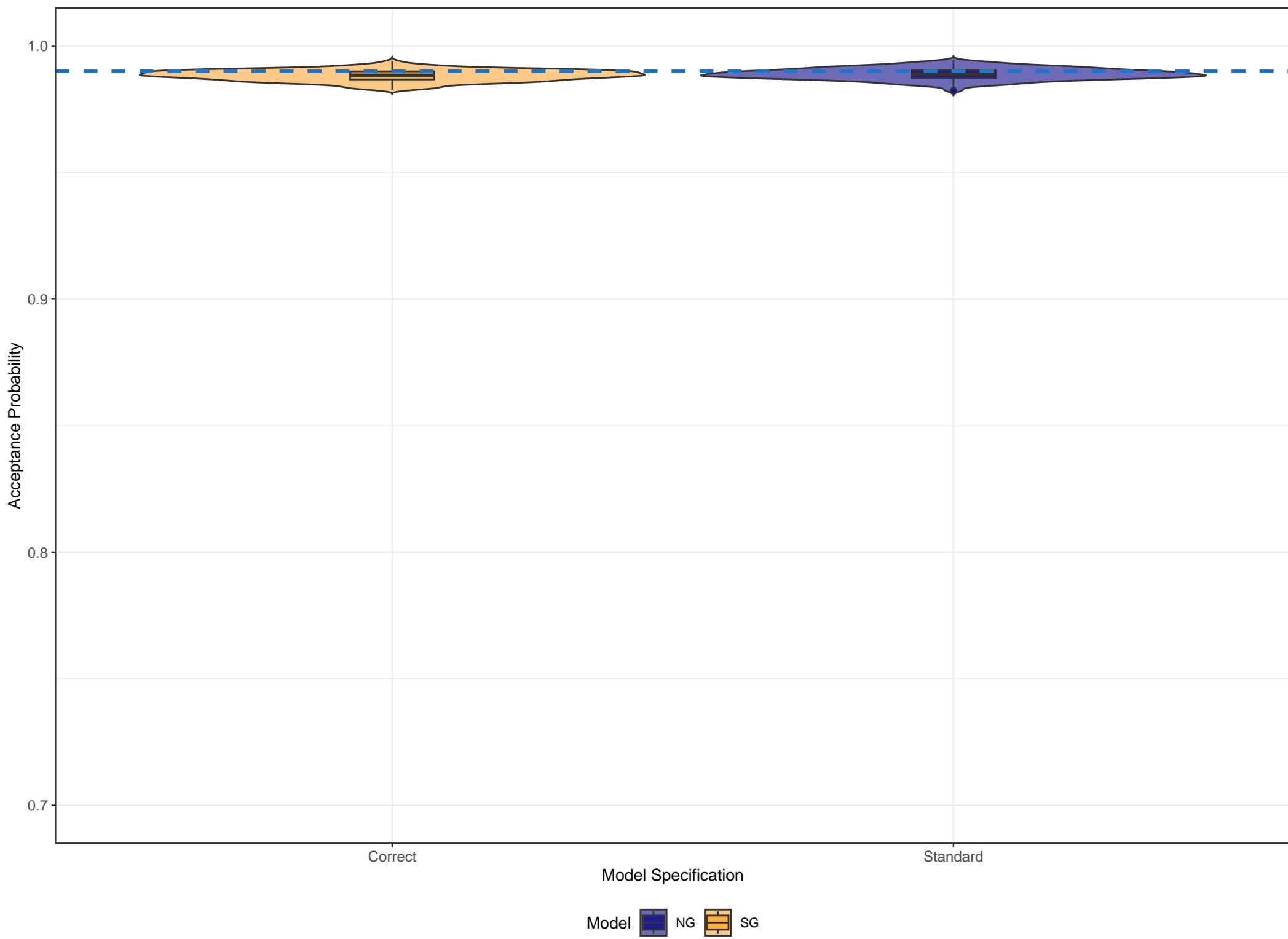
Energy Fraction of Missing Information (E-FMI)

Should be above 0.3 (blue line) for efficient exploration.



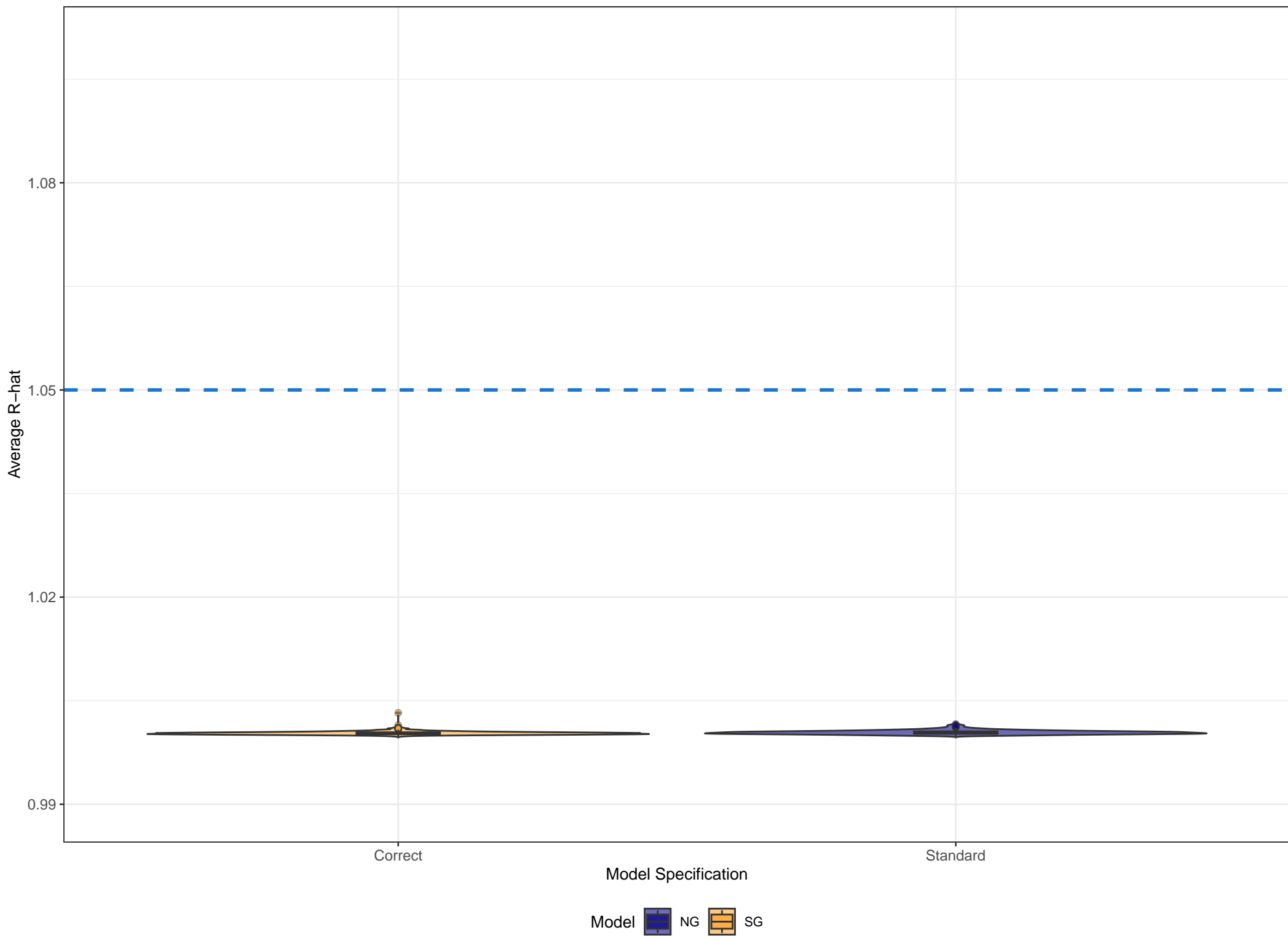
Average Acceptance Statistic

Target near 0.99 (blue line). Higher is generally better.



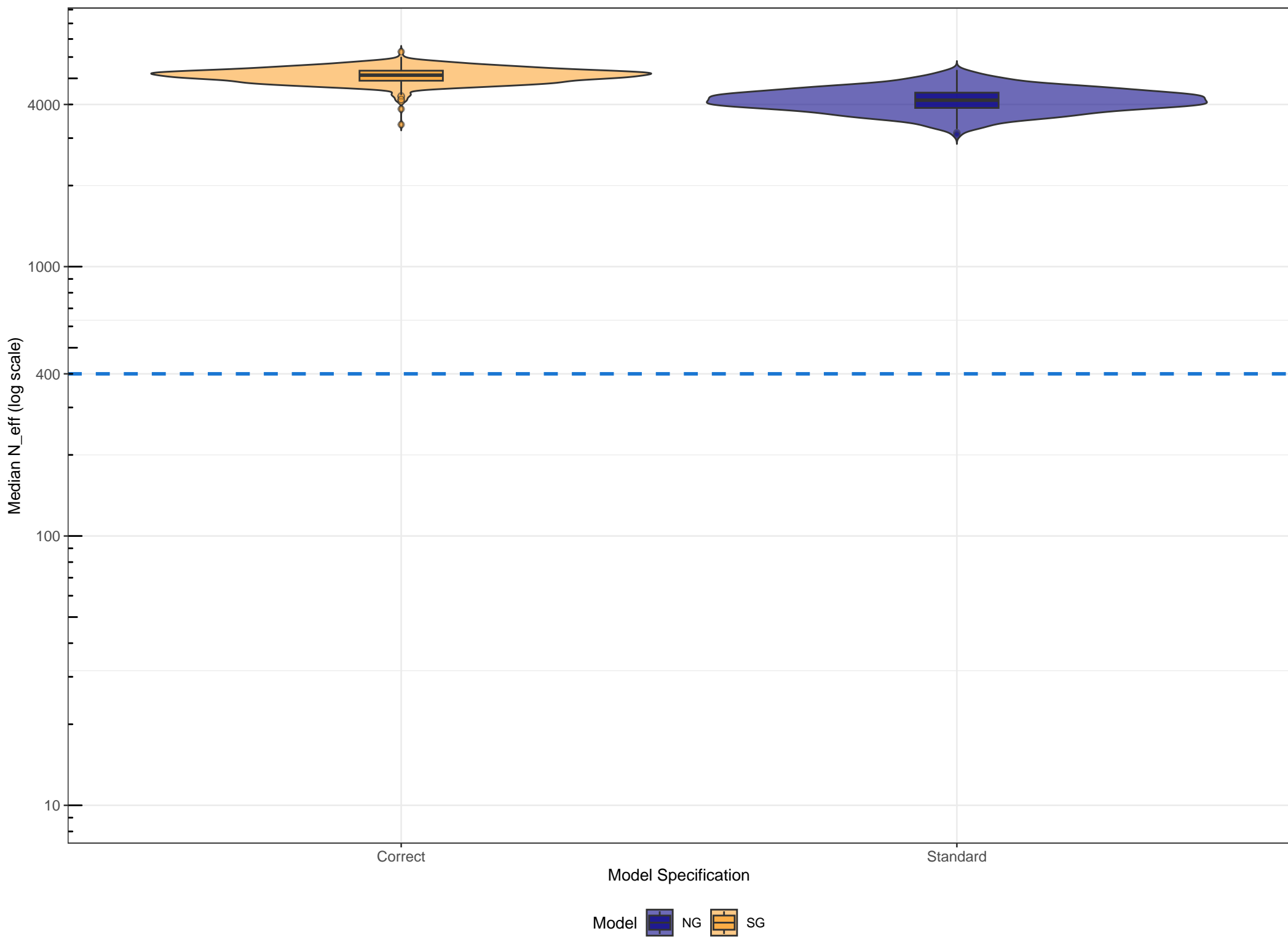
Potential Scale Reduction Factor (R-hat)

Should be < 1.05 (blue line). Average R-hat across params per replication.



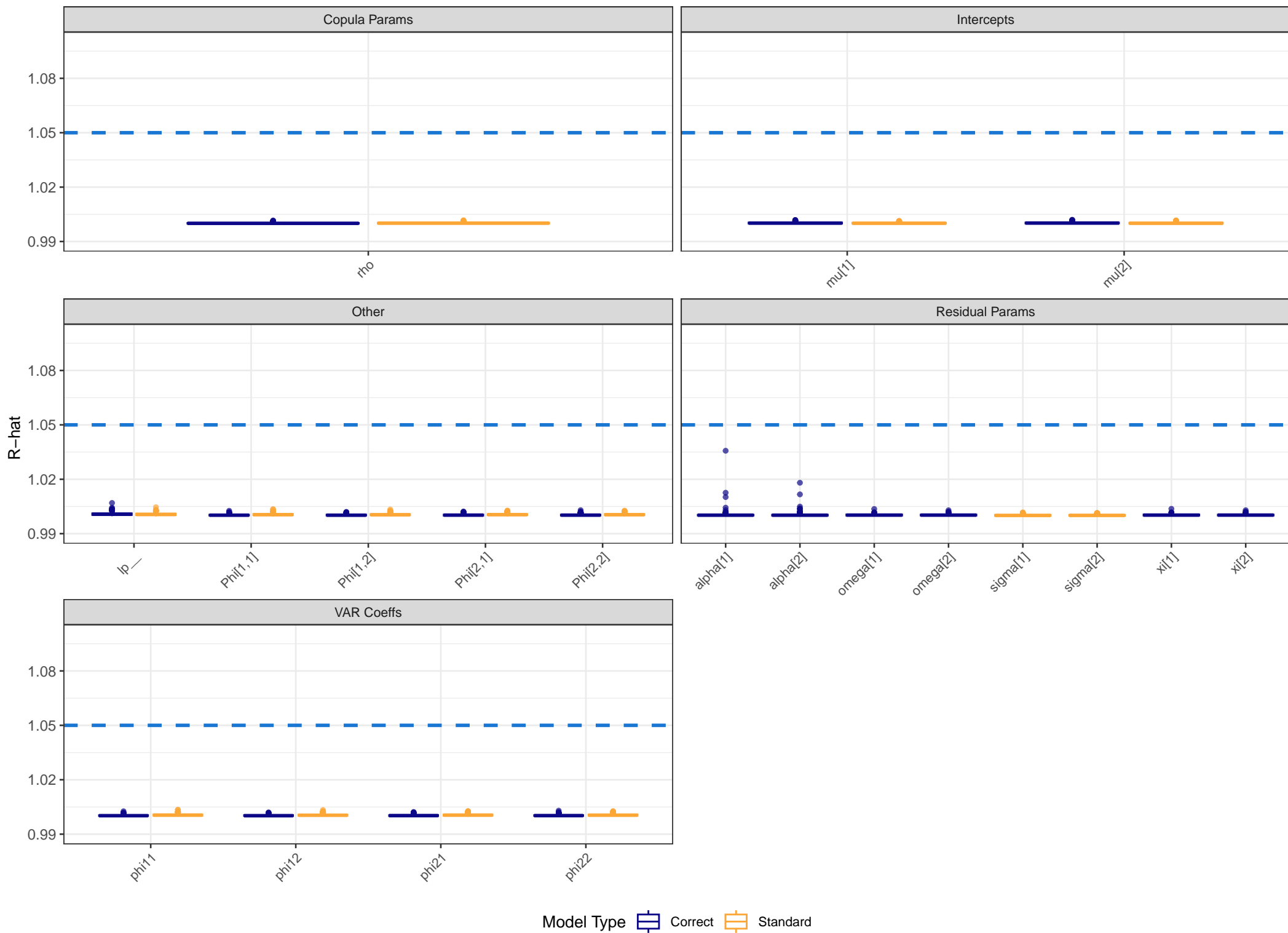
Effective Sample Size (N_eff)

Higher is better; 400+ is a common guideline (blue line).



R-hat by Parameter Category

Boxplots across replications for each parameter. Helps spot tough parameters.



Trace Plot: SG Model (Rep 206 with 1 divergences)

Looking for 'hairy caterpillar' appearance – good mixing across chains.

