Study 3: VAR(1) with Normal Margins — Gaussian vs. Clayton Copula

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0. Summary

0.1 Computational Stability

Both models exhibit excellent computational stability across all simulation conditions. The Normal-Gaussian (NG) model and the Normal-Clayton (NC) model both show no post-warmup divergent transitions and max $\hat{R} \leq 1.01$ in all replications. This stands in contrast to Studies 1-2 where some model-DGP combinations exhibited divergences.

0.2 Model Performance Under Clayton Copula DGP

Normal-Clayton (NC): The correctly specified model is approximately unbiased for all parameters including the copula parameter θ. Coverage is close to nominal (0.95) across conditions, with slight under-coverage for θ at higher dependence levels ($\theta \geq 4$) in small samples.

Normal-Gaussian (NG): The misspecified model recovers the VAR dynamics (Φ) and intercepts (μ) without substantial bias, demonstrating robustness of marginal parameter inference to copula misspecification. The copula parameter ρ has no ground truth under the Clayton DGP, but posterior means increase monotonically with θ, indicating the Gaussian copula "absorbs" the Clayton dependence structure.

0.3 Key Insights

1. **Copula misspecification does not propagate to marginal parameters**: Under normal margins, the NG model recovers μ, Φ, and σ with similar accuracy to the correctly specified NC model.

2. **The Clayton copula captures asymmetric tail dependence**: Unlike the symmetric Gaussian copula, the Clayton copula concentrates dependence in the lower tail. This feature cannot be captured by the NG model's ρ parameter.

3. **Kendall's τ provides a common dependence scale**: The relationship $\tau = \theta/(\theta+2)$ maps Clayton θ to the $[0,1]$ scale, facilitating comparison with Gaussian ρ (where $\tau = (2/\pi)\arcsin(\rho)$).

1. Introduction

This simulation study compares two Bayesian VAR(1) models under a Clayton copula DGP with normal margins: a Normal-Gaussian (NG) model (misspecified copula) and a Normal-Clayton (NC) model (correctly specified). Unlike Studies 1-2, which examined marginal distribution misspecification, Study 3 focuses on **copula misspecification** while keeping margins correctly specified in both models.

1.1. Data Generating Process (DGP)

The DGP follows the same VAR(1) structure as Studies 1-2:

$$Y_t = \mu + \Phi Y_{t-1} + \varepsilon_t, \qquad t = 2, \dots, T,$$

with $\mu = \mathbf{0}$. Innovations $\varepsilon_t = (\varepsilon_{1t}, \varepsilon_{2t})$ have standard normal margins (mean 0, variance 1) coupled through a **Clayton copula** with parameter $\theta > 0$.

ℹ Clayton Copula

The Clayton copula is an Archimedean copula with CDF:

$$C(u, v; \theta) = \left(u^{-\theta} + v^{-\theta} - 1\right)^{-1/\theta}, \qquad \theta > 0$$

It exhibits **lower-tail dependence**: extreme low values co-occur more frequently than under a Gaussian copula. The lower-tail dependence coefficient is $\lambda_L = 2^{-1/\theta}$.

❗ Kendall's Tau Relationship

For the Clayton copula, Kendall's τ relates to θ via:

$$\tau = \frac{\theta}{\theta + 2}$$

This provides a monotone mapping between $\theta \in (0, \infty)$ and $\tau \in (0, 1)$.

Table 1: Kendall's tau values for Clayton copula design parameters.

theta	tau
0.5	0.20
1.0	0.33
2.0	0.50
4.0	0.67
8.0	0.80

1.2. Simulation Design

The study employs a factorial design crossing three factors.

Table 2: Summary of the Simulation Design Factors.

Factor	Levels
Time Series Length (T)	50, 100, 200
Clayton Parameter (theta)	0.5, 1.0, 2.0, 4.0, 8.0
VAR Parameters (Phi)	Set A: phi_11=phi_22=0.40, phi_12=phi_21=0.10
Margins	Standard Normal (mean 0, variance 1)

> **i Design Simplification**
>
> Study 3 uses only VAR Set A (symmetric) and excludes skewness direction factors since all margins are symmetric normal. This yields $3 \times 5 = 15$ conditions with 200 replications each, for a total of 3,000 simulated datasets.

1.3. True Parameter Values

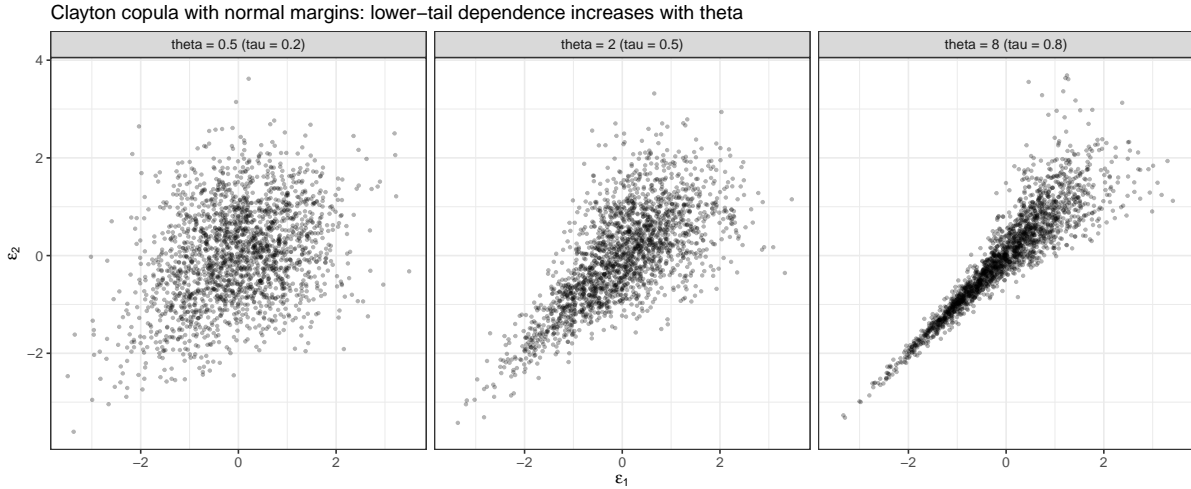Table 3: True Parameter Values Used in the Data Generating Process.

Parameter	True Value	Notes
mu_1, mu_2	0, 0	Innovations are mean-zero
phi_11, phi_22	0.40	Diagonal AR coefficients
phi_12, phi_21	0.10	Cross-effects (symmetric)
sigma_1, sigma_2	1.0, 1.0	Innovations are unit-variance

Parameter	True Value	Notes
theta (NC model)	Design value (0.5, 1, 2, 4, or 8)	Clayton copula parameter
rho (NG model)	Undefined (copula misspecified)	No ground truth under Clayton DGP

> **❗ No Ground Truth for rho in NG Model**
>
> Under the Clayton copula DGP, the Gaussian copula parameter ρ has no well-defined ground truth. The NG model is misspecified for the copula structure, so bias and coverage metrics are **not computed** for ρ. Instead, we report posterior means descriptively to show how the Gaussian copula absorbs Clayton dependence.

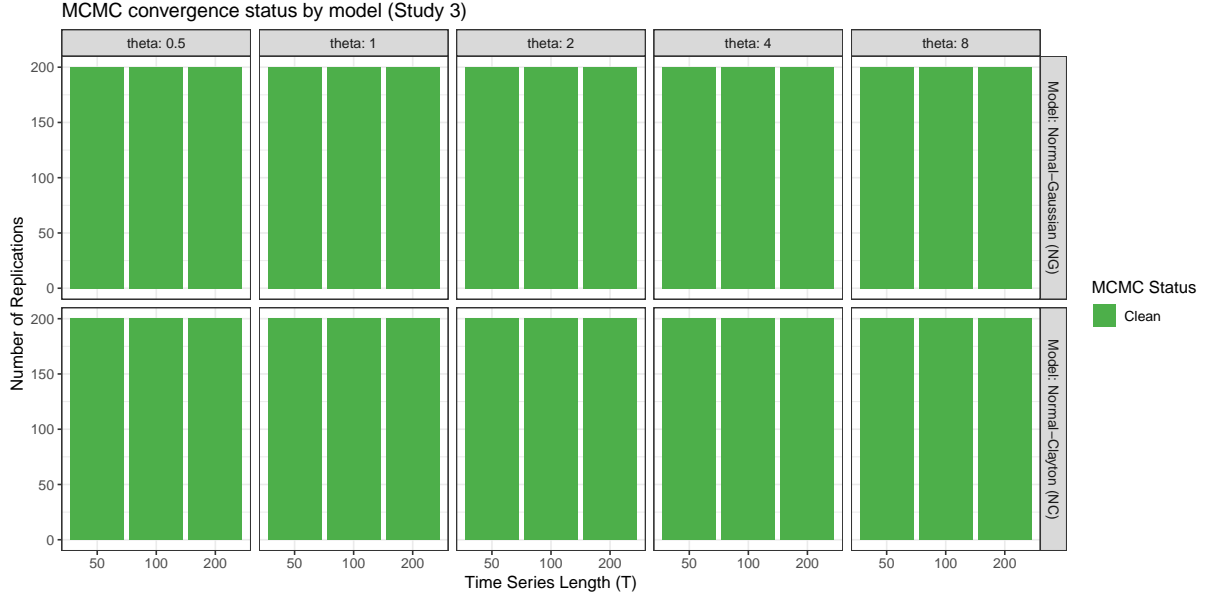## 1.4. Visual Check: Clayton Copula Dependence Structure

Clayton copula with normal margins: lower–tail dependence increases with theta

Interpretation. The Clayton copula induces asymmetric dependence concentrated in the lower-left tail. As θ increases, the clustering of extreme negative values becomes more pronounced. This lower-tail dependence cannot be captured by a symmetric Gaussian copula.

2. Data Loading and Preparation

2.1. MCMC Classification and Overview

We classify runs based on MCMC diagnostics ($\hat{R}$ and divergent transitions) using the same criteria as Studies 1-2:

- **Clean**: $\hat{R} \leq 1.01$ and no post-warmup divergences.
- **Problematic**: $\hat{R} > 1.01$ or at least one divergence.
- **Failed/Error**: Non-OK status or missing diagnostics.

MCMC convergence status by model (Study 3)

Interpretation. Both NG and NC fits are uniformly Clean across the entire design, with zero post-warmup divergent transitions. This excellent computational behavior demonstrates that both models sample efficiently under the Clayton DGP with normal margins.
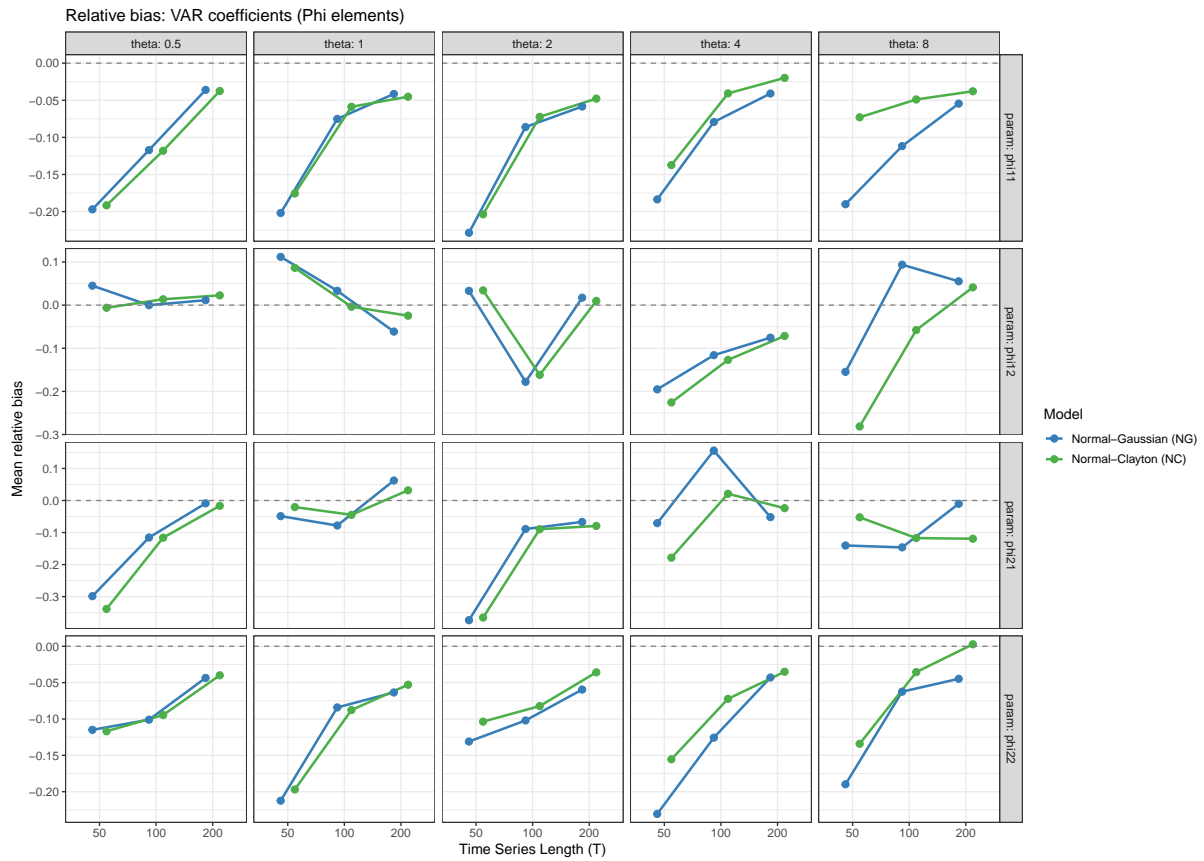
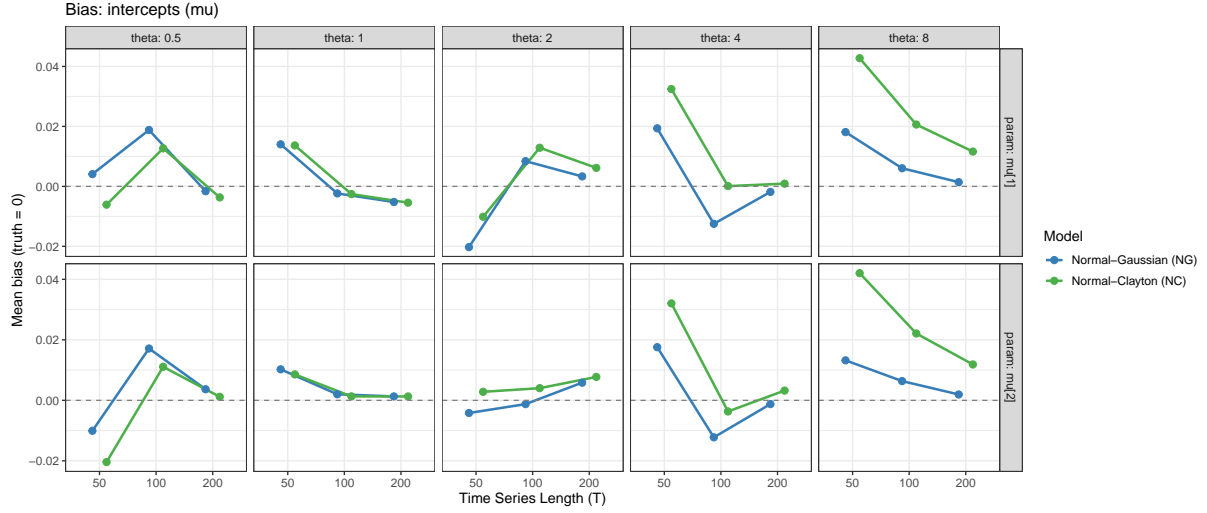Table 4: Divergence summary: All runs have zero post-warmup divergent transitions.

Model	T	N Runs	Total Divergences
Normal-Gaussian (NG)	50	1000	0
Normal-Gaussian (NG)	100	1000	0
Normal-Gaussian (NG)	200	1000	0
Normal-Clayton (NC)	50	1000	0
Normal-Clayton (NC)	100	1000	0
Normal-Clayton (NC)	200	1000	0

3. Helper Functions

4. VAR Parameters: NG vs NC Performance

4.1. Relative Bias

Relative bias: VAR coefficients (Phi elements)

Bias: intercepts (mu)

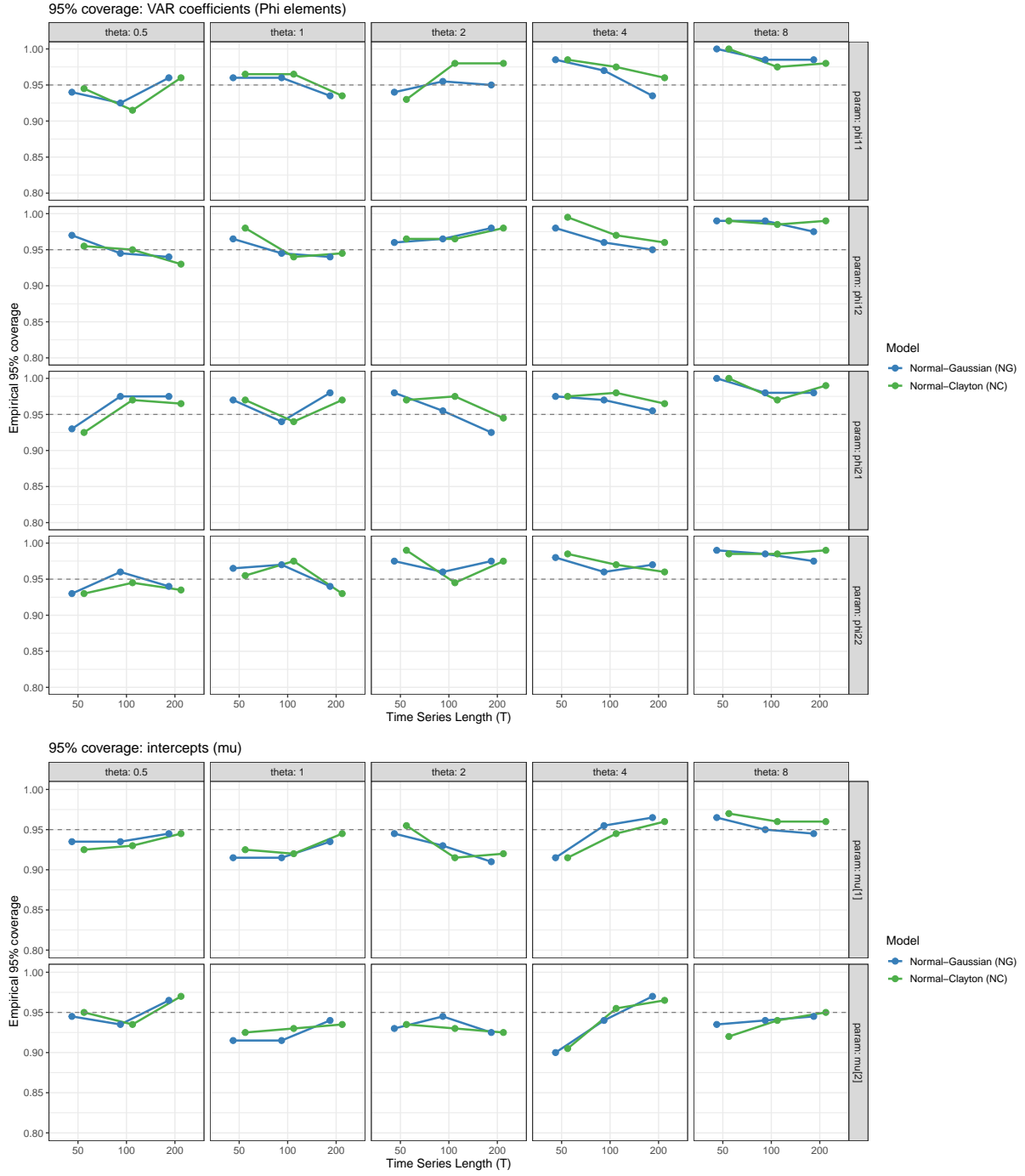**Interpretation.** Both models recover the VAR parameters with similar accuracy. The NG model (misspecified copula) shows no systematic bias disadvantage compared to NC, indicating that copula misspecification does not propagate to inference on the VAR dynamics.

4.2. 95% Coverage

95% coverage: VAR coefficients (Phi elements)

95% coverage: intercepts (mu)

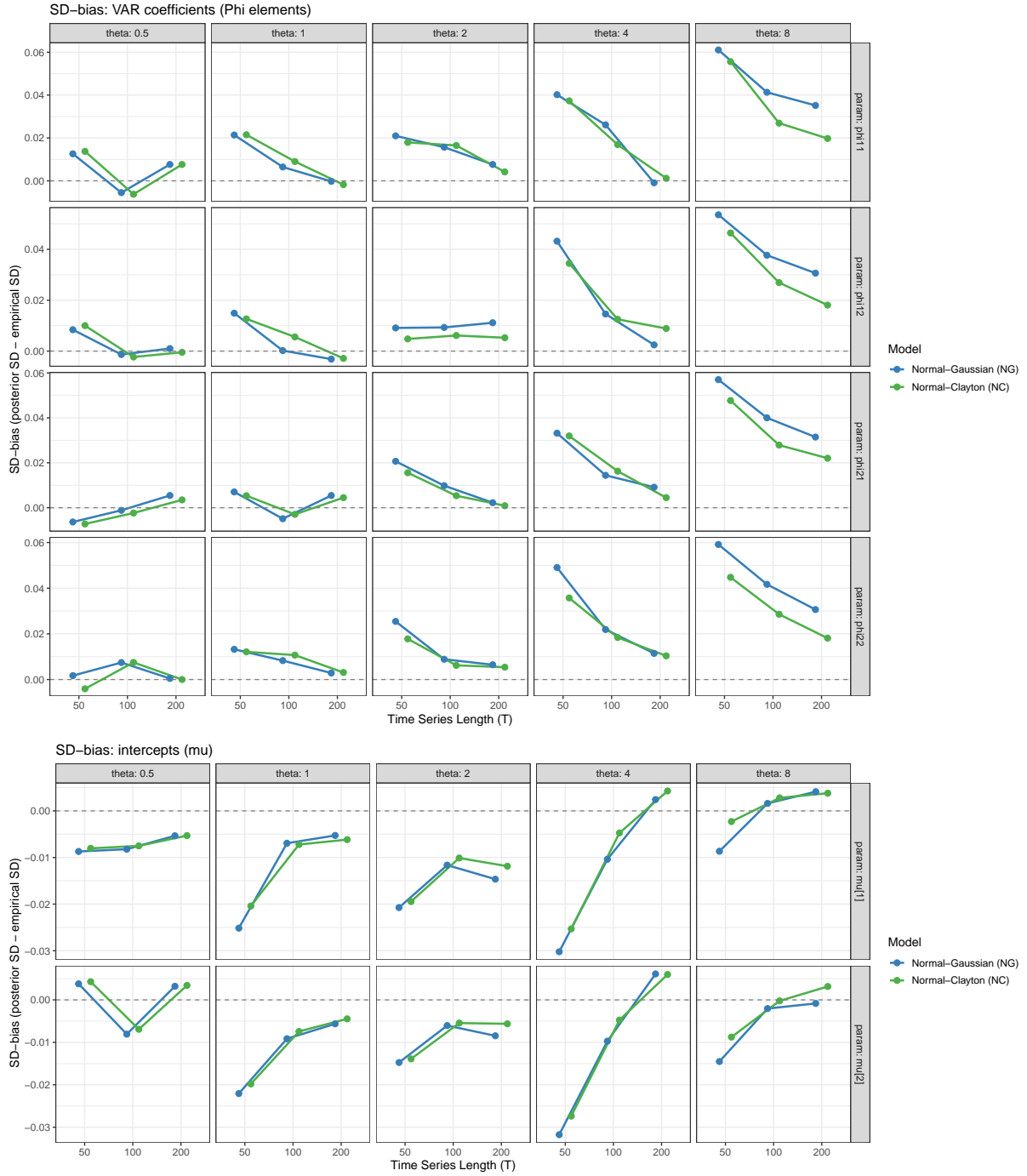**Interpretation.** Coverage is close to nominal for both models across all VAR parameters. There is no evidence that copula misspecification in NG degrades frequentist coverage for μ

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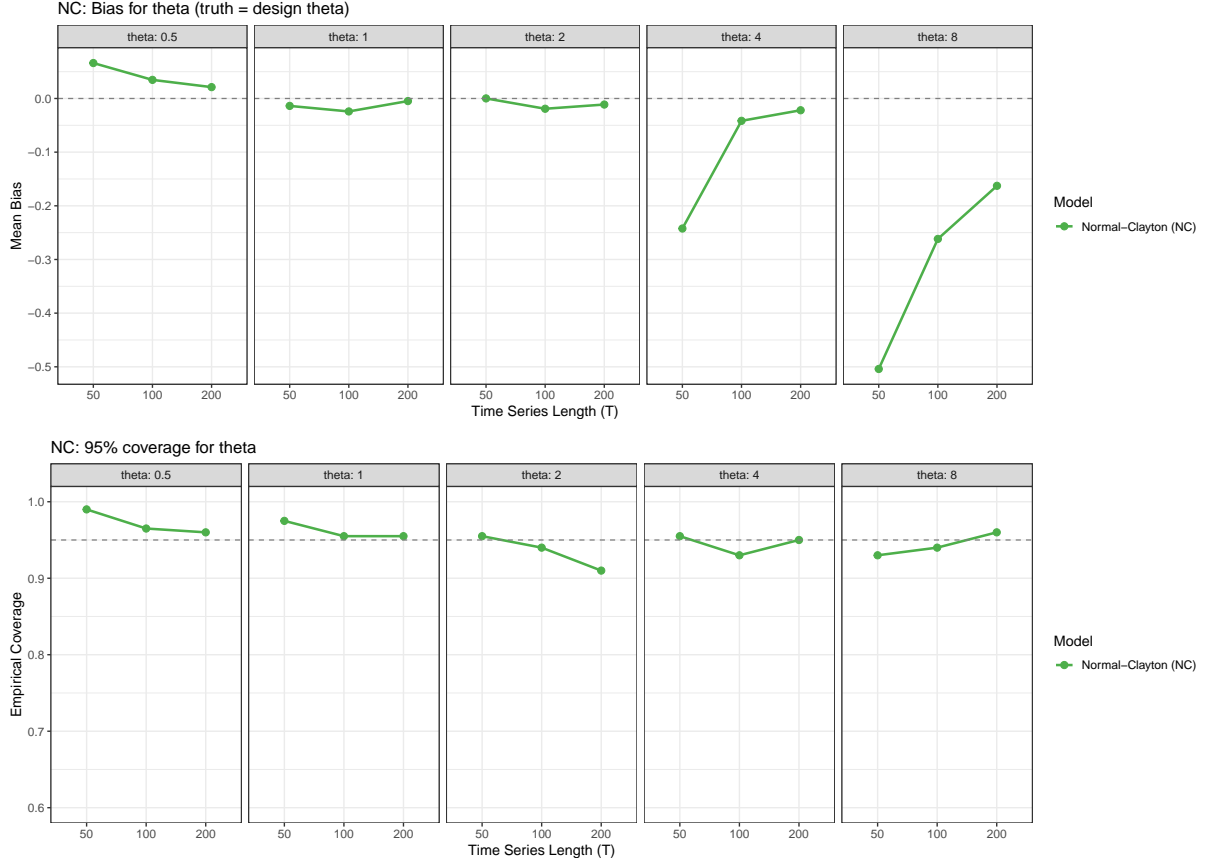
or Φ.

4.3. SD-Bias

SD−bias: VAR coefficients (Phi elements)

SD−bias: intercepts (mu)

Interpretation. Both models show similar SD-bias patterns, with slight over-estimation of posterior uncertainty at smaller T. The patterns are nearly identical between NG and NC, further confirming that copula misspecification has minimal impact on VAR parameter inference.
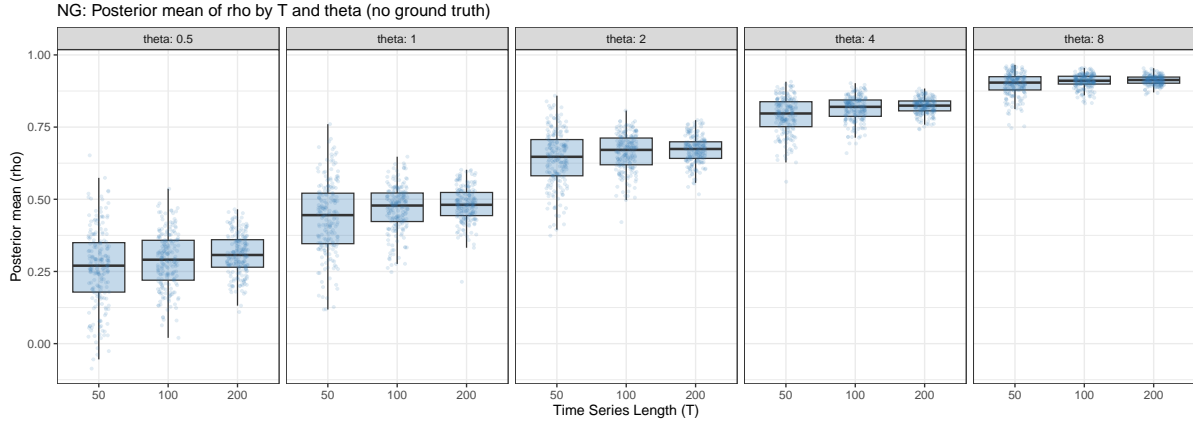
5. Copula Parameters

5.1. NC (Clayton copula): theta Recovery

NC: Bias for theta (truth = design theta)

NC: 95% coverage for theta

Interpretation. The NC model shows negative bias for θ, with the magnitude increasing with θ. This suggests the prior (Log-Normal$(0, 1)$) may provide some shrinkage toward smaller values, particularly for $\theta = 8$ which lies in the upper tail of the prior. Coverage is close to nominal for moderate θ but drops below 0.95 for $\theta = 8$ at small T, consistent with the bias pattern.
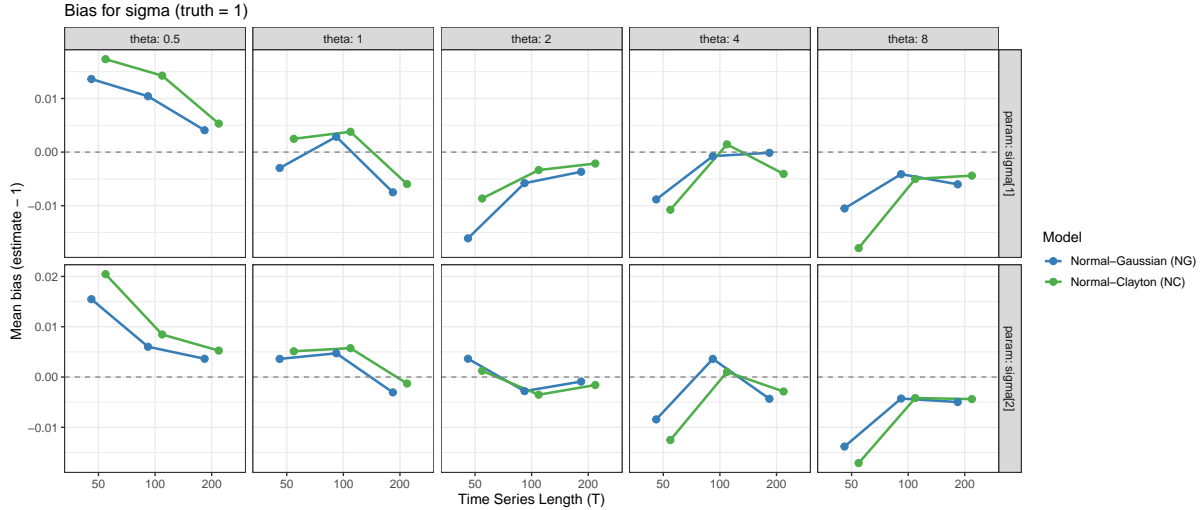
5.2. NG (Gaussian copula): rho Posterior Means

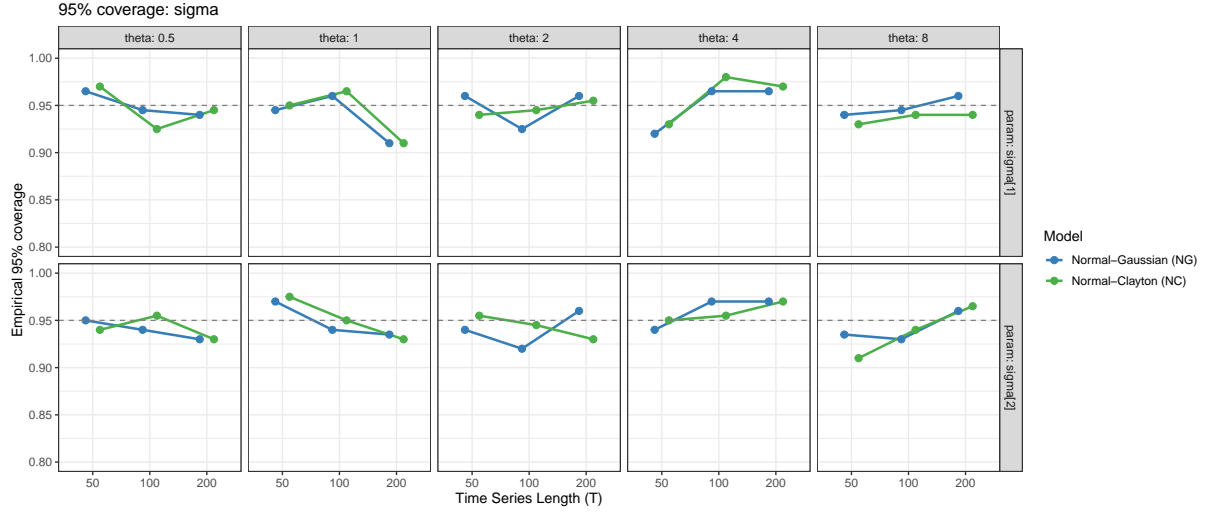Since ρ has no ground truth under the Clayton DGP, we report posterior means descriptively.

NG: Posterior mean of rho by T and theta (no ground truth)

Interpretation. The posterior mean of ρ increases monotonically with the true Clayton θ, showing how the Gaussian copula "absorbs" the Clayton dependence structure. For $\theta = 8$ (Kendall's $\tau = 0.80$), the NG model estimates $\rho \approx 0.85$, which corresponds to $\tau_{\text{Gauss}} = (2/\pi)\arcsin(0.85) \approx 0.60$ – lower than the true $\tau = 0.80$ because the Gaussian copula cannot capture the asymmetric lower-tail dependence.

6. Marginal Parameters

We report mean bias for the innovation standard deviations (σ). Under the DGP, the true value is 1.

Bias for sigma (truth = 1)

95% coverage: sigma

Interpretation. Both models recover the marginal scale parameters with minimal bias and near-nominal coverage. As in Studies 1-2, the marginal parameters are robust to copula misspecification because they depend primarily on the univariate distribution of residuals, not their dependence structure.

7. MCMC Diagnostics: Status Split

NC: Coverage split by MCMC status

Interpretation. Since all replications are classified as Clean (no divergences, $\hat{R} \leq 1.01$), there is no variation by MCMC status. This confirms excellent computational behavior for both models.

8. Export Tables

Tables exported to results/exported_tables_s3:

- `analysis_summary_aggregated.csv`: Condition-level metrics
- `analysis_summary_status_split.csv`: Metrics split by MCMC status

- `analysis_mcmc_health_counts.csv`: MCMC convergence counts

9. Details

This section provides technical details on the implementation of the simulation study.

9.1. Prior Specifications

Table 5: Prior Specifications for the Normal-Gaussian (NG) Model.

Parameter	Prior	Support	Rationale
mu_1, mu_2	Normal(0, 1)	Real line	Weakly informative; centered at true value (0)
phi_11, phi_12, phi_21, phi_22	Normal(0, 0.5)	(-1, 1)	Regularizes toward stationarity
sigma_1, sigma_2	Half-Normal(0, 1)	(0, infinity)	Weakly informative scale prior
rho	Normal(0, 0.5)	(-1, 1)	Regularizes toward independence

Table 6: Prior Specifications for the Normal-Clayton (NC) Model.

Parameter	Prior	Support	Rationale
mu_1, mu_2	Normal(0, 1)	Real line	Weakly informative
phi_11, phi_12, phi_21, phi_22	Normal(0, 0.5)	(-1, 1)	Regularizes toward stationarity
sigma_1, sigma_2	Half-Normal(0, 1)	(0, infinity)	Weakly informative scale prior
theta	Log-Normal(0, 1)	(0, infinity)	Covers design values within +/- 2 SDs

> **i** Log-Normal Prior for Clayton theta
>
> The Log-Normal(0, 1) prior has median 1 and places approximately 95% of its mass in (0.14, 7.4). This covers the design grid $\theta \in \{0.5, 1, 2, 4, 8\}$ well, with only the largest value ($\theta = 8$) lying slightly in the upper tail.

9.2. MCMC Settings

Table 7: MCMC Sampling Configuration.

Setting	Value	Description
Chains	4	Number of independent Markov chains
Total iterations	3,000	Iterations per chain (including warmup)
Warmup iterations	1,500	Discarded adaptation period
Post-warmup draws	1,500	Retained samples per chain
adapt_delta	0.98	Target acceptance probability
max_treedepth	13	Maximum tree depth for NUTS
Parallelization	Outer loop	Replications parallelized; chains sequential

9.3. Gaussian Copula Log-Density

For uniform marginals $(u, v) \in (0, 1)^2$ with $\rho \in (-1, 1)$, let $z_1 = \Phi^{-1}(u)$ and $z_2 = \Phi^{-1}(v)$:

$$\log c_{\mathrm{Gauss}}(u, v; \rho) = -\frac{1}{2}\log(1 - \rho^2) - \frac{1}{2(1 - \rho^2)}\left(z_1^2 - 2\rho z_1 z_2 + z_2^2\right) + \frac{1}{2}\left(z_1^2 + z_2^2\right)$$

9.4. Clayton Copula Log-Density

For $(u, v) \in (0, 1)^2$ with $\theta > 0$:

$$\log c_{\mathrm{Clayton}}(u, v; \theta) = \log(1 + \theta) - (1 + \theta)(\log u + \log v) - \left(2 + \frac{1}{\theta}\right)\log S$$

where $S = u^{-\theta} + v^{-\theta} - 1$.

> **i** Boundary Clamping
>
> Both copula implementations apply boundary clamping with $\varepsilon = 10^{-9}$:
>
> $$u_{\mathrm{clamped}} = \max(\varepsilon, \min(1 - \varepsilon, u))$$
>
> This prevents numerical issues when $u \to 0$ or $u \to 1$.

9.5. Reproducibility Strategy

The simulation uses deterministic seeding:

- **Global seed**: 3033 (dedicated for Study 3)
- **Init seeds**: seed_init = 7e5 + cid * 1000 + rid
- **Stan seeds**: seed_Stan = 8e5 + cid * 1000 + rid

9.6. Ground Truth Under Copula Misspecification

Table 8: Ground Truth Under Copula Misspecification.

Parameter	NG Ground Truth	NC Ground Truth
mu_1, mu_2	0	0
phi_11, phi_22	0.40	0.40
phi_12, phi_21	0.10	0.10
sigma_1, sigma_2	1.0	1.0
rho	NA (undefined)	—
theta	—	Design value

The NG model's ρ has no ground truth because the Gaussian copula is misspecified for the Clayton DGP. Bias and coverage metrics are not computed for ρ.