

Statistical Analysis Appendix

1 Statistical Model

The model:

$$y_i \sim \begin{cases} 0 & \text{with probability } 1 - \psi_i \\ \text{Gamma}(\mu_i, \varphi) & \text{with probability } \psi_i \end{cases} \begin{array}{l} \text{Probability of Wound Closure} \\ \text{Probability of Non Wound Closure} \end{array}$$

$$\begin{aligned} \text{The hurdle component: } \text{logit}(\psi_i) = \alpha_\psi & \quad (\text{Intercept}) \\ + \quad u_{\psi, \text{site}[i]} + u_{\psi, \text{subject}[i]} & \quad (\text{Random Effects for site and subject}) \\ + \quad \beta_{\psi_{\text{arm}}} \cdot \text{arm}_i & \quad (\text{Fixed Effect of Arm}) \\ + \quad \beta_{\psi_{\text{time}}} \cdot \text{time}_i & \quad (\text{Fixed Effect of Time}) \\ + \quad \beta_{\psi_{(\text{arm} \cdot \text{time})}} \cdot (\text{arm}_i \cdot \text{time}_i) & \quad (\text{Interaction Effect}) \\ + \quad \beta_{\psi_{\text{baseline area}}} \cdot \log(\text{baseline area})_i & \quad (\text{Fixed Effect of baseline area}) \end{aligned}$$

$$\begin{aligned} \text{The Gamma component: } \log(\mu_i) = \alpha_\mu & \quad (\text{Intercept}) \\ + \quad u_{\mu, \text{site}[i]} + u_{\mu, \text{subject}[i]} & \quad (\text{Random Effects for site and subject}) \\ + \quad \beta_{\mu_{\text{arm}}} \cdot \text{arm}_i & \quad (\text{Fixed Effect of Arm}) \\ + \quad \beta_{\mu_{\text{time}}} \cdot \text{time}_i & \quad (\text{Fixed Effect of Time}) \\ + \quad \beta_{\mu_{(\text{arm} \cdot \text{time})}} \cdot (\text{arm}_i \cdot \text{time}_i) & \quad (\text{Interaction Effect}) \\ + \quad \beta_{\mu_{\text{baseline area}}} \cdot \log(\text{baseline area})_i & \quad (\text{Fixed Effect of baseline area}) \end{aligned}$$

Random Effects Distributions:

$$\begin{aligned} u_{\psi, \text{site}} & \sim \text{Normal}(0, \sigma_{\psi, \text{site}}) \\ u_{\psi, \text{subject}} & \sim \text{Normal}(0, \sigma_{\psi, \text{subject}}) \\ u_{\mu, \text{site}} & \sim \text{Normal}(0, \sigma_{\mu, \text{site}}) \\ u_{\mu, \text{subject}} & \sim \text{Normal}(0, \sigma_{\mu, \text{subject}}) \end{aligned}$$

The priors are non-informative and wide on the log (wound area) and logit (wound closure) scale(s).

Priors for the Hurdle component:

$$\begin{aligned} \alpha_\psi & \sim \text{Normal}(0, 1) \\ \beta_{\psi, \text{arm}}, \beta_{\psi, \text{time}}, \beta_{\psi, \text{int}}, \beta_{\psi, \text{baseline area}} & \sim \text{Normal}(0, 1) \\ \sigma_{\psi, \text{site}}, \sigma_{\psi, \text{subject}} & \sim \text{HalfNormal}(1) \end{aligned}$$

Priors for the Gamma component:

$$\begin{aligned}\alpha_{\mu} &\sim \text{Normal}(0, 6.16) \\ \beta_{\mu, \text{ arm}}, \beta_{\mu, \text{ time}}, \beta_{\mu, \text{ int}}, \beta_{\mu, \text{ baseline area}} &\sim \text{Normal}(0, S_{\beta}) \\ \sigma_{\mu, \text{ site}}, \sigma_{\mu, \text{ subject}} &\sim \text{HalfNormal}(6.16) \\ \varphi &\sim \text{HalfCauchy}(1)\end{aligned}$$

2 Software Details

	value
Arviz Version	0.21.0
Inference Library	Pymc
Inference Library Version	5.23.0
Sampling Time (in seconds)	133.4
Tuning Steps	1000
Modeling Interface	Bambi
Modeling Interface Version	0.15.0

Figure 1: Modeling Software Information

The random seed was “1234”, with a target_accept setting of .99. The PYMC implementation of NUTS (No-U Turn Sampling) MCMC sampling was used. Sampling completed with no divergences.

```
Initializing NUTS using jitter+adapt_diag...
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [alpha, Intercept, arm, time, arm:time, log(area_baseline), 1|site_sigma, 1|site_offset, 1|subjectid_sigma, 1|subjectid_offset,
psi_Intercept, psi_arm, psi_time, psi_arm:time, psi_log(area_baseline), psi_1|site_sigma, psi_1|site_offset, psi_1|subjectid_sigma,
psi_1|subjectid_offset]
```

Progress	Draws	Divergences	Step size	Grad evals	Sampling Speed	Elapsed	Remaining
	2000	0	0.04	127	19.86 draws/s	0:01:40	0:00:00
	2000	0	0.04	127	19.27 draws/s	0:01:43	0:00:00
	2000	0	0.04	127	16.97 draws/s	0:01:57	0:00:00
	2000	0	0.04	127	16.48 draws/s	0:02:01	0:00:00

Figure 2: MCMC Sampler Screenshot

3 Diagnostics

3.1 MCMC Sampling Diagnostics

3.1.1 Diagnostic Summary

The maximum tree depth was 8, with the mode at 7. R-HAT's are all < 1.01

	MCSE MEAN	MCSE SD	ESS BULK	ESS TAIL	R HAT
Intercept	0.006	0.004	2263.0	2742.0	1.0
psi_arm[LHACM]	0.011	0.01	4526.0	3327.0	1.0
psi_time[1]	0.009	0.012	7073.0	3225.0	1.0
psi_time[2]	0.009	0.013	7167.0	3349.0	1.0
psi_time[3]	0.009	0.013	7027.0	2706.0	1.0
psi_time[4]	0.009	0.011	6284.0	3154.0	1.0
psi_time[5]	0.01	0.012	5817.0	2918.0	1.0
psi_time[6]	0.01	0.012	6043.0	3043.0	1.0
psi_time[7]	0.009	0.011	6050.0	3359.0	1.0
psi_time[8]	0.009	0.011	6733.0	3324.0	1.0
psi_time[9]	0.008	0.01	6445.0	3465.0	1.0
psi_time[10]	0.009	0.011	6206.0	3083.0	1.0
psi_time[11]	0.008	0.013	7119.0	3104.0	1.0

Figure 3: MCMC Diagnostics Summary Table

3.1.2 Traceplot

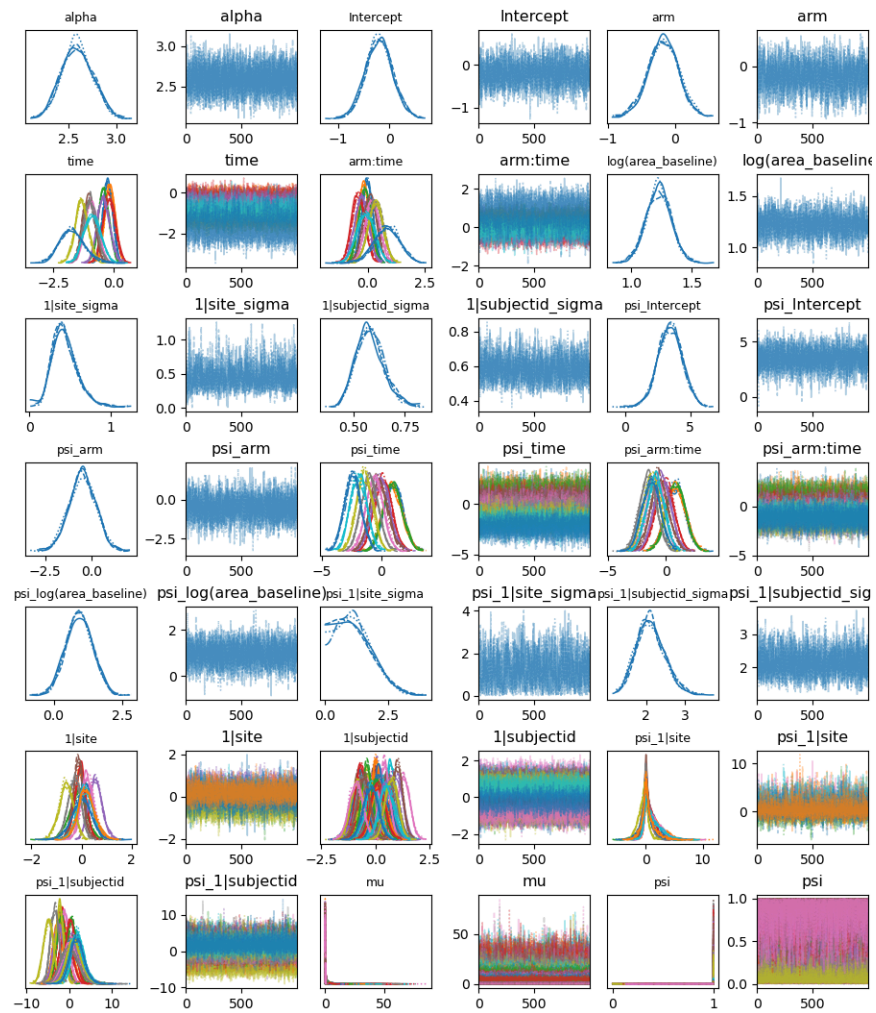


Figure 4: MCMC Trace Plot

3.1.3 Parallel Plot

The Parallel plot confirms no divergences during sampling.

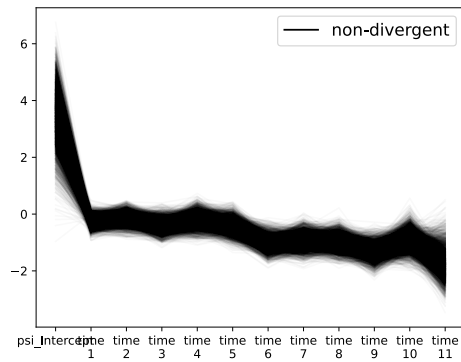


Figure 5: MCMC Parallel Plot - SOC over Time

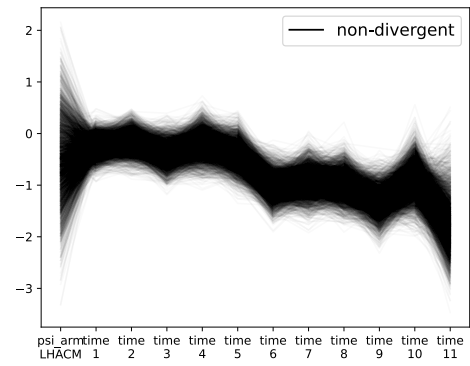


Figure 6: MCMC Parallel Plot - LHCACM over Time

3.1.4 ESS (Effective Sample Size) Evolution

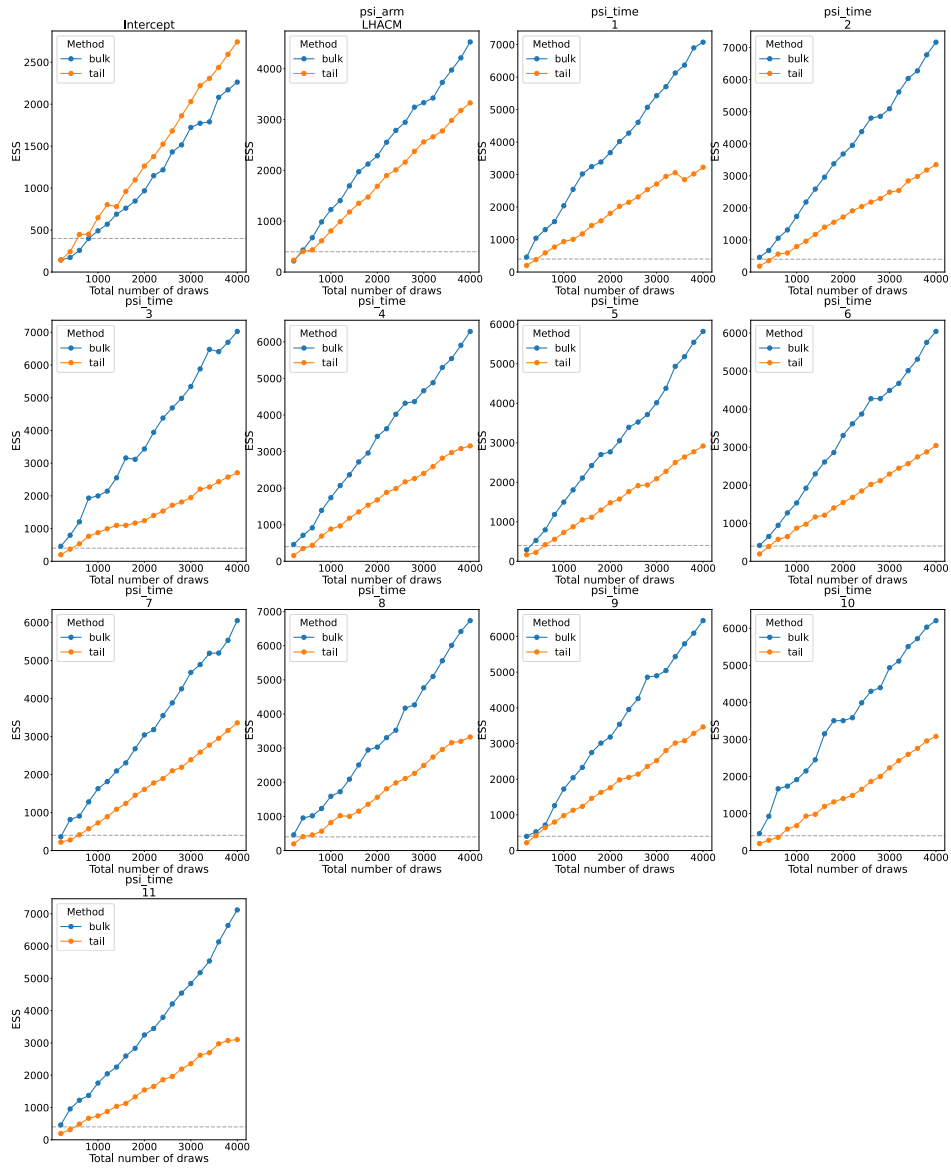


Figure 7: ESS Evolution Plot

3.1.5 Energy Plot

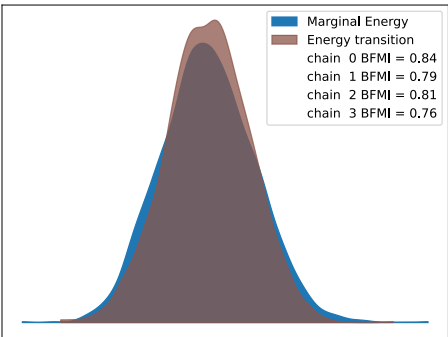


Figure 8: MCMC Energy Plot

3.1.6 Pair Plot

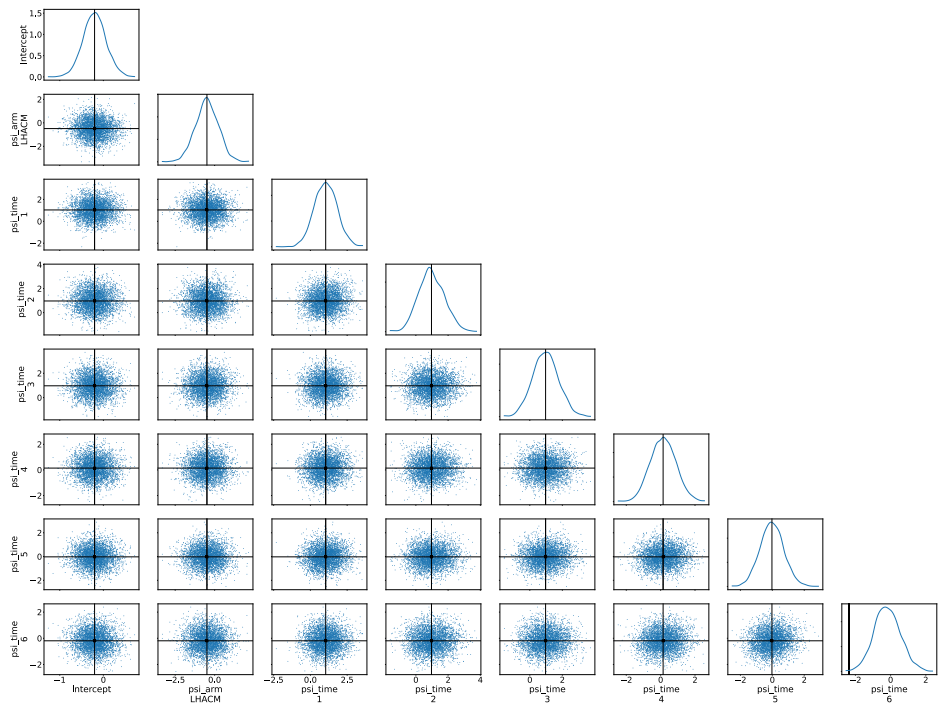


Figure 9: MCMC Scatter Plot with Marginals

3.2 Posterior Predictive Check

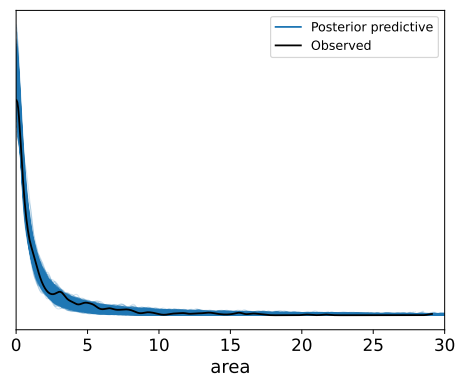


Figure 10: Posterior Predictive Check - KDE

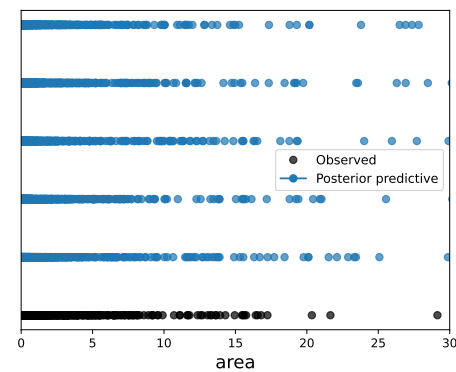


Figure 11: Posterior Predictive Check - Scatter

3.3 LOO-CV (Leave One Out Cross Validation)

3.4 LOO-CV Results

Computed from 4000 posterior samples and 597 observations log-likelihood matrix.

	Estimate	SE
elpd_loo	-756.88	32.37
p_loo	97.63	-

There has been a warning during the calculation. Please check the results.

Pareto k diagnostic values:

		Count	Pct.
(-Inf, 0.70]	(good)	586	98.2%
(0.70, 1]	(bad)	10	1.7%
(1, Inf)	(very bad)	1	0.2%

Figure 12: LOO-CV - ELPD and Pareto K Table