Table 2 - Dietary Diversity

2022-03-15

Load the **Dietary Diversity** variables

**Dietary Diversity:** This is the basic bechmarking model utilizing the default, uninformed priors

dietary\_diversity\_Bayesmodel <-   
 brm(formula = dietarydiversity | weights(samp\_wgt) ~   
 cost\_deviation + treat\_any + treat\_GK +   
 dietarydiversity\_R1 + Lhh\_wealth\_asinh + Lvill\_eligible\_ratio + Lsavingsstock\_asinh3 +   
 Lconsumpti\_x\_Ldietarydi + Lconsumpti\_x\_Lproductiv + Ldietarydi\_x\_Lassetscon +   
 (1 | vid) + (1 | block),  
 data = dietary\_diversity\_data,  
 family = gaussian("identity"),  
 seed = 1272022,  
 warmup = 1000,  
 iter = 2000,  
 thin = 1,  
 control = list(adapt\_delta = .95, max\_treedepth = 10),  
 #backend = "cmdstanr",  
 cores = 4, #overrides default 1 core  
 #threads = 3,need to get cmdstanr package working here  
 save\_pars = save\_pars(all = TRUE), # potentially allows for more post-processing functionality  
 file = "uninformed\_prior\_outcomes\\dietary\_diversity\_Bayes")

Model Summary

summary(dietary\_diversity\_Bayesmodel)

## Family: gaussian   
## Links: mu = identity; sigma = identity   
## Formula: dietarydiversity | weights(samp\_wgt) ~ cost\_deviation + treat\_any + treat\_GK + dietarydiversity\_R1 + Lhh\_wealth\_asinh + Lvill\_eligible\_ratio + Lsavingsstock\_asinh3 + Lconsumpti\_x\_Ldietarydi + Lconsumpti\_x\_Lproductiv + Ldietarydi\_x\_Lassetscon + (1 | vid) + (1 | block)   
## Data: dietary\_diversity\_data (Number of observations: 1751)   
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;  
## total post-warmup draws = 4000  
##   
## Group-Level Effects:   
## ~block (Number of levels: 22)   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sd(Intercept) 0.30 0.08 0.16 0.48 1.01 962 1425  
##   
## ~vid (Number of levels: 248)   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sd(Intercept) 0.55 0.04 0.47 0.64 1.01 1469 2187  
##   
## Population-Level Effects:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS  
## Intercept 3.19 0.22 2.75 3.62 1.00 2472  
## cost\_deviation 0.00 0.00 0.00 0.00 1.00 2392  
## treat\_any 0.26 0.12 0.02 0.48 1.00 1556  
## treat\_GK -0.03 0.12 -0.27 0.21 1.00 1837  
## dietarydiversity\_R1 -0.12 0.07 -0.26 0.02 1.00 2694  
## Lhh\_wealth\_asinh 0.01 0.01 -0.00 0.03 1.00 6416  
## Lvill\_eligible\_ratio -0.57 0.45 -1.44 0.32 1.00 1509  
## Lsavingsstock\_asinh3 0.00 0.00 0.00 0.00 1.00 4307  
## Lconsumpti\_x\_Ldietarydi 0.01 0.01 0.00 0.03 1.00 2640  
## Lconsumpti\_x\_Lproductiv 0.01 0.00 0.00 0.01 1.00 3204  
## Ldietarydi\_x\_Lassetscon 0.01 0.00 0.01 0.01 1.00 5973  
## Tail\_ESS  
## Intercept 2787  
## cost\_deviation 2866  
## treat\_any 2521  
## treat\_GK 2760  
## dietarydiversity\_R1 2588  
## Lhh\_wealth\_asinh 3066  
## Lvill\_eligible\_ratio 2411  
## Lsavingsstock\_asinh3 3074  
## Lconsumpti\_x\_Ldietarydi 2727  
## Lconsumpti\_x\_Lproductiv 3584  
## Ldietarydi\_x\_Lassetscon 3365  
##   
## Family Specific Parameters:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sigma 1.58 0.02 1.55 1.62 1.00 5245 2491  
##   
## Draws were sampled using sampling(NUTS). For each parameter, Bulk\_ESS  
## and Tail\_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).

Prior summery - how informative are priors

prior\_summary(dietary\_diversity\_Bayesmodel)

## prior class coef group resp dpar nlpar  
## (flat) b   
## (flat) b cost\_deviation   
## (flat) b dietarydiversity\_R1   
## (flat) b Lconsumpti\_x\_Ldietarydi   
## (flat) b Lconsumpti\_x\_Lproductiv   
## (flat) b Ldietarydi\_x\_Lassetscon   
## (flat) b Lhh\_wealth\_asinh   
## (flat) b Lsavingsstock\_asinh3   
## (flat) b Lvill\_eligible\_ratio   
## (flat) b treat\_any   
## (flat) b treat\_GK   
## student\_t(3, 5, 2.5) Intercept   
## student\_t(3, 0, 2.5) sd   
## student\_t(3, 0, 2.5) sd block   
## student\_t(3, 0, 2.5) sd Intercept block   
## student\_t(3, 0, 2.5) sd vid   
## student\_t(3, 0, 2.5) sd Intercept vid   
## student\_t(3, 0, 2.5) sigma   
## bound source  
## default  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## default  
## default  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## default

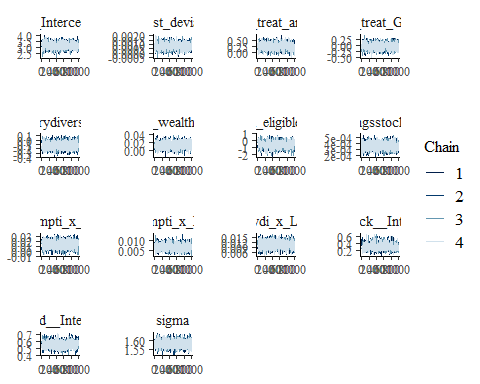
check\_prior(dietary\_diversity\_Bayesmodel)

## Warning: Some priors could not be simulated.

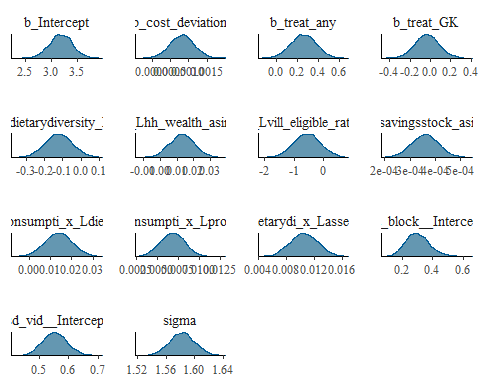
## Parameter Prior\_Quality  
## 1 b\_Intercept uninformative  
## 2 b\_cost\_deviation not determinable  
## 3 b\_treat\_any not determinable  
## 4 b\_treat\_GK not determinable  
## 5 b\_dietarydiversity\_R1 not determinable  
## 6 b\_Lhh\_wealth\_asinh not determinable  
## 7 b\_Lvill\_eligible\_ratio not determinable  
## 8 b\_Lsavingsstock\_asinh3 not determinable  
## 9 b\_Lconsumpti\_x\_Ldietarydi not determinable  
## 10 b\_Lconsumpti\_x\_Lproductiv not determinable  
## 11 b\_Ldietarydi\_x\_Lassetscon not determinable

Diagnostics

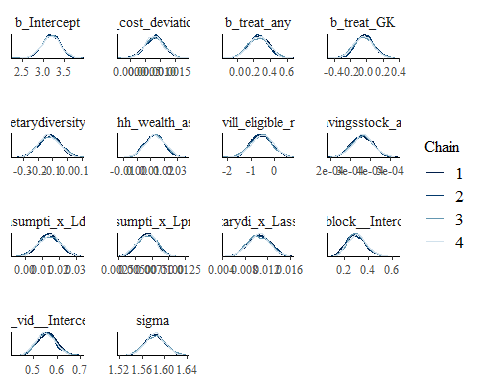
# trace diagnostic plot  
mcmc\_trace(dietary\_diversity\_Bayesmodel, n\_warmup = 0,  
 pars = c("b\_Intercept", "b\_cost\_deviation", "b\_treat\_any",   
 "b\_treat\_GK", "b\_dietarydiversity\_R1", "b\_Lhh\_wealth\_asinh",  
 "b\_Lvill\_eligible\_ratio", "b\_Lsavingsstock\_asinh3",  
 "b\_Lconsumpti\_x\_Ldietarydi", "b\_Lconsumpti\_x\_Lproductiv",   
 "b\_Ldietarydi\_x\_Lassetscon", "sd\_block\_\_Intercept",   
 "sd\_vid\_\_Intercept", "sigma"))



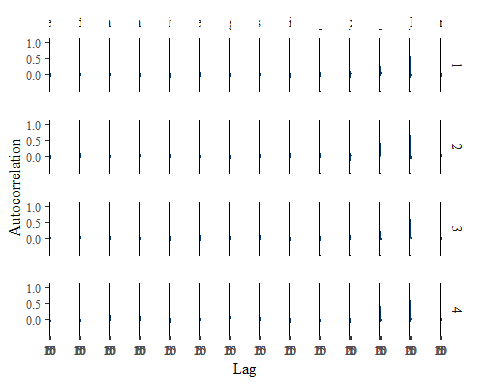
ggsave("table\_2\_diagnostics\\dietary\_div\_trace.png", plot = last\_plot(), width = 12, height = 5)  
  
#density diagnostic plot  
mcmc\_dens(dietary\_diversity\_Bayesmodel,  
 pars = c("b\_Intercept", "b\_cost\_deviation", "b\_treat\_any",   
 "b\_treat\_GK", "b\_dietarydiversity\_R1", "b\_Lhh\_wealth\_asinh",  
 "b\_Lvill\_eligible\_ratio", "b\_Lsavingsstock\_asinh3",  
 "b\_Lconsumpti\_x\_Ldietarydi", "b\_Lconsumpti\_x\_Lproductiv",   
 "b\_Ldietarydi\_x\_Lassetscon", "sd\_block\_\_Intercept",   
 "sd\_vid\_\_Intercept", "sigma"))



ggsave("table\_2\_diagnostics\\dietary\_div\_dens.png", plot = last\_plot(), width = 12, height = 5)  
  
mcmc\_dens\_overlay(dietary\_diversity\_Bayesmodel,  
 pars = c("b\_Intercept", "b\_cost\_deviation", "b\_treat\_any",   
 "b\_treat\_GK", "b\_dietarydiversity\_R1", "b\_Lhh\_wealth\_asinh",  
 "b\_Lvill\_eligible\_ratio", "b\_Lsavingsstock\_asinh3",  
 "b\_Lconsumpti\_x\_Ldietarydi", "b\_Lconsumpti\_x\_Lproductiv",   
 "b\_Ldietarydi\_x\_Lassetscon", "sd\_block\_\_Intercept",   
 "sd\_vid\_\_Intercept", "sigma"))



ggsave("table\_2\_diagnostics\\dietary\_div\_overlay.png", plot = last\_plot(), width = 12, height = 5)  
  
  
#acf (auto-correlation) diagnostic plot  
mcmc\_acf(dietary\_diversity\_Bayesmodel,  
 pars = c("b\_Intercept", "b\_cost\_deviation", "b\_treat\_any",   
 "b\_treat\_GK", "b\_dietarydiversity\_R1", "b\_Lhh\_wealth\_asinh",  
 "b\_Lvill\_eligible\_ratio", "b\_Lsavingsstock\_asinh3",  
 "b\_Lconsumpti\_x\_Ldietarydi", "b\_Lconsumpti\_x\_Lproductiv",   
 "b\_Ldietarydi\_x\_Lassetscon", "sd\_block\_\_Intercept",   
 "sd\_vid\_\_Intercept", "sigma"))

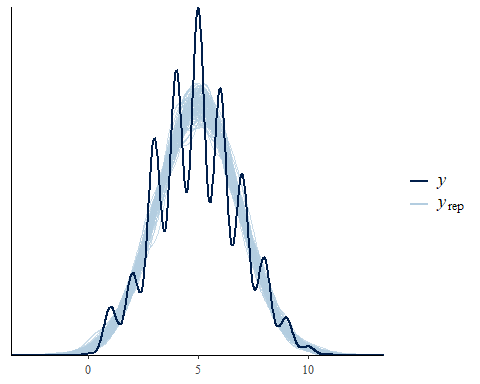


ggsave("table\_2\_diagnostics\\dietary\_div\_acf.png", plot = last\_plot(), width = 12, height = 5)

posterior predictive checks

pp\_check(dietary\_diversity\_Bayesmodel, nsamples = 100)

## Warning: Argument 'nsamples' is deprecated. Please use argument 'ndraws'  
## instead.



pp\_check(dietary\_diversity\_Bayesmodel, nsamples = 10, type = 'error\_scatter\_avg', alpha = .1)

## Warning: Argument 'nsamples' is deprecated. Please use argument 'ndraws'  
## instead.

