

Ch. 1 - Model comparisons

Wade VanderWright

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Model Comparisons

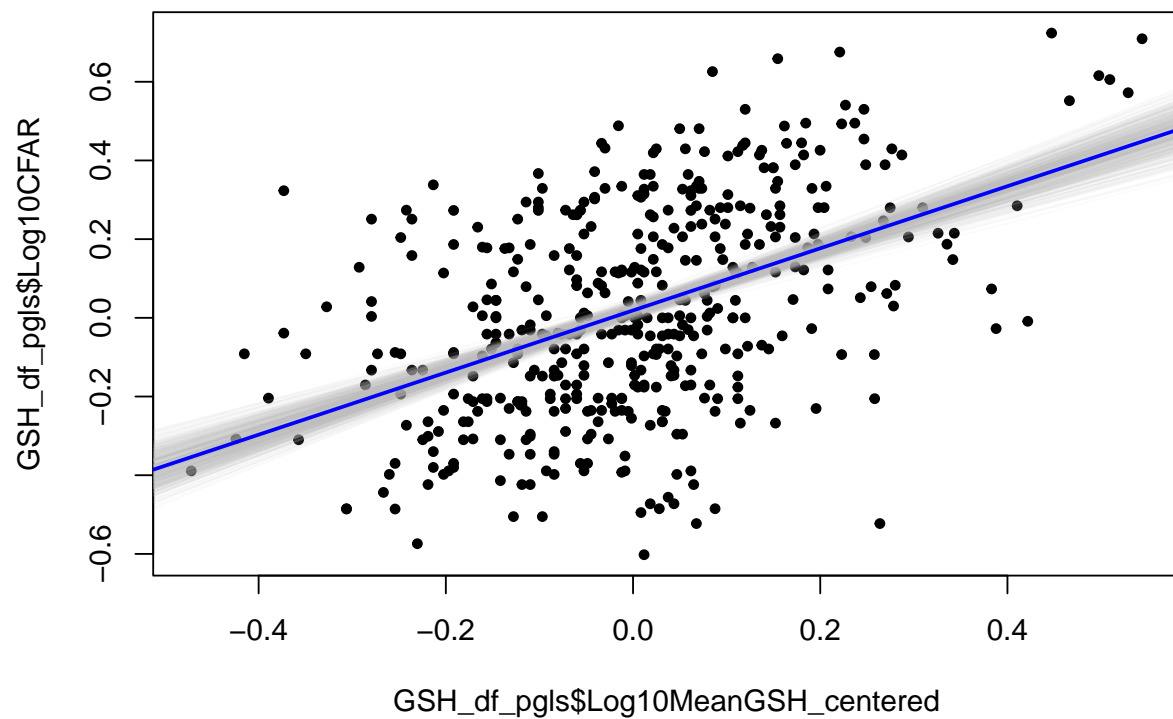
Model 1 - CFAR ~ GSH

1. brms model

```
Model_plain <- brm(Log10CFAR ~ Log10MeanGSH_centered,  
  data = GSH_df_pgls,  
  family = gaussian(),  
  prior = Plain_prior  
)
```

```
fixef(Model_plain, summary = T)
```

```
##              Estimate Est.Error      Q2.5      Q97.5  
## Intercept          0.01878724 0.01121401 -0.003048758 0.04068312  
## Log10MeanGSH_centered 0.78943177 0.06909079 0.653733169 0.92180824
```



2. STAN model

Data considered

```
data {
  int <lower=1> N;
  vector[N] x;
  vector[N] y;
}
```

The parameters accepted by the model

```
parameters {
  real alpha;
  real beta;
  real<lower=0> sigma;
}
```

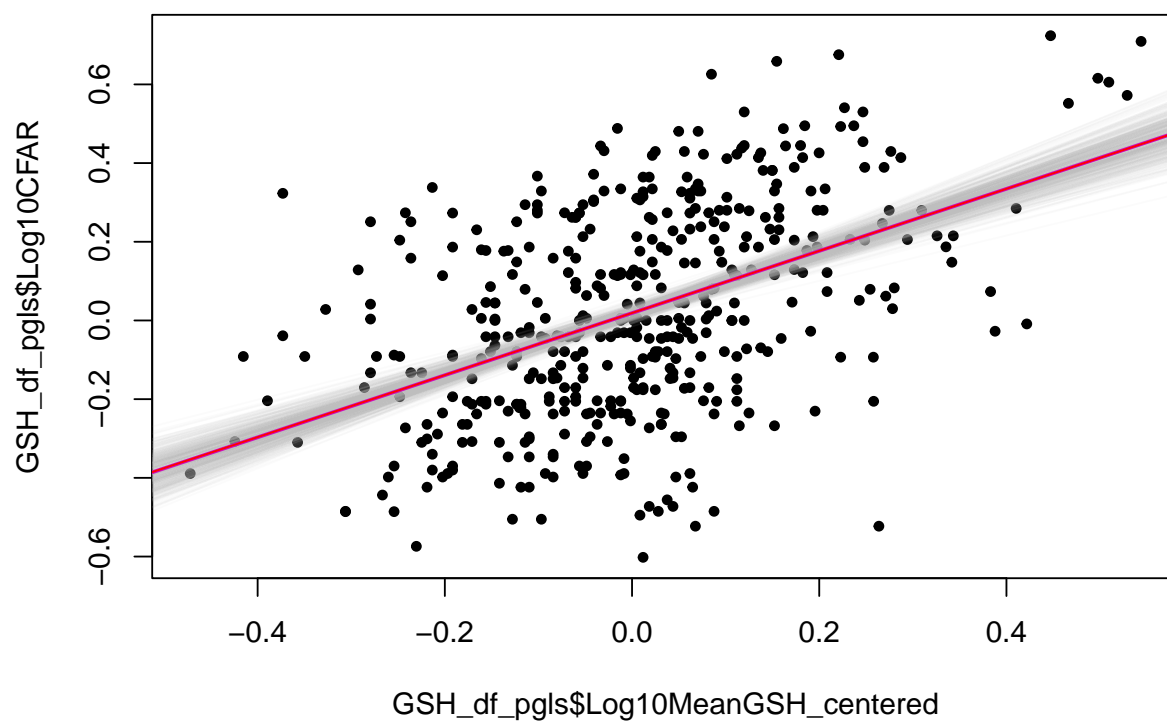
Model form:

```
model {
  sigma ~ student_t(3, 0, 10);
```

```
y ~ normal(alpha + x * beta , sigma);
}
```

```
fit1_summary <- summary(fit1, pars = c("alpha", "beta", "sigma"), probs = c(0.05, 0.95))$summary
print(fit1_summary)
```

```
##           mean      se_mean      sd      5%      95%    n_eff
## alpha 0.01900869 0.0002460092 0.011114187 0.001013608 0.03747443 2041.046
## beta  0.78894370 0.0017257508 0.071948028 0.669736389 0.90516905 1738.128
## sigma 0.23579844 0.0001758531 0.007734538 0.223108150 0.24878671 1934.501
##           Rhat
## alpha 1.0004828
## beta  0.9988377
## sigma 0.9998605
```



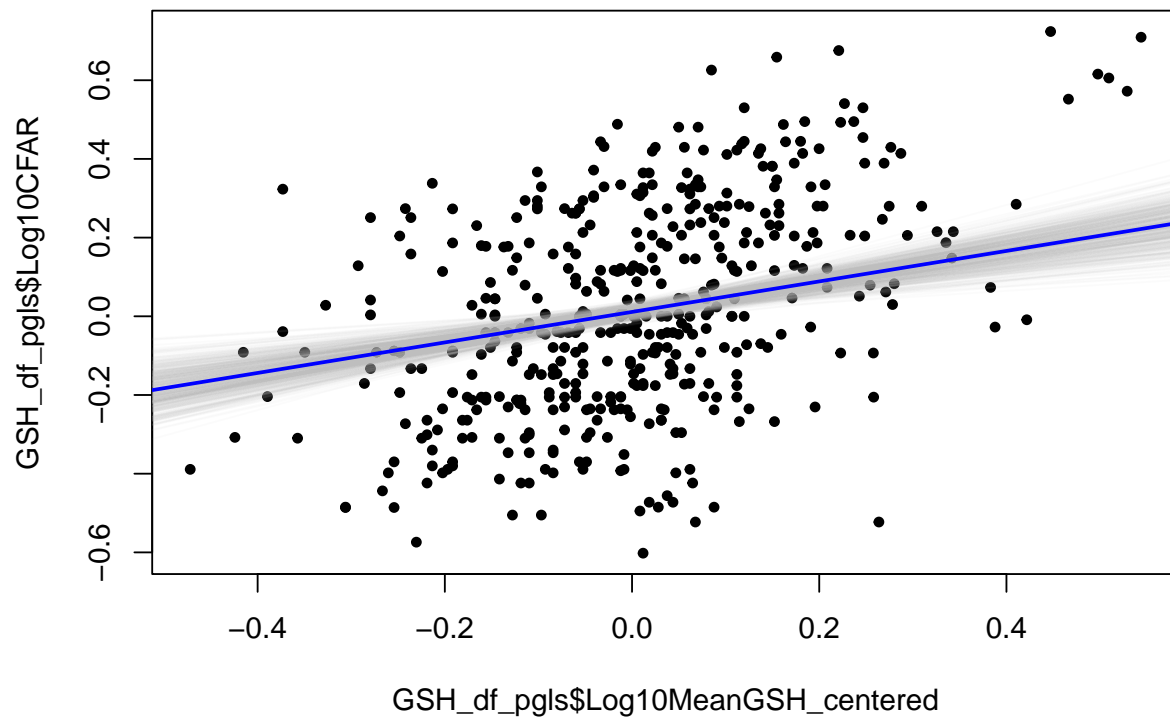
Model 2 - CFAR ~ GSH * Max Size

1. brms model

```
Model_size <- brm(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered,  
  data = GSH_df_pgls,  
  family = gaussian(),  
  prior = Size_prior  
)
```

```
fixef(Model_size, summary = T)
```

##	Estimate	Est.Error	Q2.5
## Intercept	0.01107801	0.01158262	-0.01069365
## Log10MeanGSH_centered	0.38761087	0.08262037	0.22932179
## Log10MaxSize_centered	0.30460627	0.04281846	0.22222482
## Log10MeanGSH_centered:Log10MaxSize_centered	0.26628115	0.16406086	-0.05284798
##	Q97.5		
## Intercept	0.03436049		
## Log10MeanGSH_centered	0.55212619		
## Log10MaxSize_centered	0.38716498		
## Log10MeanGSH_centered:Log10MaxSize_centered	0.58368860		



2. STAN model

Data considered

```
data {  
  int <lower=0> N; // number of data points  
  int <lower=0> K; // number of predictors  
  matrix[N,K] x; // predictor matrix  
  vector[N] y; // CFAR  
}
```

The parameters accepted by the model.

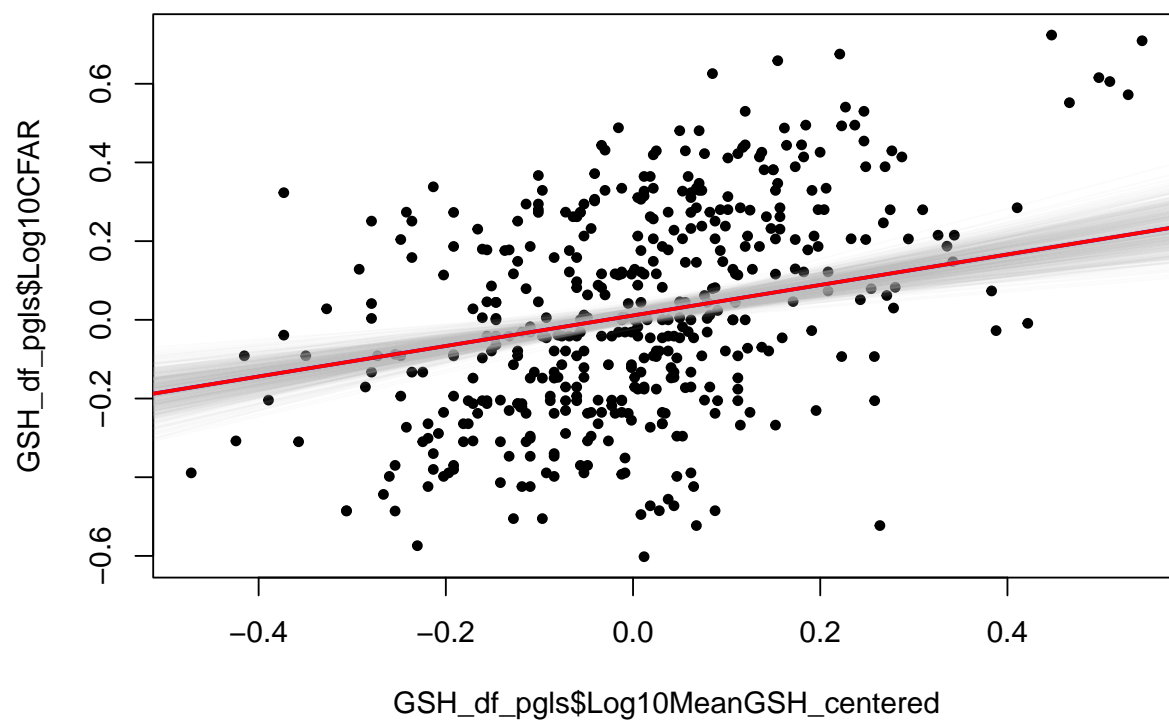
```
parameters {  
  real alpha;  
  vector[K] beta;  
  real<lower=0> sigma;  
}
```

The model to be estimated. We model the output 'y' to be normally distributed with mean 'mu' and standard deviation 'sigma'.

```
model {  
  
  sigma ~ student_t(3, 0, 10);  
  
  y ~ normal(alpha + x * beta , sigma);  
}
```

```
fit2_summary <- summary(fit2, pars = c("beta[1]", "beta[2]", "beta[3]", "beta[4]", "sigma"), probs = c(0.0, 0.025, 0.975, 1.0))  
print(fit2_summary)
```

##		mean	se_mean	sd	5%	95%	n_eff
##	beta[1]	0.01104707	0.0002537778	0.011373020	-0.007366795	0.02975656	2008.373
##	beta[2]	0.38772105	0.0019673695	0.082329451	0.254362486	0.52129402	1751.211
##	beta[3]	0.30513071	0.0010166417	0.043336491	0.231788976	0.37746503	1817.070
##	beta[4]	0.25558541	0.0037875546	0.158011884	-0.003275980	0.51150818	1740.451
##	sigma	0.22114731	0.0001653446	0.007578203	0.209154790	0.23385828	2100.645
##		Rhat					
##	beta[1]	0.9984008					
##	beta[2]	0.9999482					
##	beta[3]	1.0004711					
##	beta[4]	0.9990472					
##	sigma	0.9996704					



Model 3 - CFAR ~ GSH + Max Size (No interaction)

1. brms model

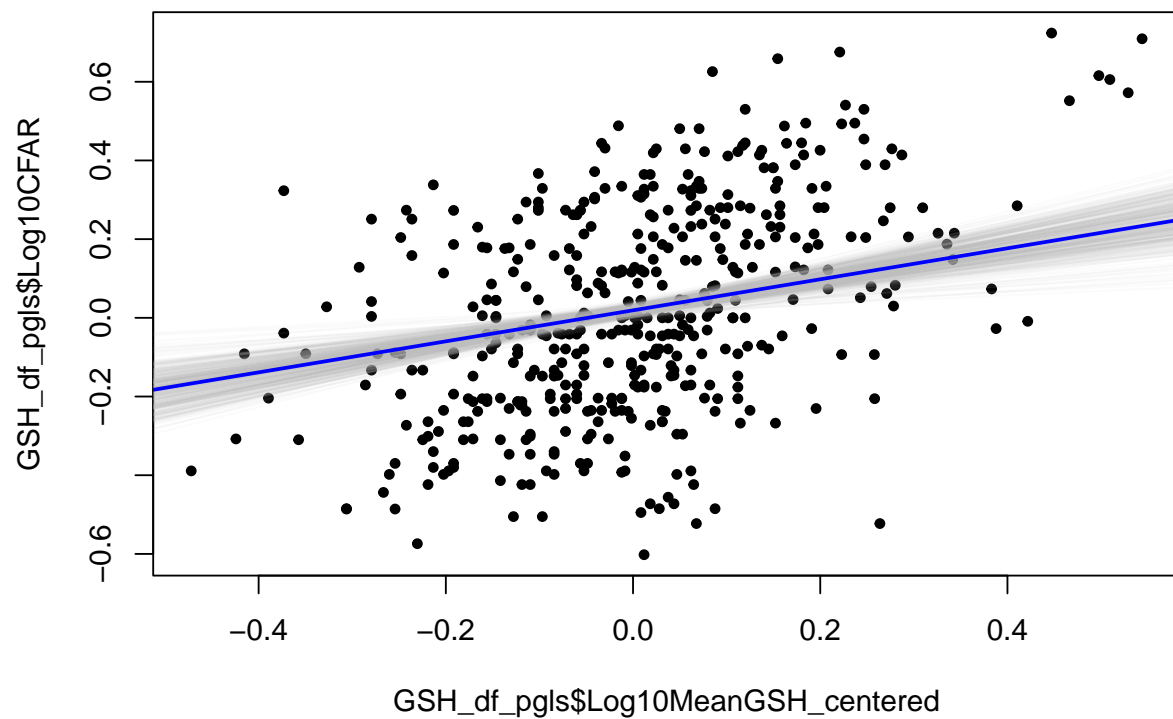
```
Model_size_2 <- brm(Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered,  
  data = GSH_df_pgls,  
  family = gaussian(),  
  prior = Size_prior_2)
```

```
summary(Model_size_2)
```

```
## Family: gaussian  
## Links: mu = identity; sigma = identity  
## Formula: Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered  
## Data: GSH_df_pgls (Number of observations: 456)  
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;  
## total post-warmup draws = 4000  
##  
## Population-Level Effects:  
##
```

	Estimate	Est.Error	1-95% CI	u-95% CI	Rhat	Bulk_ESS
## Intercept	0.02	0.01	-0.00	0.04	1.00	3526
## Log10MeanGSH_centered	0.39	0.08	0.24	0.55	1.00	3567
## Log10MaxSize_centered	0.33	0.04	0.25	0.40	1.00	3528

```
## Tail_ESS  
## Intercept 2556  
## Log10MeanGSH_centered 2768  
## Log10MaxSize_centered 3043  
##  
## Family Specific Parameters:  
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS  
## sigma 0.22 0.01 0.21 0.24 1.00 3652 2981  
##  
## 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).
```



2. STAN model

Data considered

```
data {
  int <lower=0> N; // number of data points
  int <lower=0> K; // number of predictors
  matrix[N,K] x; // predictor matrix
  vector[N] y; // CFAR
}
```

The parameters accepted by the model.

```
parameters {
  real alpha;
  vector[K] beta;
  real<lower=0> sigma;
}
```

The model to be estimated. We model the output 'y' to be normally distributed with mean 'mu' and standard deviation 'sigma'.

```
model {
```



```

sigma ~ student_t(3, 0, 10);

y ~ normal(alpha + x * beta , sigma);
}

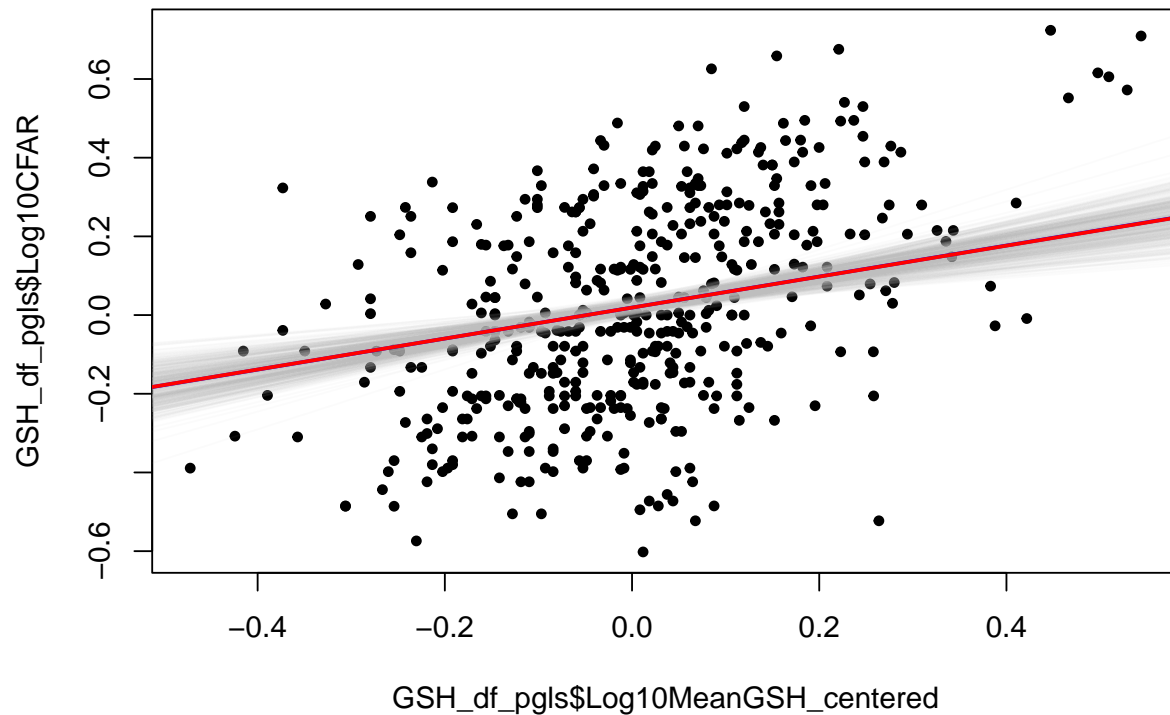
```

```
fit3
```

```

## Inference for Stan model: StanModel2.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##               mean se_mean   sd  2.5%  25%   50%   75%  97.5% n_eff Rhat
## alpha         0.02    0.00 0.01   0.00  0.01  0.02  0.03  0.04  2075   1
## beta[1]       0.39    0.00 0.08   0.23  0.34  0.39  0.45  0.55  1620   1
## beta[2]       0.32    0.00 0.04   0.24  0.30  0.32  0.35  0.40  1550   1
## sigma         0.22    0.00 0.01   0.21  0.22  0.22  0.23  0.24  1790   1
## lp__         458.67    0.05 1.41 455.06 458.03 458.99 459.70 460.42   948   1
##
## Samples were drawn using NUTS(diag_e) at Wed Mar 02 11:22:15 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).

```



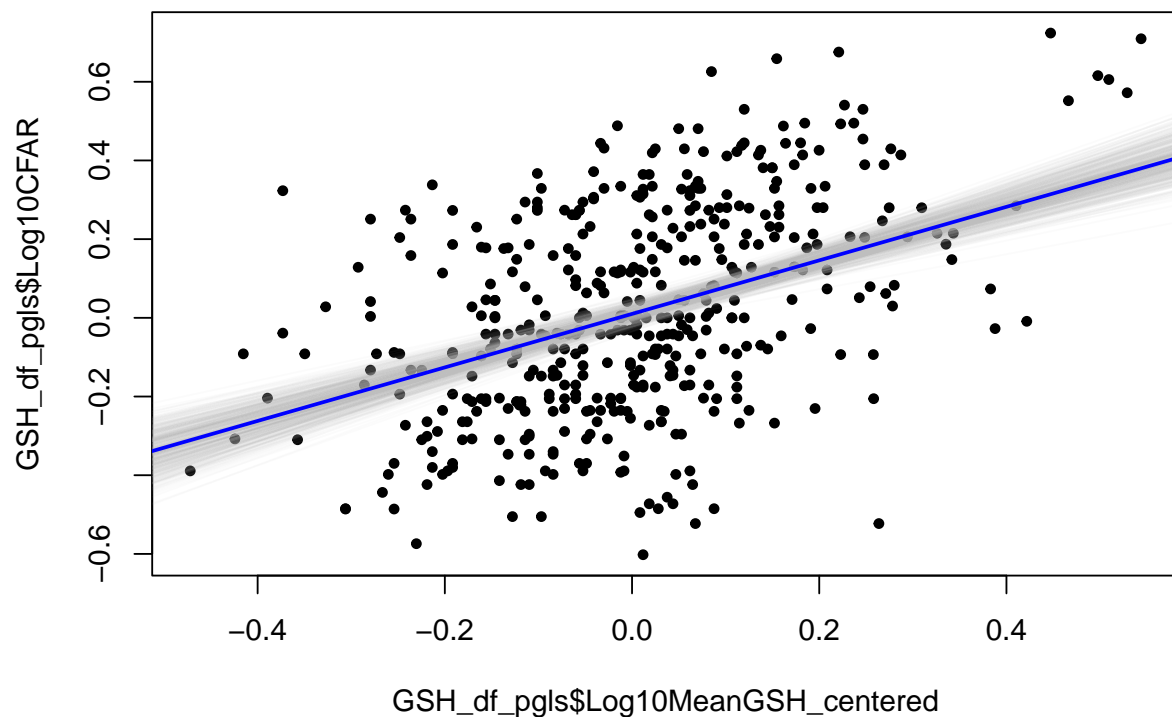
Model 4 - CFAR ~ GSH + PrimaryHabitat (No interaction)

1. brms model

```
habitat_model <- brm(Log10CFAR ~ Log10MeanGSH_centered + PrimaryHabitat,
  data = GSH_df_pgls,
  family = gaussian(),
  prior = habitat_prior,
  cores = 2)
```

```
summary(habitat_model)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: Log10CFAR ~ Log10MeanGSH_centered + PrimaryHabitat
## Data: GSH_df_pgls (Number of observations: 456)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Population-Level Effects:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept           0.01      0.02   -0.02    0.04 1.00     4027
## Log10MeanGSH_centered 0.68      0.07    0.54    0.83 1.00     4122
## PrimaryHabitatDeepwater -0.01     0.02   -0.06    0.04 1.00     3851
## PrimaryHabitatPelagic  0.25      0.05    0.16    0.34 1.00     4558
##
##           Tail_ESS
## Intercept       2871
## Log10MeanGSH_centered 2943
## PrimaryHabitatDeepwater 3151
## PrimaryHabitatPelagic 3159
##
## Family Specific Parameters:
##           Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma      0.23      0.01    0.21    0.25 1.00     3991     2793
##
## 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).
```



2. STAN model

Data considered

```
data {
  int <lower=0> N; // number of data points
  int <lower=0> K; // number of predictors
  matrix[N,K] x; // predictor matrix
  vector[N] y; // CFAR
}
```

The parameters accepted by the model.

```
parameters {
  real alpha;
  vector[K] beta;
  real<lower=0> sigma;
}
```

The model to be estimated. We model the output 'y' to be normally distributed with mean 'mu' and standard deviation 'sigma'.

```
model {
```

```

sigma ~ student_t(3, 0, 10);

y ~ normal(alpha + x * beta , sigma);
}

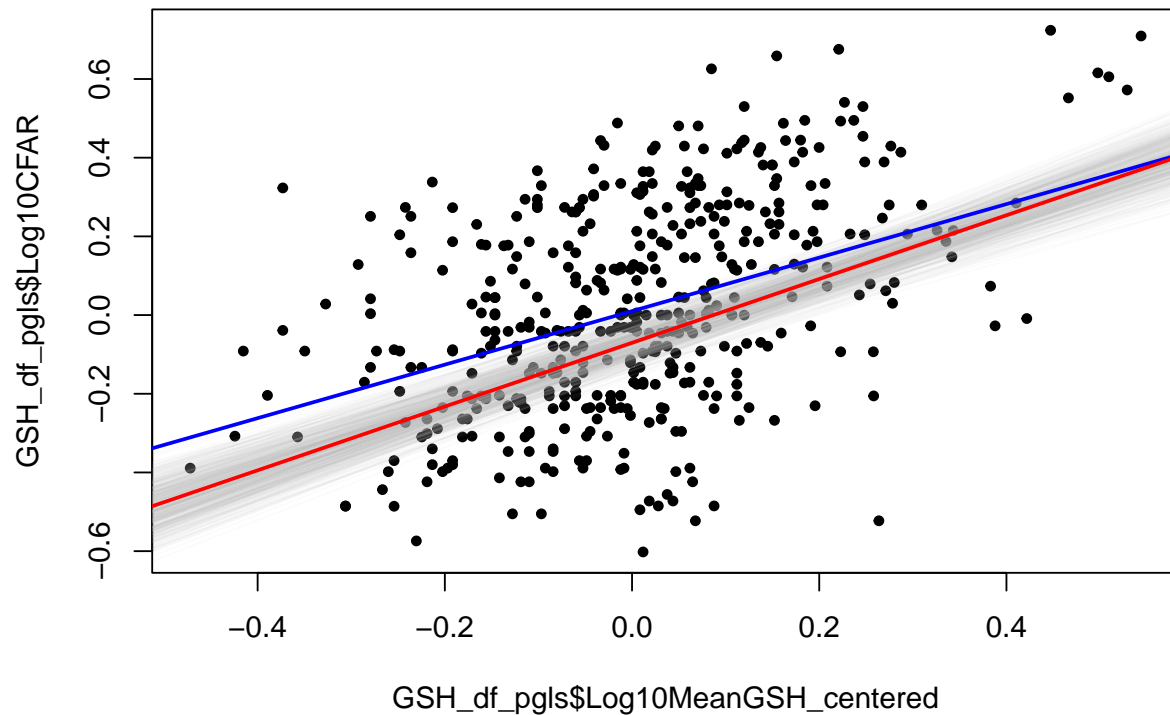
```

```
fit6
```

```

## Inference for Stan model: StanModel2.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##               mean se_mean   sd  2.5%  25%   50%   75%  97.5% n_eff Rhat
## alpha       -0.07   0.00 0.03  -0.13 -0.09 -0.07 -0.05 -0.01   903 1.00
## beta[1]      0.81   0.00 0.07   0.67  0.76  0.81  0.86  0.94  1396 1.00
## beta[2]      0.05   0.00 0.02   0.02  0.04  0.05  0.07  0.09   979 1.00
## sigma        0.23   0.00 0.01   0.22  0.23  0.23  0.24  0.25  1463 1.00
## lp__        433.52   0.05 1.43 430.05 432.77 433.84 434.58 435.32   725 1.01
##
## Samples were drawn using NUTS(diag_e) at Fri Mar 18 14:02:20 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).

```



Model 5 - CFAR ~ GSH * PrimaryHabitat

1. brms model

```
habitat_model_2 <- brm(Log10CFAR ~ Log10MeanGSH_centered * PrimaryHabitat,
  data = GSH_df_pgls,
  family = gaussian(),
  prior = habitat_prior2,
  cores = 2)
```

```
summary(habitat_model_2)
```

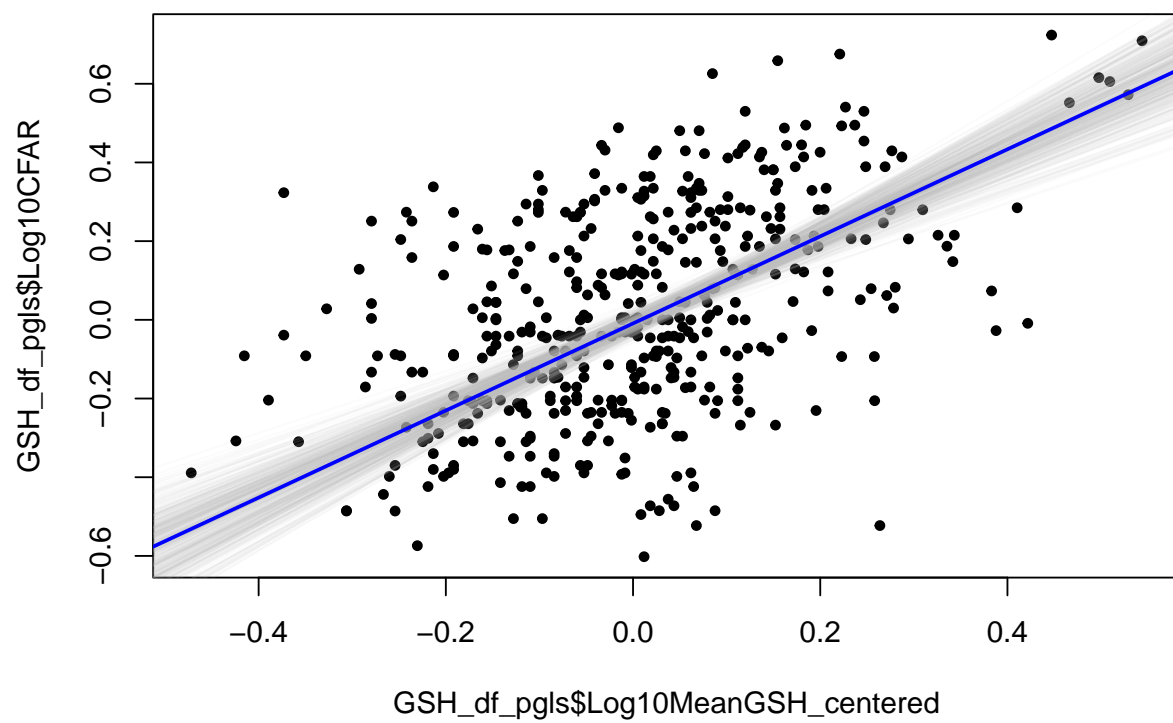
```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: Log10CFAR ~ Log10MeanGSH_centered * PrimaryHabitat
## Data: GSH_df_pgls (Number of observations: 456)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Population-Level Effects:
##
```

	Estimate	Est.Error	1-95% CI
## Intercept	-0.01	0.02	-0.04
## Log10MeanGSH_centered	1.11	0.13	0.85
## PrimaryHabitatDeepwater	-0.00	0.02	-0.05
## PrimaryHabitatPelagic	0.29	0.06	0.18
## Log10MeanGSH_centered:PrimaryHabitatDeepwater	-0.64	0.16	-0.96
## Log10MeanGSH_centered:PrimaryHabitatPelagic	-0.56	0.22	-1.00

```
##
```

	u-95% CI	Rhat	Bulk_ESS	Tail_ESS
## Intercept	0.02	1.00	3731	3045
## Log10MeanGSH_centered	1.36	1.00	2427	2696
## PrimaryHabitatDeepwater	0.04	1.00	3866	2861
## PrimaryHabitatPelagic	0.40	1.00	3449	3073
## Log10MeanGSH_centered:PrimaryHabitatDeepwater	-0.32	1.00	2630	2589
## Log10MeanGSH_centered:PrimaryHabitatPelagic	-0.10	1.00	2539	2375

```
##
## Family Specific Parameters:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma 0.23 0.01 0.21 0.24 1.00 3731 2813
##
## 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).
```



2. STAN model

TBD

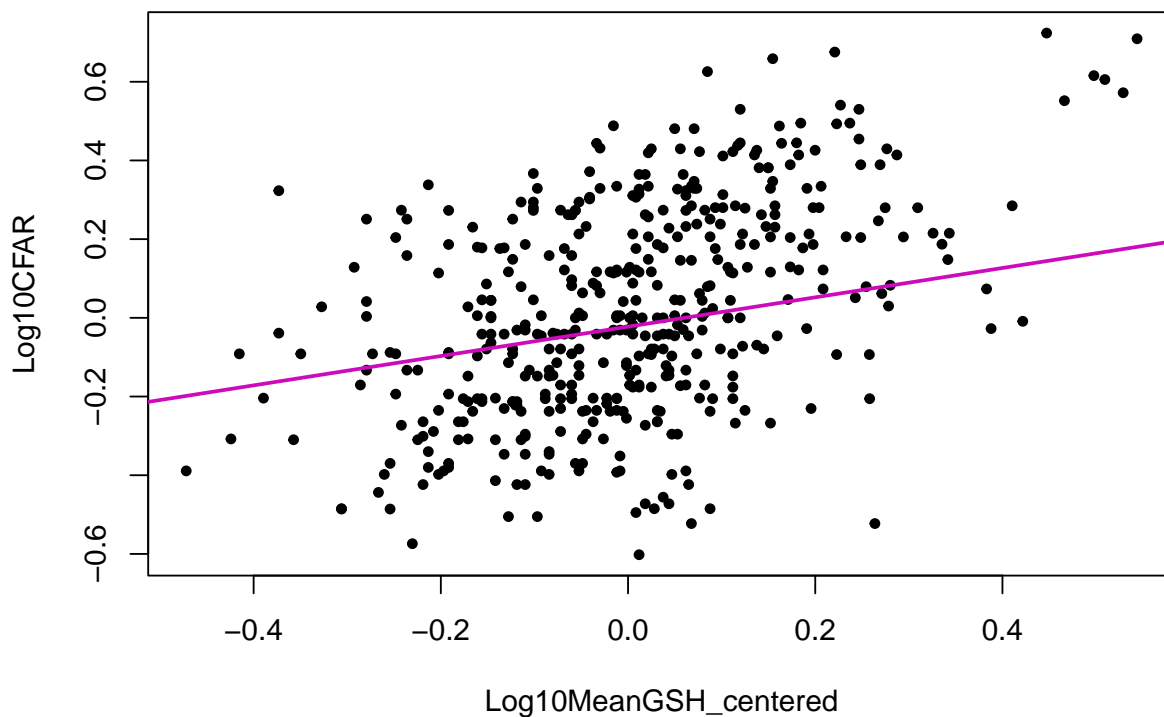
Model 6 - CFAR ~ GSH + Phylogeny

1. PGLS model

```
pglsMod1 <- gls(Log10CFAR ~ Log10MeanGSH_centered, correlation = corPagel(phy = SampleTree, value = 0.5
```

```
summary(pglsMod1)
```

```
## Generalized least squares fit by maximum likelihood
## Model: Log10CFAR ~ Log10MeanGSH_centered
## Data: GSH_df_pgls
##      AIC      BIC    logLik
## -427.4206 -410.9306 217.7103
##
## Correlation Structure: corPagel
## Formula: ~Binomial
## Parameter estimate(s):
##      lambda
## 0.7030228
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)   -0.0224754 0.06282858 -0.357726  0.7207
## Log10MeanGSH_centered 0.3728837 0.05950418  6.266513  0.0000
##
## Correlation:
##              (Intr)
## Log10MeanGSH_centered -0.065
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.7884571 -0.6933649  0.1151372  1.0885641  2.9034051
##
## Residual standard error: 0.2147249
## Degrees of freedom: 456 total; 454 residual
```



2. brms model

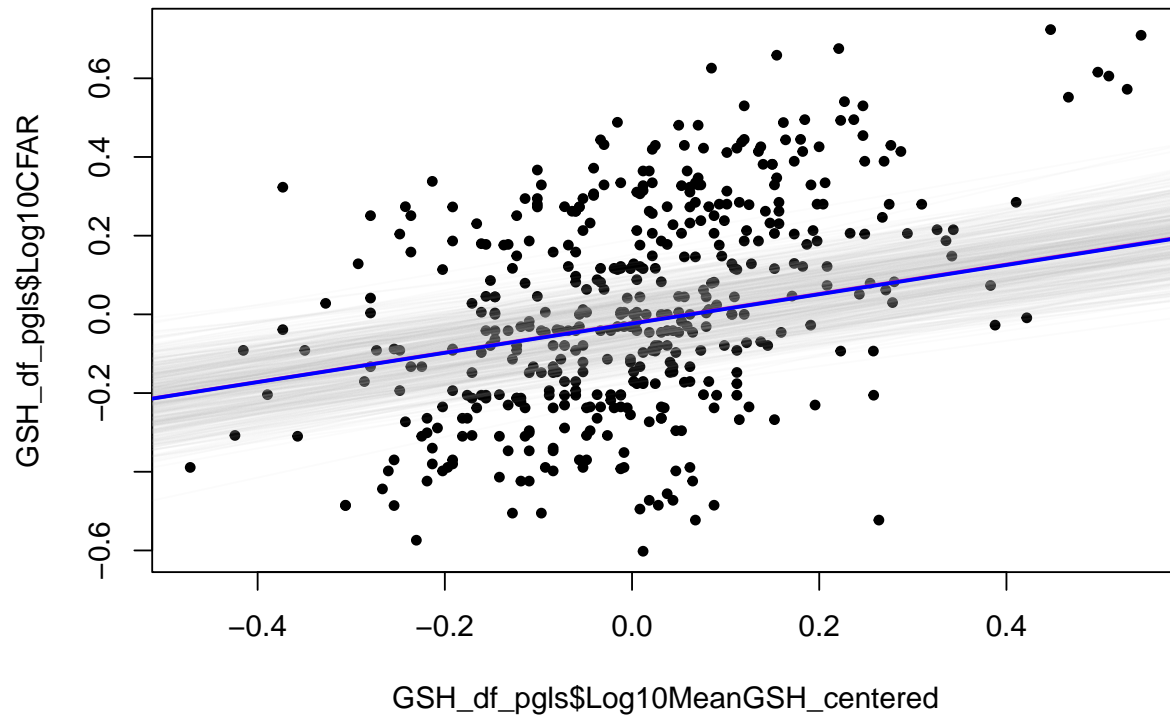
```
Model_simple <- brm(Log10CFAR ~ Log10MeanGSH_centered + (1|gr(Binomial, cov = A)),
  data = GSH_df_pgls,
  family = gaussian(),
  data2 = list(A = A),
  prior = Simple_prior,
  cores = 2)
```

```
summary(Model_simple)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: Log10CFAR ~ Log10MeanGSH_centered + (1 | gr(Binomial, cov = A))
## Data: GSH_df_pgls (Number of observations: 456)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Group-Level Effects:
## ~Binomial (Number of levels: 456)
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.01 0.00 0.01 0.01 1.00 1200 1938
##
## Population-Level Effects:
```



```
##               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept          -0.02    0.06   -0.15    0.10 1.00    1257
## Log10MeanGSH_centered 0.37    0.06    0.25    0.49 1.00    4238
##               Tail_ESS
## Intercept           2076
## Log10MeanGSH_centered 3483
##
## Family Specific Parameters:
##               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma           0.12    0.01    0.11    0.13 1.00    1717    2848
##
## 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).
```



3. STAN model

Data considered

```
data {
  int <lower=0> N; // number of data points
  int <lower=0> K; // number of predictors
  matrix[N,K] x; // predictor matrix
  vector[N] y; // outcome (CFAR)
```

```

matrix[N, N] d_mat; // sigma matrix
matrix[N, N] A; // vcov matrix
}

```

The parameters accepted by the model.

```

parameters {
  real alpha;
  vector[K] beta; // coefficients
  real<lower=0> sigma; // error
  real<lower=0,upper=1> lambda; // phylogenetic signal
}

transformed parameters {

  matrix[N, N] sigma_mat;
  matrix[N, N] sigma_total;

  vector[N] mu_y;

  sigma_mat = (1-lambda)*d_mat + lambda*A;
  sigma_total = sigma*sigma_mat;

}

```

The model to be estimated. We model the output ‘y’ to be normally distributed with mean ‘mu’ and standard deviation ‘sigma’.

```

model {
  beta ~ student_t(3, 0, 10);
  lambda ~ uniform(0,1);
  sigma ~ student_t(3, 0, 2.5);

  y ~ multi_normal(alpha + x * beta, sigma_total);
}

```

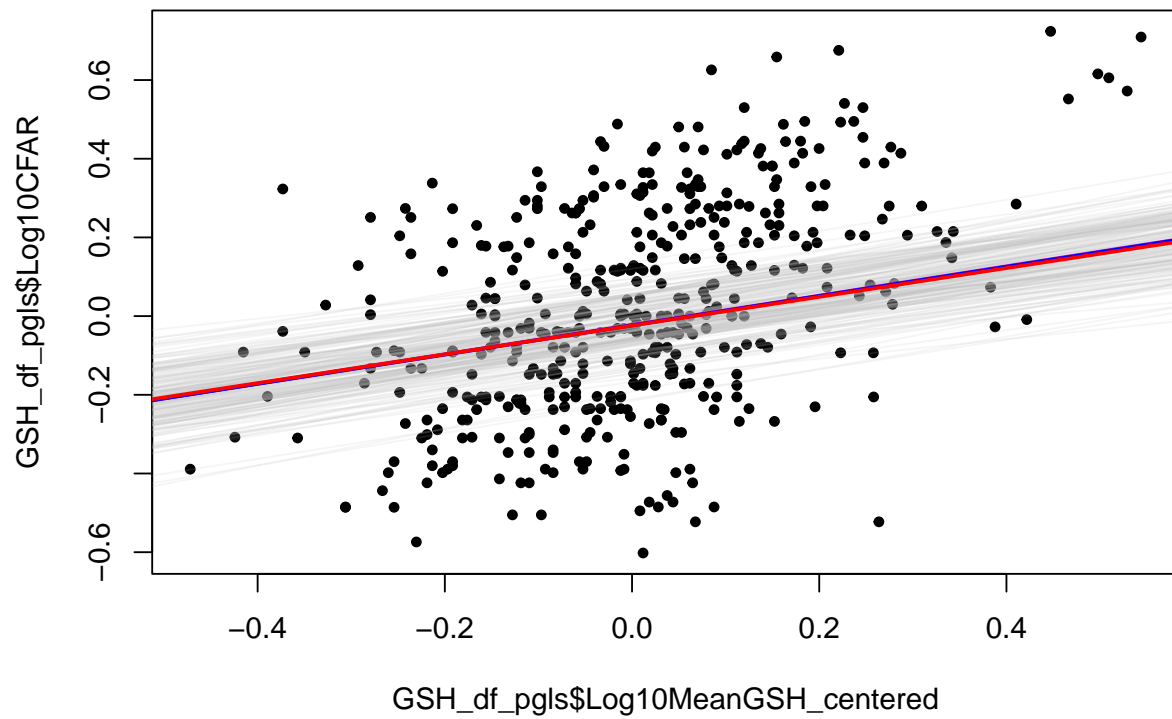
```
fit4
```

```

## Inference for Stan model: StanModel3.
## 4 chains, each with iter=1000; warmup=500; thin=10;
## post-warmup draws per chain=50, total post-warmup draws=200.
##
##           mean se_mean   sd  2.5%   25%   50%   75%  97.5% n_eff Rhat
## alpha    -0.02     0.0 0.06  -0.15  -0.06  -0.03   0.02   0.09   219 0.99
## beta[1]    0.37     0.0 0.06   0.25   0.33   0.36   0.41   0.47   216 1.01
## lp__      625.81     0.1 1.36 622.82 625.03 626.10 626.84 627.47   193 1.02
##

```

```
## Samples were drawn using NUTS(diag_e) at Thu Mar 03 14:30:50 2022.  
## For each parameter, n_eff is a crude measure of effective sample size,  
## and Rhat is the potential scale reduction factor on split chains (at  
## convergence, Rhat=1).
```



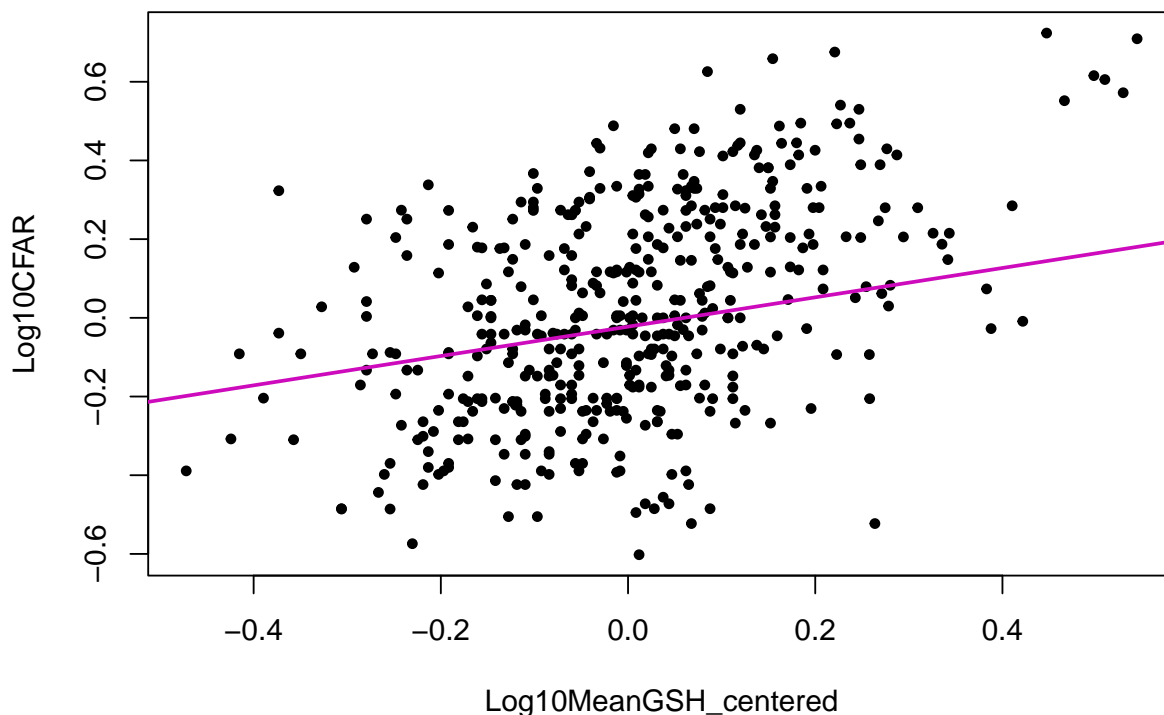
Model 7 - CFAR ~ GSH * Max Size + Phylogeny

1. PGLS model

```
pglsMod2 <- gls(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered, correlation = corPagel(phy =
```

```
summary(pglsMod2)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: y ~ x
##   Data: GSH_df_pgls
##           AIC      BIC    logLik
##   -427.4206 -410.9306 217.7103
##
## Correlation Structure: corPagel
##   Formula: ~Binomial
##   Parameter estimate(s):
##     lambda
## 0.7030228
##
## Coefficients:
##               Value Std.Error   t-value p-value
## (Intercept) -0.0224754 0.06282858 -0.357726  0.7207
## x           0.3728837 0.05950418  6.266513  0.0000
##
## Correlation:
##   (Intr)
## x -0.065
##
## Standardized residuals:
##           Min           Q1           Med           Q3           Max
## -2.7884572 -0.6933649  0.1151373  1.0885641  2.9034051
##
## Residual standard error: 0.2147249
## Degrees of freedom: 456 total; 454 residual
```



2. brms model

```
Model_BS <- brm(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered + (1|gr(Binomial, cov = A)),
  data = GSH_df_pgls,
  family = gaussian(),
  data2 = list(A = A),
  prior = BS_prior,
  sample_prior = TRUE, chains = 4, cores = 2)
```

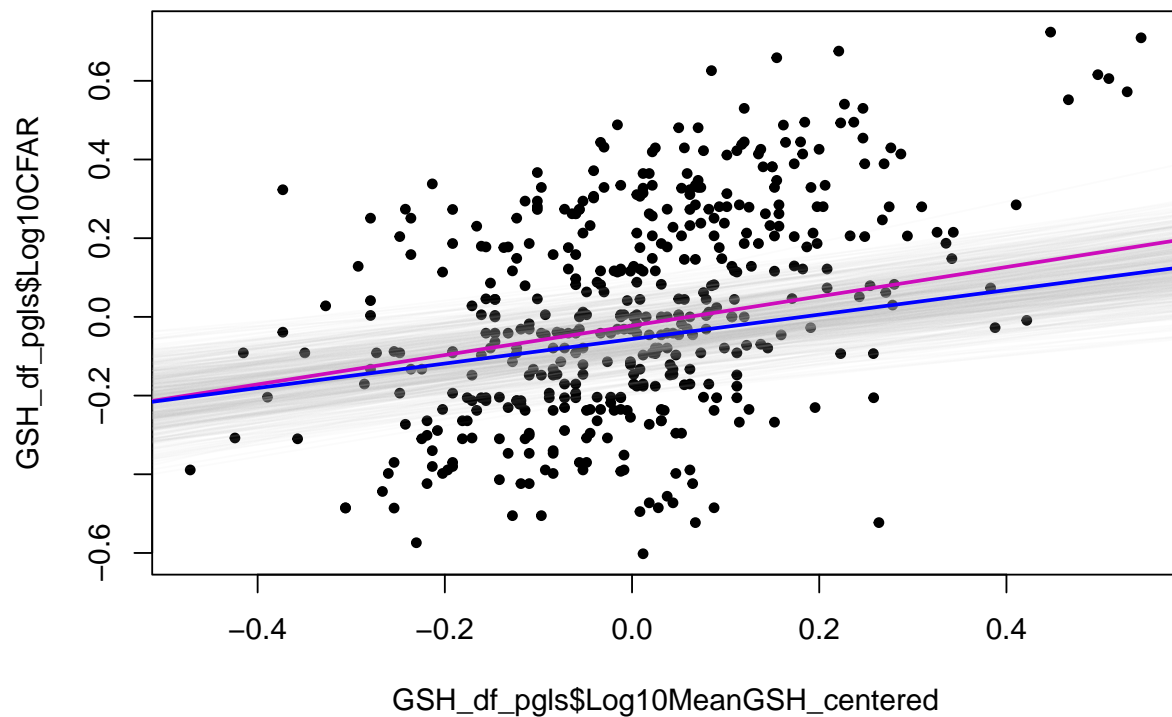
```
summary(Model_BS)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered + (1 | gr(Binomial, cov = A))
## Data: GSH_df_pgls (Number of observations: 456)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Group-Level Effects:
## ~Binomial (Number of levels: 456)
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.01 0.00 0.01 0.01 1.00 1303 2376
##
## Population-Level Effects:
```

```

##                                Estimate Est.Error l-95% CI
## Intercept                     -0.06      0.06    -0.17
## Log10MeanGSH_centered         0.31      0.06     0.19
## Log10MaxSize_centered         0.13      0.04     0.06
## Log10MeanGSH_centered:Log10MaxSize_centered 0.43      0.12     0.20
##                                u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept                     0.05 1.00     1824    2402
## Log10MeanGSH_centered         0.43 1.00     6595    3478
## Log10MaxSize_centered         0.20 1.00     4866    3342
## Log10MeanGSH_centered:Log10MaxSize_centered 0.67 1.00     5734    3590
##
## Family Specific Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma    0.12      0.01     0.11    0.13 1.00     2164    3283
##
## 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).

```



3. STAN model

Data considered

```
data {
```

```

int <lower=0> N; // number of data points
int <lower=0> K; // number of predictors
matrix[N,K] x; // predictor matrix
vector[N] y; // outcome (CFAR)
matrix[N, N] d_mat; // sigma matrix
matrix[N, N] A; // vcov matrix
}

```

The parameters accepted by the model.

```

parameters {
  real alpha;
  vector[K] beta; // coefficients
  real<lower=0> sigma; // error
  real<lower=0,upper=1> lambda; // phylogenetic signal
}

transformed parameters {

  matrix[N, N] sigma_mat;
  matrix[N, N] sigma_total;

  vector[N] mu_y;

  sigma_mat = (1-lambda)*d_mat + lambda*A;
  sigma_total = sigma*sigma_mat;

}

```

The model to be estimated. We model the output ‘y’ to be normally distributed with mean ‘mu’ and standard deviation ‘sigma’.

```

model {

  beta ~ student_t(3, 0, 10);
  lambda ~ uniform(0,1);
  sigma ~ student_t(3, 0, 2.5);

  y ~ multi_normal(alpha + x * beta, sigma_total);
}

```

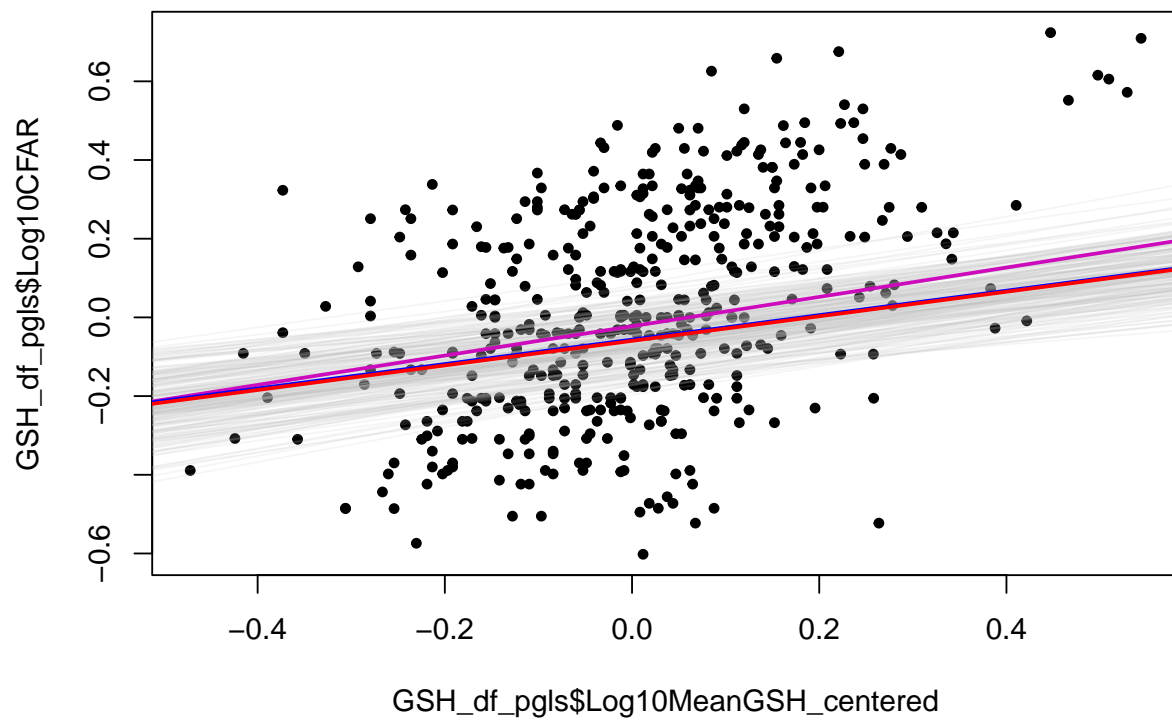
```
fit5
```

```

## Inference for Stan model: StanModel3.
## 4 chains, each with iter=1000; warmup=500; thin=10;
## post-warmup draws per chain=50, total post-warmup draws=200.
##
##           mean se_mean   sd  2.5%   25%   50%   75%  97.5% n_eff Rhat

```

```
## alpha      -0.06      0.00 0.06  -0.17  -0.10  -0.06  -0.02   0.05   154 1.01
## beta[1]     0.31      0.00 0.06   0.20   0.26   0.32   0.35   0.44   272 0.99
## beta[2]     0.12      0.00 0.04   0.06   0.10   0.12   0.15   0.20   194 0.99
## beta[3]     0.43      0.01 0.12   0.22   0.35   0.44   0.51   0.65   210 0.99
## lp__        641.68     0.12 1.76 637.09 640.81 642.00 643.00 643.99   199 1.00
##
## Samples were drawn using NUTS(diag_e) at Mon Mar 07 12:09:07 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```



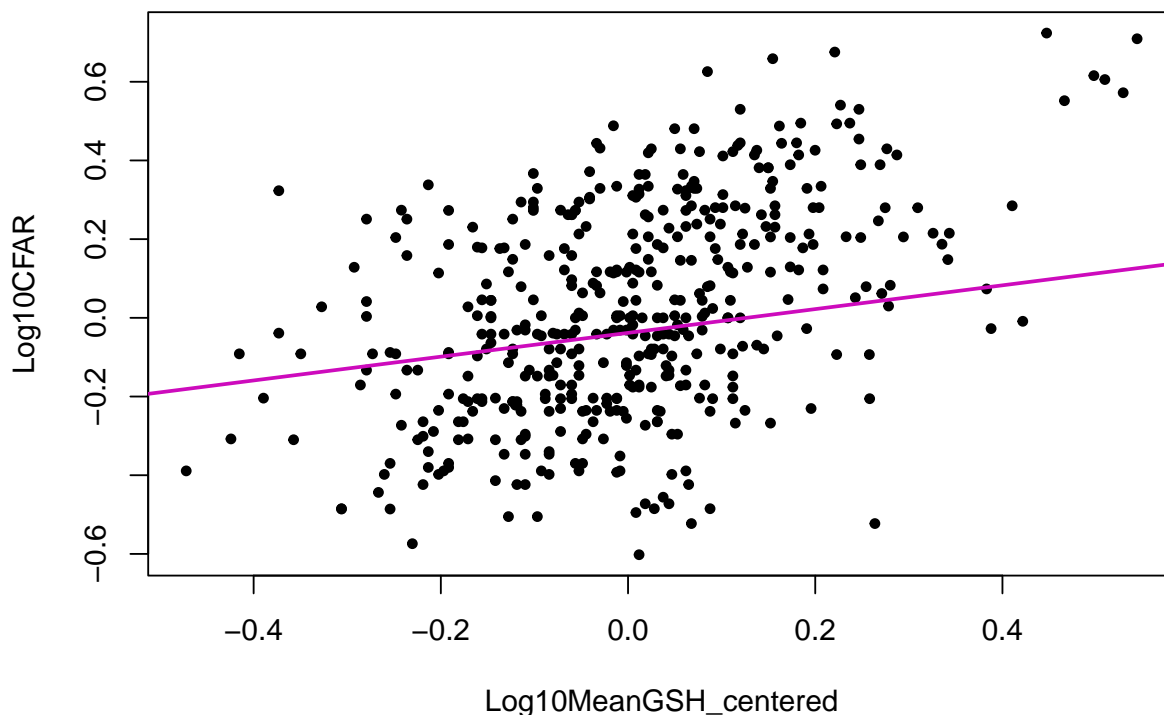
Model 8 - CFAR ~ GSH + Max Size + Phylogeny

1. PGLS model

```
pglsMod3 <- gls(Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered, correlation = corPagel(phy =
```

```
summary(pglsMod3)
```

```
## Generalized least squares fit by maximum likelihood
## Model: Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered
## Data: GSH_df_pgls
##      AIC      BIC    logLik
## -447.4392 -426.8268 228.7196
##
## Correlation Structure: corPagel
## Formula: ~Binomial
## Parameter estimate(s):
##      lambda
## 0.6786106
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  -0.03827951 0.05915461 -0.647110  0.5179
## Log10MeanGSH_centered  0.30222706 0.06034147  5.008613  0.0000
## Log10MaxSize_centered  0.16260955 0.03412415  4.765233  0.0000
##
## Correlation:
##              (Intr) L10MGS
## Log10MeanGSH_centered -0.050
## Log10MaxSize_centered -0.056 -0.268
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.8353741 -0.5472167  0.2440250  1.1919410  2.8367324
##
## Residual standard error: 0.2047976
## Degrees of freedom: 456 total; 453 residual
```



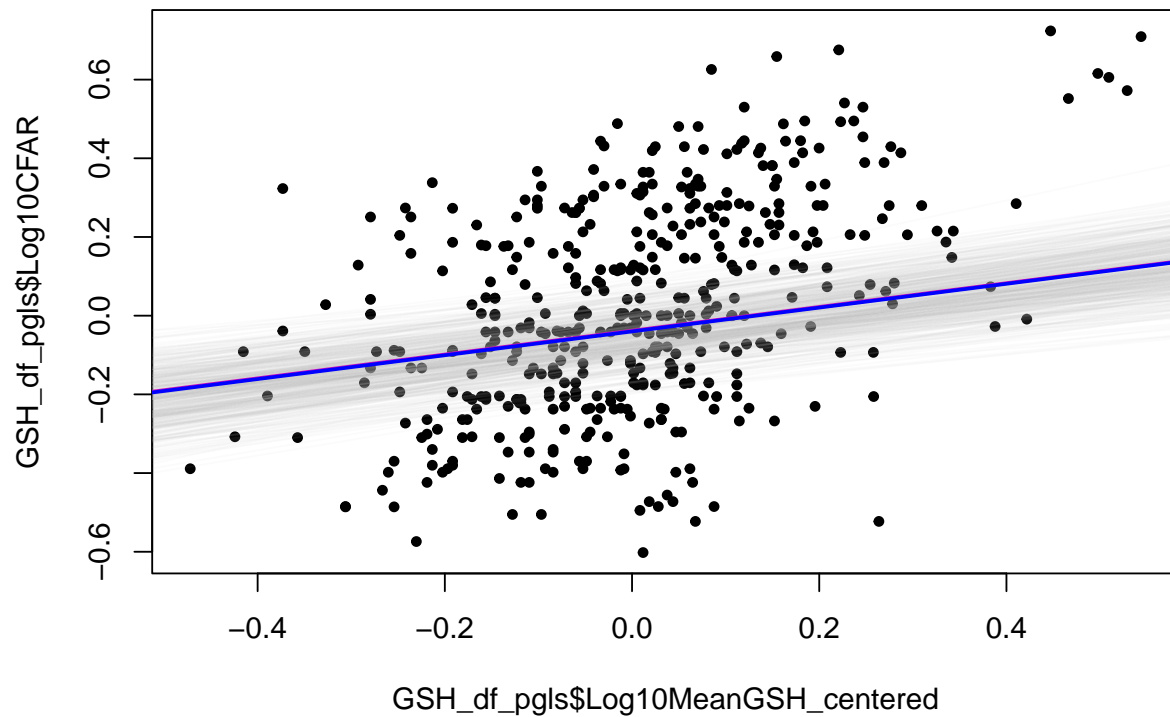
2. brms model

```
Model_BS <- brm(Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered + (1|gr(Binomial, cov = A)),
  data = GSH_df_pgls,
  family = gaussian(),
  data2 = list(A = A),
  prior = BS_prior,
  sample_prior = TRUE, chains = 4, cores = 2)
```

```
summary(Model_BS2)
```

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered + (1 | gr(Binomial, cov = A))
## Data: GSH_df_pgls (Number of observations: 456)
## Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
## total post-warmup draws = 4000
##
## Group-Level Effects:
## ~Binomial (Number of levels: 456)
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.01 0.00 0.01 0.01 1.00 1186 1678
##
## Population-Level Effects:
```

```
##               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS
## Intercept          -0.04     0.06   -0.16    0.08 1.00    1283
## Log10MeanGSH_centered  0.30     0.06    0.19    0.42 1.00    3622
## Log10MaxSize_centered  0.16     0.03    0.10    0.23 1.00    3812
##               Tail_ESS
## Intercept           2054
## Log10MeanGSH_centered 3227
## Log10MaxSize_centered 3414
##
## Family Specific Parameters:
##               Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma          0.12     0.01    0.11    0.13 1.00    1686    2672
##
## 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).
```



3. STAN model

TBD

Model 9 - CFAR \sim GSH + PrimaryHabitat + Phylogeny

Model 10 - CFAR \sim GSH * PrimaryHabitat + Phylogeny

Model 11 - CFAR \sim GSH * MaxSize + PrimaryHabitat + Phylogeny