

Ch. 1 - Model comparisons

Wade VanderWright

2022-02-25

Contents

Hypothesis summaries	2
No Phylogeny	2
With Phylogeny	2
Model Comparisons	3
No Phylogeny	3
With phylogeny	19

Hypothesis summaries

No Phylogeny

Model	Hypothesis
Log10CFAR ~ Log10GSH	Activity only varies with gill slit height
Log10CFAR ~ Log10GSH * MaxSize	Activity varies with gill slit height and maximum size and the effect of gill slit height varies with maximum size
Log10CFAR ~ Log10GSH + MaxSize	Activity varies with gill slit height and maximum size
Log10CFAR ~ Log10GSH + PrimaryHabitat	Activity varies with gill slit height and primary habitat
Log10CFAR ~ Log10GSH * PrimaryHabitat	Activity varies with gill slit height and primary habitat and the effect of gill slit height varies with primary habitat

With Phylogeny

Model	Hypothesis
Log10CFAR ~ Log10GSH + Phylogeny	Activity only varies with gill slit height and is conserved across evolutionary history
Log10CFAR ~ Log10GSH * MaxSize + Phylogeny	Activity varies with gill slit height and maximum size and the effect of gill slit height varies with maximum size and is conserved across evolutionary history
Log10CFAR ~ Log10GSH + MaxSize + Phylogeny	Activity varies with gill slit height and maximum size and is conserved across evolutionary history
Log10CFAR ~ Log10GSH + PrimaryHabitat + Phylogeny	Activity varies with gill slit height and primary habitat and is conserved across evolutionary history
Log10CFAR ~ Log10GSH * PrimaryHabitat + Phylogeny	Activity varies with gill slit height and primary habitat and the effect of gill slit height varies with primary habitat and is conserved across evolutionary history
Log10CFAR ~ Log10GSH * MaxSize + PrimaryHabitat + Phylogeny	Activity varies with gill slit height, maximum size, and primary habitat, and the effect of gill slit height varies with maximum size and is conserved across evolutionary history

Model Comparisons

No Phylogeny

Model 1 - CFAR ~ GSH

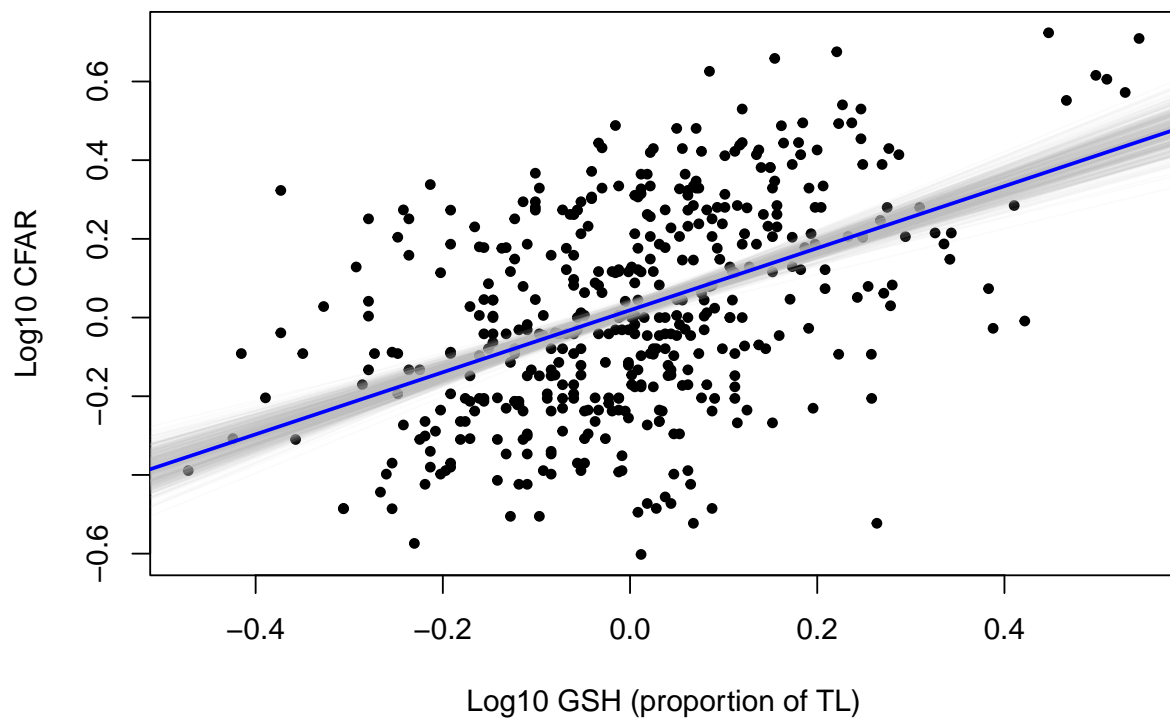
1. brms model

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

Table 1: brms model summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	0.0186040	0.0114242	-0.003649	0.0401433
Log10MeanGSH_centered	0.7884163	0.0697968	0.651545	0.9267644

Correlation= 0.471640472505464



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:

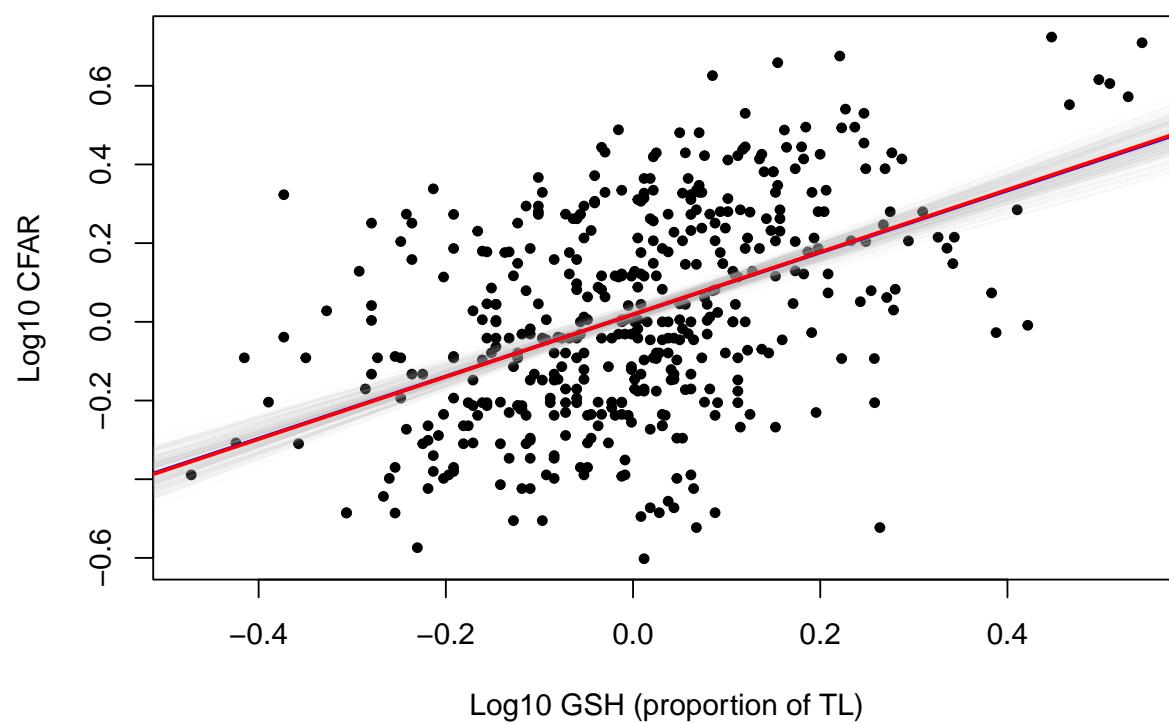
```
model {
  sigma ~ student_t(3, 0, 10);

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

Table 2: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0188158	0.0001937	0.0110817	-0.0031703	0.0406778	3274.674	0.9984189
beta	0.7922521	0.0017679	0.0665245	0.6608094	0.9182969	1415.881	1.0050079
sigma	0.2358616	0.0001837	0.0078292	0.2210460	0.2517663	1817.402	1.0015645

Correlation= 0.471640472505464



Model 2 - CFAR ~ GSH * Max Size

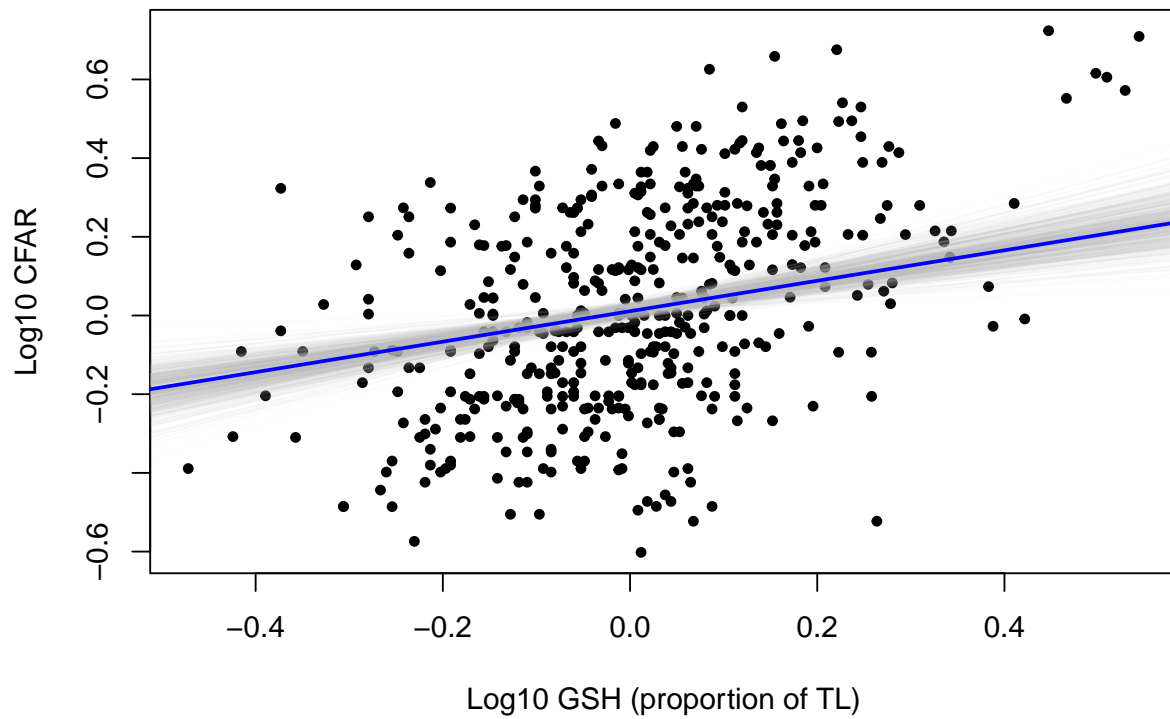
1. brms model

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

Table 3: brms model 2 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	0.0108613	0.0116288	-0.0116655	0.0338328
Log10MeanGSH_centered	0.3870415	0.0813134	0.2282266	0.5479091
Log10MaxSize_centered	0.3052711	0.0431941	0.2182414	0.3891395
Log10MeanGSH_centered:Log10MaxSize_centered	0.263756	0.1662728	-0.0681492	0.5881496

Correlation= 0.471640472505464



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);

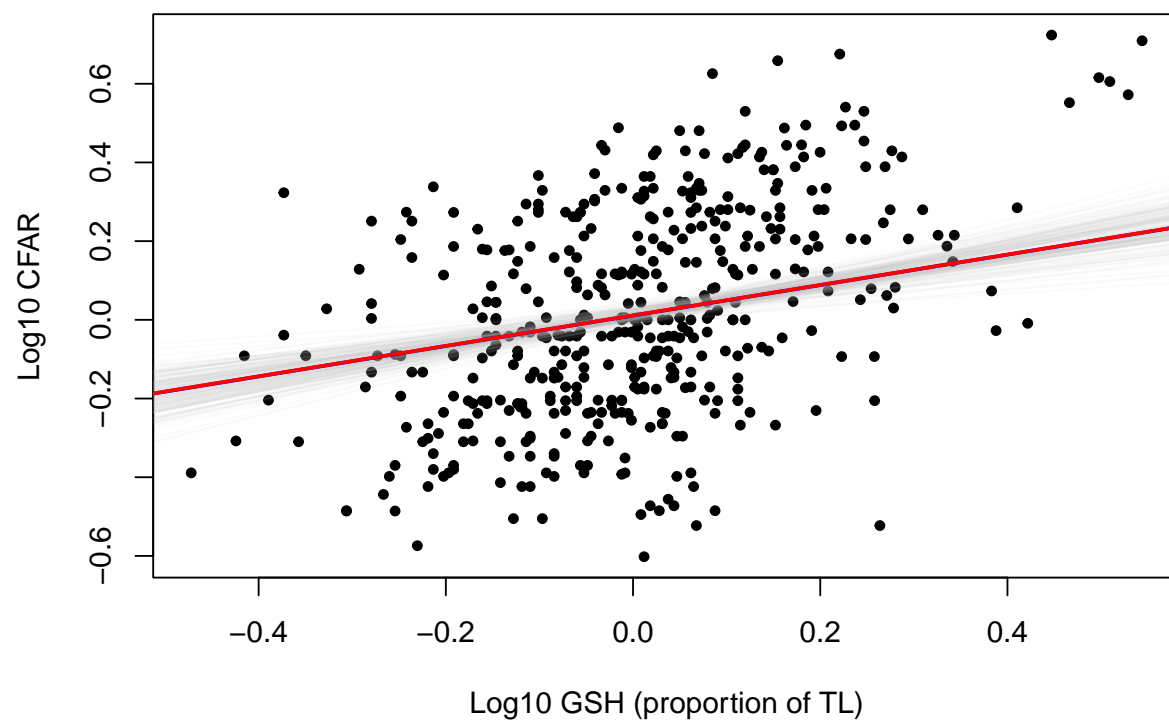
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 4: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0112357	0.0002557	0.0114051	-0.0115889	0.0333155	1988.829	0.9993611
beta	0.3868145	0.0019944	0.0817741	0.2251650	0.5436388	1681.167	0.9995647
beta2	0.3052701	0.0011185	0.0436857	0.2179698	0.3925311	1525.506	0.9995208
(size)							
GSH:Size	0.2621950	0.0041698	0.1644755	-0.0673900	0.5828360	1555.845	1.0006233
sigma	0.2213459	0.0001514	0.0074170	0.2072423	0.2362991	2399.682	1.0013515

Correlation= 0.471640472505464



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

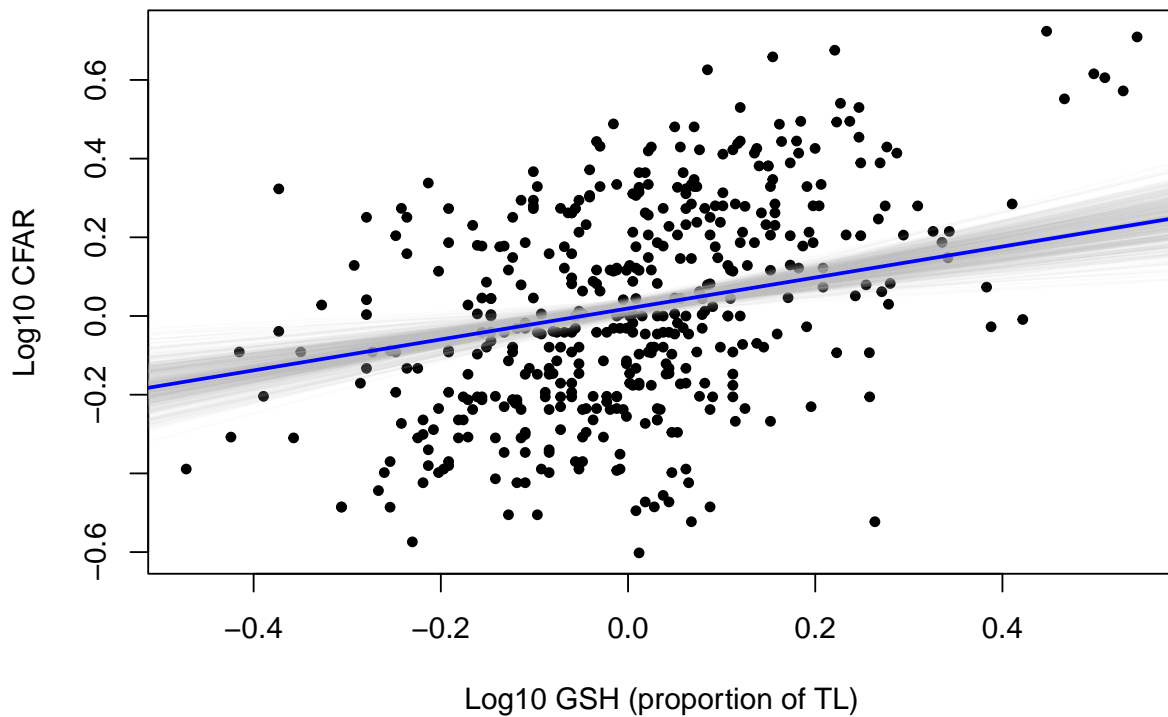
1. brms model

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

Table 5: brms model 3 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	0.0191592	0.0105502	-0.0012029	0.0391889
Log10MeanGSH_centered	0.3933932	0.0813047	0.2321998	0.5565847
Log10MaxSize_centered	0.3256492	0.0409817	0.2463013	0.4055545

Correlation= 0.471640472505464



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);

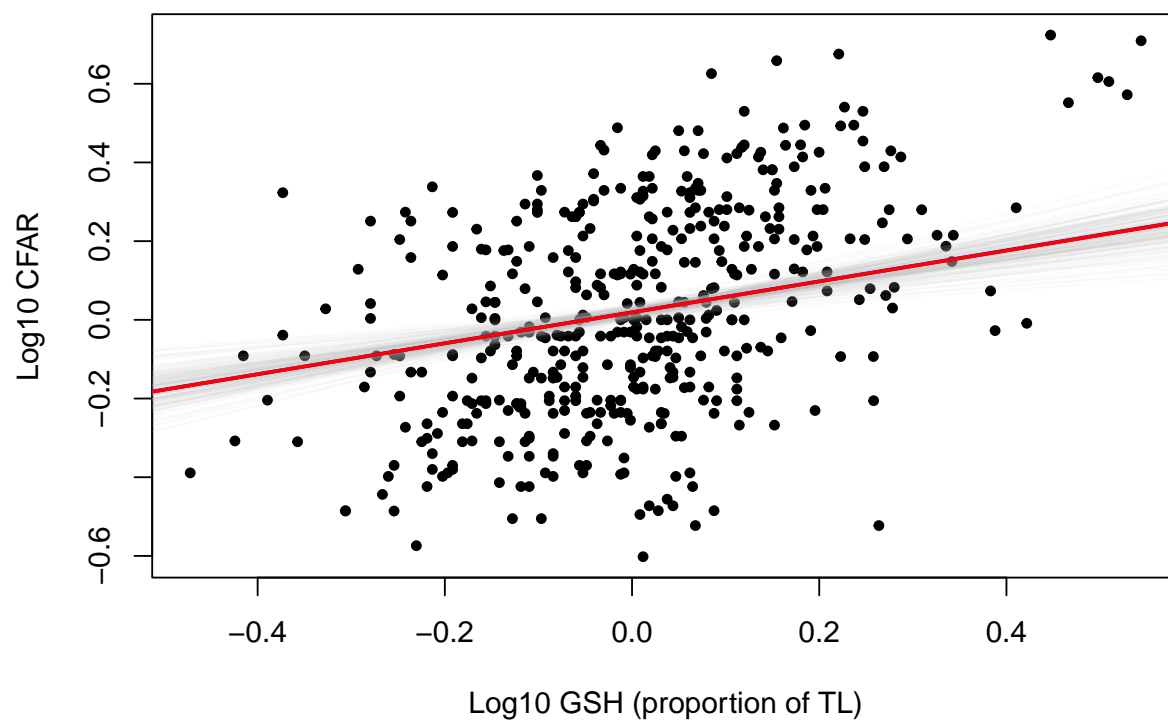
    y ~ normal(alpha + x * beta , sigma);
}

```

Table 6: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0188396	0.0002374	0.0102310	-0.0012143	0.0392767	1857.446	0.9991824
beta	0.3927498	0.0019778	0.0783052	0.2334579	0.5461124	1567.571	1.0044142
beta2	0.3253207	0.0010034	0.0410548	0.2433716	0.4054188	1674.104	0.9994939
(size)							
sigma	0.2212969	0.0001638	0.0074071	0.2075136	0.2365912	2045.035	0.9989518

Correlation= 0.471640472505464



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

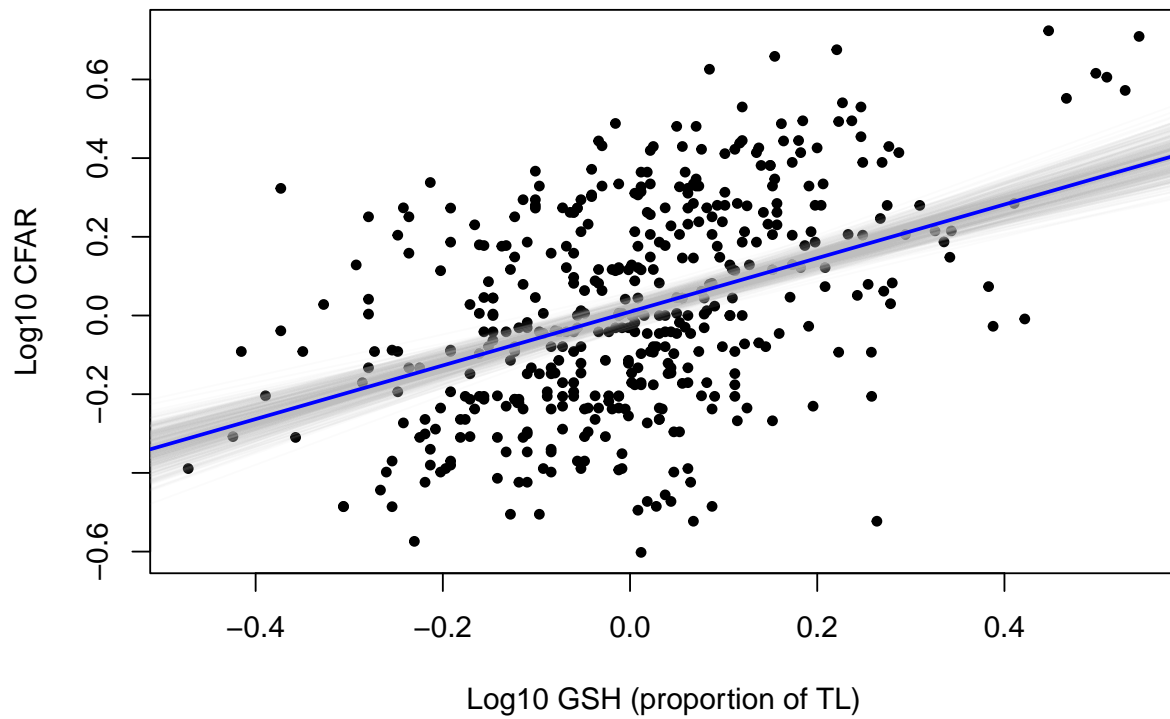
1. brms model

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

Table 7: brms model 4 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	0.0094310	0.0162116	-0.0213733	0.0416329
Log10MeanGSH_centered	0.6817737	0.0715856	0.5417254	0.8220336
PrimaryHabitatDeepwater	-0.0090850	0.0229203	-0.0534812	0.0359128
PrimaryHabitatPelagic	0.2506187	0.0496865	0.1519708	0.3509502

Correlation= 0.471640472505464



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);

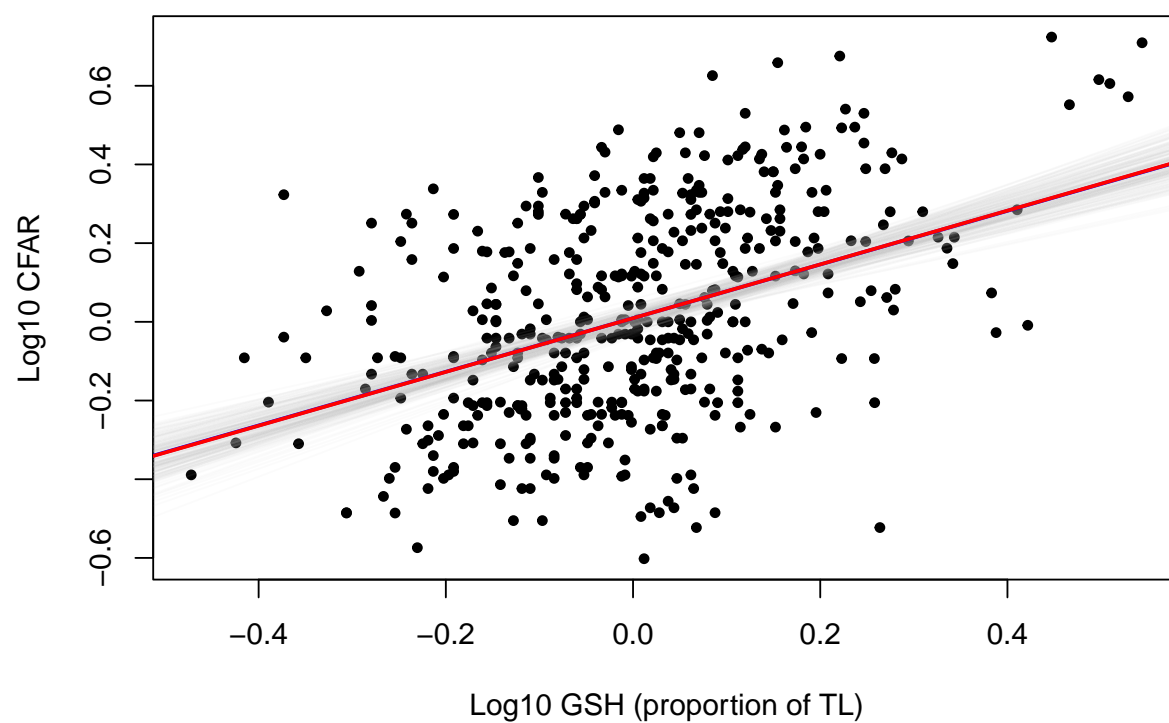
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 8: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0093064	0.0004752	0.0164154	-0.0229501	0.0409012	1193.296	1.003653
beta	0.6833951	0.0017509	0.0731667	0.5406023	0.8252357	1746.240	1.000578
deepwater	-0.0090020	0.0006501	0.0234225	-0.0542237	0.0353749	1298.224	1.001620
pelagic	0.2492132	0.0011411	0.0483598	0.1557461	0.3421209	1795.947	1.001240
sigma	0.2293517	0.0001706	0.0077231	0.2149873	0.2447730	2050.060	1.001779

Correlation= 0.471640472505464



Model 5 - CFAR ~ GSH * PrimaryHabitat

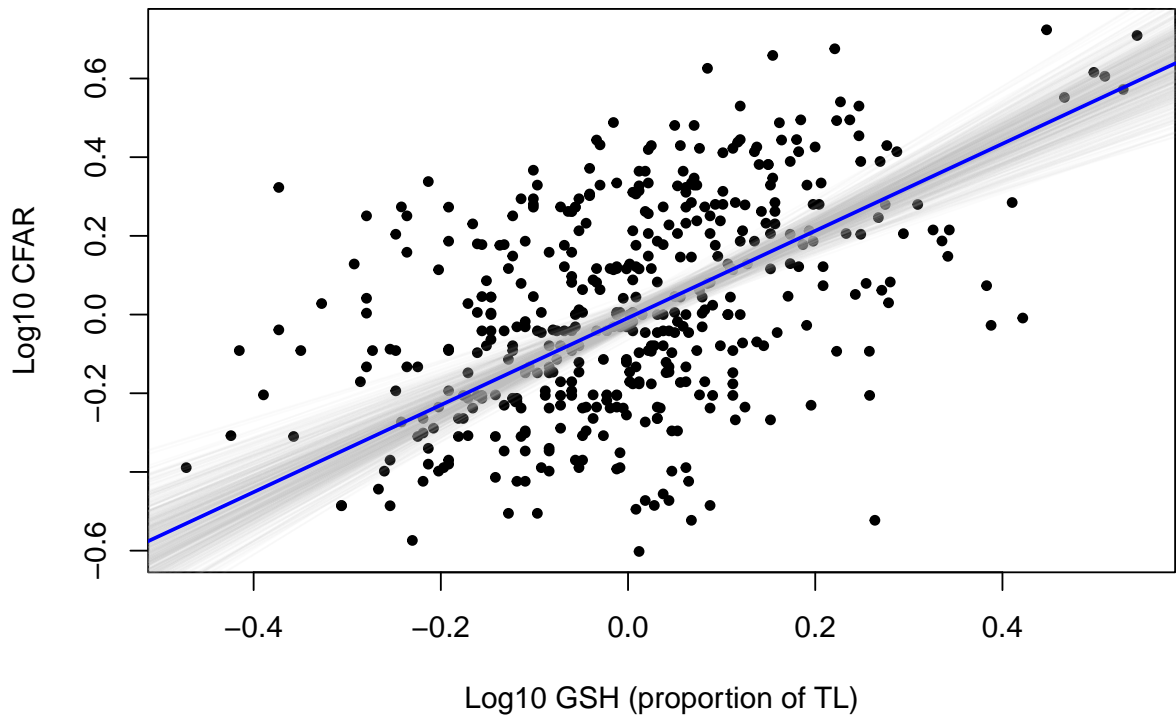
1. brms model

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

Table 9: brms model 5 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0085535	0.0168304	-0.0417676	0.0251176
Log10MeanGSH_centered	1.1067339	0.1325830	0.8451767	1.3691526
PrimaryHabitatDeepwater	-0.0034605	0.0231775	-0.0491468	0.0425060
PrimaryHabitatPelagic	0.2917904	0.0565341	0.1835352	0.4041409
Log10MeanGSH_centered:PrimaryHabitatDeepwater	-0.6421565	0.1661818	-0.9654556	-0.3042642
Log10MeanGSH_centered:PrimaryHabitatPelagic	-0.5641885	0.2255462	-1.0076427	-0.1251787

Correlation= 0.471640472505464



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);

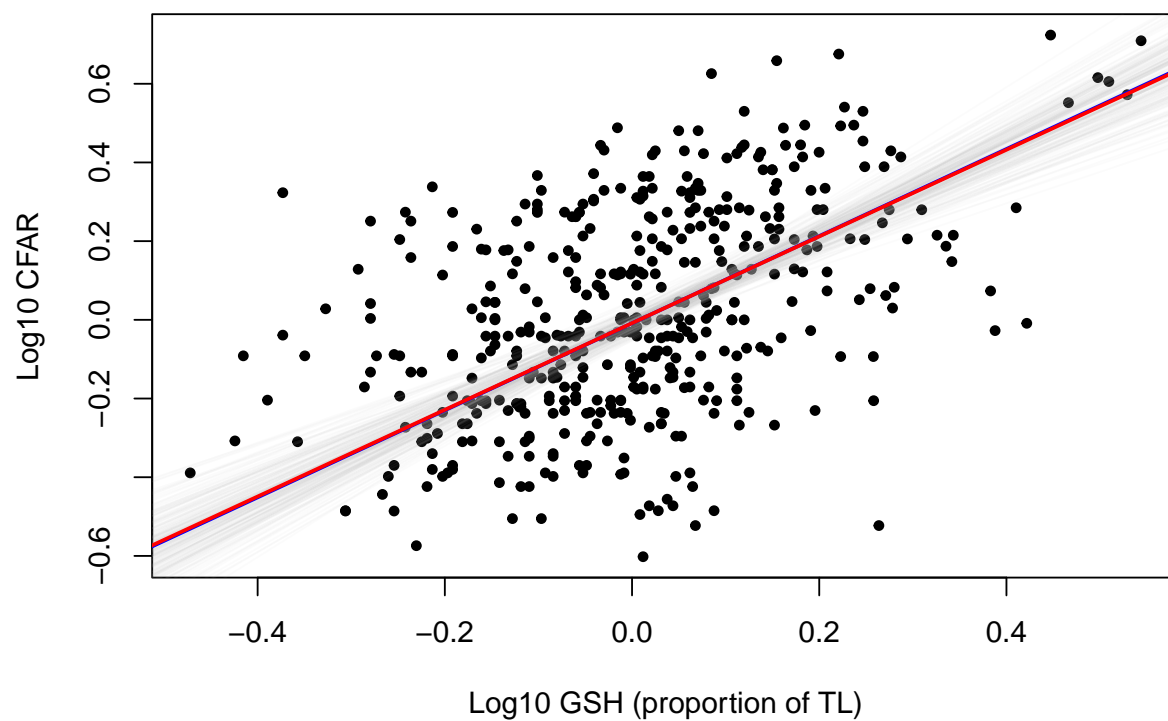
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 10: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0083782	0.0004424	0.0169187	-0.0422139	0.0252893	1462.451	0.9992744
beta	1.1015835	0.0038217	0.1254782	0.8610416	1.3588685	1078.017	1.0021302
deepwater	-0.0036666	0.0005806	0.0230853	-0.0500280	0.0404861	1580.752	0.9995743
pelagic	0.2920746	0.0014158	0.0561438	0.1837302	0.4050651	1572.518	1.0016054
GSH:deepwater	0.6327790	0.0045439	0.1636559	-0.9752255	-0.3220716	1297.214	1.0014948
GSH:pelagic	-0.5547668	0.0066944	0.2173005	-0.9867699	-0.1316071	1053.656	1.0029185
sigma	0.2260972	0.0001929	0.0077090	0.2118355	0.2422684	1596.831	1.0001837

Correlation= 0.471640472505464



	elpd_diff	se_diff	elpd_loo	se_elpd_loo	p_loo	se_p_loo	looic	se_looic
Model_size	0.0000000	0.000000	39.42096	13.07853	4.763323	0.4957700	-78.84191	26.15706
Model_size_2	-0.2180412	1.620030	39.20292	13.30920	3.710303	0.3352244	-78.40583	26.61840
habitat_model_2	-10.2608587	7.934863	29.16010	13.58205	5.628635	0.4769462	-58.32020	27.16410
habitat_model	-16.4485437	7.444745	22.97241	13.51326	4.094816	0.3453095	-45.94483	27.02652
Model_plain	-28.6190606	7.164067	10.80190	13.35951	2.835150	0.2725939	-21.60379	26.71903

BRMS LOO analysis

LOO compare

```
fit1_loo <- loo(Model_plain)
fit2_loo <- loo(Model_size)
fit3_loo <- loo(Model_size_2)
fit4_loo <- loo(habitat_model)
fit5_loo <- loo(habitat_model_2)

brms_loo_nonphylo_list <- list(fit1_loo, fit2_loo, fit3_loo, fit4_loo, fit5_loo)
brms_loo_nonphylo <- loo_compare(brms_loo_nonphylo_list)

kbl(brms_loo_nonphylo, booktabs = T, linesep = "") %>%
  kable_styling(latex_options = c("scale_down", "hold_position"))
```

LOO model weights

```
loo_model_weights(brms_loo_nonphylo_list)
```

```
## Method: stacking
## -----
##          weight
## model1 0.000
## model2 0.022
## model3 0.675
## model4 0.000
## model5 0.303
```

Table 11: PGLS summary

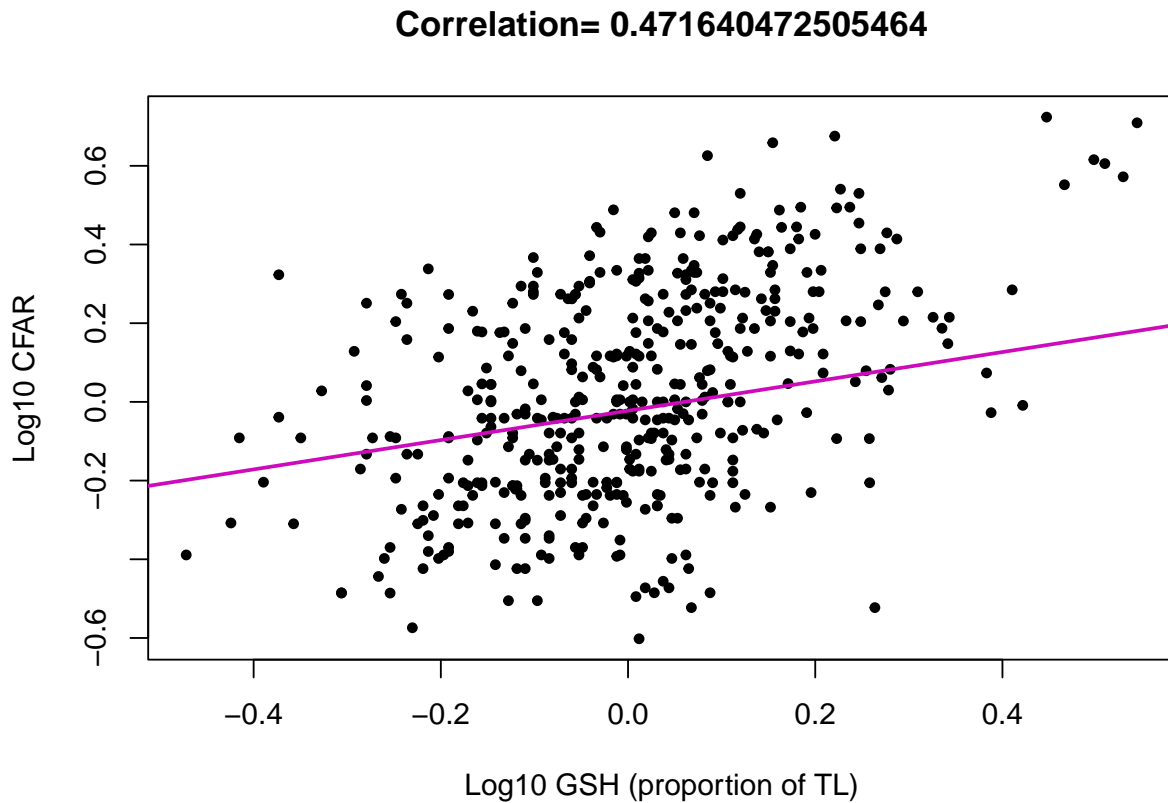
	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0224754	0.0628286	-0.3577261	0.7207146	-0.1456172	0.1006663
Log10MeanGSH_centered	0.3728837	0.0595042	6.2665128	0.0000000	0.2562576	0.4895097

With phylogeny

Model 6 - CFAR ~ GSH + Phylogeny

1. PGLS model

```
pglsMod1 <- gls(Log10CFAR ~ Log10MeanGSH_centered, correlation = corPagel(phy = SampleTree, value = 0.5),
  data = GSH_df_pgls, method = "ML")
```



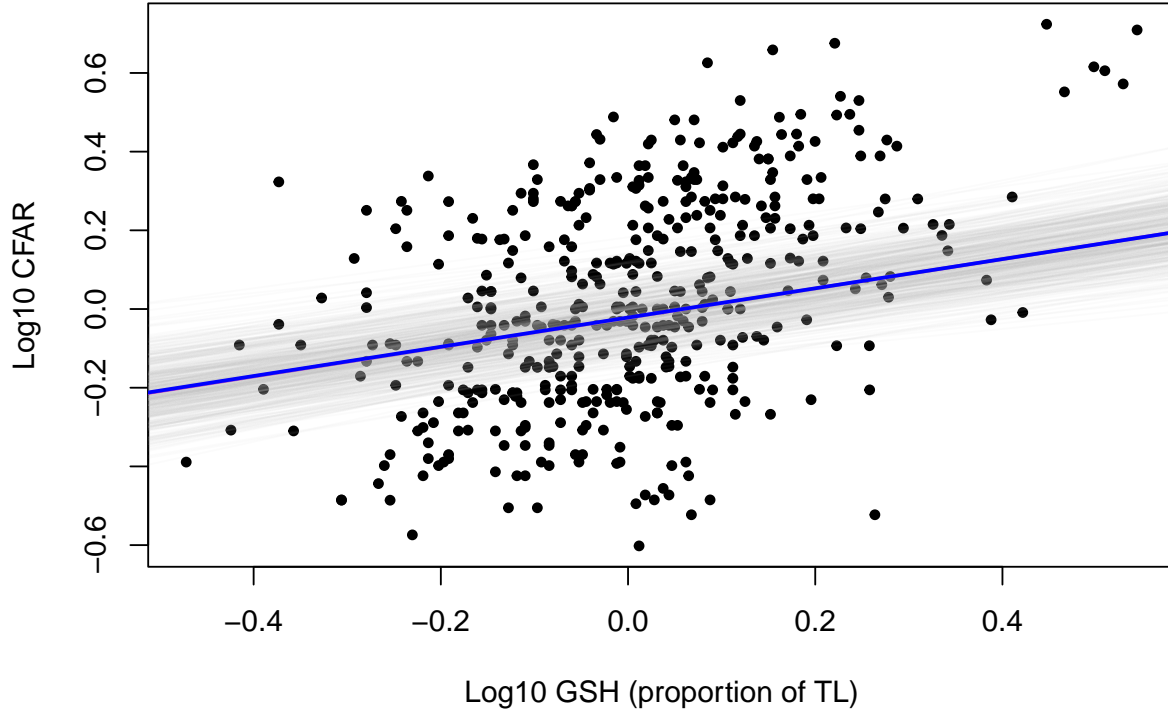
2. brms model

```
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)
```

Table 12: brms model 6 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0216233	0.0641111	-0.1484133	0.1086491
Log10MeanGSH_centered	0.3714871	0.0609867	0.2510932	0.4920521

Correlation= 0.471640472505464



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 {
```

Table 13: STAN model 6 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0212663	0.0026451	0.0637752	-0.1443539	0.0993291	581.3101	1.0083253
beta	0.3762973	0.0024778	0.0603920	0.2642602	0.4999318	594.0789	0.9957055
sigma	0.0474796	0.0002165	0.0050428	0.0394590	0.0584414	542.7036	1.0011663
lambda	0.7039053	0.0018043	0.0422913	0.6151044	0.7800027	549.3910	1.0072163

```

    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);
}

```

Correlation= 0.471640472505464

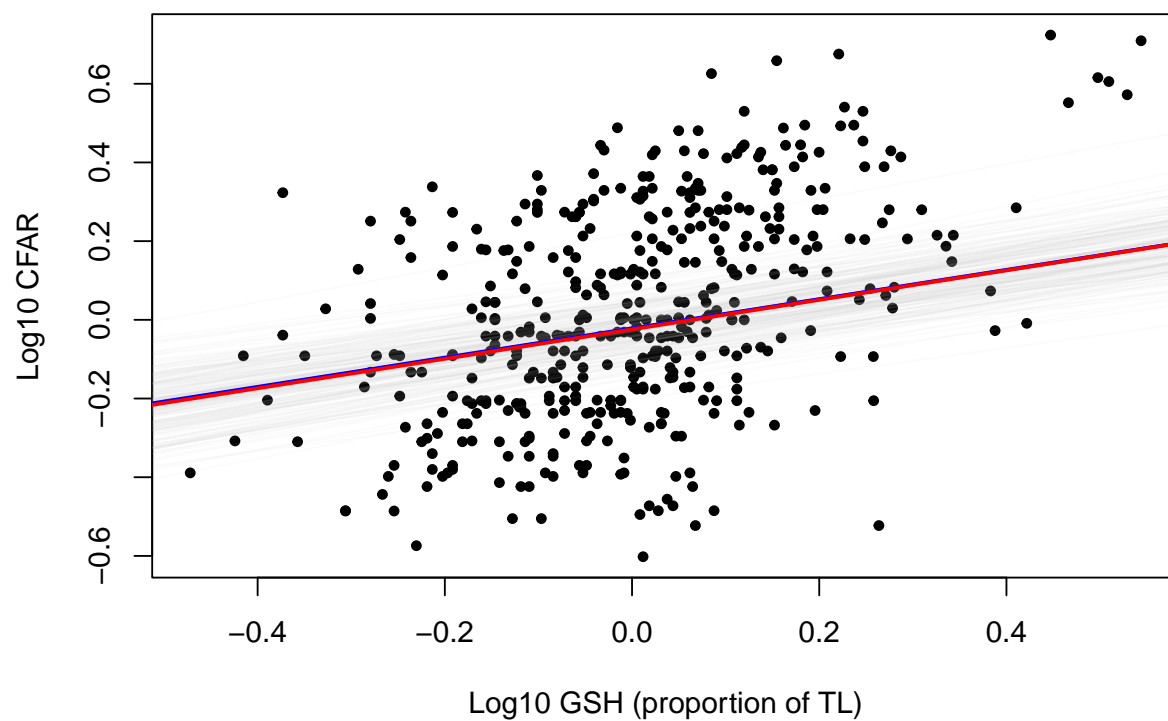


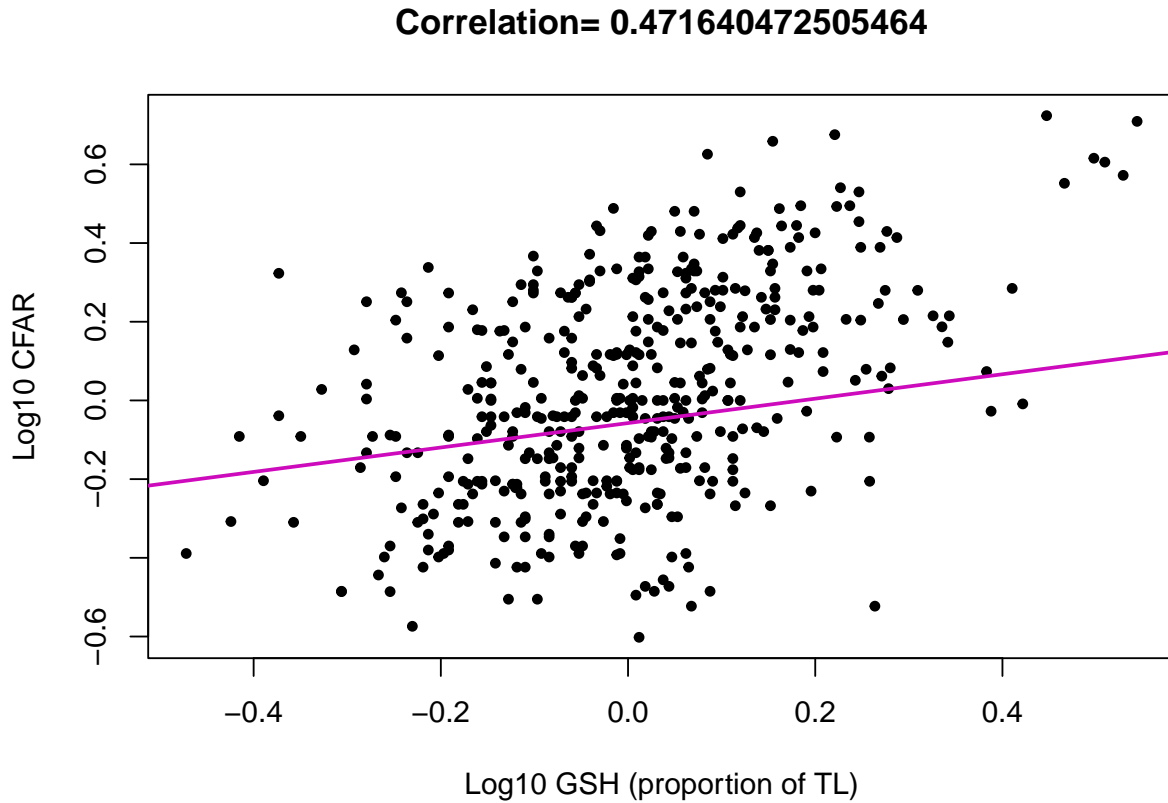
Table 14: PGLS summary

	Value	Std.Error	t-value	p-value	2.5 %	9.75 %
(Intercept)	-0.0575841	0.0576548	-0.998773	0.3184390	-0.1705854	0.0544282
Log10MeanGSH_centered	0.3102797	0.0596610	5.200711	0.0000003	0.1933462	0.4272132
Log10MaxSize_centered	0.1272174	0.0352490	3.609111	0.0003416	0.0581307	0.1963041
Log10MeanGSH_centered:Log10MaxSize_centered	0.4334147	0.1232626	3.516191	0.0004820	0.1918245	0.6750047

Model 7 - CFAR ~ GSH * Max Size + Phylogeny

1. PGLS model

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

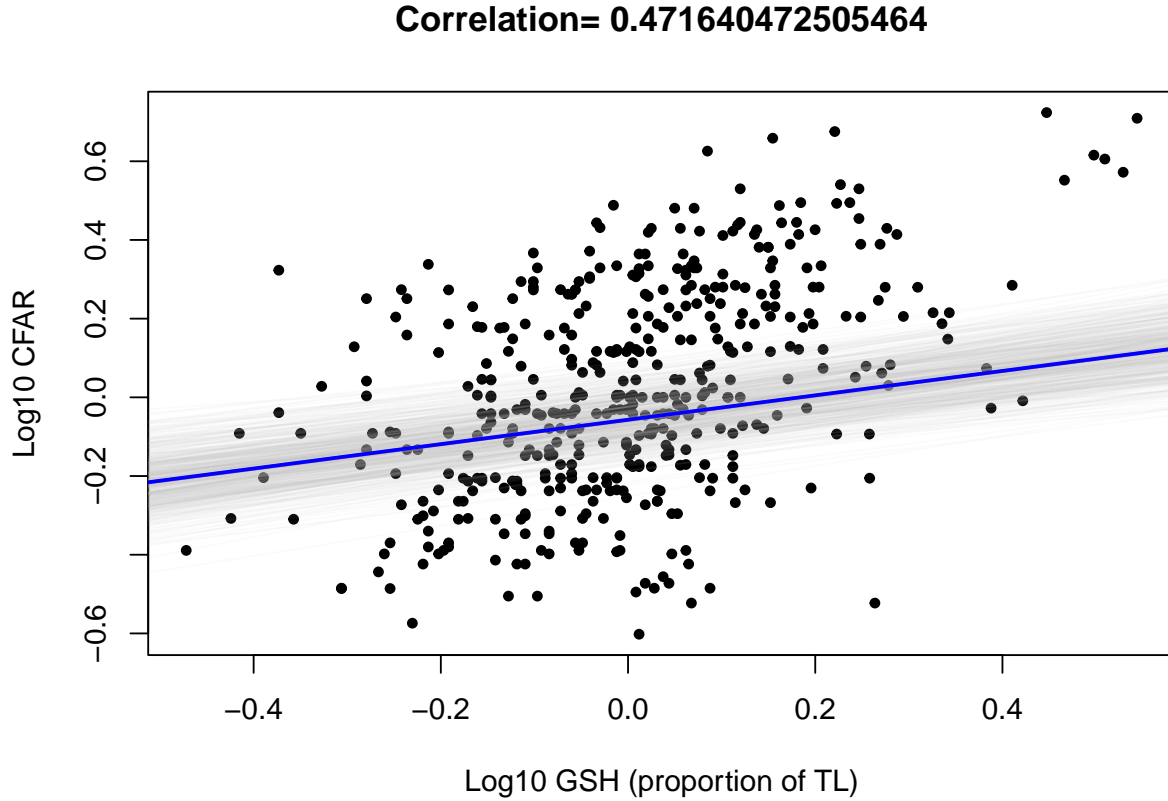


2. brms model

```
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)
```

Table 15: brms model 7 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0568821	0.0579540	-0.1725123	0.0580787
Log10MeanGSH_centered	0.3100289	0.0602294	0.1866072	0.4273601
Log10MaxSize_centered	0.1267622	0.0351696	0.0576869	0.1957255
Log10MeanGSH_centered:Log10MaxSize_centered	0.0337519	0.1237383	0.1928571	0.6781341



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.

Table 16: STAN model 7 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0576060	0.0012582	0.0567142	-0.1748269	0.0517834	2031.745	0.9993214
beta	0.3119275	0.0013463	0.0594781	0.1937403	0.4318569	1951.703	1.0003062
beta2	0.1273933	0.0008116	0.0352748	0.0598826	0.1959810	1889.054	0.9994723
(size)							
GSH:MaxSize	0.4296080	0.0028943	0.1292687	0.1804127	0.6753124	1994.770	0.9993773
sigma	0.0413515	0.0001330	0.0044842	0.0335414	0.0512851	1136.097	0.9987187
lambda	0.6693168	0.0014095	0.0471767	0.5708993	0.7571727	1120.349	0.9996346

```

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);
}

```

Correlation= 0.471640472505464

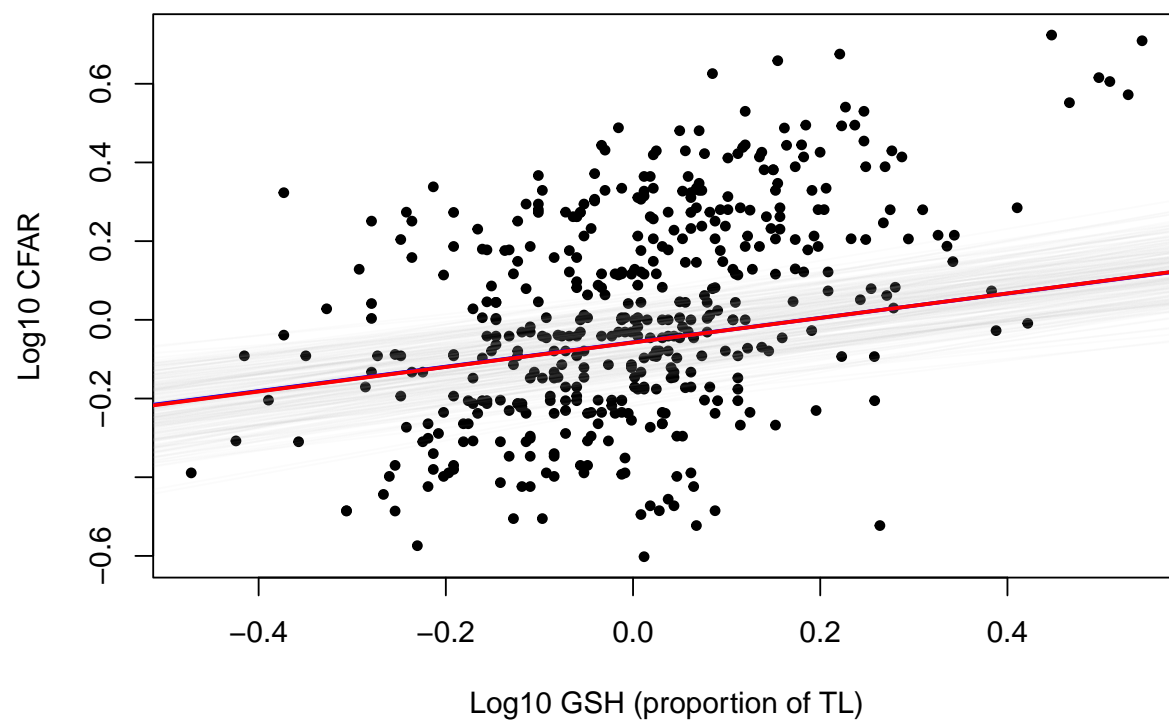


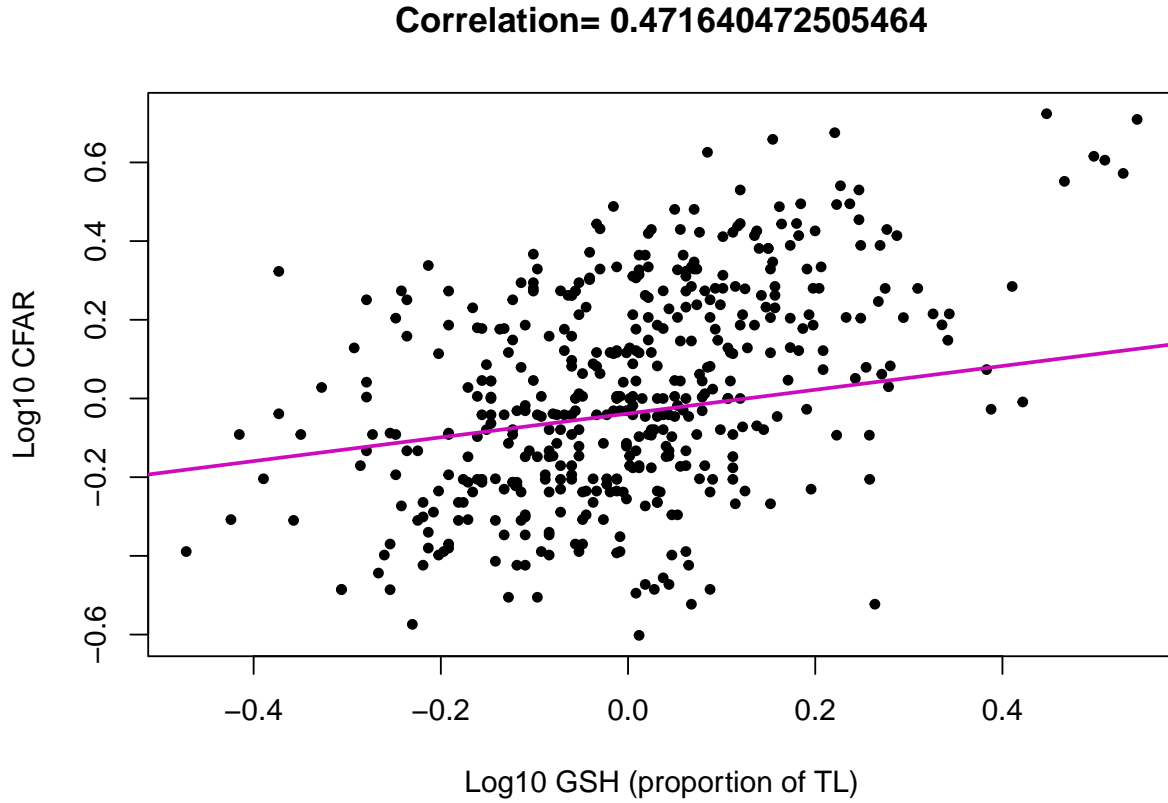
Table 17: PGLS summary

	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0382795	0.0591546	-0.6471096	0.5178888	-0.1542204	0.0776614
Log10MeanGSH_centered	0.3022271	0.0603415	5.0086129	0.0000008	0.1839600	0.4204942
Log10MaxSize_centered	0.1626095	0.0341242	4.7652331	0.0000025	0.0957274	0.2294917

Model 8 - CFAR ~ GSH + Max Size + Phylogeny

1. PGLS model

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

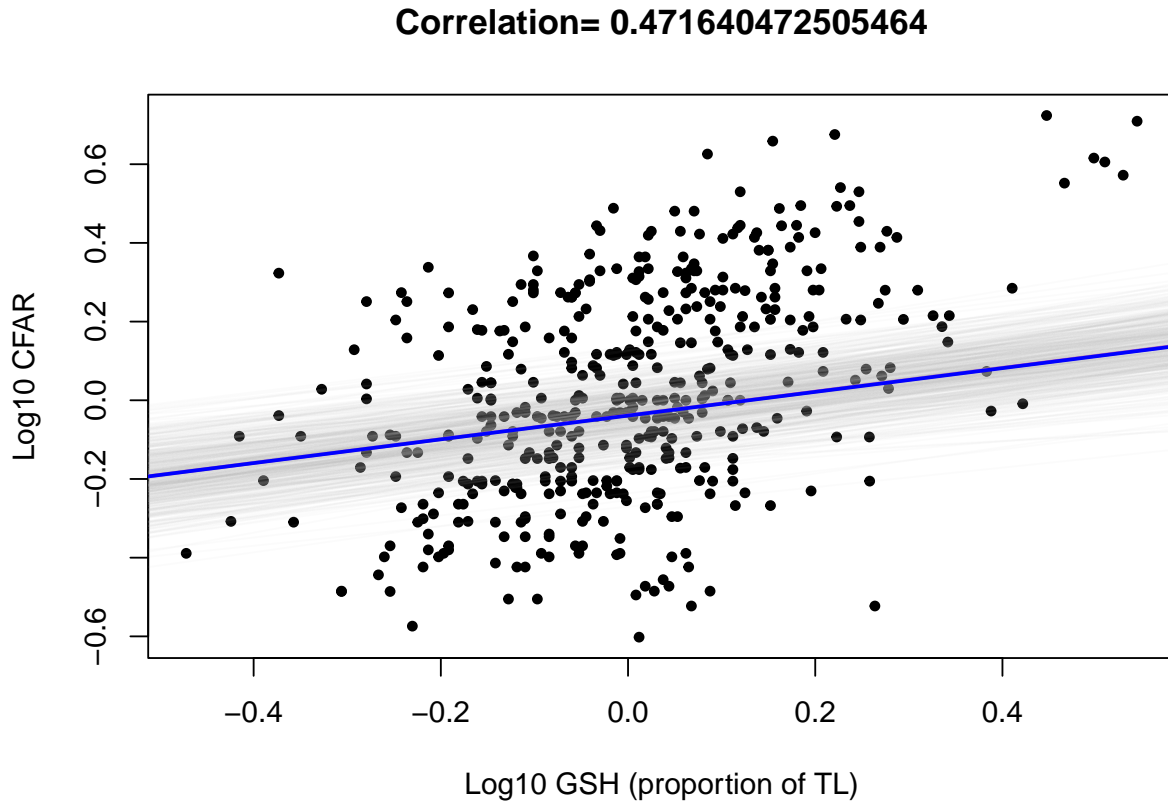


2. brms model

```
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)
```

Table 18: brms model 8 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0389619	0.0603196	-0.1579793	0.0801359
Log10MeanGSH_centered	0.3016207	0.0592575	0.1873177	0.4200445
Log10MaxSize_centered	0.1619811	0.0340442	0.0964249	0.2283516



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 {
```

Table 19: STAN model 8 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0378307	0.0015482	0.0639088	-0.1601034	0.0888579	1703.918	0.9990736
beta	0.3024532	0.0014609	0.0609542	0.1826927	0.4261175	1740.966	1.0011061
beta2 (size)	0.1624285	0.0007494	0.0332792	0.0980794	0.2285594	1971.954	0.9993628
sigma	0.0434596	0.0001544	0.0048400	0.0348521	0.0542975	982.300	1.0019873
lambda	0.6821638	0.0014381	0.0464156	0.5919477	0.7694996	1041.699	1.0033275

```

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);
}

```

Correlation= 0.471640472505464

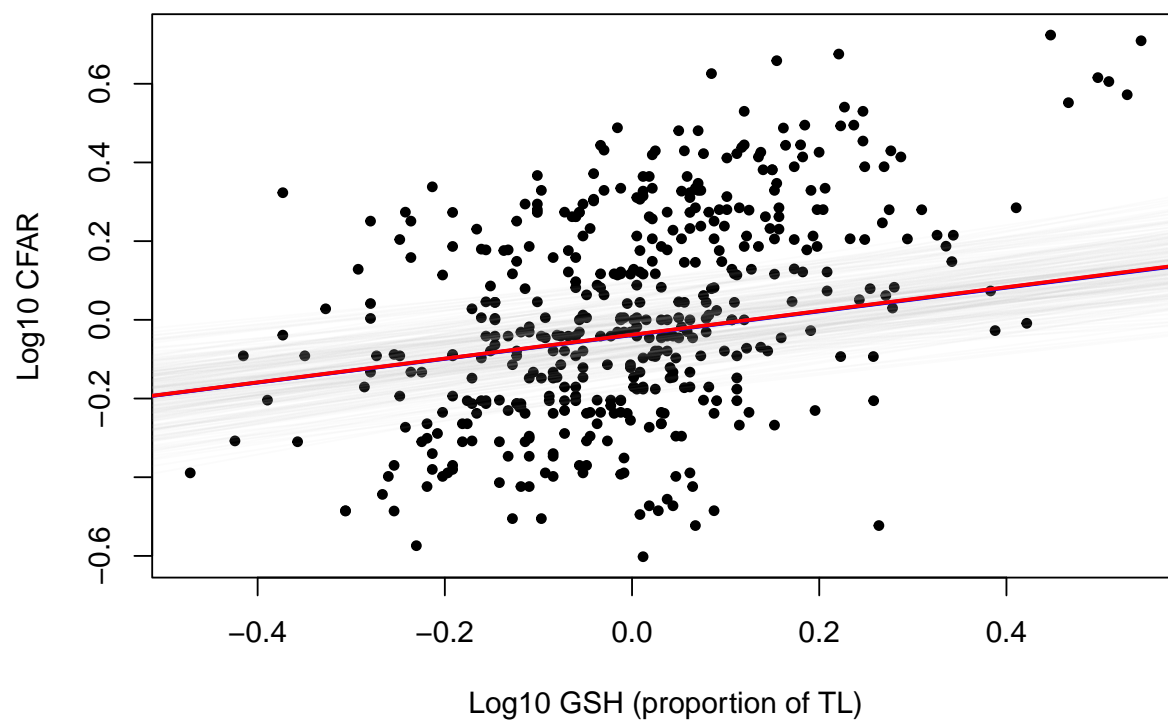


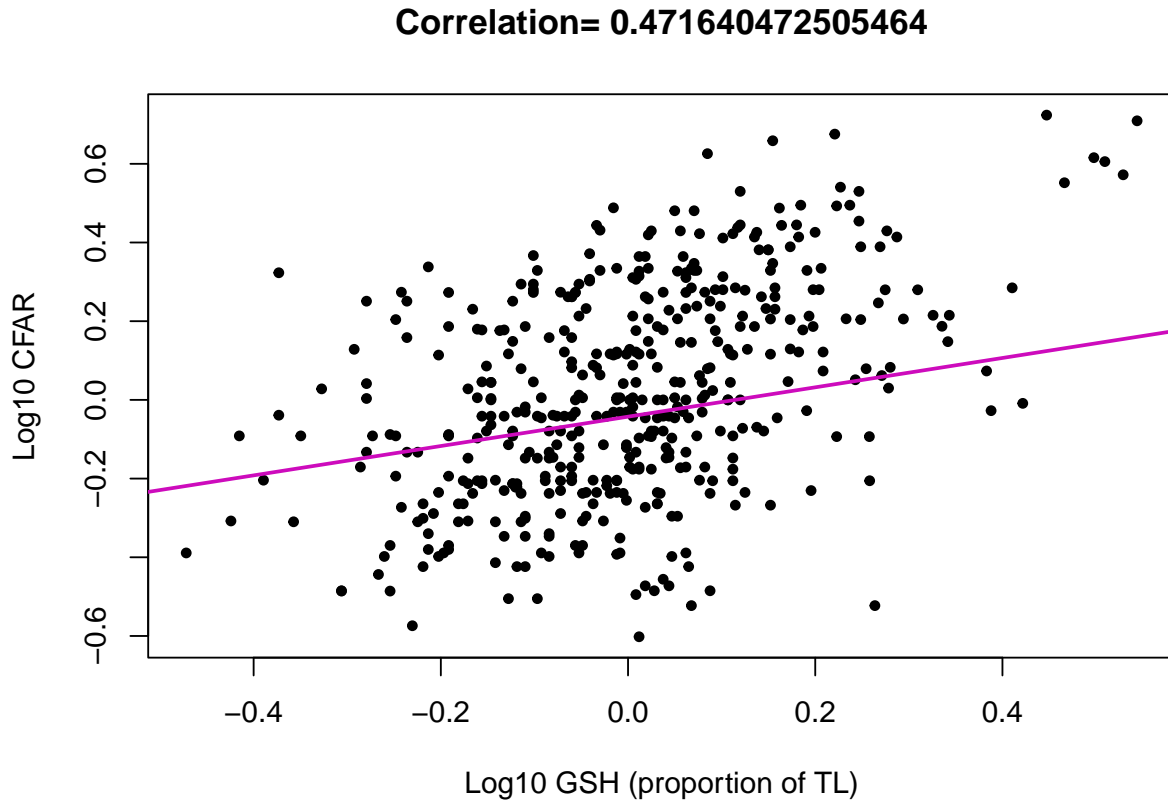
Table 20: PGLS summary

	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0426521	0.0610948	-0.6981305	0.4854546	-0.1623957	0.0770914
Log10MeanGSH_centered	0.3729626	0.0587488	6.3484281	0.0000000	0.2578170	0.4881081
PrimaryHabitatDeepwater	0.0139319	0.0264094	0.5275378	0.5980790	-0.0378295	0.0656934
PrimaryHabitatPelagic	0.1500620	0.0390274	3.8450405	0.0001378	0.0735697	0.2265543

Model 9 - CFAR ~ GSH + PrimaryHabitat + Phylogeny

1. PGLS model

```
pglsMod5 <- gls(Log10CFAR ~ Log10MeanGSH_centered + PrimaryHabitat,
  correlation = corPagel(phy = SampleTree, value = 0.5, fixed = F, form = ~Binomial),
  data = GSH_df_pgls, method = "ML")
```



2. brms model

```
HabitatPhylo <- brm(Log10CFAR ~ Log10MeanGSH_centered + Log10MaxSize_centered + (1|gr(Binomial, cov = A)),
  data = GSH_df_pgls,
  family = gaussian(),
  data2 = list(A = A),
  prior = BS_prior2,
  sample_prior = TRUE, chains = 4, cores = 2)
```

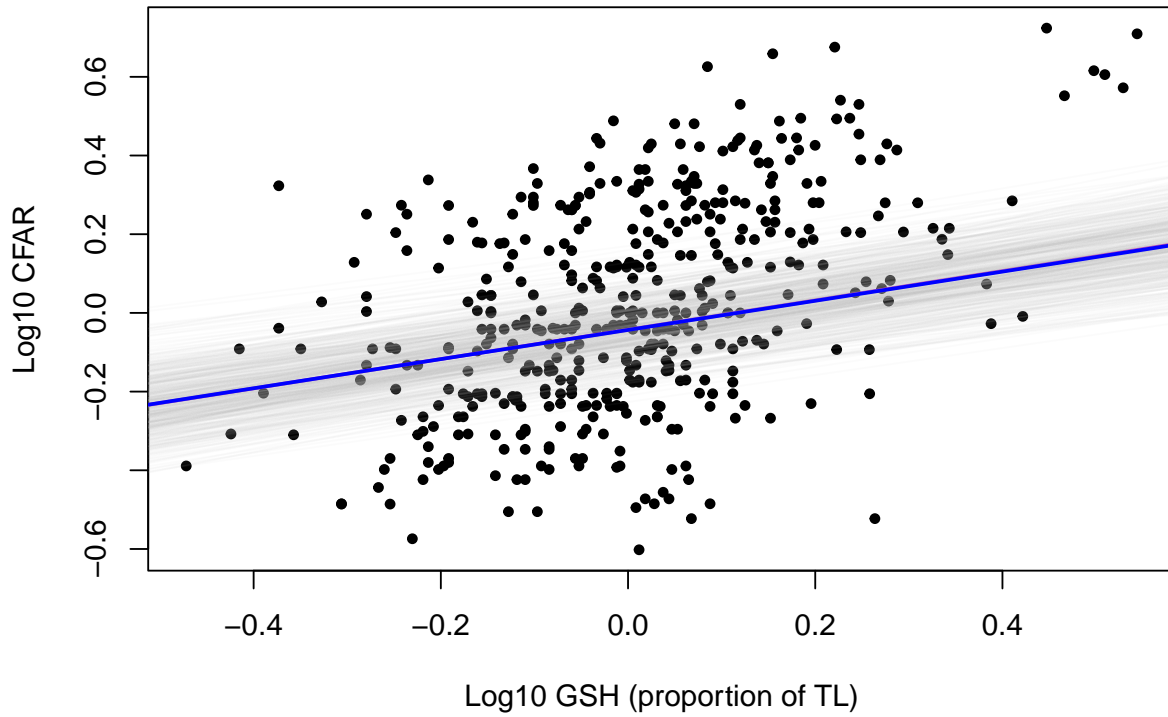
Table 21: brms model 9 summary

	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0433191	0.0623802	-0.1642391	0.0811959
Log10MeanGSH_centered	0.3706046	0.0604604	0.2538407	0.4864557
PrimaryHabitatDeepwater	0.0134363	0.0266982	-0.0361910	0.0659098
PrimaryHabitatPelagic	0.1495636	0.0396811	0.0750472	0.2276969

Table 22: STAN model 8 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0432051	0.0013669	0.0639528	-0.1698045	0.0849299	2189.068	1.0006248
beta	0.3719482	0.0013547	0.0609737	0.2505965	0.4928009	2025.682	1.0011433
deepwater	0.0152370	0.0005615	0.0262145	-0.0367034	0.0678131	2179.493	0.9997415
pelagic	0.1505860	0.0008176	0.0394523	0.0719386	0.2262333	2328.220	1.0006759
sigma	0.0438643	0.0001305	0.0049446	0.0354849	0.0542555	1436.673	0.9985969
lambda	0.6791834	0.0012515	0.0478577	0.5819305	0.7682589	1462.287	0.9989043

Correlation= 0.471640472505464



3. STAN Model

Correlation= 0.471640472505464

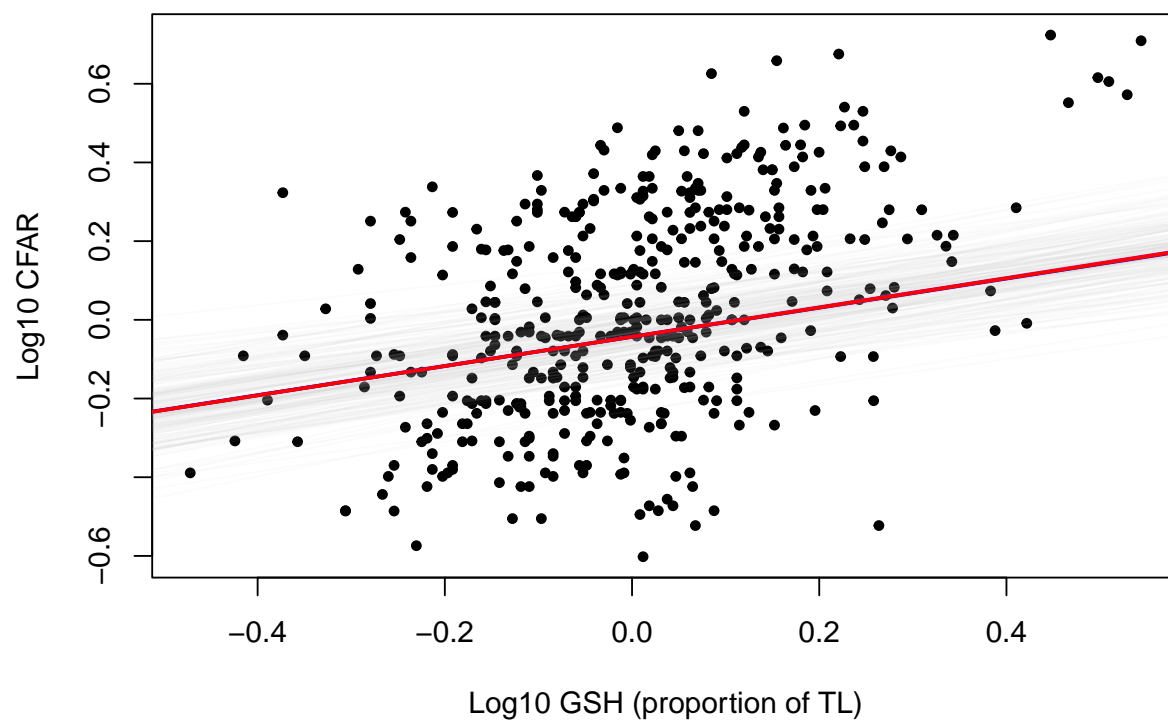


Table 23: PGLS summary

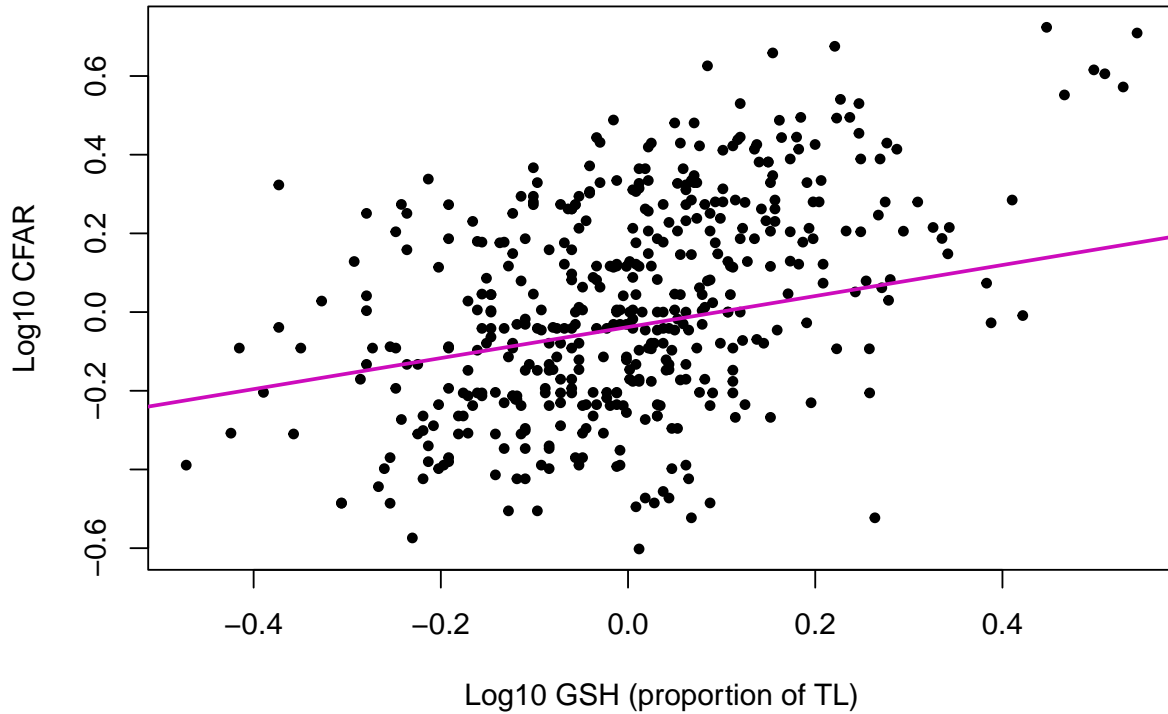
	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0380642	0.0600813	-0.6335439	0.5267004	-0.1558215	0.0796931
Log10MeanGSH_centered	0.3942985	0.1149440	3.4303530	0.0006584	0.1690124	0.6195846
PrimaryHabitatDeepwater	-0.0012632	0.0270931	-0.0466234	0.9628340	-0.0543646	0.0518382
PrimaryHabitatPelagic	0.1089660	0.0431700	2.5241114	0.0119421	0.0243543	0.1935777
Log10MeanGSH_centered:PrimaryHabitatDeepwater	-0.0946536	0.1297042	-0.7297649	0.4659136	-0.3488692	0.1595520
Log10MeanGSH_centered:PrimaryHabitatPelagic	0.3197980	0.1808652	1.7681563	0.0777123	-0.0346913	0.6940806

Model 10 - CFAR ~ GSH * PrimaryHabitat + Phylogeny

1. PGLS model

```
pglsMod6 <- gls(Log10CFAR ~ Log10MeanGSH_centered * PrimaryHabitat,
  correlation = corPagel(phy = SampleTree, value = 0.5, fixed = F, form = ~Binomial),
  data = GSH_df_pgls, method = "ML")
```

Correlation= 0.471640472505464



2. BRMS Model

```
HabitatPhylo2 <- brm(Log10CFAR ~ Log10MeanGSH_centered * PrimaryHabitat + (1|gr(Binomial, cov = A)),
  data = GSH_df_pgls,
```

Table 24: brms model 10 summary

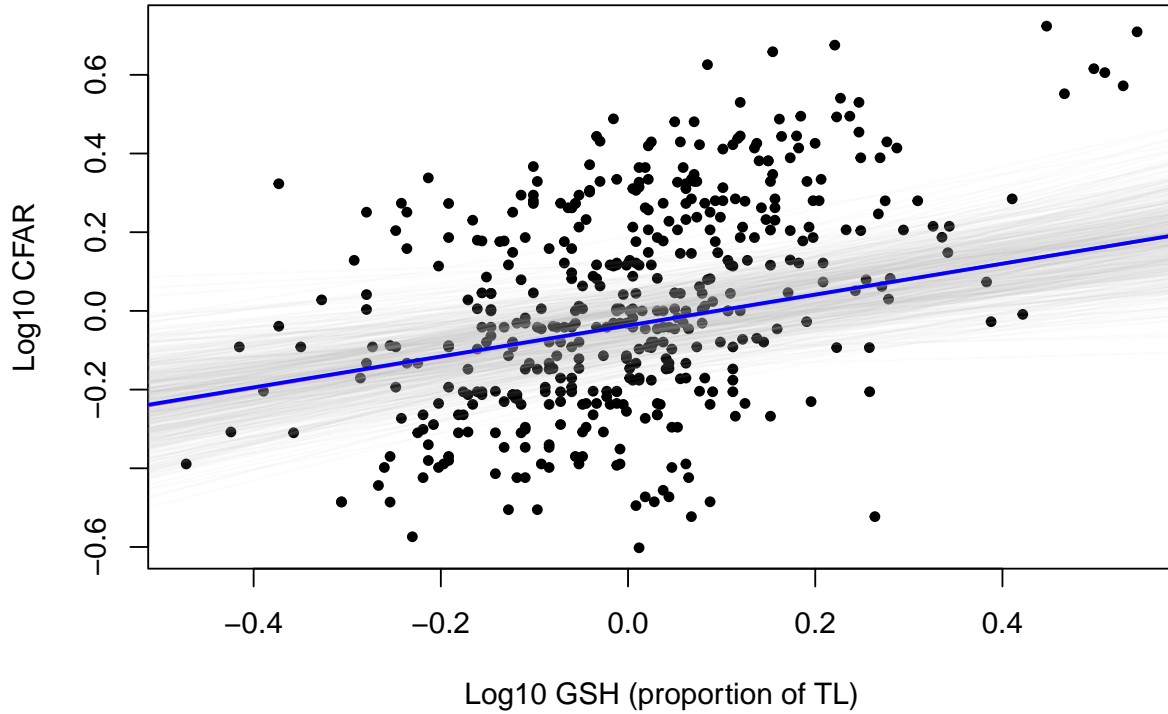
	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0370099	0.0629477	-0.1631366	0.0823122
Log10MeanGSH_centered	0.3930570	0.1194236	0.1502121	0.6230306
PrimaryHabitatDeepwater	-0.0009378	0.0274507	-0.0539797	0.0527488
PrimaryHabitatPelagic	0.1086930	0.0431179	0.0264042	0.1928199
Log10MeanGSH_centered:PrimaryHabitatDeepwater	-0.0931295	0.1334098	-0.3523780	0.1707157
Log10MeanGSH_centered:PrimaryHabitatPelagic	0.371813	0.1831236	-0.0368259	0.6889472

```

family = gaussian(),
data2 = list(A = A),
prior = HabitatPhylo_prior2,
sample_prior = TRUE, chains = 4, cores = 4)

```

Correlation= 0.471640472505464



3. STAN Model

Table 25: STAN model 8 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0353942	0.0013946	0.0606516	-0.1567340	0.0809660	1891.374	0.9990718
beta	0.3923793	0.0028290	0.1121529	0.1746769	0.6117809	1571.697	1.0023520
deepwater	-0.0025071	0.0006547	0.0278236	-0.0572648	0.0497482	1806.228	0.9988779
pelagic	0.1061112	0.0010039	0.0434120	0.0235064	0.1933592	1870.157	1.0003583
GSH:deepwater	0.0921483	0.0031392	0.1246842	-0.3383413	0.1490137	1577.579	1.0035480
GSH:pelagic	0.3230165	0.0043783	0.1768289	-0.0299055	0.6558215	1631.154	1.0027676
sigma	0.0432303	0.0001250	0.0048897	0.0344387	0.0537310	1531.313	1.0005741
lambda	0.6748741	0.0011765	0.0480115	0.5765192	0.7619337	1665.233	1.0001277

Correlation= 0.471640472505464

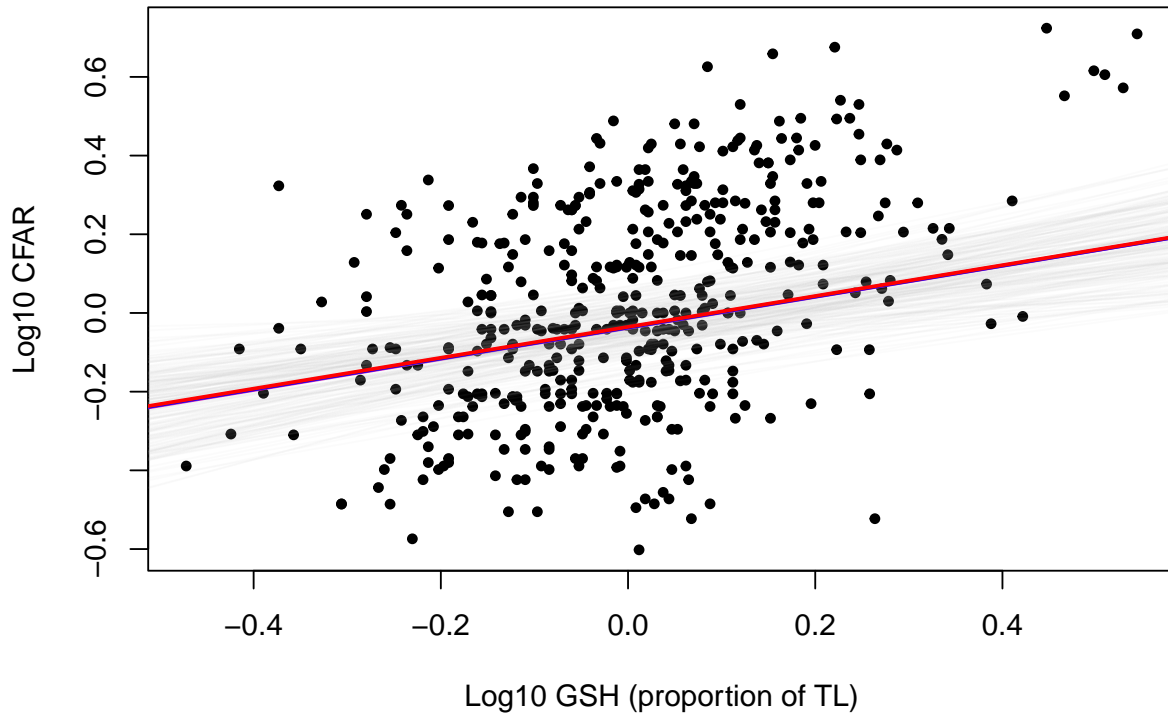


Table 26: PGLS summary

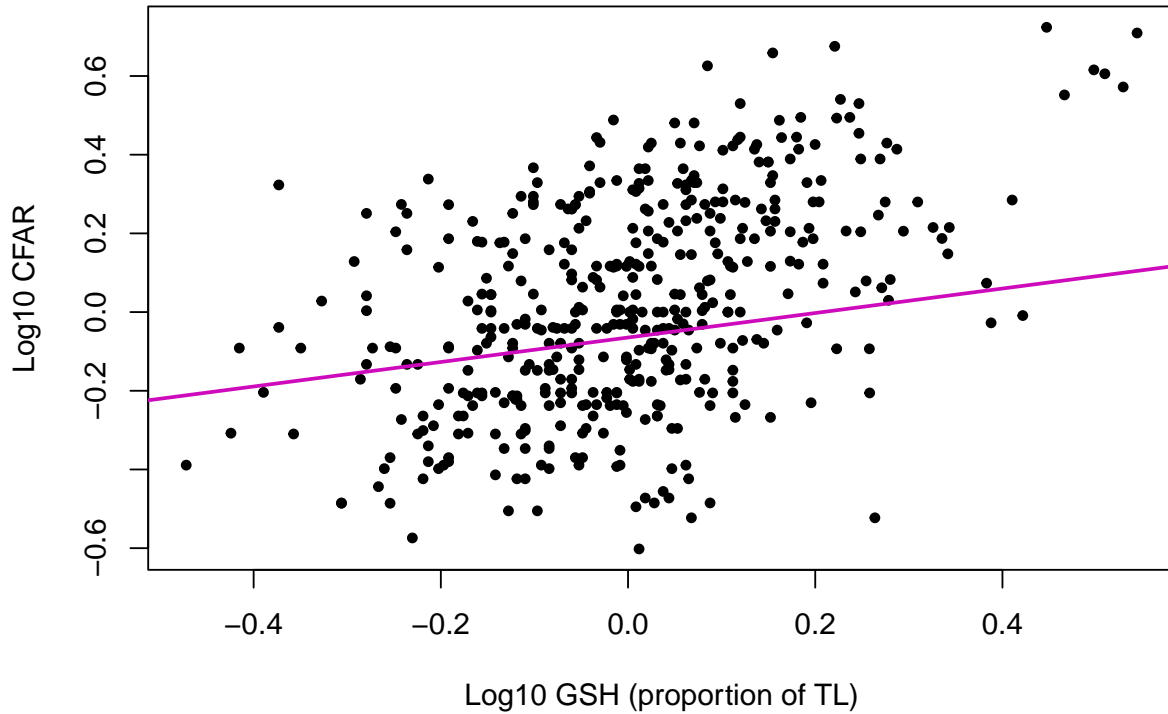
	Value	Std.Error	t-value	p-value	2.5 %	
(Intercept)	-0.0646193	0.0577730	-1.1185034	0.2639488	-0.1778522	0.0
Log10MeanGSH_centered	0.3111825	0.0594286	5.2362390	0.0000003	0.1947045	0.4
Log10MaxSize_centered	0.1234860	0.0351974	3.5083817	0.0004962	0.0545003	0.1
PrimaryHabitatDeepwater	0.0069539	0.0258660	0.2688422	0.7881743	-0.0437425	0.0
PrimaryHabitatPelagic	0.0990615	0.0399968	2.4767337	0.0136256	0.0206692	0.1
Log10MeanGSH_centered:Log10MaxSize_centered	0.3443064	0.1284790	2.6798657	0.0076353	0.0924922	0.5

Model 11 - CFAR ~ GSH * MaxSize + PrimaryHabitat + Phylogeny

1. PGLS model

```
pglsMod8 <- gls(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered + PrimaryHabitat,
  correlation = corPagel(phy = SampleTree, value = 0.5, fixed = F, form = ~Binomial),
  data = GSH_df_pgls, method = "ML")
```

Correlation= 0.471640472505464



2. BRMS Model

```
SizeHabitatModel <- brm(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered + PrimaryHabitat + (1
  data = GSH_df_pgls,
```

Table 27: brms model 11 summary

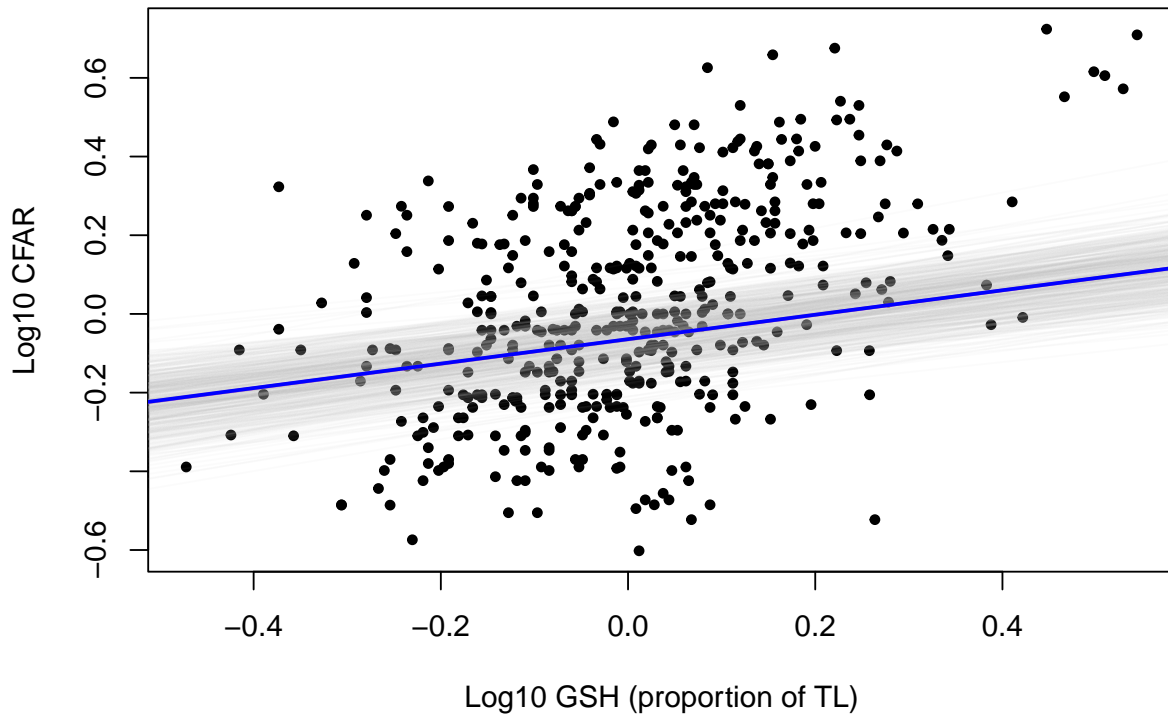
	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0641073	0.0581580	-0.1799243	0.0481271
Log10MeanGSH_centered	0.3107214	0.0595552	0.1927469	0.4271668
Log10MaxSize_centered	0.1234986	0.0356178	0.0534569	0.1925711
PrimaryHabitatDeepwater	0.0070842	0.0268180	-0.0460209	0.0592925
PrimaryHabitatPelagic	0.0991838	0.0418159	0.0166001	0.1807377
Log10MeanGSH_centered:Log10MaxSize_centered	0.1270241	0.0906405	0.0906405	0.5860575

```

family = gaussian(),
data2 = list(A = A),
prior = SizeHabitatMod_prior,
sample_prior = TRUE, chains = 4, cores = 4)

```

Correlation= 0.471640472505464

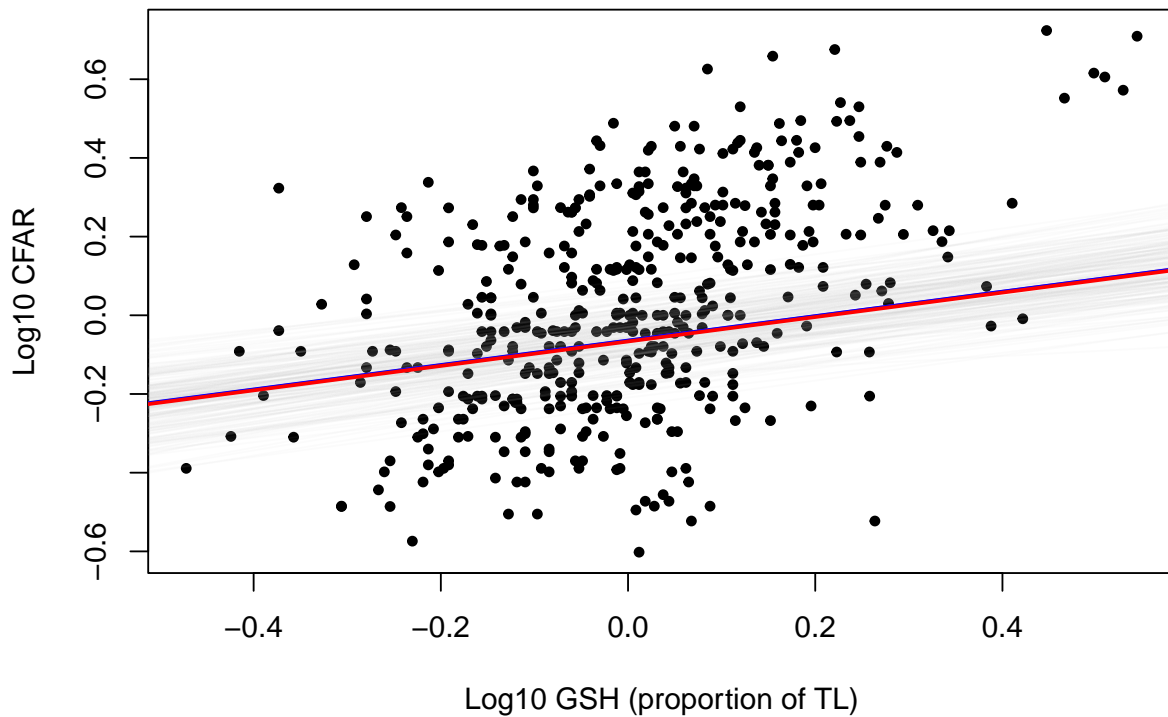


3. STAN Model

Table 28: STAN model 8 summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0665577	0.0023477	0.0596609	-0.1803131	0.0444530	645.8081	1.0027281
beta	0.3106144	0.0022482	0.0571246	0.2034375	0.4171056	645.5966	0.9997237
beta2 (size)	0.1221065	0.0014753	0.0360779	0.0525489	0.1910845	597.9881	0.9991238
deepwater	0.0085882	0.0011085	0.0253557	-0.0396565	0.0574381	523.2269	1.0042187
pelagic	0.1010546	0.0016374	0.0373201	0.0266434	0.1804577	519.4994	1.0036065
GSH:MaxSize	0.3419927	0.0047183	0.1251360	0.0907834	0.5877307	703.3822	0.9988565
sigma	0.0405081	0.0001881	0.0045690	0.0325699	0.0507079	590.0525	1.0019658
lambda	0.6622346	0.0019413	0.0501537	0.5575898	0.7547391	667.4532	1.0045633

Correlation= 0.471640472505464



BRMS LOO analysis

LOO compare

```
## Warning: Found 13 observations with a pareto_k > 0.7 in model 'Model_simple'. It
## is recommended to set 'moment_match = TRUE' in order to perform moment matching
## for problematic observations.
```

```
## Warning: Found 9 observations with a pareto_k > 0.7 in model 'Model_BS'. It is
## recommended to set 'moment_match = TRUE' in order to perform moment matching for
```

```
## problematic observations.
```

```
## Warning: Found 12 observations with a pareto_k > 0.7 in model 'Model_BS2'. It is
## recommended to set 'moment_match = TRUE' in order to perform moment matching for
## problematic observations.
```

```
## Warning: Found 7 observations with a pareto_k > 0.7 in model 'HabitatPhylo'. It
## is recommended to set 'moment_match = TRUE' in order to perform moment matching
## for problematic observations.
```

```
## Warning: Found 11 observations with a pareto_k > 0.7 in model 'HabitatPhylo2'.
## It is recommended to set 'moment_match = TRUE' in order to perform moment
## matching for problematic observations.
```

```
## Warning: Found 8 observations with a pareto_k > 0.7 in model 'SizeHabitatModel'.
## It is recommended to set 'moment_match = TRUE' in order to perform moment
## matching for problematic observations.
```

	elpd_diff	se_diff	elpd_loo	se_elpd_loo	p_loo	se_p_loo	looic	se_looic
SizeHabitatModel	0.000000	0.000000	264.9064	14.69849	112.2488	6.201853	-	29.39698
Model_BS	-	2.606531	263.5209	14.65287	114.7254	6.257732	529.8129	-
Model_BS2	1.385534	-	260.3270	15.27443	117.3638	6.964097	527.0418	-
HabitatPhylo	4.579458	5.653521	255.1556	15.08340	117.7633	7.086189	-	30.54885
HabitatPhylo2	9.750859	-	254.8301	14.28666	117.5718	6.447159	520.6539	-
Model_simple	10.076306	5.341777	251.6618	16.18877	124.2187	8.200400	510.3111	-
	13.244643	9.727113					509.6602	32.37753
							503.3236	

LOO model weights

```
loo_model_weights(brms_loo_phylo_list)
```

```
## Method: stacking
```

```
## -----
```

```
##          weight
```

```
## model1 0.197
```

```
## model2 0.000
```

```
## model3 0.147
```

```
## model4 0.000
```

```
## model5 0.000
```

```
## model6 0.656
```