

# Ch. 1 - Model comparisons

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## 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

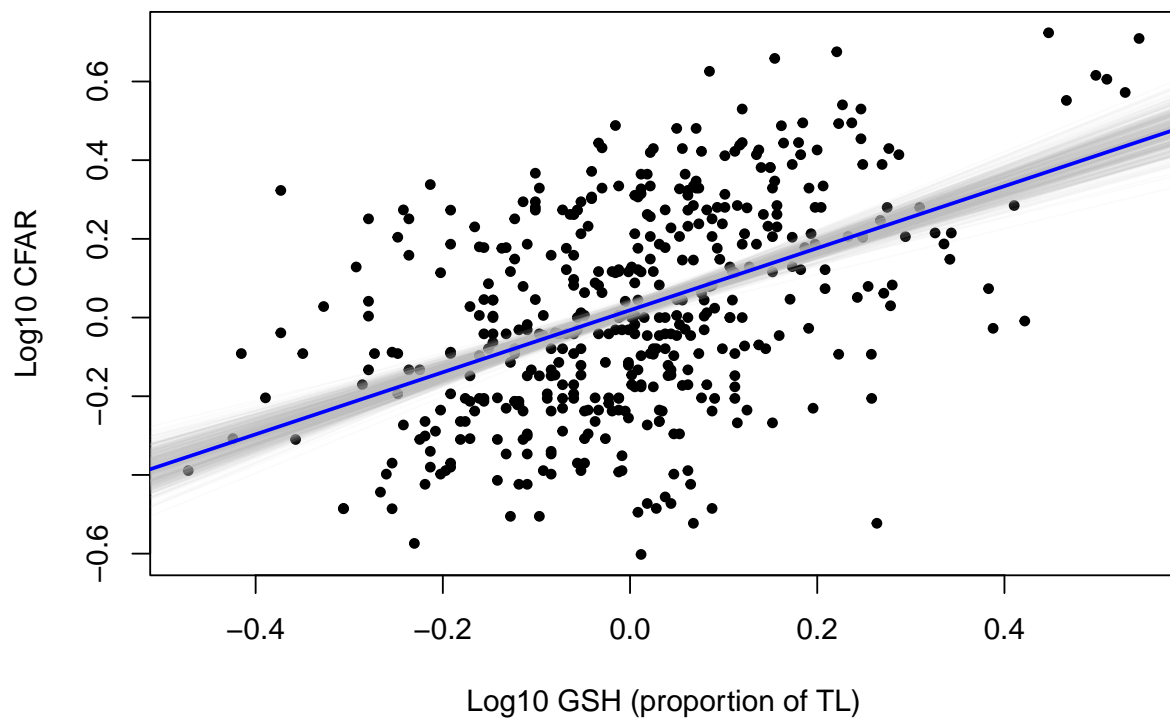
1. brms model

```
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);

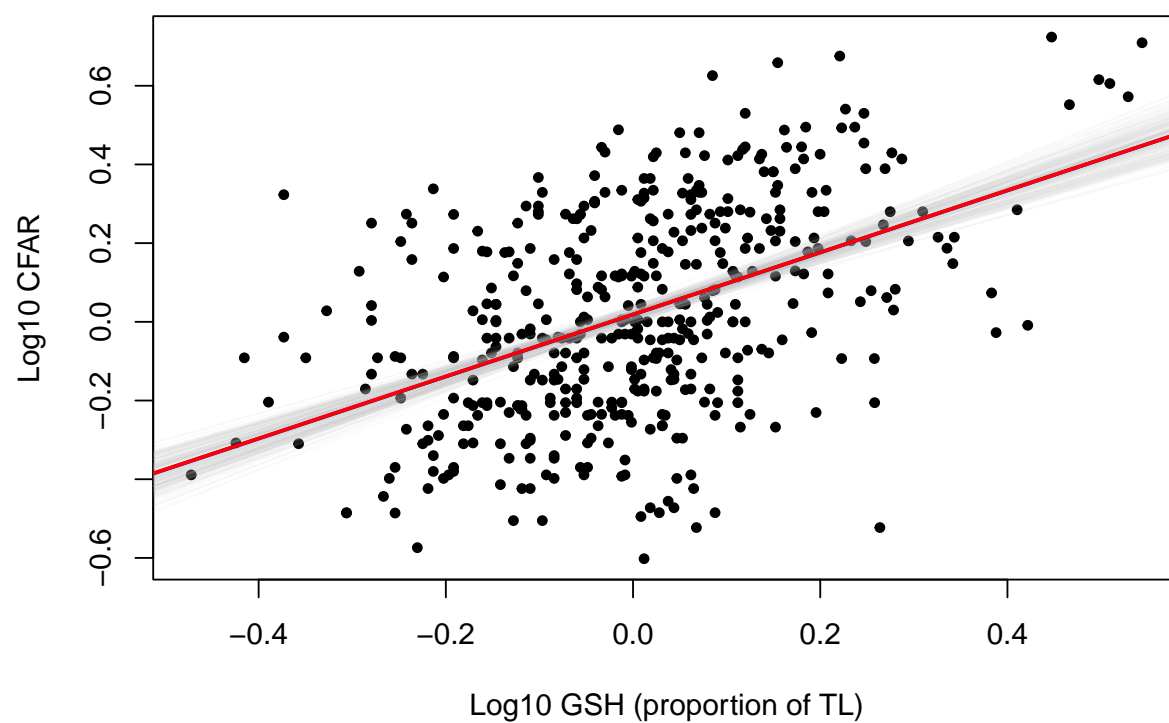
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 2: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0189506	0.0000841	0.0111648	-0.0026424	0.0408163	17615.82	0.9999231
beta	0.7883361	0.0005644	0.0695872	0.6515938	0.9243961	15201.24	1.0000195
sigma	0.2359767	0.0000613	0.0079081	0.2209879	0.2520731	16623.76	0.9999651

**Correlation= 0.471640472505464**



## Model 2 - CFAR ~ GSH \* Max Size

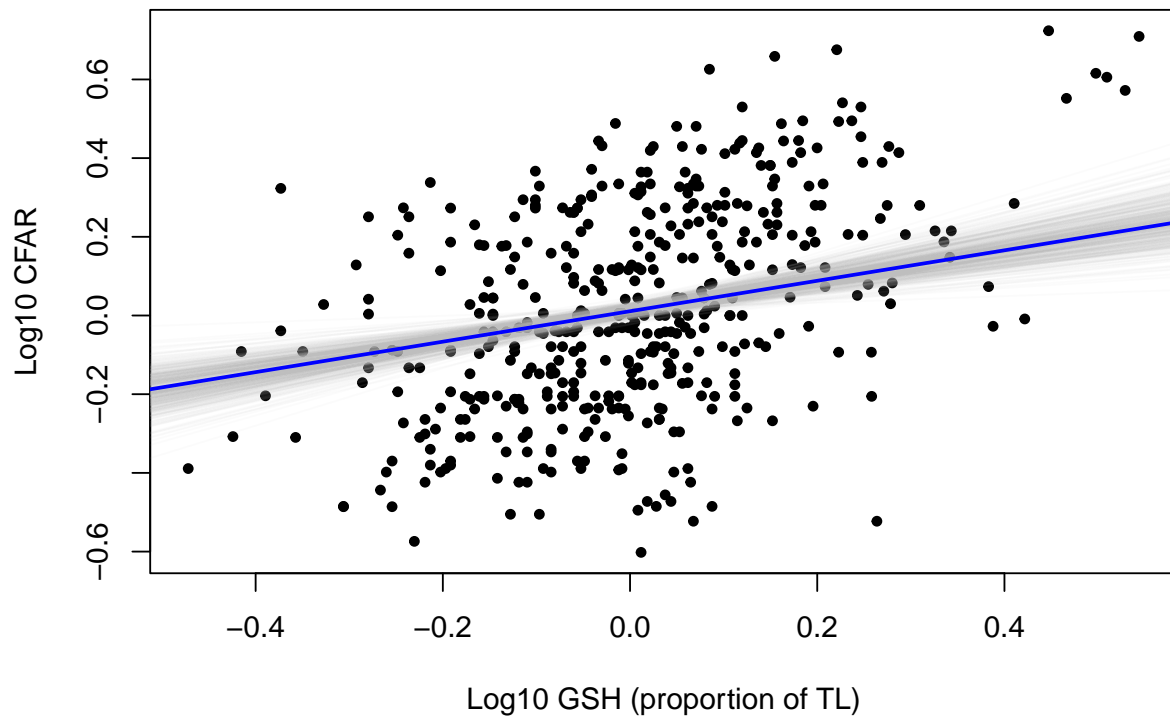
### 1. brms model

```
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);

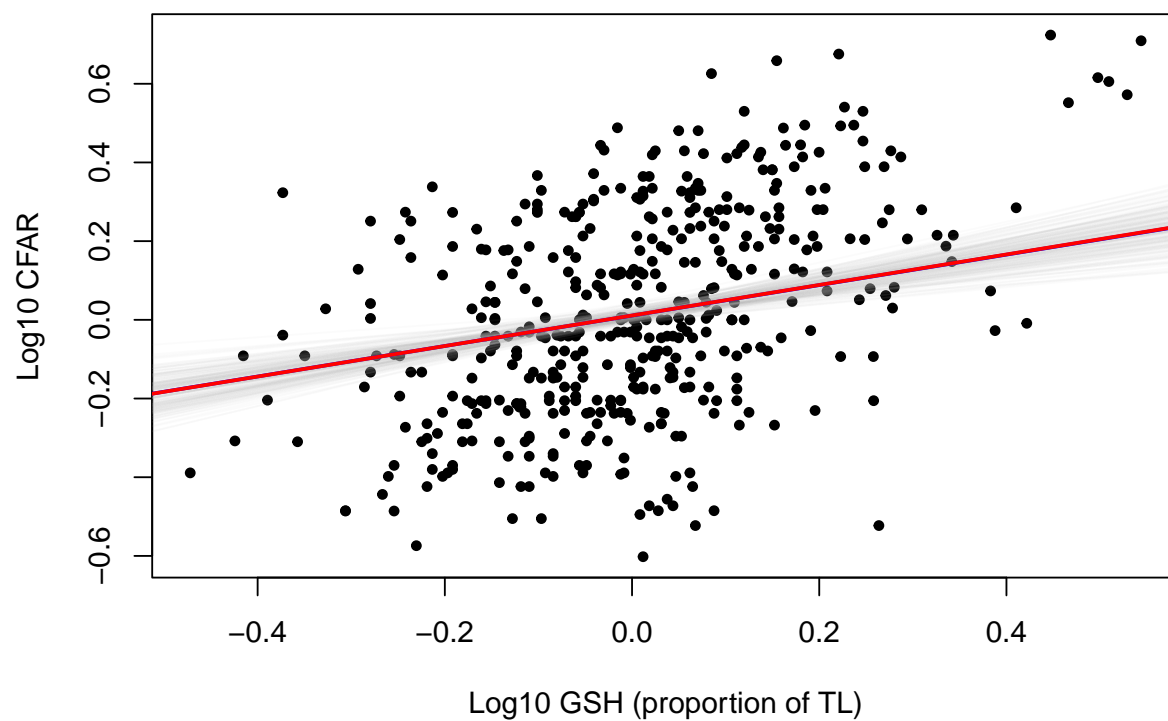
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 4: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0110269	0.0000920	0.0115361	-0.0113001	0.0335334	15731.13	0.9999386
beta	0.3880005	0.0006566	0.0819559	0.2280443	0.5475787	15577.48	1.0000483
beta2	0.3045951	0.0003623	0.0435066	0.2209701	0.3905040	14421.90	1.0000831
(size)							
GSH:Size	0.2626225	0.0013903	0.1648556	-0.0604101	0.5849597	14060.55	1.0001111
sigma	0.2211292	0.0000583	0.0073257	0.2074078	0.2362670	15764.83	1.0001402

Correlation= 0.471640472505464





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

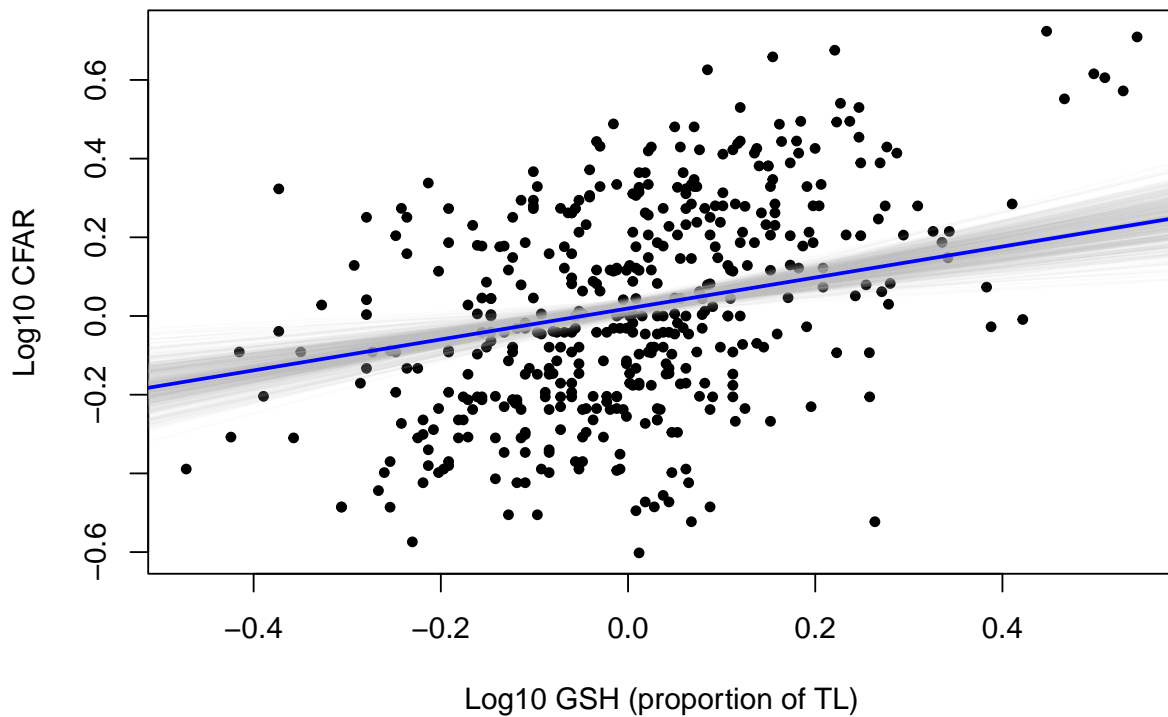
#### 1. brms model

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

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);

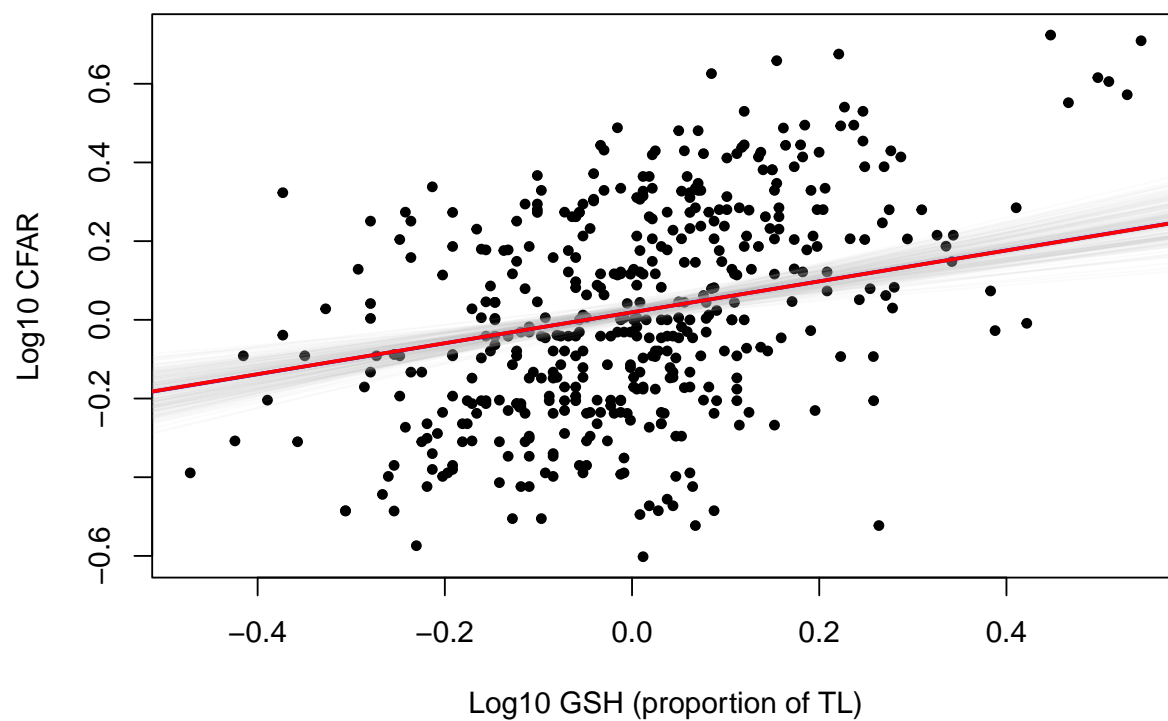
    y ~ normal(alpha + x * beta , sigma);
}

```

Table 6: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0191617	0.0000906	0.0105192	-0.0013327	0.0400324	13478.94	0.9999506
beta	0.3927275	0.0007432	0.0817446	0.2336588	0.5511781	12096.35	1.0000262
beta2	0.3254458	0.0003768	0.0411819	0.2450405	0.4056256	11947.87	1.0000978
(size)							
sigma	0.2214230	0.0000601	0.0073302	0.2075638	0.2363629	14864.18	0.9999069

Correlation= 0.471640472505464



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

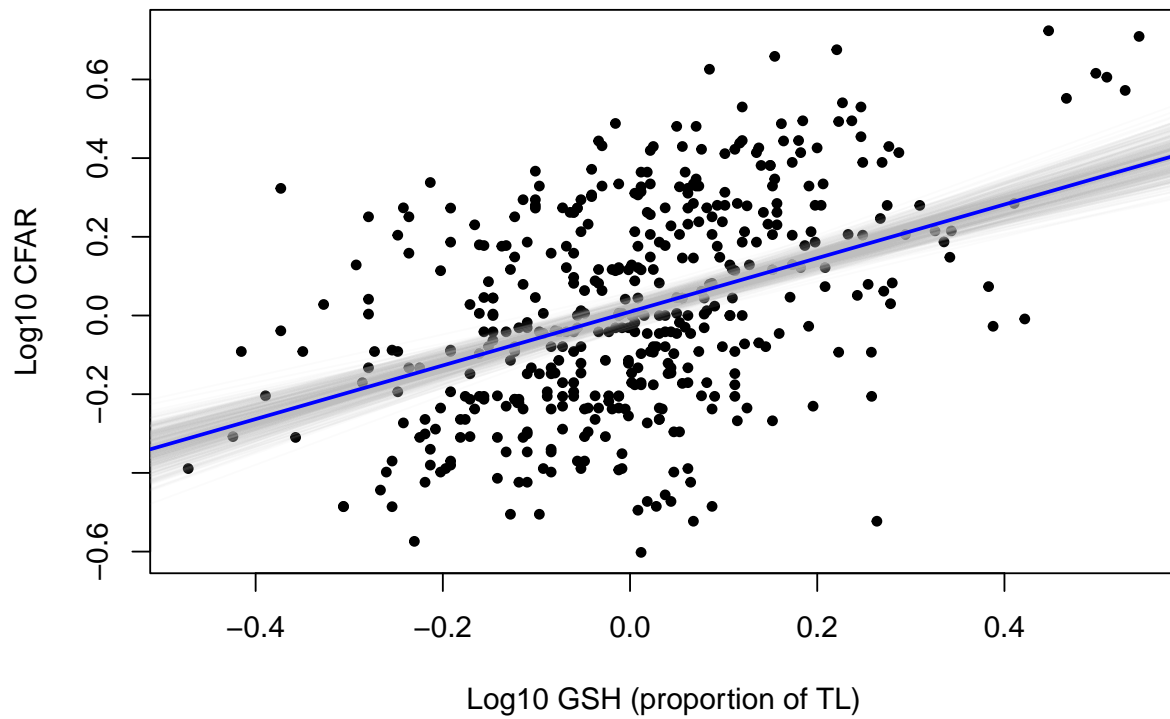
### 1. brms model

```
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);

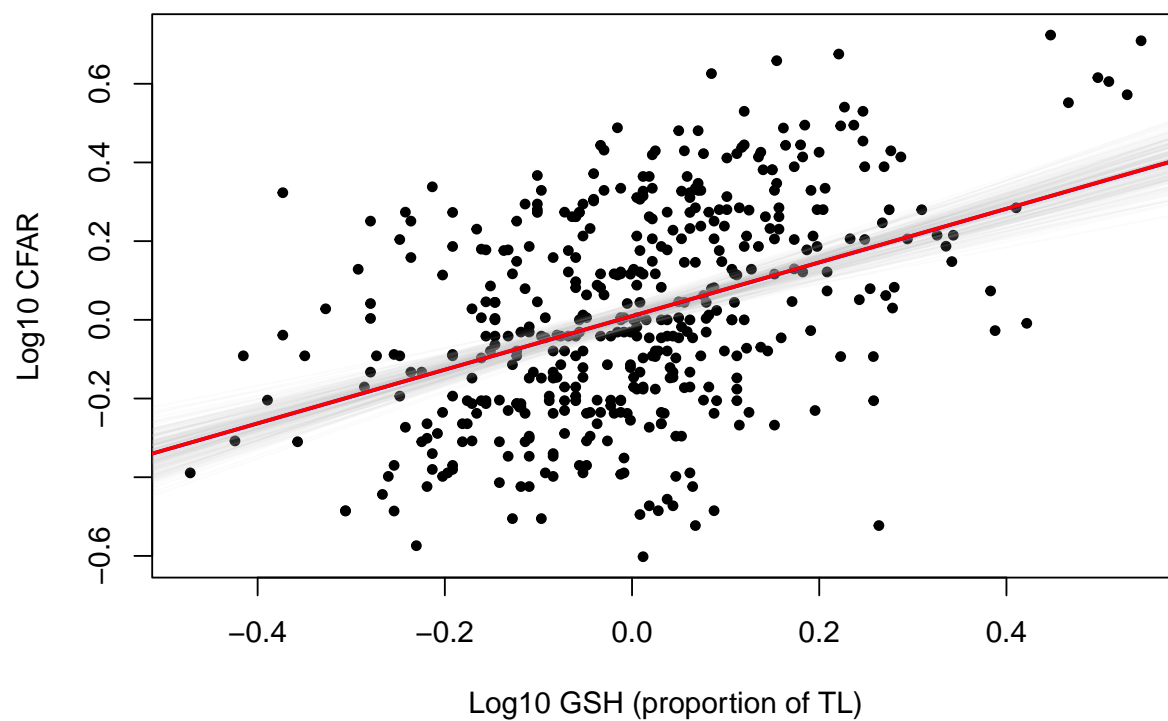
  y ~ normal(alpha + x * beta , sigma);
}

```

Table 8: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	0.0097769	0.0001614	0.0163755	-0.0223144	0.0417903	10298.56	0.9999514
beta	0.6820382	0.0006386	0.0740327	0.5372126	0.8296146	13438.32	0.9999372
deepwater	-0.0099067	0.0002293	0.0230925	-0.0550870	0.0354064	10144.70	0.9999298
pelagic	0.2490748	0.0004065	0.0487259	0.1533813	0.3426777	14365.85	0.9999028
sigma	0.2294194	0.0000637	0.0076547	0.2151361	0.2450414	14462.87	1.0000201

**Correlation= 0.471640472505464**



Model 5 - CFAR ~ GSH \* PrimaryHabitat

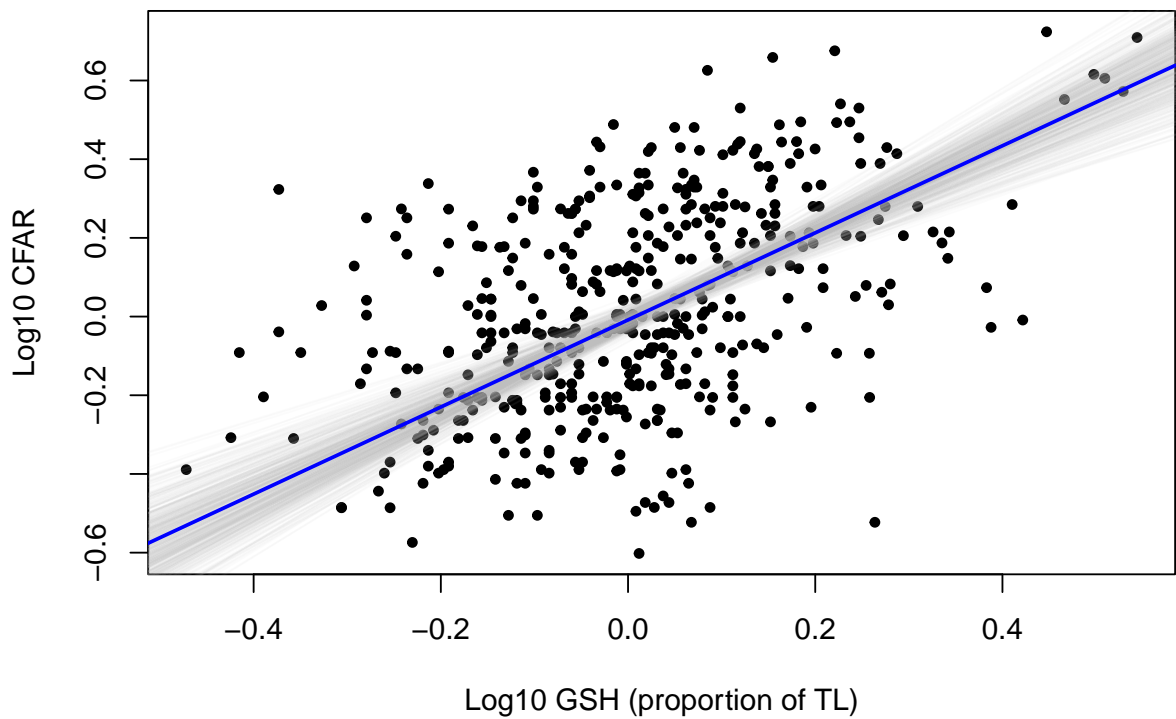
1. brms model

```
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);
}

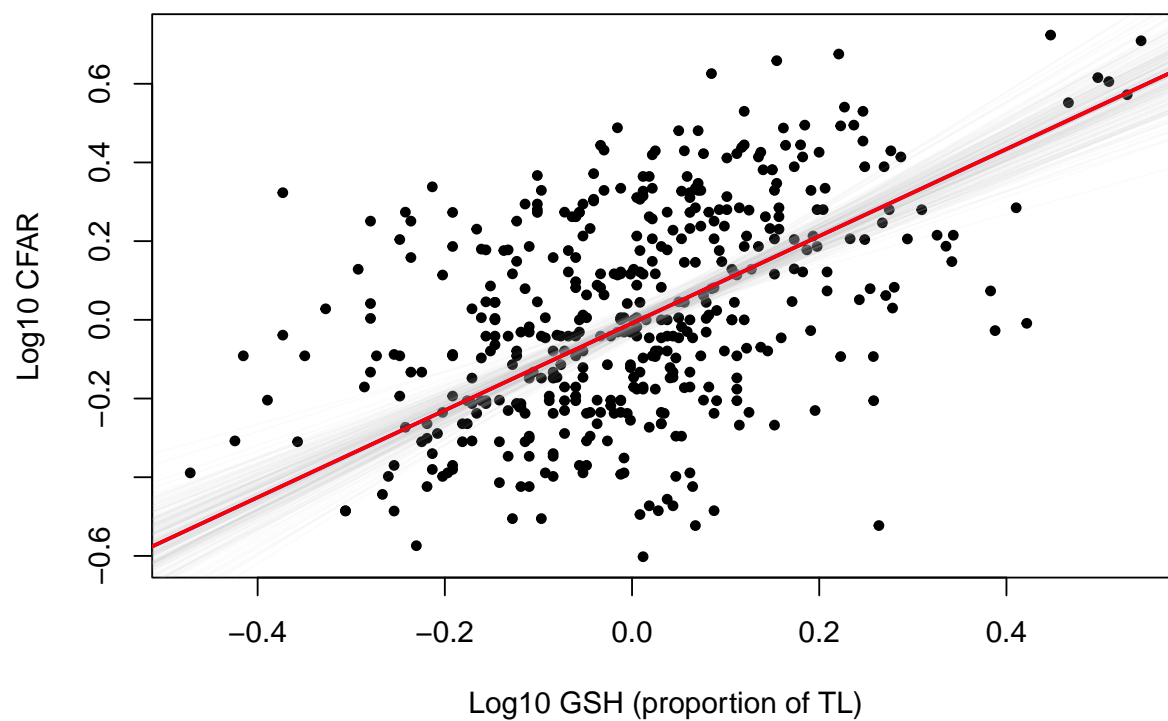
```

Table 10: STAN model summary

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
alpha	-0.0086716	0.0001626	0.0169351	-0.0418434	0.0252055	10846.907	1.0004082
beta	1.1064165	0.0012963	0.1275497	0.8589251	1.3624717	9681.178	1.0000406
deepwater	-0.0031396	0.0002169	0.0231841	-0.0483342	0.0423330	11421.254	1.0001209
pelagic	0.2909246	0.0005196	0.0567046	0.1782580	0.4013676	11911.013	1.0002852
GSH:deepwater	0.6386898	0.0015781	0.1613494	-0.9593101	-0.3311171	10453.536	0.9999643
GSH:pelagic	-0.5625077	0.0022335	0.2226852	-0.9989797	-0.1223004	9940.345	0.9999787
sigma	0.2258792	0.0000638	0.0076499	0.2114378	0.2412959	14384.468	1.0001323



**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_postion"))
```

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

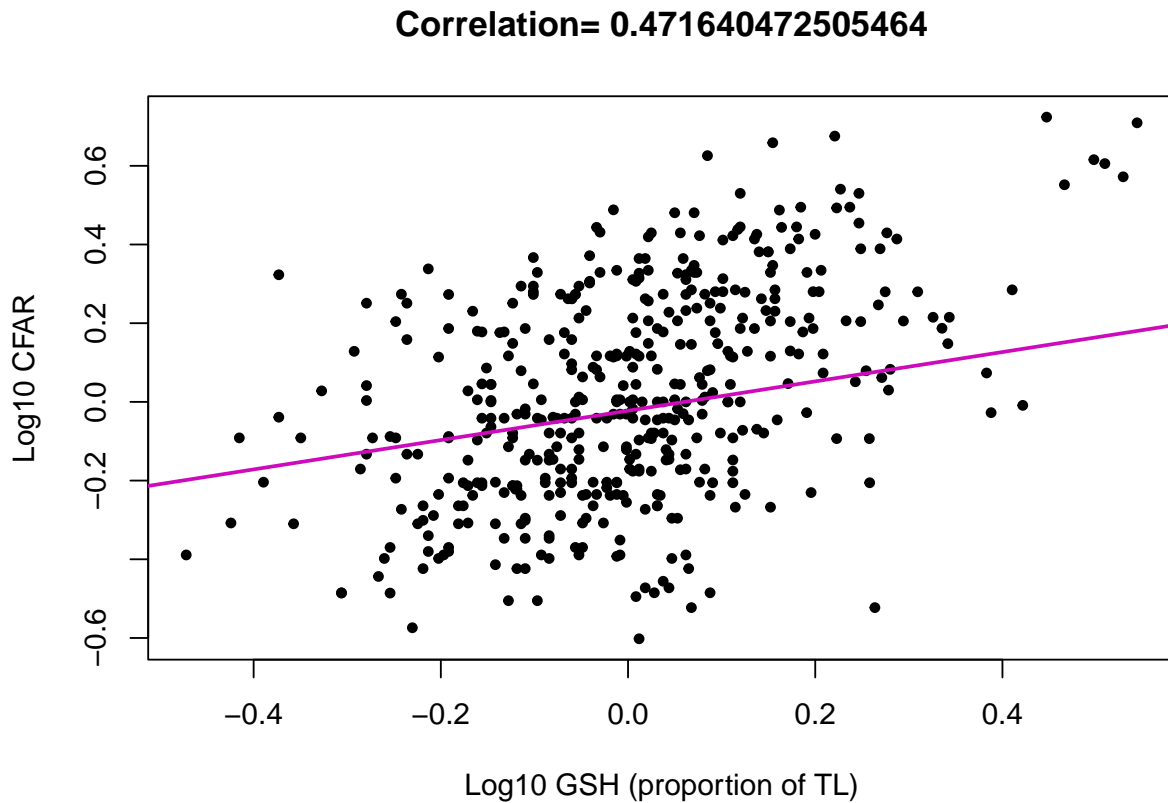
	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0224754	0.0628286	-0.3577261	0.7207146	-0.1456172	0.1006663
Log10MeanGSH_centered	0.3728837	0.0595042	6.2665128	0.0000000	0.2562576	0.4895097

## 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")
```



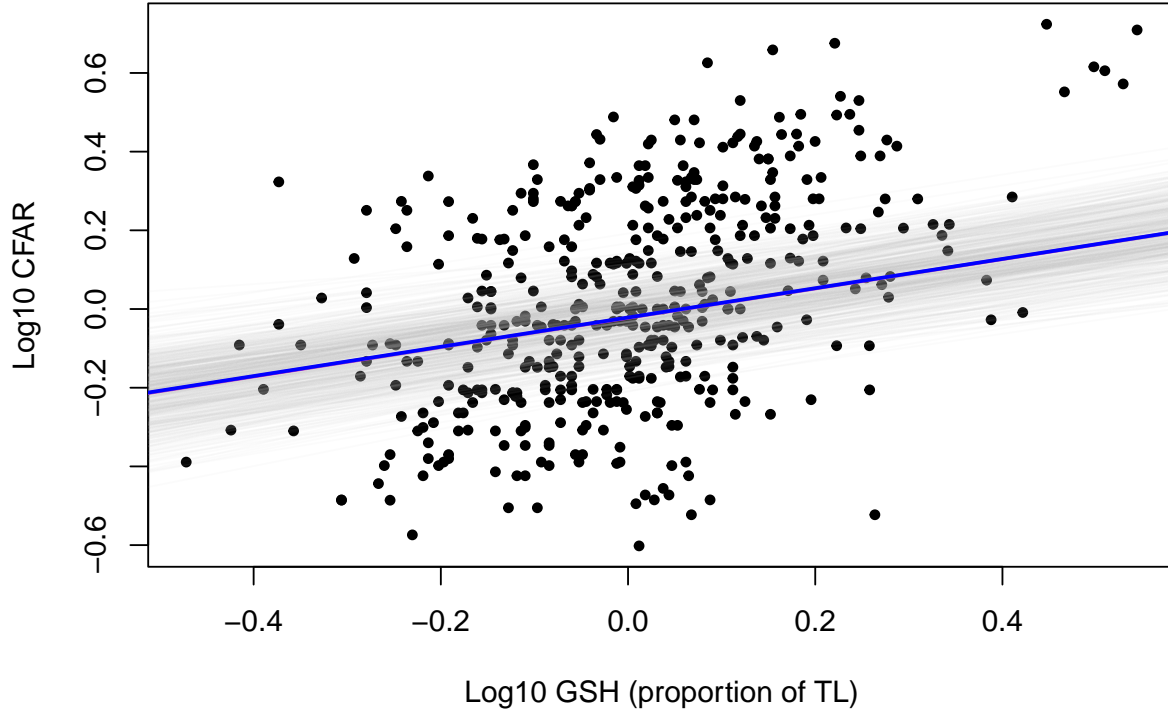
#### 2. brms model

```
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	-0.0214910	0.0635787	-0.1460351	0.1025128
Log10MeanGSH_centered	0.3721942	0.0612686	0.2520485	0.4937324

**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	-0.0224102	0.0005257	0.0629641	-0.1461487	0.1014901	14346.624	0.9998965
beta	0.3729818	0.0005293	0.0610750	0.2560190	0.4946870	13312.186	1.0000800
sigma	0.0474255	0.0000571	0.0052967	0.0382611	0.0589428	8611.627	1.0001556
lambda	0.7049128	0.0004727	0.0440888	0.6143114	0.7865885	8698.670	1.0001259

```

    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**

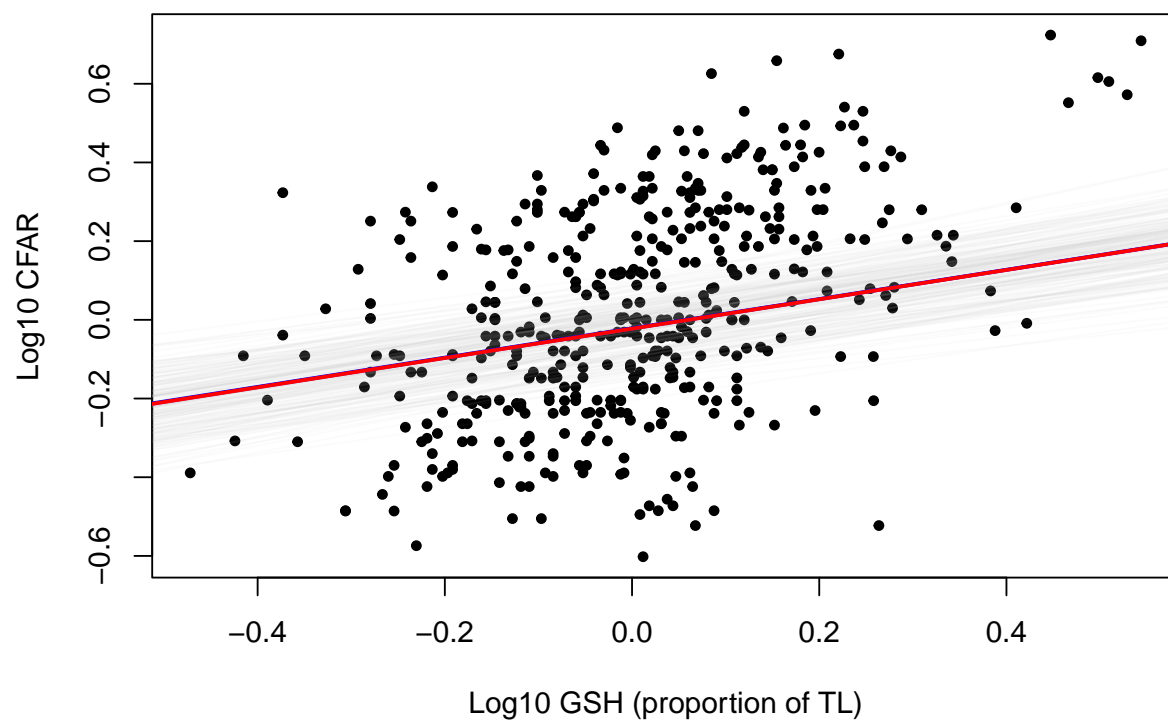


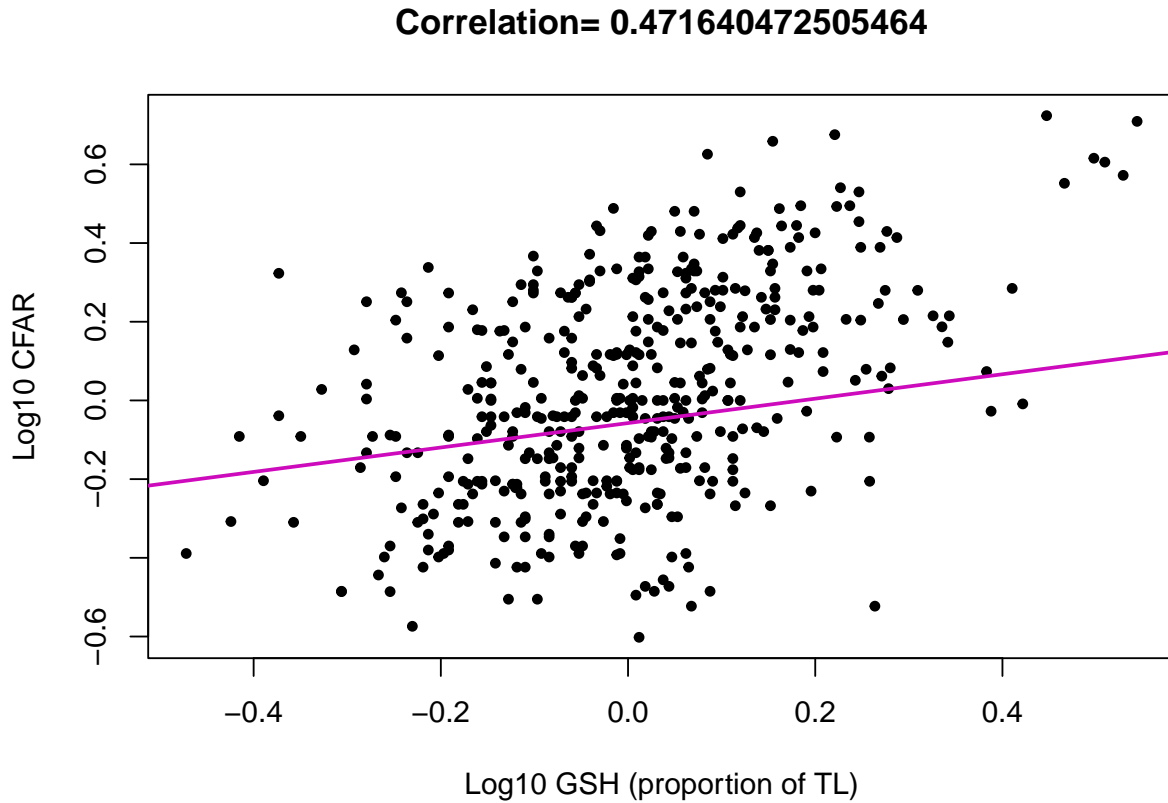
Table 14: PGLS summary

	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 =
```

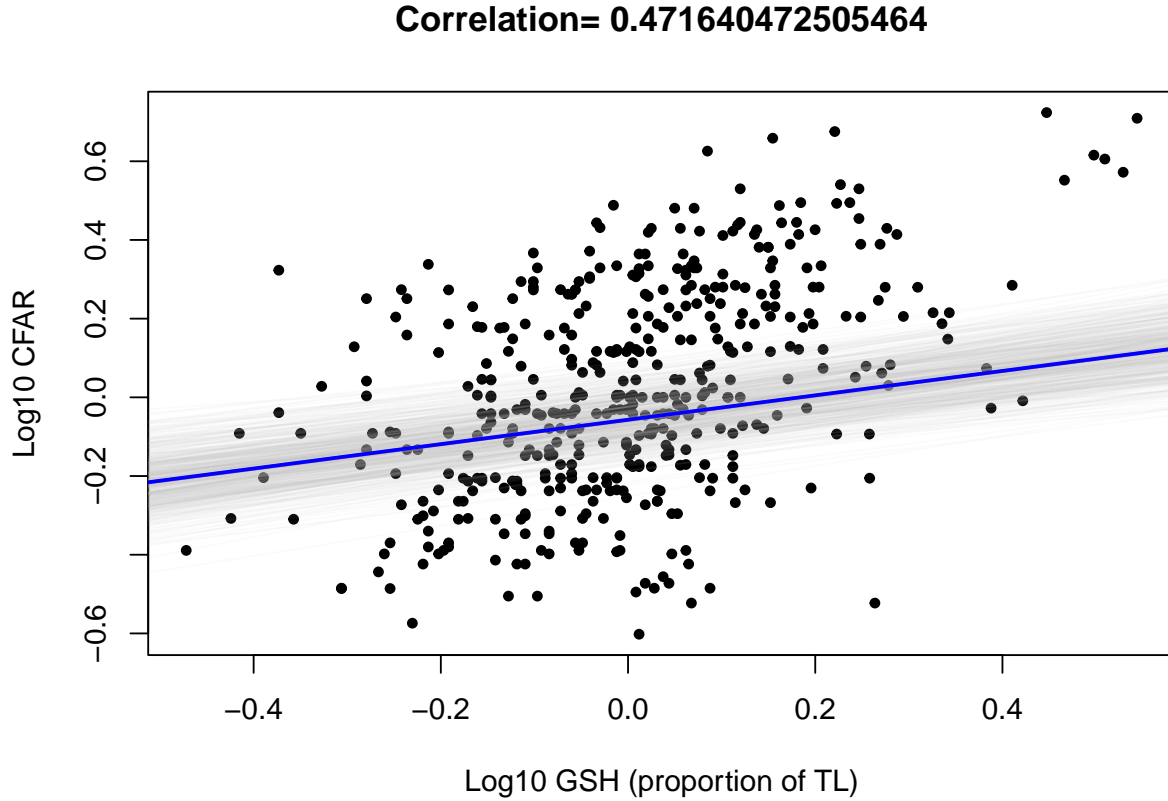


#### 2. brms model

```
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

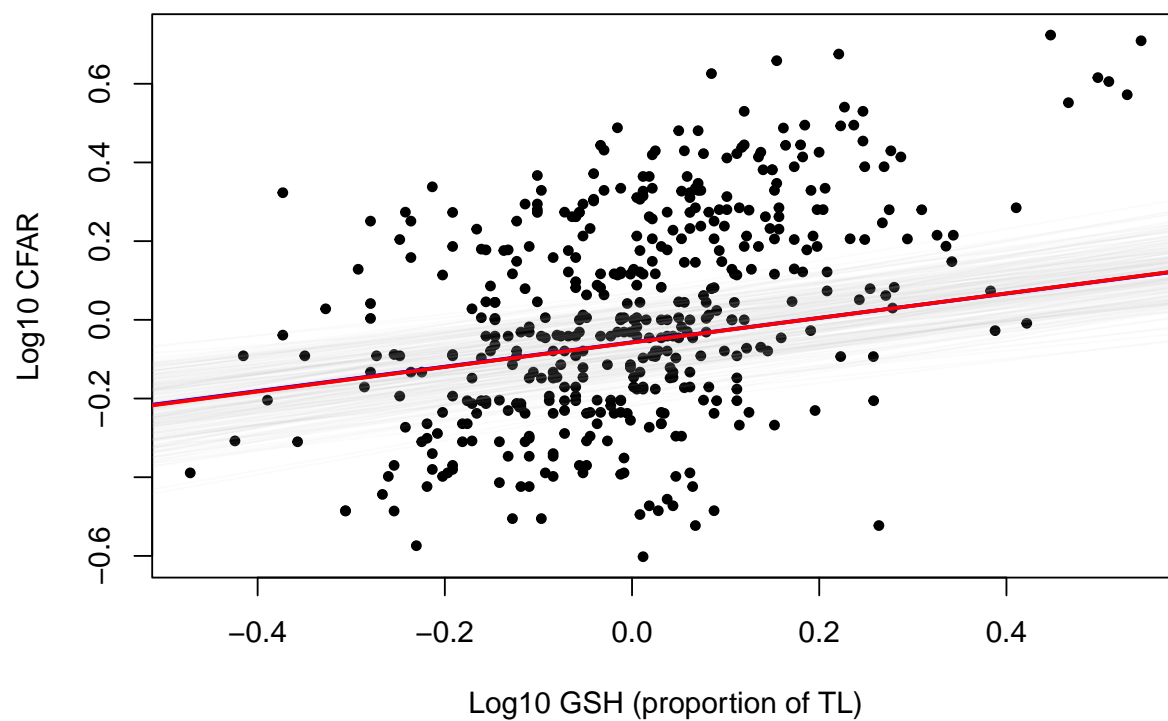


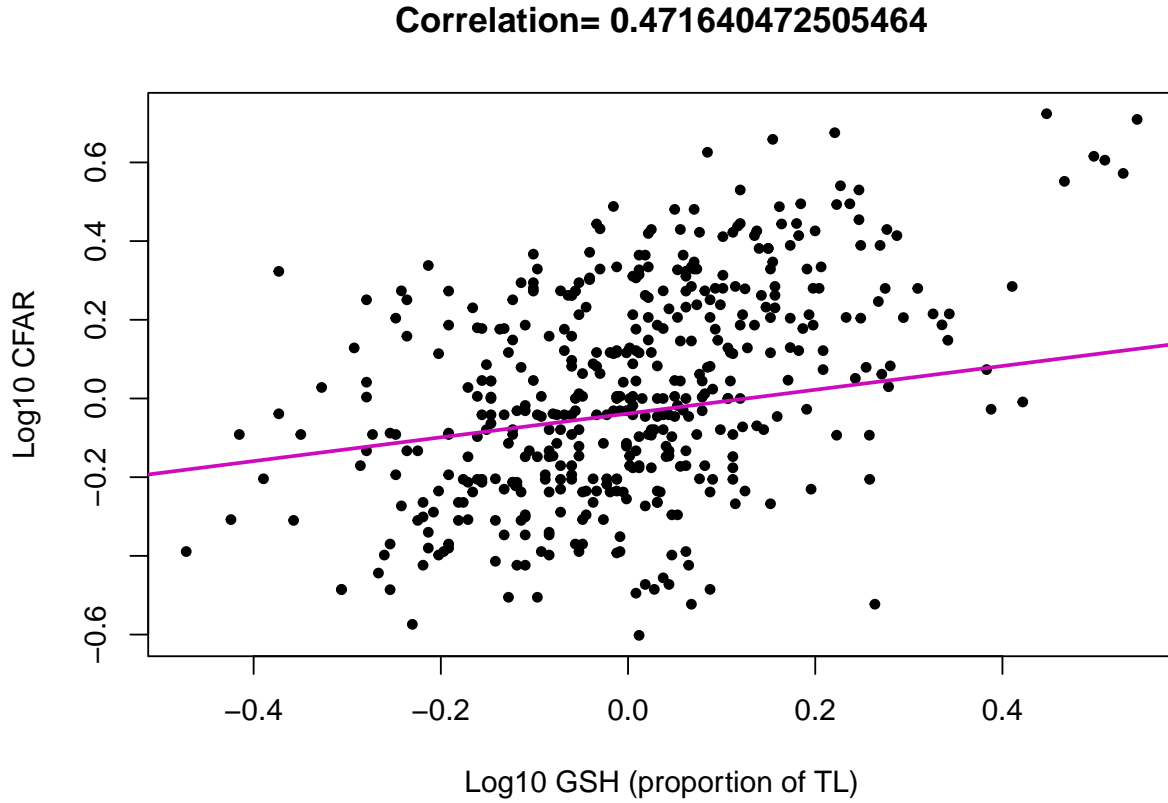
Table 17: PGLS summary

	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 =
```

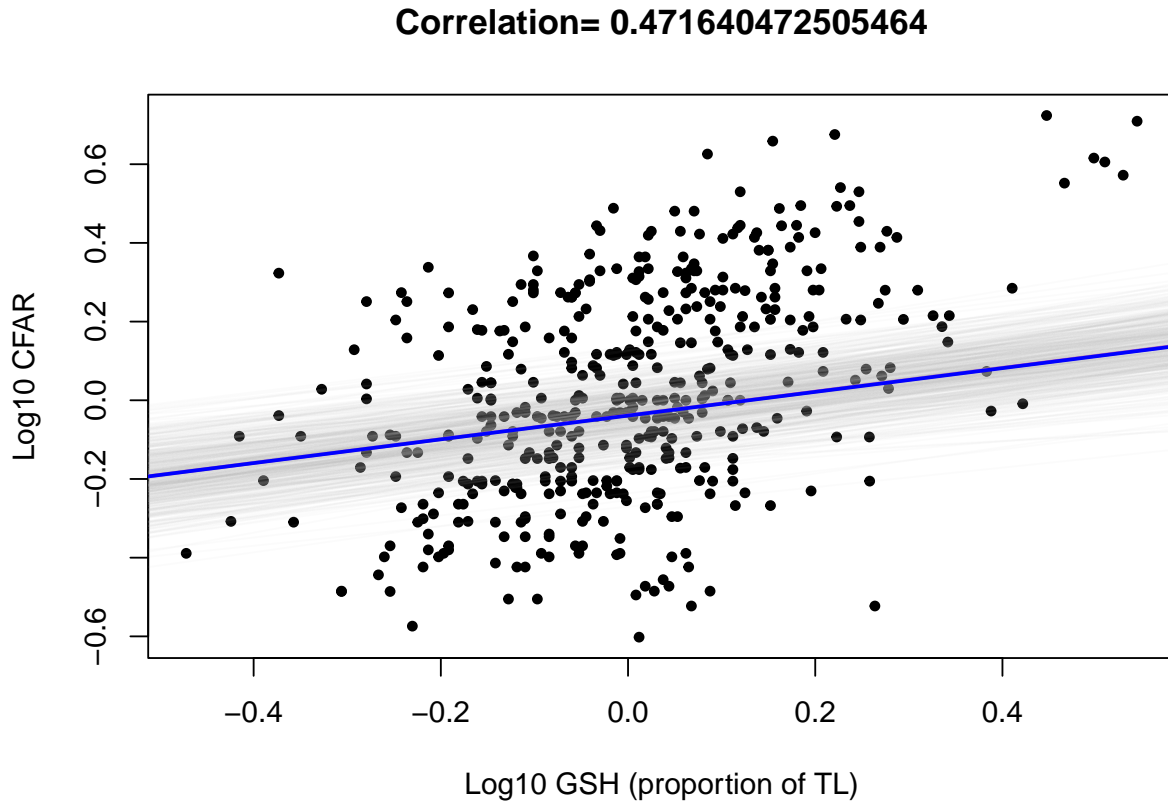


### 2. brms model

```
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**

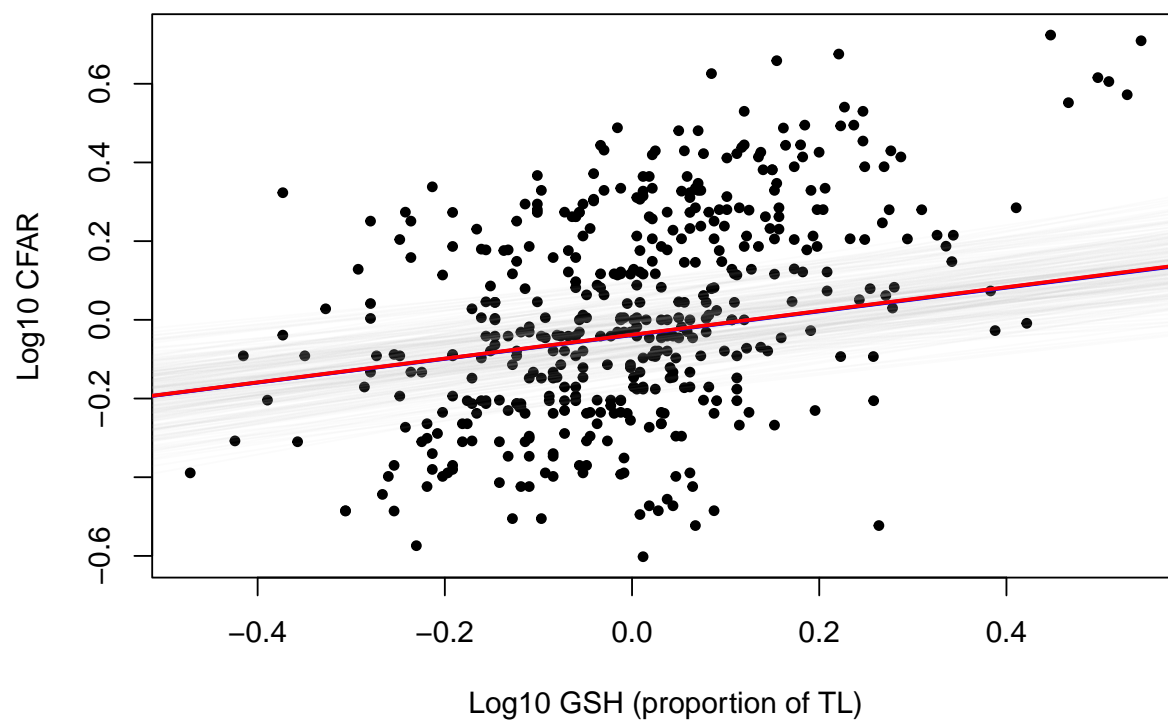


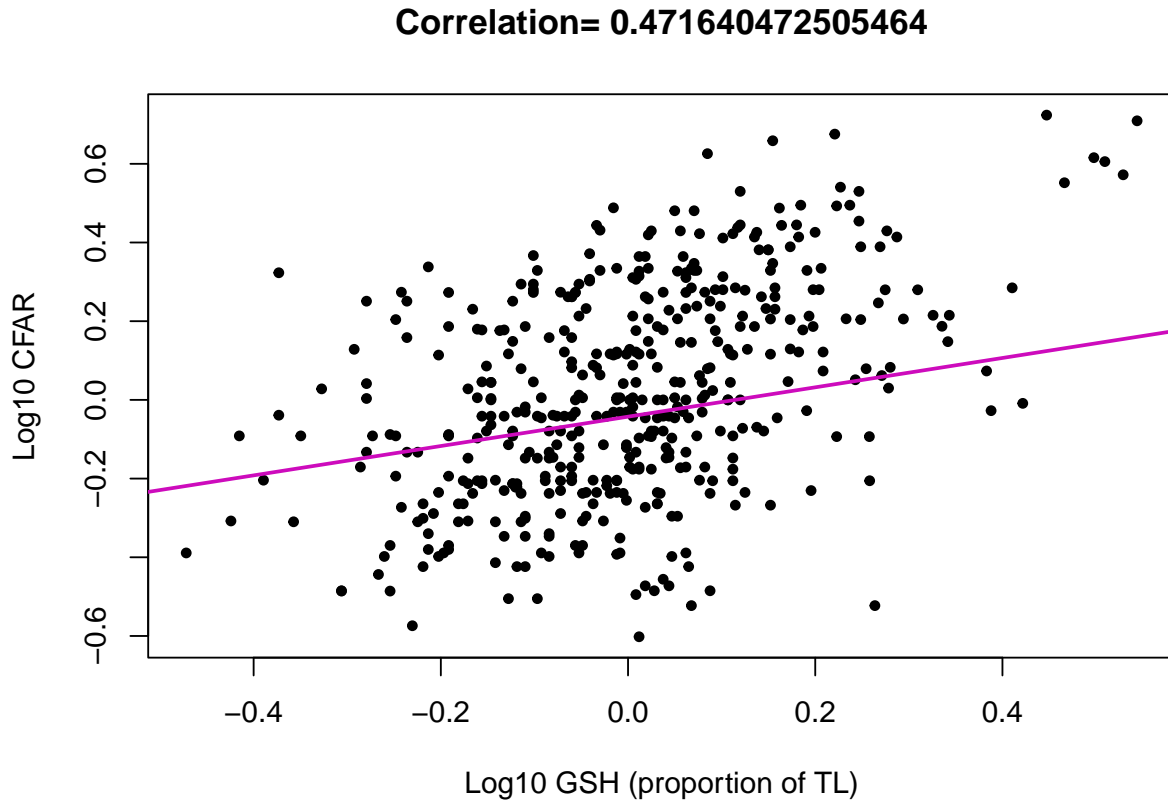
Table 20: PGLS summary

	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)
```

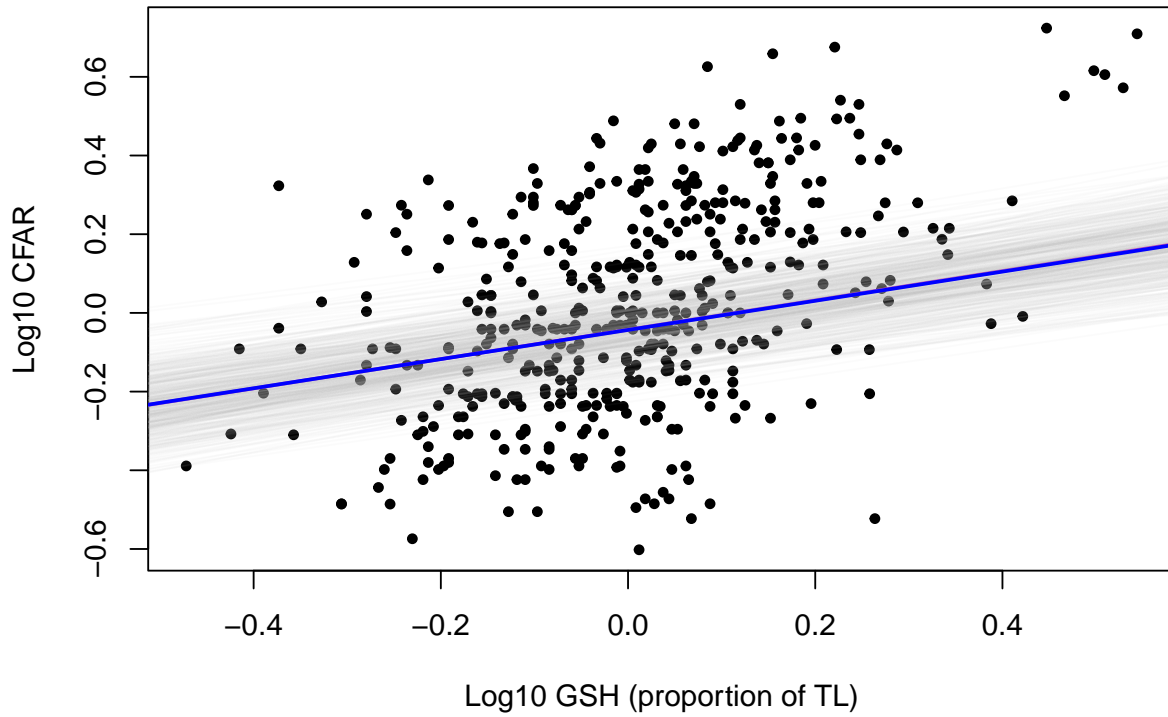
Table 21: brms model 9 summary

	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**

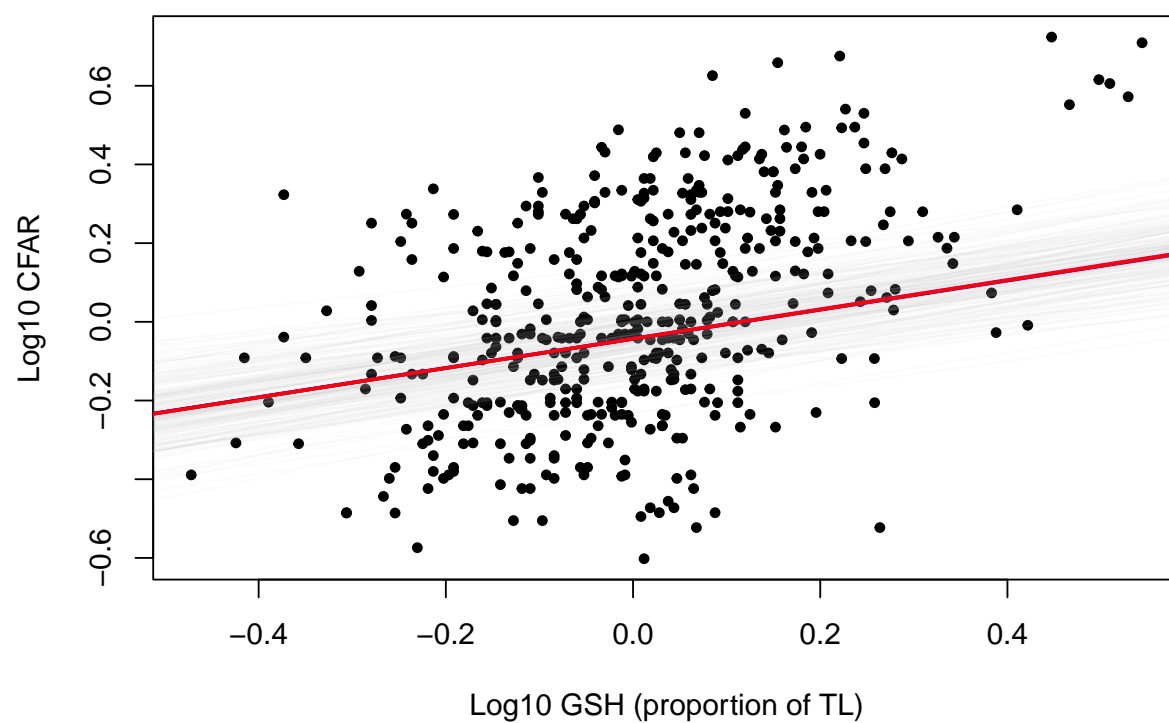


Table 23: PGLS summary

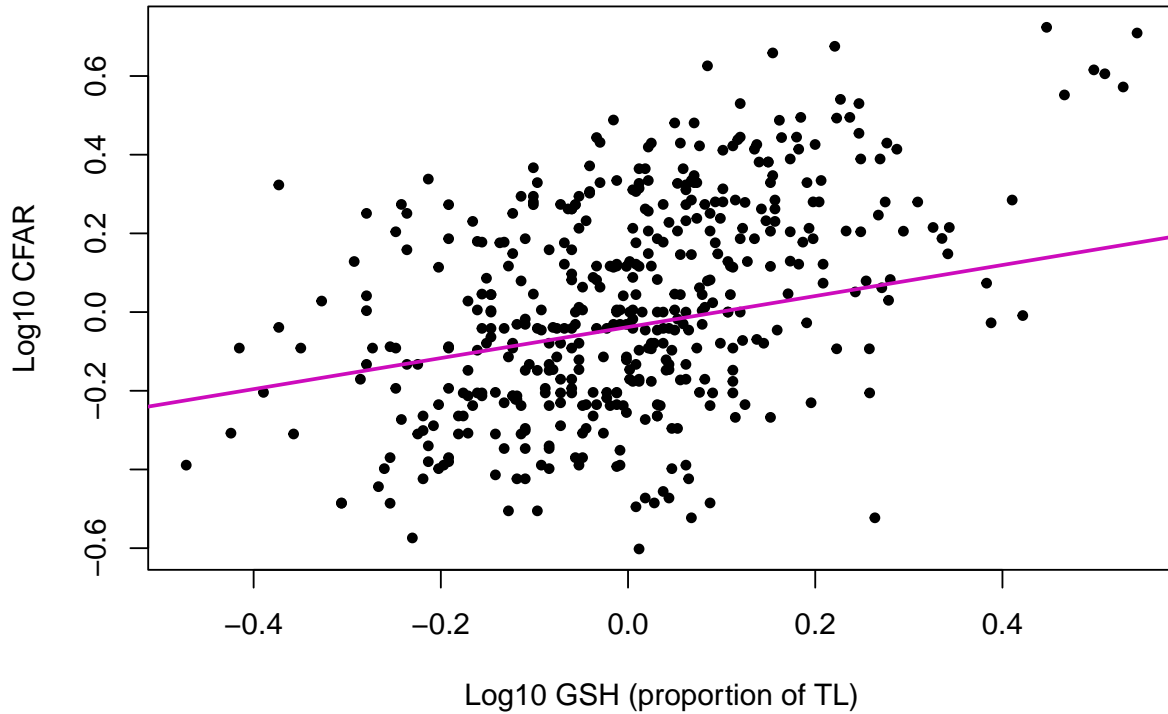
	Value	Std.Error	t-value	p-value	2.5 %	97.5 %
(Intercept)	-0.0380642	0.0600813	-0.6335439	0.5267004	-0.1558215	0.0796931
Log10MeanGSH_centered	0.3942985	0.1149440	3.4303530	0.0006584	0.1690124	0.6195846
PrimaryHabitatDeepwater	-0.0012632	0.0270931	-0.0466234	0.9628340	-0.0543646	0.0518382
PrimaryHabitatPelagic	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	0.6890806

### 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

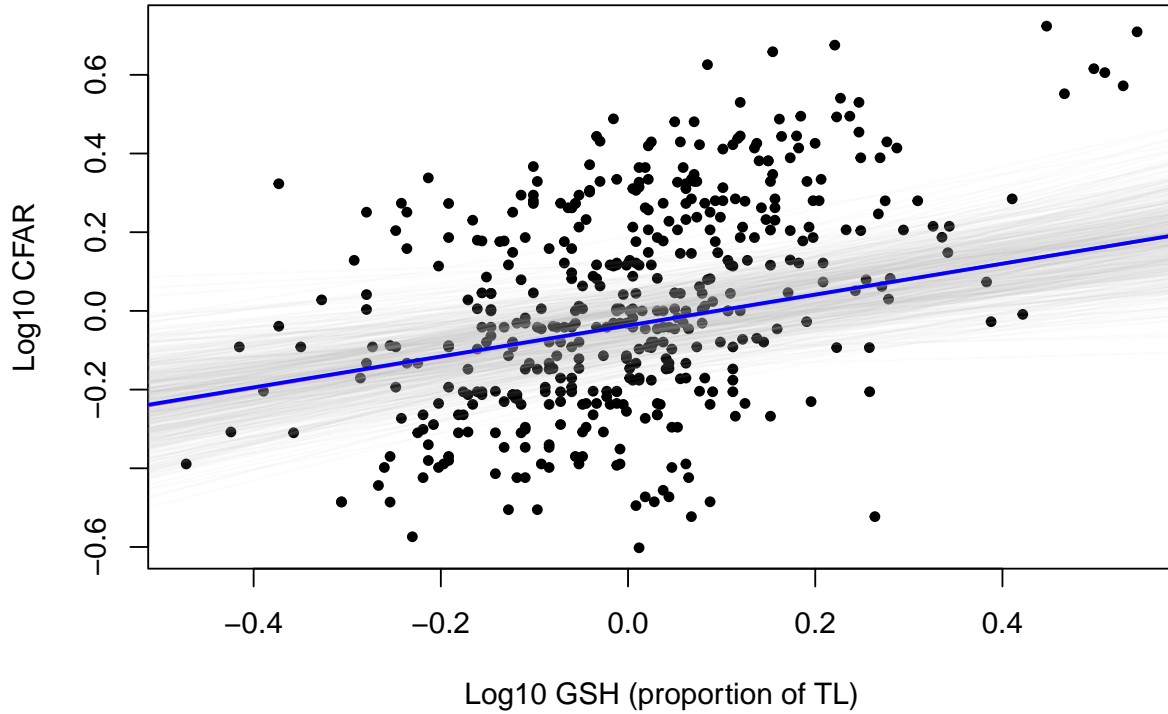
	Estimate	Est.Error	Q2.5	Q97.5
Intercept	-0.0370099	0.0629477	-0.1631366	0.0823122
Log10MeanGSH_centered	0.3930570	0.1194236	0.1502121	0.6230306
PrimaryHabitatDeepwater	-0.0009378	0.0274507	-0.0539797	0.0527488
PrimaryHabitatPelagic	0.1086930	0.0431179	0.0264042	0.1928199
Log10MeanGSH_centered:PrimaryHabitatDeepwater	-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**

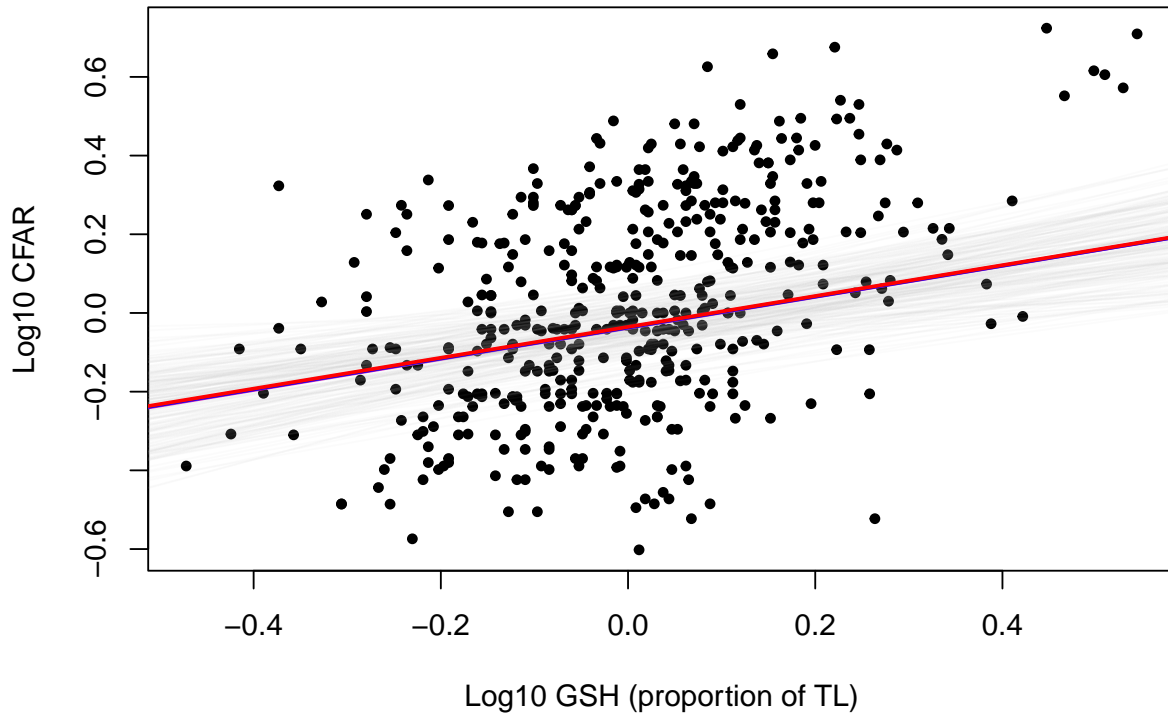


Table 26: PGLS summary

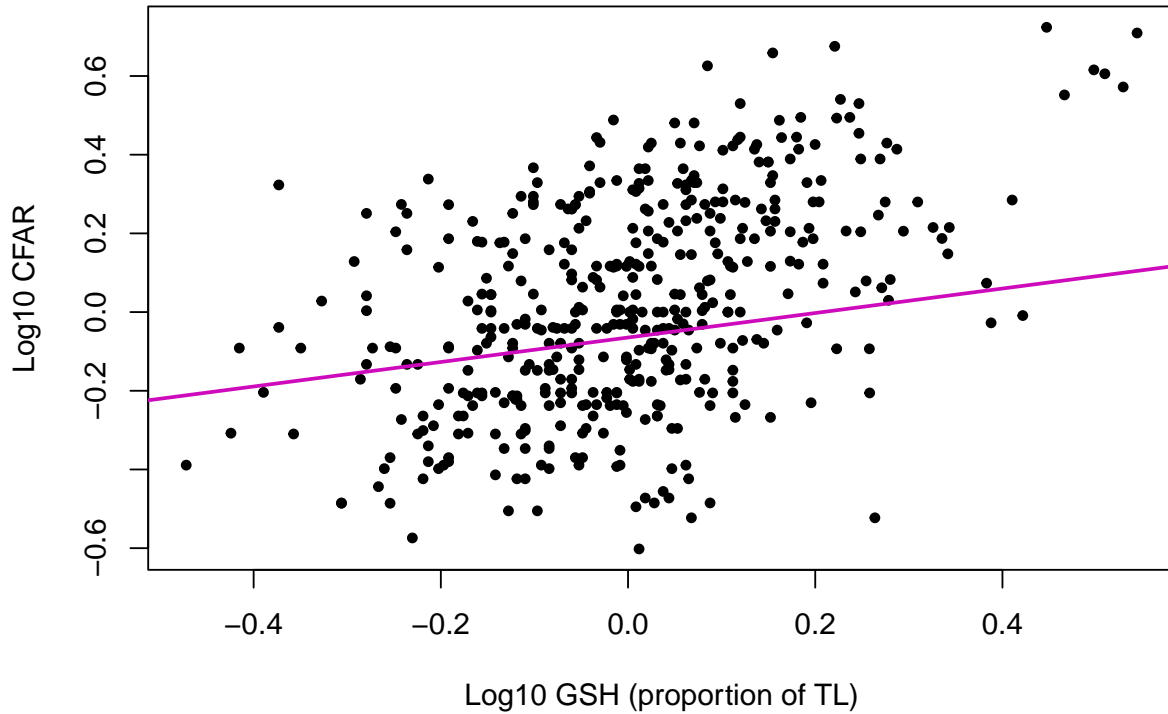
	Value	Std.Error	t-value	p-value	2.5 %	
(Intercept)	-0.0646193	0.0577730	-1.1185034	0.2639488	-0.1778522	0.0
Log10MeanGSH_centered	0.3111825	0.0594286	5.2362390	0.0000003	0.1947045	0.4
Log10MaxSize_centered	0.1234860	0.0351974	3.5083817	0.0004962	0.0545003	0.1
PrimaryHabitatDeepwater	0.0069539	0.0258660	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

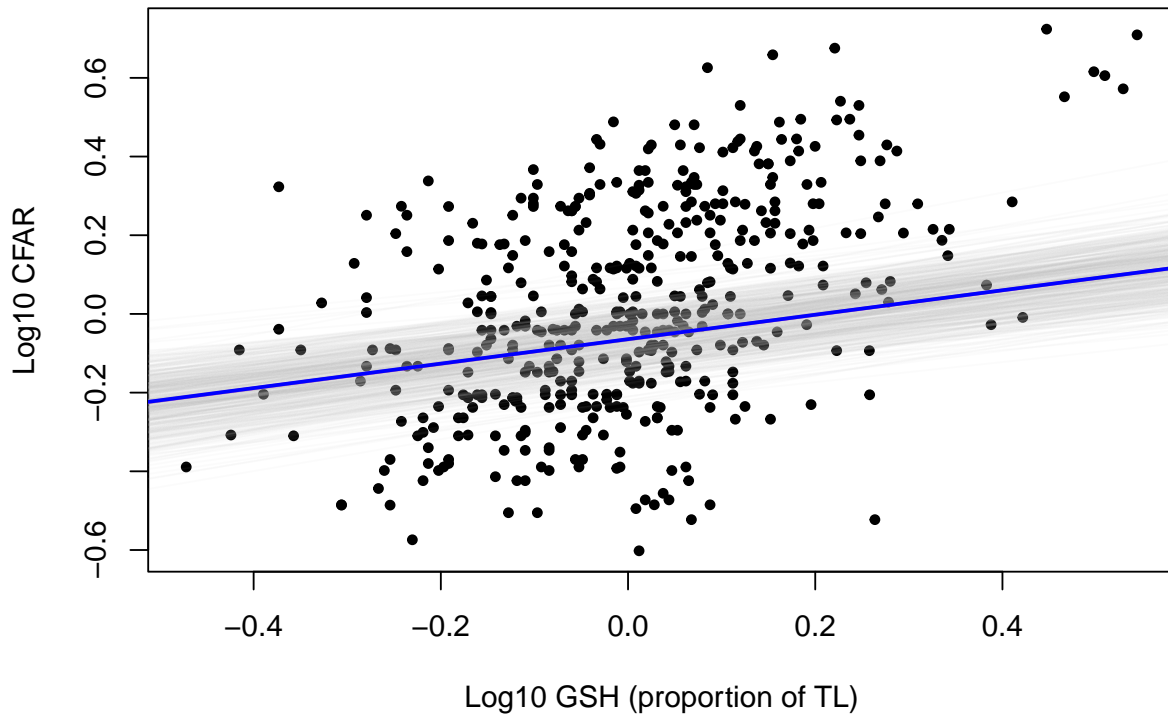
```
SizeHabitatModel <- brm(Log10CFAR ~ Log10MeanGSH_centered * Log10MaxSize_centered + PrimaryHabitat + (1
  data = GSH_df_pgls,
```

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**

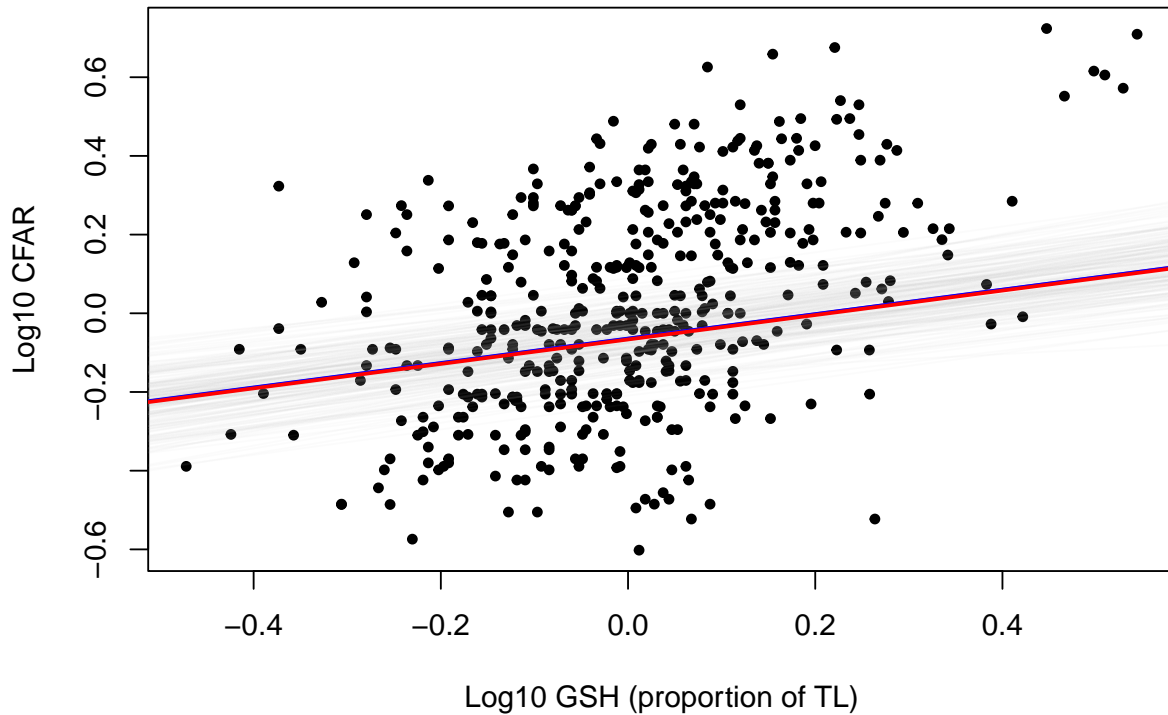


### 3. STAN Model

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	520.6539	-
HabitatPhylo2	9.750859	-	254.8301	14.28666	117.5718	6.447159	510.3111	-
Model_simple	10.076306	5.341777	252.6024	15.81492	122.6211	7.758200	509.6602	-
	12.304013	9.250782					505.2048	31.62985

LOO model weights

```
loo_model_weights(brms_loo_phylo_list)
```

```
## Method: stacking
```

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

```
##          weight
```

```
## model1 0.224
```

```
## model2 0.000
```

```
## model3 0.119
```

```
## model4 0.000
```

```
## model5 0.000
```

```
## model6 0.657
```