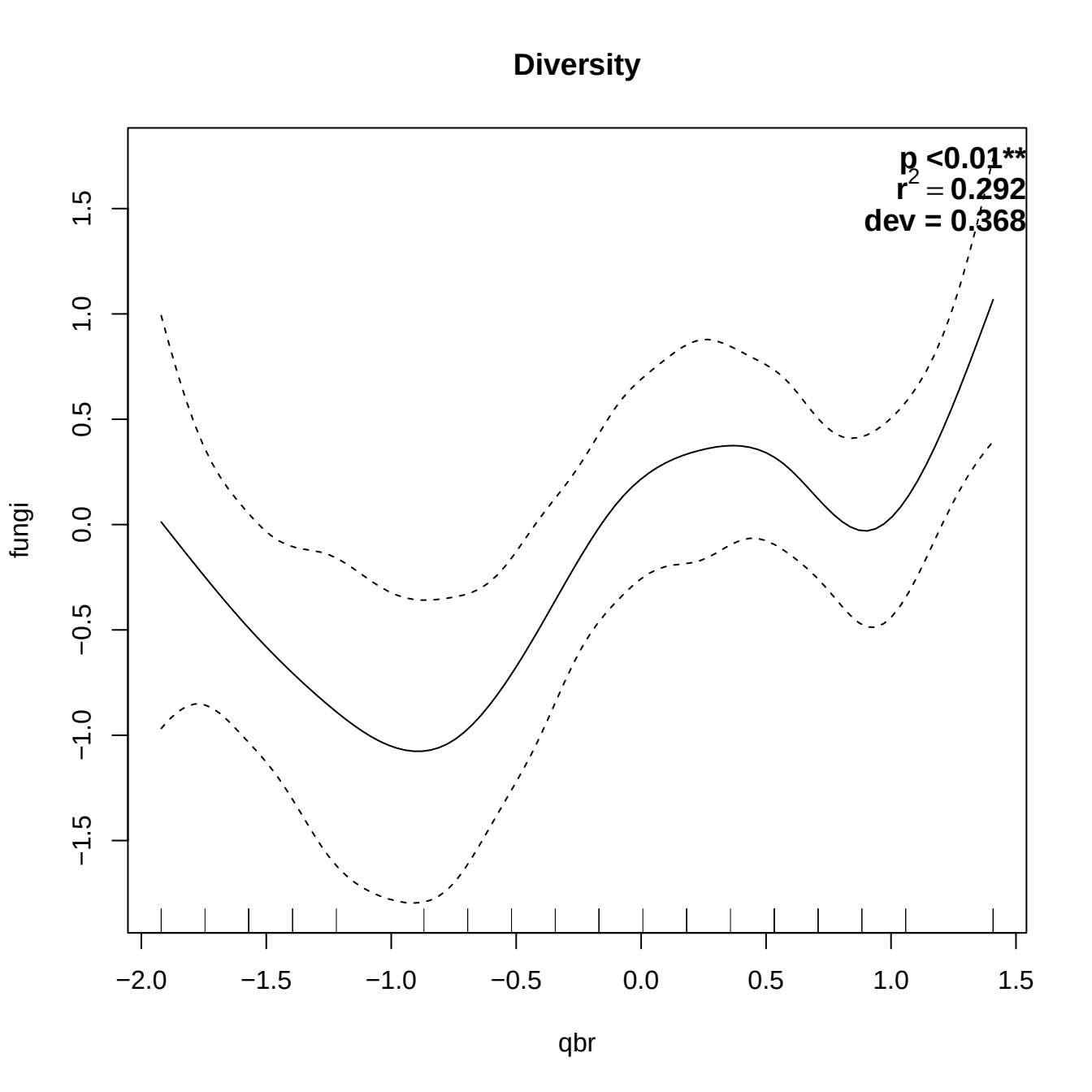
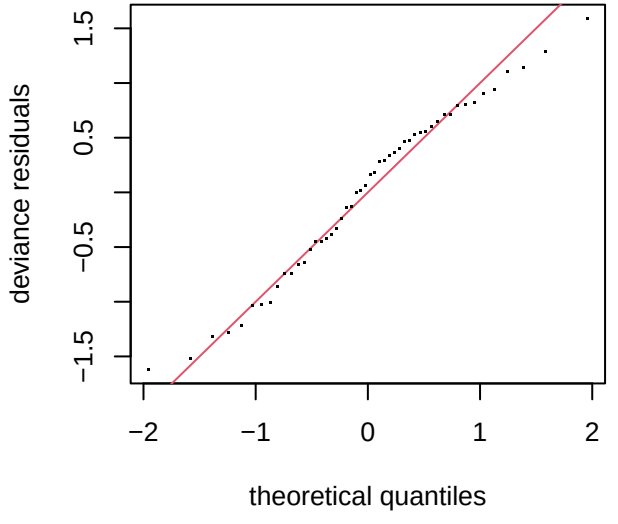
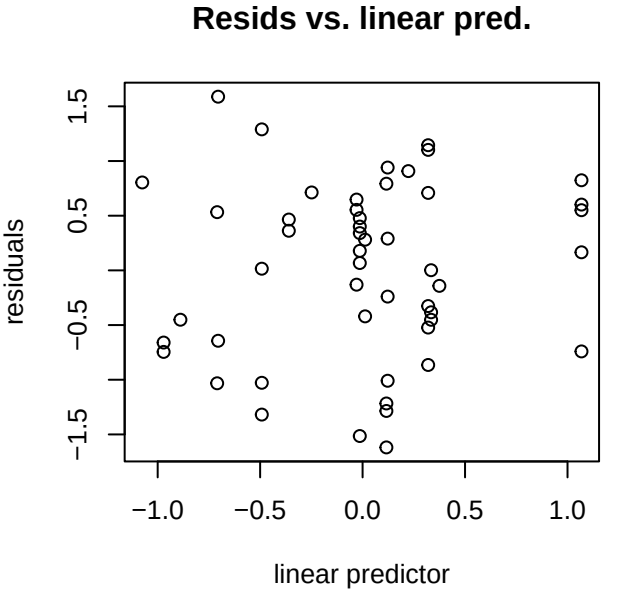
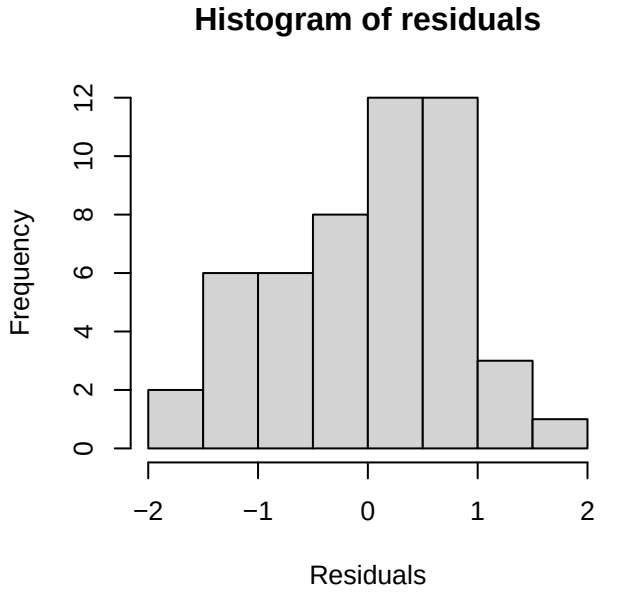
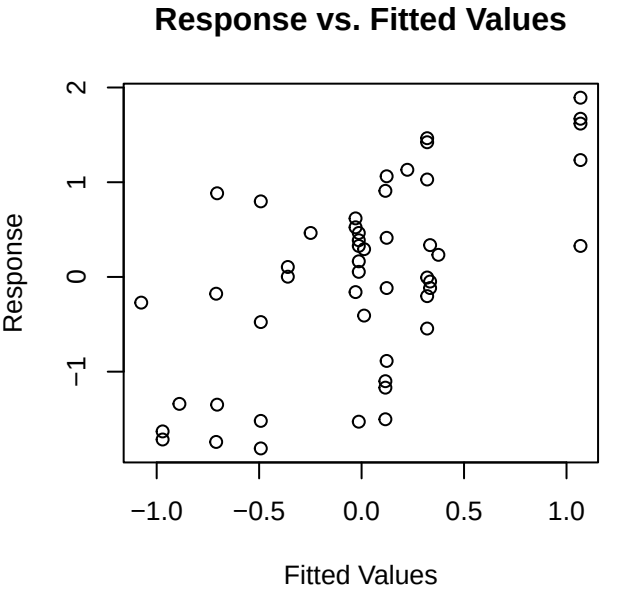
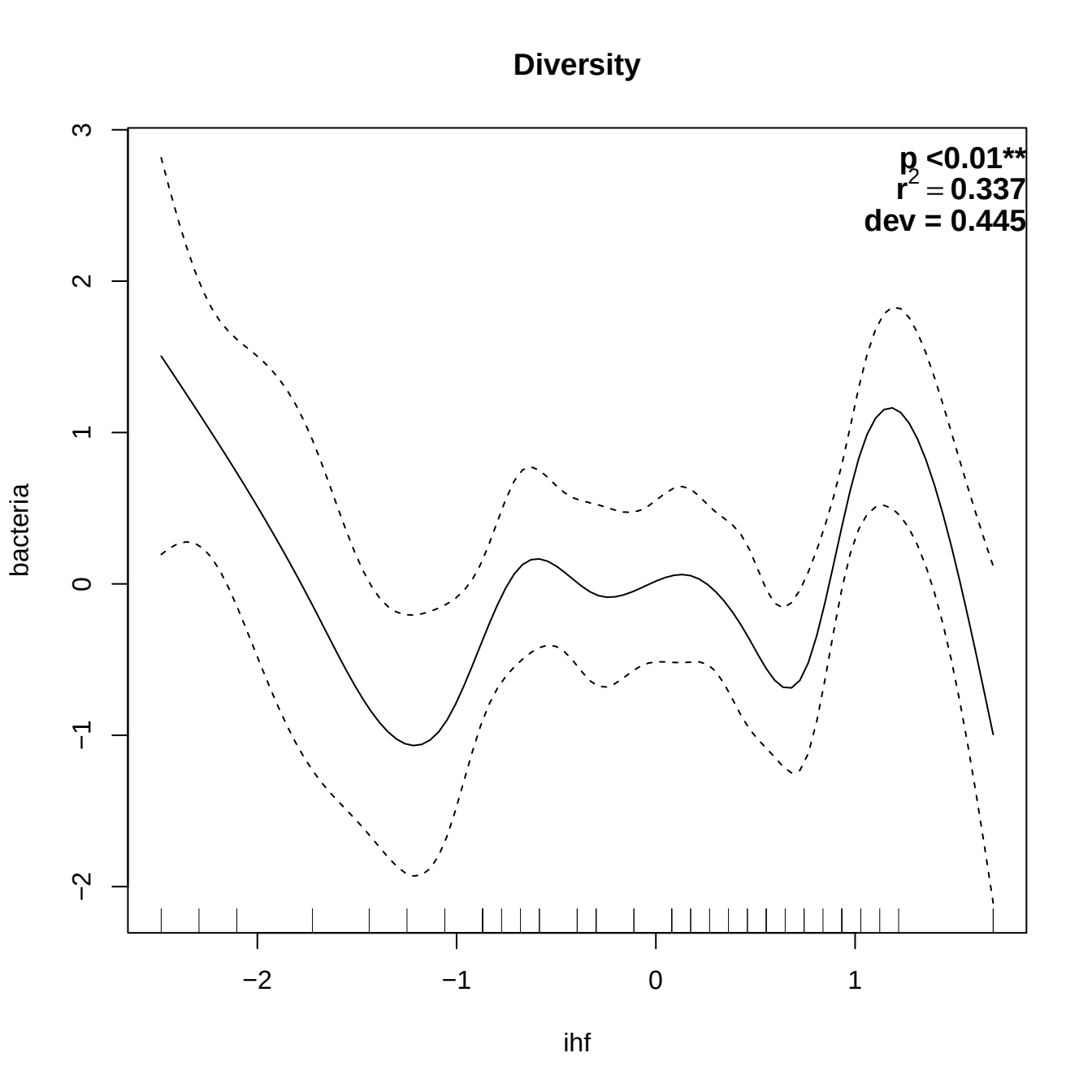

Diversity
p <0.01**
r2 = 0.292
dev = 0.368
fungi
qbr
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5

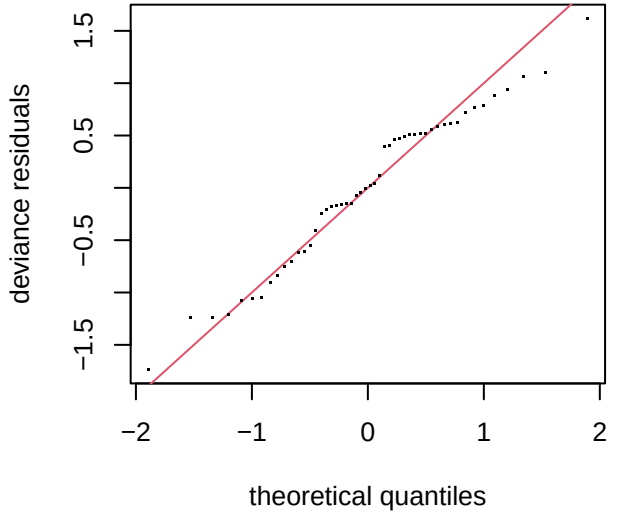

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

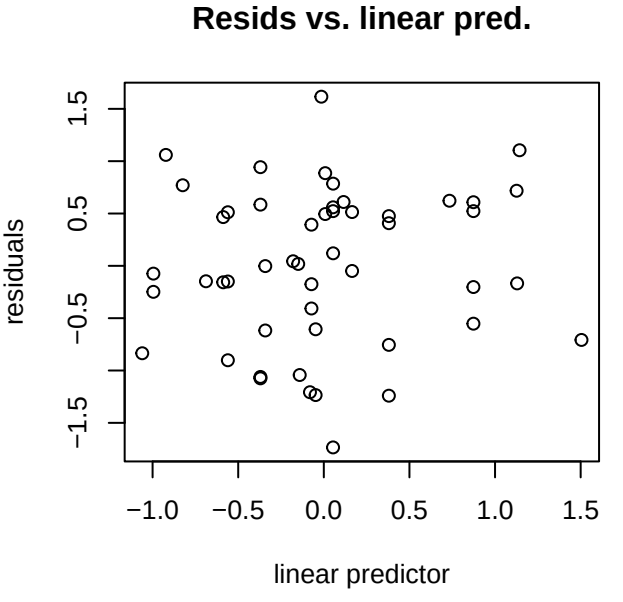

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
linear predictor

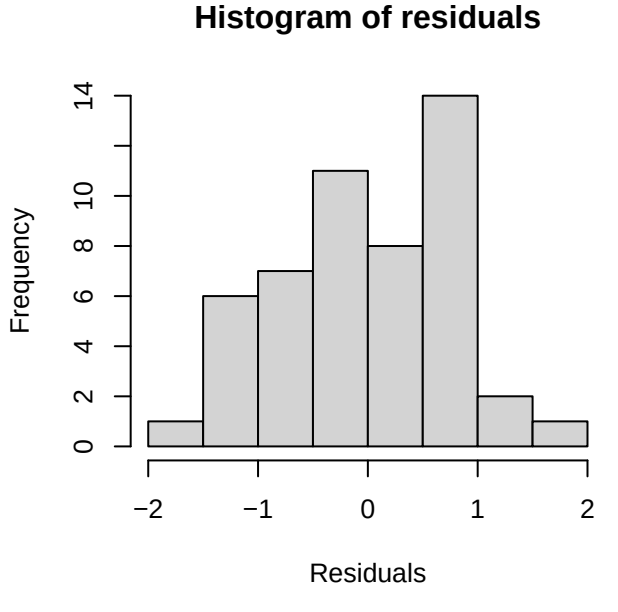

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

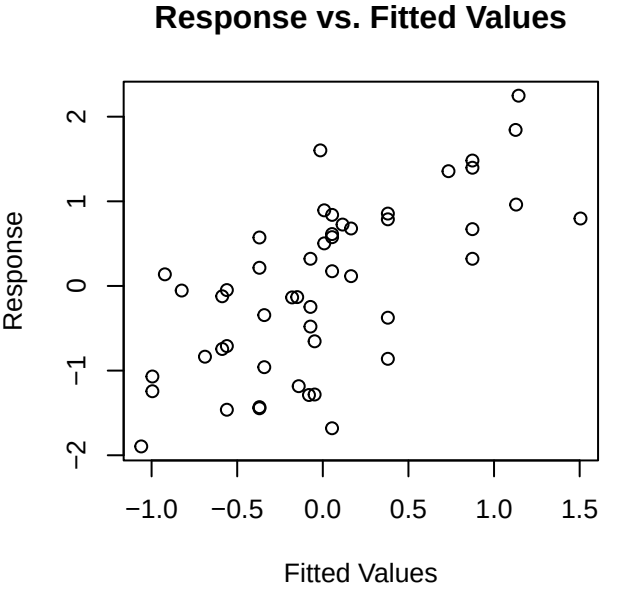

Response vs. Fitted Values
Response
2
1
0
−1
−1.0
−0.5
0.0
0.5
1.0
Fitted Values

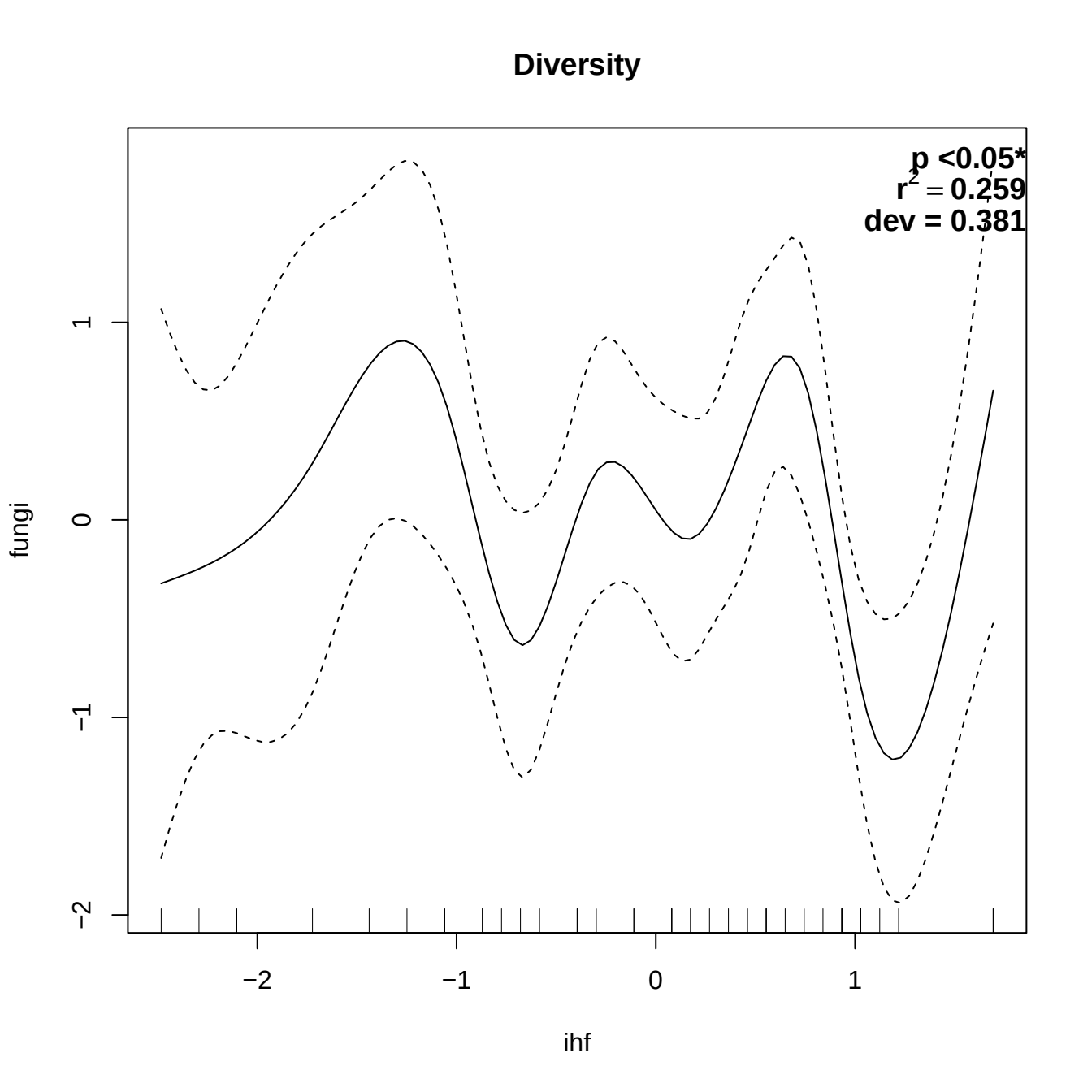

Diversity
p <0.01**
r2 = 0.337
dev = 0.445
bacteria
ihf
3
2
1
0
−1
−2
−2
−1
0
1

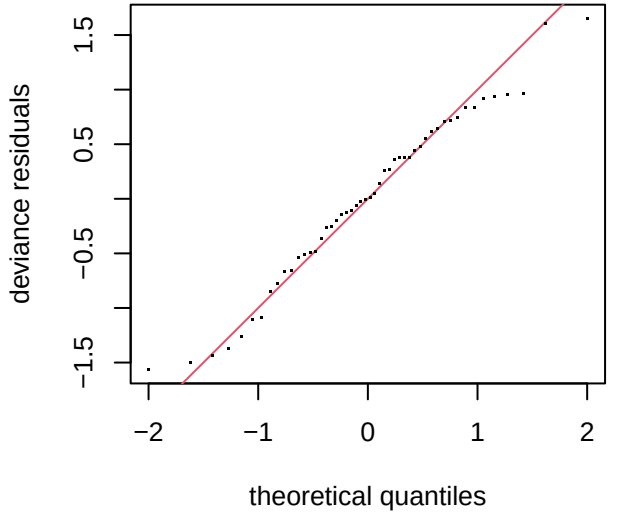

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

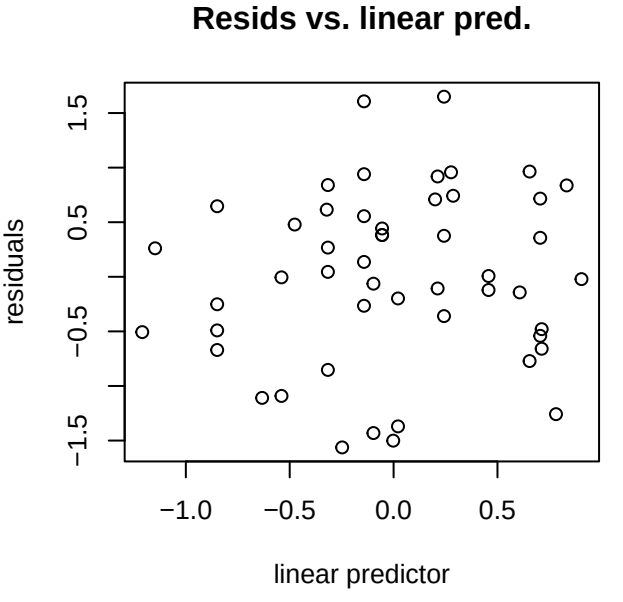

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
linear predictor

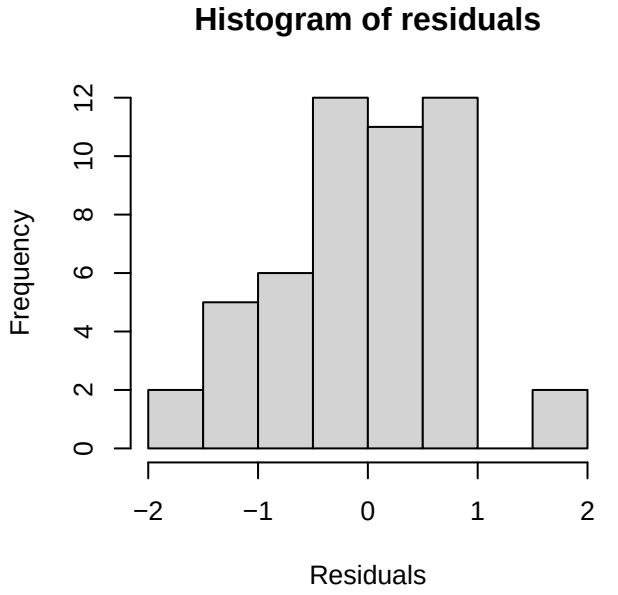

Histogram of residuals
Frequency
14
10
8
6
4
2
0
−2
−1
0
1
2
Residuals

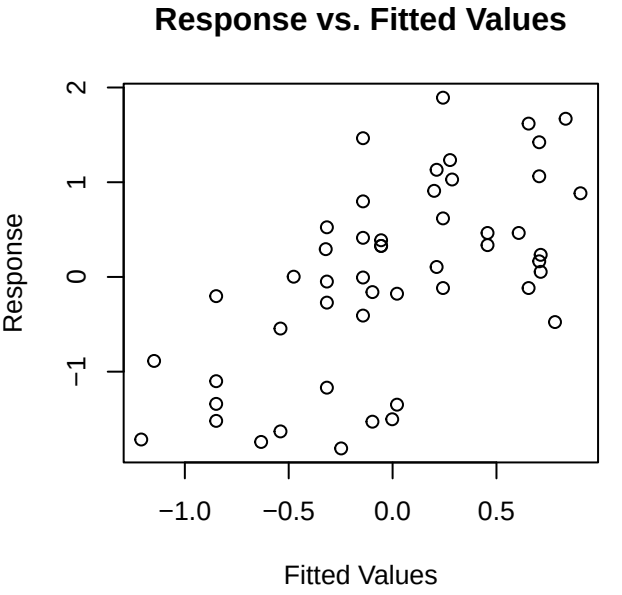

Response vs. Fitted Values
Response
2
1
0
−1
−2
−1.0
−0.5
0.0
0.5
1.0
1.5
Fitted Values

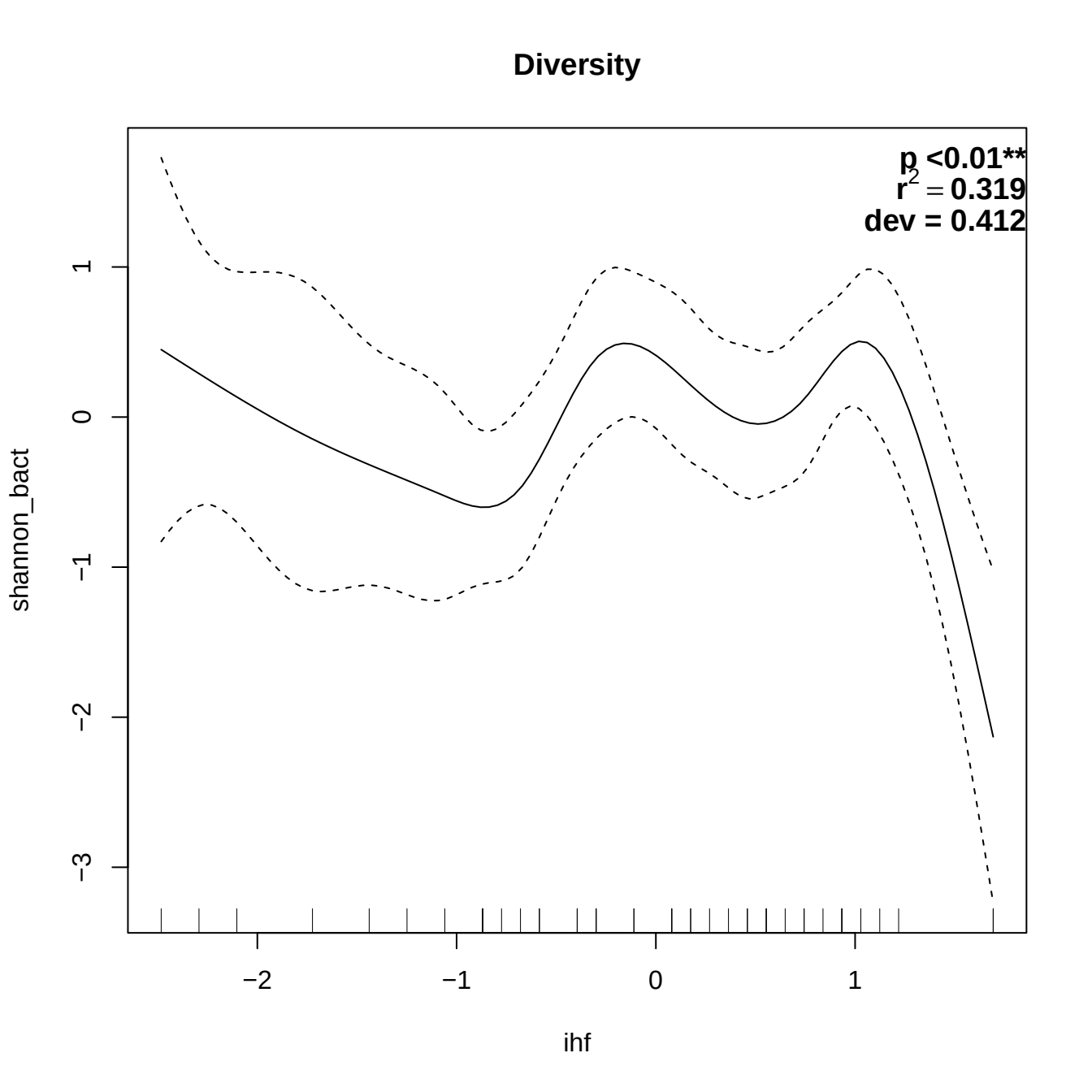

Diversity
p <0.05*
r2 = 0.259
dev = 0.381
fungi
ihf
−2
−1
0
1
−2
−1
0
1

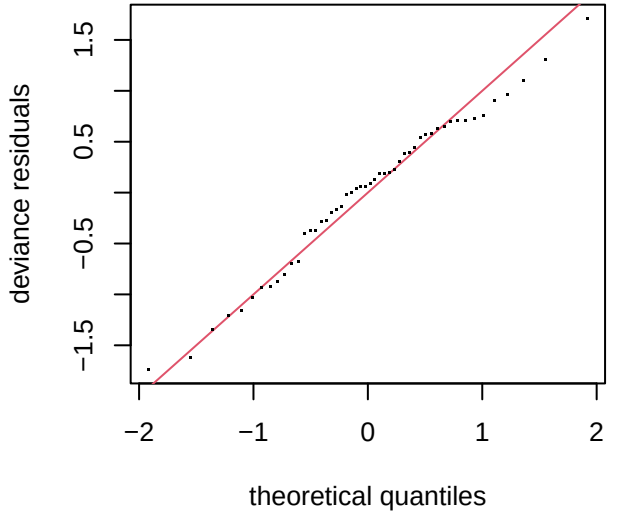

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

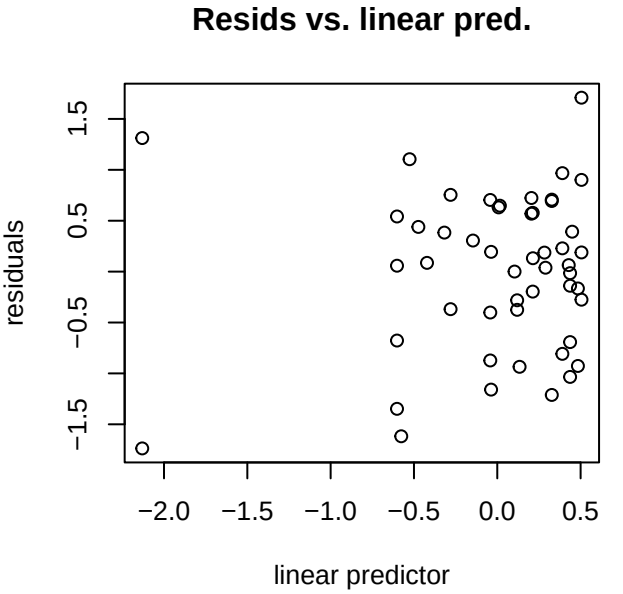

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−1.0
−0.5
0.0
0.5
linear predictor

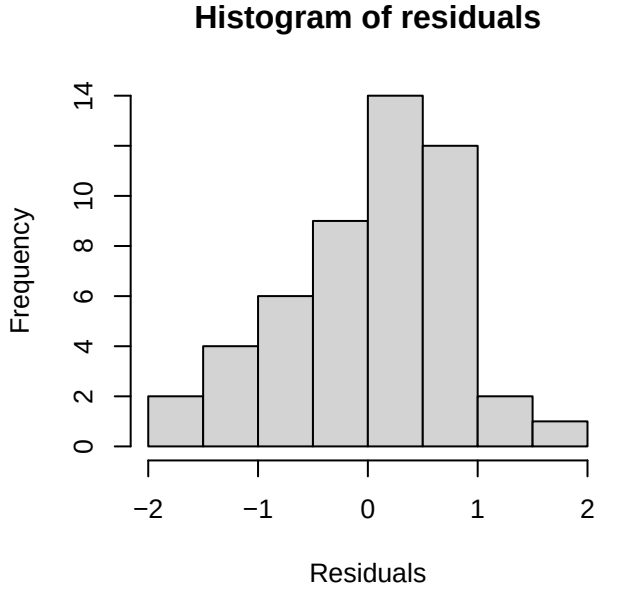

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

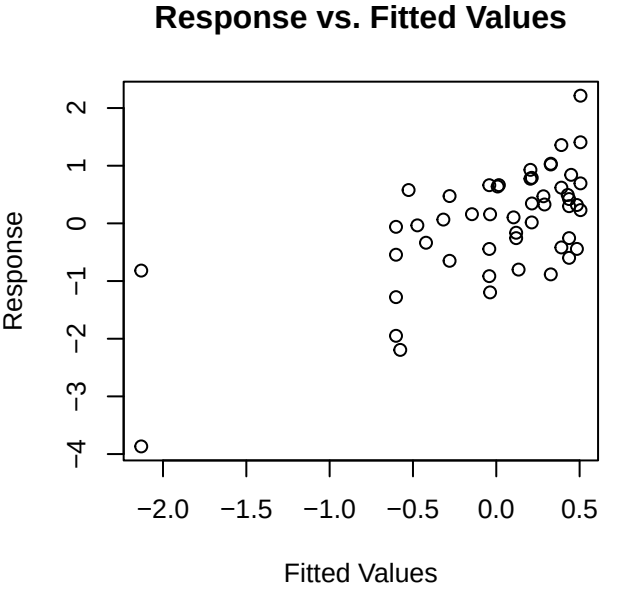

Response vs. Fitted Values
Response
2
1
0
−1
−1.0
−0.5
0.0
0.5
Fitted Values

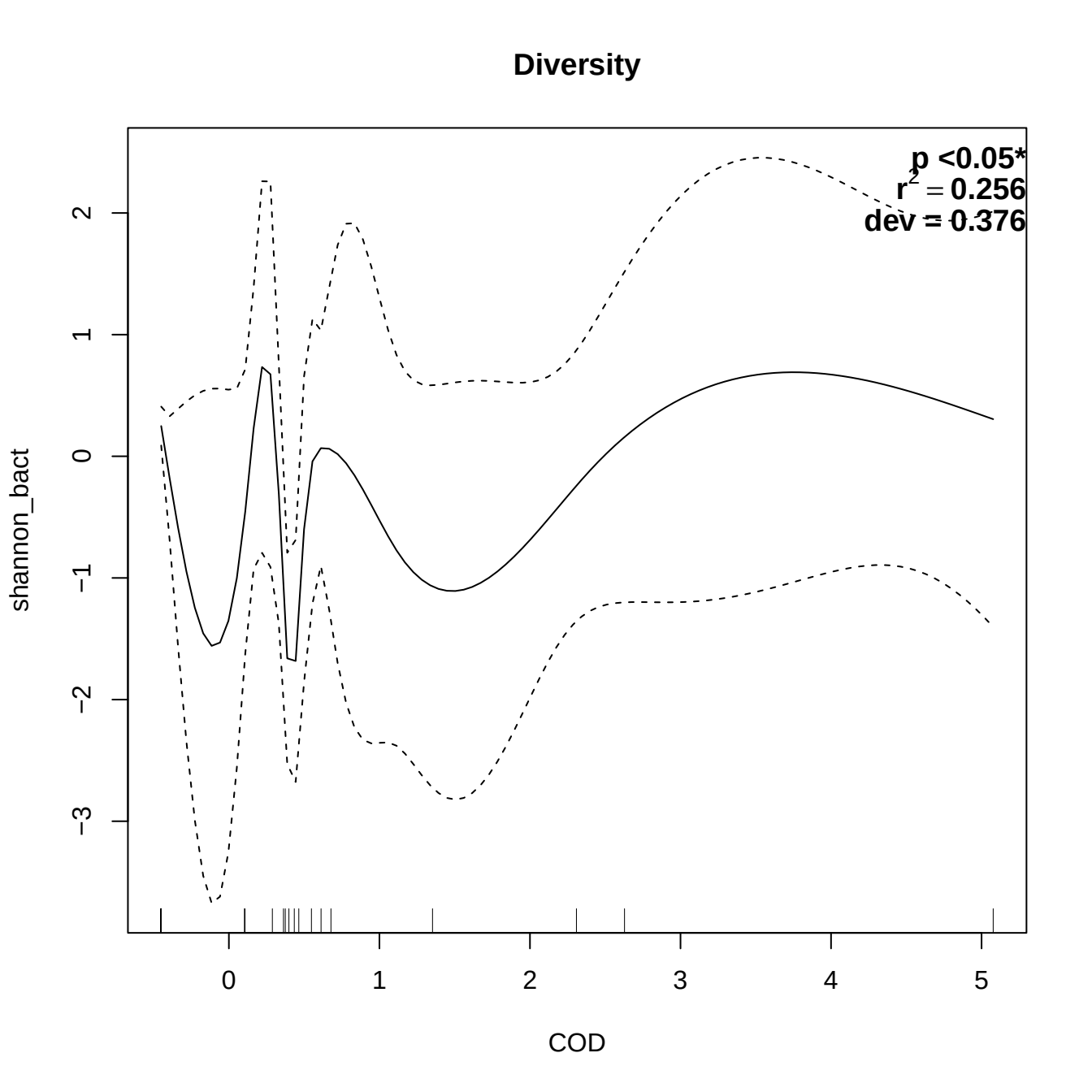

Diversity
p <0.01**
r2 = 0.319
dev = 0.412
shannon_bact
ihf
1
0
−1
−2
−3
−2
−1
0
1

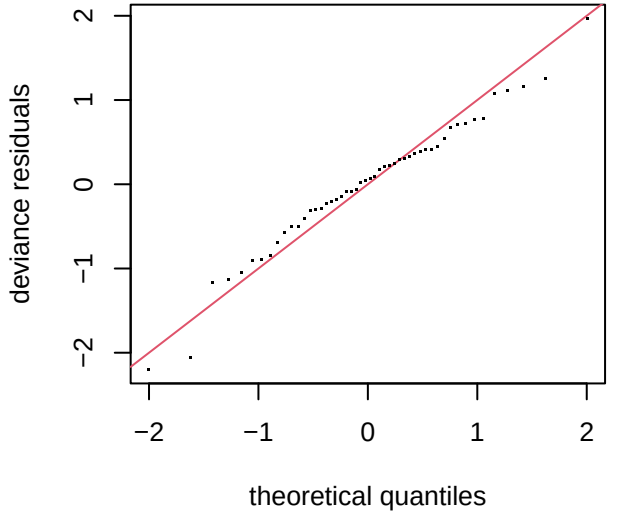

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

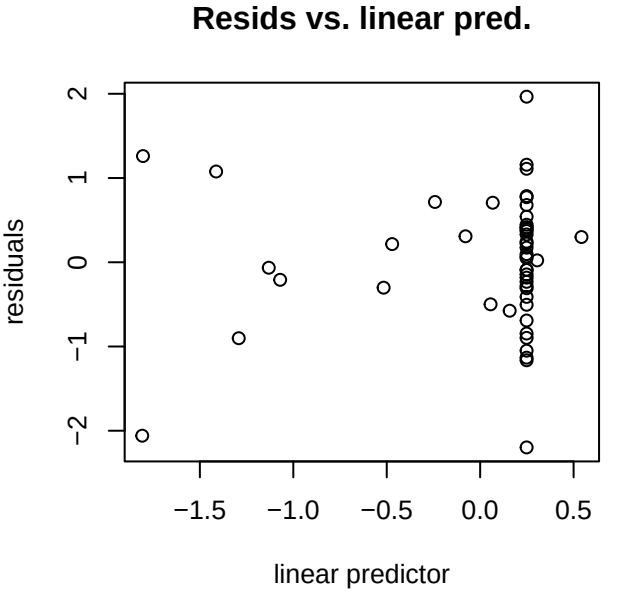

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−2.0
−1.5
−1.0
−0.5
0.0
0.5
linear predictor

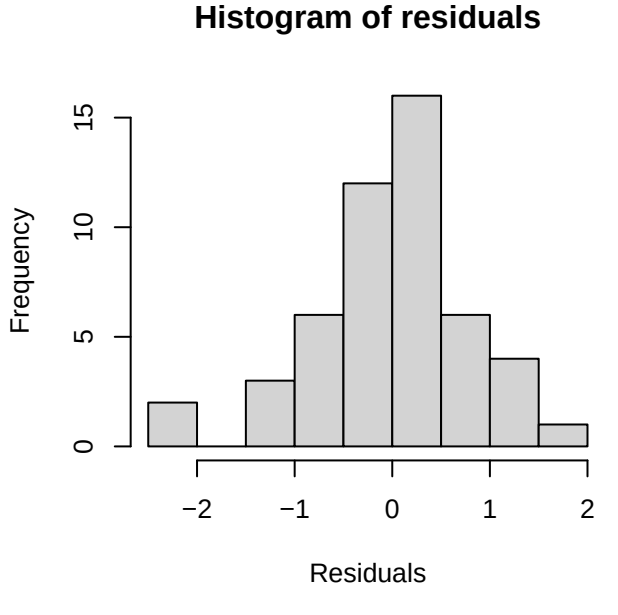

Histogram of residuals
Frequency
0
2
4
6
8
10
14
−2
−1
0
1
2
Residuals

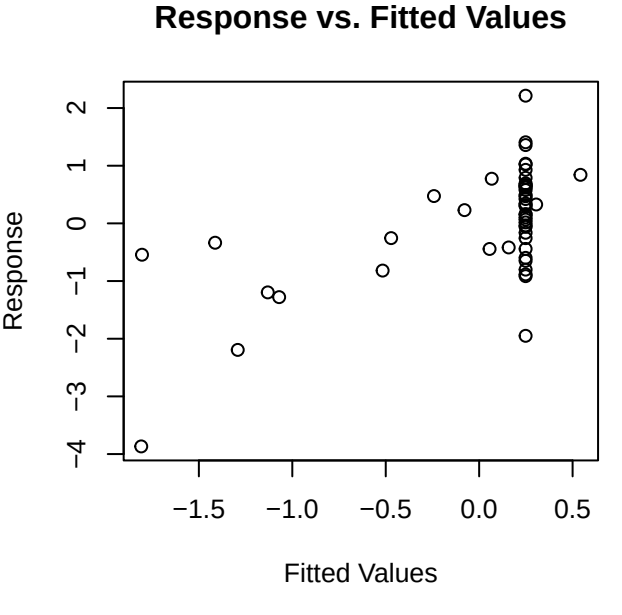

Response vs. Fitted Values
Response
2
1
0
−1
−2
−3
−4
−2.0
−1.5
−1.0
−0.5
0.0
0.5
Fitted Values

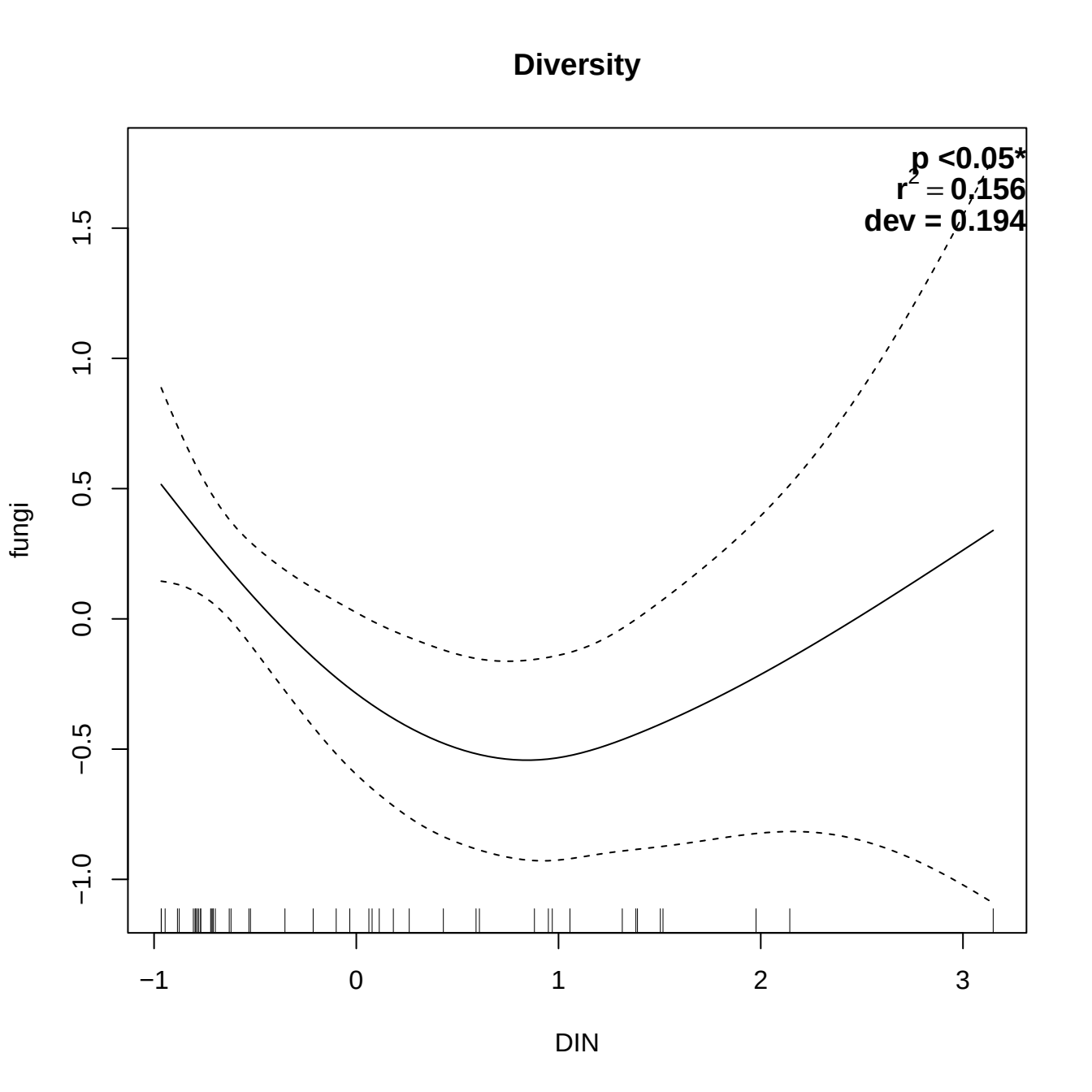

Diversity
p <0.05*
r2 = 0.256
dev = 0.376
shannon_bact
COD
2
1
0
−1
−2
−3
0
1
2
3
4
5

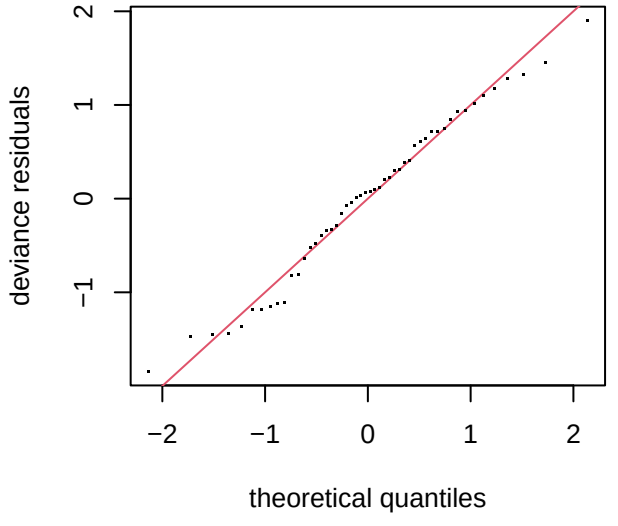

deviance residuals
theoretical quantiles

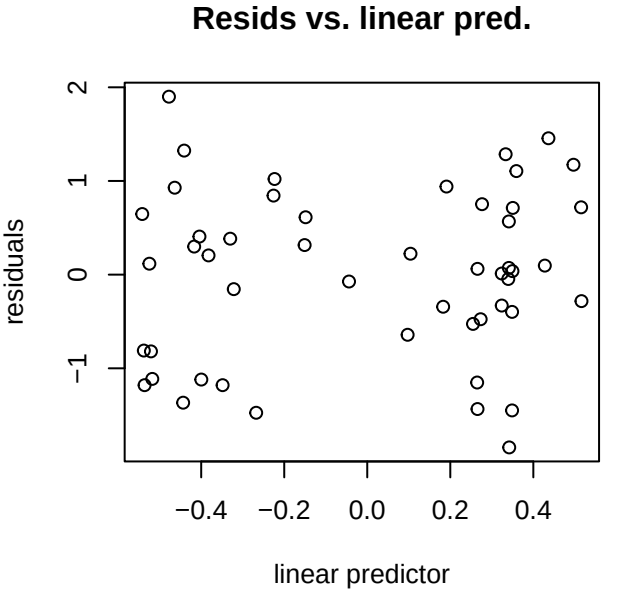

Resids vs. linear pred.
residuals
linear predictor

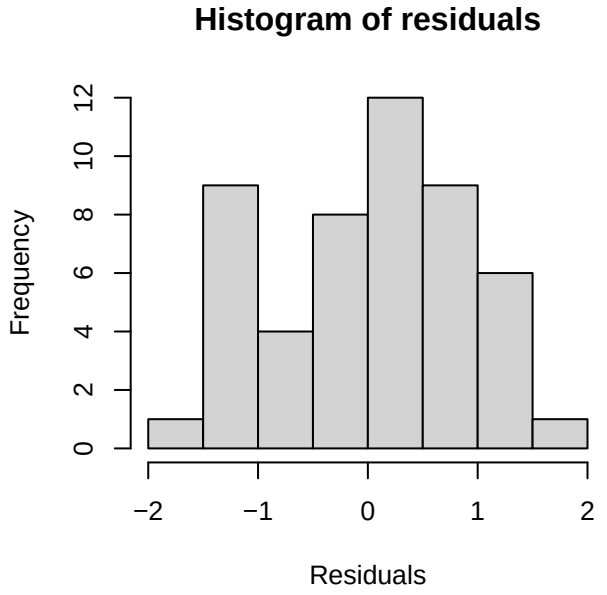

Histogram of residuals
Frequency
Residuals

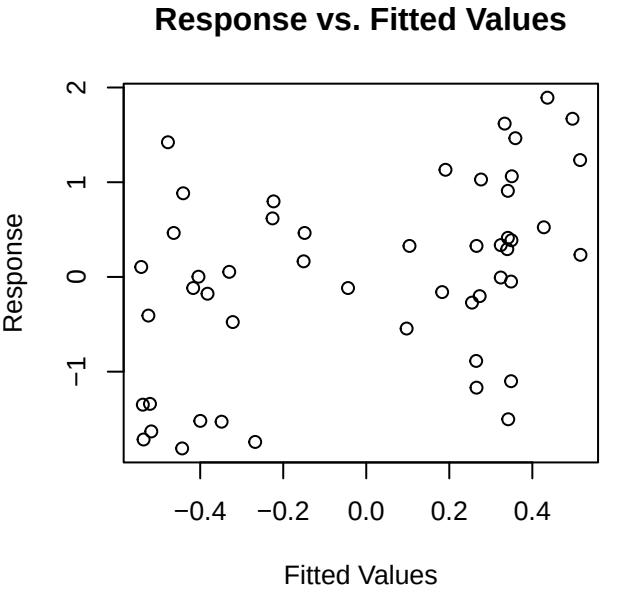

Response vs. Fitted Values
Response
Fitted Values

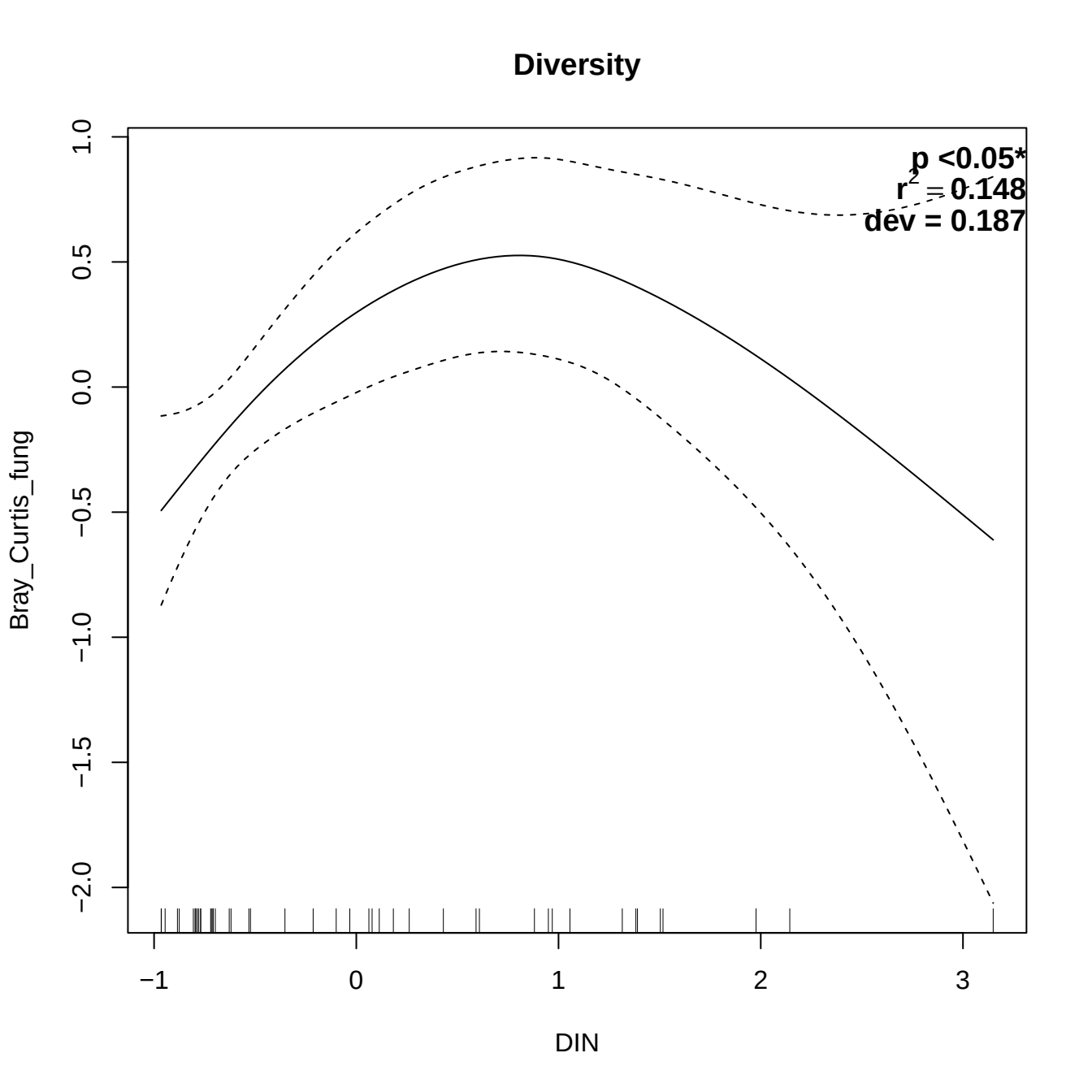

Diversity
p <0.05*
r2 = 0,156
dev = 0.194
fungi
1.5
1.0
0.5
0.0
−0.5
−1.0
−1
0
1
2
3
DIN

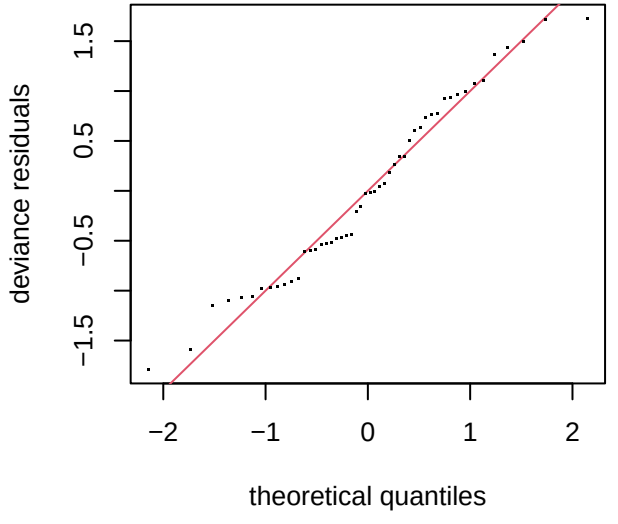

deviance residuals
theoretical quantiles

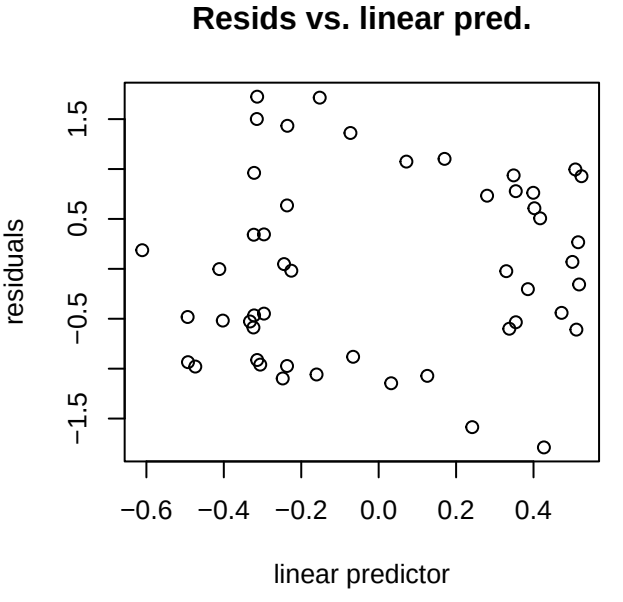

Resids vs. linear pred.
residuals
linear predictor

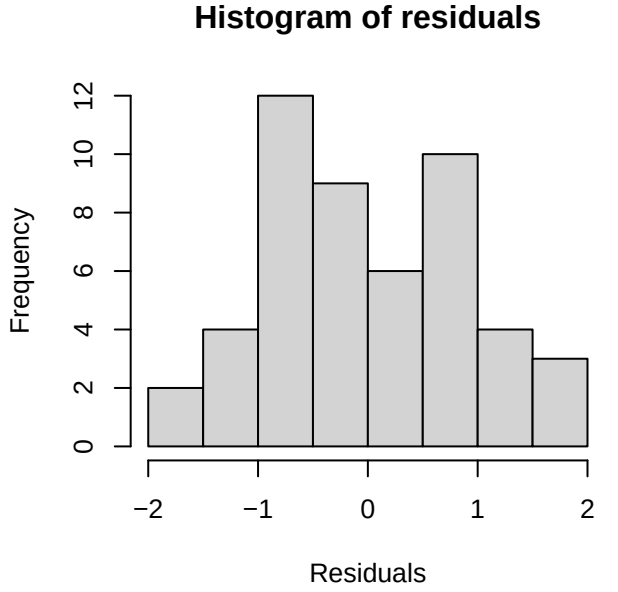

Histogram of residuals
Frequency
Residuals

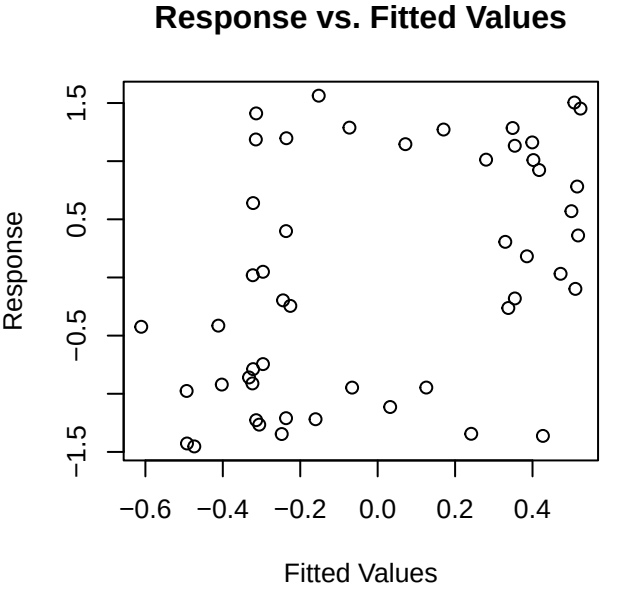

Response vs. Fitted Values
Response
Fitted Values

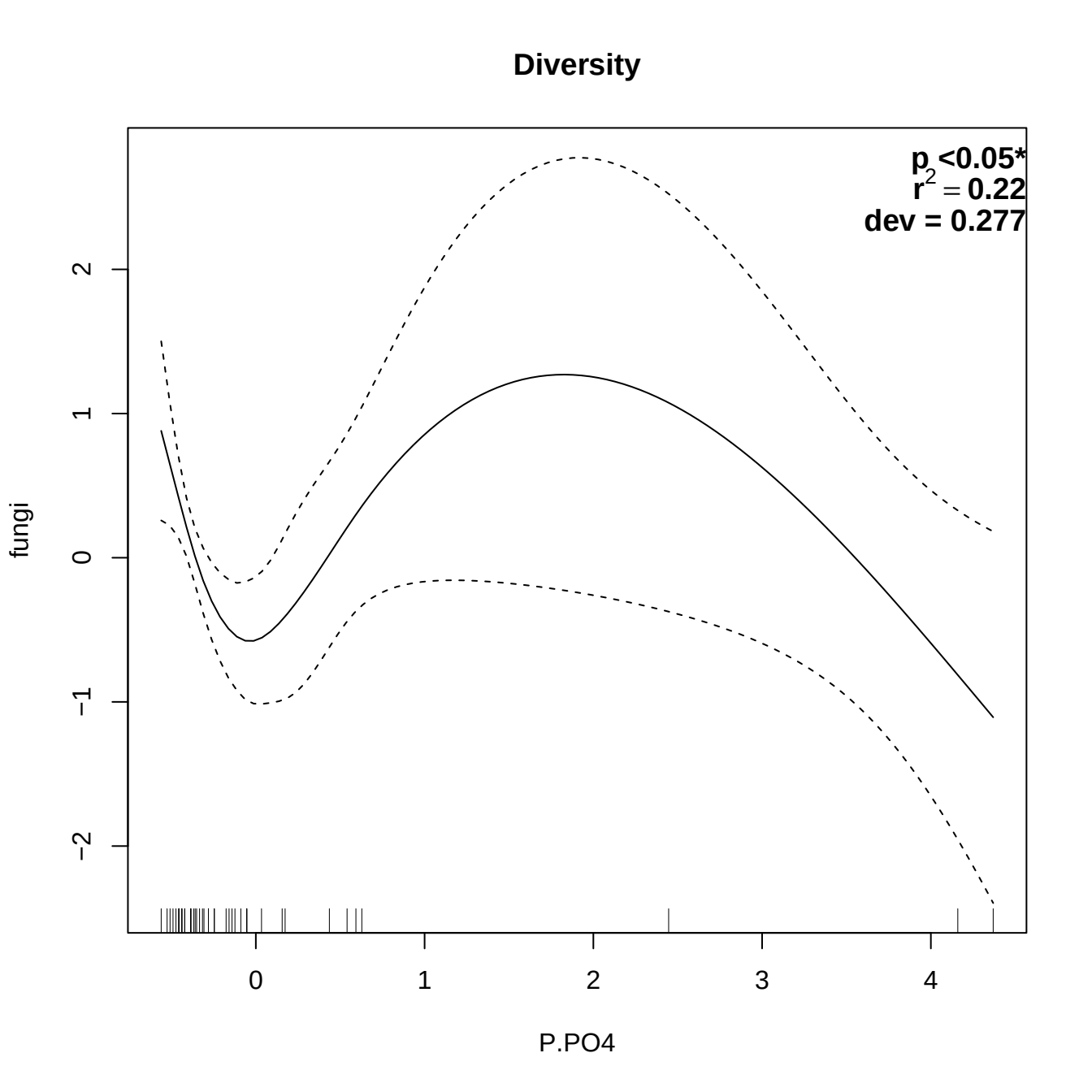

Diversity
p <0.05*
r2 = 0.148
dev = 0.187
Bray_Curtis_fung
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−1
0
1
2
3
DIN

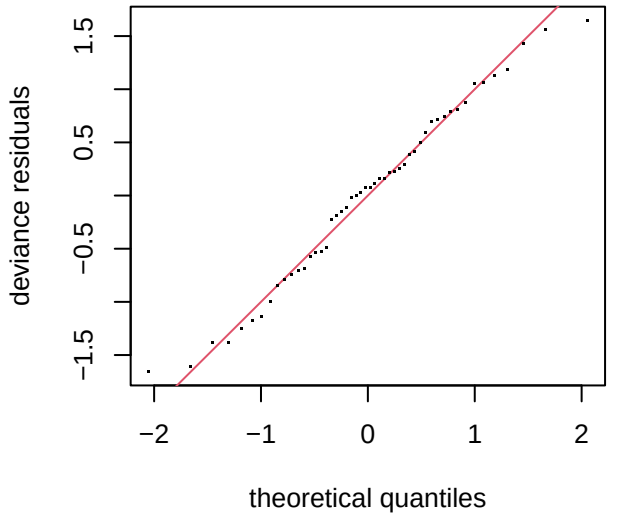

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

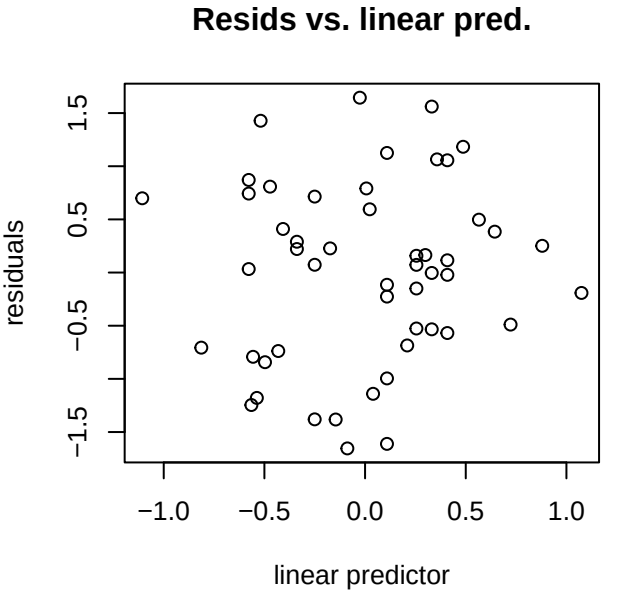

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
linear predictor

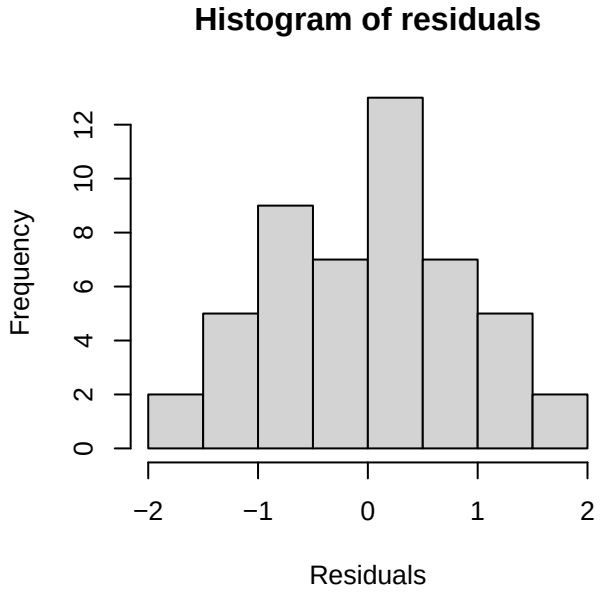

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

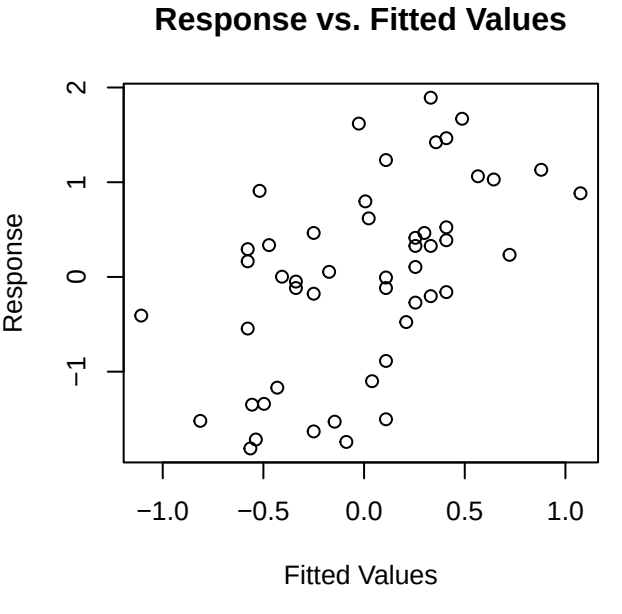

Response vs. Fitted Values
Response
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
Fitted Values

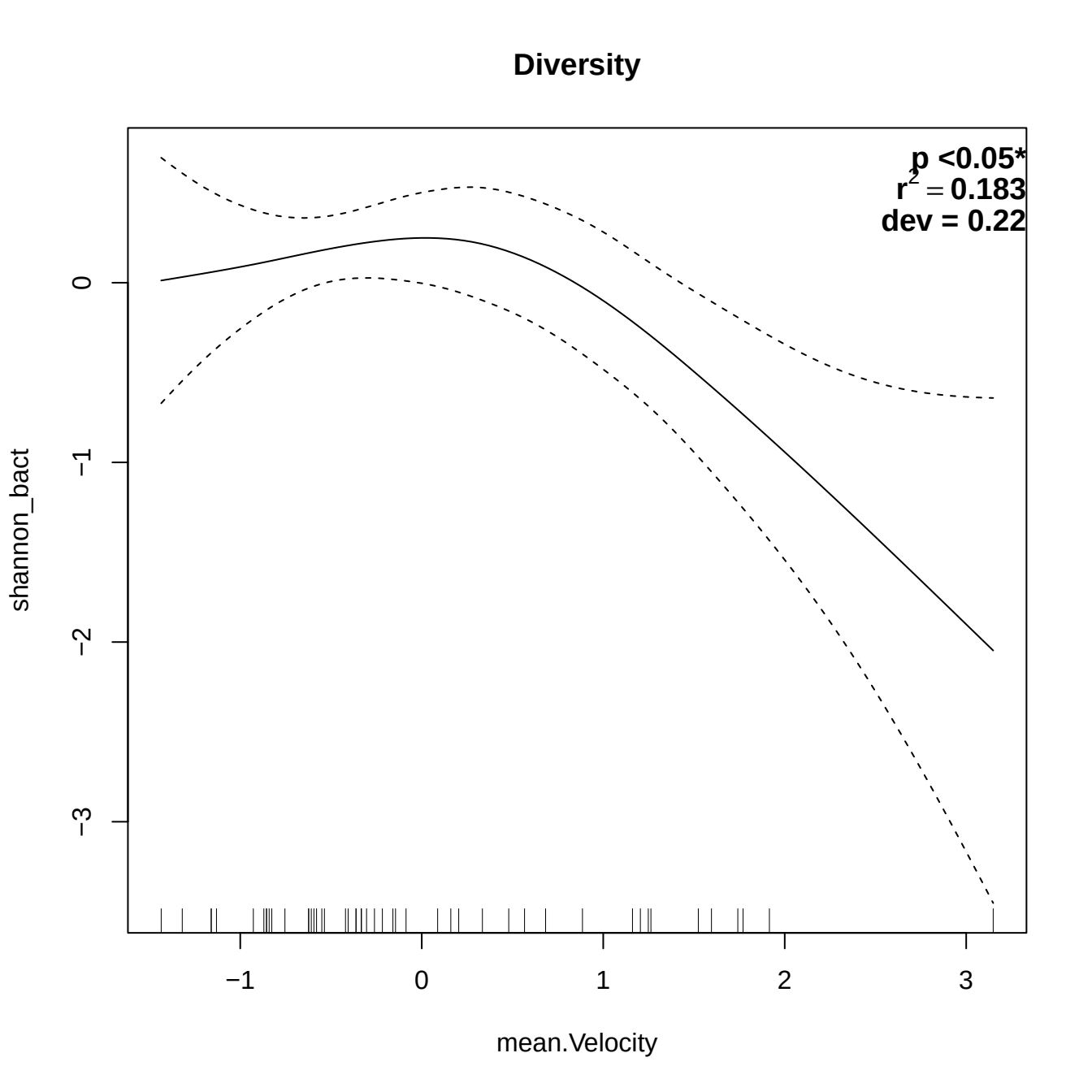

Diversity
p <0.05*
r2 = 0.22
dev = 0.277
fungi
2
1
0
−1
−2
0
1
2
3
4
P.PO4

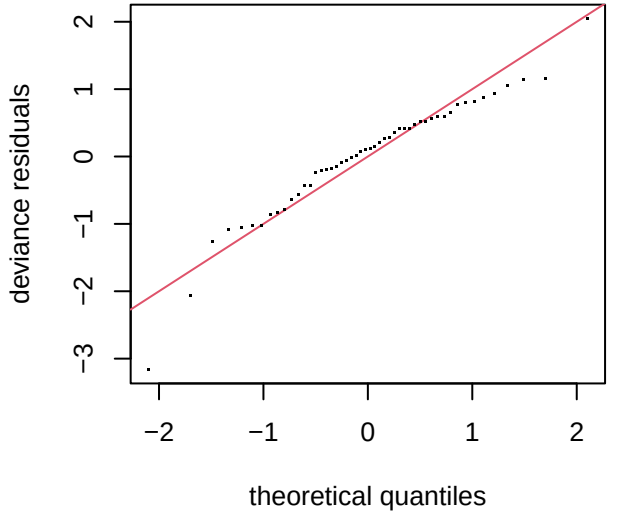

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

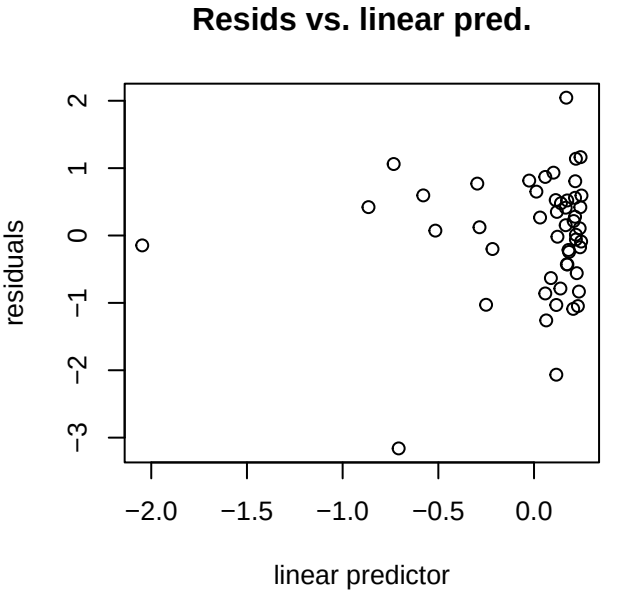

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
linear predictor

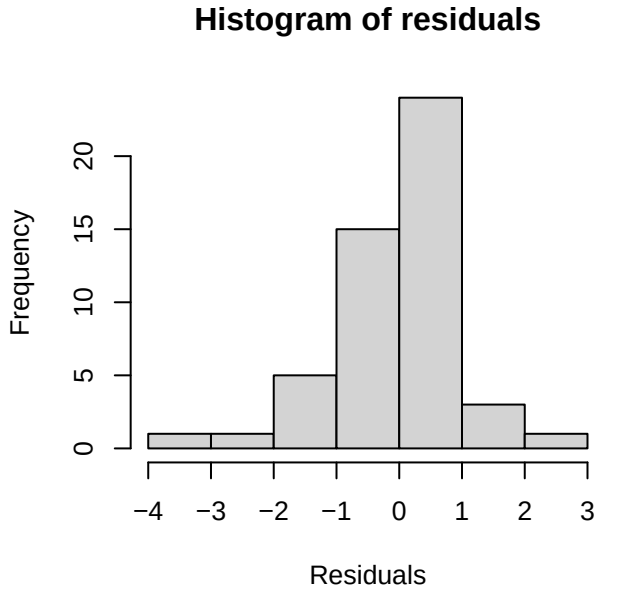

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

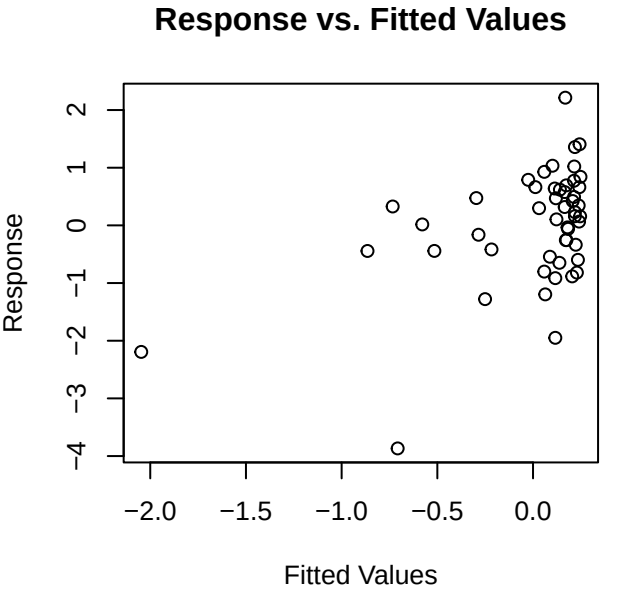

Response vs. Fitted Values
Response
2
1
0
−1
−1.0
−0.5
0.0
0.5
1.0
Fitted Values

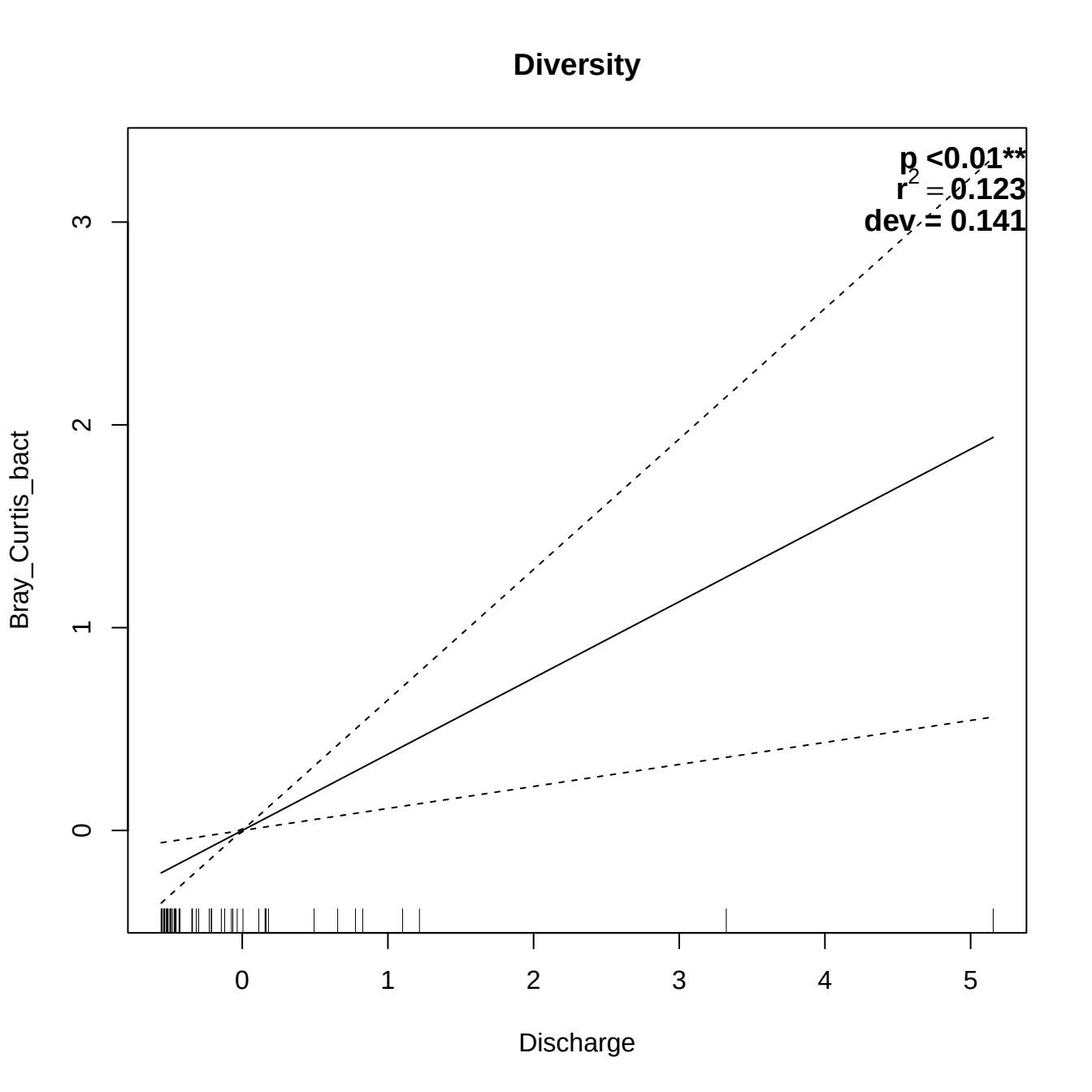

Diversity
p <0.05*
r2 = 0.183
dev = 0.22
shannon_bact
0
−1
−2
−3
−1
0
1
2
3
mean.Velocity

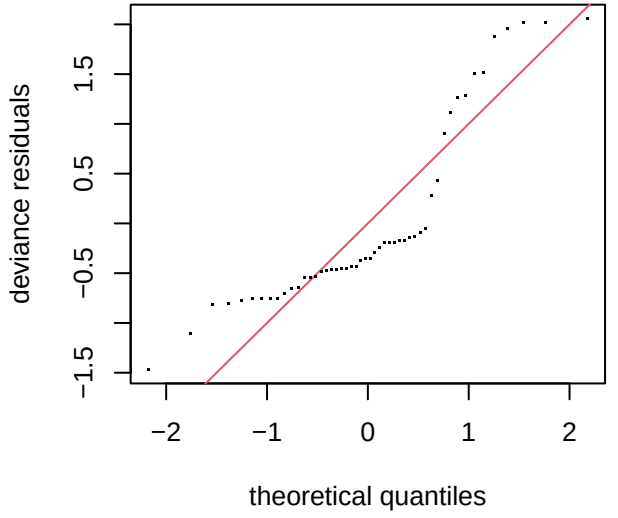

deviance residuals
theoretical quantiles

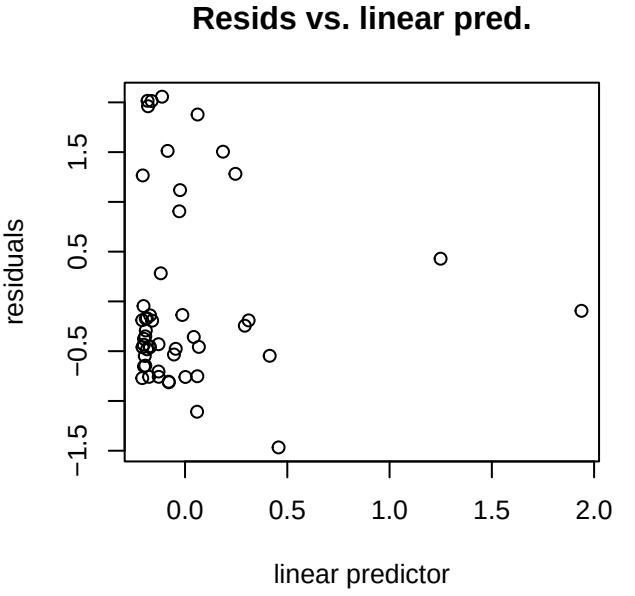

Resids vs. linear pred.
residuals
linear predictor

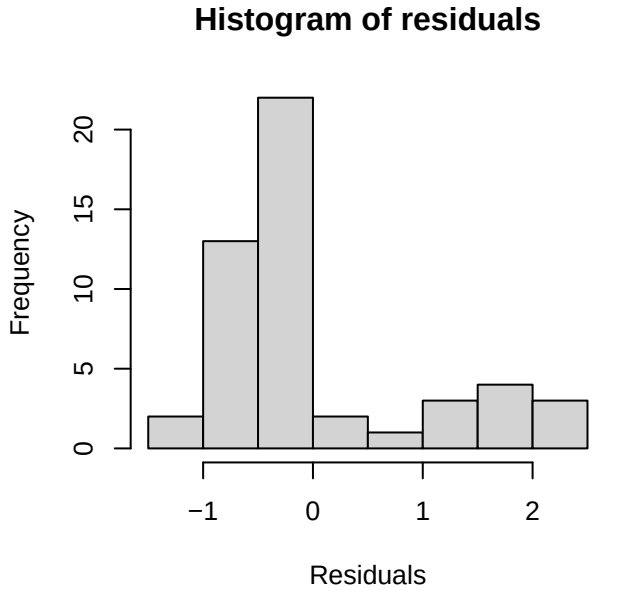

Histogram of residuals
Frequency
Residuals

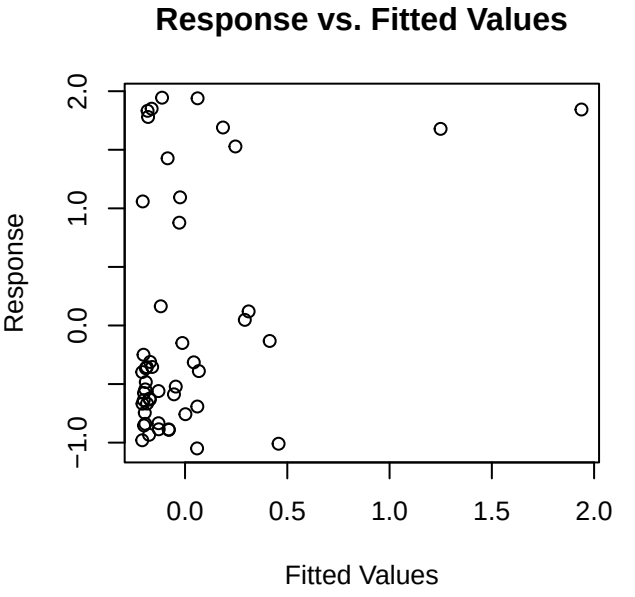

Response vs. Fitted Values
Response
Fitted Values

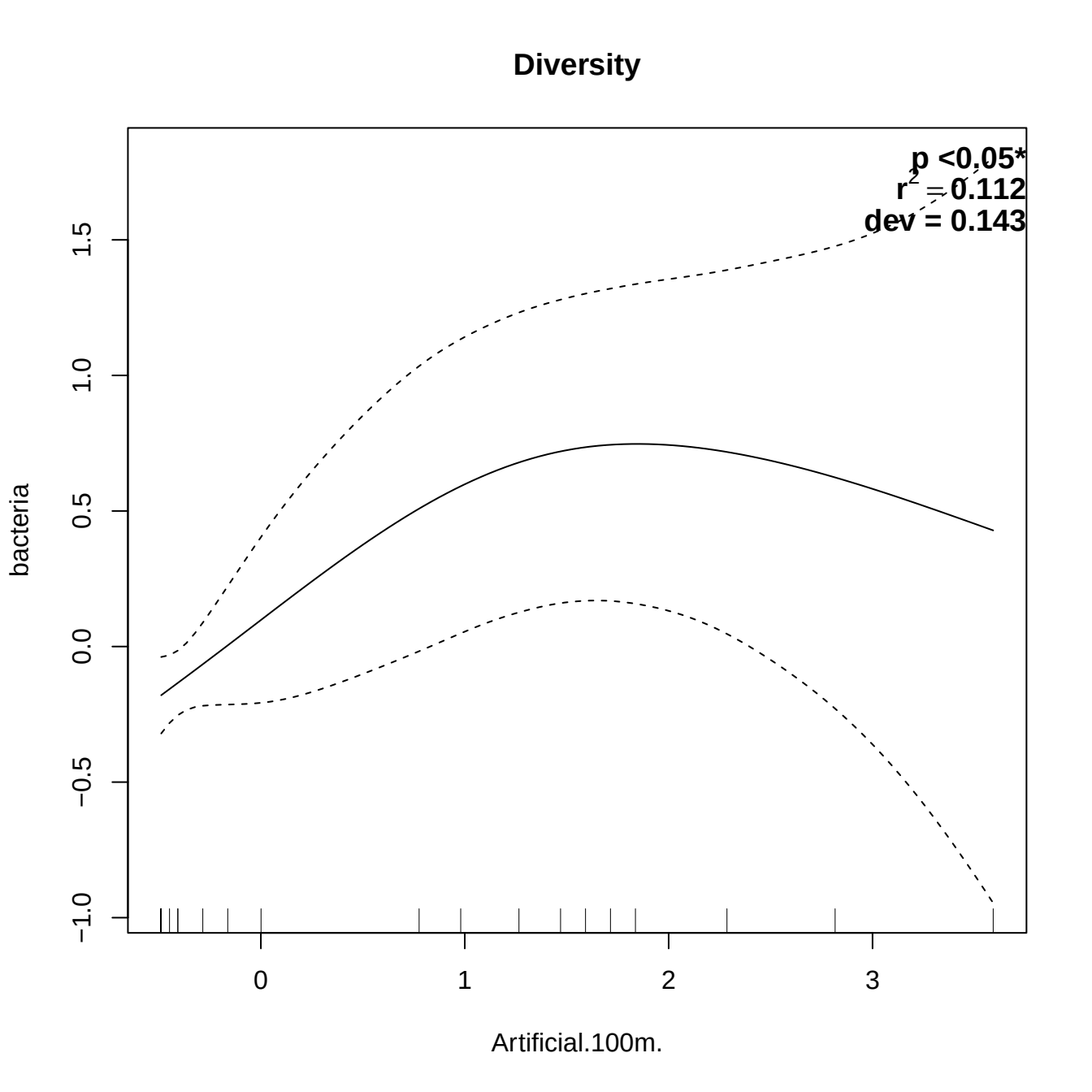

Diversity
p <0.01**
r2 = 0.123
dev = 0.141
Bray_Curtis_bact
Discharge
0
1
2
3
4
5

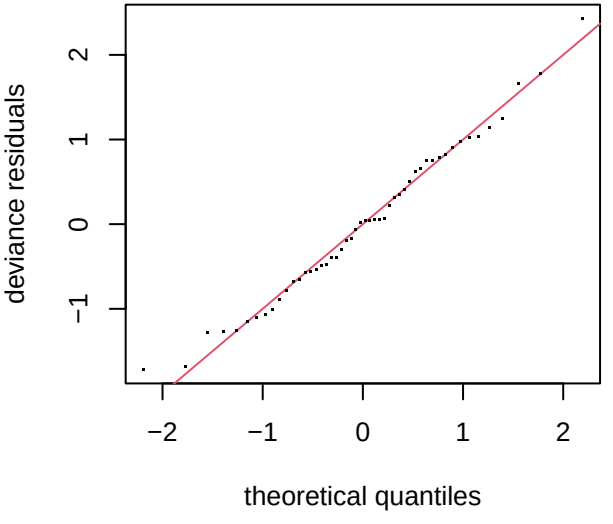

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

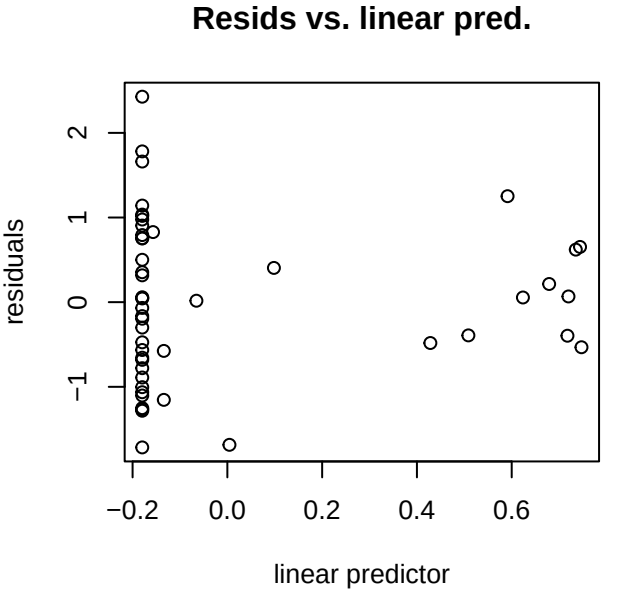

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
0.0
0.5
1.0
1.5
2.0
linear predictor

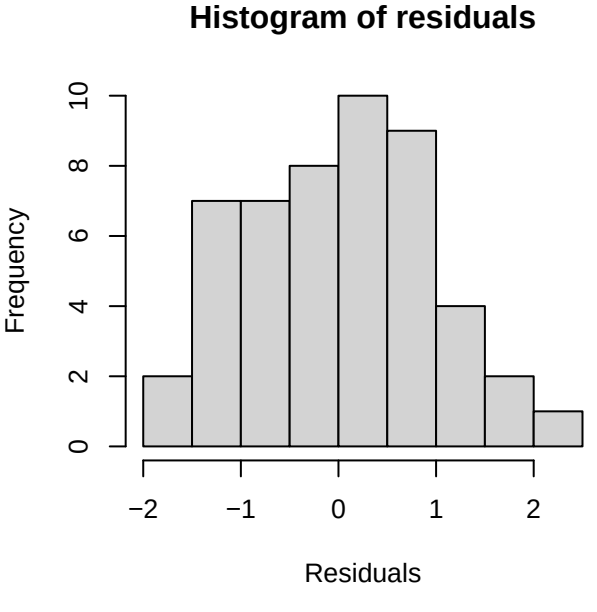

Histogram of residuals
Frequency
0
5
10
15
20
−1
0
1
2
Residuals

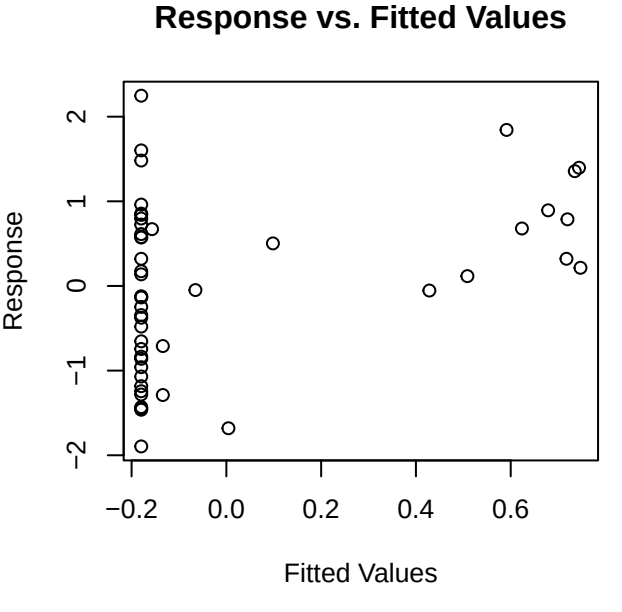

Response vs. Fitted Values
Response
2.0
1.0
0.0
−1.0
0.0
0.5
1.0
1.5
2.0
Fitted Values

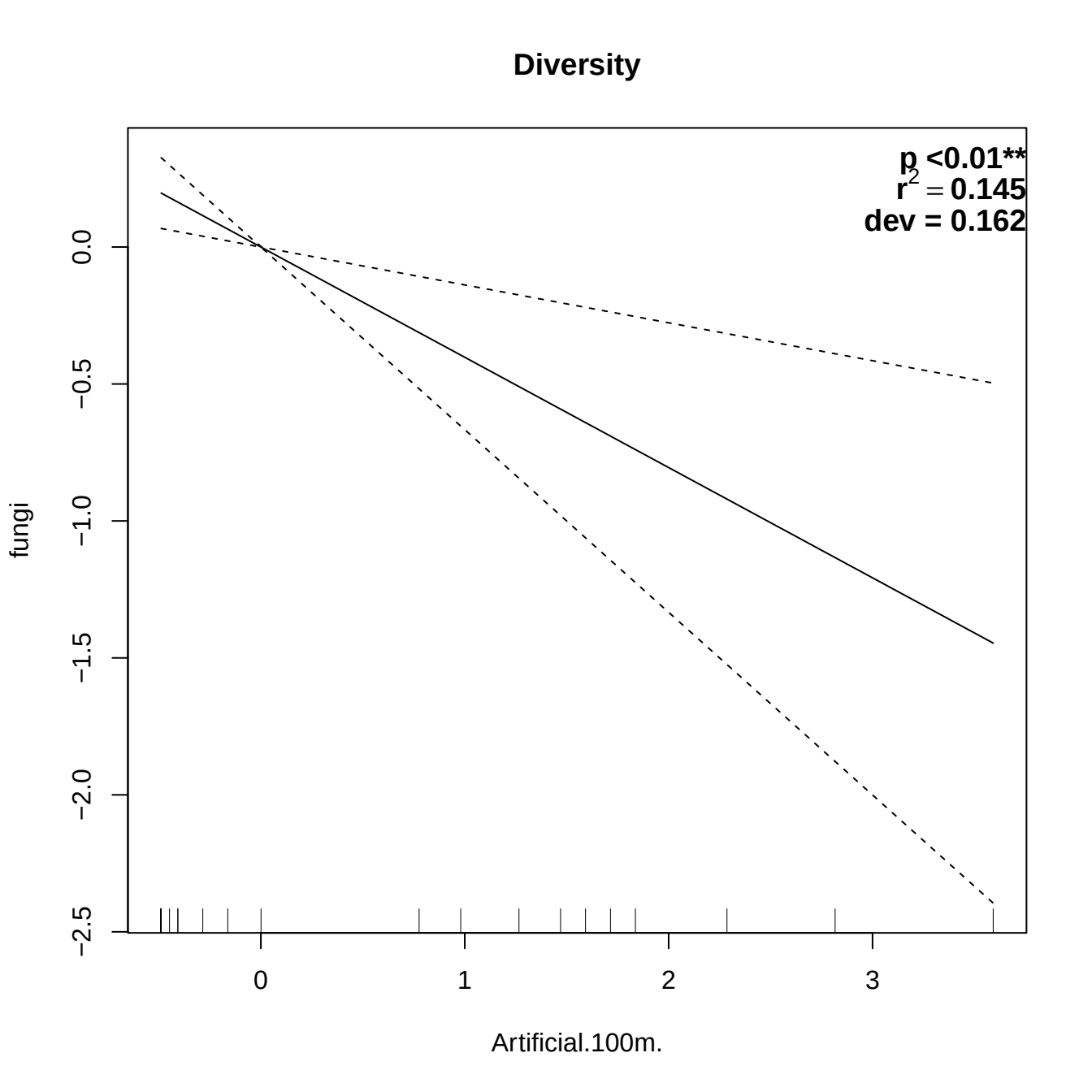

Diversity
p <0,05*
r2 = 0.112
dev = 0.143
bacteria
1.5
1.0
0.5
0.0
−0.5
−1.0
0
1
2
3
Artificial.100m.

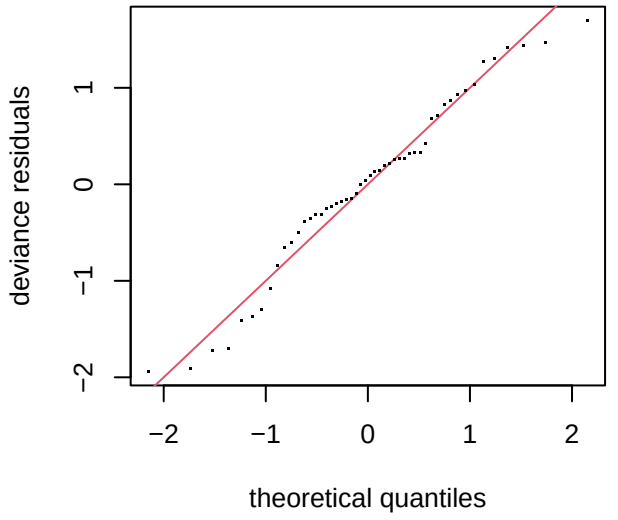

deviance residuals
theoretical quantiles

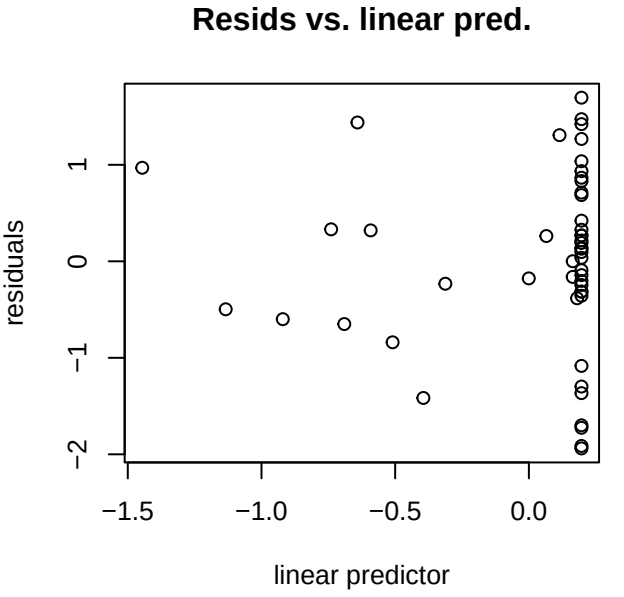

Resids vs. linear pred.
residuals
linear predictor

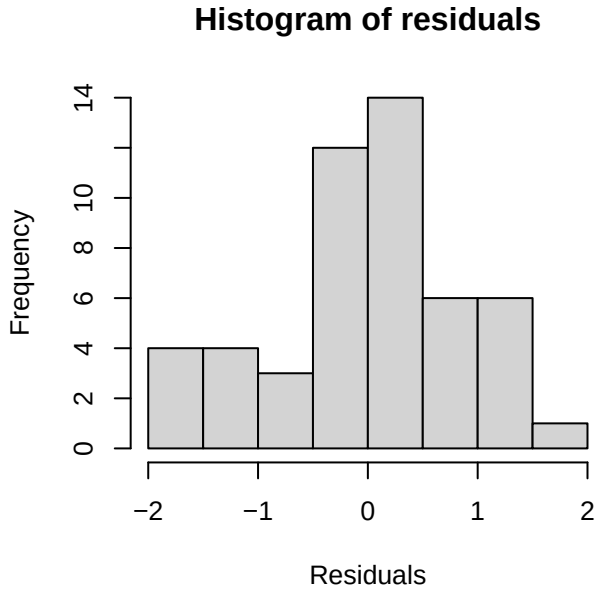

Histogram of residuals
Frequency
Residuals

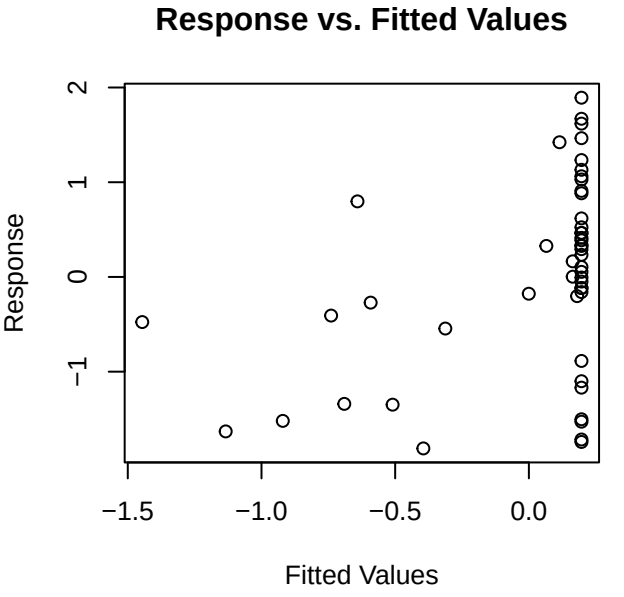

Response vs. Fitted Values
Response
Fitted Values

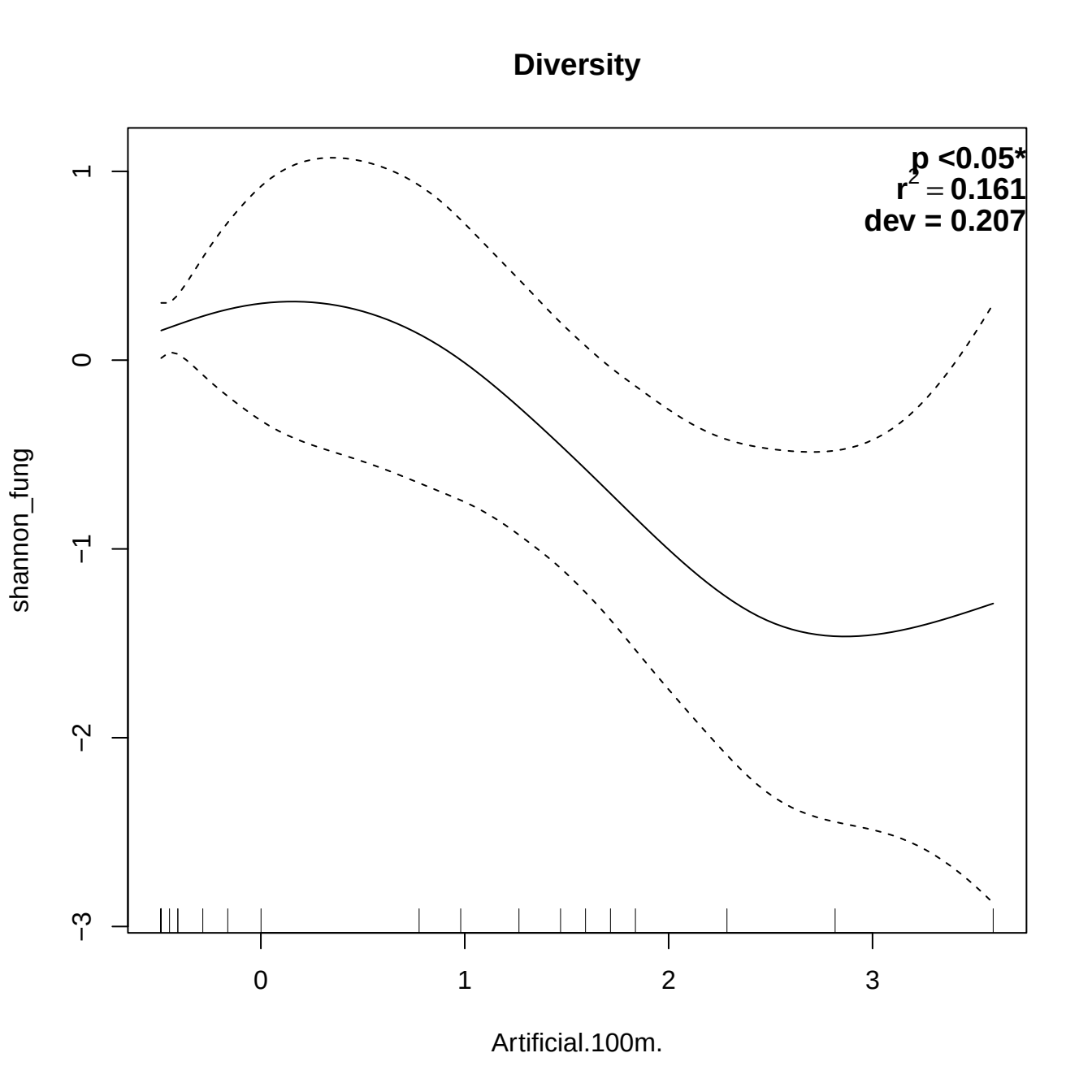

Diversity
p <0.01**
r2 = 0.145
dev = 0.162
fungi
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0
1
2
3
Artificial.100m.

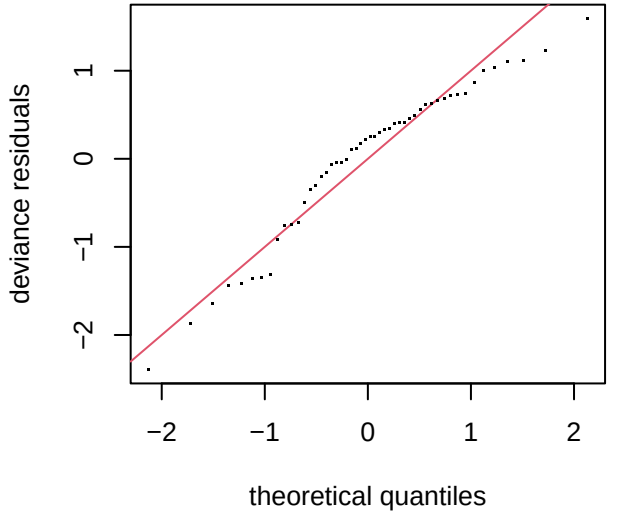

deviance residuals
theoretical quantiles

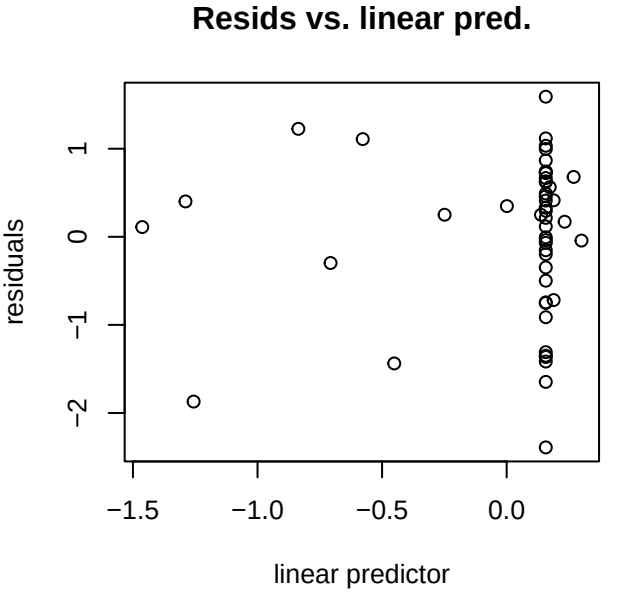

Resids vs. linear pred.
residuals
linear predictor

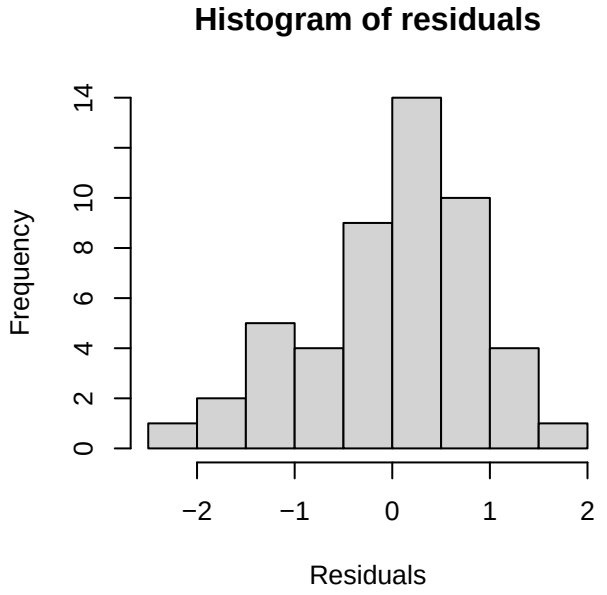

Histogram of residuals
Frequency
Residuals

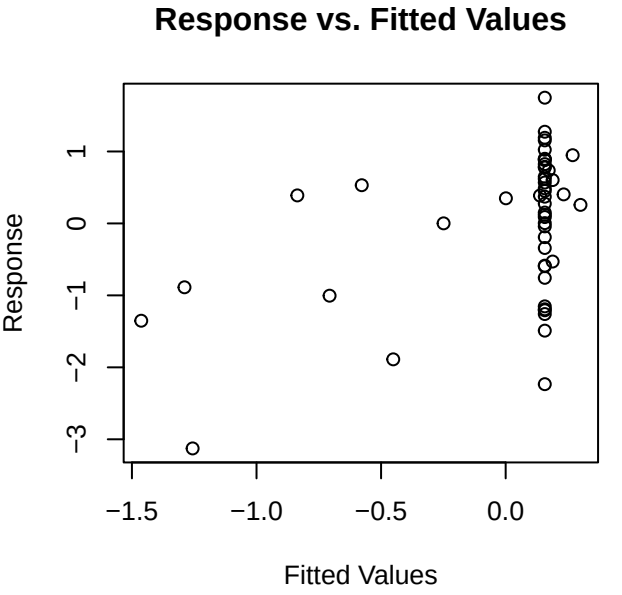

Response vs. Fitted Values
Response
Fitted Values

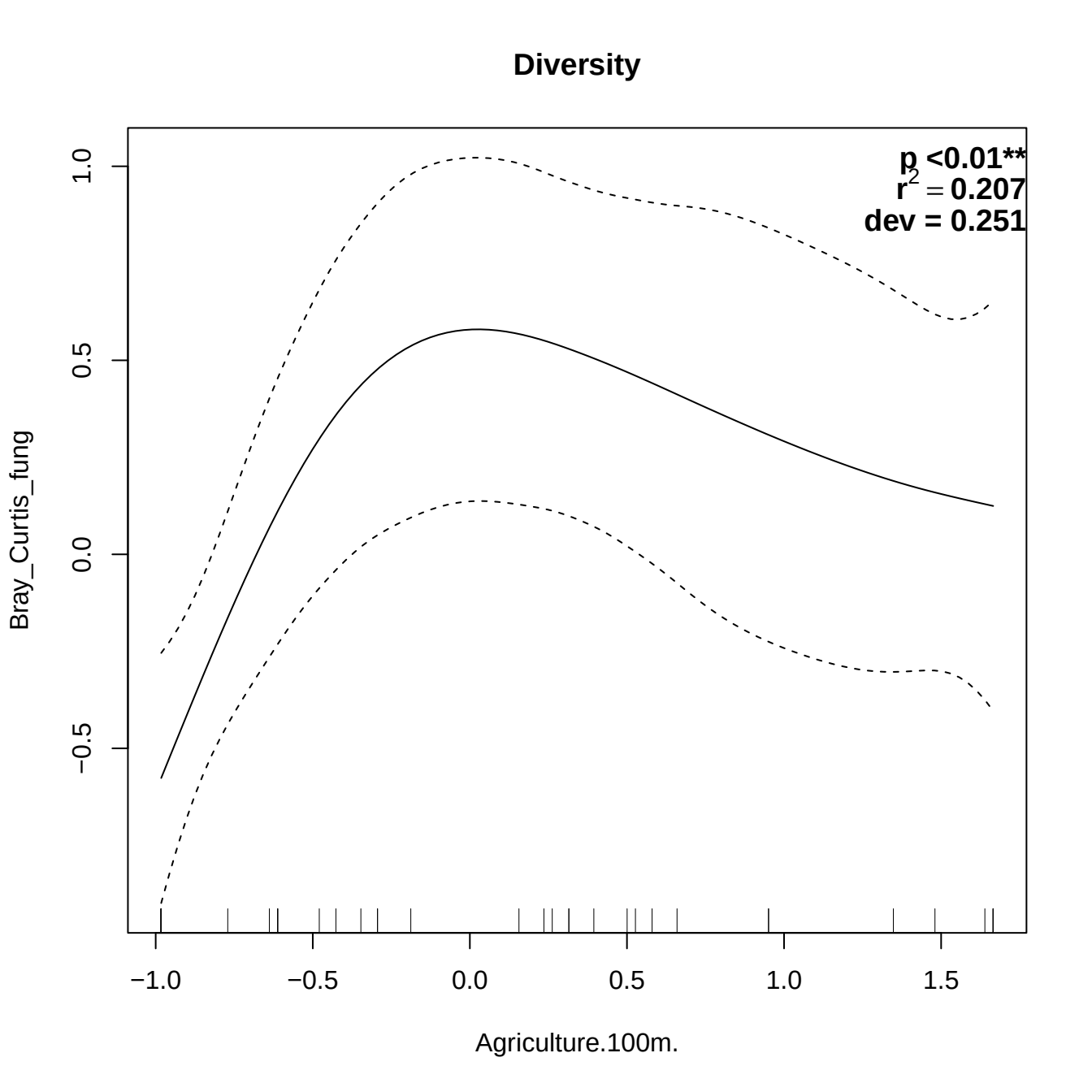

Diversity
p <0.05*
r2 = 0.161
dev = 0.207
shannon_fung
1
0
−1
−2
−3
0
1
2
3
Artificial.100m.

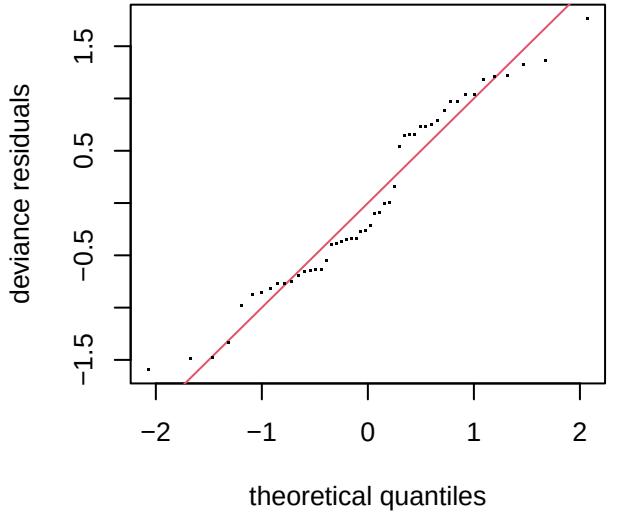

deviance residuals
theoretical quantiles

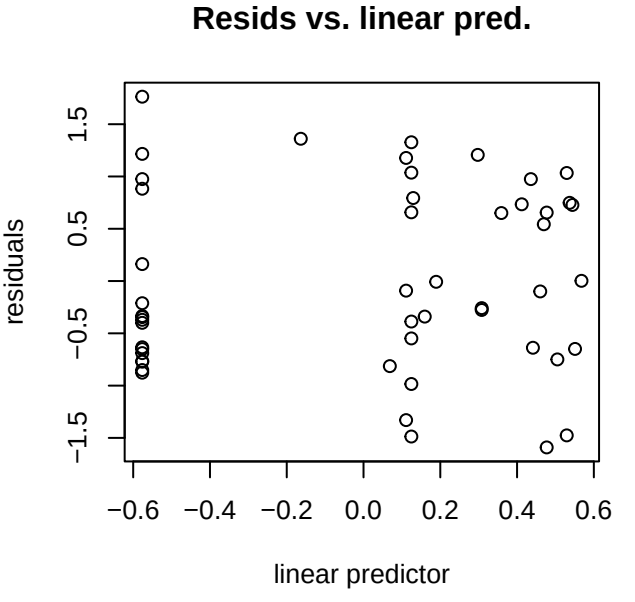

Resids vs. linear pred.
residuals
linear predictor

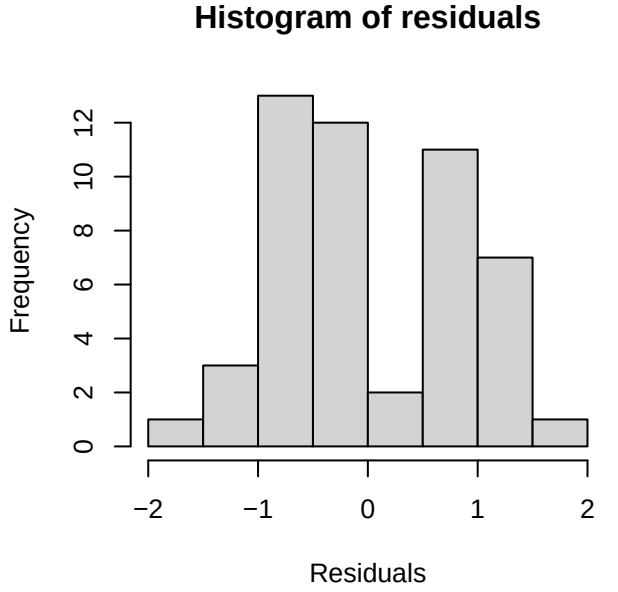

Histogram of residuals
Frequency
Residuals

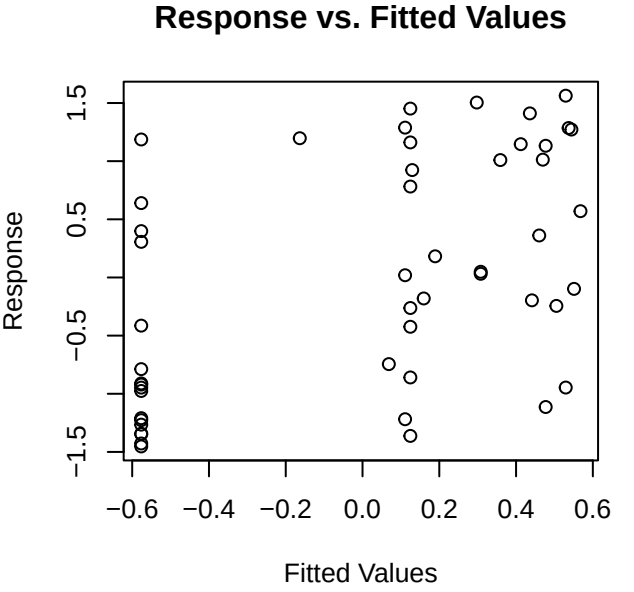

Response vs. Fitted Values
Response
Fitted Values

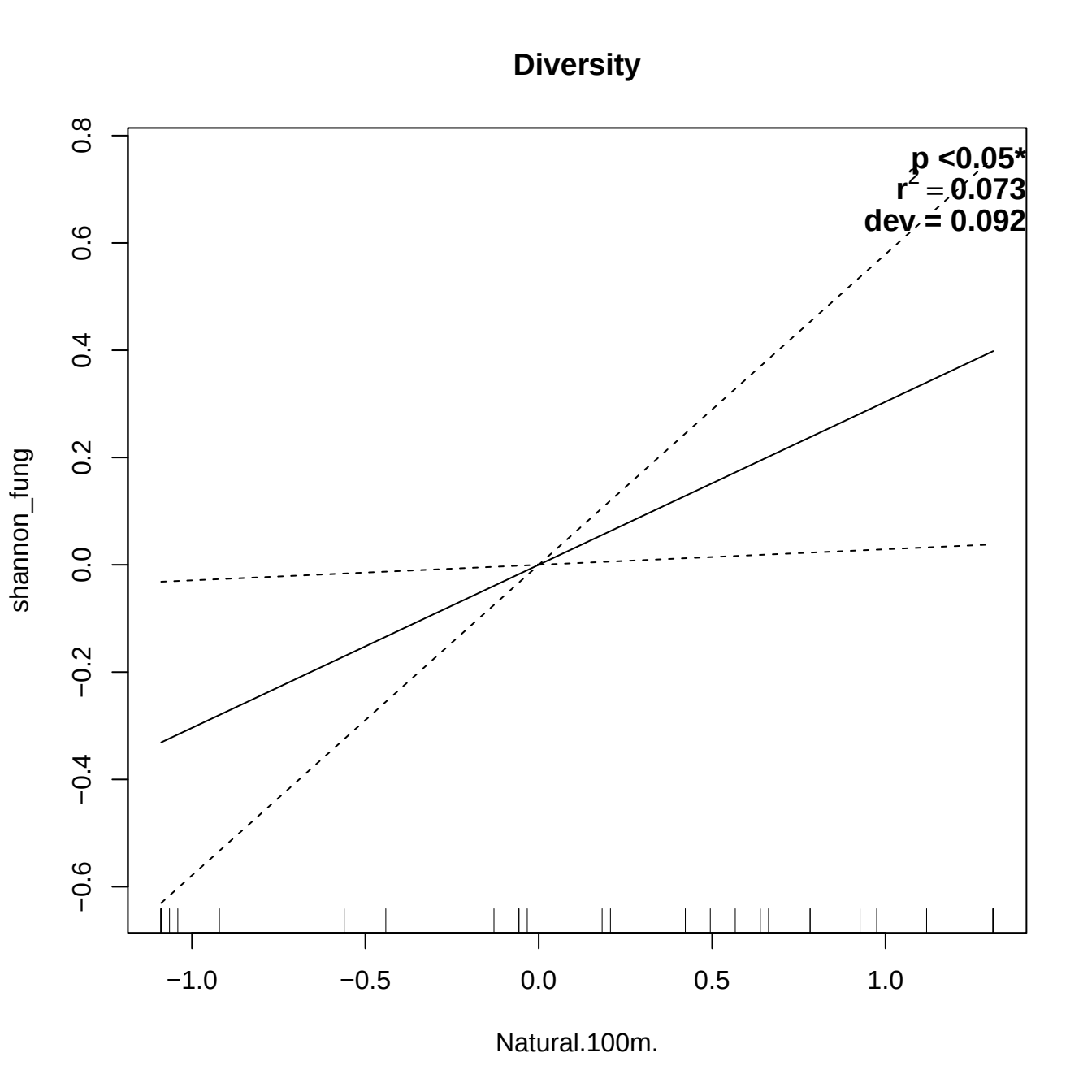

Diversity
p <0.01**
r2 = 0.207
dev = 0.251
Bray_Curtis_fung
1.0
0.5
0.0
−0.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Agriculture.100m.

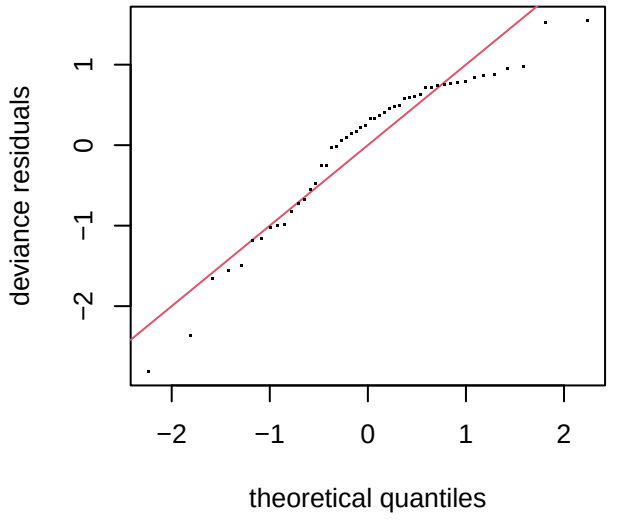

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

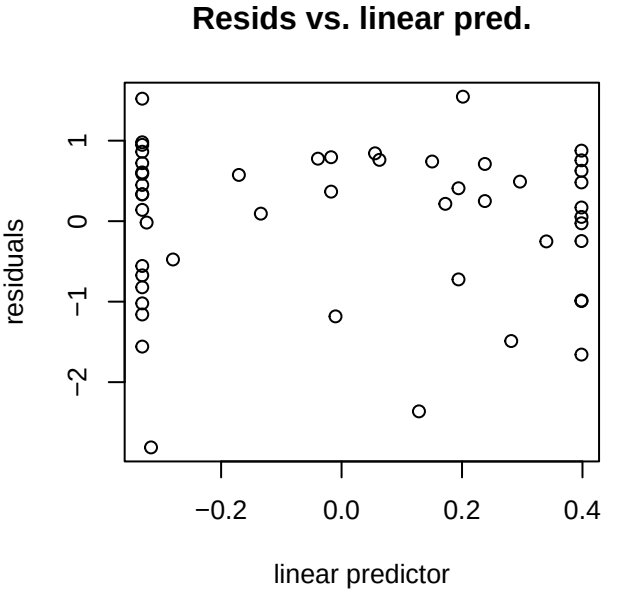

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
linear predictor

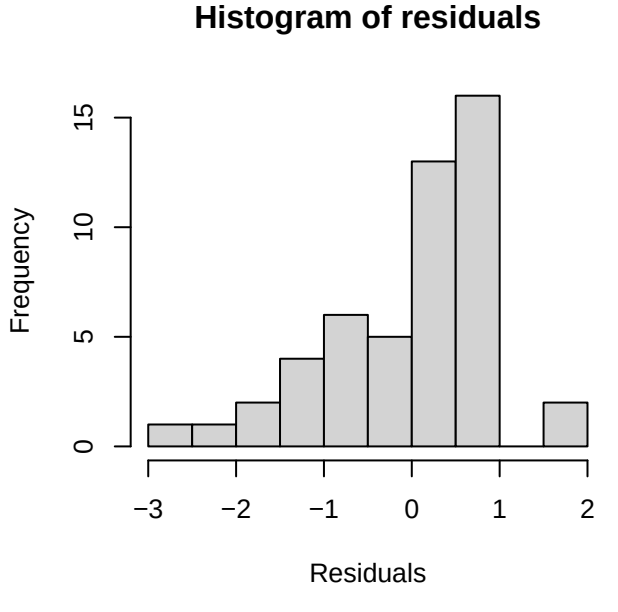

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

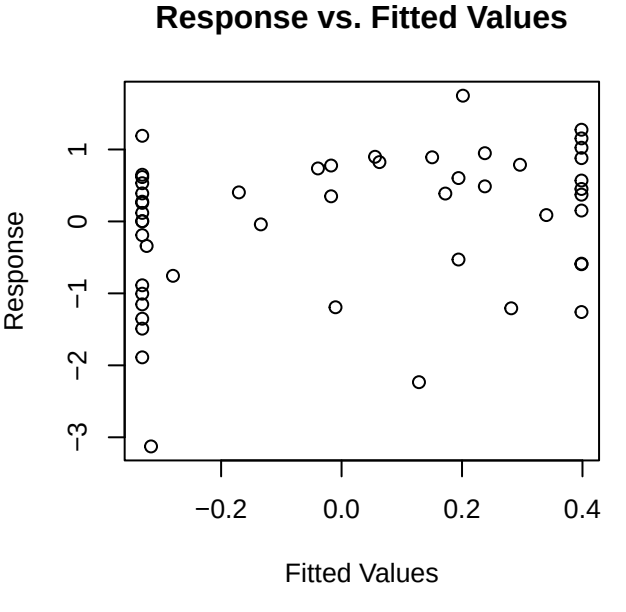

Response vs. Fitted Values
Response
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
Fitted Values

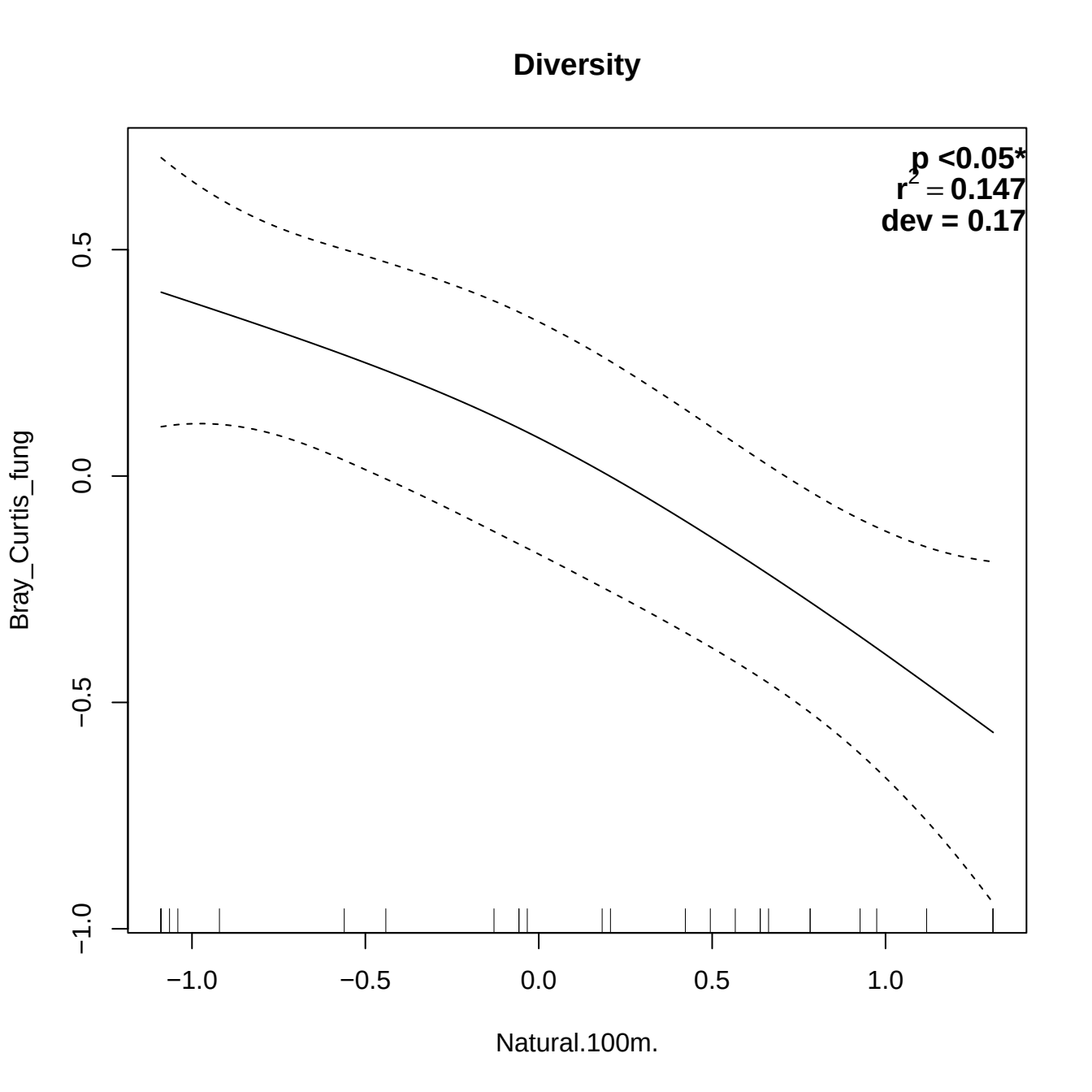

Diversity
p <0.05*
r2 = 0.073
dev = 0.092
shannon_fung
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−1.0
−0.5
0.0
0.5
1.0
Natural.100m.

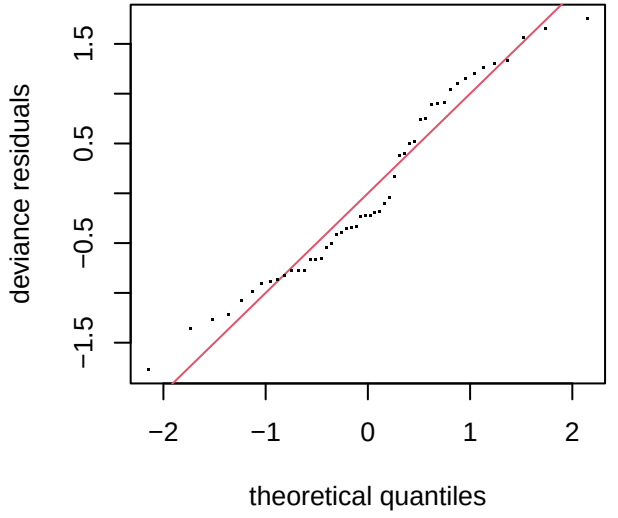

deviance residuals
theoretical quantiles

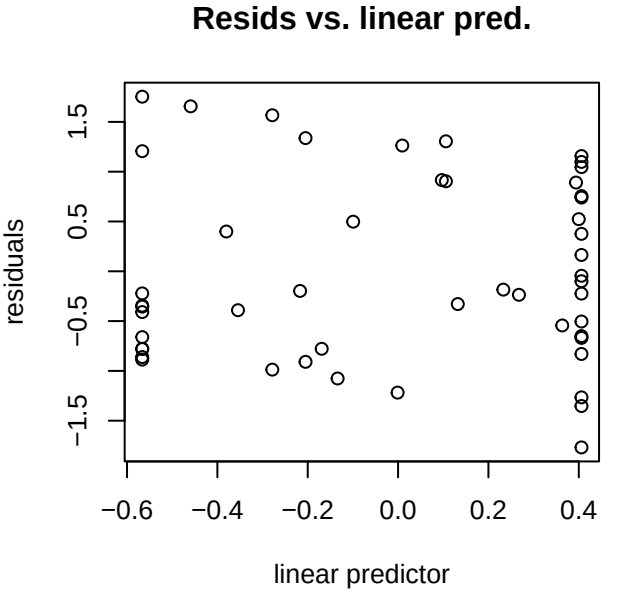

Resids vs. linear pred.
residuals
linear predictor

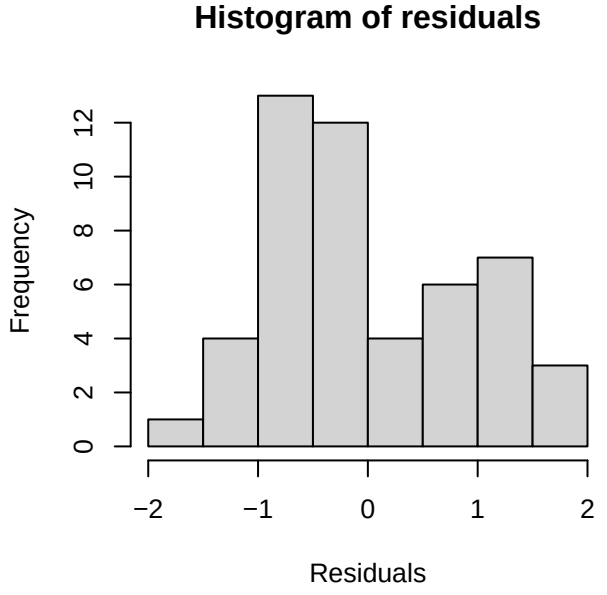

Histogram of residuals
Frequency
Residuals

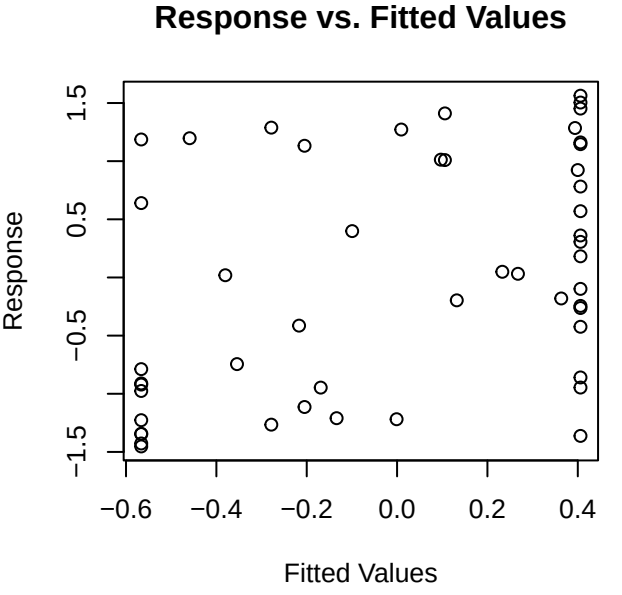

Response vs. Fitted Values
Response
Fitted Values

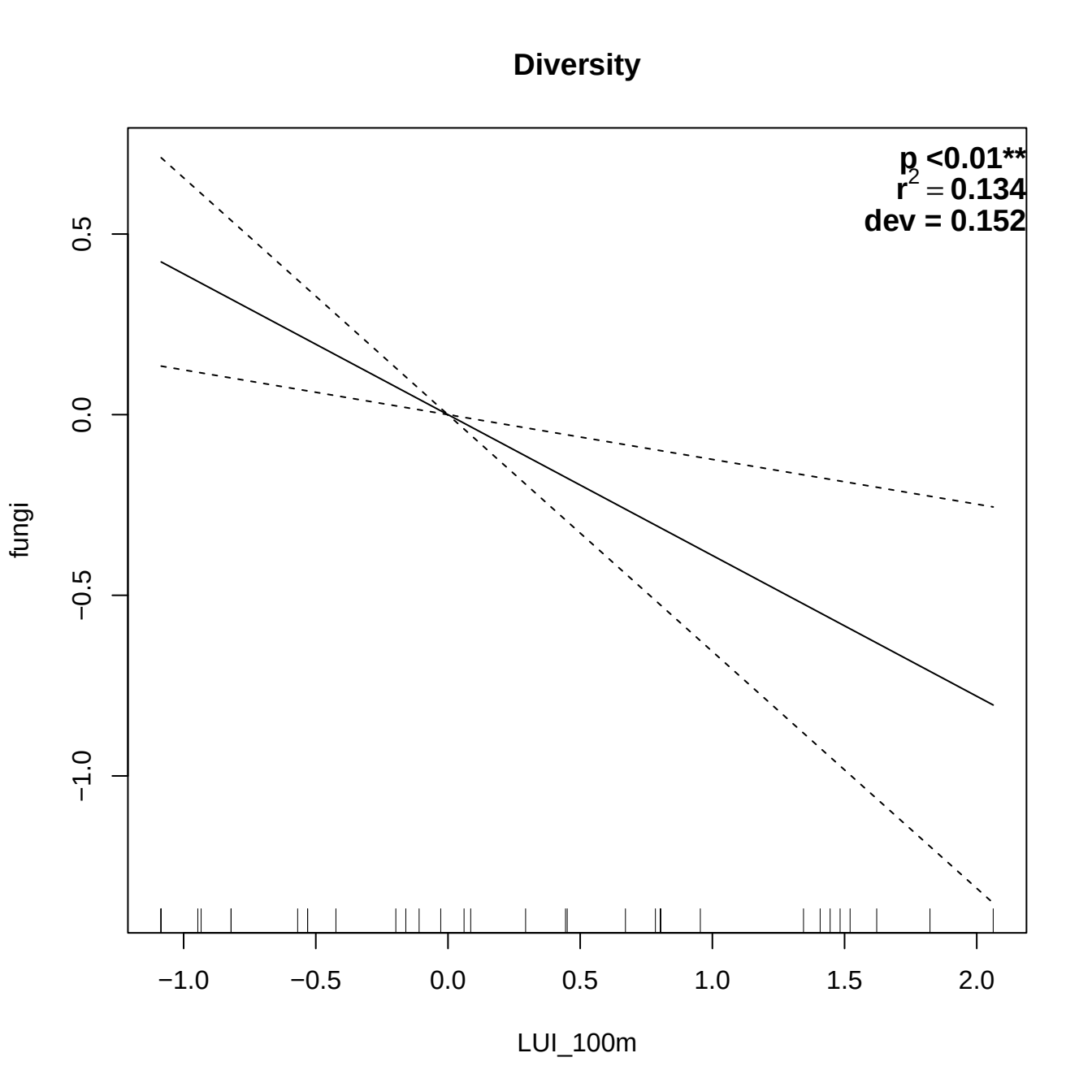

Diversity
p <0.05*
r2 = 0.147
dev = 0.17
Bray_Curtis_fung
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0
Natural.100m.

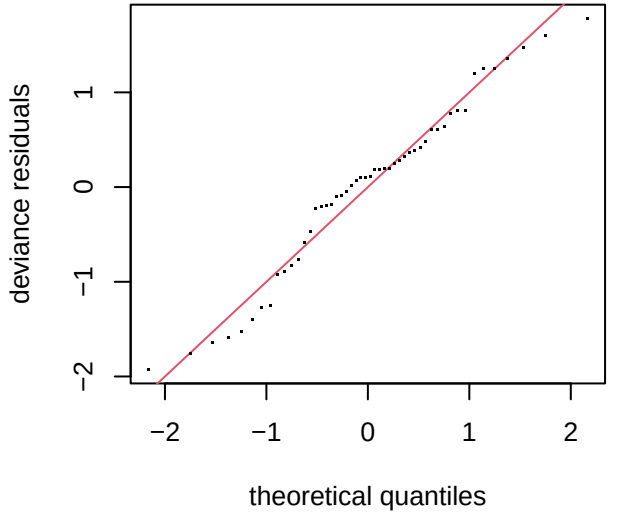

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

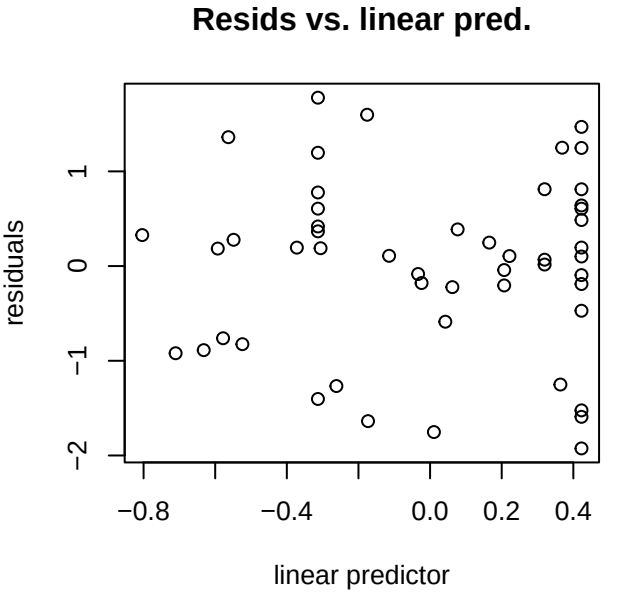

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
linear predictor

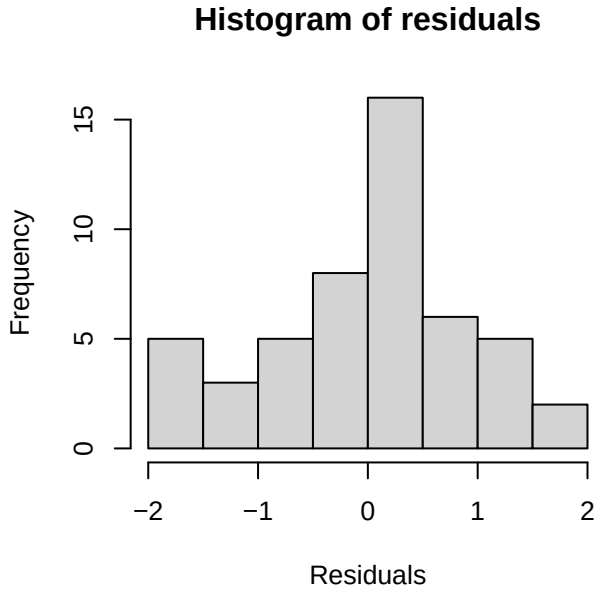

Histogram of residuals
Frequency
0
2
4
6
8
10
12
−2
−1
0
1
2
Residuals

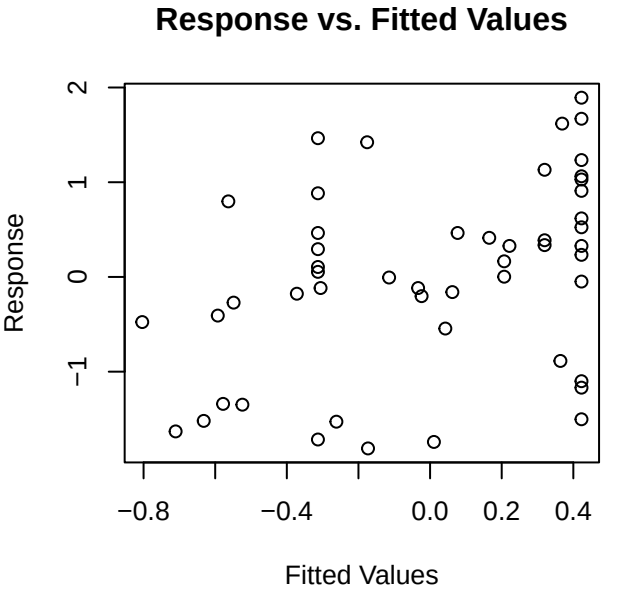

Response vs. Fitted Values
Response
1.5
0.5
−0.5
−1.5
−0.6
−0.4
−0.2
0.0
0.2
0.4
Fitted Values

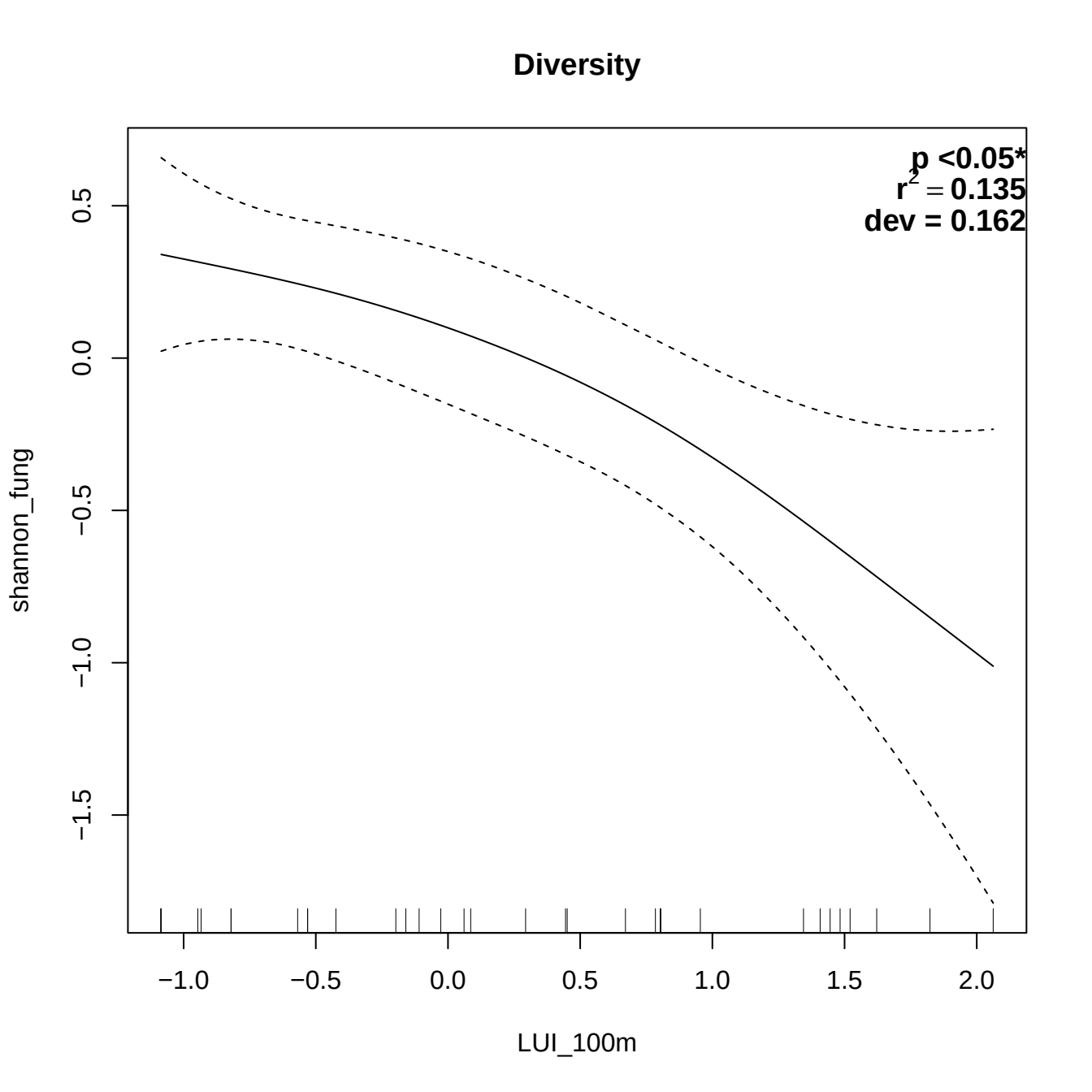

Diversity
p <0.01**
r2 = 0.134
dev = 0.152
fungi
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
LUI_100m

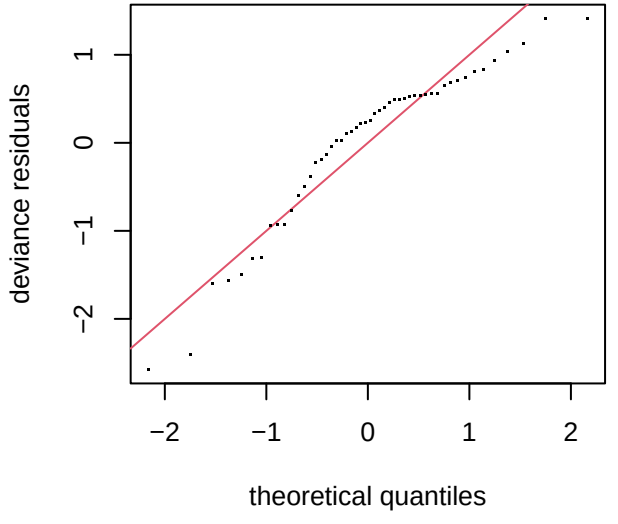

deviance residuals
−2
−1
0
1
−2
−1
0
1
2
theoretical quantiles

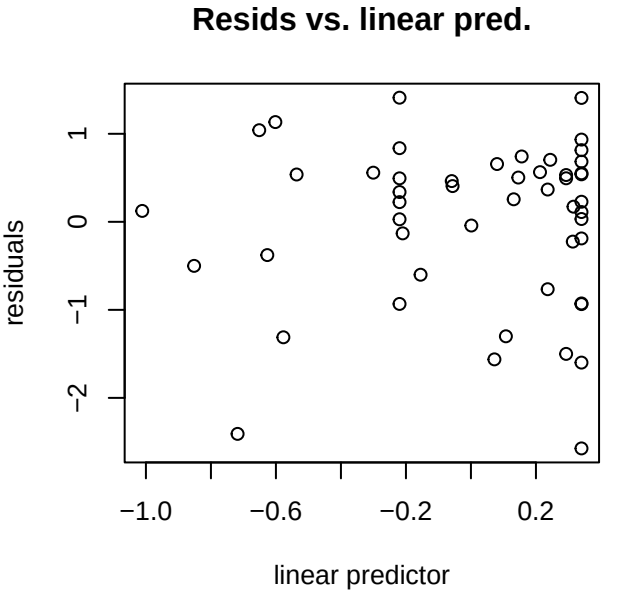

Resids vs. linear pred.
residuals
−2
−1
0
1
−0.8
−0.4
0.0
0.2
0.4
linear predictor

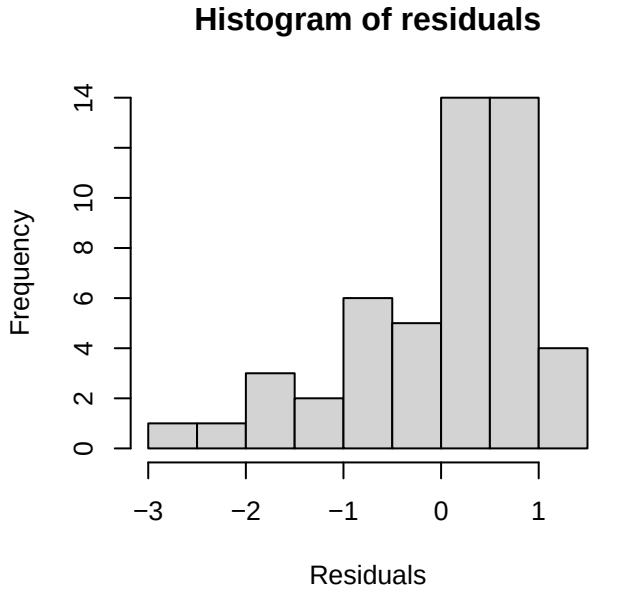

Histogram of residuals
Frequency
0
5
10
15
−2
−1
0
1
2
Residuals

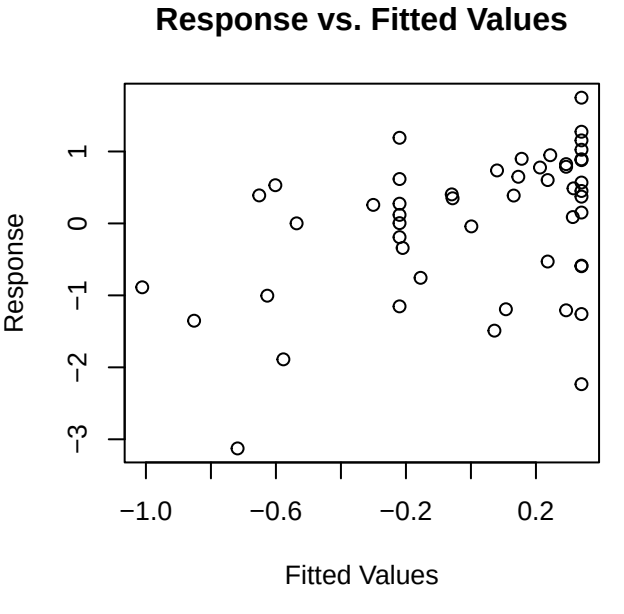

Response vs. Fitted Values
Response
−1
0
1
2
−0.8
−0.4
0.0
0.2
0.4
Fitted Values

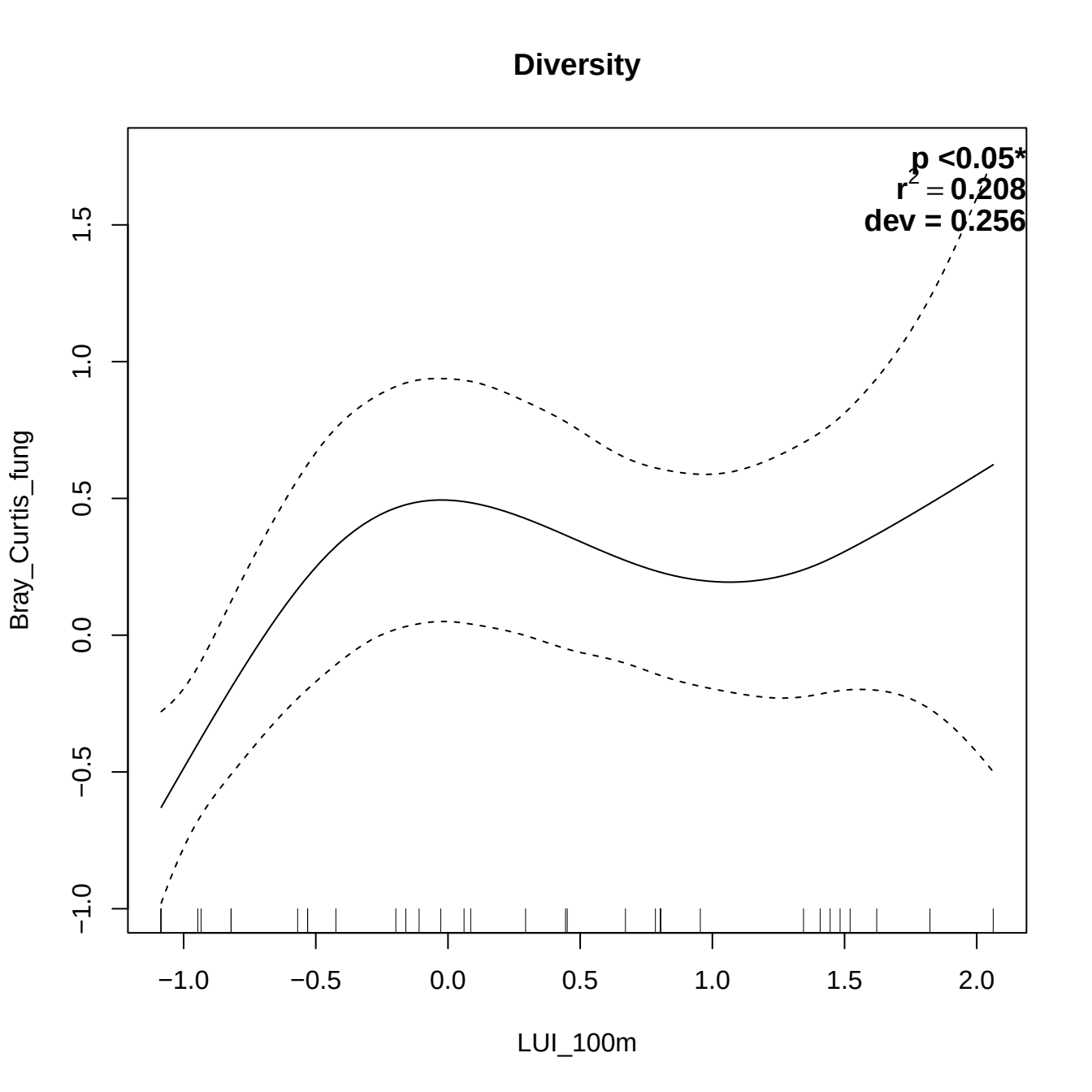

Diversity
p <0.05*
r2 = 0.135
dev = 0.162
shannon_fung
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
LUI_100m

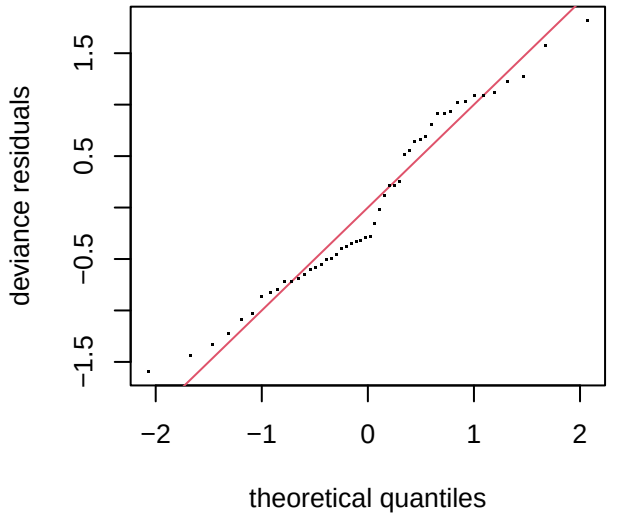

deviance residuals
theoretical quantiles

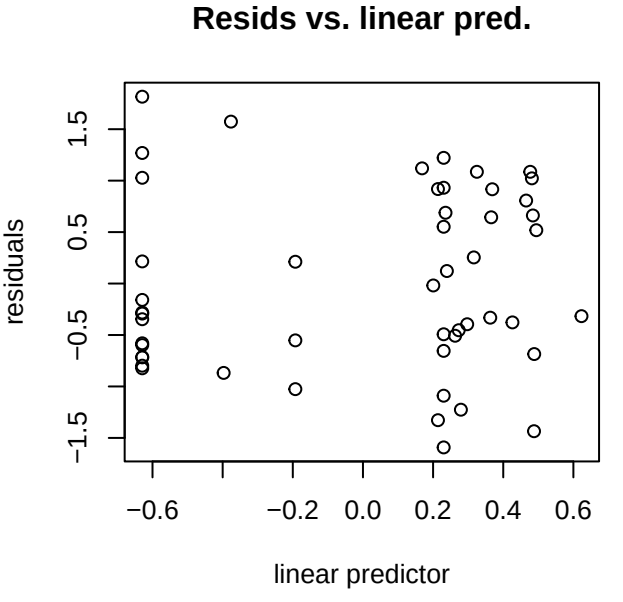

Resids vs. linear pred.
residuals
linear predictor

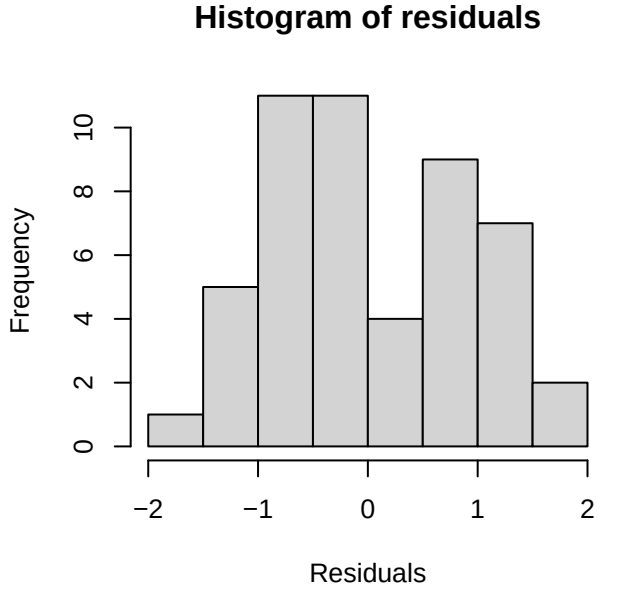

Histogram of residuals
Frequency
Residuals

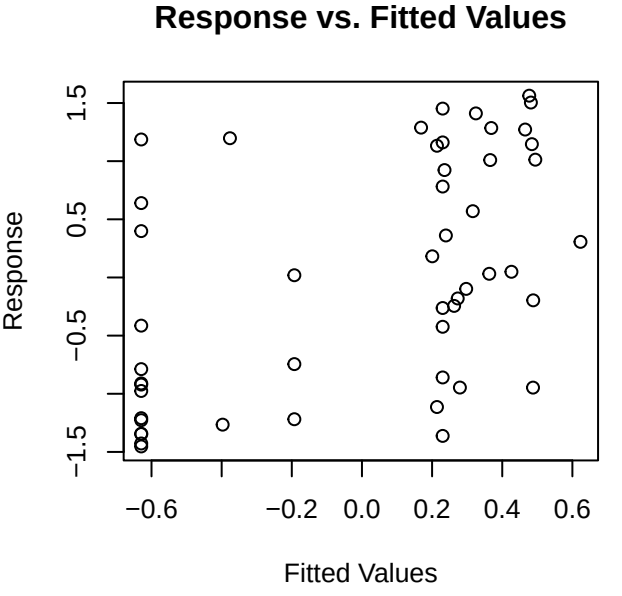

Response vs. Fitted Values
Response
Fitted Values

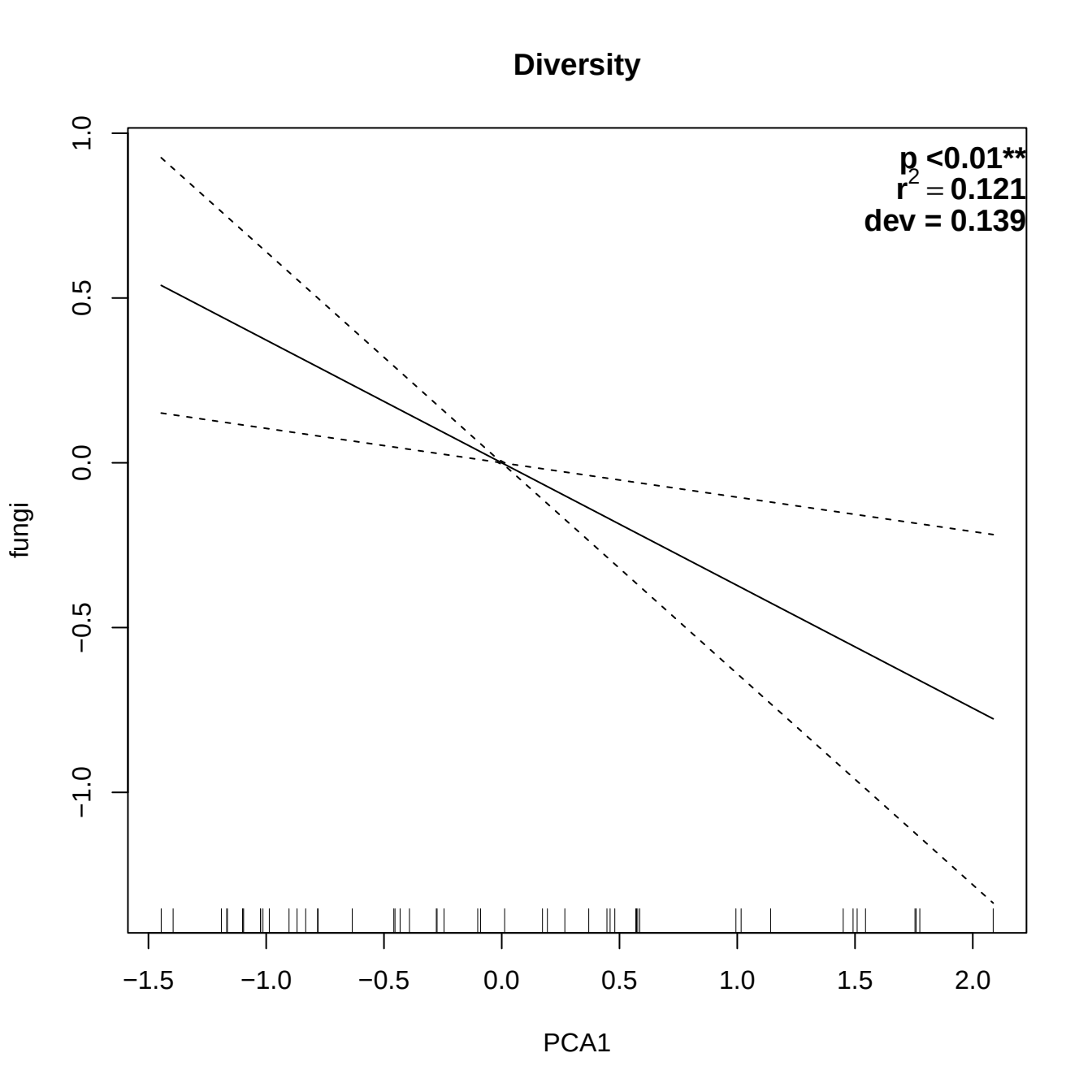

Diversity
p <0.05*
r2 = 0.208
dev = 0.256
Bray_Curtis_fung
LUI_100m
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0

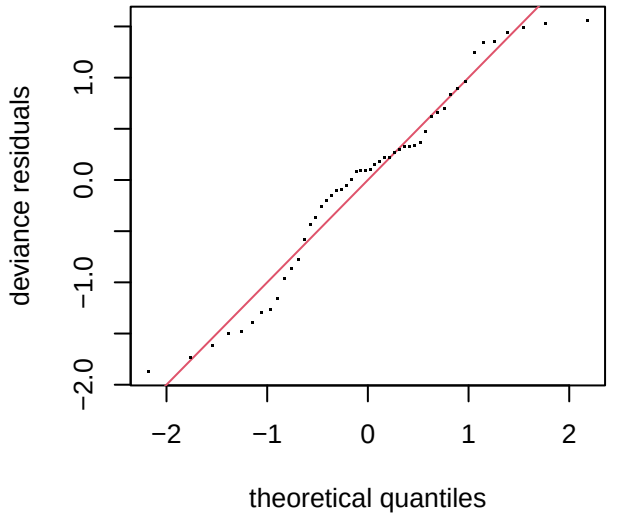

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

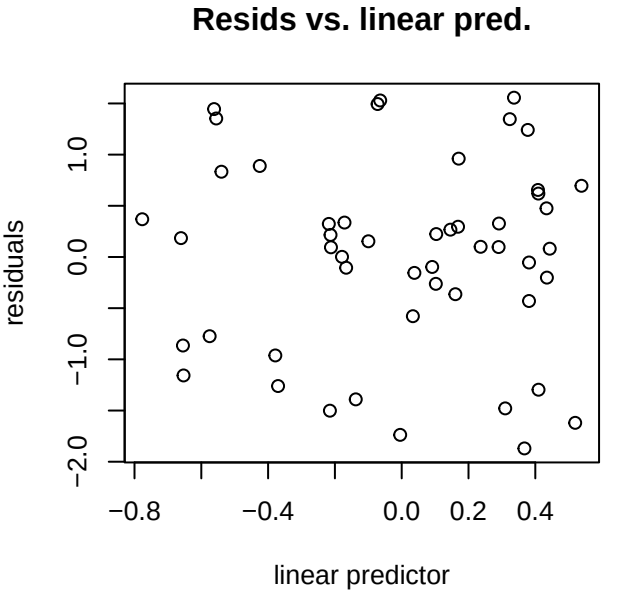

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−0.6
−0.2
0.0
0.2
0.4
0.6
linear predictor

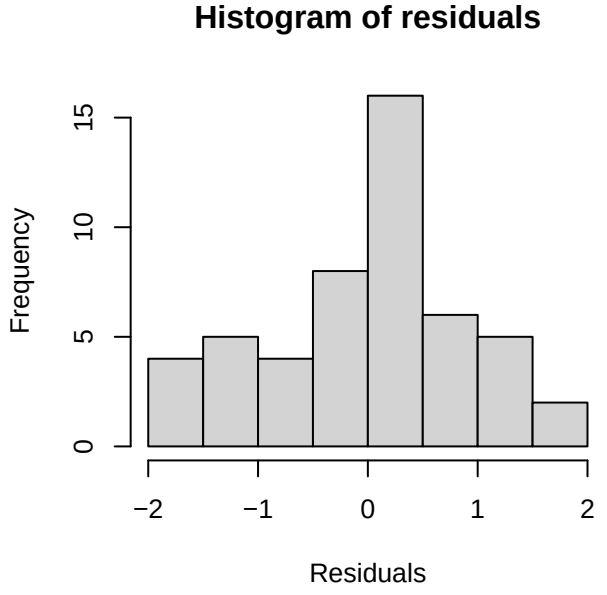

Histogram of residuals
Frequency
0
2
4
6
8
10
−2
−1
0
1
2
Residuals

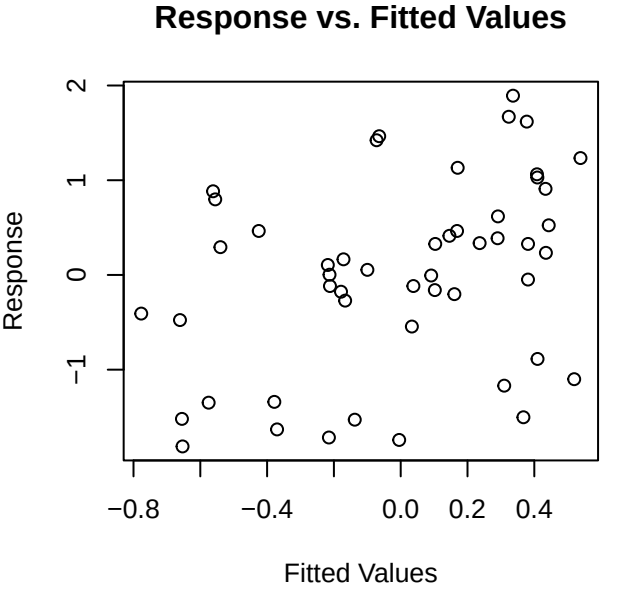

Response vs. Fitted Values
Response
1.5
0.5
−0.5
−1.5
−0.6
−0.2
0.0
0.2
0.4
0.6
Fitted Values

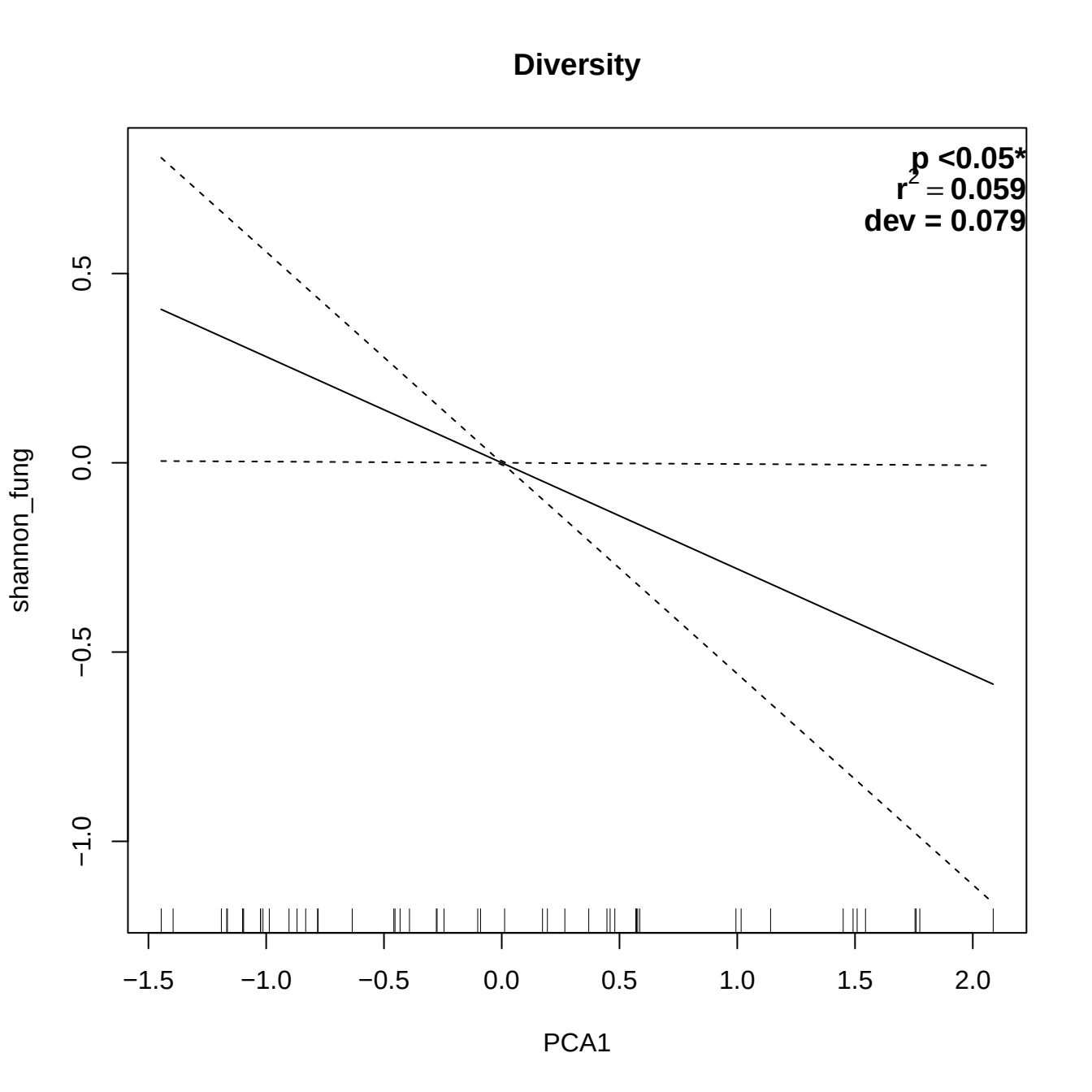

Diversity
p <0.01**
r2 = 0.121
dev = 0.139
fungi
PCA1
1.0
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0

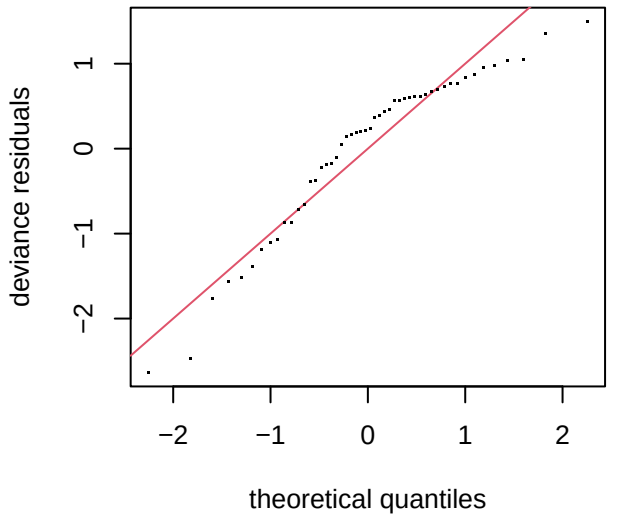

deviance residuals
1.0
0.0
−1.0
−2.0
−2
−1
0
1
2
theoretical quantiles

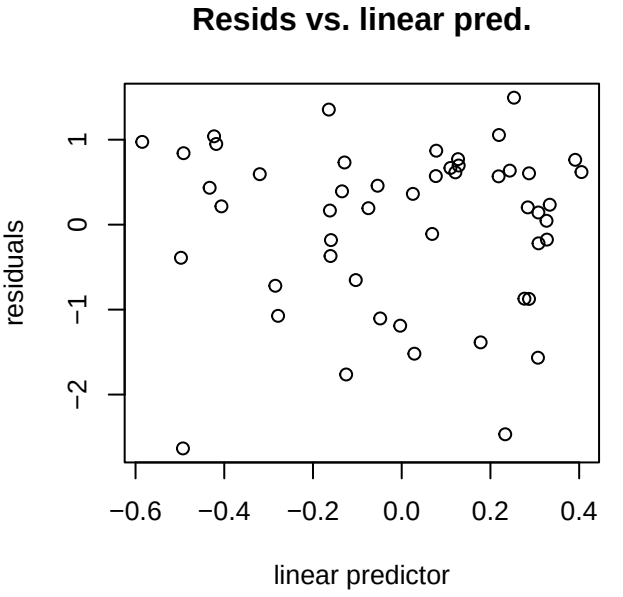

Resids vs. linear pred.
residuals
1.0
0.0
−1.0
−2.0
−0.8
−0.4
0.0
0.2
0.4
linear predictor

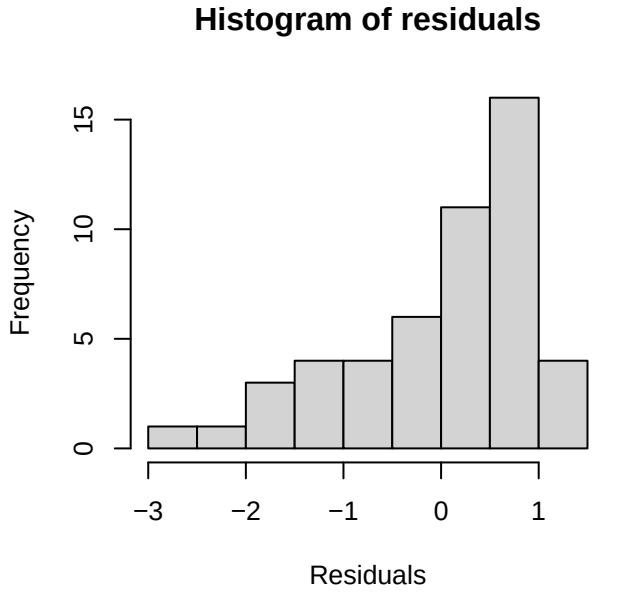

Histogram of residuals
Frequency
15
10
5
0
−2
−1
0
1
2
Residuals

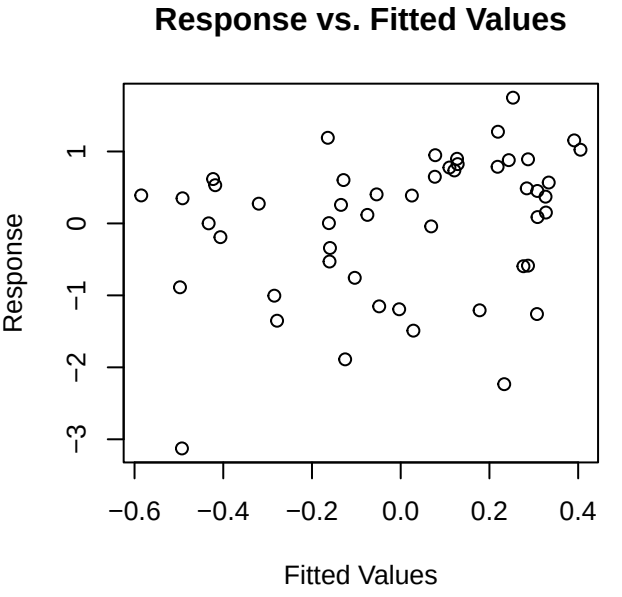

Response vs. Fitted Values
Response
2
1
0
−1
−0.8
−0.4
0.0
0.2
0.4
Fitted Values

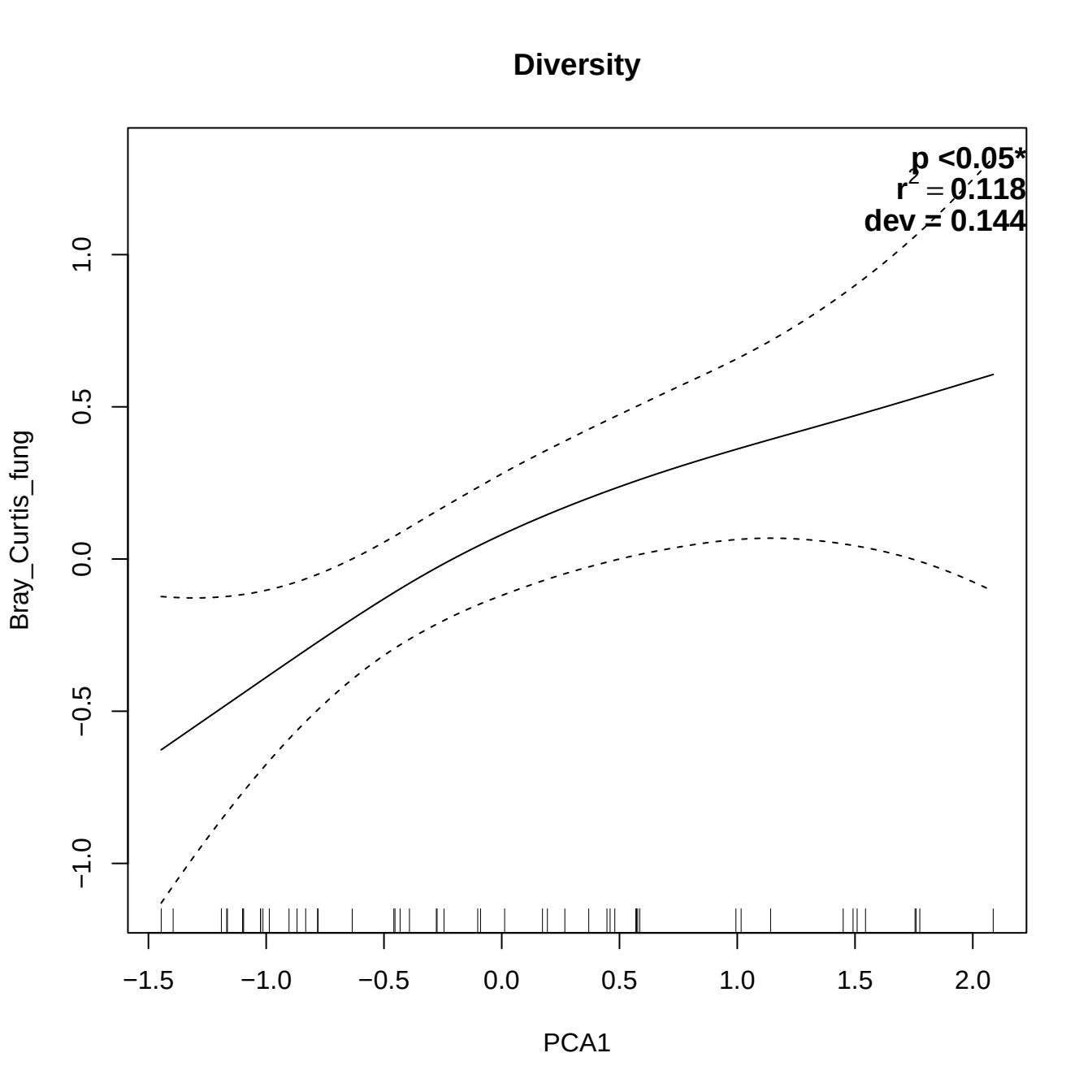

Diversity
p <0.05*
r2 = 0.059
dev = 0.079
shannon_fung
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
PCA1

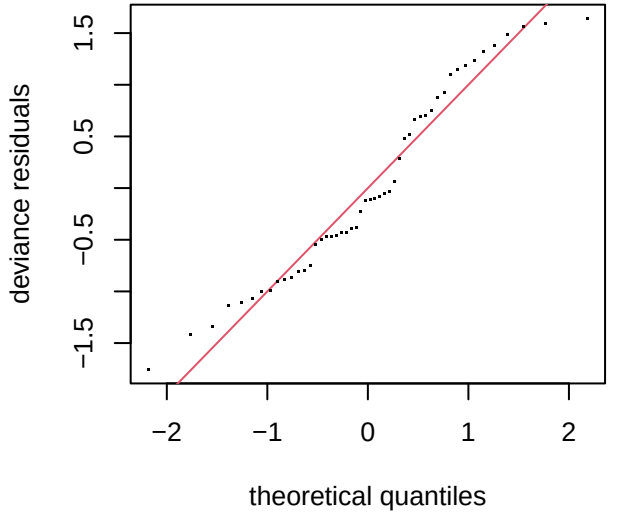

deviance residuals
theoretical quantiles

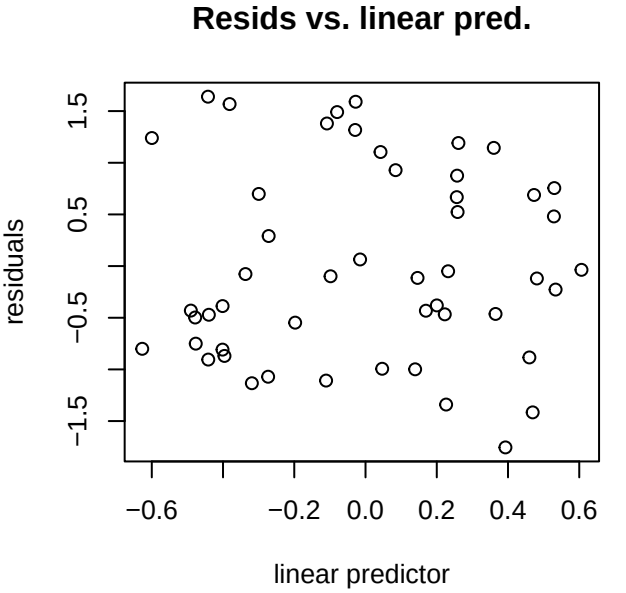

Resids vs. linear pred.
residuals
linear predictor

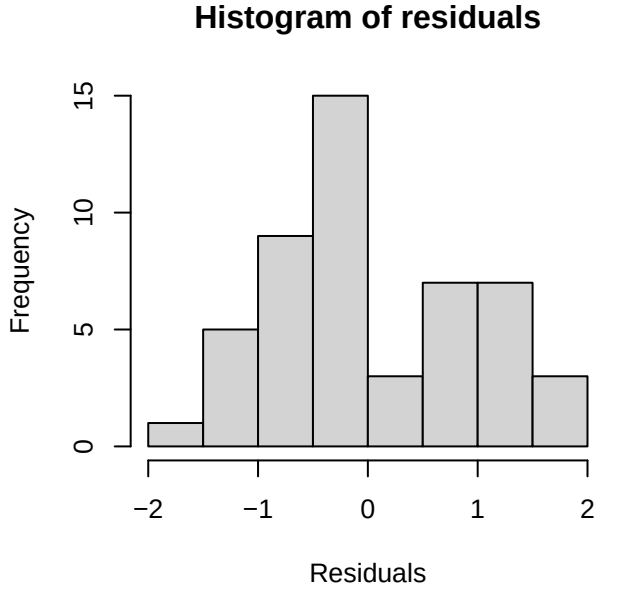

Histogram of residuals
Frequency
Residuals

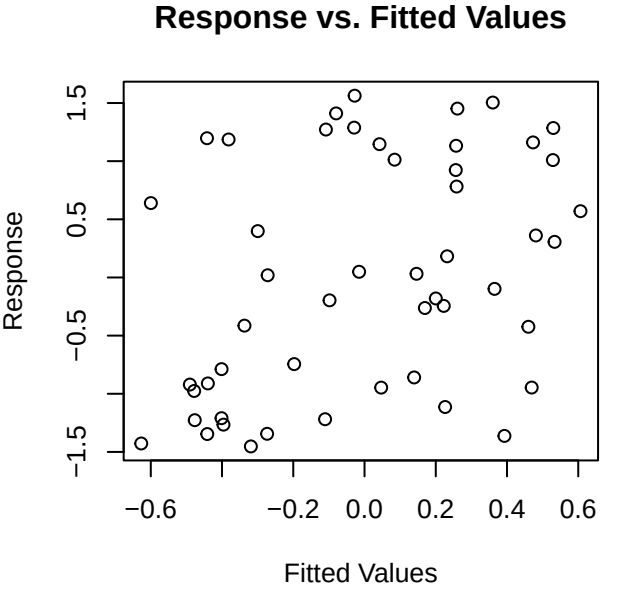

Response vs. Fitted Values
Response
Fitted Values

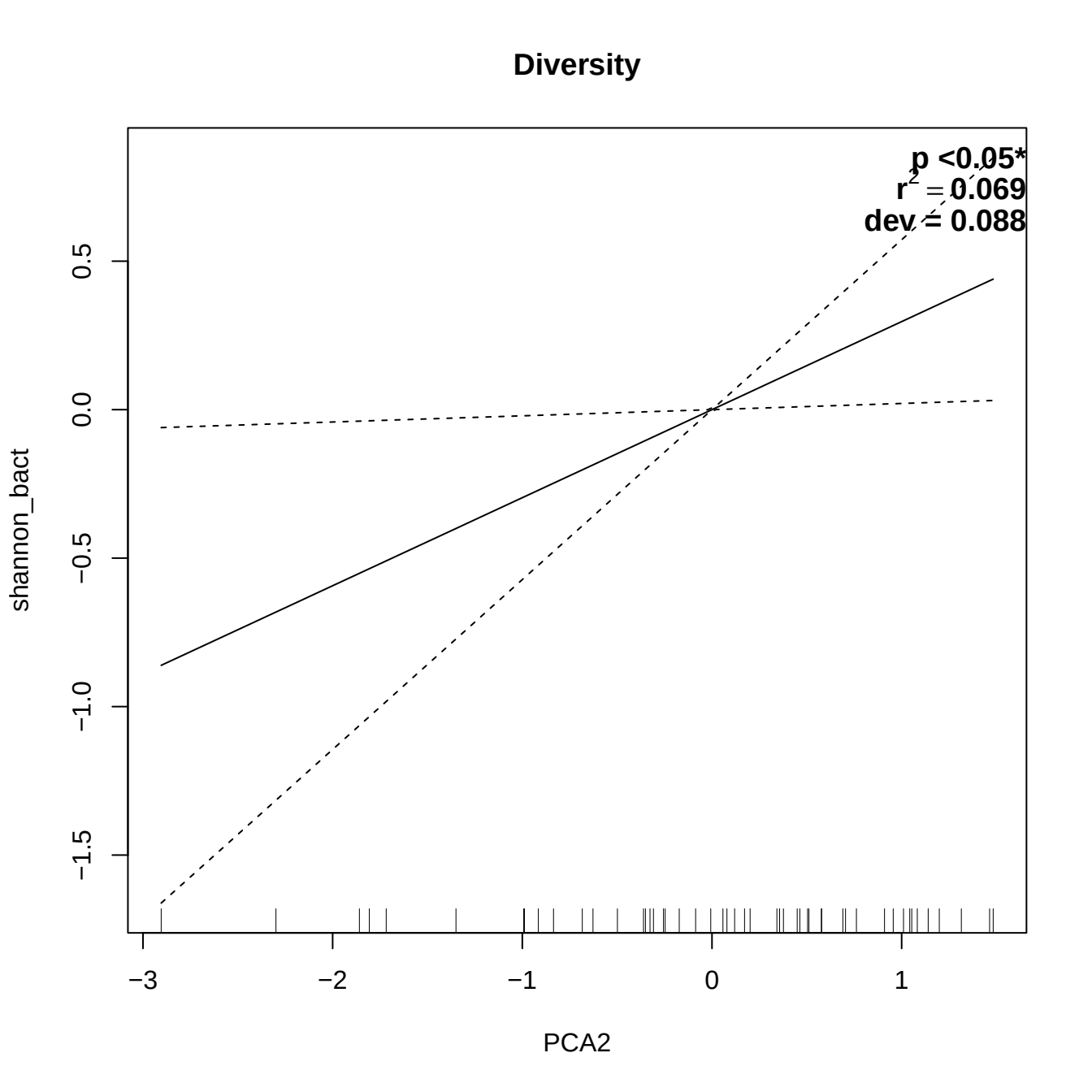

Diversity
p <0.05*
r2 = 0.118
dev = 0.144
Bray_Curtis_fung
1.0
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
PCA1

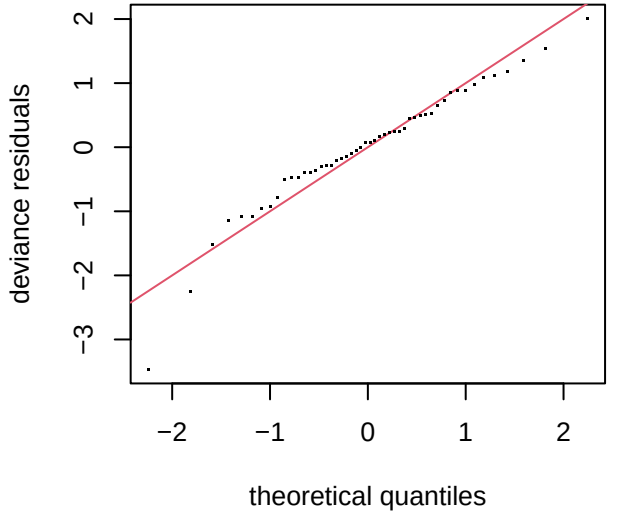

deviance residuals
1.5
0.5
−0.5
−1.5
−2
−1
0
1
2
theoretical quantiles

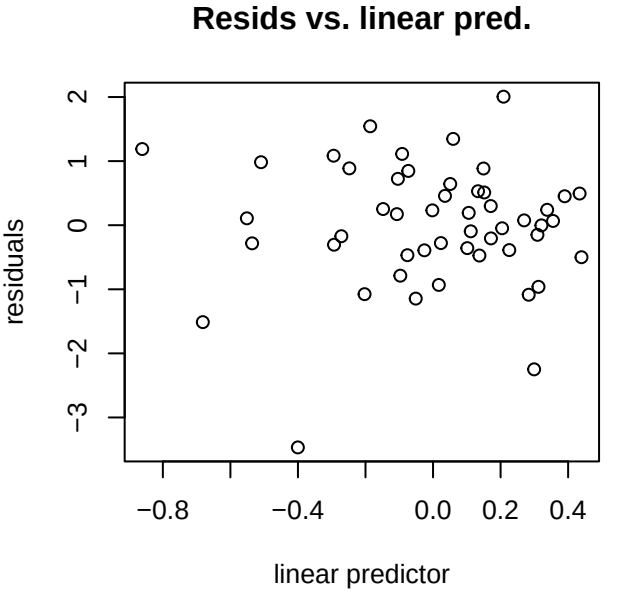

Resids vs. linear pred.
residuals
1.5
0.5
−0.5
−1.5
−0.6
−0.2
0.0
0.2
0.4
0.6
linear predictor

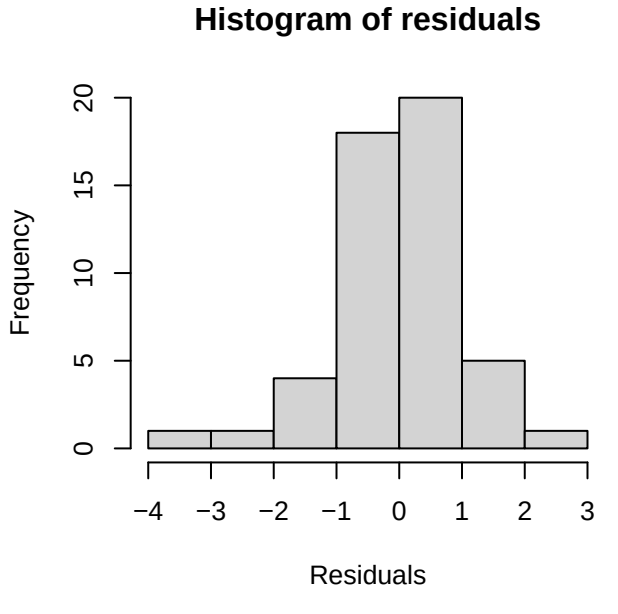

Histogram of residuals
Frequency
15
10
5
0
−2
−1
0
1
2
Residuals

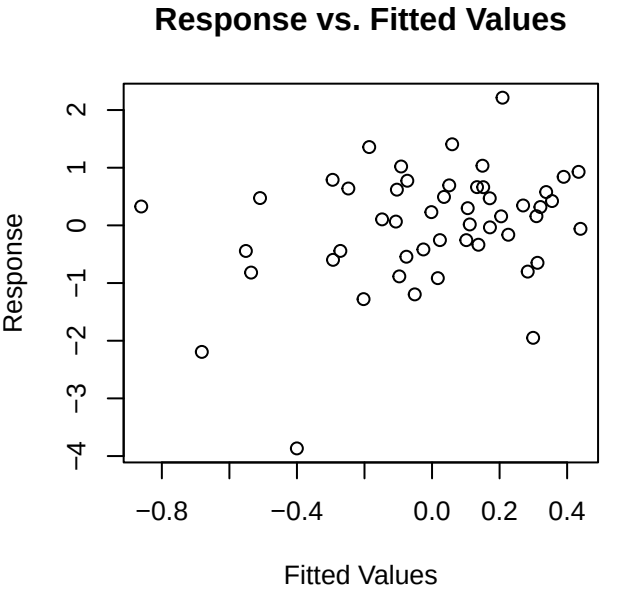

Response vs. Fitted Values
Response
1.5
0.5
−0.5
−1.5
−0.6
−0.2
0.0
0.2
0.4
0.6
Fitted Values

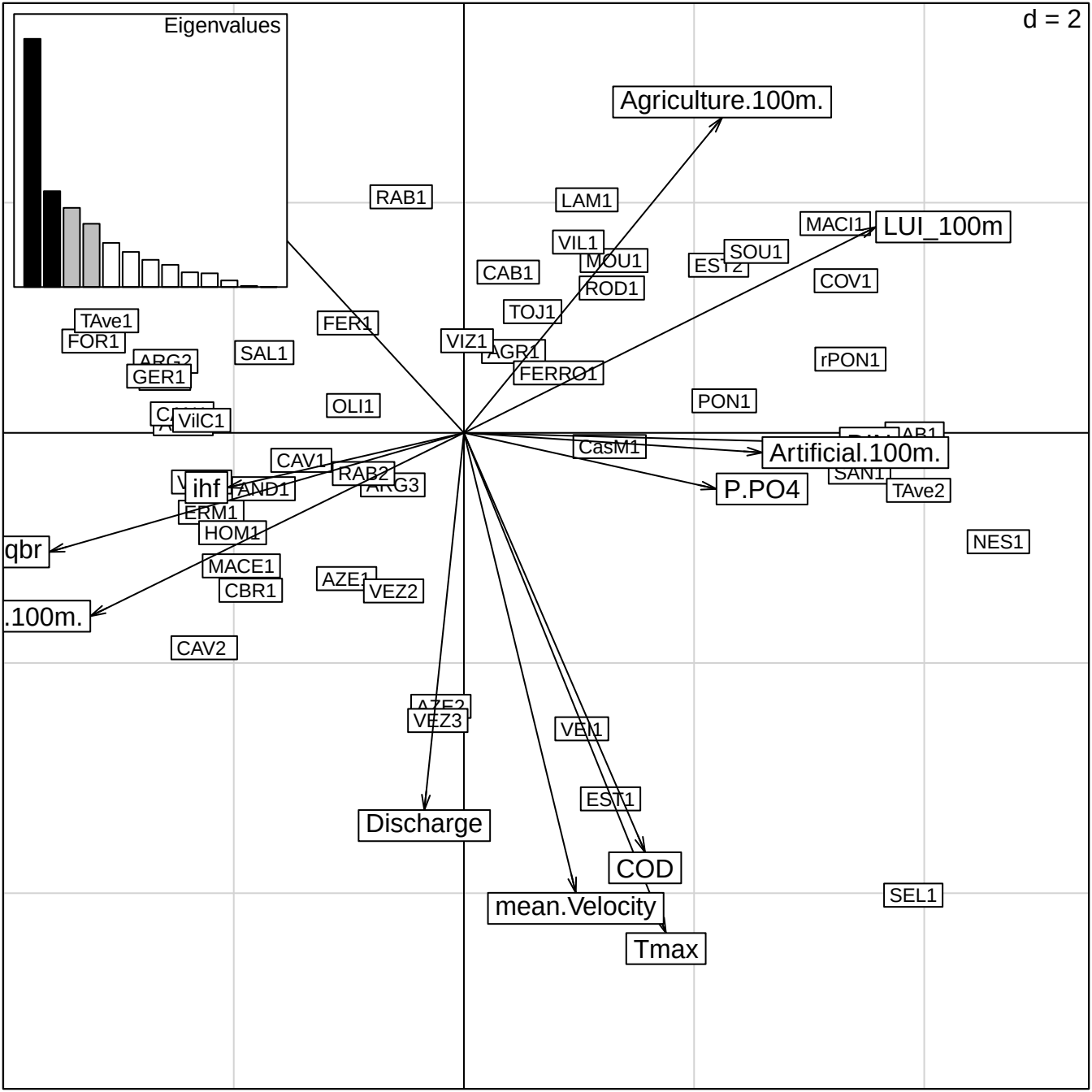

Diversity
p <0.05*
r2 = 0.069
dev = 0.088
shannon_bact
0.5
0.0
−0.5
−1.0
−1.5
−3
−2
−1
0
1
PCA2


deviance residuals
theoretical quantiles


Resids vs. linear pred.
residuals
linear predictor


Histogram of residuals
Frequency
Residuals


Response vs. Fitted Values
Response
Fitted Values


Eigenvalues
d = 2
Agriculture.100m.
LUI_100m
Artificial.100m.
P.PO4
Discharge
COD
mean.Velocity
Tmax
RAB1
LAM1
MACI1
VIL1
SOU1
MOU1
ESTZ
CAB1
COV1
ROD1
TOJ1
TAve1
FOR1
FER1
VIZ1
AGR1
SAL1
ARG2
GER1
FERRO1
rPON1
OLI1
PON1
VilC1
CasM1
CAV1
RAB2
ihf
ARG3
SAN1
TAve2
ERM1
HOM1
qbr
NES1
MACE1
AZE1
CBR1
VEZ2
.100m.
CAV2
VEZ3
VEL1
EST1
SEL1