

Multivariate Statistics in Ecology and Quantitative Genetics

Mixed-effects models

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Contents

The random effect of the beach

How to select a mixed-effects model

Nested Anova of a split-plot experiment.

Generalized linear mixed-effects models

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On every beach, 5 plots were sampled in the intertidal range.

Each plot was sampled only once. Thus, each line in the data table corresponds to one plot.

```

> rikz <- read.csv("RIKZ_Tab4.csv")
> rikz$Beach <- factor(rikz$Beach)
> rikz$Week <- factor(rikz$Week)
> str(rikz)
'data.frame': 45 obs. of 15 variables:
 $ ShannonW      : num  0.76 0.72 0.85 0.53 0.74 0.13 0.4 0.29 1.02
 $ Richness      : int   11 10 13 11 10 8 9 8 19 17 ...
 $ angle1       : int   32 62 65 55 23 129 126 52 26 143 ...
 $ angle2       : int   96 96 96 96 96 89 89 89 89 89 ...
 $ exposure     : int   10 10 10 10 10 8 8 8 8 8 ...
 $ salinity     : num  29.4 29.4 29.4 29.4 29.4 29.6 29.6 29.6 29.6
 $ temperature  : num  17.5 17.5 17.5 17.5 17.5 20.8 20.8 20.8 20.8
 $ NAP         : num  0.045 -1.036 -1.336 0.616 -0.684 ...
 $ penetrability: num  254 227 237 249 252 ...
 $ grainsize   : num  222 200 194 221 202 ...
 $ humus       : num  0.05 0.3 0.1 0.15 0.05 0.1 0.1 0.1 0.15 0 ..
 $ chalk       : num  2.05 2.5 3.45 1.6 2.45 2.5 1.85 1.7 2.3 2.6
 $ sorting1    : num  69.8 59 59.2 67.8 57.8 ...
 $ Beach      : Factor w/ 9 levels "1","2","3","4",...: 1 1 1 1 1
 $ Week      : Factor w/ 4 levels "1","2","3","4": 1 1 1 1 1 1 1

```


Today we use the following columns:

ShannonW A biodiversity index based on the Shannon entropy.

Richness The number of species.

Beach Which beach.

NAP The altitude of the plot compared to the average sea level.

exposure An index composed of wave action, length of the surf zone, slope, grain size, depth of the anaerobic layer.

salinity Salt contents.

humus Fraction of organic material.

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In an earlier analysis, NAP turned out to have an impact on species richness. Does ShannonW also depend on NAP?

```
> mod1 <- lm(ShannonW~NAP,data=rikz)
```

```
> summary(mod1)
```

```
[..]
```

```
Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.47141	0.03627	12.996	< 2e-16	***
NAP	-0.22583	0.03478	-6.493	7.01e-08	***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.2294 on 43 degrees of freedom
```

```
Multiple R-squared: 0.4951, Adjusted R-squared: 0.4833
```

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F-statistic: 42.16 on 1 and 43 DF, p-value: 7.01e-08
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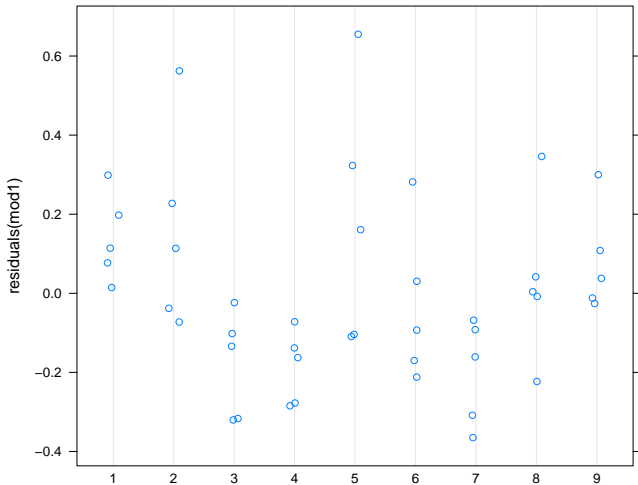
```
Residual standard error: 0.2294 on 43 degrees of freedom
```

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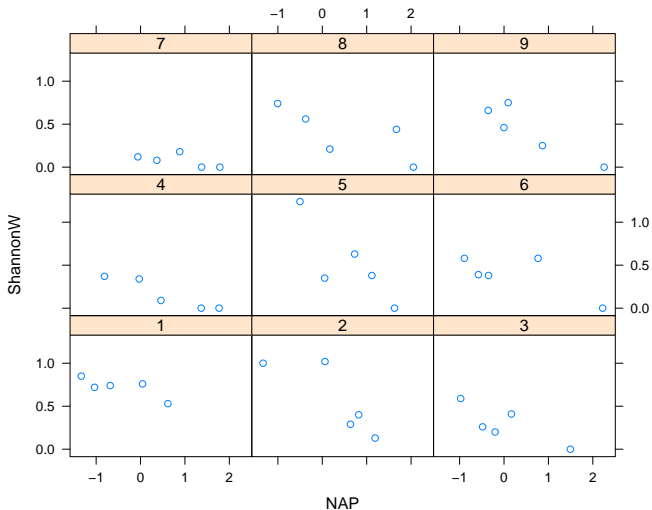
```
F-statistic: 42.16 on 1 and 43 DF,  p-value: 7.01e-08
```

Can we really pool the data from the different beaches?

```
> library(lattice)  
> dotplot(residuals(mod1)~rikz$Beach, jitter.x=TRUE, pch=1)
```



```
> xyplot(ShannonW~NAP|Beach,data=rikz)
```



```
> mod2 <- lm(ShannonW~NAP+Beach,data=rikz)
```

```
> summary(mod2)
```

```
[..]
```

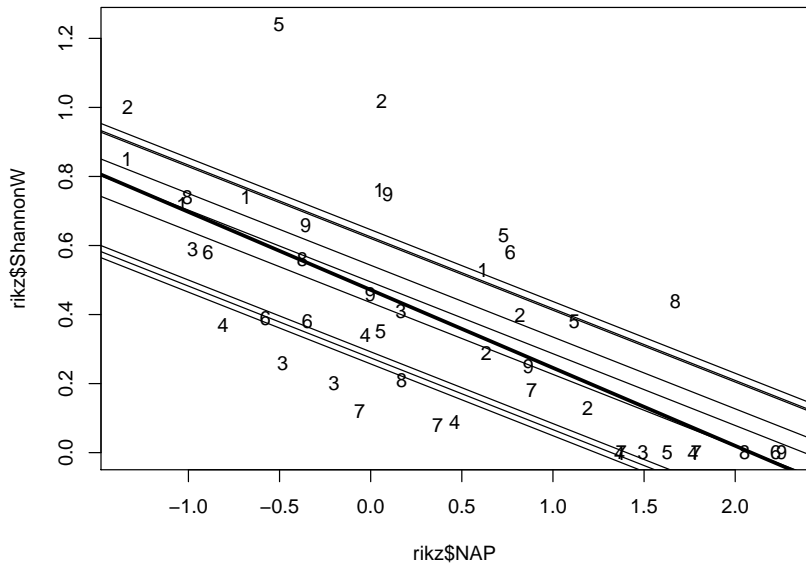
	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.620395	0.086771	7.150	2.45e-08	***
NAP	-0.207945	0.031366	-6.630	1.15e-07	***
Beach2	0.004665	0.123148	0.038	0.96999	
Beach3	-0.328311	0.121791	-2.696	0.01072	*
Beach4	-0.345859	0.125102	-2.765	0.00903	**
Beach5	0.025370	0.125550	0.202	0.84103	
Beach6	-0.185777	0.122910	-1.511	0.13964	
Beach7	-0.363441	0.128055	-2.838	0.00750	**
Beach8	-0.125882	0.124720	-1.009	0.31975	
Beach9	-0.077617	0.125268	-0.620	0.53953	

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.1911 on 35 degrees of freedom
```

The random effect of the beach



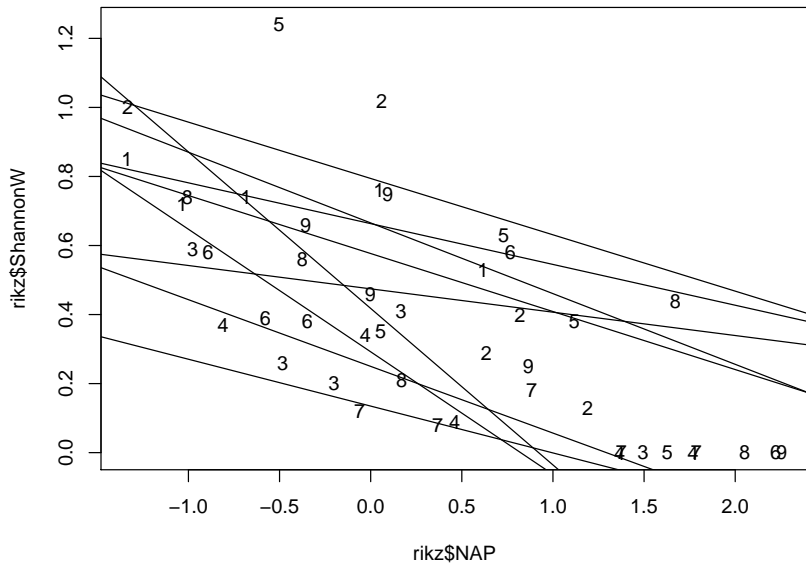

```
> mod3 <- lm(ShannonW~NAP*Beach,data=rikz)
```

```
> summary(mod3)
```

```
[..]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.663388	0.097592	6.798	2.67e-07	***
NAP	-0.118188	0.113333	-1.043	0.30627	
Beach2	0.002042	0.129370	0.016	0.98752	
Beach3	-0.371311	0.126891	-2.926	0.00688	**
Beach4	-0.413504	0.135632	-3.049	0.00510	**
Beach5	0.130807	0.142539	0.918	0.36691	
Beach6	-0.245660	0.127976	-1.920	0.06554	.
Beach7	-0.528549	0.165405	-3.195	0.00354	**
Beach8	-0.188925	0.131537	-1.436	0.16241	
Beach9	-0.086618	0.136291	-0.636	0.53043	
NAP:Beach2	-0.236876	0.145877	-1.624	0.11604	
NAP:Beach3	-0.075049	0.149266	-0.503	0.61919	
NAP:Beach4	-0.044999	0.142857	-0.315	0.75519	
NAP:Beach5	-0.335176	0.156110	-2.147	0.04093	*
NAP:Beach6	-0.017519	0.133795	-0.131	0.89679	
NAP:Beach7	0.050573	0.166465	0.304	0.76361	
NAP:Beach8	-0.049864	0.132654	-0.376	0.70993	

The random effect of the beach



```

> anova(mod1,mod2,mod3)
[.]
Model 1: ShannonW ~ NAP
Model 2: ShannonW ~ NAP + Beach
Model 3: ShannonW ~ NAP * Beach
  Res.Df    RSS Df Sum of Sq    F Pr(>F)
1      43 2.26293
2      35 1.27812  8    0.98481 3.7433 0.00458 **
3      27 0.88792  8    0.39020 1.4831 0.20951
[.]
> AIC(mod1,mod2,mod3)
      df      AIC
mod1  3  -0.8457103
mod2 11 -10.5528837
mod3 19 -10.9445763

```

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- ▶ Model 2 (where beaches have an additive effect) is significantly better than model 1, and model 3 is not significantly better than model 2.
- ▶ AIC favours (takes the lowest value for) model 3.
- ▶ How can AIC be negative? It is still defined as $-2 \cdot \log(L) + 2 \cdot d$, whereas d is the number of parameters and L is the likelihood of the ML parameter estimate in the model. Since the response variable ShannonW has a continuous distribution (assumed to be normal), the likelihood is the probability *density* of the data given the parameter values. Densities can be larger than 1. If $L > 1$, then $\log(L) > 0$ and AIC can be negative.

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- ▶ We do not want to estimate 8 extra parameters for the beaches
- ▶ Is there another way to take the difference between the beaches into account?
- ▶ Assume that the effect α_k of beach k is random. Do not estimate all α_k but only their standard deviation σ_α .

Mixed-effects model

Let S_i and N_i be the ShannonW and the NAP observed at plot i , which is on beach k .

$$S_i = a + b \cdot N_i + \alpha_k + \varepsilon_i$$

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Mixed-effects: a and b are *deterministic*, $\alpha_1, \alpha_2, \dots, \alpha_9$ are *random*.

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Mixed-effects: a and b are *deterministic*, $\alpha_1, \alpha_2, \dots, \alpha_9$ are *random*.

To be estimated: $a, b, \sigma_\alpha, \sigma$.


```
> library(lme4)
> mmod0 <- lmer(ShannonW~1+NAP+(1|Beach),
+               data=rikz,verbose=TRUE)
0:    -3.0154190: 0.730297
1:    -3.0321775: 0.694973
2:    -3.0321844: 0.694215
3:    -3.0321844: 0.694257
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```

It may be necessary to first install the lme4 package:

```
> install.packages("lme4")
```

This will only work if the R version installed is not too old.

```

> summary(mmod0)
Linear mixed model fit by REML
Formula: ShannonW ~ 1 + NAP + (1 | Beach)
  Data: rikz
      AIC   BIC logLik deviance REMLdev
4.968 12.19  1.516   -12.27   -3.032
Random effects:
Groups   Name             Variance Std.Dev.
Beach    (Intercept)  0.017595 0.13264
Residual                   0.036504 0.19106
Number of obs: 45, groups: Beach, 9

Fixed effects:
              Estimate Std. Error t value
(Intercept)  0.46722    0.05366   8.707
NAP          -0.21380    0.03060  -6.987

Correlation of Fixed Effects:
      (Intr)
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What is REML?

```

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```

What is REML?

Why are there
t-values but no
p-values?

REML vs. ML

- ▶ ML (Maximum Likelihood): estimate all parameters (here a , b , σ_α , σ) by maximizing their joint likelihood.

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- ▶ Comparable to estimation of σ^2 from sample X_1, \dots, X_n by $\frac{1}{n-1} \sum_i (\mu_X - X_i)^2$ instead of the biased ML estimator $\frac{1}{n} \sum_i (\mu_X - X_i)^2$

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- ▶ Also for fitting parameters of mixed-effects models, ML estimation is biased and REML is usually preferred.
- ▶ ML estimation should be used when a likelihood ratio test shall be applied to models with different fixed effects and the same random effects.

Why no p -values for the t -values?

- ▶ The t -values computed like in the usual linear model, but in the case of mixed-effects models they are in general not t -distributed (under the null hypothesis). Thus, it is not clear how to get p -values from the t -values.

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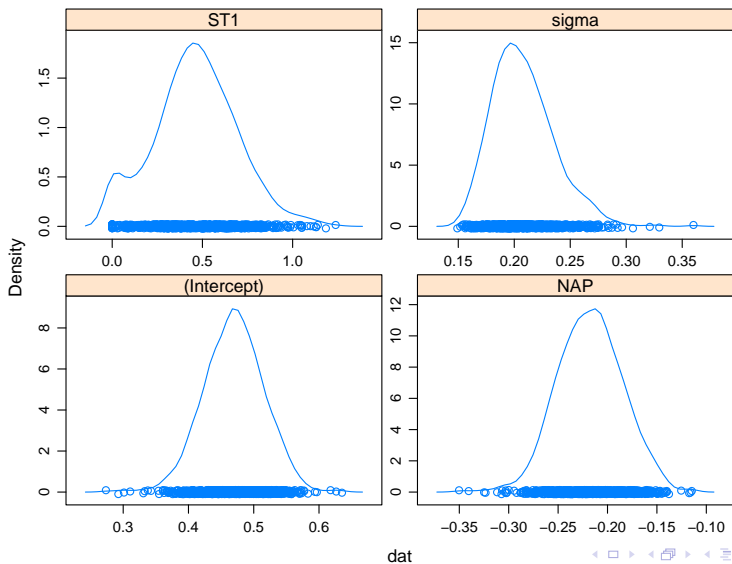
- ▶ The t -values computed like in the usual linear model, but in the case of mixed-effects models they are in general not t -distributed (under the null hypothesis). Thus, it is not clear how to get p -values from the t -values.
- ▶ Some other programs give p -values which can be very imprecise.
- ▶ Exception: small balanced datasets. Here, t -values are approximately t -distributed and $|t| > 2$ usually indicates significance on the 5% level.

One possibility to visualize the estimations for the parameter and to assess their significance is based on sampling parameter values from their posterior distribution by an MCMC method.

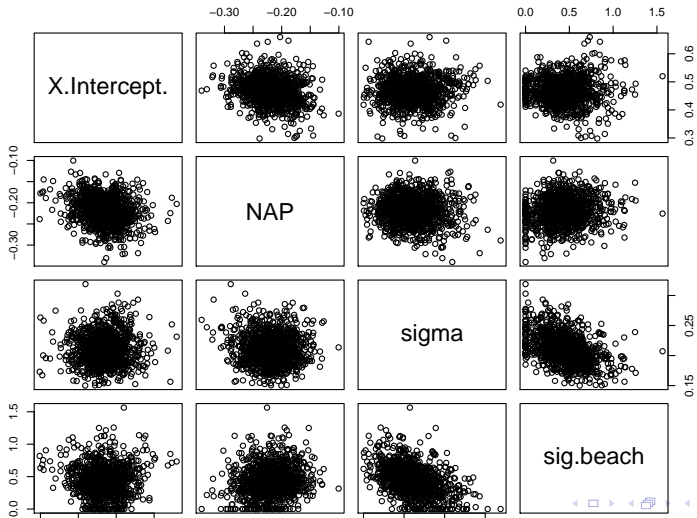
One possibility to visualize the estimations for the parameter and to assess their significance is based on sampling parameter values from their posterior distribution by an MCMC method.

In contrast to most other methods discussed in this lecture, this is a Bayesian approach and thus needs prior distributions for the parameter values (or at least pseudo priors).

```
> samp <- mcmcsamp(mmod0,1000)
> densityplot(samp)
```




```
> sampdf <- data.frame(t(samp@fixef),  
+                       sigma=t(samp@sigma),sig.beach=t(samp@ST))  
> plot(sampdf)
```



Upcoming versions of lme4 offer more comfortable possibilities to visualize results. The following two plots can be generated with a version lme4 that is available via

```
svn checkout svn://svn.r-forge.r-project.org/svnroot/lme4
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or with older alpha versions lme4a.

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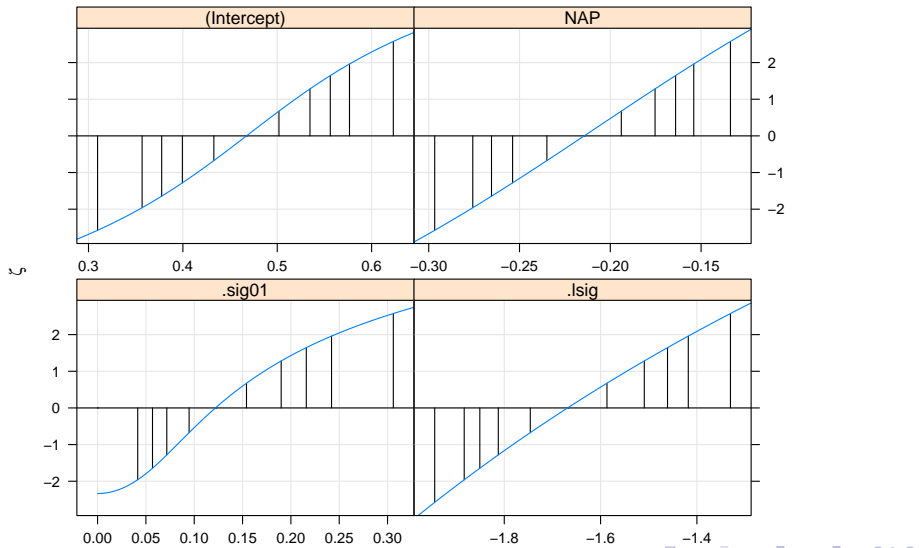
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or with older alpha versions lme4a.

The profiles in the first plots are likelihood ratios.

Vertical lines indicate 50%, 80%, 90%, 95%, and 99% confidence intervals.

```
> pr0 <- profile(mmod0)  
> xyplot(pr0)
```



Display confidence intervals (per default 95%).

```
> confint(pr0)
```

	2.5 %	97.5 %
.sig01	0.0415353	0.2420610
.lsig	-1.8831563	-1.4178656
(Intercept)	0.3568131	0.5765609
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The next plot shows pairwise confidence ranges (again 50%, 80%, 90%, 95%, and 99%).

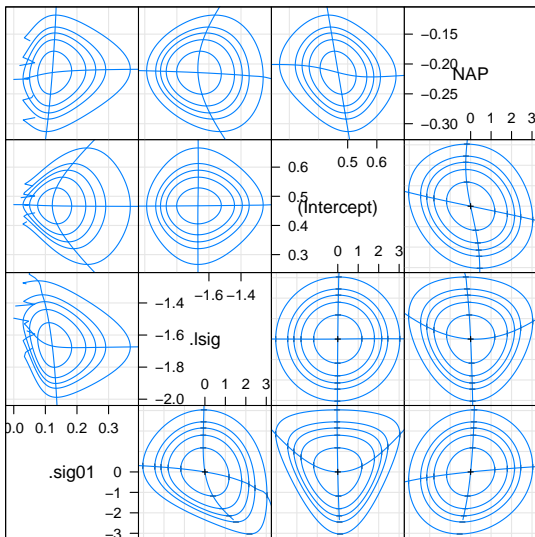
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The next plot shows pairwise confidence ranges (again 50%, 80%, 90%, 95%, and 99%).

Panels above the diagonal are in the original scale of the parameters, panels below the diagonal are on the $\sqrt{\text{likelihoodratio}}$ scale.


```
> splom(pr0)
```

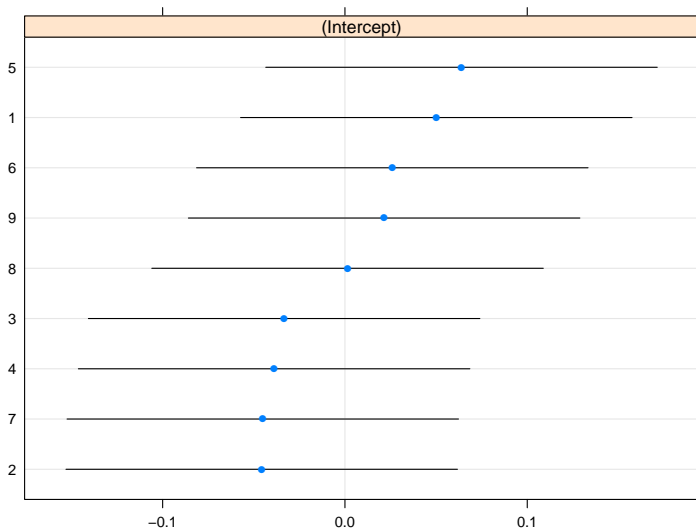


Sturdiagramm-Matrix

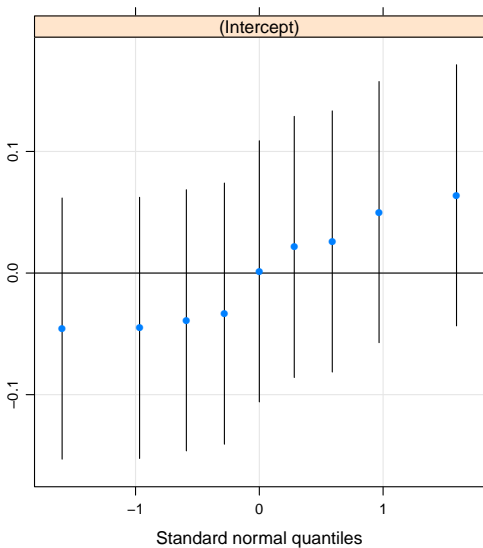
Back to what is possible with older version of lme4.

The next two plots visualize estimates for the random effects of the beaches.

```
> dotplot(ranef(B1,postVar=TRUE))
```



```
> qqmath(ranef(B1,postVar=TRUE))
```



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General considerations

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 1. Making predictions as precise as possible
 2. or to understand what the most influential parameters are?
- ▶ In the first case AIC may be appropriate.
- ▶ In the second case it may be better to use likelihood-ratio tests and remove all parameters which do not significantly improve the fit.

General considerations

- ▶ What is the purpose of the model?
 1. Making predictions as precise as possible
 2. or to understand what the most influential parameters are?
- ▶ In the first case AIC may be appropriate.
- ▶ In the second case it may be better to use likelihood-ratio tests and remove all parameters which do not significantly improve the fit.
- ▶ Variable selection should not only depend on statistics but also on the relevance of the parameter for the biological question.

We begin with a comparison of two nested models with the same random parameters

We begin with a comparison of two nested models with the same random parameters

```
> B0 <- lmer(ShannonW~1+exposure*NAP+(1|Beach),  
+           data=rikz,verbose=TRUE)  
0:      -3.1079878: 0.730297  
1:      -3.9300741: 0.431067  
2:      -3.9406377: 0.471682  
3:      -3.9424344: 0.460627  
4:      -3.9424352: 0.460386  
5:      -3.9424352: 0.460388
```

```
> summary(B0)
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
```

```
Data: rikz
```

```
AIC    BIC logLik deviance REMLdev
```

```
8.058 18.90  1.971   -23.54   -3.942
```

```
Random effects:
```

Groups	Name	Variance	Std.Dev.
--------	------	----------	----------

Beach	(Intercept)	0.0069857	0.08358
-------	-------------	-----------	---------

Residual		0.0329581	0.18154
----------	--	-----------	---------

```
Number of obs: 45, groups: Beach, 9
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
--	----------	------------	---------

(Intercept)	1.92603	0.44765	4.303
-------------	---------	---------	-------

exposure	-0.14294	0.04368	-3.272
----------	----------	---------	--------

```
[..]
```

```
> summary(B0)
```

```
[..]
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	1.92603	0.44765	4.303
exposure	-0.14294	0.04368	-3.272
NAP	-0.89673	0.33620	-2.667
exposure:NAP	0.06661	0.03270	2.037

```
Correlation of Fixed Effects:
```

	(Intr)	exposr	NAP
exposure	-0.996		
NAP	-0.233	0.235	
exposur:NAP	0.235	-0.238	-0.996

```
> B1 <- update(B0, ~.-exposure:NAP)
0:      -3.5739227: 0.730297
1:      -4.1112507: 0.00000
2:      -4.1112507: 3.65618e-06
3:      -4.1112511: 0.000144407
4:      -4.1650501: 0.0555603
5:      -4.7984144: 0.246592
6:      -5.0104872: 0.374551
7:      -5.0104967: 0.373651
8:      -5.0104968: 0.373725
9:      -5.0104968: 0.373722
```

```

> summary(B1)
Linear mixed model fit by REML
Formula: ShannonW ~ exposure + NAP + (1 | Beach)
Data: rikz
AIC   BIC logLik deviance REMLdev
4.99 14.02  2.505  -19.62  -5.01
Random effects:
Groups   Name             Variance Std.Dev.
Beach    (Intercept)  0.0050958 0.071385
Residual                   0.0364847 0.191010
Number of obs: 45, groups: Beach, 9

Fixed effects:
              Estimate Std. Error t value
(Intercept)  1.71143    0.41570   4.117
exposure     -0.12166    0.04053  -3.001
NAP          -0.21555    0.02990  -7.209

Correlation of Fixed Effects:
      (Intr) exposr
exposure -0.996

```

```
> anova(B0,B1)
```

```
Data: rikz
```

```
Models:
```

```
B1: ShannonW ~ exposure + NAP + (1 | Beach)
```

```
B0: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B1	5	-9.6222	-0.58886	9.8111				
B0	6	-11.5446	-0.70461	11.7723	3.9224		1	0.04765

```
---
```

```
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
```



```

> anova(B0,B1)
Data: rikz
Models:
B1: ShannonW ~ exposure + NAP + (1 | Beach)
B0: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
   Df      AIC      BIC  logLik  Chisq Chi Df Pr(>Chisq)
B1  5  -9.6222 -0.58886  9.8111
B0  6 -11.5446 -0.70461 11.7723 3.9224    1  0.04765
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

```

The p -value of 0.04765 may be imprecise because REML was used.

```

> anova(B0,B1)
Data: rikz
Models:
B1: ShannonW ~ exposure + NAP + (1 | Beach)
B0: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
   Df      AIC      BIC  logLik  Chisq Chi Df Pr(>Chisq)
B1  5  -9.6222 -0.58886  9.8111
B0  6 -11.5446 -0.70461 11.7723 3.9224    1  0.04765
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

```

The p -value of 0.04765 may be imprecise because REML was used. To get a slightly more reliable p -value we fit both models with ML.

```
> B1ML <- update(B1,REML=FALSE)
0:    -16.875166: 0.730297
1:    -19.518802: 0.00000
2:    -19.518802: 3.18807e-06
```

```
> B0ML <- update(B0,REML=FALSE)
0:    -21.820395: 0.730297
1:    -22.739010: 0.00000
2:    -22.739010: 7.52231e-06
3:    -22.739011: 0.000259128
4:    -22.880262: 0.0868904
5:    -23.616152: 0.288666
6:    -23.703097: 0.366825
7:    -23.703443: 0.361997
8:    -23.703444: 0.362261
9:    -23.703444: 0.362262
```

```
> anova(B1ML,B0ML)
```

```
Data: rikz
```

```
Models:
```

```
B1ML: ShannonW ~ exposure + NAP + (1 | Beach)
```

```
B0ML: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B1ML	5	-9.5188	-0.48549	9.7594				
B0ML	6	-11.7034	-0.86347	11.8517	4.1846		1	0.04079 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> anova(B1ML,B0ML)
```

```
Data: rikz
```

```
Models:
```

```
B1ML: ShannonW ~ exposure + NAP + (1 | Beach)
```

```
B0ML: ShannonW ~ 1 + exposure * NAP + (1 | Beach)
```

	Df	AIC	BIC	logLik	Chisq	Chi Df	Pr(>Chisq)
B1ML	5	-9.5188	-0.48549	9.7594			
B0ML	6	-11.7034	-0.86347	11.8517	4.1846	1	0.04079 *


```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The model B0 (or B0ML) with interaction between NAP and exposure fits significantly better.

Zuur *et al.*¹ recommend the following strategy for the selection of random and fixed parameters.

1. Start with a model that contains as many of the relevant parameters and interactions as possible.
2. First select random parameters. To decide between models which have different random parameters, fit models with REML and choose model of minimal AIC.
3. Now select fixed parameters. This can be done with the help of AIC or with likelihood ratio tests. If likelihood ratio tests are used, apply ML to fit the models to the data.
4. Never remove covariates that are still involved in interactions.
5. Fit the final model with REML.

¹A.F. Zuur, E.N. Ieno, N.J. Walker, A.A. Saveliev, G.M. Smith (2009) *Mixed effects models and extensions in ecology with R*. Springer. 

```
> B2 <- lmer(ShannonW~1+(exposure+salinity+NAP+humus)^2+(
+           .... [TRUNCATED]
0:      -5.8942807: 0.730297
1:      -5.8978355: 0.838579
2:      -5.9174068: 0.789454
3:      -5.9175376: 0.784845
4:      -5.9175385: 0.785156
5:      -5.9175385: 0.785156
```

```
> summary(B2)
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
                                     + (1 | Beach)
```

```
Data: rikz
```

```
AIC    BIC logLik deviance REMLdev
```

```
20.08 43.57  2.959   -37.55  -5.918
```

```
Random effects:
```

```
Groups   Name          Variance Std.Dev.
```

```
Beach    (Intercept) 0.015652 0.12511
```

```
Residual                0.025390 0.15934
```

```
Number of obs: 45, groups: Beach, 9
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	40.32851	21.45346	1.880
exposure	-4.16161	2.12543	-1.958
salinity	-1.38750	0.74706	-1.857
NAP	0.65692	0.92037	0.714
humus	40.36916	16.33692	2.471
exposure:salinity	0.14522	0.07425	1.956

[..]

Correlation of Fixed Effects:

	(Intr)	exposr	salnty	NAP	humus	expsr:s	ex:NAP	expsr
exposure	-0.998							
salinity	-0.999	0.998						
NAP	-0.079	0.062	0.074					
humus	0.117	-0.142	-0.129	0.152				
expsr:slnty	0.996	-0.999	-0.998	-0.057	0.155			
exposur:NAP	0.173	-0.165	-0.177	-0.661	0.067	0.167		
exposur:hms	-0.285	0.295	0.306	-0.008	-0.694	-0.315	-0.331	
salinty:NAP	0.005	0.012	0.003	-0.920	-0.224	-0.020	0.316	0.18
salinty:hms	0.025	0.002	-0.022	-0.197	-0.888	-0.006	0.128	0.28
NAP:humus	0.149	-0.145	-0.158	0.109	-0.119	0.154	0.215	-0.14

slnty:

exposure
 salinity
 NAP
 humus
 expsr:slnty
 exposur:NAP
 exposur:hms

```

> B3 <- lmer(ShannonW~1+(exposure+salinity+NAP+humus)^2
+           +(1+NAP|Beach), data=rikz,verbose=TRUE)
0:      -1.5323306: 0.730297 0.700275 0.00000
1:      -5.4597824: 1.16363 0.00000 -0.193541
2:      -5.7892458: 1.04081 4.21403e-06 -0.0735358
3:      -5.9531543: 0.913041 6.58205e-06 -0.188264
[. . .]
12:     -6.0798268: 0.829521 0.00000 -0.109646
13:     -6.0798268: 0.829519 0.00000 -0.109651
14:     -6.0798268: 0.829519 0.00000 -0.109651

```

Next, we fit a model where there is not only a random intercept for every beach but also a random coefficient of NAP. Again, let S_i and N_i be the ShannonW and the NAP observed at plot i , which is on beach k . The model says

$$S_i = a + [\text{fixed effects terms}] + \alpha_k + \beta_k \cdot N_i + \varepsilon_i.$$

$\varepsilon_1, \dots, \varepsilon_{45}$ are independently $\mathcal{N}(0, \sigma^2)$ -distributed,

$\alpha_1, \dots, \alpha_9$ are independently $\mathcal{N}(0, \sigma_\alpha^2)$ -distributed,

β_1, \dots, β_9 are independently $\mathcal{N}(0, \sigma_\beta^2)$ -distributed,

Next, we fit a model where there is not only a random intercept for every beach but also a random coefficient of NAP. Again, let S_i and N_i be the ShannonW and the NAP observed at plot i , which is on beach k . The model says

$$S_i = a + [\text{fixed effects terms}] + \alpha_k + \beta_k \cdot N_i + \varepsilon_i.$$

$\varepsilon_1, \dots, \varepsilon_{45}$ are independently $\mathcal{N}(0, \sigma^2)$ -distributed,

$\alpha_1, \dots, \alpha_9$ are independently $\mathcal{N}(0, \sigma_\alpha^2)$ -distributed,

β_1, \dots, β_9 are independently $\mathcal{N}(0, \sigma_\beta^2)$ -distributed,

Besides the fixed-effects coefficients we have to estimate σ , σ_α and σ_β .

```
> summary(B3)
```

```
[..]
```

	AIC	BIC	logLik	deviance	REMLdev
	23.92	51.02	3.04	-37.69	-6.08

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Beach	(Intercept)	0.01730652	0.131554	
	NAP	0.00020808	0.014425	-1.000
Residual		0.02515108	0.158591	

Number of obs: 45, groups: Beach, 9

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	40.93936	21.72964	1.884
exposure	-4.22455	2.15239	-1.963
salinity	-1.40881	0.75753	-1.860
NAP	0.67896	0.93389	0.727
humus	40.42412	16.30099	2.480
exposure:salinity	0.14742	0.07528	1.958
exposure:NAP	0.08480	0.03663	2.315
exposure:humus	-2.10698	0.78447	-2.686

```

> B4 <- lmer(ShannonW~1+(exposure+salinity+NAP+humus)^2
+           +(1+NAP+exposure|Beach),data=rikz,verbose=TRUE)
0:   -1.6536097: 0.730297 0.700275 0.0711568 0.00000 0.00000
1:   -3.4551238: 0.700827 0.500322 0.00000 -0.0225207 -0.207903
2:   -5.5427746: 0.630604 0.176807 0.00000 -0.00365199 -0.00670
3:   -5.7754683: 0.635022 0.175143 0.00000 -0.00439670 0.027882
[...]
267: -6.2309242: 0.0242437 1.71415e-05 7.45081e-05 -3.81706 3.1
268: -6.2309242: 0.0242437 1.71415e-05 7.45081e-05 -3.81706 3.1
269: -6.2309242: 0.0242437 1.71415e-05 7.45081e-05 -3.81706 3.1

```

```
> summary(B4)
```

```
[..]
```

	AIC	BIC	logLik	deviance	REMLdev
	29.77	62.29	3.115	-38.41	-6.231

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Beach	(Intercept)	1.4754e-05	0.0038411	
	NAP	2.1496e-04	0.0146616	-1.000
	exposure	1.4259e-04	0.0119410	1.000 -1.000
Residual		2.5102e-02	0.1584364	

Number of obs: 45, groups: Beach, 9

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	42.77575	20.81776	2.055
exposure	-4.41472	2.06398	-2.139
salinity	-1.47464	0.72415	-2.036
NAP	0.67731	0.93297	0.726
humus	40.48334	16.27068	2.488
exposure:salinity	0.15425	0.07203	2.142
exposure:NAP	0.08472	0.03662	2.313

```

> B5 <- lmer(ShannonW~1+(exposure+salinity+NAP+humus)^2
+           +(1+NAP+exposure|Beach)+(1|Week),data=rikz,verbose=TRUE)
0:    -1.9949020: 0.730297 0.700275 0.0711568 0.00000 0.00000
1:    -2.5896994: 0.696448 0.572039 0.00000 -0.0146206 -0.256429
2:    -5.3531758: 0.661521 0.525272 0.00000 -0.00132594 -0.10653
[... ]
62:   -9.1285182: 4.30055 1.60825e-07 0.00000 0.0323185 -0.0979
63:   -9.1285182: 4.30055 1.49005e-08 5.79252e-07 0.0323201 -0.0
64:   -9.1285182: 4.30055 0.00000 0.00000 0.0323202 -0.0979503

```



```
> summary(B5)
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
          + (1 + NAP + exposure | Beach) + (1 | Week)
```

```
Data: rikz
```

```
AIC BIC logLik deviance REMLdev
```

```
28.87 63.2 4.564 -40.07 -9.129
```

```
Random effects:
```

Groups	Name	Variance	Std.Dev.	Corr
Beach	(Intercept)	0.44901920	0.670089	
	NAP	0.00046904	0.021657	1.000
	exposure	0.00430800	0.065635	-1.000 -1.000
Week	(Intercept)	0.02093924	0.144704	
Residual		0.02427827	0.155815	

```
Number of obs: 45, groups: Beach, 9; Week, 4
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	21.42334	15.49344	1.383
exposure	-2.34537	1.53851	-1.524
salinity	-0.74919	0.54787	-1.367

```
> anova(B2,B3,B4,B5)
```

```
Data: rikz
```

```
Models:
```

```
B2: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
      + (1 | Beach)
```

```
B3: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
      + (1 + NAP | Beach)
```

```
B4: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
      + (1 + NAP + exposure | Beach)
```

```
B5: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
      + (1 + NAP + exposure | Beach) + (1 | Week)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B2	13	-11.5528	11.934	18.776				
B3	15	-7.6911	19.409	18.846	0.1383		2	0.9332
B4	18	-2.4079	30.112	19.204	0.7168		3	0.8693
B5	19	-2.0744	32.252	20.037	1.6665		1	0.1967

Don't trust the p -values on the previous slide! The problem is not only that the models were fitted with REML. The main problem is that the null hypotheses (e.g. $\sigma_\beta = 0$ in the case of B2/B3) are on the boundary of the parameter space. σ_β can only be ≥ 0 , and deviations from $\sigma_\beta = 0$ are thus only possible in one direction. The χ^2 -approximation of likelihood ratio tests are only reliable when deviations from the expectation under the null hypothesis are possible in all directions, for example if the null hypothesis $\theta = 0$ is tested for some parameter θ , and estimates of θ can lead to positive as well as negative values.

Don't trust the p -values on the previous slide! The problem is not only that the models were fitted with REML. The main problem is that the null hypotheses (e.g. $\sigma_\beta = 0$ in the case of B2/B3) are on the boundary of the parameter space. σ_β can only be ≥ 0 , and deviations from $\sigma_\beta = 0$ are thus only possible in one direction. The χ^2 -approximation of likelihood ratio tests are only reliable when deviations from the expectation under the null hypothesis are possible in all directions, for example if the null hypothesis $\theta = 0$ is tested for some parameter θ , and estimates of θ can lead to positive as well as negative values.

Thus, we rather base our decision on the AIC values. This is, of course, also not stringent. However, in our case, all criteria favor model B2.

Now we keep the random effects “(1 | Beach)” and search for a good selection of fixed effects. Here, our aim is to get a simple, understandable model. Therefore apply a strict criterion and remove all variables which do not significantly improve the model fit on the 5% level.

Now we keep the random effects “(1 | Beach)” and search for a good selection of fixed effects. Here, our aim is to get a simple, understandable model. Therefore apply a strict criterion and remove all variables which do not significantly improve the model fit on the 5% level.

(If our aim was a model to make good predictions, we would rather take AIC as a criterion, which leaves more parameters in.)

```
> summary(B2)
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2
+ (1 | Beach)
```

```
[..]
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	40.32851	21.45346	1.880
exposure	-4.16161	2.12543	-1.958
salinity	-1.38750	0.74706	-1.857
NAP	0.65692	0.92037	0.714
humus	40.36916	16.33692	2.471
exposure:salinity	0.14522	0.07425	1.956
exposure:NAP	0.08357	0.03615	2.312
exposure:humus	-2.06931	0.78148	-2.648
salinity:NAP	-0.06337	0.02639	-2.401
salinity:humus	-0.67100	0.43169	-1.554
NAP:humus	1.01589	0.59247	1.715

```
[..]
```

```
> B6 <- update(B2, ~.-salinity:humus)
0:      -3.3840456: 0.730297
1:      -3.3848655: 0.748586
2:      -3.3851681: 0.742306
3:      -3.3851681: 0.742296
4:      -3.3851681: 0.742299
5:      -3.3851681: 0.742299
```



```
> anova(B6,B2)
```

```
Data: rikz
```

```
Models:
```

```
B6: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B6:     exposure:salinity + exposure:NAP + exposure:humus + salinity
```

```
B6:     NAP:humus
```

```
B2: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2 + (1 | Beach)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B6	12	-10.720	10.960	17.360				
B2	13	-11.553	11.934	18.776	2.8329		1	0.09235 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remember that we should better use ML instead of REML if we want to apply likelihood ratio tests!

```
> B2ML <- update(B2,REML=FALSE)
```

```
0:    -37.815253: 0.730297
```

```
1:    -38.227458: 0.520323
```

```
2:    -38.238951: 0.555035
```

```
3:    -38.239535: 0.548840
```

```
4:    -38.239535: 0.548745
```

```
5:    -38.239535: 0.548714
```

```
6:    -38.239535: 0.548724
```

```
> B6ML <- update(B6,REML=FALSE)
```

```
0:    -34.786862: 0.730297
```

```
1:    -35.481002: 0.455308
```

```
2:    -35.502068: 0.503911
```

```
3:    -35.503579: 0.494055
```

```
4:    -35.503579: 0.493868
```

```
5:    -35.503579: 0.493857
```

```
6:    -35.503579: 0.493844
```

```
7:    -35.503579: 0.493844
```

```
> anova(B6ML,B2ML)
```

```
Data: rikz
```

```
Models:
```

```
B6ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B6ML:      exposure:salinity + exposure:NAP + exposure:humus + salin
```

```
B6ML:      NAP:humus
```

```
B2ML: ShannonW ~ 1 + (exposure + salinity + NAP + humus)^2 + (1 | B
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B6ML	12	-11.504	10.176	17.752				
B2ML	13	-12.239	11.247	19.120	2.736		1	0.09811 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(B6)
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach)
        exposure:salinity + exposure:NAP + exposure:humus + salinity:NAP
        NAP:humus
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	40.98076	21.18993	1.934
exposure	-4.13572	2.10009	-1.969
salinity	-1.40592	0.73832	-1.904
NAP	0.37102	0.92444	0.401
humus	17.61688	7.69600	2.289
exposure:salinity	0.14382	0.07340	1.959
exposure:NAP	0.09008	0.03673	2.453
exposure:humus	-1.70126	0.76643	-2.220
salinity:NAP	-0.05584	0.02661	-2.098
NAP:humus	1.24688	0.58490	2.132

```
[..]
```

```
> B7 <- update(B6, ~.-exposure:salinity)
```

```
0:    -3.0026064: 0.730297
```

```
1:    -3.2146723:  1.04756
```

```
2:    -3.2845341: 0.957924
```

```
3:    -3.2886569: 0.926746
```

```
4:    -3.2887713: 0.931248
```

```
5:    -3.2887715: 0.931100
```

```
6:    -3.2887715: 0.931099
```

```
> B7ML <- update(B7, REML=FALSE)
```

```
0:   -30.038157: 0.730297
```

```
1:   -30.038162: 0.725726
```

```
2:   -30.038210: 0.727949
```

```
3:   -30.038210: 0.727947
```

```
> anova(B7ML,B6ML)
```

```
Data: rikz
```

```
Models:
```

```
B7ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B7ML:      exposure:NAP + exposure:humus + salinity:NAP + NAP:humus
```

```
B6ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B6ML:      exposure:salinity + exposure:NAP + exposure:humus + salin
```

```
B6ML:      NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B7ML	11	-8.0382	11.835	15.019				
B6ML	12	-11.5036	10.176	17.752	5.4654		1	0.01940 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> B8 <- update(B6, ~.-salinity:NAP)
0:      -4.5729780: 0.730297
1:      -4.6975945: 0.596090
2:      -4.6982261: 0.606261
3:      -4.6982498: 0.604628
4:      -4.6982498: 0.604628
5:      -4.6982498: 0.604628
```



```
> B8ML <- update(B8,REML=FALSE)
0:    -29.489856: 0.730297
1:    -30.710552: 0.00000
2:    -30.710552: 2.50994e-05
3:    -30.710558: 0.000649769
4:    -31.015846: 0.162724
5:    -31.356389: 0.335700
6:    -31.356637: 0.345734
7:    -31.356869: 0.341604
8:    -31.356869: 0.341641
9:    -31.356869: 0.341630
```

```
> anova(B8ML,B6ML)
```

```
Data: rikz
```

```
Models:
```

```
B8ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B8ML:      exposure:salinity + exposure:NAP + exposure:humus + NAP:h
```

```
B6ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B6ML:      exposure:salinity + exposure:NAP + exposure:humus + salin
```

```
B6ML:      NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B8ML	11	-9.3569	10.516	15.678				
B6ML	12	-11.5036	10.176	17.752	4.1467		1	0.04172 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(B6)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	40.98076	21.18993	1.934
exposure	-4.13572	2.10009	-1.969
salinity	-1.40592	0.73832	-1.904
NAP	0.37102	0.92444	0.401
humus	17.61688	7.69600	2.289
exposure:salinity	0.14382	0.07340	1.959
exposure:NAP	0.09008	0.03673	2.453
exposure:humus	-1.70126	0.76643	-2.220
salinity:NAP	-0.05584	0.02661	-2.098
NAP:humus	1.24688	0.58490	2.132

```
[...]
```

```
> B9 <- update(B6, ~.-NAP:humus)
0:      1.7262210: 0.730297
1:      1.4342459: 0.527474
2:      1.4326078: 0.545056
3:      1.4324476: 0.540992
4:      1.4324476: 0.540993
5:      1.4324476: 0.540993
6:      1.4324476: 0.540993
```

```
> B9ML <- update(B9,REML=FALSE)
0:    -29.340922: 0.730297
1:    -31.445430: 0.00000
2:    -31.445430: 1.57944e-05
3:    -31.445431: 0.000268510
4:    -31.471347: 0.0479773
5:    -31.646917: 0.147977
6:    -31.778206: 0.347977
7:    -31.821753: 0.257110
8:    -31.831799: 0.282988
9:    -31.831884: 0.285733
10:   -31.831884: 0.285584
11:   -31.831884: 0.285537
12:   -31.831884: 0.285545
```

```
> anova(B9ML,B6ML)
```

```
Data: rikz
```

```
Models:
```

```
B9ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B9ML:      exposure:salinity + exposure:NAP + exposure:humus + salin
```

```
B6ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B6ML:      exposure:salinity + exposure:NAP + exposure:humus + salin
```

```
B6ML:      NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B9ML	11	-9.8319	10.041	15.916				
B6ML	12	-11.5036	10.176	17.752	3.6717		1	0.05534 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(B9)
```

```
[..]
```

	Estimate	Std. Error	t value
(Intercept)	33.46430	18.61198	1.798
exposure	-3.37260	1.84346	-1.829
salinity	-1.12647	0.64909	-1.735
NAP	0.02515	0.96985	0.026
humus	12.41735	7.87781	1.576
exposure:salinity	0.11548	0.06449	1.791
exposure:NAP	0.07247	0.03847	1.884
exposure:humus	-1.21902	0.78897	-1.545
salinity:NAP	-0.03552	0.02661	-1.335

```
[..]
```

```
> B10 <- update(B9, ~.-salinity:NAP)
```

```
0:    -1.7647565: 0.730297
```

```
1:    -2.2271740: 0.471298
```

```
2:    -2.2311842: 0.500273
```

```
3:    -2.2317909: 0.492691
```

```
4:    -2.2317912: 0.492525
```

```
5:    -2.2317912: 0.492501
```

```
6:    -2.2317912: 0.492501
```

```
> B10ML <- update(B10, REML=FALSE)
```

```
0:   -26.956276: 0.730297
```

```
1:   -29.939179: 0.00000
```

```
2:   -29.939179: 1.55125e-06
```

```
3:   -29.939179: 1.55125e-06
```



```
> anova(B10ML,B9ML)
```

```
Data: rikz
```

```
Models:
```

```
B10ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B10ML:      exposure:salinity + exposure:NAP + exposure:humus
```

```
B9ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B9ML:      exposure:salinity + exposure:NAP + exposure:humus
```

```
B9ML      + salinity:NAP
```

```
      Df      AIC      BIC logLik  Chisq Chi Df Pr(>Chisq)
```

```
B10ML 10 -9.9392  8.1274 14.970
```

```
B9ML  11 -9.8319 10.0414 15.916 1.8927      1      0.1689
```

```
> summary(B10)
[...]
```

(Intercept)	34.86718	18.02729	1.934
exposure	-3.47464	1.78723	-1.944
salinity	-1.17017	0.62943	-1.859
NAP	-1.16367	0.37065	-3.139
humus	11.46664	7.96861	1.439
exposure:salinity	0.11852	0.06259	1.894
exposure:NAP	0.09198	0.03577	2.571
exposure:humus	-1.12149	0.79790	-1.406

```
[...]
```

```
> B11 <- update(B10, ~.-exposure:humus)
0:      1.9746978: 0.730297
1:      1.8085855: 0.00000
2:      1.8085855: 0.00000

> B11ML <- update(B11, REML=FALSE)
0:     -24.123141: 0.730297
1:     -28.644278: 0.00000
2:     -28.644278: 0.00000
```

```
> anova(B11ML,B10ML)
```

```
Data: rikz
```

```
Models:
```

```
B11ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B11ML:      exposure:salinity + exposure:NAP
```

```
B10ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B10ML:      exposure:salinity + exposure:NAP + exposure:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B11ML	9	-10.6443	5.6157	14.322				
B10ML	10	-9.9392	8.1274	14.970	1.2949		1	0.2551

```
> B11
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach)
+ exposure:salinity + exposure:NAP
```

```
[..]
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	25.44676	12.14435	2.095
exposure	-2.53976	1.20472	-2.108
salinity	-0.82116	0.41941	-1.958
NAP	-0.89459	0.35486	-2.521
humus	0.26450	0.51705	0.511
exposure:salinity	0.08385	0.04175	2.008
exposure:NAP	0.06663	0.03459	1.926

```
[...]
```

```
> B12 <- update(B11, ~.-exposure:salinity)
```

```
0: -0.098587691: 0.730297
```

```
1: -0.66093519: 0.474219
```

```
2: -0.66484670: 0.500408
```

```
3: -0.66548356: 0.493367
```

```
4: -0.66548380: 0.493228
```

```
5: -0.66548380: 0.493229
```

```
> B12ML <- update(B12, REML=FALSE)
```

```
0: -22.593499: 0.730297
```

```
1: -24.104251: 0.00000
```

```
2: -24.104251: 6.18232e-06
```

```
3: -24.104252: 0.000170993
```

```
4: -24.139061: 0.0457497
```

```
5: -24.470138: 0.165738
```

```
6: -24.715631: 0.405714
```

```
7: -24.801367: 0.303438
```

```
8: -24.811567: 0.328111
```

```
> anova(B12ML,B11ML)
```

```
Data: rikz
```

```
Models:
```

```
B12ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B12ML:     exposure:NAP
```

```
B11ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B11ML:     exposure:salinity + exposure:NAP
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B12ML	8	-8.8116	5.6417	12.406				
B11ML	9	-10.6443	5.6157	14.322	3.8327		1	0.05026 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> B12
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ exposure + salinity + NAP + humus +  
        (1 | Beach) + exposure:NAP
```

```
[..]
```

	Estimate	Std. Error	t value
(Intercept)	1.15024	1.46738	0.784
exposure	-0.12376	0.05269	-2.349
salinity	0.01993	0.04045	0.493
NAP	-0.93216	0.34402	-2.710
humus	0.35074	0.51842	0.677
exposure:NAP	0.07059	0.03354	2.105

```
[..]
```



```
> B13 <- update(B12, ~.-salinity)
```

```
0:      -4.0925532: 0.730297
```

```
1:      -5.0279973: 0.406952
```

```
2:      -5.0421919: 0.454465
```

```
3:      -5.0447002: 0.441360
```

```
4:      -5.0447011: 0.441102
```

```
5:      -5.0447011: 0.441104
```

```
> B13ML <- update(B13, REML=FALSE)
```

```
0:     -22.405729: 0.730297
```

```
1:     -23.632872: 0.00000
```

```
2:     -23.632872: 6.82081e-06
```

```
3:     -23.632873: 0.000209714
```

```
4:     -23.702115: 0.0625813
```

```
5:     -24.233233: 0.221826
```

```
6:     -24.453896: 0.338432
```

```
7:     -24.454528: 0.346503
```

```
8:     -24.454571: 0.344888
```

```
> anova(B13ML,B12ML)
```

```
Data: rikz
```

```
Models:
```

```
B13ML: ShannonW ~ exposure + NAP + humus + (1 | Beach) + exposure:N
```

```
B12ML: ShannonW ~ exposure + salinity + NAP + humus + (1 | Beach) +
```

```
B12ML:      exposure:NAP
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B13ML	7	-10.4546	2.1921	12.227				
B12ML	8	-8.8116	5.6417	12.406	0.357		1	0.5502

```
> B13
```

```
Linear mixed model fit by REML
```

```
Formula: ShannonW ~ exposure + NAP + humus +  
          (1 | Beach) + exposure:NAP
```

```
[..]
```

	Estimate	Std. Error	t value
(Intercept)	1.82886	0.45860	3.988
exposure	-0.13557	0.04412	-3.073
NAP	-0.93632	0.34287	-2.731
humus	0.40236	0.50705	0.794
exposure:NAP	0.07087	0.03343	2.120

```
[..]
```

```
> B14 <- update(B13, ~.-humus)
0:      -3.1079878: 0.730297
1:      -3.9300741: 0.431067
2:      -3.9406377: 0.471682
3:      -3.9424344: 0.460627
4:      -3.9424352: 0.460386
5:      -3.9424352: 0.460388

> B14ML <- update(B14, REML=FALSE)
0:      -21.820395: 0.730297
1:      -22.739010: 0.00000
2:      -22.739010: 7.52231e-06
3:      -22.739011: 0.000259128
4:      -22.880262: 0.0868904
5:      -23.616152: 0.288666
6:      -23.703097: 0.366825
7:      -23.703443: 0.361997
8:      -23.703444: 0.362261
```

```
> anova(B14ML,B13ML)
```

```
Data: rikz
```

```
Models:
```

```
B14ML: ShannonW ~ exposure + NAP + (1 | Beach) + exposure:NAP
```

```
B13ML: ShannonW ~ exposure + NAP + humus + (1 | Beach) + exposure:N
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B14ML	6	-11.703	-0.86347	11.852				
B13ML	7	-10.455	2.19207	12.227	0.7511		1	0.3861

```
> B14
```

```
[..]
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	1.92603	0.44765	4.303
exposure	-0.14294	0.04368	-3.272
NAP	-0.89673	0.33620	-2.667
exposure:NAP	0.06661	0.03270	2.037

```
[..]
```

```
> B15 <- update(B14, ~.-exposure:NAP)
```

```
0:    -3.5739227: 0.730297  
1:    -4.1112507: 0.00000  
2:    -4.1112507: 3.65618e-06  
3:    -4.1112511: 0.000144407  
4:    -4.1650501: 0.0555603  
5:    -4.7984144: 0.246592  
6:    -5.0104872: 0.374551  
7:    -5.0104967: 0.373651  
8:    -5.0104968: 0.373725  
9:    -5.0104968: 0.373722
```

```
> B15ML <- update(B15, REML=FALSE)
```

```
0:    -16.875166: 0.730297  
1:    -19.518802: 0.00000  
2:    -19.518802: 3.18807e-06
```

```
> anova(B15ML,B14ML)
```

```
Data: rikz
```

```
Models:
```

```
B15ML: ShannonW ~ exposure + NAP + (1 | Beach)
```

```
B14ML: ShannonW ~ exposure + NAP + (1 | Beach) + exposure:NAP
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
B15ML	5	-9.5188	-0.48549	9.7594				
B14ML	6	-11.7034	-0.86347	11.8517	4.1846		1	0.04079 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
> summary(B14)
```

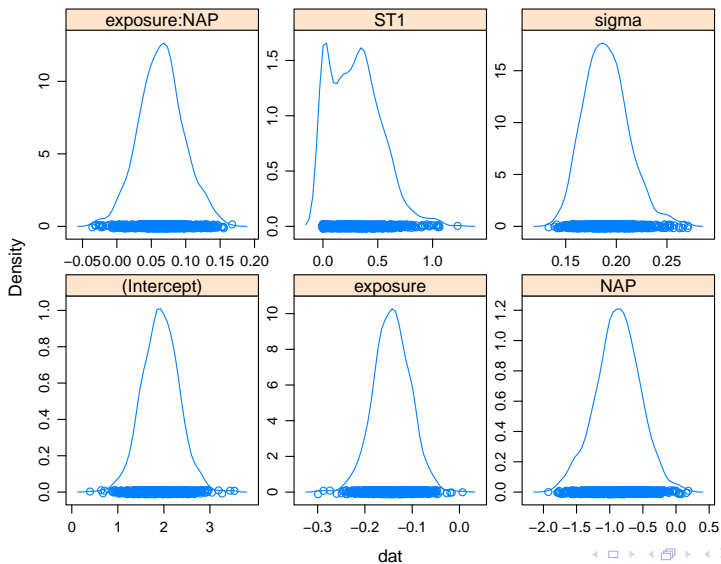
```
[..]
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	1.92603	0.44765	4.303
exposure	-0.14294	0.04368	-3.272
NAP	-0.89673	0.33620	-2.667
exposure:NAP	0.06661	0.03270	2.037

```
[..]
```

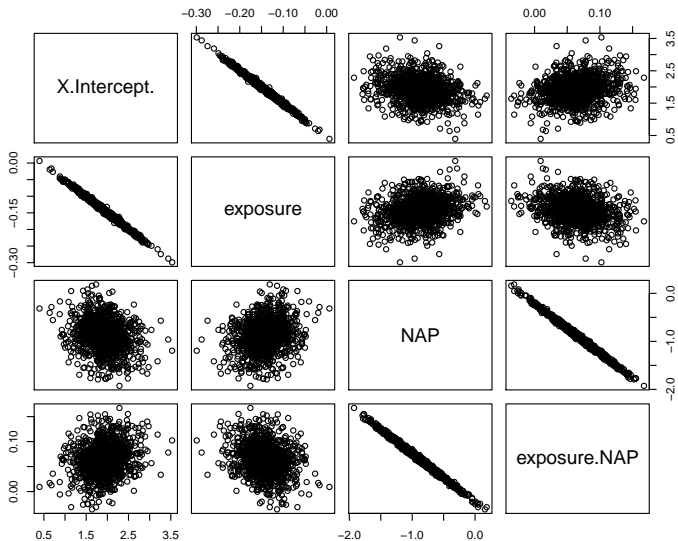
```
> samp14 <- mcmcSamp(B14,1000)
> densityplot(samp14)
```



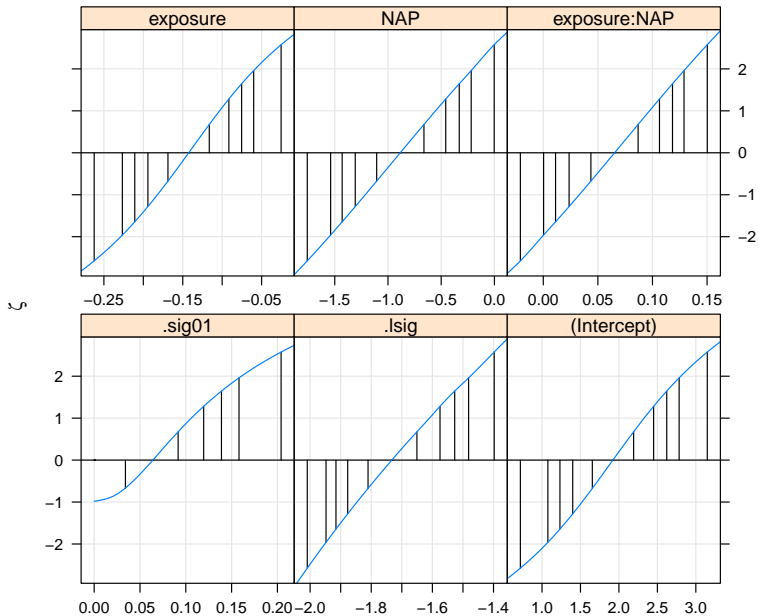
```
> sum(samp14@ST==0)/1000  
[1] 0.153
```

15.3% of the sampled parameter sets have $\sigma_\alpha = 0$. This means, with a posterior probability of 15.3% there is no beach effect.

```
> plot(data.frame(t(samp14@fixef)))
```



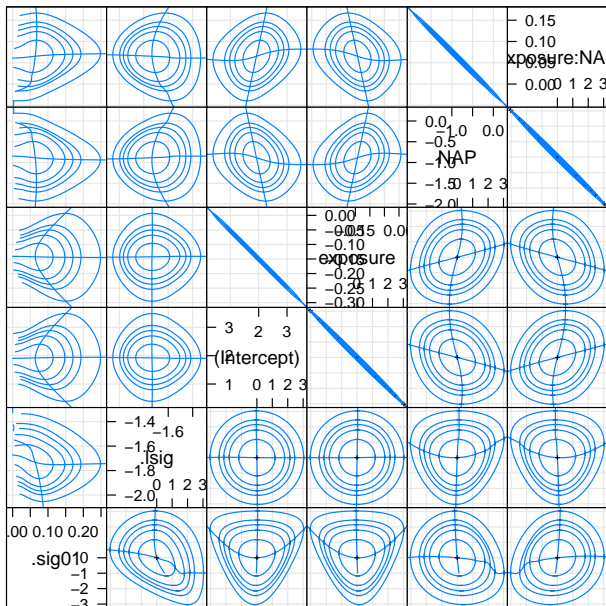
How to select a mixed-effects model



```
> confint(pr14)
```

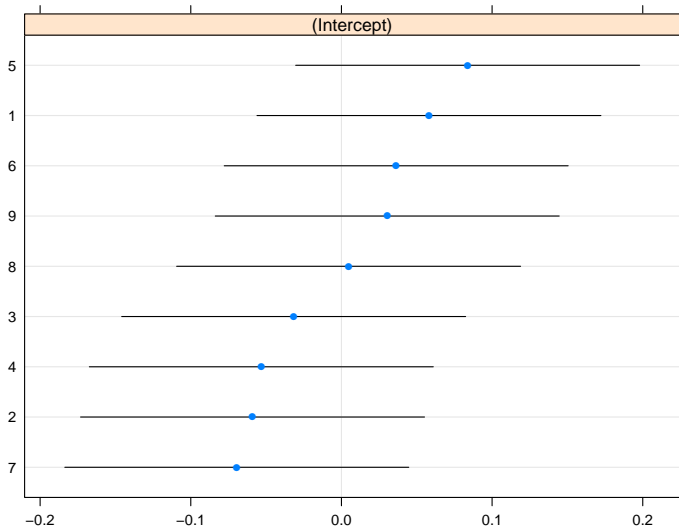
	2.5 %	97.5 %
.sig01	NA	0.15806902
.lsig	-1.9478665471	-1.48146028
(Intercept)	1.0759293994	2.78295226
exposure	-0.2265797054	-0.06004775
NAP	-1.5386892998	-0.21810411
exposure:NAP	0.0003071935	0.12889265

How to select a mixed-effects model

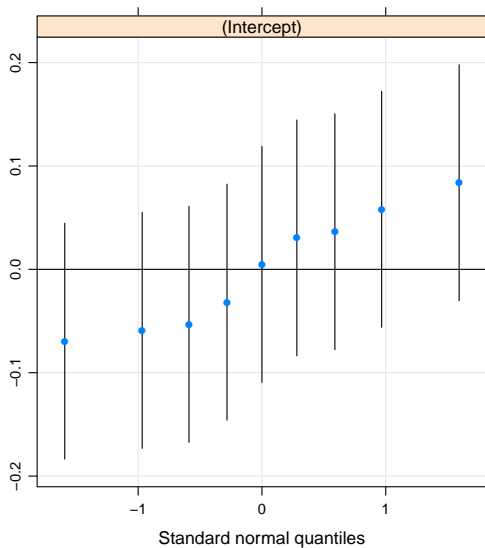


Streudiagramm-Matrix

```
> dotplot(ranef(B14,postVar=TRUE))
```




```
> qqmath(ranef(B14,postVar=TRUE))
```



Contents

The random effect of the beach

How to select a mixed-effects model

Nested Anova of a split-plot experiment.

Generalized linear mixed-effects models

```
> library(MASS)
> oats.aov <- aov(Y~N+V+Error(B/V),data=oats,qr=T)
> model.tables(oats.aov,type="mean")
```

```
Grand mean
103.9722
```

```
N
0.0cwt 0.2cwt 0.4cwt 0.6cwt
 79.39  98.89 114.22 123.39
```

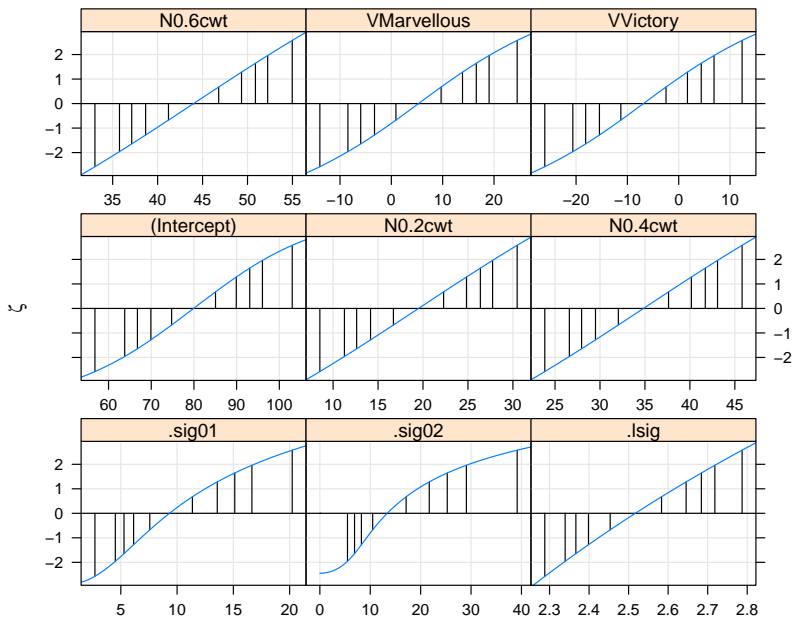
```
V
Golden.rain  Marvellous      Victory
      104.50      109.79      97.63
```

```
> oats.lmer <- lmer(Y~N+V+(1 | B/V),data=oats)
> fixef(oats.lmer)
(Interc) N0.2cwt N0.4cwt N0.6cwt VMarvellous VVictory
 79.917   19.50   34.83   44.0      5.292   -6.875
```

```
> oats.pr <- profile(oats.lmer)
> confint(oats.pr)

                2.5 %    97.5 %
.sig01          4.511185 16.646920
.sig02          5.482973 29.072479
.lsig           2.339491  2.718178
(Intercept)    63.786567 96.046767
N0.2cwt        11.258823 27.741177
N0.4cwt        26.592156 43.074511
N0.6cwt        35.758823 52.241177
VMarvellous   -8.461640 19.045023
VVictory      -20.628307  6.878357
```

Nested Anova of a split-plot experiment.



Contents

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How to select a mixed-effects model

Nested Anova of a split-plot experiment.

Generalized linear mixed-effects models

- ▶ Generalized linear mixed-effects models can be fitted with the `glmer` command in the `lme4` package.

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- ▶ Generalized linear mixed-effects models can be fitted with the `glmer` command in the `lme4` package.
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- ▶ All p -values can be very imprecise, so do not trust them too much, especially if they are close to the significance level.
- ▶ Mcmc methods or other nice methods to visualize the results of a mixed-effects GLM are not yet implemented in `lme4`.
- ▶ As an example we fit an overdispersed Poisson model to the RIKZ data with Richness as the response variable.

```

> mmod11 <- glmer(Richness~1+(exposure+salinity+NAP+humus)^2
+                 +(1 | Beach),
+                 family=quasipoisson,data=rikz,verbose=TRUE)
 0: 49.833560: 0.730297 64.4576 -6.91148 -2.16330 2.32707[.
 1: 49.818337: 0.730288 64.4576 -6.91149 -2.16331 2.32707[.
 2: 49.813761: 0.730246 64.4576 -6.91148 -2.16330 2.32707[.
[...]
```

52:	32.698606:	2.36530e-08	64.4582	-6.91155	-2.16332	2.32[.
53:	32.698606:	1.27632e-08	64.4582	-6.91155	-2.16332	2.32[.
54:	32.698606:	2.55421e-09	64.4582	-6.91155	-2.16332	2.32[.

```
> summary(mmod11)
```

Generalized linear mixed model fit by the Laplace approximation

Formula: Richness ~ 1 + (exposure + salinity + NAP + humus)^2
+ (1 | Beach)

Data: rikz

AIC BIC logLik deviance

58.7 82.19 -16.35 32.7

Random effects:

Groups	Name	Variance	Std.Dev.
--------	------	----------	----------

Beach	(Intercept)	1.2605e-17	3.5504e-09
-------	-------------	------------	------------

Residual		1.9321e+00	1.3900e+00
----------	--	------------	------------

Number of obs: 45, groups: Beach, 9

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	64.45819	45.35670	1.421
exposure	-6.91155	4.44718	-1.554
salinity	-2.16332	1.56826	-1.379
NAP	2.32704	4.22804	0.550
humus	62.83613	49.51439	1.269
exposure:salinity	0.23884	0.15421	1.549

```

> mmod12 <- glmer(Richness~1+(exposure+salinity+NAP+humus)^2
+                 +(1+NAP | Beach),
+                 family=quasipoisson,data=rikz,verbose=TRUE)
 0: 59.544991: 0.730297 0.700275 0.00000 64.4576 -6.91148 -2
 1: 59.537494: 0.730285 0.700265 -5.54163e-08 64.4576 -6.9114
 2: 59.531152: 0.730266 0.700248 -2.01145e-07 64.4576 -6.9114
[...]
```

59:	32.698606:	0.00000	0.00000	0.134189	64.4553	-6.91124	-2
60:	32.698606:	0.00000	0.00000	0.134153	64.4577	-6.91148	-2
61:	32.698606:	0.00000	7.78293e-09	0.134153	64.4577	-6.91148	
62:	32.698606:	0.00000	6.42409e-09	0.134153	64.4577	-6.91148	

```
> summary(mmod12)
```

Generalized linear mixed model fit by the Laplace approximation

Formula: Richness ~ 1 + (exposure + salinity + NAP + humus)^2
 + (1 + NAP | Beach)

Data: rikz

AIC BIC logLik deviance

62.7 89.8 -16.35 32.7

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
Beach	(Intercept)	0.0000e+00	0.0000e+00	
	NAP	7.9737e-17	8.9296e-09	NaN
Residual		1.9321e+00	1.3900e+00	

Number of obs: 45, groups: Beach, 9

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	64.45774	45.35664	1.421
exposure	-6.91148	4.44718	-1.554
salinity	-2.16330	1.56826	-1.379
NAP	2.32709	4.22804	0.550
humus	62.83178	49.51448	1.269

```
> anova(mmod11,mmod12)
```

```
Data: rikz
```

```
Models:
```

```
mmod11: Richness ~ 1 + (exposure + salinity + NAP + humus)^2
          + (1 | Beach)
```

```
mmod12: Richness ~ 1 + (exposure + salinity + NAP + humus)^2
          + (1 + NAP | Beach)
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
mmod11	13	58.699	82.185	-16.349				
mmod12	15	62.699	89.799	-16.349	4.148e-10		2	1


```
> summary(mmod11)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	64.45819	45.35670	1.421
exposure	-6.91155	4.44718	-1.554
salinity	-2.16332	1.56826	-1.379
NAP	2.32704	4.22804	0.550
humus	62.83613	49.51439	1.269
exposure:salinity	0.23884	0.15421	1.549
exposure:NAP	-0.01075	0.13433	-0.080
exposure:humus	-3.34134	2.07648	-1.609
salinity:NAP	-0.10649	0.12179	-0.874
salinity:humus	-0.93055	1.39050	-0.669
NAP:humus	4.47479	2.36577	1.892

```
[...]
```

```
> mmod13 <- update(mmod11, ~.-exposure:NAP)
  0:    49.843351: 0.730297  64.9374 -6.96048 -2.18191  2.08793[.
  1:    49.827666: 0.730288  64.9374 -6.96048 -2.18192  2.08793[.
  2:    49.820544: 0.730200  64.9374 -6.96048 -2.18190  2.08794[.
[...]
```

56:	32.710979:	3.62620e-05	64.9381	-6.96054	-2.18195	2.08291
57:	32.710979:	0.00000	64.9381	-6.96056	-2.18193	2.08813[.
58:	32.710979:	0.00000	64.9381	-6.96055	-2.18194	2.08799[.
59:	32.710979:	0.00000	64.9381	-6.96056	-2.18193	2.08798[.
60:	32.710979:	0.00000	64.9381	-6.96056	-2.18193	2.08794[.

```
> anova(mmod13,mmod11)
```

```
Data: rikz
```

```
Models:
```

```
mmod13: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod13:      exposure:salinity + exposure:humus + salinity:NAP +
```

```
mmod13:      salinity:humus + NAP:humus
```

```
mmod11: Richness ~ 1 + (exposure + salinity + NAP + humus)^2 + (1 |
```

```
      Df      AIC      BIC  logLik  Chisq Chi Df Pr(>Chisq)
```

```
mmod13 12 56.711 78.391 -16.355
```

```
mmod11 13 58.699 82.185 -16.349 0.0124      1      0.9114
```

```
> summary(mmod13)
```

Generalized linear mixed model fit by the Laplace approximation

Formula: Richness ~ exposure + salinity + NAP + humus +

(1 | Beach) + exposure:salinity + exposure:humus +

salinity:NAP + salinity:humus + NAP:humus

```
[..]
```

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	64.9381	45.1037	1.440
exposure	-6.9606	4.4192	-1.575
salinity	-2.1819	1.5560	-1.402
NAP	2.0879	3.0016	0.696
humus	63.5644	48.7489	1.304
exposure:salinity	0.2407	0.1529	1.575
exposure:humus	-3.4145	1.8665	-1.829
salinity:NAP	-0.1018	0.1073	-0.949
salinity:humus	-0.9299	1.3925	-0.668
NAP:humus	4.4724	2.3660	1.890

```
[..]
```

```

> mmod14 <- update(mmod13, ~.-salinity:humus)
0:      50.977682: 0.730297  68.3906 -7.14795 -2.29828  2.41247  3
1:      50.963879: 0.730289  68.3906 -7.14795 -2.29829  2.41247  3
2:      50.963059: 0.730193  68.3906 -7.14795 -2.29828  2.41247  3
3:      50.007435: 0.636302  68.3910 -7.14725 -2.29102  2.41331  3
4:      47.892486: 0.542366  68.3913 -7.14654 -2.28372  2.41404  3
5:      39.995619: 0.166545  68.3925 -7.14406 -2.25563  2.41702  3
6:      39.769482: 0.166545  68.3925 -7.14406 -2.25565  2.41702  3
7:      39.647185: 0.166543  68.3925 -7.14406 -2.25566  2.41701  3
0.242384 -3.00727 -0
[...]
62:     33.567645: 1.55968e-07  68.3895 -7.14784 -2.29824  2.41238
63:     33.567645: 0.00000  68.3904 -7.14793 -2.29827  2.41247  3
64:     33.567645: 1.19137e-09  68.3906 -7.14795 -2.29828  2.41247

```

```
> anova(mmod14,mmod13)
```

```
Data: rikz
```

```
Models:
```

```
mmod14: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod14:      exposure:salinity + exposure:humus + salinity:NAP + NAP
```

```
mmod13: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod13:      exposure:salinity + exposure:humus + salinity:NAP + sal
```

```
mmod13:      NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
mmod14	11	55.568	75.441	-16.784				
mmod13	12	56.711	78.391	-16.355	0.8567		1	0.3547

```
> summary(mmod14)
```

```
[..]
```

	Estimate	Std. Error	t value
(Intercept)	68.3906	45.2987	1.510
exposure	-7.1479	4.4665	-1.600
salinity	-2.2983	1.5638	-1.470
NAP	2.4125	3.0405	0.794
humus	33.2900	17.8258	1.867
exposure:salinity	0.2468	0.1546	1.596
exposure:humus	-3.0208	1.7998	-1.678
salinity:NAP	-0.1145	0.1088	-1.052
NAP:humus	5.1862	2.1676	2.393

```
[..]
```

```
> mmod15 <- update(mmod14, ~.-salinity:NAP)
  0:    54.119609: 0.730297  64.2333 -6.76223 -2.13153 -
  1:    54.105967: 0.730289  64.2333 -6.76224 -2.13154 -
  2:    54.105023: 0.730191  64.2333 -6.76223 -2.13154 -
[...]
```

33:	35.825219:	0.00000	64.2334	-6.76224	-2.13154	-
34:	35.825219:	0.00000	64.2333	-6.76223	-2.13153	-


```
> anova(mmod15,mmod14)
```

```
Data: rikz
```

```
Models:
```

```
mmod15: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod15:      exposure:salinity + exposure:humus + NAP:humus
```

```
mmod14: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod14:      exposure:salinity + exposure:humus + salinity:NAP + NAP
```

```
      Df      AIC      BIC  logLik  Chisq Chi Df Pr(>Chisq)
```

```
mmod15 10 55.825 73.892 -17.913
```

```
mmod14 11 55.568 75.441 -16.784 2.2576      1      0.1330
```

```
> summary(mmod15)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	64.2333	45.8648	1.400
exposure	-6.7622	4.5261	-1.494
salinity	-2.1315	1.5821	-1.347
NAP	-0.7919	0.1650	-4.800
humus	26.3211	17.2232	1.528
exposure:salinity	0.2313	0.1566	1.477
exposure:humus	-2.3704	1.7606	-1.346
NAP:humus	4.1208	1.9210	2.145

```
[...]
```

```
> mmod16 <- update(mmod15, ~.-exposure:humus)
```

```
0:      58.266620: 0.730297  46.8934 -5.01697 -1.48258 -
```

```
1:      58.254732: 0.730288  46.8934 -5.01698 -1.48259 -
```

```
2:      58.235790: 0.728826  46.8934 -5.01694 -1.48244 -
```

```
3:      46.756746: 0.120192  46.8961 -5.00220 -1.42242 -
```

```
[...]
```

```
28:     39.633451: 0.00000  46.8961 -5.01723 -1.48267 -
```

```
29:     39.633451: 0.00000  46.8945 -5.01709 -1.48262 -
```

```
30:     39.633451: 0.00000  46.8935 -5.01699 -1.48259 -
```

```
> anova(mmod16,mmod15)
```

```
Data: rikz
```

```
Models:
```

```
mmod16: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod16:      exposure:salinity + NAP:humus
```

```
mmod15: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod15:      exposure:salinity + exposure:humus + NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
mmod16	9	57.633	73.893	-19.817				
mmod15	10	55.825	73.892	-17.913	3.8082		1	0.051 .

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(mmod16)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	46.8935	47.4863	0.988
exposure	-5.0170	4.6770	-1.073
salinity	-1.4826	1.6240	-0.913
NAP	-0.7177	0.1653	-4.341
humus	3.2326	1.7443	1.853
exposure:salinity	0.1658	0.1604	1.034
NAP:humus	4.0391	2.0136	2.006

```
[...]
```

```
> mmod17 <- update(mmod16, ~.-exposure:salinity)
  0:      58.637737:  0.730297 -2.14684 -0.183246  0.196099
  1:      58.598479:  0.729260 -2.14690 -0.183880  0.194558
  2:      58.564423:  0.727583 -2.14686 -0.183644  0.195548
[...]
```

33:	42.290178:	8.33188e-06	-2.14646	-0.183254	0.196099
34:	42.290178:	3.01290e-06	-2.14671	-0.183249	0.196099
35:	42.290178:	2.25278e-09	-2.14684	-0.183246	0.196099
36:	42.290178:	1.36106e-11	-2.14684	-0.183246	0.196099

```
> anova(mmod17,mmod16)
```

```
Data: rikz
```

```
Models:
```

```
mmod17: Richness ~ exposure + salinity + NAP + humus + (1
```

```
mmod17:     NAP:humus
```

```
mmod16: Richness ~ exposure + salinity + NAP + humus + (1
```

```
mmod16:     exposure:salinity + NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
mmod17	8	58.290	72.743	-21.145				
mmod16	9	57.633	73.893	-19.817	2.6567		1	0.1031

```
> summary(mmod17)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	-2.1468	4.0782	-0.526
exposure	-0.1832	0.1281	-1.430
salinity	0.1961	0.1137	1.725
NAP	-0.7116	0.1780	-3.997
humus	3.4743	1.8951	1.833
NAP:humus	3.8253	2.1777	1.757

```
[...]
```



```
> mmod18 <- update(mmod17, ~.-exposure)
```

```
0: 59.363947: 0.730297 -6.50861 0.283750 -0.782548
1: 59.309792: 0.729344 -6.50868 0.281666 -0.782629
2: 59.249973: 0.724342 -6.50859 0.283825 -0.783080
3: 49.314348: 0.249654 -6.50743 0.281775 -0.821932
4: 49.028180: 0.0874159 -6.50621 0.286181 -0.768039
5: 47.878333: 0.0874274 -6.50630 0.283516 -0.768044
6: 47.829181: 0.111395 -6.50597 0.283569 -0.776400
7: 47.811523: 0.108337 -6.48757 0.282663 -0.780176
8: 47.782569: 0.107177 -6.38537 0.279448 -0.780133
9: 47.771312: 0.120894 -6.28677 0.276050 -0.770252
10: 47.770238: 0.117932 -6.26689 0.275277 -0.772068
11: 47.769283: 0.116689 -6.25496 0.274892 -0.775140
12: 47.768895: 0.118127 -6.25212 0.274784 -0.773427
13: 47.768886: 0.118026 -6.24913 0.274674 -0.773555
14: 47.768886: 0.118044 -6.24792 0.274631 -0.773578
15: 47.768885: 0.118049 -6.24780 0.274626 -0.773576
16: 47.768885: 0.118049 -6.24780 0.274626 -0.773576
```

```
> anova(mmod18,mmod17)
```

```
Data: rikz
```

```
Models:
```

```
mmod18: Richness ~ salinity + NAP + humus + (1 | Beach) + NAP:humus
```

```
mmod17: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
mmod17:      NAP:humus
```

	Df	AIC	BIC	logLik	Chisq	Chi	Df	Pr(>Chisq)
mmod18	7	61.769	74.416	-23.884				
mmod17	8	58.290	72.743	-21.145	5.4787		1	0.01925 *

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
> summary(mmod17)
```

```
[...]
```

	Estimate	Std. Error	t value
(Intercept)	-2.1468	4.0782	-0.526
exposure	-0.1832	0.1281	-1.430
salinity	0.1961	0.1137	1.725
NAP	-0.7116	0.1780	-3.997
humus	3.4743	1.8951	1.833
NAP:humus	3.8253	2.1777	1.757

```
[..]
```

```
> mmod19 <- update(mmod17, ~.-NAP:humus)
0:      69.899155:  0.730297 -0.528882 -0.288714  0.180644 -0.498037
1:      69.858054:  0.729229 -0.528938 -0.289361  0.179067 -0.498187
2:      69.822146:  0.727528 -0.528902 -0.289110  0.180093 -0.498425
3:      69.752883:  0.723874 -0.528954 -0.289891  0.178653 -0.498916
4:      59.543657:  0.331011 -0.528734 -0.314567  0.189047 -0.545780
5:      56.406034:  0.224112 -0.528678 -0.320623  0.190064 -0.550253
6:      54.889391:  0.136913 -0.528511 -0.324521  0.195036 -0.558595
7:      54.771875:  0.0497220 -0.528591 -0.329548  0.191390 -0.56709
8:      53.704231:  0.00628396 -0.528348 -0.325059  0.194014 -0.5708
9:      52.557547:  0.0391547 -0.528090 -0.298380  0.183467 -0.56589
10:     52.326076:  0.00000 -0.527933 -0.291355  0.181607 -0.563221
11:     52.106386:  0.00000 -0.528402 -0.324021  0.191978 -0.491460
12:     52.008303:  3.46690e-15 -0.528380 -0.323749  0.192565 -0.491
13:     51.758028:  4.00663e-13 -0.528270 -0.314098  0.188878 -0.492
14:     51.716750:  0.00000 -0.528142 -0.305373  0.187209 -0.488564
15:     51.457747:  0.00000 -0.527829 -0.297049  0.183507 -0.489009
16:     51.427700:  0.00000 -0.527500 -0.294752  0.182725 -0.496743
17:     51.426304:  0.00277884 -0.527461 -0.294440  0.182564 -0.4964
18:     51.418913:  0.00000 -0.527550 -0.291428  0.181696 -0.495694
19:     51.411862:  0.00000 -0.527743 -0.288447  0.180484 -0.495154
```

```

> mmod20 <- update(mmod17, ~.-salinity)
0:      59.931609: 0.730297  4.64070 -0.307879 -0.705878  3.87577
1:      59.686506: 0.720204  4.63974 -0.318464 -0.705170  3.87486
2:      59.438573: 0.708236  4.64065 -0.310064 -0.704618  3.87391
3:      58.974741: 0.681684  4.63965 -0.322306 -0.703439  3.87166
4:      53.658984:  0.00000  4.65615 -0.299096 -0.648086  3.71811
5:      51.878726: 6.21175e-08  4.65523 -0.308198 -0.648525  3.718
6:      51.089349:  0.00000  4.66017 -0.308044 -0.704827  3.70271
7:      51.085319:  0.00000  4.65088 -0.309370 -0.704784  3.74770
8:      51.005801:  0.00000  4.64691 -0.307597 -0.704035  3.77021
9:      50.974766:  0.00000  4.64425 -0.307696 -0.711910  3.79163
10:     50.607459: 0.0432925  4.62618 -0.307252 -0.698582  3.96917
11:     50.157784: 0.0897194  4.60979 -0.305835 -0.686628  4.13325
12:     50.124822: 0.0902944  4.60961 -0.307876 -0.686690  4.13318
13:     50.106719: 0.0905979  4.60987 -0.306959 -0.686892  4.13179
14:     50.087485: 0.0919311  4.61015 -0.307911 -0.687372  4.12889
15:     50.068168: 0.0915007  4.61097 -0.307049 -0.687990  4.12263
16:     50.043262: 0.0918963  4.61239 -0.308146 -0.689342  4.11006
17:     50.022777: 0.0885245  4.61654 -0.307269 -0.691585  4.08530
18:     49.988336: 0.0991556  4.61353 -0.308123 -0.687550  4.13588
19:     49.914042: 0.0956507  4.62255 -0.307547 -0.692348  4.08647

```

```
> mmod17
```

```
Generalized linear mixed model fit by the Laplace approximation
```

```
Formula: Richness ~ exposure + salinity + NAP + humus + (1 | Beach)
```

```
Data: rikz
```

```
AIC BIC logLik deviance
```

```
58.29 72.74 -21.15 42.29
```

```
Random effects:
```

Groups	Name	Variance	Std.Dev.
Beach	(Intercept)	5.2533e-22	2.2920e-11
	Residual	2.8358e+00	1.6840e+00

```
Number of obs: 45, groups: Beach, 9
```

```
Fixed effects:
```

	Estimate	Std. Error	t value
(Intercept)	-2.1468	4.0782	-0.526
exposure	-0.1832	0.1281	-1.430
salinity	0.1961	0.1137	1.725
NAP	-0.7116	0.1780	-3.997
humus	3.4743	1.8951	1.833
NAP:humus	3.8253	2.1777	1.757