

# Review of linear models

5 Sep 2024



Licensed under the [Creative Commons attribution-noncommercial license](#).  
Please share & remix noncommercially, mentioning its origin.

```
## it's nice to include packages at the top  
## (and NOT automatically install them)  
## try not to carry over packages you don't use  
library(faux)  
library(brglm2) ## for lizards data  
library(ggplot2); theme_set(theme_bw())  
## diagnostics  
library(performance)  
library(DHARMA)  
## downstream model evaluation  
library(broom)  
library(dotwhisker)  
library(emmeans)  
library(effects)  
library(marginaleffects)  
library(parameters)  
## library(ggeffects)
```

# Why linear models? (Lindeløv 2019)

## Common statistical tests are linear models

Last updated: 02 April, 2019

See worked examples and more details at the accompanying notebook: <https://lindeløv.github.io/tests-as-linear>

	Common name	Built-in function in R	Equivalent linear model in R	Exact?	The linear model in words	Icon
Simple regression: $\text{lm}(y \sim 1 + x)$	<b>y is independent of x</b> P: One-sample t-test N: Wilcoxon signed-rank	t.test(y) wilcox.test(y)	$\text{lm}(y \sim 1)$ $\text{lm}(\text{signed\_rank}(y) \sim 1)$	✓ for $N \geq 14$	One number (intercept, i.e., the mean) predicts y. - (Same, but it predicts the <i>signed rank</i> of y.)	
	P: Paired-sample t-test N: Wilcoxon matched pairs	t.test(y1, y2, paired=TRUE) wilcox.test(y1, y2, paired=TRUE)	$\text{lm}(y_2 - y_1 \sim 1)$ $\text{lm}(\text{signed\_rank}(y_2 - y_1) \sim 1)$	✓ for $N \geq 14$	One intercept predicts the pairwise $y_2 - y_1$ differences. - (Same, but it predicts the <i>signed rank</i> of $y_2 - y_1$ .)	
	<b>y ~ continuous x</b> P: Pearson correlation N: Spearman correlation	cor.test(x, y, method='Pearson') cor.test(x, y, method='Spearman')	$\text{lm}(y \sim 1 + x)$ $\text{lm}(\text{rank}(y) \sim 1 + \text{rank}(x))$	✓ for $N \geq 10$	One intercept plus x multiplied by a number (slope) predicts y. - (Same, but with <i>ranked x</i> and y)	
	<b>y ~ discrete x</b> P: Two-sample t-test P: Welch's t-test N: Mann-Whitney U	t.test(y1, y2, var.equal=TRUE) t.test(y1, y2, var.equal=FALSE) wilcox.test(y1, y2)	$\text{lm}(y \sim 1 + G_1)^4$ $\text{glm}(y \sim 1 + G_1, \text{weights}=\dots)^4$ $\text{lm}(\text{signed\_rank}(y) \sim 1 + G_1)^4$	✓ for $N \geq 11$	An intercept for <b>group 1</b> (plus a difference if <b>group 2</b> ) predicts y. - (Same, but with one variance <i>per group</i> instead of one common.) - (Same, but it predicts the <i>signed rank</i> of y.)	
Multiple regression: $\text{lm}(y \sim 1 + x_1 + x_2 + \dots)$	P: One-way ANOVA N: Kruskal-Wallis	aov(y ~ group) kruskal.test(y ~ group)	$\text{lm}(y \sim 1 + G_1 + G_2 + \dots + G_n)^4$ $\text{lm}(\text{rank}(y) \sim 1 + G_1 + G_2 + \dots + G_n)^4$	✓ for $N \geq 11$	An intercept for <b>group 1</b> (plus a difference if <b>group 2</b> ) predicts y. - (Same, but it predicts the <i>rank</i> of y.)	
	P: One-way ANCOVA	aov(y ~ group + x)	$\text{lm}(y \sim 1 + G_1 + G_2 + \dots + G_n + x)^4$	✓	- (Same, but plus a slope on x.) Note: this is discrete AND continuous. ANCOVAs are ANOVAs with a continuous x.	
	P: Two-way ANOVA	aov(y ~ group * sex)	$\text{lm}(y \sim 1 + G_1 + G_2 + \dots + G_n + S_1 + S_2 + \dots + S_k + G_1:S_1 + G_1:S_2 + \dots + G_n:S_k)$	✓	Interaction term: changing <b>sex</b> changes the <b>y ~ group</b> parameters. Note: $G_{1:k}$ is an indicator (0 or 1) for each non-intercept levels of the <b>group</b> variable. Similarly for $S_{1:k}$ for <b>sex</b> . The first line (with $G_1$ ) is main effect of group, the second (with $S_1$ ) for sex and the third is the <b>group * sex</b> interaction. For two levels (e.g. male/female), line 2 would just be " $S_1$ " and line 3 would be " $S_1$ multiplied with each $G_i$ ."	[Coming]
	<b>Counts ~ discrete x</b> N: Chi-square test	chisq.test(groupXsex_table)	<b>Equivalent log-linear model</b> $\text{glm}(y \sim 1 + G_1 + G_2 + \dots + G_n + S_1 + S_2 + \dots + S_k + G_1:S_1 + G_1:S_2 + \dots + G_n:S_k, \text{family}=\dots)^4$	✓	Interaction term: (Same as Two-way ANOVA.) Note: Run glm using the following arguments: <code>glm(model, family=poisson())</code> . As linear-model, the Chi-square test is $\log(y) = \log(N) + \log(a) + \log(\beta) + \log(a\beta)$ where $a_i$ and $\beta_j$ are proportions. See more info in the accompanying notebook.	Same as Two-way ANOVA
	N: Goodness of fit	chisq.test(y)	$\text{glm}(y \sim 1 + G_1 + G_2 + \dots + G_n, \text{family}=\dots)^4$	✓	(Same as One-way ANOVA and see Chi-Square note.)	1W-ANOVA

List of common parametric (P) non-parametric (N) tests and equivalent linear models. The notation  $y \sim 1 + x$  is R shorthand for  $y = 1 + a \cdot x$  which most of us learned in school. Models in similar colors are highly similar, but really, notice how similar they all are across colors! For non-parametric models, the linear models are reasonable approximations for non-small sample sizes (see "Exact" column and click links to see simulations). Other less accurate approximations exist, e.g., Wilcoxon for the sign test and Goodness-of-fit for the binomial test. The signed rank function is  $\text{signed\_rank} = \text{function}(x) \{ \text{sign}(x) * \text{rank}(\text{abs}(x)) \}$ . The variables  $G_i$  and  $S_i$  are "dummy coded" indicator variables (either 0 or 1) exploiting the fact that when  $\Delta x = 1$  between categories the difference equals the slope. Subscripts (e.g.,  $G_2$  or  $y_1$ ) indicate different columns in data.  $\text{lm}$  requires long-format data for all non-continuous models. All of this is exposed in greater detail and worked examples at <https://lindeløv.github.io/tests-as-linear>.

<sup>4</sup> See the note to the two-way ANOVA for explanation of the notation.

<sup>8</sup> Same model, but with one variance per group: `glm(value ~ 1 + G1, weights = varIdent(form = ~1|group), method="ML")`.



Jonas Kristoffer Lindeløv  
<https://lindeløv.net>

## Basics

- assume  $\mathbf{y} \sim \text{Normal}(\mathbf{X}\beta, \sigma)$ <sup>1</sup>
- $\mathbf{X}$  is the *model matrix*, can be anything we want it to be
- the *Gauss-Markov theorem* (Wikipedia) makes weaker assumptions:  $\mathbf{y} = \mathbf{X}\beta + \epsilon$ ; as long as  $\epsilon$  is mean-zero, homoscedastic with finite variance, and uncorrelated ... then the OLS solution

$$\hat{\beta} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{y}$$

is the BLUE (or MVUE).

- we'll embrace the assumptions (which are needed for inference!)

## Computation

- matrix decompositions (QR with pivoting; see [here](#))
- big problems: `biglm`, `speedglm`, `RcppEigen::fastLm`

<sup>1</sup>Notation-abuse warning ...

- optimized BLAS, kernel trick, etc.
- memory vs speed vs robustness ...
- $p$  vs.  $n$  vs. many-small-regressions vs. ...

## Inference

- $\sigma^2$  (residual variance) is  $\text{RSS}/(n - p)$
- The covariance matrix is  $\Sigma = \sigma^2(\mathbf{X}^\top \mathbf{X})^{-1}$ .
- Individual coefficients are  $t$ -distributed
- Linear combinations of coefficients (contrasts or predictions) are  $t$ -distributed with covariance matrix  $\mathbf{C}^\top \Sigma^{-1} \mathbf{C}$
- Joint hypotheses on coefficients are  $F$ -distributed
- Wald and likelihood ratio test comparisons are equivalent (but need to be careful about marginality)

## Model matrices

- model definition converted to  $\mathbf{X}$  before we start
- **input variables** vs **predictor variables** (Schielzeth (2010), Gelman and Hill (2006), [CV](#))
  - transformations
  - encoding of categorical variables: **contrasts**
  - interactions
  - basis expansions (e.g. polynomials)

## Wilkinson-Rogers formulas

- Wilkinson and Rogers (1973), updated by Chambers and Hastie (1991, ch. 2)
- operators:  $+$ ,  $*$ ,  $:$ ,  $/$ ,  $-$ ,  $\wedge$
- $\text{I}()$

## Contrasts

### treatment contrasts

- intercept = baseline, subsequent values are differences
- $\{\beta_0 = \mu_0, \beta_i = \mu_i - \mu_0 \text{ for } i > 0\}$
- equivalently:  $\{\mu_0 = \beta_0, \mu_i = \beta_0 + \beta_i \text{ for } i > 0\}$
- **contrast matrix:**

$$\mathbf{C}\beta = \begin{pmatrix} 1 & 0 & 0 & \dots \\ 1 & 1 & 0 & \dots \\ 1 & 0 & 1 & \dots \\ \vdots & \vdots & \vdots & \ddots \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \dots \end{pmatrix} = \begin{pmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \\ \dots \end{pmatrix} .$$

Maybe easier to start from the **inverse** contrast matrix:  $\beta = \mathbf{C}^{-1}\mu$ .

```
C <- cbind(1, contr.treatment(3)) ## R omits the intercept by default
solve(C)
```

```
      1 2 3
      1 0 0
2 -1 1 0
3 -1 0 1
```

We have to specify the baseline level (contr.treatment uses first level of a factor; contr.SAS() uses the last level).

It's nice when contrasts are *orthogonal*, i.e. all rows are independent  $\rightarrow \mathbf{C}^\top \mathbf{C}$  is diagonal.

### Sum-to-zero contrasts

- intercept is the (unweighted!) average rather than baseline value ( $\sum \mu_i/n$ )
- other parameters are differences between mean of level  $i$  and intercept ( $\mu_i - \sum_j \mu_j/n$ )
- **last** level is dropped

```
mfun <- function(C) MASS::fractions(solve(C))
(C <- cbind(1,contr.sum(3)))
```

```
      [,1] [,2] [,3]
1      1      1      0
2      1      0      1
3      1     -1     -1
```

```
mfun(C)
```

```
      1      2      3
[1,] 1/3 1/3 1/3
[2,] 2/3 -1/3 -1/3
[3,] -1/3 2/3 -1/3
```

## Helmert contrasts

- Weird but orthogonal
- intercept, diff of first two levels, diff of level 3 from 1 & 2, ...

```
(C <- cbind(1,contr.helmert(3)))
```

```
  [,1] [,2] [,3]
1     1    -1    -1
2     1     1    -1
3     1     0     2
```

```
mfun(C)
```

```
      1      2      3
[1,] 1/3 1/3 1/3
[2,] -1/2 1/2 0
[3,] -1/6 -1/6 1/3
```

## others

- `MASS::contr.sdif()` (successive-differences)
- `contr.poly()` (orthogonal polynomial contrasts)
- custom (e.g., “none” vs “symbiont effect” vs “crabs vs shrimp” vs “two-symbiont effect”) (McKeon et al. (2012); data [here](#))

```
cc_inv <- matrix(c(1/4,1/4,1/4,1/4,
                  1,-1/3,-1/3,-1/3,
                  0,1,-1,0,
                  0,1/2,1/2,-1),
                byrow=TRUE,
                nrow=4,
                dimnames=list(c("intercept","avg_symb","C.vs.S","twosymb"),
                             c("none","C","S","CS"))
## inverse contrast matrix
MASS::fractions(cc_inv)
```

	none	C	S	CS
intercept	1/4	1/4	1/4	1/4
avg_symb	1	-1/3	-1/3	-1/3
C.vs.S	0	1	-1	0
twosymb	0	1/2	1/2	-1

```
## contrast matrix
mfun(cc_inv)
```

	intercept	avg_symb	C.vs.S	twosymb
none	1	3/4	0	0
C	1	-1/4	1/2	1/3
S	1	-1/4	-1/2	1/3
CS	1	-1/4	0	-2/3

## practical issues

- too many ways to set contrasts (`options()`, `contrasts(f) <- lm(..., contrasts = list(...))`)
- terrible naming conventions: you can get used to it or use the `faux` package
- OK to fit models and later use `emmeans` to recover desired contrasts (switching linear bases)

```
mtcars$fcyl <- factor(mtcars$cyl)
lm0 <- lm(mpg ~ fcyl, mtcars)
cn <- function(x) names(coef(x))
cn(lm0)
```

```
[1] "(Intercept)" "fcyl6"      "fcyl8"
```

```
update(lm0, contrasts = list(fcyl = contr.sum(3))) |> cn()
```

```
[1] "(Intercept)" "fcyl1"      "fcyl2"
```

```
update(lm0, contrasts = list(fcyl = contr.helmert(3))) |> cn()
```

```
[1] "(Intercept)" "fcyl1"      "fcyl2"
```

## using faux

```
update(lm0, data = transform(mtcars, fcyl = contr_code_sum(fcyl))) |> cn()
```

```
[1] "(Intercept)"      "fcyl.4-intercept" "fcyl.6-intercept"
```

```
update(lm0, data = transform(mtcars, fcyl = contr_code_helmert(fcyl))) |> cn()
```

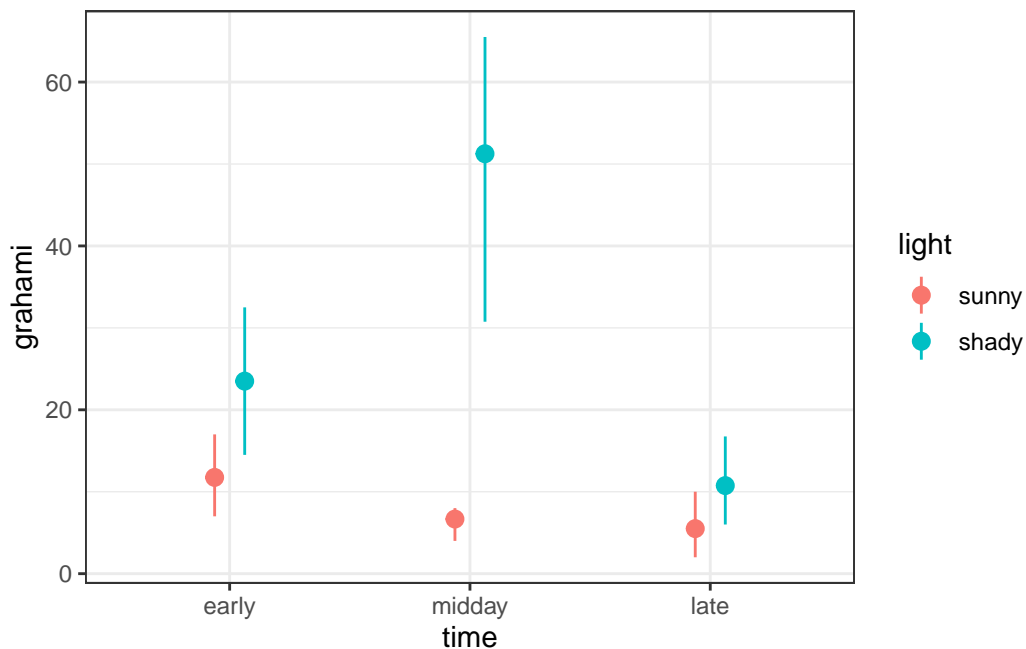
```
[1] "(Intercept)" "fcyl.6-4"    "fcyl.8-4.6"
```

## Interactions

- differences in differences
- parameter values of main effects (and  $p$  values etc.) depend on contrasts/centering!
- overall model fit ( $R^2$ , predictions, etc.) is invariant

Lizard data (Schoener (1970), from the `brglm2` package):

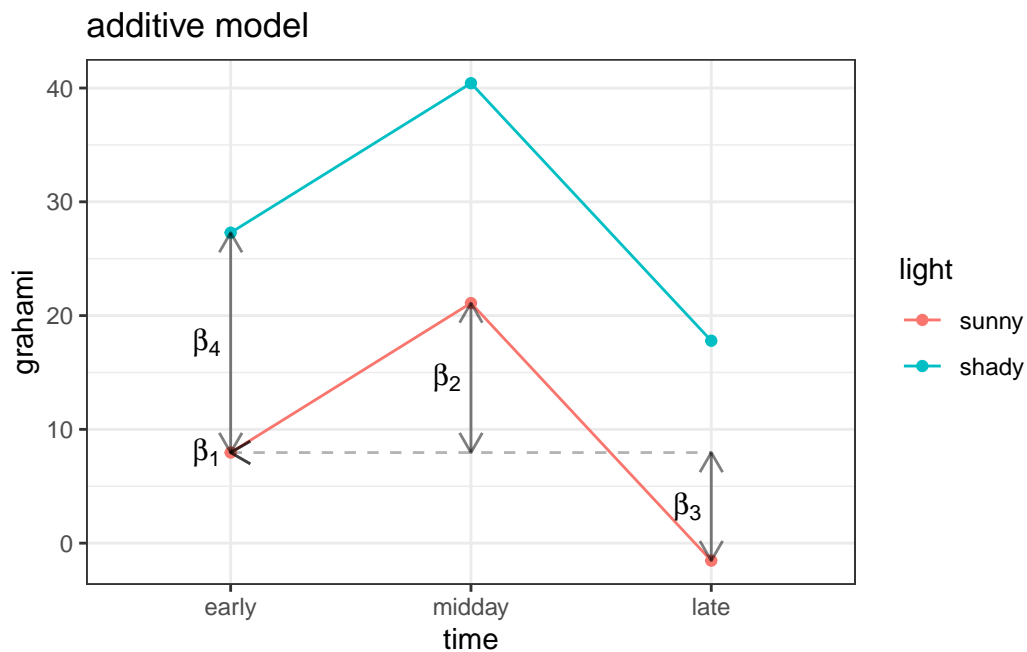
```
data("lizards", package = "brglm2")
ggplot(lizards, aes(time, grahami, colour = light)) +
  stat_summary(fun.data = mean_cl_boot,
              position = position_dodge(width = 0.25))
```



```

data("lizards", package = "brglm2")
lmTL1 <- lm(grahami~time+light,data=lizards)
pp <- with(lizards,expand.grid(time=levels(time),light=levels(light)))
pp$grahami <- predict(lmTL1,newdata=pp)
cc <- as.list(plyr::rename(coef(lmTL1),c(`(Intercept)`="int")))
labelpos <- with(cc,
  list(x=c(1,2,3,1),xend=c(1,2,3,1),
    y=c(int,int,int,int),
    yend=c(int,int+timemidday,int+timelate,int+lightshady)))
xpos <- -0.1
ggplot(pp,aes(x=time,y=grahami,colour=light))+geom_point()+
  geom_line(aes(group=light))+
  annotate("segment",x=labelpos$x,xend=labelpos$xend,y=labelpos$y,
    yend=labelpos$yend,alpha=0.5,
    arrow=arrow(length = unit(0.3,"cm"),ends="both"))+
  annotate("text",x=with(labelpos,(x+xend)/2)+xpos,y=with(labelpos,(y+yend)/2),
  label=paste0("beta[",1:4,"]"),parse=TRUE)+
  annotate("segment",x=labelpos$x[1],xend=labelpos$x[3],y=labelpos$y[1],
    yend=labelpos$y[1],alpha=0.3,lty=2) +
  labs(title = "additive model")

```



```

lmTL2 <- lm(grahami~time*light,data=lizards)
gg_color_hue <- function(n) {

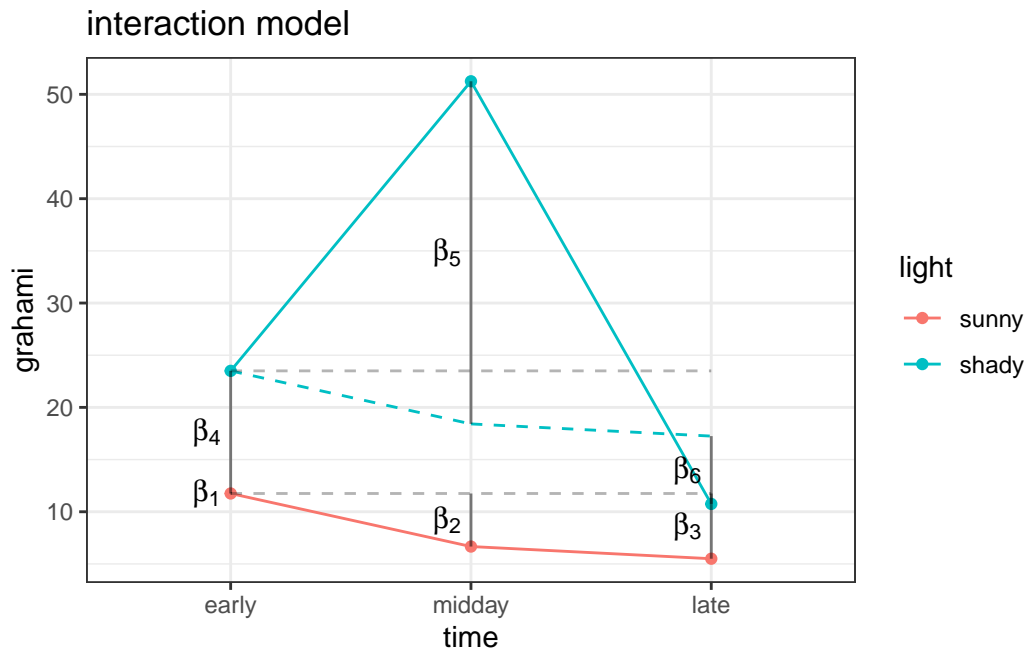
```



```

hues = seq(15, 375, length=n+1)
hcl(h=hues, l=65, c=100)[1:n]
}
pp2 <- pp
pp2$grahami <- predict(lmTL2,newdata=pp)
cc <- as.list(plyr::rename(coef(lmTL2),c(`(Intercept)`="int",
    `timemidday:lightshady`="midshady",`timelate:lightshady`="lateshady"))))
labelpos <- with(cc,
  list(x=c(1,2,3,1,2,3),xend=c(1,2,3,1,2,3),
    y=c(int,int,int,int,int+lightshady+timemidday,int+lightshady+timelate),
    yend=c(int,int+timemidday,int+timelate,int+lightshady,
      int+timemidday+lightshady+midshady,int+timelate+lightshady+lateshady)))
xpos <- -0.1
ggplot(pp2,aes(x=time,y=grahami,colour=light))+geom_point()+
  geom_line(aes(group=light))+
  annotate("segment",x=1:2,xend=2:3,
    y=with(cc,c(int+lightshady,int+timemidday+lightshady)),
    yend=with(cc,c(int+timemidday+lightshady,int+timelate+lightshady)),
    colour=gg_color_hue(2)[2],lty=2)+
  annotate("segment",x=labelpos$x,xend=labelpos$xend,y=labelpos$y,
    yend=labelpos$yend,alpha=0.5) +
    ## arrow=arrow(length = unit(0.3,"cm"),ends="both"))+
  annotate("text",x=with(labelpos,(x+xend)/2)+xpos,y=with(labelpos,(y+yend)/2),
label=paste0("beta[",1:6,"]"),parse=TRUE)+
  annotate("segment",x=rep(labelpos$x[1],2),
    xend=rep(labelpos$x[3],2),
    y=labelpos$yend[c(1,4)],
    yend=labelpos$yend[c(1,4)],alpha=0.3,lty=2) +
  labs(title = "interaction model")

```



## Marginality

- Venables (1998)
- 'type (X) sums of squares'
- scaling and centering (Schielzeth 2010) alleviates many problems; sum-to-zero contrasts (weighted or unweighted?)

## Making life easier with emmeans

- important to understand contrasts
- **but** easier to compute *expected marginal means*, contrasts via emmeans package
- contrasts expressed in terms of *group means*
- e.g.
- good documentation, vignettes

## Model interpretation, visualization, testing

### Diagnostics

- linearity > heteroscedasticity, outliers > normality

- upstream problems can induce downstream problems first
- universal plots are universal, but less interpretable than problem-specific exploration (try to identify problematic predictors/groups/etc.)

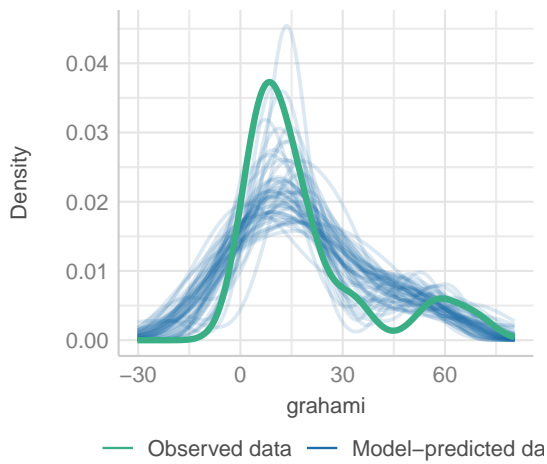
## Graphical diagnostics

- base R: `stats::plot.lm()`
- `performance::check_model()`
- DHARMA (`simulateResiduals(., plot = TRUE)`)
  - (`plotResiduals(simout, form = pred_var)`)
- `broom::augment()` + plot-your-own (ggplot2)

```
performance::check_model(lmTL2)
```

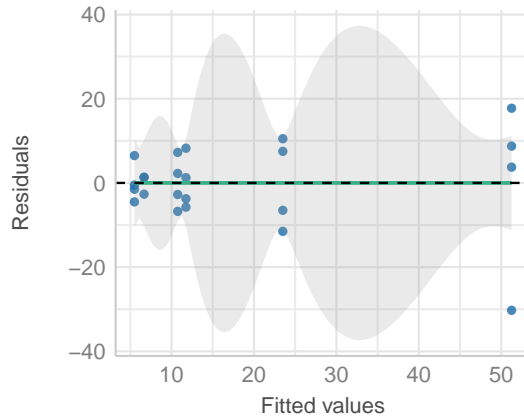
### Posterior Predictive Check

Model-predicted lines should resemble observed data



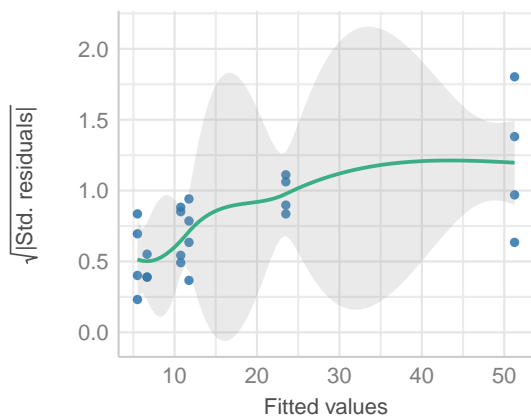
### Linearity

Reference line should be flat and horizontal



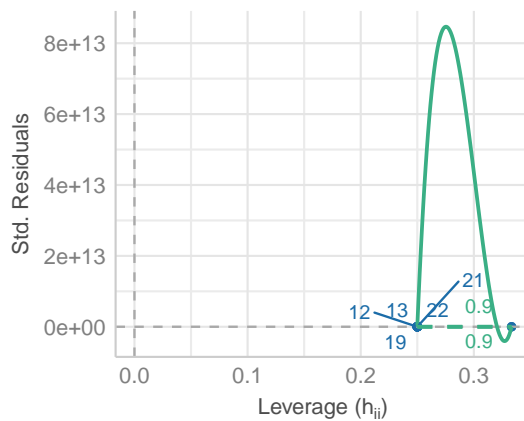
### Homogeneity of Variance

Reference line should be flat and horizontal



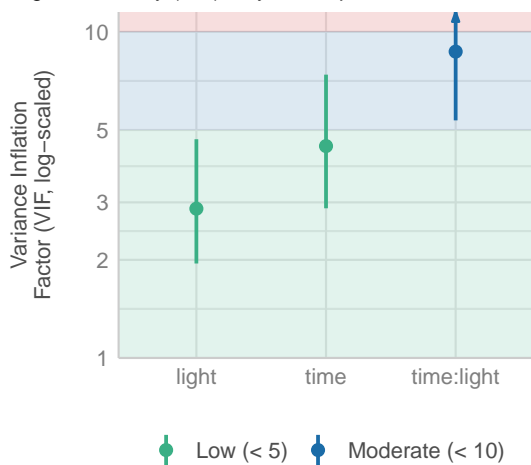
### Influential Observations

Points should be inside the contour lines



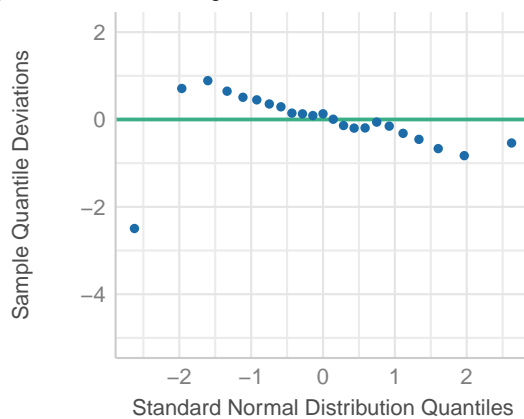
### Collinearity

High collinearity (VIF) may inflate parameter uncertainty



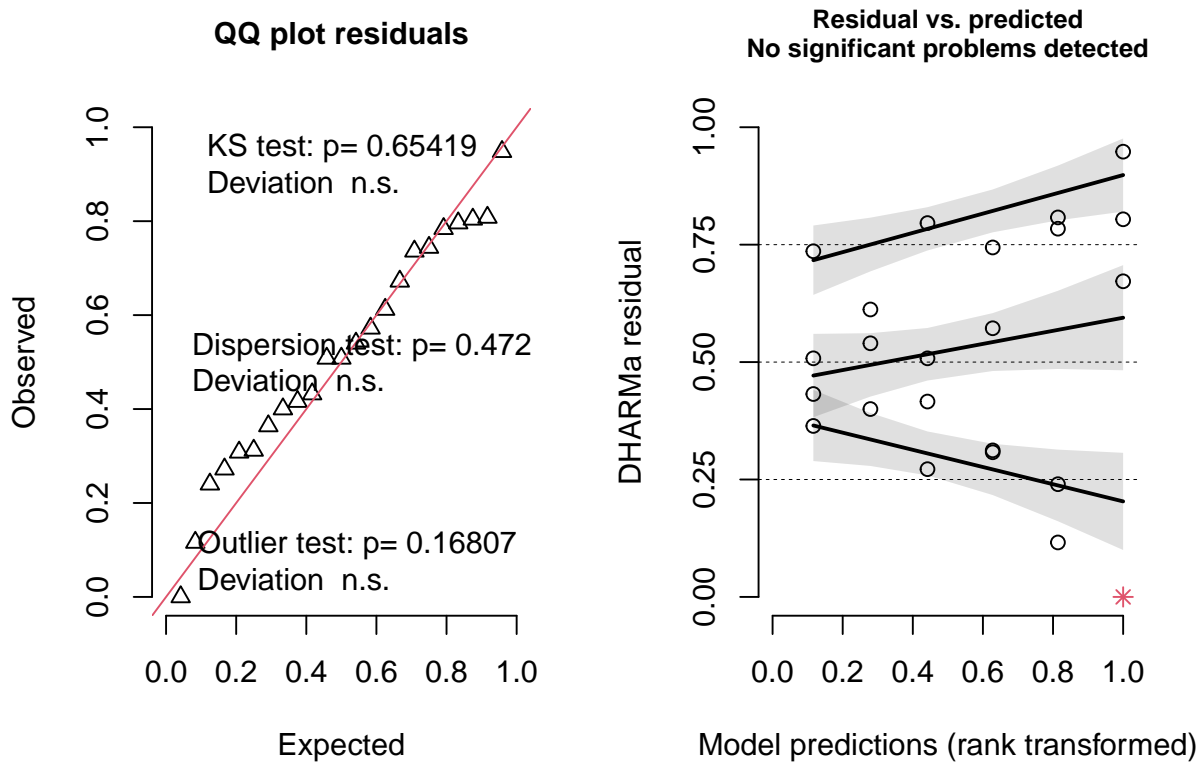
### Normality of Residuals

Dots should fall along the line



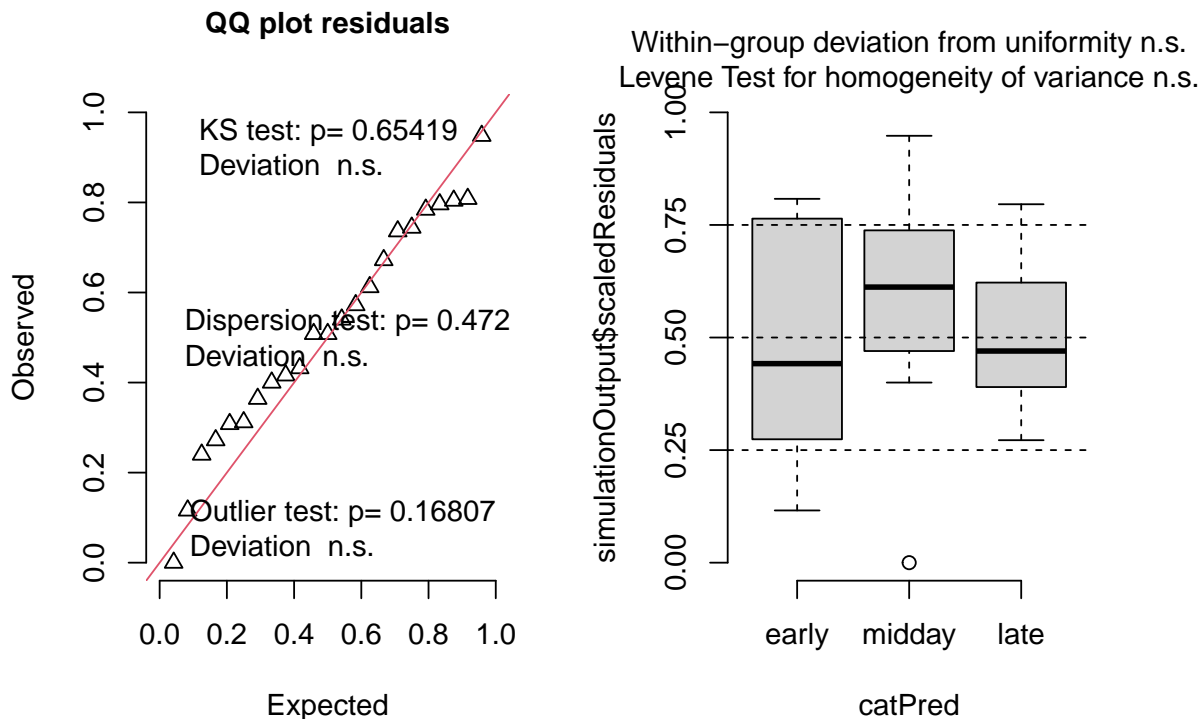
```
ss <- simulateResiduals(lmTL2)
plot(ss)
```

### DHARMA residual



```
plot(ss, form = lizards$time)
```

## DHARMA residual



## Solutions to problems

- **nonlinearity:** transformation, add covariates (??), add interactions, add polynomial terms etc.
- **outliers:** drop values (report both!), use robust regression
- **heteroscedasticity:** transformation, model dispersion explicitly, GLMs
- **non-Normality:** transformation, GLMs

## Transformation

- May do too much at once (GLMs and GAMs allow more flexibility)
- Log-transformation is often interpretable and solves problems
- Transforming boundary values (e.g.  $\log(0)$ ) is problematic
- **Box-Cox transformations:**  $y \rightarrow \frac{y^{\lambda-1}}{\lambda}$  (include Jacobian term  $GM^{\lambda-1}$  in denominator to keep log-likelihood comparable)
  - flexible
  - in practice people often use ‘round numbers’:  $\lambda = 0$  (log),  $1/2$  (square root), etc.

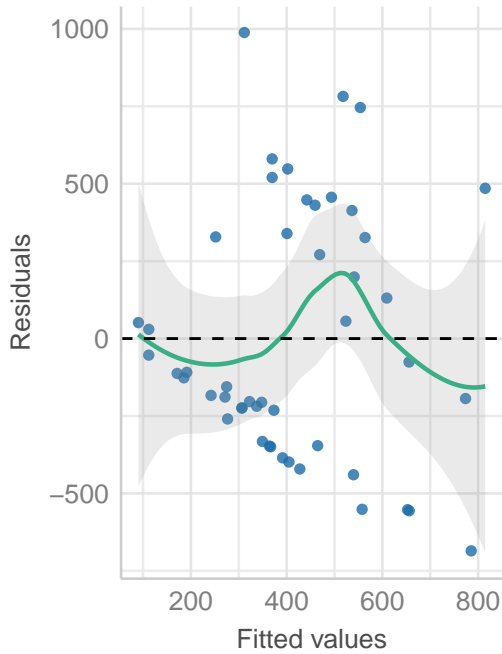
- MASS::boxcox()
- hard to interpret!

## Example

```
library(faraway)
m1 <- lm(perm ~ area, rock)
performance::check_model(m1, check = c("linearity", "homogeneity", "outliers", "qq"))
```

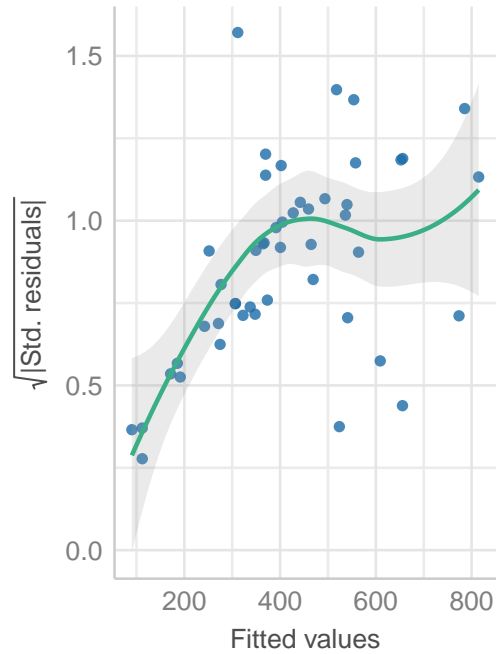
### Linearity

Reference line should be flat and horizontal



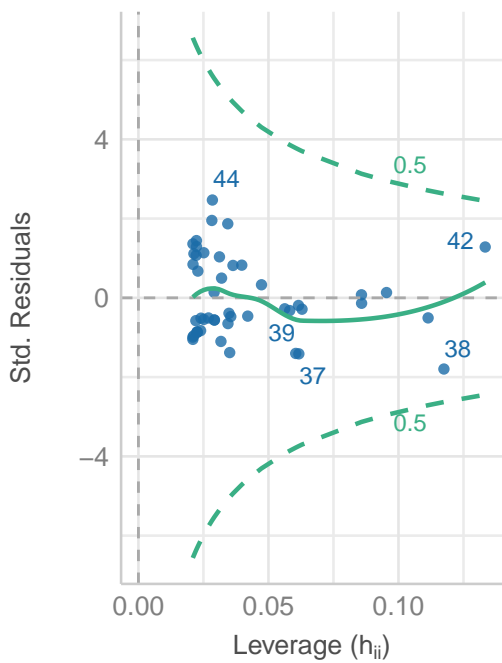
### Homogeneity of Variance

Reference line should be flat and horizontal



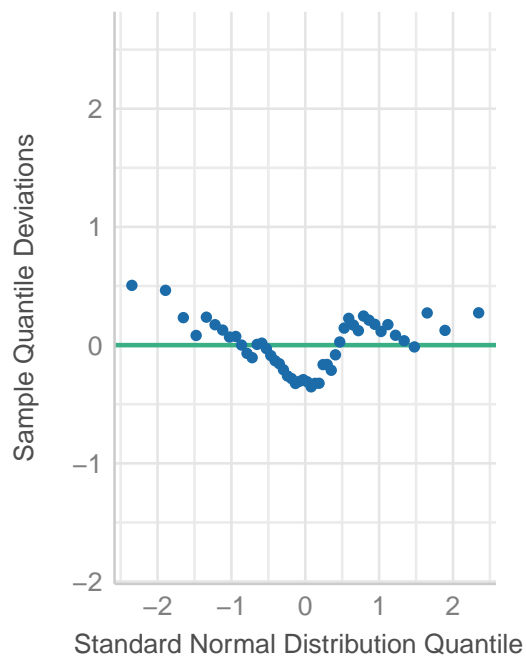
### Influential Observations

Points should be inside the contour lines



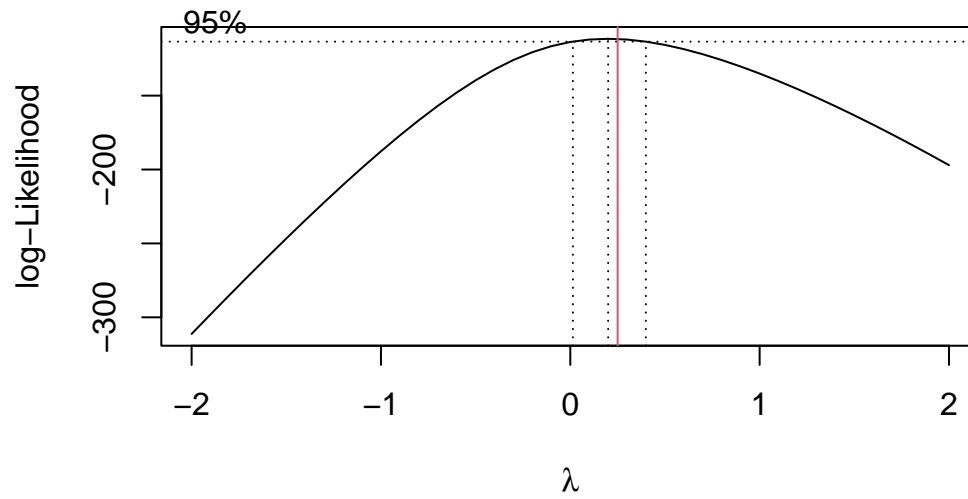
### Normality of Residuals

Dots should fall along the line





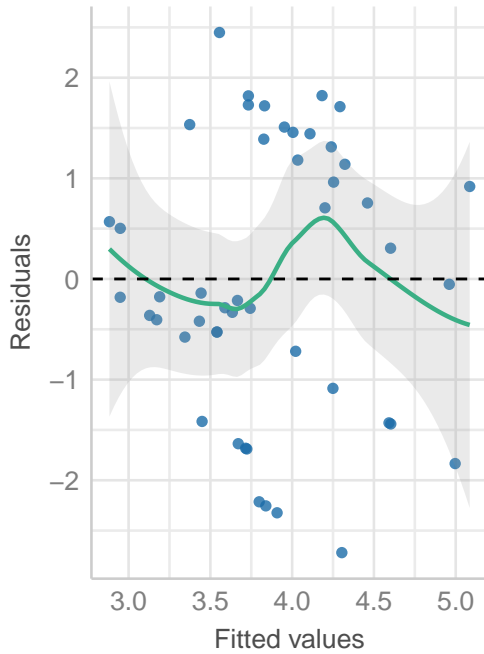
```
m <- MASS::boxcox(m1, interp = FALSE)
abline(v=1/4, col = 2)
```



```
m2 <- update(m1, perm^(1/4) ~ .)
performance::check_model(m2, check = c("linearity", "homogeneity", "outliers", "qq"))
```

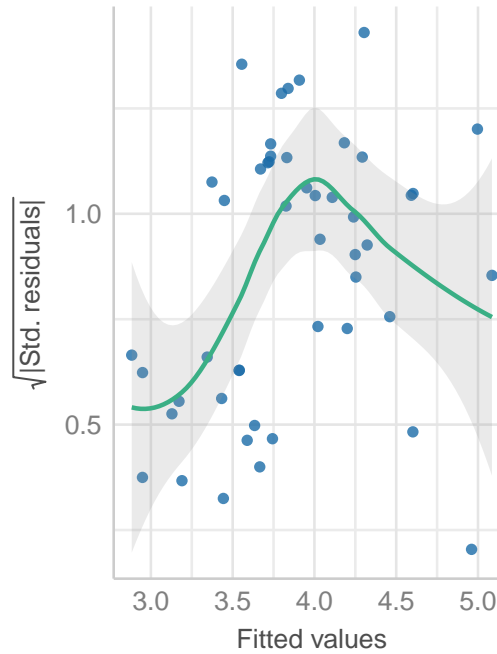
### Linearity

Reference line should be flat and horizontal



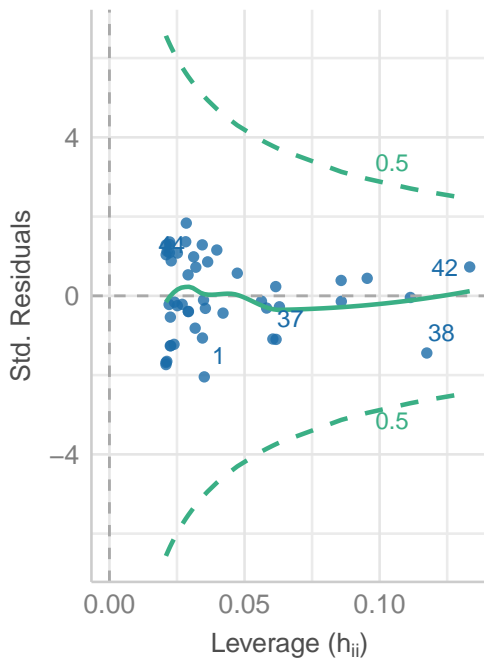
### Homogeneity of Variance

Reference line should be flat and horizontal



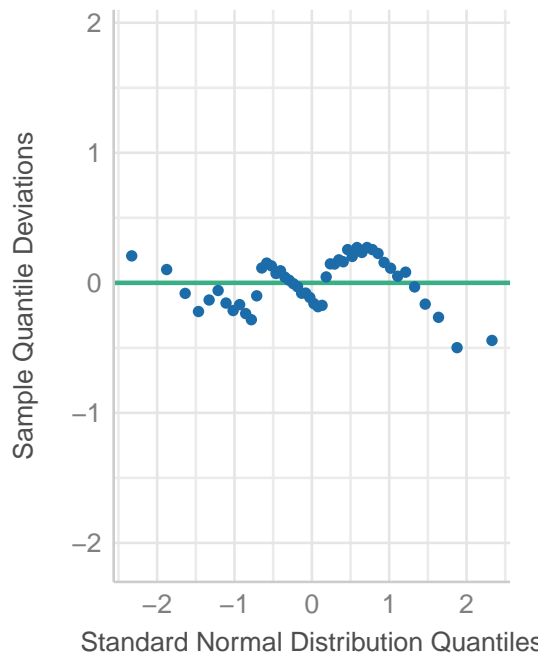
### Influential Observations

Points should be inside the contour lines



### Normality of Residuals

Dots should fall along the line



When we transform we have to add the logs of the *Jacobian* of the transform to the log-

likelihood, or subtract  $\sum \log(J_i)$  from the negative log-likelihood. e.g. if we log-transform,  $\sum \log(J(y_i)) = \sum \log(\partial(\log(y_i))/\partial y) = \sum \log(1/y_i) = -\sum \log y_i$ . In this case  $\sum \log(J(y_i)) = \sum \log((1/4)P^i - 3/4) = -N \log 4 - 3/4 \sum \log(P)$ :

Check:

```
logJ <- -(nrow(rock)*log(4) + 3/4*sum(log(rock$perm)))
lm2 <- logLik(m2) + logJ
lm1 <- logLik(m1)
lm2-lm1
```

```
'log Lik.' 23.3844 (df=3)
```

```
## difference from Box-Cox sequence
max(m$y)-m$y[m$x==1]
```

```
[1] 23.52213
```

## Reminder about parameter scaling

- Schielzeth (2010), Gelman (2008)
- centering ensures no problems with marginality (analogous to sum-to-zero contrasts)
- scaling predictors gives coefficients equal units (analogous to Cohen's  $d$ )
- scaling response makes coefficients *standardized partial regression coefficients* (equal to partial correlation coefficients if predictors are independent)
- scaling by 2 SD makes coefficients equivalent to those from balanced binary predictors
- scaling inputs or scaling predictors?

## What about correlated predictors?

- Can compute *variance inflation factors* (VIFs)
- Dropping correlated factors is dubious: Graham (2003), Dormann et al. (2012), Morrissey and Ruxton (2018), Vanhove (2021)
- perfect collinearity gets handled automatically by R's pivoting, but may want to change contrasts/model setup

```
summary(lmTL2)
```

Call:

```
lm(formula = grahami ~ time * light, data = lizards)
```

Residuals:

Min	1Q	Median	3Q	Max
-30.250	-4.125	1.250	6.875	17.750

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	11.750	5.375	2.186	0.04311 *
timemidday	-5.083	8.211	-0.619	0.54408
timelate	-6.250	7.602	-0.822	0.42238
lightshady	11.750	7.602	1.546	0.14061
timemidday:lightshady	32.833	11.190	2.934	0.00927 **
timelate:lightshady	-6.500	10.751	-0.605	0.55343

---

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

Residual standard error: 10.75 on 17 degrees of freedom

Multiple R-squared: 0.7504, Adjusted R-squared: 0.677

F-statistic: 10.22 on 5 and 17 DF, p-value: 0.0001179

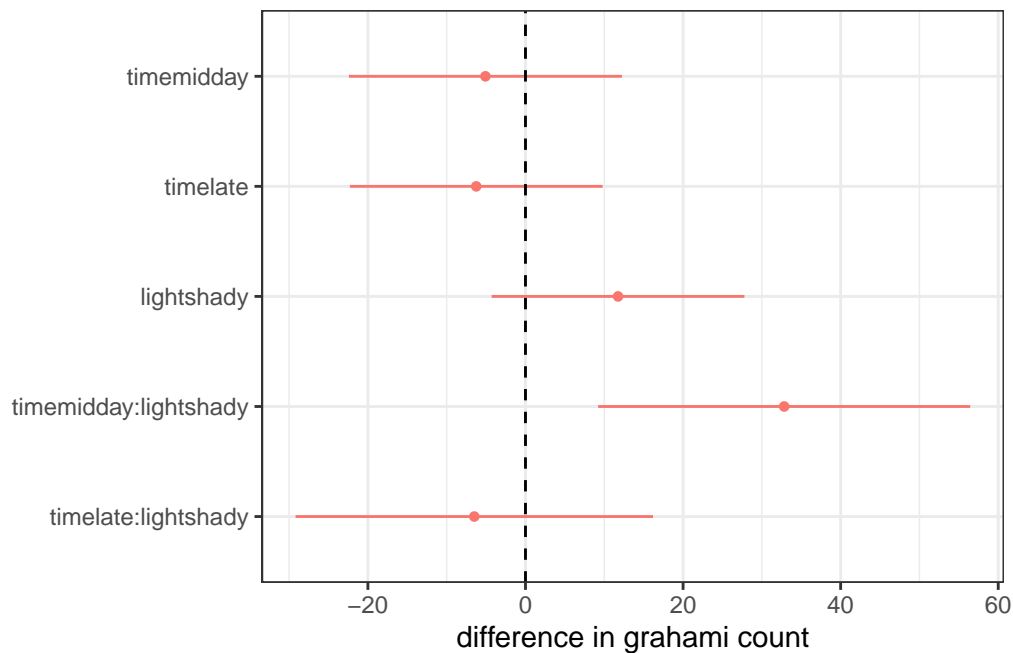
```
broom::tidy(lmTL2)
```

# A tibble: 6 x 5

term	estimate	std.error	statistic	p.value
<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1 (Intercept)	11.8	5.38	2.19	0.0431
2 timemidday	-5.08	8.21	-0.619	0.544
3 timelate	-6.25	7.60	-0.822	0.422
4 lightshady	11.8	7.60	1.55	0.141
5 timemidday:lightshady	32.8	11.2	2.93	0.00927
6 timelate:lightshady	-6.50	10.8	-0.605	0.553

## automatically drop intercept; optional by\_2sd argument

```
dotwhisker::dwplot(lmTL2) + geom_vline(xintercept = 0, lty = 2) +  
  labs(x="difference in grahami count")
```



## Interpretation and testing

- Look at coefficient tables: `summary()` or `coef(summary())`
- model comparison: `drop1()`, `anova()`, `car::Anova()`
- coefficient *plots*: `broom` + `ggplot2`, `dotwhisker`

## Downstream methods

- plot predictions **with data**
- partial residuals plots (e.g. [remef package](#))
- prediction, effects plots
- uncertainty of predictions
- `emmeans`, `marginaleffects`, `effects`, `sjPlot` ...

## References

Chambers, J. M., and T. J. Hastie, eds. 1991. *Statistical Models in S*. 1st ed. Chapman & Hall/CRC.

- Dormann, Carsten F., Jane Elith, Sven Bacher, Carsten Buchmann, Gudrun Carl, Gabriel Carré, Jaime R. García Marquéz, et al. 2012. "Collinearity: A Review of Methods to Deal with It and a Simulation Study Evaluating Their Performance." *Ecography*, no-. <https://doi.org/10.1111/j.1600-0587.2012.07348.x>.
- Gelman, Andrew. 2008. "Scaling Regression Inputs by Dividing by Two Standard Deviations." *Statistics in Medicine* 27 (15): 2865–73. <https://doi.org/10.1002/sim.3107>.
- Gelman, Andrew, and Jennifer Hill. 2006. *Data Analysis Using Regression and Multi-level/Hierarchical Models*. Cambridge, England: Cambridge University Press.
- Graham, Michael H. 2003. "Confronting Multicollinearity in Ecological Multiple Regression." *Ecology* 84 (11): 2809–15. <https://doi.org/10.1890/02-3114>.
- Lindeløv, Jonas Kristoffer. 2019. "Common Statistical Tests Are Linear Models (or: How to Teach Stats)." <https://lindeloev.github.io/tests-as-linear/>.
- McKeon, C., Adrian Stier, Shelby McIlroy, and Benjamin Bolker. 2012. "Multiple Defender Effects: Synergistic Coral Defense by Mutualist Crustaceans." *Oecologia* 169 (4): 1095–1103. <https://doi.org/10.1007/s00442-012-2275-2>.
- Morrissey, Michael B., and Graeme D. Ruxton. 2018. "Multiple Regression Is Not Multiple Regressions: The Meaning of Multiple Regression and the Non-Problem of Collinearity." *Philosophy, Theory, and Practice in Biology* 10 (3).
- Schielzeth, Holger. 2010. "Simple Means to Improve the Interpretability of Regression Coefficients: Interpretation of Regression Coefficients." *Methods in Ecology and Evolution* 1 (2): 103–13. <https://doi.org/10.1111/j.2041-210X.2010.00012.x>.
- Schoener, Thomas W. 1970. "Nonsynchronous Spatial Overlap of Lizards in Patchy Habitats." *Ecology* 51 (3): 408–18. <https://doi.org/10.2307/1935376>.
- Vanhove, Jan. 2021. "Collinearity Isn't a Disease That Needs Curing." *Meta-Psychology* 5 (April). <https://doi.org/10.15626/MP.2021.2548>.
- Venables, W. N. 1998. "Exegeses on Linear Models." In. 1998 International S-PLUS User Conference. Washington, DC. <http://www.stats.ox.ac.uk/pub/MASS3/Exegeses.pdf>.
- Wilkinson, G. N., and C. E. Rogers. 1973. "Symbolic Description of Factorial Models for Analysis of Variance." *Journal of the Royal Statistical Society. Series C (Applied Statistics)* 22 (3): 392–99. <https://doi.org/10.2307/2346786>.