Extended statistical reports

Code

Setup

Load libraries

Hide

```
library(tidyverse)
```

```
package ã¤¼ã‚±tidyverseã¤¼ã‚² was built under R version 3.5.3□[30m-- □[1mAttaching packages□[22
m ------------------------------------- tidyverse 1.2.1 --□[39m
□[30m□[32mv□[30m □[34mggplot2□[30m 3.2.0     □[32mv□[30m □[34mpurrr  □[30m 0.3.2
□[32mv□[30m □[34mtibble □[30m 2.1.3     □[32mv□[30m □[34mdplyr  □[30m 0.8.1
□[32mv□[30m □[34mtidyr  □[30m 0.8.3     □[32mv□[30m □[34mstringr□[30m 1.4.0
□[32mv□[30m □[34mreadr  □[30m 1.3.1     □[32mv□[30m □[34mforcats□[30m 0.4.0□[39m
package ã¤¼ã‚±ggplot2ã¤¼ã‚² was built under R version 3.5.3package ã¤¼ã‚±tibbleã¤¼ã‚² was built
under R version 3.5.3package ã¤¼ã‚±tidyrã¤¼ã‚² was built under R version 3.5.3package ã¤¼ã‚±read
rã¤¼ã‚² was built under R version 3.5.3package ã¤¼ã‚±purrrã¤¼ã‚² was built under R version 3.5.3
package ã¤¼ã‚±dplyrã¤¼ã‚² was built under R version 3.5.3package ã¤¼ã‚±stringrã¤¼ã‚² was built u
nder R version 3.5.3package ã¤¼ã‚±forcatsã¤¼ã‚² was built under R version 3.5.3□[30m-- □[1mConf
licts□[22m ---------------------------------------- tidyverse_conflicts() --
□[31mx□[30m □[34mdplyr□[30m::□[32mfilter()□[30m masks □[34mstats□[30m::filter()
□[31mx□[30m □[34mdplyr□[30m::□[32mlag()□[30m    masks □[34mstats□[30m::lag()□[39m
```

Hide

```
library(knitr)
```

```
package ã¤¼ã‚±knitrã¤¼ã‚² was built under R version 3.5.3
```

Hide

```
library(nlme)
```

```
package ã¤¼ã‚±nlmeã¤¼ã‚² was built under R version 3.5.3
Attaching package: ã¤¼ã‚±nlmeã¤¼ã‚²

The following object is masked from ã¤¼ã‚±package:dplyrã¤¼ã‚²:

    collapse
```

Hide

```
library(ggbeeswarm)
```

```
package ã¤¼ã‚±ggbeeswarmã¤¼ã‚² was built under R version 3.5.3
```

Hide

```
library(emmeans)
```

```
package ã¤ã‚±ã‚emmeansã¤ã‚² was built under R version 3.5.3
```

Hide

```
library(kableExtra)
```

```
package ã¤ã‚±ã‚kableExtraã¤ã‚² was built under R version 3.5.3
Attaching package: ã¤ã‚±ã‚kableExtraã¤ã‚²

The following object is masked from ã¤ã‚±ã‚package:dplyrã¤ã‚²:

    group_rows
```

Hide

```
library(GGally)
```

```
package ã¤ã‚±ã‚GGallyã¤ã‚² was built under R version 3.5.3
Attaching package: ã¤ã‚±ã‚GGallyã¤ã‚²

The following object is masked from ã¤ã‚±ã‚package:emmeansã¤ã‚²:

    pigs

The following object is masked from ã¤ã‚±ã‚package:dplyrã¤ã‚²:

    nasa
```

Hide

```
library(qqplotr)
```

```
package ã¤ã‚±ã‚qqplotrã¤ã‚² was built under R version 3.5.3
Attaching package: ã¤ã‚±ã‚qqplotrã¤ã‚²

The following objects are masked from ã¤ã‚±ã‚package:ggplot2ã¤ã‚²:

    stat_qq_line, StatQqLine
```

Hide

```
library(gridExtra)
```

```
package ã¤¼ã‚±gridExtraã¤¼ã‚² was built under R version 3.5.3
Attaching package: ã¤¼ã‚±gridExtraã¤¼ã‚²

The following object is masked from ã¤¼ã‚±package:dplyrã¤¼ã‚²:

    combine
```

Hide

```
library(RColorBrewer)
```

```
package ã¤¼ã‚±RColorBrewerã¤¼ã‚² was built under R version 3.5.2
```

Hide

```
library(car)
```

```
package ã¤¼ã‚±carã¤¼ã‚² was built under R version 3.5.3Loading required package: carData
package ã¤¼ã‚±carDataã¤¼ã‚² was built under R version 3.5.2
Attaching package: ã¤¼ã‚±carã¤¼ã‚²

The following object is masked from ã¤¼ã‚±package:dplyrã¤¼ã‚²:

    recode

The following object is masked from ã¤¼ã‚±package:purrrã¤¼ã‚²:

    some
```

Hide

```
library(effects)
```

```
package ã¤¼ã‚±effectsã¤¼ã‚² was built under R version 3.5.3lattice theme set by effectsTheme()
See ?effectsTheme for details.
```

Load in the fish data

Hide

```
master_data <- read_csv("C:/Users/kelse/Desktop/fishData_compiledForStats_v6.csv")
```

```
Missing column names filled in: 'X1' [1]Parsed with column specification:
cols(
  .default = col_double(),
  sequence = □[31mcol_character()□[39m,
  individual = □[31mcol_character()□[39m,
  species = □[31mcol_character()□[39m,
  side = □[31mcol_character()□[39m,
  forceType = □[31mcol_character()□[39m,
  pressType = □[31mcol_character()□[39m
)
See spec(...) for full column specifications.
```

Get rid of the indexing column from Python

Hide

```
master_data$X1 <- NULL
```

Make some variables that read in as numerics into factors (categorical variables)

Hide

```
master_data$speed <- factor(master_data$speed)
master_data$segment <- factor(master_data$segment)
```

Just in case, let's make two smaller tables - one for bluegill, one for trout

Hide

```
bluegill_data <- master_data %>%
  filter(species == "bluegill")
trout_data <- master_data %>%
  filter(species == "trout")
```

Set up some basic themes for plots

Hide

```
papertheme <- theme_bw() + theme(axis.line = element_line(color="gray"),
                                 axis.ticks = element_line(color="gray"),
                                 panel.border = element_blank(),
                                 strip.background = element_blank(),
                                 legend.title = element_blank())
```

Let's drop left/right distinction from final data set.

Hide

```
master_data_nosides <- master_data %>%

  select(species, individual, sequence, speed, period, freq, waveSpeed, waveLength, tbamp, Re, S
t,
         netCFxWholeBody, p1maxCFxWholeBody, p1minCFxWholeBody,
         p1maxTimeCFxWholeBody, p1minTimeCFxWholeBody,
         p2maxCFxWholeBody, p2minCFxWholeBody, p2maxTimeCFxWholeBody, p2minTimeCFxWholeBody,
         netCFyWholeBody, maxCFyWholeBody, minCFyWholeBody, maxTimeCFyWholeBody, minTimeCFyWhole
Body,
         segment, pressType, forceType,
         ampInSegm, ampMaxTimeInSegm, ampMinTimeInSegm, bodyAngleInSegm,
         bodyAngleMaxTimeInSegm, bodyAngleMinTimeInSegm,
         AoAInSegm, AoAMaxTimeInSegm, AoAMinTimeInSegm,
         meanCpsInSegmSidesAvg, absMeanCpsInSegmSidesAvg,
         maxCpsInSegmSidesAvg, minCpsInSegmSidesAvg,
         maxTimeCpsInSegmSidesAvg, minTimeCpsInSegmSidesAvg,
         meanCFxInSegmSidesAvg, netCFxInSegmSidesAvg, meanCFxByMechSidesAvg, netCFxByMechSidesAv
g,
         meanCFyInSegmSidesAvg, netCFyInSegmSidesAvg,
         absMeanCFxByMechSidesAvg, absNetCFxByMechSidesAvg, absPeakCFxByMechSidesAvg,
         peakCFxByMechSidesAvg, peakTimeCFxByMechSidesAvg, areaUnderCurveByMechSidesAvg,
         ampAtPeakByMechSidesAvg, angleAtPeakByMechSidesAvg
         ) %>%
  unique()
bluegill_data_nosides <- master_data_nosides %>%
  filter(species == 'bluegill')
trout_data_nosides <- master_data_nosides %>%
  filter(species == 'trout')
thrust_data_nosides <- master_data_nosides %>%
  filter(forceType == 'thrust')
drag_data_nosides <- master_data_nosides %>%
  filter(forceType == 'drag')
speciescomp_data_nosides <- master_data_nosides %>%
  filter(speed == "2.5")
```

CFx models

Questions/Hypotheses we're interested in: -How does force change in each segment across speed or species? -How does thrust/drag compare across high to low pressure type? -How does thrust/drag in segments compare across pressure type?

Stats analysis completed following the protocol in Zuur et al. Zuur, A. F., Ieno, E. N., Walker, N., Saveliev, A. A. and Smith, G. M. (2009). Mixed effects models and extensions in ecology with R. New York, NY: Springer New York.

CFx (species comparison) model

Do a test for NA values - see if we have missing data

Hide

```
sc_test_for_na <- speciescomp_data_nosides %>%
  group_by(forceType, pressType, species, segment) %>%
  summarize(n=sum(!is.na(absMeanCFxByMechSidesAvg))) %>%
  filter(n<24)
sc_test_for_na
```

forceType <chr>	pressType <chr>	species <chr>	segment <fctr>	n <int>
drag	hi	bluegill	1	15
drag	hi	bluegill	2	15
drag	hi	bluegill	3	15
drag	hi	bluegill	4	15
drag	hi	bluegill	5	15
drag	hi	bluegill	6	15
drag	hi	bluegill	7	15
drag	hi	trout	1	9
drag	hi	trout	2	9
drag	hi	trout	3	9
drag	hi	trout	4	9
drag	hi	trout	5	9
drag	hi	trout	6	9
drag	hi	trout	7	9
drag	lo	bluegill	1	15
drag	lo	bluegill	2	15
drag	lo	bluegill	3	15
drag	lo	bluegill	4	15
drag	lo	bluegill	5	15
drag	lo	bluegill	6	15
drag	lo	bluegill	7	15
drag	lo	trout	1	9
drag	lo	trout	2	9
drag	lo	trout	3	9
drag	lo	trout	4	9
drag	lo	trout	5	9

forceType <chr>	pressType <chr>	species <chr>	segment <fctr>	n <int>
drag	lo	trout	6	9
drag	lo	trout	7	9
thrust	hi	bluegill	1	15
thrust	hi	bluegill	2	15
thrust	hi	bluegill	3	15
thrust	hi	bluegill	4	15
thrust	hi	bluegill	5	15
thrust	hi	bluegill	6	15
thrust	hi	bluegill	7	15
thrust	hi	trout	1	9
thrust	hi	trout	2	9
thrust	hi	trout	3	9
thrust	hi	trout	4	9
thrust	hi	trout	5	9
thrust	hi	trout	6	9
thrust	hi	trout	7	9
thrust	lo	bluegill	1	15
thrust	lo	bluegill	2	15
thrust	lo	bluegill	3	15
thrust	lo	bluegill	4	15
thrust	lo	bluegill	5	15
thrust	lo	bluegill	6	15
thrust	lo	bluegill	7	15
thrust	lo	trout	1	9
thrust	lo	trout	2	9
thrust	lo	trout	3	9
thrust	lo	trout	4	9
thrust	lo	trout	5	9
thrust	lo	trout	6	9

forceType <chr>	pressType <chr>	species <chr>	segment <fctr>	n <int>
thrust	lo	trout	7	9

1-56 of 56 rows

Do a test for 0's - see how many we have

Hide

```
sc_test_for_zero <- speciescomp_data_nosides %>%
  group_by(forceType, pressType, species, segment) %>%
  summarize(n=sum(absMeanCFxByMechSidesAvg==0)) %>%
  filter(n>0)
sc_test_for_zero
```

forceType <chr>	pressType <chr>	species <chr>	segment <fctr>	n <int>
drag	hi	bluegill	2	3
drag	hi	bluegill	3	9
drag	hi	bluegill	4	4
drag	hi	trout	2	3
drag	hi	trout	3	3
drag	hi	trout	4	4
drag	lo	bluegill	1	15
drag	lo	trout	1	8
drag	lo	trout	7	1
thrust	hi	bluegill	1	15
thrust	hi	bluegill	2	13
thrust	hi	trout	1	9
thrust	hi	trout	2	7
thrust	hi	trout	3	1

1-14 of 14 rows

build model

Find random term structure

Start with a basic linear model and a basic mixed effects model for comparisons (we believe that individual has to be a random effect).

Hide

```
m2 <- gls(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment, data = speciescomp_dat
a_nosides)
```

Hide

```
m3 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
                          random = ~1|individual, data = speciescomp_data_nosides)
```

compare models

Hide

```
anova(m2,m3)
```

	Model <int>	df <dbl>	AIC <chr>	BIC <chr>	logLik <chr>	Test <fctr>	L.Ratio <chr>	p-value <chr>
m2	1	57	-7344.703	-7092.578	3729.352			
m3	2	58	-7348.925	-7092.377	3732.463	1 vs 2	6.221797	0.0126

2 rows

Do a p-value correction for testing on the boundary

Hide

```
0.5*(1-pchisq(6.221792, 1))
```

```
[1] 0.006309367
```

This p-value is still below our significance threshold, so we accept individual as a random intercept term.

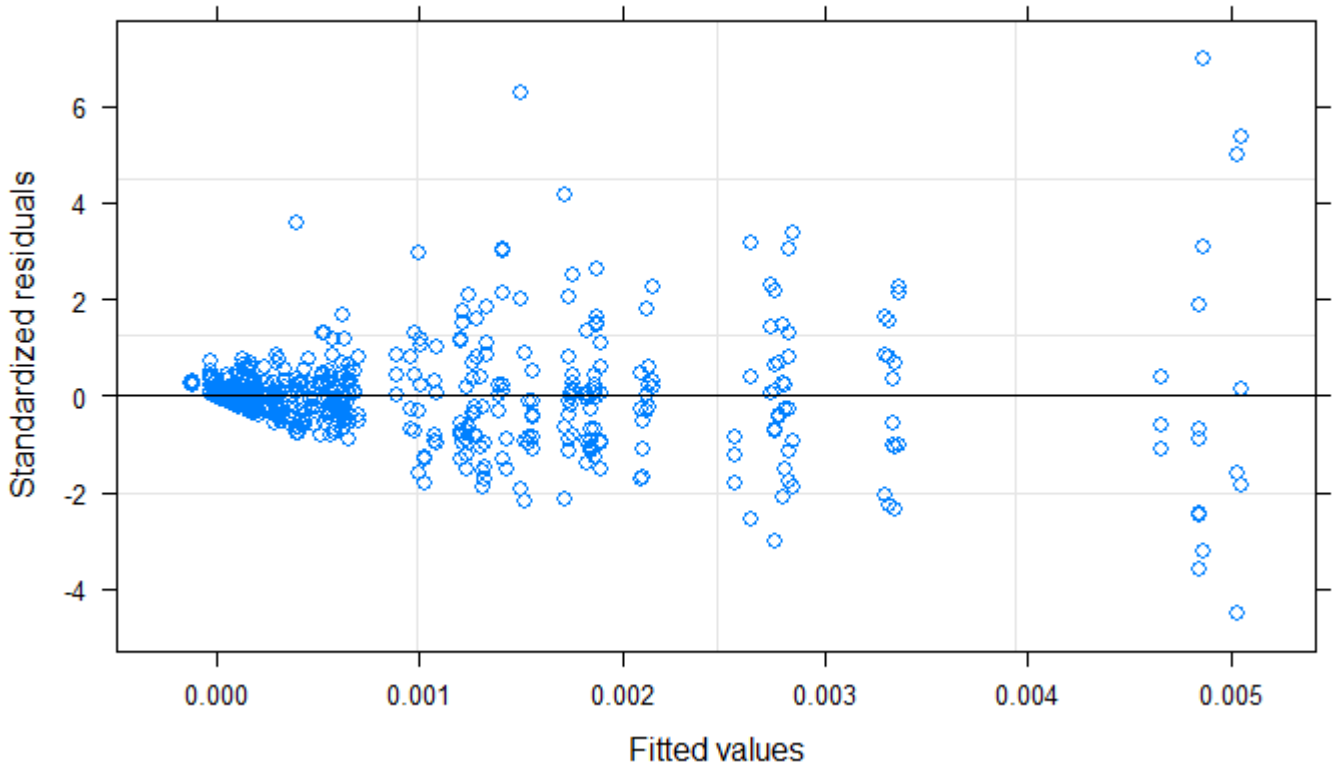
We are data-limited, so take this as our random structure (we don’t have enough data to fit random slopes)

Check for heterogeneity

Plot residuals

Hide

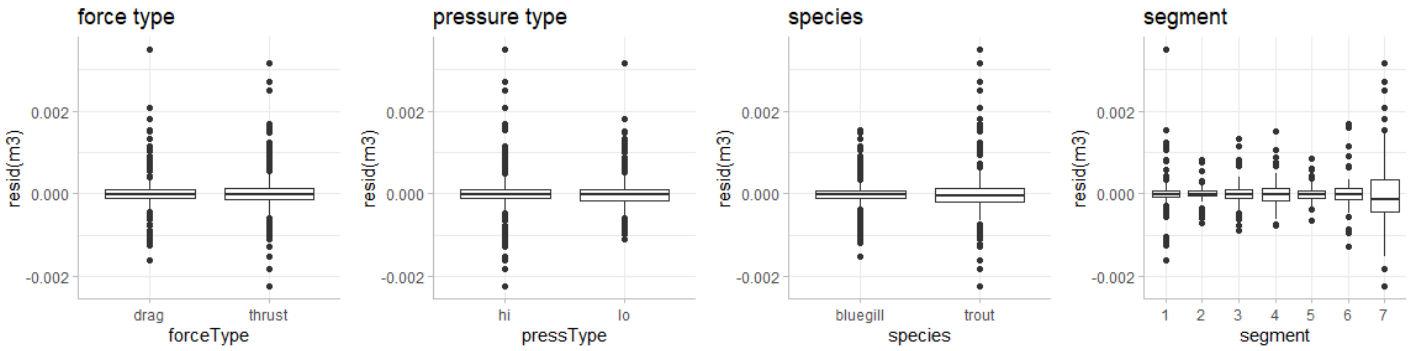
```
plot(m3)
```



So, we see there is heteroskedasticity. But where does it come from?

Hide

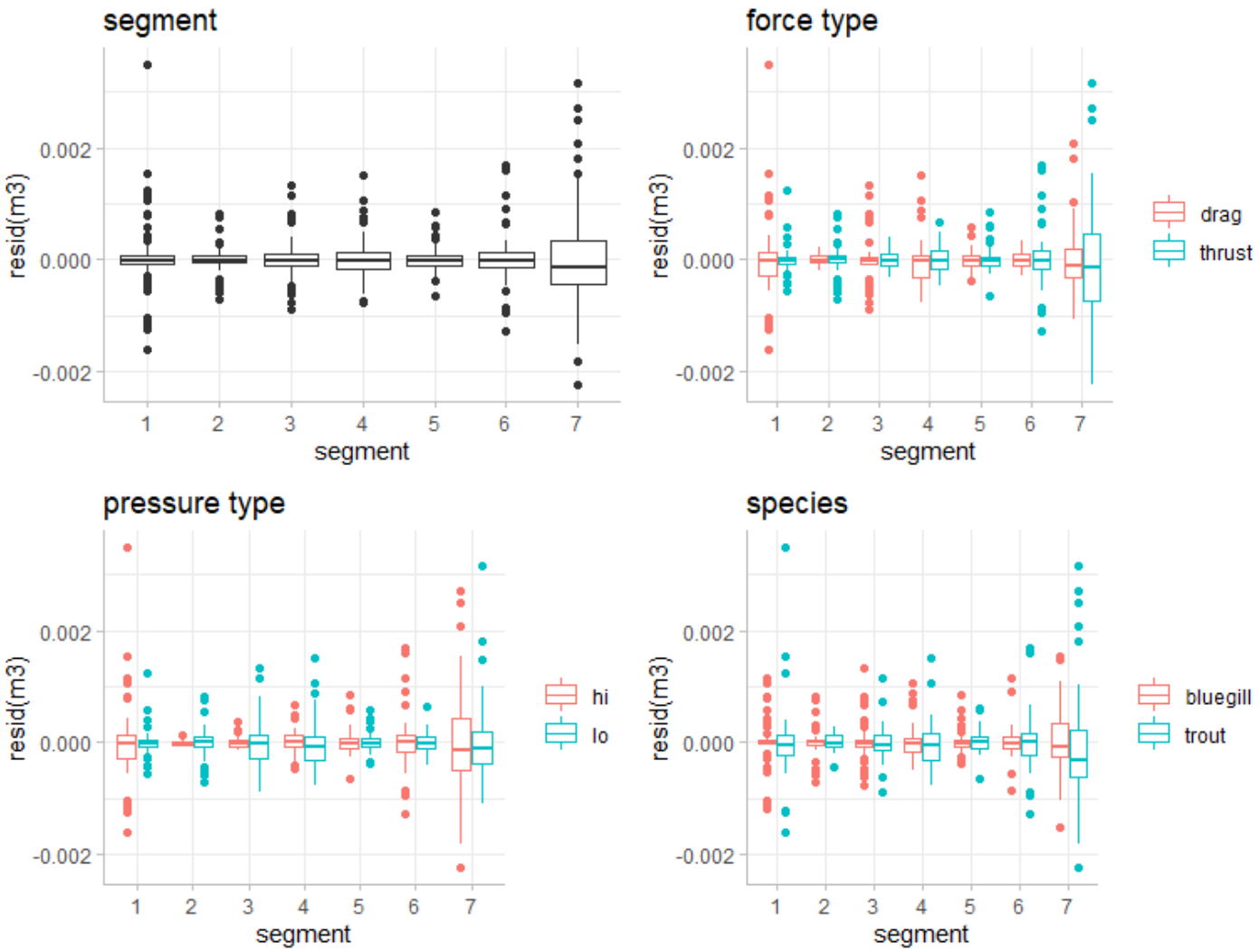
```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = forceType, y = resid(m3)))
    + geom_boxplot() + papertheme + ggtitle("force type"),

  ggplot(speciescomp_data_nosides, aes(x = pressType, y = resid(m3)))
    + geom_boxplot() + papertheme + ggtitle("pressure type"),

  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(m3)))
    + geom_boxplot() +papertheme + ggtitle("species"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(m3)))
    + geom_boxplot() + papertheme + ggtitle("segment"),


  ncol=4
)
```



Ok, so it seems like all factors have some level of unequal variances. Segment particularly, and maybe species and pressType.

Hide

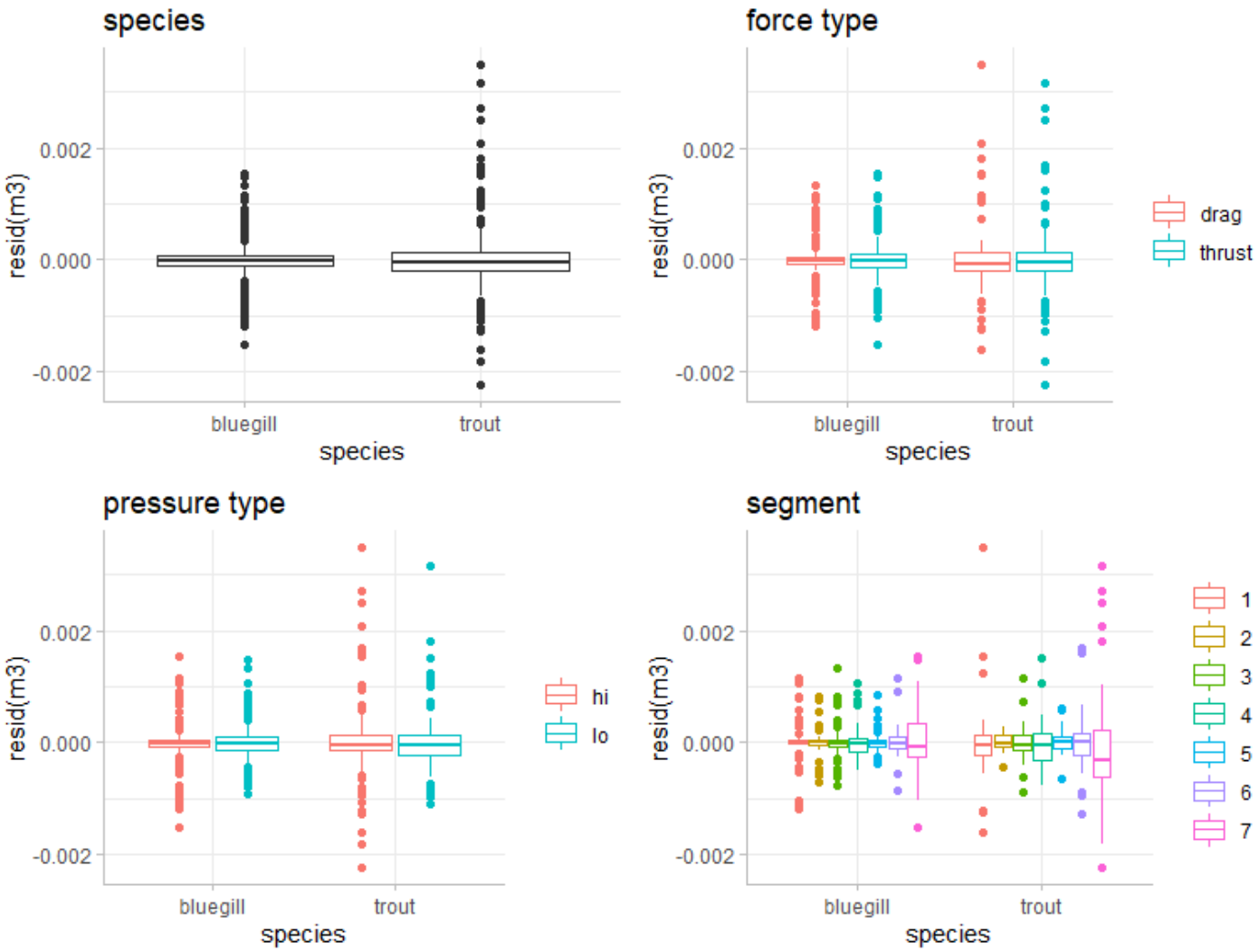
```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(m3)))
    + geom_boxplot() + papertheme + ggtitle("segment"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(m3), color = forceType))
    + geom_boxplot() + papertheme + ggtitle("force type"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(m3), color = pressType))
    + geom_boxplot() + papertheme + ggtitle("pressure type"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(m3), color = species))
    + geom_boxplot() +papertheme + ggtitle("species"),

  ncol=2
)
```



The patterns vs segment didn't change much when broken up by the other factors. Trout seems to consistently have more variance than bluegill. Pressure type doesn't have a consistent pattern - lo and hi both have larger variances depending on the segment. Force type is pretty equal except in the last segment.

Hide

```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(m3)))
    + geom_boxplot() + papertheme + ggtitle("species"),

  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(m3), color = forceType))
    + geom_boxplot() + papertheme + ggtitle("force type"),

  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(m3), color = pressType))
    + geom_boxplot() + papertheme + ggtitle("pressure type"),

  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(m3), color = segment))
    + geom_boxplot() +papertheme + ggtitle("segment"),

  ncol=2
)
```



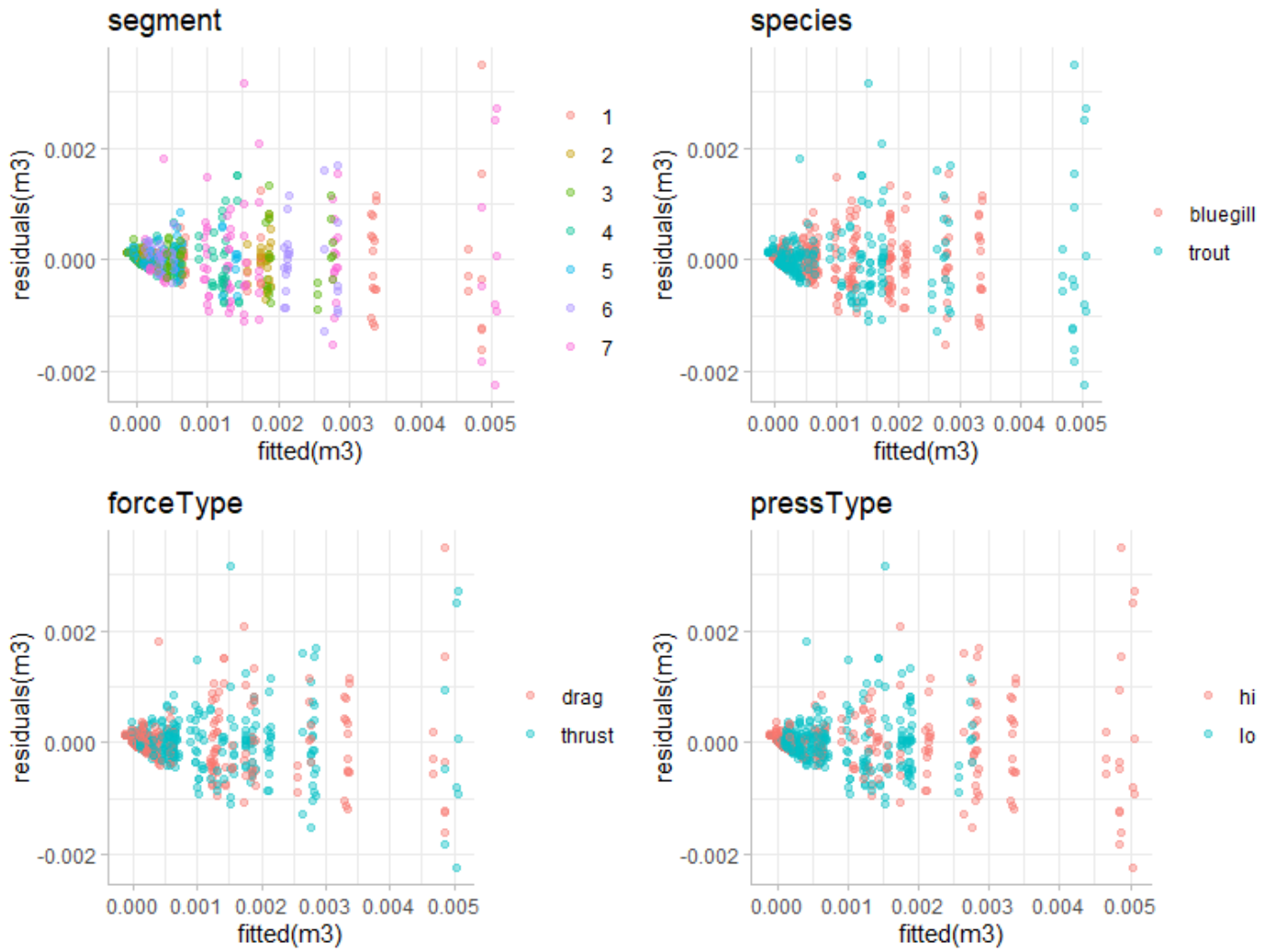
As above, see that trout variance is larger vs segments, but hard to say what the difference is between species based on pressType or forceType.

Find variance structure

Look for what could be causing issues with residuals by marking them up with color.

Hide

```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = fitted(m3), y = residuals(m3), color = segment))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("segment"),

  ggplot(speciescomp_data_nosides, aes(x = fitted(m3), y = residuals(m3), color = species))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("species"),

  ggplot(speciescomp_data_nosides, aes(x = fitted(m3), y = residuals(m3), color = forceType))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("forceType"),

  ggplot(speciescomp_data_nosides, aes(x = fitted(m3), y = residuals(m3), color = pressType))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("pressType"),

  ncol = 2
)
```



Segment and pressType are probably the issue (the really big values all from segment 1 and 7, hi pressure), but trout does have some larger residuals than bluegill

Let's try some variance structures out.

Note: varIdent(form =~ 1|forceType*pressType*species*segment) nor varIdent(form =~ 1|pressType*species*segment) nor varIdent(form =~ 1|pressType*segment)

converge. So, let's do what we can…

Let's do groups of 2 and then single.

Hide

```
vfsc1 <- varIdent(form =~ 1|species*segment)
vfsc2 <- varIdent(form =~ 1|pressType*species)
vfsc3 <- varIdent(form =~ 1|segment)
vfsc4 <- varIdent(form =~ 1|pressType)
vfsc5 <- varIdent(form =~ 1|species)
```

Set up REML models with different variance structures.

Hide

```
m3.1 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
               random = ~1|individual,
               data = speciescomp_data_nosides,
               weights = vfsc1)
m3.2 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
               random = ~1|individual,
               data = speciescomp_data_nosides,
               weights = vfsc2)
m3.3 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
               random = ~1|individual,
               data = speciescomp_data_nosides,
               weights = vfsc3)
m3.4 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
               random = ~1|individual,
               data = speciescomp_data_nosides,
               weights = vfsc4)
m3.5 <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segment,
               random = ~1|individual,
               data = speciescomp_data_nosides,
               weights = vfsc5)
```

Compare using AIC

Hide

```
AIC(m3, m3.1, m3.2, m3.3, m3.4, m3.5)
```

	df <dbl>	AIC <dbl>
m3	58	-7348.925
m3.1	71	-7695.483
m3.2	61	-7471.708
m3.3	64	-7613.016
m3.4	59	-7365.740
m3.5	59	-7463.706

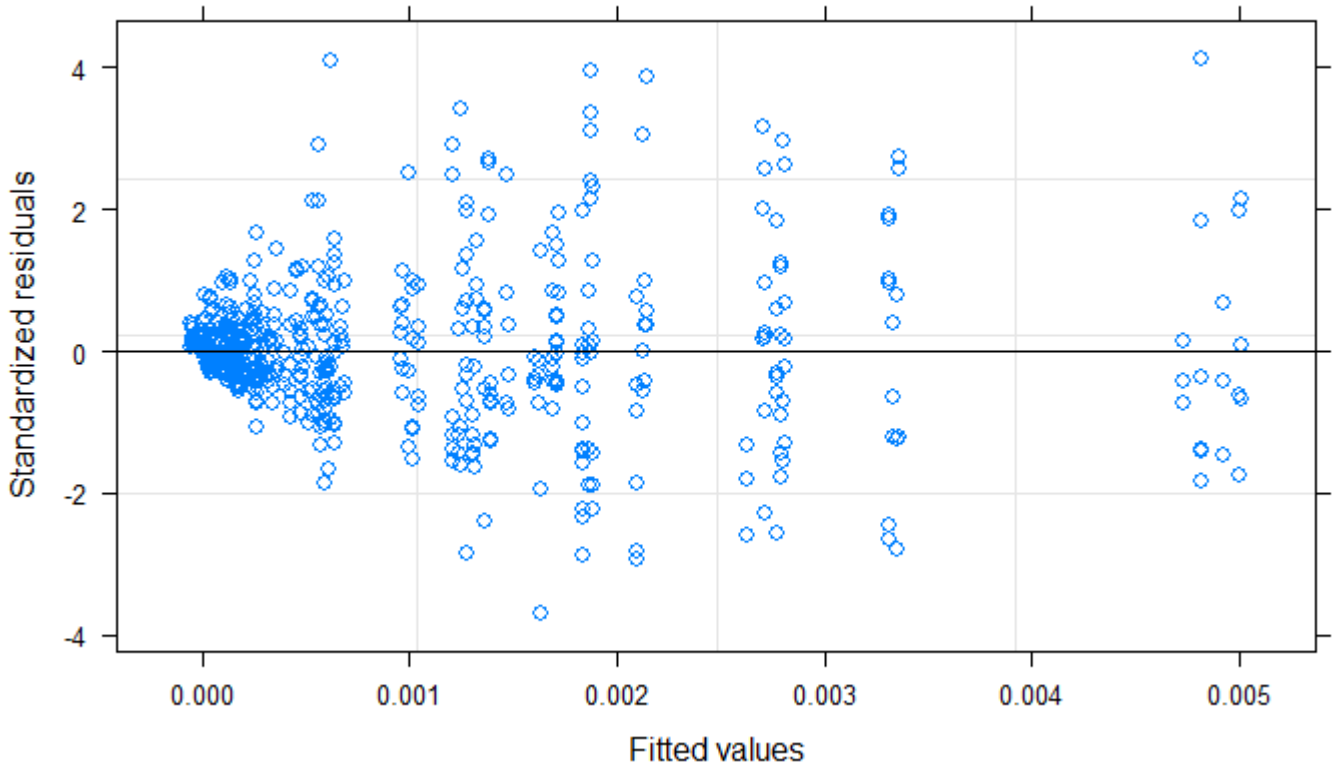
6 rows

The m3.1 model wins.

Check residuals.

Hide

```
plot(m3.1)
```



Better than model without the unequal variance specification.

Look for optimal fixed structure

Start by finding out if highest-order interaction term is significant.

Hide

```
anova(m3.1)
```

	num… <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	610	878.4873	<.0001
forceType	1	610	177.7870	<.0001
pressType	1	610	151.8519	<.0001
species	1	6	0.4284	0.5370
segment	6	610	62.6071	<.0001
forceType:pressType	1	610	1.5198	0.2181
forceType:species	1	610	52.6994	<.0001
pressType:species	1	610	105.0629	<.0001
forceType:segment	6	610	137.4509	<.0001
pressType:segment	6	610	206.9643	<.0001

	num… <int>	denDF <dbl>	F-value <chr>	p-value <chr>
species:segment	6	610	6.2332	<.0001
forceType:pressType:species	1	610	67.2642	<.0001
forceType:pressType:segment	6	610	245.4993	<.0001
forceType:species:segment	6	610	7.6620	<.0001
pressType:species:segment	6	610	4.8774	0.0001
forceType:pressType:species:segment	6	610	4.1312	0.0004

1-16 of 16 rows

4-way interaction term is significant, so nothing can be dropped.

For fun, let's do a goodness-of-fit test for the model terms:

Hide

```
car::Anova(m3.1)
```

```
Analysis of Deviance Table (Type II tests)

Response: absMeanCFxByMechSidesAvg
                                     Chisq Df Pr(>Chisq)
forceType                         177.7870  1  < 2.2e-16 ***
pressType                         151.8519  1  < 2.2e-16 ***
species                             9.9572  1  0.0016022 **
segment                           375.6424  6  < 2.2e-16 ***
forceType:pressType                 1.5198  1  0.2176477
forceType:species                   2.7506  1  0.0972201 .
pressType:species                   4.7293  1  0.0296534 *
forceType:segment                 824.7053  6  < 2.2e-16 ***
pressType:segment                1241.7857  6  < 2.2e-16 ***
species:segment                    37.3992  6  1.472e-06 ***
forceType:pressType:species         7.2366  1  0.0071431 **
forceType:pressType:segment      1472.9961  6  < 2.2e-16 ***
forceType:species:segment          45.9720  6  2.999e-08 ***
pressType:species:segment          29.2642  6  5.422e-05 ***
forceType:pressType:species:segment   24.7870  6  0.0003739 ***
---
Signif. codes:  0 â□□***â□□ 0.001 â□□**â□□ 0.01 â□□*â□□ 0.05 â□□.â□□ 0.1 â□□ â□□ 1
```

Again, 4-way interaction is highly significant, so we keep all the terms.

Final descriptive CFx model (species comparison)

Force magnitude depends on force type, pressure type, species, and segment when the effect of individuals is controlled for, and we allow for differing variances across segments and species.

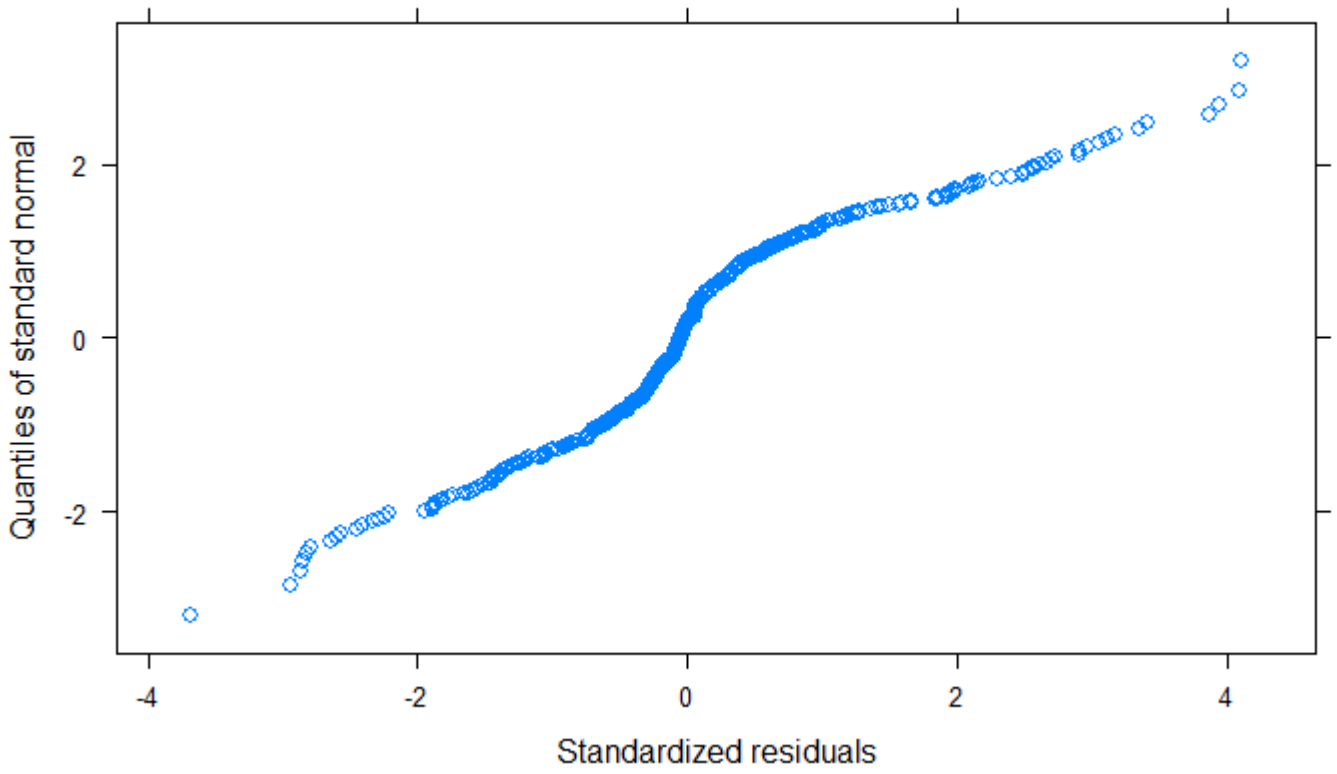
Hide

```
speciescomp_CFx_descriptive <- lme(absMeanCFxByMechSidesAvg ~ forceType*pressType*species*segmen
t,
                          random = ~1|individual,
                          data = speciescomp_data_nosides,
                          weights = varIdent(form =~ 1|species*segment))
```

One last check - qq plot

Hide

```
qqnorm(speciescomp_CFx_descriptive)
```



Ok, still not fabulous, but there may be enough data to not worry about non-normality.

Hide

```
summary(speciescomp_CFx_descriptive)
```

```
Linear mixed-effects model fit by REML
 Data: speciescomp_data_nosides
```

AIC	BIC	logLik
<dbl>	<dbl>	<dbl>
-7695.483	-7381.433	3918.742

1 row

```
Random effects:
 Formula: ~1 | individual
         (Intercept)     Residual
StdDev: 4.174885e-05 0.0004227267

Variance function:
 Structure: Different standard deviations per stratum
 Formula: ~1 | species * segment
 Parameter estimates:
bluegill*1 bluegill*2 bluegill*3 bluegill*4 bluegill*5 bluegill*6 bluegill*7    trout*1    trout
*2    trout*3
 1.0000000  0.5800407  0.7950462  0.7337566  0.4893385  0.7015150  1.3993632  2.0388809  0.32839
55  0.8898430
   trout*4    trout*5    trout*6    trout*7
 1.3610684  0.5981036  1.3954356  3.0198877
Fixed effects: absMeanCFxByMechSidesAvg ~ forceType * pressType * species *      segment
```

	Value <chr>	**Std.Error** <chr>	**…** <chr>	**t-** <chr>
(Intercept)	0.003332736	0.0001107329	610	30
forceTypethrust	-0.003332736	0.0001543580	610	-2
pressTypelo	-0.003332736	0.0001543580	610	-2
speciestrout	0.001454916	0.0003088398	6	4.
segment2	-0.003310153	0.0001261798	610	-2
segment3	-0.003330676	0.0001394399	610	-2
segment4	-0.003329945	0.0001353781	610	-2
segment5	-0.003301121	0.0001215147	610	-2
segment6	-0.003171698	0.0001333265	610	-2
segment7	-0.002032506	0.0001877280	610	-1
forceTypethrust:pressTypelo	0.003995550	0.0002182951	610	18
forceTypethrust:speciestrout	-0.001454916	0.0004346319	610	-3
pressTypelo:speciestrout	-0.001454908	0.0004346319	610	-3
forceTypethrust:segment2	0.003310236	0.0001784452	610	18
forceTypethrust:segment3	0.003407696	0.0001971979	610	17
forceTypethrust:segment4	0.003882413	0.0001914536	610	20
forceTypethrust:segment5	0.003918632	0.0001718478	610	22
forceTypethrust:segment6	0.005291250	0.0001885521	610	28
forceTypethrust:segment7	0.004822431	0.0002654875	610	18

	Value <chr>	Std.Error <chr>	… t- <chr>
pressTypelo:segment2	0.003409895	0.0001784452	610 19
pressTypelo:segment3	0.005191446	0.0001971979	610 26
pressTypelo:segment4	0.004561770	0.0001914536	610 23
pressTypelo:segment5	0.003886336	0.0001718478	610 22
pressTypelo:segment6	0.003333421	0.0001885521	610 17
pressTypelo:segment7	0.002172451	0.0002654875	610 8.
speciestrout:segment2	-0.001466019	0.0003171780	610 -4
speciestrout:segment3	-0.001448440	0.0003430810	610 -4
speciestrout:segment4	-0.001446099	0.0003710102	610 -3
speciestrout:segment5	-0.001387905	0.0003231221	610 -4
speciestrout:segment6	-0.001317863	0.0003727979	610 -3
speciestrout:segment7	-0.001091596	0.0005466772	610 -1
forceTypethrust:pressTypelo:speciestrout	0.002475922	0.0006146623	610 4.
forceTypethrust:pressTypelo:segment2	-0.002212581	0.0002523596	610 -8
forceTypethrust:pressTypelo:segment3	-0.005477318	0.0002788799	610 -1
forceTypethrust:pressTypelo:segment4	-0.005636280	0.0002707562	610 -2
forceTypethrust:pressTypelo:segment5	-0.005123643	0.0002430294	610 -2
forceTypethrust:pressTypelo:segment6	-0.005883103	0.0002666529	610 -2
forceTypethrust:pressTypelo:segment7	-0.004632299	0.0003754560	610 -1
forceTypethrust:speciestrout:segment2	0.001466353	0.0004485574	610 3.
forceTypethrust:speciestrout:segment3	0.001468133	0.0004851898	610 3.
forceTypethrust:speciestrout:segment4	0.001909416	0.0005246877	610 3.
forceTypethrust:speciestrout:segment5	0.002106150	0.0004569636	610 4.
forceTypethrust:speciestrout:segment6	0.001963842	0.0005272158	610 3.
forceTypethrust:speciestrout:segment7	0.003281009	0.0007731184	610 4.
pressTypelo:speciestrout:segment2	0.001595733	0.0004485574	610 3.
pressTypelo:speciestrout:segment3	0.002267895	0.0004851898	610 4.
pressTypelo:speciestrout:segment4	0.001573521	0.0005246877	610 2.
pressTypelo:speciestrout:segment5	0.001120549	0.0004569636	610 2.

	Value <chr>	Std.Error <chr>	… t- <chr>
pressTypelo:speciestrout:segment6	0.001414151	0.0005272158	610 2.
pressTypelo:speciestrout:segment7	0.001285265	0.0007731184	610 1.
forceTypethrust:pressTypelo:speciestrout:segment2	-0.002791667	0.0006343559	610 -4
forceTypethrust:pressTypelo:speciestrout:segment3	-0.003195758	0.0006861621	610 -4
forceTypethrust:pressTypelo:speciestrout:segment4	-0.002973220	0.0007420205	610 -4
forceTypethrust:pressTypelo:speciestrout:segment5	-0.002667311	0.0006462442	610 -4
forceTypethrust:pressTypelo:speciestrout:segment6	-0.002859067	0.0007455958	610 -3
forceTypethrust:pressTypelo:speciestrout:segment7	-0.004041676	0.0010933545	610 -3

1-56 of 56 rows

```
 Correlation:
                                          (Intr) frcTyp prssTy spcstr sgmnt2 sgmnt3 sgmn
t4 sgmnt5
forceTypethrust                           -0.697
pressTypelo                               -0.697  0.500
speciestrout                              -0.359  0.250  0.250
segment2                                  -0.853  0.612  0.612  0.306
segment3                                  -0.772  0.553  0.553  0.277  0.677
segment4                                  -0.795  0.570  0.570  0.285  0.697  0.631
segment5                                  -0.885  0.635  0.635  0.317  0.777  0.703  0.7
24
segment6                                  -0.807  0.579  0.579  0.289  0.708  0.641  0.6
60  0.735
segment7                                  -0.573  0.411  0.411  0.205  0.503  0.455  0.4
69  0.522
forceTypethrust:pressTypelo                0.493 -0.707 -0.707 -0.177 -0.433 -0.391 -0.4
03 -0.449
forceTypethrust:speciestrout               0.248 -0.355 -0.178 -0.704 -0.217 -0.197 -0.2
02 -0.226
pressTypelo:speciestrout                   0.248 -0.178 -0.355 -0.704 -0.217 -0.197 -0.2
02 -0.226
forceTypethrust:segment2                   0.603 -0.865 -0.433 -0.216 -0.707 -0.479 -0.4
93 -0.549
forceTypethrust:segment3                   0.546 -0.783 -0.391 -0.196 -0.479 -0.707 -0.4
46 -0.497
forceTypethrust:segment4                   0.562 -0.806 -0.403 -0.201 -0.493 -0.446 -0.7
07 -0.512
forceTypethrust:segment5                   0.626 -0.898 -0.449 -0.224 -0.549 -0.497 -0.5
12 -0.707
forceTypethrust:segment6                   0.571 -0.819 -0.409 -0.205 -0.501 -0.453 -0.4
67 -0.520
forceTypethrust:segment7                   0.405 -0.581 -0.291 -0.145 -0.356 -0.322 -0.3
31 -0.369
                                          sgmnt6 sgmnt7 frcT:T frcTy: prssT: frcT:2 frc
T:3 frcT:4
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7                                   0.476
forceTypethrust:pressTypelo               -0.409 -0.291
forceTypethrust:speciestrout              -0.206 -0.146  0.251
pressTypelo:speciestrout                  -0.206 -0.146  0.251  0.500
forceTypethrust:segment2                  -0.501 -0.356  0.612  0.307  0.154
forceTypethrust:segment3                  -0.453 -0.322  0.553  0.278  0.139  0.677
forceTypethrust:segment4                  -0.467 -0.331  0.570  0.286  0.143  0.697  0.6
31
forceTypethrust:segment5                  -0.520 -0.369  0.635  0.319  0.160  0.777  0.7
03  0.724
```

```
forceTypethrust:segment6                          -0.707 -0.337  0.579  0.291  0.145  0.708  0.6
41  0.660
forceTypethrust:segment7                          -0.337 -0.707  0.411  0.206  0.103  0.503  0.4
55  0.469
                                                  frcT:5 frcT:6 frcT:7 prsT:2 prsT:3 prsT:4 prs
T:5 prsT:6
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7
forceTypethrust:pressTypelo
forceTypethrust:speciestrout
pressTypelo:speciestrout
forceTypethrust:segment2
forceTypethrust:segment3
forceTypethrust:segment4
forceTypethrust:segment5
forceTypethrust:segment6                           0.735
forceTypethrust:segment7                           0.522  0.476
                                                  prsT:7 spcs:2 spcs:3 spcs:4 spcs:5 spcs:6 spc
s:7 frT:T:
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7
forceTypethrust:pressTypelo
forceTypethrust:speciestrout
pressTypelo:speciestrout
forceTypethrust:segment2
forceTypethrust:segment3
forceTypethrust:segment4
forceTypethrust:segment5
forceTypethrust:segment6
forceTypethrust:segment7
                                                  fT:T:2 fT:T:3 fT:T:4 fT:T:5 fT:T:6 fT:T:7 fr
T::2 frT::3
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
```

```
segment7
forceTypethrust:pressTypelo
forceTypethrust:speciestrout
pressTypelo:speciestrout
forceTypethrust:segment2
forceTypethrust:segment3
forceTypethrust:segment4
forceTypethrust:segment5
forceTypethrust:segment6
forceTypethrust:segment7
                                                    frT::4 frT::5 frT::6 frT::7 prT::2 prT::3 pr
T::4 prT::5
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7
forceTypethrust:pressTypelo
forceTypethrust:speciestrout
pressTypelo:speciestrout
forceTypethrust:segment2
forceTypethrust:segment3
forceTypethrust:segment4
forceTypethrust:segment5
forceTypethrust:segment6
forceTypethrust:segment7
                                                    prT::6 prT::7 fT:T::2 fT:T::3 fT:T::4 fT:T::5
fT:T::6
forceTypethrust
pressTypelo
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7
forceTypethrust:pressTypelo
forceTypethrust:speciestrout
pressTypelo:speciestrout
forceTypethrust:segment2
forceTypethrust:segment3
forceTypethrust:segment4
forceTypethrust:segment5
forceTypethrust:segment6
forceTypethrust:segment7
 [ reached getOption("max.print") -- omitted 37 rows ]

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
```

```
-3.68502270 -0.32884478 -0.04988586  0.26360019  4.11126464

Number of Observations: 672
Number of Groups: 8
```

Hide

```
anova(speciescomp_CFx_descriptive)
```

	num… <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	610	878.4873	<.0001
forceType	1	610	177.7870	<.0001
pressType	1	610	151.8519	<.0001
species	1	6	0.4284	0.5370
segment	6	610	62.6071	<.0001
forceType:pressType	1	610	1.5198	0.2181
forceType:species	1	610	52.6994	<.0001
pressType:species	1	610	105.0629	<.0001
forceType:segment	6	610	137.4509	<.0001
pressType:segment	6	610	206.9643	<.0001
species:segment	6	610	6.2332	<.0001
forceType:pressType:species	1	610	67.2642	<.0001
forceType:pressType:segment	6	610	245.4993	<.0001
forceType:species:segment	6	610	7.6620	<.0001
pressType:species:segment	6	610	4.8774	0.0001
forceType:pressType:species:segment	6	610	4.1312	0.0004

1-16 of 16 rows

Post-hoc tests

Do post-hoc tests so we can get a sense of what's going on in the model.

Hide

```
CLD(emmeans(speciescomp_CFx_descriptive, specs = ~ forceType*pressType | segment*species), adjus
t = "fdr")
```

```
'CLD' will be deprecated. Its use is discouraged.
See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
segment = 1, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      lo        0.00e+00 1.11e-04  7 -3.69e-04 0.000369  1
 thrust    hi        0.00e+00 1.11e-04  7 -3.69e-04 0.000369  1
 thrust    lo        6.63e-04 1.11e-04  7  2.93e-04 0.001032   2
 drag      hi        3.33e-03 1.11e-04  7  2.96e-03 0.003702    3

segment = 1, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 thrust    hi        0.00e+00 2.88e-04  6 -1.02e-03 0.001015  1
 drag      lo        8.00e-09 2.88e-04  6 -1.02e-03 0.001015  1
 thrust    lo        1.68e-03 2.88e-04  6  6.69e-04 0.002699   2
 drag      hi        4.79e-03 2.88e-04  6  3.77e-03 0.005803    3

segment = 2, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 thrust    hi        8.30e-08 6.60e-05  7 -2.20e-04 0.000220  1
 drag      hi        2.26e-05 6.60e-05  7 -1.98e-04 0.000243  1
 drag      lo        9.97e-05 6.60e-05  7 -1.20e-04 0.000320  1
 thrust    lo        1.86e-03 6.60e-05  7  1.64e-03 0.002080   2

segment = 2, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 thrust    hi        4.17e-07 5.22e-05  6 -1.83e-04 0.000184  1
 drag      hi        1.15e-05 5.22e-05  6 -1.72e-04 0.000195  1
 drag      lo        2.29e-04 5.22e-05  6  4.57e-05 0.000413   2
 thrust    lo        1.69e-03 5.22e-05  6  1.50e-03 0.001869    3

segment = 3, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        2.06e-06 8.88e-05  7 -2.94e-04 0.000298  1
 thrust    hi        7.70e-05 8.88e-05  7 -2.19e-04 0.000373  1
 thrust    lo        4.54e-04 8.88e-05  7  1.58e-04 0.000750   2
 drag      lo        1.86e-03 8.88e-05  7  1.56e-03 0.002157    3

segment = 3, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        8.54e-06 1.28e-04  6 -4.41e-04 0.000458  1
 thrust    hi        9.67e-05 1.28e-04  6 -3.53e-04 0.000546  1
 thrust    lo        5.67e-04 1.28e-04  6  1.17e-04 0.001016   2
 drag      lo        2.68e-03 1.28e-04  6  2.23e-03 0.003130    3

segment = 4, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        2.79e-06 8.22e-05  7 -2.71e-04 0.000277  1
 thrust    lo        1.41e-04 8.22e-05  7 -1.34e-04 0.000415  1
 thrust    hi        5.52e-04 8.22e-05  7  2.78e-04 0.000827   2
 drag      lo        1.23e-03 8.22e-05  7  9.58e-04 0.001506    3

segment = 4, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        1.16e-05 1.93e-04  6 -6.69e-04 0.000692  1
 thrust    lo        2.25e-04 1.93e-04  6 -4.55e-04 0.000906  1
```

```
 thrust    hi        1.02e-03 1.93e-04  6  3.35e-04 0.001696   2
 drag      lo        1.36e-03 1.93e-04  6  6.79e-04 0.002040   2

segment = 5, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        3.16e-05 5.66e-05  7 -1.57e-04 0.000220  1
 thrust    lo        4.30e-05 5.66e-05  7 -1.46e-04 0.000232  1
 drag      lo        5.85e-04 5.66e-05  7  3.97e-04 0.000774   2
 thrust    hi        6.18e-04 5.66e-05  7  4.29e-04 0.000806   2

segment = 5, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        9.86e-05 8.77e-05  6 -2.10e-04 0.000407  1
 thrust    lo        2.36e-04 8.77e-05  6 -7.31e-05 0.000544  1
 drag      lo        3.18e-04 8.77e-05  6  9.21e-06 0.000627  1
 thrust    hi        1.34e-03 8.77e-05  6  1.03e-03 0.001644   2

segment = 6, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      hi        1.61e-04 7.88e-05  7 -1.02e-04 0.000424  1
 drag      lo        1.62e-04 7.88e-05  7 -1.01e-04 0.000425  1
 thrust    lo        2.33e-04 7.88e-05  7 -3.02e-05 0.000496  1
 thrust    hi        2.12e-03 7.88e-05  7  1.86e-03 0.002382   2

segment = 6, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      lo        2.58e-04 1.98e-04  6 -4.40e-04 0.000956  1
 drag      hi        2.98e-04 1.98e-04  6 -3.99e-04 0.000996  1
 thrust    lo        4.55e-04 1.98e-04  6 -2.43e-04 0.001152  1
 thrust    hi        2.77e-03 1.98e-04  6  2.07e-03 0.003463   2

segment = 7, species = bluegill:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      lo        1.40e-04 1.54e-04  7 -3.73e-04 0.000653  1
 thrust    lo        9.93e-04 1.54e-04  7  4.80e-04 0.001506   2
 drag      hi        1.30e-03 1.54e-04  7  7.87e-04 0.001813   2
 thrust    hi        2.79e-03 1.54e-04  7  2.28e-03 0.003303    3

segment = 7, species = trout:
 forceType pressType   emmean       SE df  lower.CL upper.CL .group
 drag      lo        3.34e-04 4.26e-04  6 -1.17e-03 0.001834  1
 thrust    lo        1.45e-03 4.26e-04  6 -5.39e-05 0.002948  12
 drag      hi        1.66e-03 4.26e-04  6  1.63e-04 0.003164   2
 thrust    hi        4.98e-03 4.26e-04  6  3.48e-03 0.006480    3

d.f. method: containment
Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 4 estimates
P value adjustment: fdr method for 6 tests
significance level used: alpha = 0.05
```

Hide

```
CLD(emmeans(speciescomp_CFx_descriptive, specs = ~ species | segment*forceType*pressType), adjus
t = "fdr")
```

```
'CLD' will be deprecated. Its use is discouraged.
See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
segment = 1, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 3.33e-03 1.11e-04  7  3.02e-03 0.003647  1
 trout    4.79e-03 2.88e-04  6  3.93e-03 0.005644   2

segment = 1, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 0.00e+00 1.11e-04  7 -3.15e-04 0.000315  1
 trout    8.00e-09 2.88e-04  6 -8.56e-04 0.000856  1

segment = 1, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 trout    0.00e+00 2.88e-04  6 -8.56e-04 0.000856  1
 bluegill 0.00e+00 1.11e-04  7 -3.15e-04 0.000315  1

segment = 1, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 6.63e-04 1.11e-04  7  3.48e-04 0.000977  1
 trout    1.68e-03 2.88e-04  6  8.28e-04 0.002540   2

segment = 2, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 trout    1.15e-05 5.22e-05  6 -1.43e-04 0.000166  1
 bluegill 2.26e-05 6.60e-05  7 -1.65e-04 0.000210  1

segment = 2, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 9.97e-05 6.60e-05  7 -8.78e-05 0.000287  1
 trout    2.29e-04 5.22e-05  6  7.46e-05 0.000384  1

segment = 2, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 8.30e-08 6.60e-05  7 -1.87e-04 0.000188  1
 trout    4.17e-07 5.22e-05  6 -1.54e-04 0.000155  1

segment = 2, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 trout    1.69e-03 5.22e-05  6  1.53e-03 0.001841  1
 bluegill 1.86e-03 6.60e-05  7  1.67e-03 0.002048  1

segment = 3, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 2.06e-06 8.88e-05  7 -2.50e-04 0.000254  1
 trout    8.54e-06 1.28e-04  6 -3.71e-04 0.000388  1

segment = 3, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.86e-03 8.88e-05  7  1.61e-03 0.002113  1
 trout    2.68e-03 1.28e-04  6  2.30e-03 0.003059   2

segment = 3, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 7.70e-05 8.88e-05  7 -1.75e-04 0.000329  1
```

```
 trout    9.67e-05 1.28e-04  6 -2.82e-04 0.000476  1

segment = 3, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 4.54e-04 8.88e-05  7  2.02e-04 0.000706  1
 trout    5.67e-04 1.28e-04  6  1.88e-04 0.000946  1

segment = 4, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 2.79e-06 8.22e-05  7 -2.31e-04 0.000236  1
 trout    1.16e-05 1.93e-04  6 -5.62e-04 0.000585  1

segment = 4, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.23e-03 8.22e-05  7  9.98e-04 0.001465  1
 trout    1.36e-03 1.93e-04  6  7.85e-04 0.001933  1

segment = 4, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 5.52e-04 8.22e-05  7  3.19e-04 0.000786  1
 trout    1.02e-03 1.93e-04  6  4.42e-04 0.001590  1

segment = 4, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.41e-04 8.22e-05  7 -9.29e-05 0.000374  1
 trout    2.25e-04 1.93e-04  6 -3.48e-04 0.000799  1

segment = 5, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 3.16e-05 5.66e-05  7 -1.29e-04 0.000192  1
 trout    9.86e-05 8.77e-05  6 -1.62e-04 0.000359  1

segment = 5, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 trout    3.18e-04 8.77e-05  6  5.76e-05 0.000578  1
 bluegill 5.85e-04 5.66e-05  7  4.24e-04 0.000746   2

segment = 5, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 6.18e-04 5.66e-05  7  4.57e-04 0.000778  1
 trout    1.34e-03 8.77e-05  6  1.08e-03 0.001596   2

segment = 5, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 4.30e-05 5.66e-05  7 -1.18e-04 0.000204  1
 trout    2.36e-04 8.77e-05  6 -2.47e-05 0.000496  1

segment = 6, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.61e-04 7.88e-05  7 -6.29e-05 0.000385  1
 trout    2.98e-04 1.98e-04  6 -2.90e-04 0.000886  1

segment = 6, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
```

```
 bluegill 1.62e-04 7.88e-05  7 -6.22e-05 0.000386  1
 trout    2.58e-04 1.98e-04  6 -3.30e-04 0.000846  1

segment = 6, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 2.12e-03 7.88e-05  7  1.90e-03 0.002343  1
 trout    2.77e-03 1.98e-04  6  2.18e-03 0.003354   2

segment = 6, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 2.33e-04 7.88e-05  7  8.76e-06 0.000457  1
 trout    4.55e-04 1.98e-04  6 -1.33e-04 0.001043  1

segment = 7, forceType = drag, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.30e-03 1.54e-04  7  8.63e-04 0.001737  1
 trout    1.66e-03 4.26e-04  6  3.98e-04 0.002929  1

segment = 7, forceType = drag, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 1.40e-04 1.54e-04  7 -2.97e-04 0.000577  1
 trout    3.34e-04 4.26e-04  6 -9.32e-04 0.001599  1

segment = 7, forceType = thrust, pressType = hi:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 2.79e-03 1.54e-04  7  2.35e-03 0.003227  1
 trout    4.98e-03 4.26e-04  6  3.71e-03 0.006245   2

segment = 7, forceType = thrust, pressType = lo:
 species    emmean       SE df  lower.CL upper.CL .group
 bluegill 9.93e-04 1.54e-04  7  5.56e-04 0.001430  1
 trout    1.45e-03 4.26e-04  6  1.82e-04 0.002712  1

d.f. method: containment
Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 2 estimates
significance level used: alpha = 0.05
```

CFx (total) models

build model

Find random effects

Assume individual is a random effect, but let's demonstrate it.

Hide

```
testCFxBgTr_0 <- gls(meanCFxInSegmSidesAvg ~ species + segment + species:segment, data = species
comp_data_nosides)
testCFxBgTr_1 <- lme(meanCFxInSegmSidesAvg ~ species + segment + species:segment,
                         random = ~1|individual, data = speciescomp_data_nosides)
```

compare models

Hide

```
anova(testCFxBgTr_0,testCFxBgTr_1)
```

	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
	<int>	<dbl>	<chr>	<chr>	<chr>	<fctr>	<chr>	<chr>
testCFxBgTr_0	1	15	-7146.537	-7079.199	3588.268			
testCFxBgTr_1	2	16	-7150.782	-7078.955	3591.391	1 vs 2	6.24547	0.0125

2 rows

Do a p-value correction for testing on the boundary

Hide

```
0.5*(1-pchisq(6.24547, 1))
```

```
[1] 0.006225567
```

This p-value is still below our significance threshold, so we accept individual as a random intercept term.

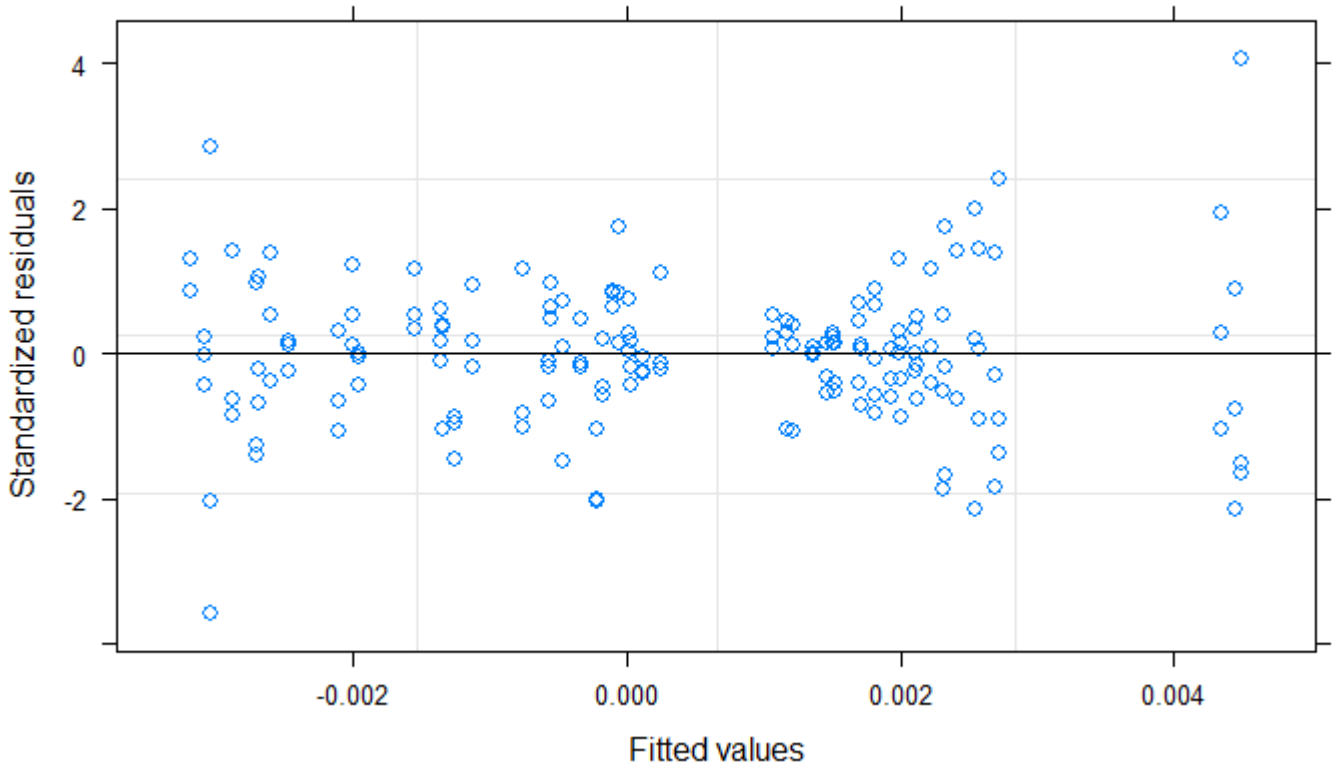
We are data-limited, so take this as our random structure (we don’t have enough data to fit random slopes)

Check for heterogeneity

Plot residuals

Hide

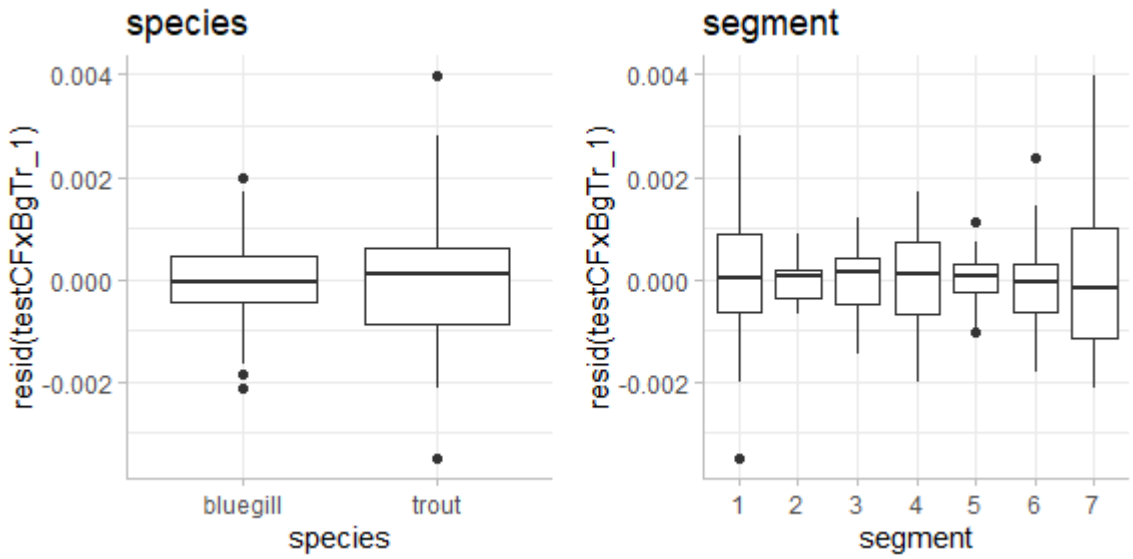
```
plot(testCFxBgTr_1)
```



Possibly some heterogeneity. Hard to tell if other issues are in play too. Let's see if there is a cause for heterogeneity.

Hide

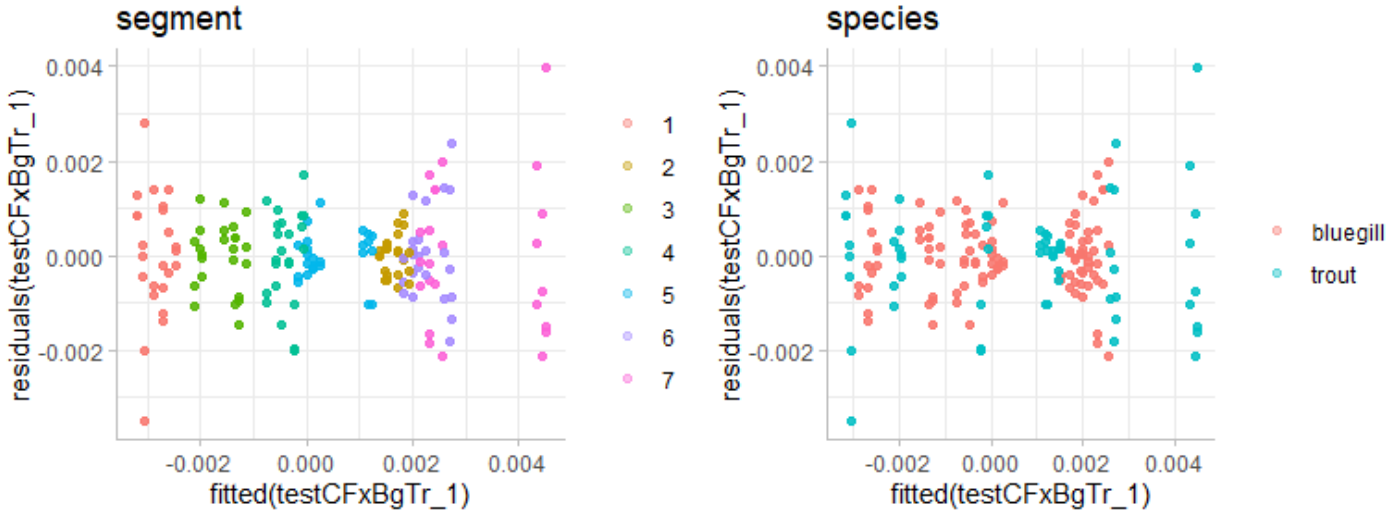
```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(testCFxBgTr_1)))
    + geom_boxplot() +papertheme + ggtitle("species"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(testCFxBgTr_1)))
    + geom_boxplot() + papertheme + ggtitle("segment"),


  ncol=2
)
```



Variances are unequal across segments and species

Hide

```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = fitted(testCFxBgTr_1), y = residuals(testCFxBgTr_1),
color = segment))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("segment"),

  ggplot(speciescomp_data_nosides, aes(x = fitted(testCFxBgTr_1), y = residuals(testCFxBgTr_1),
 color = species))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("species"),

  ncol = 2
)
```



Definitely issues due to both segments and species.

Let's see if adding a variance structure helps.

Hide

```
testCFxBgTr_1a <- lme(meanCFxInSegmSidesAvg ~ species + segment + species:segment,
                      weights = varIdent(form = ~1|species),
                      random = ~1|individual, data = speciescomp_data_nosides)
testCFxBgTr_1b <- lme(meanCFxInSegmSidesAvg ~ species + segment + species:segment,
                      weights = varIdent(form = ~1|segment),
                      random = ~1|individual, data = speciescomp_data_nosides)
testCFxBgTr_1c <- lme(meanCFxInSegmSidesAvg ~ species + segment + species:segment,
                      weights = varIdent(form = ~1|species*segment),
                      random = ~1|individual, data = speciescomp_data_nosides)
```

Compare models

Hide

```
AIC(testCFxBgTr_1, testCFxBgTr_1a, testCFxBgTr_1b, testCFxBgTr_1c)
```

	df <dbl>	**AIC** <dbl>
testCFxBgTr_1	16	-7150.782
testCFxBgTr_1a	17	-7224.206
testCFxBgTr_1b	22	-7372.424
testCFxBgTr_1c	29	-7468.704

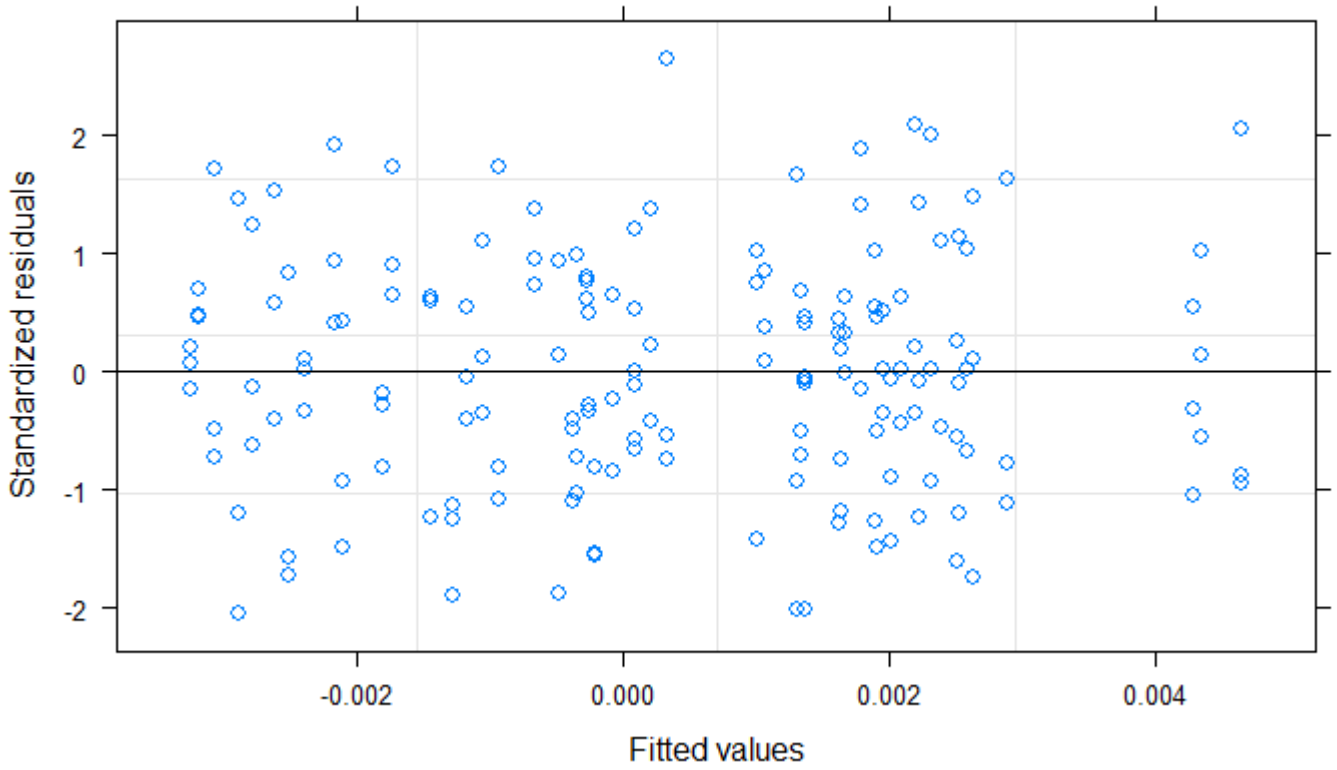
4 rows

Model with the variance allowed to vary across species*segments is best by AIC score.

So, look at residuals.

Hide

```
plot(testCFxBgTr_1c)
```



Better.

Check fixed effects structure

Hide

```
anova(testCFxBgTr_1c)
```

	numDF <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	652	75.6472	<.0001
species	1	6	13.8559	0.0098
segment	6	652	551.5447	<.0001
species:segment	6	652	30.3929	<.0001

4 rows

The interaction term is highly significant - so we need all the terms in our model.

Final bg vs tr CFx (total) model

Hide

```
speciescomp_CFx_descriptive <- lme(meanCFxInSegmSidesAvg ~ species + segment + species:segment,
                                   weights = varIdent(form = ~1|species*segment),
                                   random = ~1|individual, data = speciescomp_data_nosides)
```

Hide

```
summary(speciescomp_CFx_descriptive)
```

```
Linear mixed-effects model fit by REML
 Data: speciescomp_data_nosides
```

AIC	BIC	logLik
<dbl>	<dbl>	<dbl>
-7468.704	-7338.517	3763.352

1 row

```
Random effects:
 Formula: ~1 | individual
        (Intercept)     Residual
StdDev: 0.000248256 0.0009126358

Variance function:
 Structure: Different standard deviations per stratum
 Formula: ~1 | species * segment
 Parameter estimates:
bluegill*1 bluegill*2 bluegill*3 bluegill*4 bluegill*5 bluegill*6 bluegill*7    trout*1    trout
*2    trout*3
 1.0000000  0.5161889  0.8319911  0.8392432  0.4254090  0.5786035  1.3950638  1.9751950  0.20199
94  0.7870665
   trout*4    trout*5    trout*6    trout*7
 1.4151603  0.6571500  1.4917796  2.0480929
Fixed effects: meanCFxInSegmSidesAvg ~ species + segment + species:segment
```

	Value	Std.Error	DF	t-value	p-value
	<chr>	<chr>	<chr>	<chr>	<chr>
(Intercept)	-0.002669922	0.0001618887	652	-16.49234	0.0000
speciestrout	-0.000433909	0.0003701556	6	-1.17224	0.2855
segment2	0.004407892	0.0001325916	652	33.24412	0.0000
segment3	0.001338073	0.0001532671	652	8.73033	0.0000
segment4	0.002128546	0.0001538150	652	13.83836	0.0000
segment5	0.002713620	0.0001280389	652	21.19372	0.0000
segment6	0.004699396	0.0001361216	652	34.52351	0.0000
segment7	0.005012563	0.0002022335	652	24.78601	0.0000
speciestrout:segment2	0.000141038	0.0003298305	652	0.42761	0.6691
speciestrout:segment3	-0.000259492	0.0003578919	652	-0.72506	0.4687

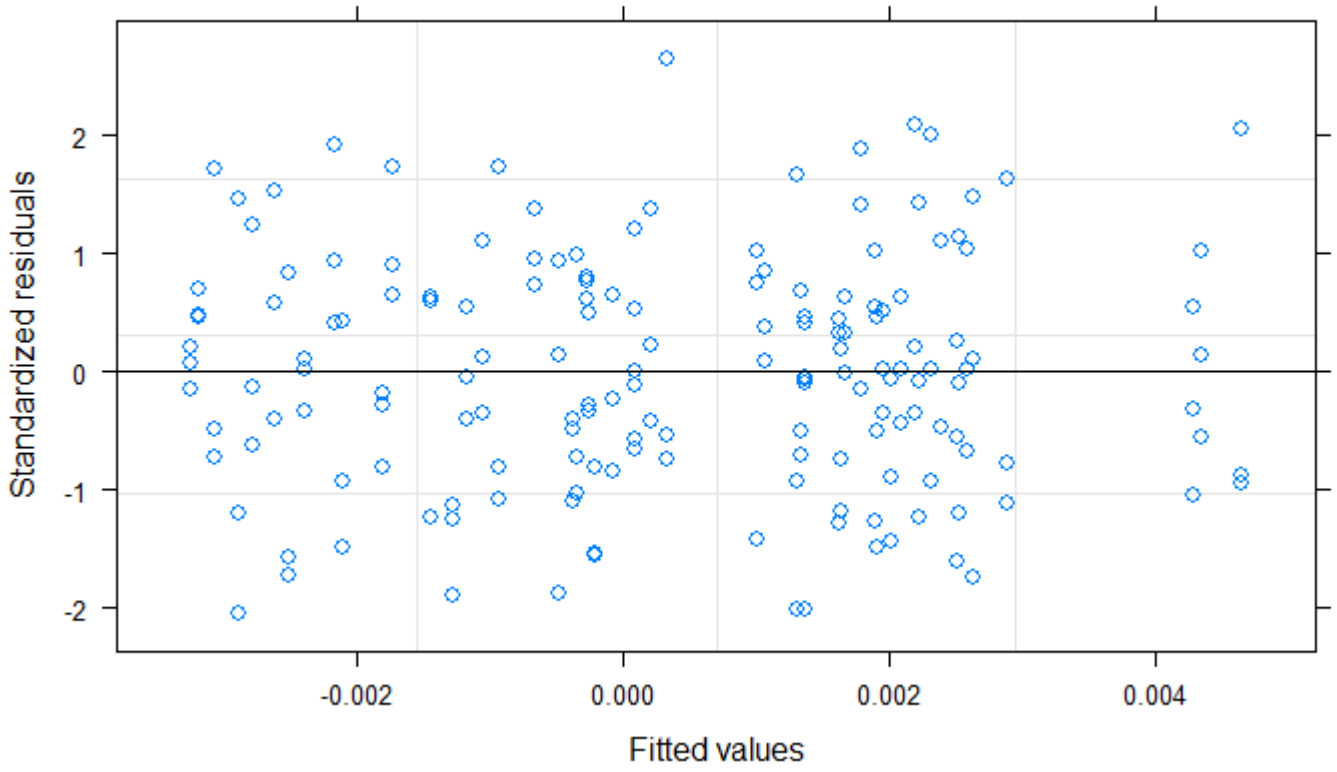
	Value <chr>	Std.Error <chr>	DF <chr>	t-value <chr>	p-value <chr>
speciestrout:segment4	0.000845613	0.0004003211	652	2.11234	0.0350
speciestrout:segment5	0.001544988	0.0003415389	652	4.52361	0.0000
speciestrout:segment6	0.001068616	0.0004003500	652	2.66921	0.0078
speciestrout:segment7	0.002520342	0.0004777145	652	5.27583	0.0000

1-14 of 14 rows

```
 Correlation:
                     (Intr) spcstr sgmnt2 sgmnt3 sgmnt4 sgmnt5 sgmnt6 sgmnt7 spcs:2 spcs:3 spc
s:4 spcs:5
speciestrout          -0.437
segment2              -0.647  0.283
segment3              -0.559  0.245  0.683
segment4              -0.557  0.244  0.681  0.589
segment5              -0.670  0.293  0.818  0.707  0.705
segment6              -0.630  0.276  0.769  0.665  0.663  0.796
segment7              -0.424  0.185  0.518  0.448  0.446  0.536  0.504
speciestrout:segment2  0.260 -0.853 -0.402 -0.275 -0.274 -0.329 -0.309 -0.208
speciestrout:segment3  0.240 -0.786 -0.293 -0.428 -0.252 -0.303 -0.285 -0.192  0.882
speciestrout:segment4  0.214 -0.703 -0.262 -0.226 -0.384 -0.271 -0.255 -0.171  0.789  0.727
speciestrout:segment5  0.251 -0.824 -0.307 -0.265 -0.264 -0.375 -0.299 -0.201  0.925  0.852  0.7
62
speciestrout:segment6  0.214 -0.703 -0.262 -0.226 -0.225 -0.271 -0.340 -0.171  0.789  0.727  0.6
50  0.762
speciestrout:segment7  0.179 -0.589 -0.219 -0.190 -0.189 -0.227 -0.213 -0.423  0.661  0.609  0.5
45  0.638
                     spcs:6
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7
speciestrout:segment2
speciestrout:segment3
speciestrout:segment4
speciestrout:segment5
speciestrout:segment6
speciestrout:segment7  0.545

Standardized Within-Group Residuals:
         Min           Q1          Med           Q3          Max
-2.034214001 -0.731015526 -0.003541536  0.652244218  2.635508542

Number of Observations: 672
Number of Groups: 8
```

Hide

```
plot(speciescomp_CFx_descriptive)
```



Hide

```
anova(speciescomp_CFx_descriptive)
```

	numDF <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	652	75.6472	<.0001
species	1	6	13.8559	0.0098
segment	6	652	551.5447	<.0001
species:segment	6	652	30.3929	<.0001

4 rows

Hide

```
CLD(emmeans(speciescomp_CFx_descriptive, specs = ~ species | segment), adjust = "fdr")
```

```
'CLD' will be deprecated. Its use is discouraged.
See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
segment = 1:
 species     emmean       SE df  lower.CL  upper.CL .group
 trout    -3.10e-03 0.000333  6 -0.004092 -0.002116  1
 bluegill -2.67e-03 0.000162  7 -0.003130 -0.002210  1

segment = 2:
 species     emmean       SE df  lower.CL  upper.CL .group
 trout     1.45e-03 0.000147  6  0.001010  0.001880  1
 bluegill  1.74e-03 0.000127  7  0.001378  0.002098  1

segment = 3:
 species     emmean       SE df  lower.CL  upper.CL .group
 trout    -2.03e-03 0.000187  6 -0.002580 -0.001471  1
 bluegill -1.33e-03 0.000148  7 -0.001753 -0.000911   2

segment = 4:
 species     emmean       SE df  lower.CL  upper.CL .group
 bluegill -5.41e-04 0.000149  7 -0.000964 -0.000119  1
 trout    -1.30e-04 0.000259  6 -0.000897  0.000638  1

segment = 5:
 species     emmean       SE df  lower.CL  upper.CL .group
 bluegill  4.37e-05 0.000122  7 -0.000302  0.000390  1
 trout     1.15e-03 0.000175  6  0.000636  0.001674   2

segment = 6:
 species     emmean       SE df  lower.CL  upper.CL .group
 bluegill  2.03e-03 0.000130  7  0.001659  0.002400  1
 trout     2.66e-03 0.000268  6  0.001867  0.003461  1

segment = 7:
 species     emmean       SE df  lower.CL  upper.CL .group
 bluegill  2.34e-03 0.000198  7  0.001779  0.002906  1
 trout     4.43e-03 0.000343  6  0.003411  0.005447   2

d.f. method: containment
Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 2 estimates
significance level used: alpha = 0.05
```

CFy models

We don’t care if force is going left or right, just the magnitude. So let’s take the absolute value of CFy.

Hide

```
bluegill_data_nosides$absMeanCFyInSegmSidesAvg <- abs(bluegill_data_nosides$meanCFyInSegmSidesAv
g)
speciescomp_data_nosides$absMeanCFyInSegmSidesAvg <- abs(speciescomp_data_nosides$meanCFyInSegmS
idesAvg)
```

build model

Find random effects

Assume individual is a random effect, but let's demonstrate it.

Hide

```
testCFyBgTr_0 <- gls(absMeanCFyInSegmSidesAvg ~ species + segment + species:segment, data = spec
iescomp_data_nosides)
testCFyBgTr_1 <- lme(absMeanCFyInSegmSidesAvg ~ species + segment + species:segment,
                         random = ~1|individual, data = speciescomp_data_nosides)
```

compare models

Hide

```
anova(testCFyBgTr_0,testCFyBgTr_1)
```

	Mo… <int>	df <dbl>	AIC <chr>	BIC <chr>	logLik <chr>	Test <fctr>	L.Ratio <chr>	p-value <chr>
testCFyBgTr_0	1	15	-4660.817	-4593.479	2345.409			
testCFyBgTr_1	2	16	-4811.128	-4739.301	2421.564	1 vs 2	152.3107	<.0001

2 rows

Do a p-value correction for testing on the boundary

Hide

```
0.5*(1-pchisq(153.3107, 1))
```

```
[1] 0
```

This p-value is still below our significance threshold, so we accept individual as a random intercept term.

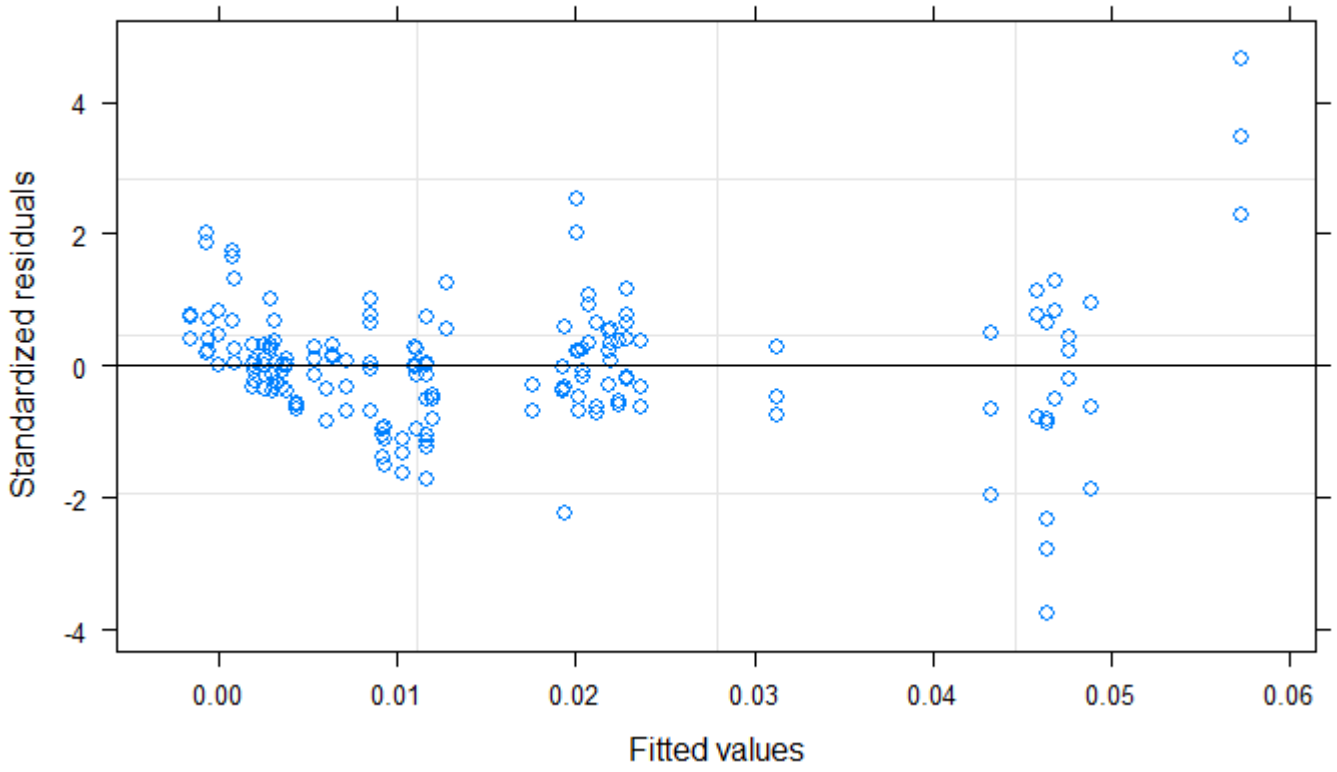
We are data-limited, so take this as our random structure (we don't have enough data to fit random slopes)

Check for heterogeneity

Plot residuals

Hide

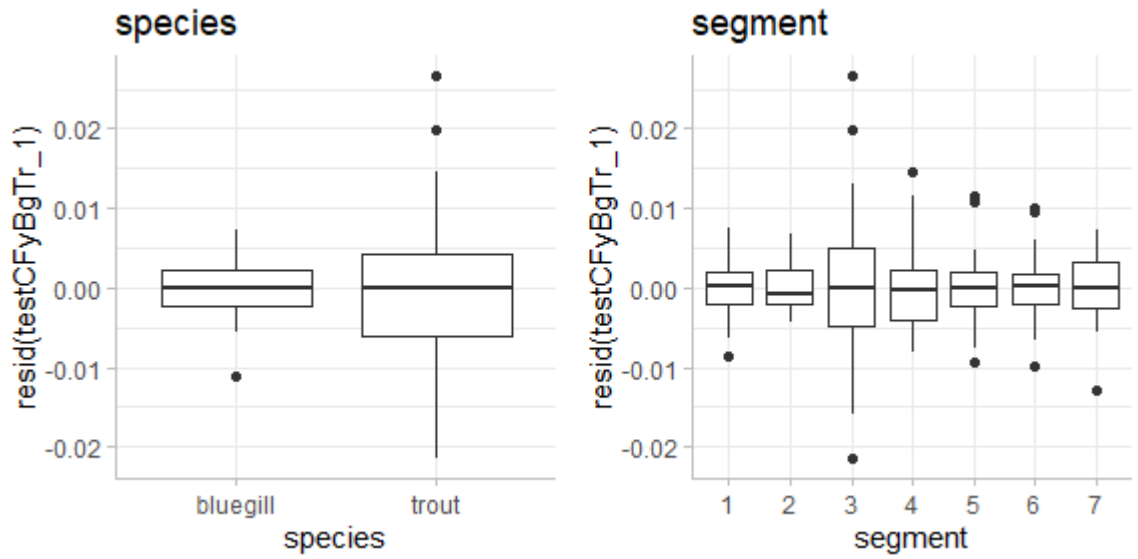
```
plot(testCFyBgTr_1)
```



Really bizarre. For sure some heterogeneity. Hard to tell if other issues are in play too. Let's see if there is a cause for heterogeneity.

Hide

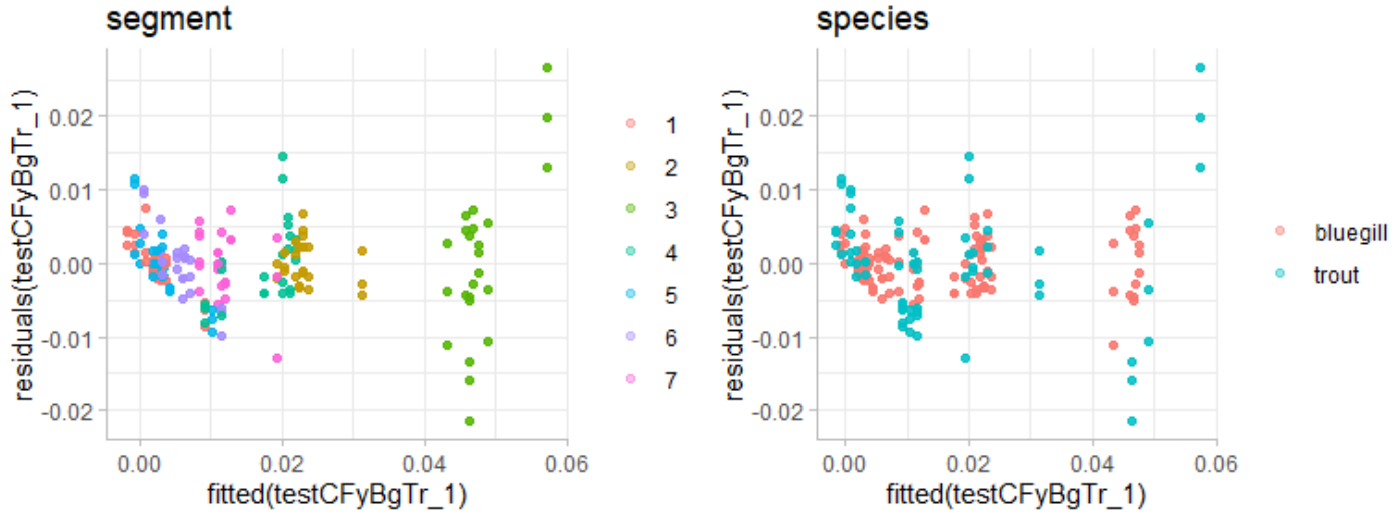
```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = species, y = resid(testCFyBgTr_1)))
    + geom_boxplot() +papertheme + ggtitle("species"),

  ggplot(speciescomp_data_nosides, aes(x = segment, y = resid(testCFyBgTr_1)))
    + geom_boxplot() + papertheme + ggtitle("segment"),


  ncol=2
)
```



Variances are unequal across segments and species

Hide

```
grid.arrange(
  ggplot(speciescomp_data_nosides, aes(x = fitted(testCFyBgTr_1), y = residuals(testCFyBgTr_1),
color = segment))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("segment"),

  ggplot(speciescomp_data_nosides, aes(x = fitted(testCFyBgTr_1), y = residuals(testCFyBgTr_1),
 color = species))
    + geom_point(alpha = 0.4) + papertheme + ggtitle("species"),

  ncol = 2
)
```



Definitely issues due to both segments and species.

Let's see if adding a variance structure helps. Note that varIdent(form = ~1|species*segment) does not converge.

Hide

```
testCFyBgTr_1a <- lme(absMeanCFyInSegmSidesAvg ~ species + segment + species:segment,
                      weights = varIdent(form = ~1|species),
                      random = ~1|individual, data = speciescomp_data_nosides)
testCFyBgTr_1b <- lme(absMeanCFyInSegmSidesAvg ~ species + segment + species:segment,
                      weights = varIdent(form = ~1|segment),
                      random = ~1|individual, data = speciescomp_data_nosides)
```

Compare models

Hide

```
AIC(testCFyBgTr_1, testCFyBgTr_1a, testCFyBgTr_1b)
```

	df <dbl>	AIC <dbl>
testCFyBgTr_1	16	-4811.128
testCFyBgTr_1a	17	-5069.278
testCFyBgTr_1b	22	-5236.370

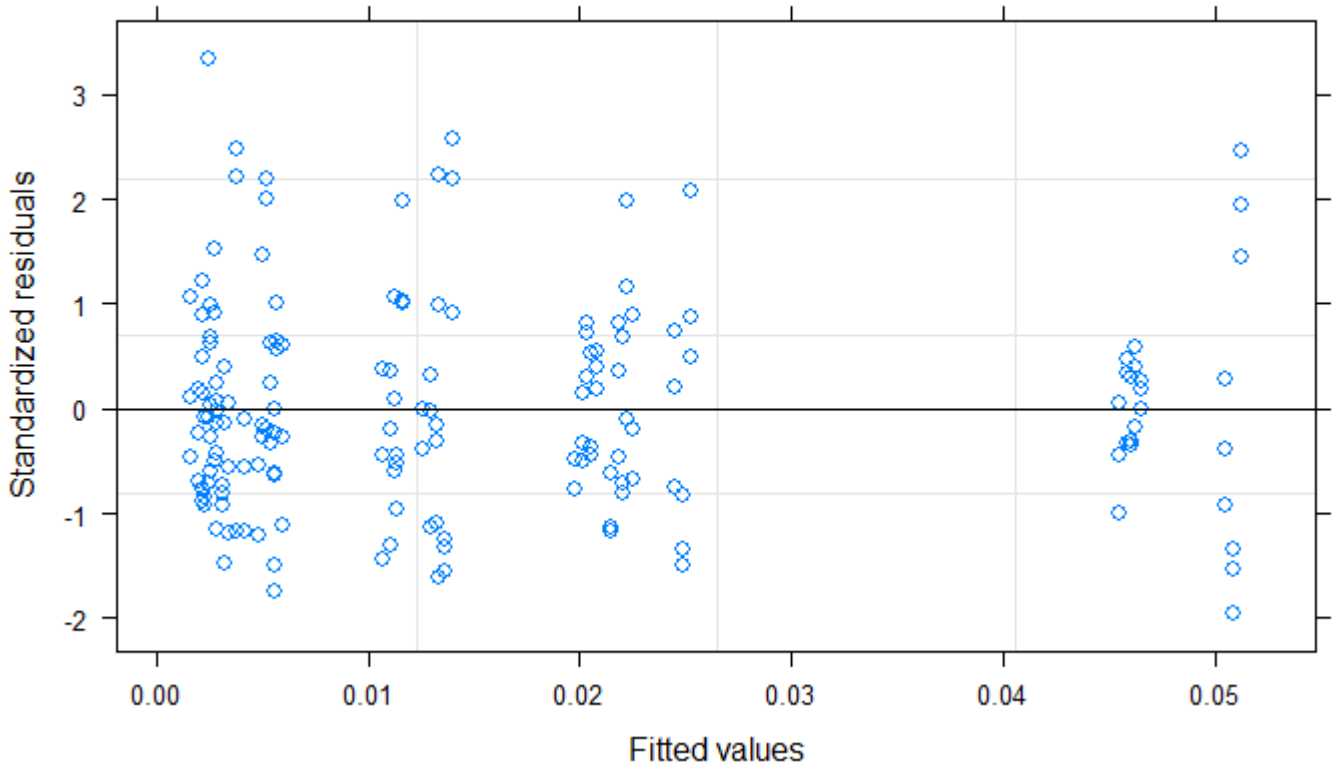
3 rows

Model with the variance allowed to vary across segments is best by AIC score - HUGE improvement.

So, look at residuals.

Hide

```
plot(testCFyBgTr_1b)
```



Better. Still some patchiness - likely because our data is sparse. Vertical spread is much improved.

Check fixed effects structure

Hide

```
anova(testCFyBgTr_1b)
```

	numDF <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	652	1067.9798	<.0001
species	1	6	3.0050	0.1337
segment	6	652	635.9902	<.0001
species:segment	6	652	5.7877	<.0001

4 rows

The interaction term is highly significant - so we need all the terms in our model.

Final bg vs tr CFy model

Hide

```
speciescomp_CFy_descriptive <- lme(absMeanCFyInSegmSidesAvg ~ species + segment + species:segmen
t,
                                   weights = varIdent(form = ~1|segment),
                                   random = ~1|individual, data = speciescomp_data_nosides)
```

Hide

```
summary(speciescomp_CFy_descriptive)
```

```
Linear mixed-effects model fit by REML
 Data: speciescomp_data_nosides
```

AIC	BIC	logLik
<dbl>	<dbl>	<dbl>
-5236.37	-5137.607	2640.185

1 row

```
Random effects:
 Formula: ~1 | individual
         (Intercept)    Residual
StdDev: 0.0004582594 0.001801651

Variance function:
 Structure: Different standard deviations per stratum
 Formula: ~1 | segment
 Parameter estimates:
       1        2        3        4        5        6        7
1.000000 2.066099 7.434360 4.463250 1.587533 1.407129 2.370348
Fixed effects: absMeanCFyInSegmSidesAvg ~ species + segment + species:segment
```

	Value	Std.Error	DF	t-value	p-value
	<chr>	<chr>	<chr>	<chr>	<chr>
(Intercept)	0.00212731	0.0003099991	652	6.86231	0.0000
speciestrout	0.00072350	0.0005062264	6	1.42920	0.2029
segment2	0.01990252	0.0005338871	652	37.27852	0.0000
segment3	0.04391672	0.0017447464	652	25.17083	0.0000
segment4	0.01820190	0.0010638541	652	17.10940	0.0000
segment5	0.00058603	0.0004363977	652	1.34287	0.1798
segment6	0.00341898	0.0004015171	652	8.51515	0.0000
segment7	0.00907832	0.0005983790	652	15.17152	0.0000
speciestrout:segment2	0.00214298	0.0008718340	652	2.45801	0.0142
speciestrout:segment3	0.00412880	0.0028491589	652	1.44913	0.1478
speciestrout:segment4	-0.00745202	0.0017372665	652	-4.28951	0.0000
speciestrout:segment5	0.00037095	0.0007126345	652	0.52053	0.6029

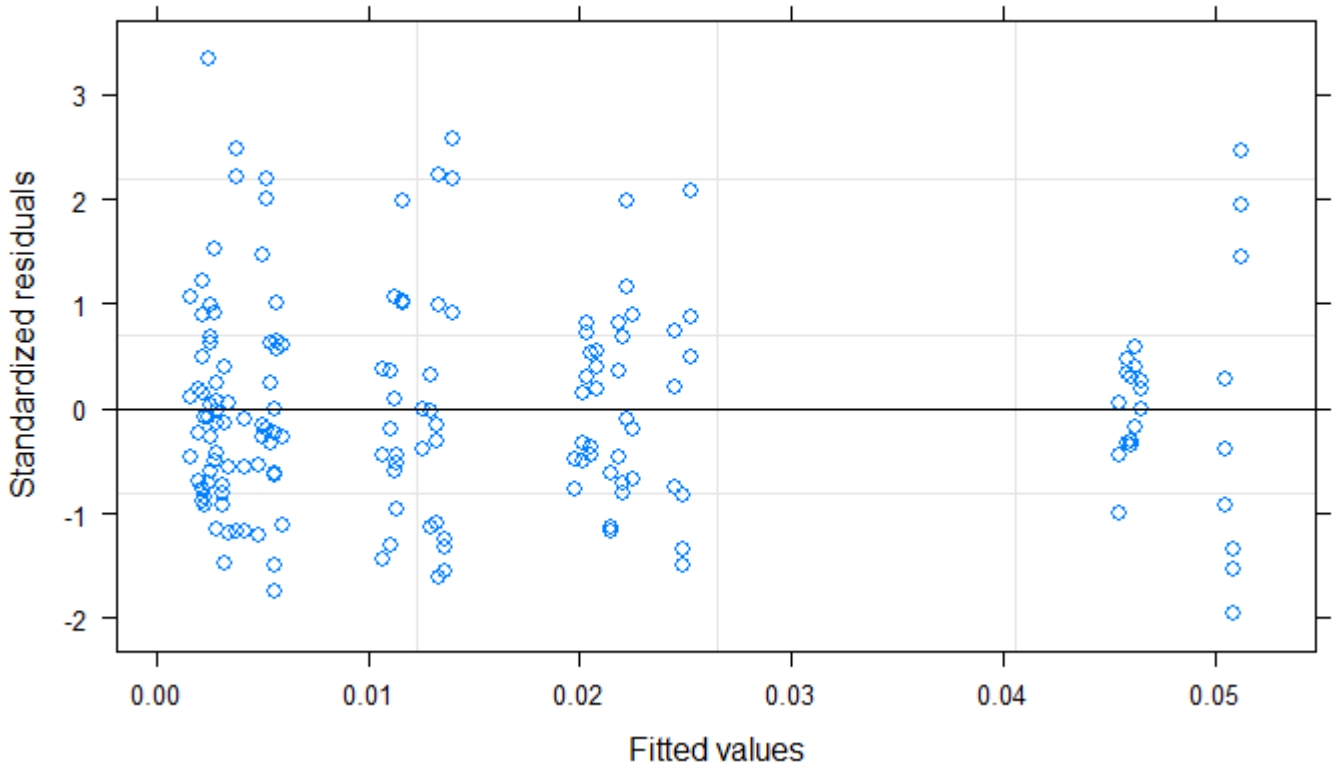
	Value <chr>	Std.Error <chr>	DF <chr>	t-value <chr>	p-value <chr>
speciestrout:segment6	-0.00107839	0.0006556746	652	-1.64471	0.1005
speciestrout:segment7	0.00104907	0.0009771489	652	1.07360	0.2834

1-14 of 14 rows

```
 Correlation:
                     (Intr) spcstr sgmnt2 sgmnt3 sgmnt4 sgmnt5 sgmnt6 sgmnt7 spcs:2 spcs:3 spc
s:4 spcs:5
speciestrout         -0.612
segment2             -0.327  0.200
segment3             -0.100  0.061  0.058
segment4             -0.164  0.100  0.095  0.029
segment5             -0.400  0.245  0.232  0.071  0.117
segment6             -0.435  0.266  0.252  0.077  0.127  0.309
segment7             -0.292  0.179  0.169  0.052  0.085  0.207  0.225
speciestrout:segment2  0.200 -0.327 -0.612 -0.036 -0.058 -0.142 -0.155 -0.104
speciestrout:segment3  0.061 -0.100 -0.036 -0.612 -0.018 -0.044 -0.047 -0.032  0.058
speciestrout:segment4  0.100 -0.164 -0.058 -0.018 -0.612 -0.071 -0.078 -0.052  0.095  0.029
speciestrout:segment5  0.245 -0.400 -0.142 -0.044 -0.071 -0.612 -0.189 -0.127  0.232  0.071  0.1
17
speciestrout:segment6  0.266 -0.435 -0.155 -0.047 -0.078 -0.189 -0.612 -0.138  0.252  0.077  0.1
27  0.309
speciestrout:segment7  0.179 -0.292 -0.104 -0.032 -0.052 -0.127 -0.138 -0.612  0.169  0.052  0.0
85  0.207
                     spcs:6
speciestrout
segment2
segment3
segment4
segment5
segment6
segment7

speciestrout:segment2
speciestrout:segment3
speciestrout:segment4
speciestrout:segment5
speciestrout:segment6
speciestrout:segment7  0.225

Standardized Within-Group Residuals:
       Min         Q1        Med         Q3        Max
-1.9449104 -0.6861456 -0.1488635  0.5522995  3.3301286

Number of Observations: 672
Number of Groups: 8
```

Hide

```
plot(speciescomp_CFy_descriptive)
```



Hide

```
anova(speciescomp_CFy_descriptive)
```

	numDF <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	652	1067.9798	<.0001
species	1	6	3.0050	0.1337
segment	6	652	635.9902	<.0001
species:segment	6	652	5.7877	<.0001

4 rows

Hide

```
CLD(emmeans(speciescomp_CFy_descriptive, specs = ~ species | segment), adjust = "fdr")
```

```
'CLD' will be deprecated. Its use is discouraged.
See '? CLD' for an explanation. Use 'pwpp' or 'multcomp::cld' instead.
```

```
segment = 1:
 species   emmean       SE df lower.CL upper.CL .group
 bluegill 0.00213 0.000310  7  0.00125  0.00301  1
 trout    0.00285 0.000400  6  0.00166  0.00404  1

segment = 2:
 species   emmean       SE df lower.CL upper.CL .group
 bluegill 0.02203 0.000522  7  0.02055  0.02351  1
 trout    0.02490 0.000674  6  0.02289  0.02690   2

segment = 3:
 species   emmean       SE df lower.CL upper.CL .group
 bluegill 0.04604 0.001741  7  0.04110  0.05099  1
 trout    0.05090 0.002248  6  0.04422  0.05757  1

segment = 4:
 species   emmean       SE df lower.CL upper.CL .group
 trout    0.01360 0.001366  6  0.00955  0.01766  1
 bluegill 0.02033 0.001058  7  0.01732  0.02334   2

segment = 5:
 species   emmean       SE df lower.CL upper.CL .group
 bluegill 0.00271 0.000422  7  0.00151  0.00391  1
 trout    0.00381 0.000545  6  0.00219  0.00543  1

segment = 6:
 species   emmean       SE df lower.CL upper.CL .group
 trout    0.00519 0.000499  6  0.00371  0.00667  1
 bluegill 0.00555 0.000386  7  0.00445  0.00664  1

segment = 7:
 species   emmean       SE df lower.CL upper.CL .group
 bluegill 0.01121 0.000588  7  0.00953  0.01288  1
 trout    0.01298 0.000759  6  0.01072  0.01523  1

d.f. method: containment
Confidence level used: 0.95
Conf-level adjustment: bonferroni method for 2 estimates
significance level used: alpha = 0.05
```

Efficiency models

Load efficiency data

Hide

```
efficiency_master_data <- read_csv("C:/Users/kelse/Desktop/power_eff_2.5_v2.csv")
```

```
Missing column names filled in: 'X1' [1]Parsed with column specification:
cols(
  X1 = □[32mcol_double()□[39m,
  sequence = □[31mcol_character()□[39m,
  individual = □[31mcol_character()□[39m,
  species = □[31mcol_character()□[39m,
  thrust_power = □[32mcol_double()□[39m,
  axial_power = □[32mcol_double()□[39m,
  lateral_power = □[32mcol_double()□[39m,
  efficiency = □[32mcol_double()□[39m
)
```

Get rid of the indexing column from Python

Hide

```
efficiency_master_data$X1 <- NULL
```

build model

Find random effects

Assume individual is a random effect, but let's demonstrate it.

Hide

```
testEffBgTr_0 <- gls(efficiency ~ species, data = efficiency_master_data)
testEffBgTr_1 <- lme(efficiency ~ species, random = ~1|individual, data = efficiency_master_dat
a)
```

compare models

Hide

```
anova(testEffBgTr_0,testEffBgTr_1)
```

	Mo… <int>	df <dbl>	AIC <chr>	BIC <chr>	logLik <chr>	Test <fctr>	L.Ratio <chr>	p-value <chr>
testEffBgTr_0	1	3	-87.13033	-83.85720	46.56516			
testEffBgTr_1	2	4	-91.16368	-86.79951	49.58184	1 vs 2	6.033351	0.014

2 rows

Do a p-value correction for testing on the boundary

Hide

```
0.5*(1-pchisq(6.033351, 1))
```

```
[1] 0.007019029
```

This p-value is still below our significance threshold, so we accept individual as a random intercept term.

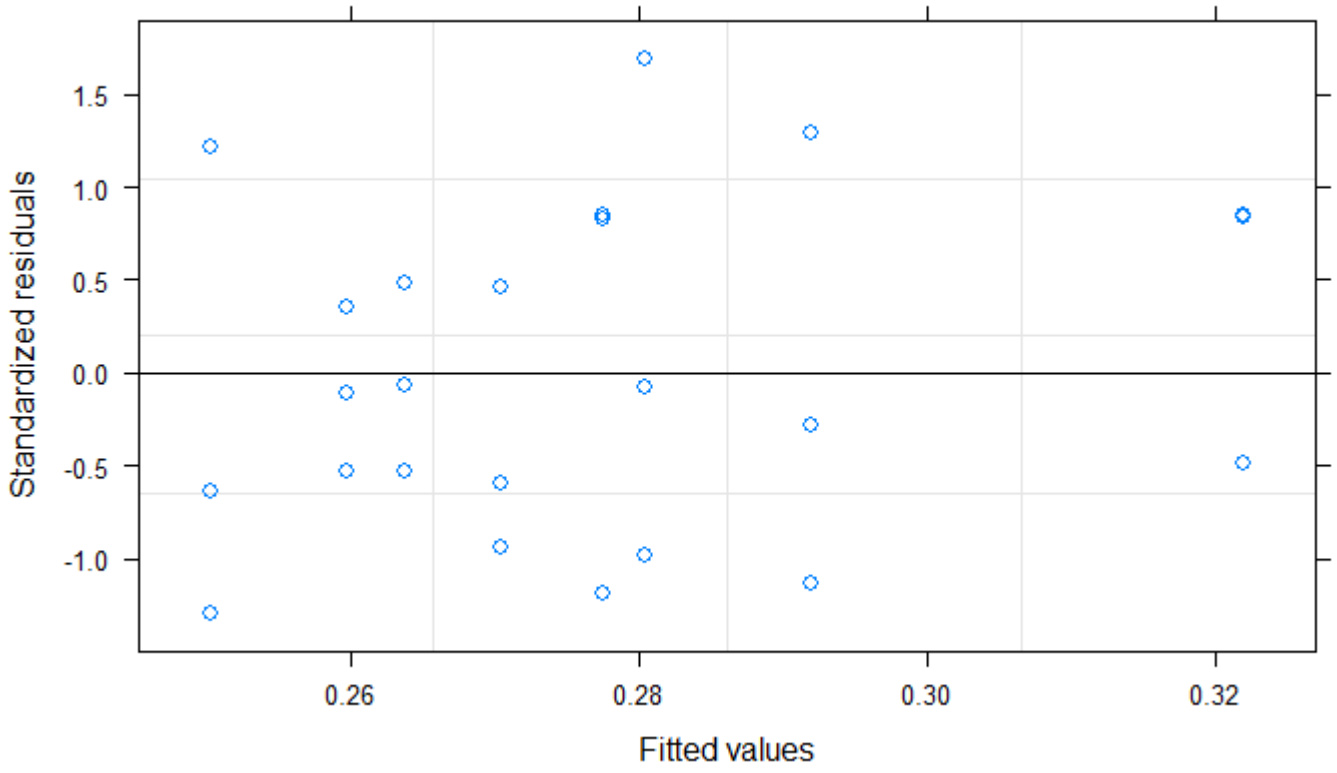
We are data-limited, so take this as our random structure (we don't have enough data to fit random slopes)

Check for heterogeneity

Plot residuals

Hide

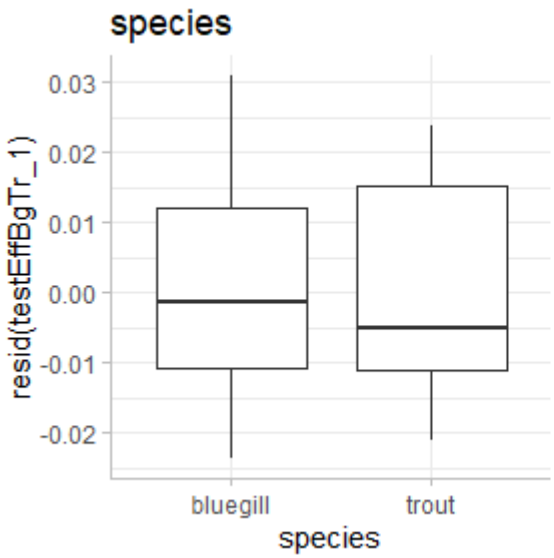
```
plot(testEffBgTr_1)
```



Hard to tell if there's heterogeneity here - but probably not.

Hide

```
grid.arrange(
  ggplot(efficiency_master_data, aes(x = species, y = resid(testEffBgTr_1)))
    + geom_boxplot() +papertheme + ggtitle("species"),


  ncol=2
)
```



Variances are equal across species

Check fixed effects structure

Hide

```
anova(testEffBgTr_1)
```

	numDF <int>	denDF <dbl>	F-value <chr>	p-value <chr>
(Intercept)	1	16	1159.8579	<.0001
species	1	6	2.8599	0.1418

2 rows

Species is not significant.

Final bg vs tr efficiency model

Hide

```
efficiency_model <- lme(efficiency ~ species, random = ~1|individual, data = efficiency_master_d
ata)
```

Hide

```
summary(efficiency_model)
```

```
Linear mixed-effects model fit by REML
 Data: efficiency_master_data
```

AIC <dbl>	BIC <dbl>	logLik <dbl>
-91.16368	-86.79951	49.58184

1 row

```
Random effects:
 Formula: ~1 | individual
        (Intercept)   Residual
StdDev:  0.02040063 0.01841369

Fixed effects: efficiency ~ species
```

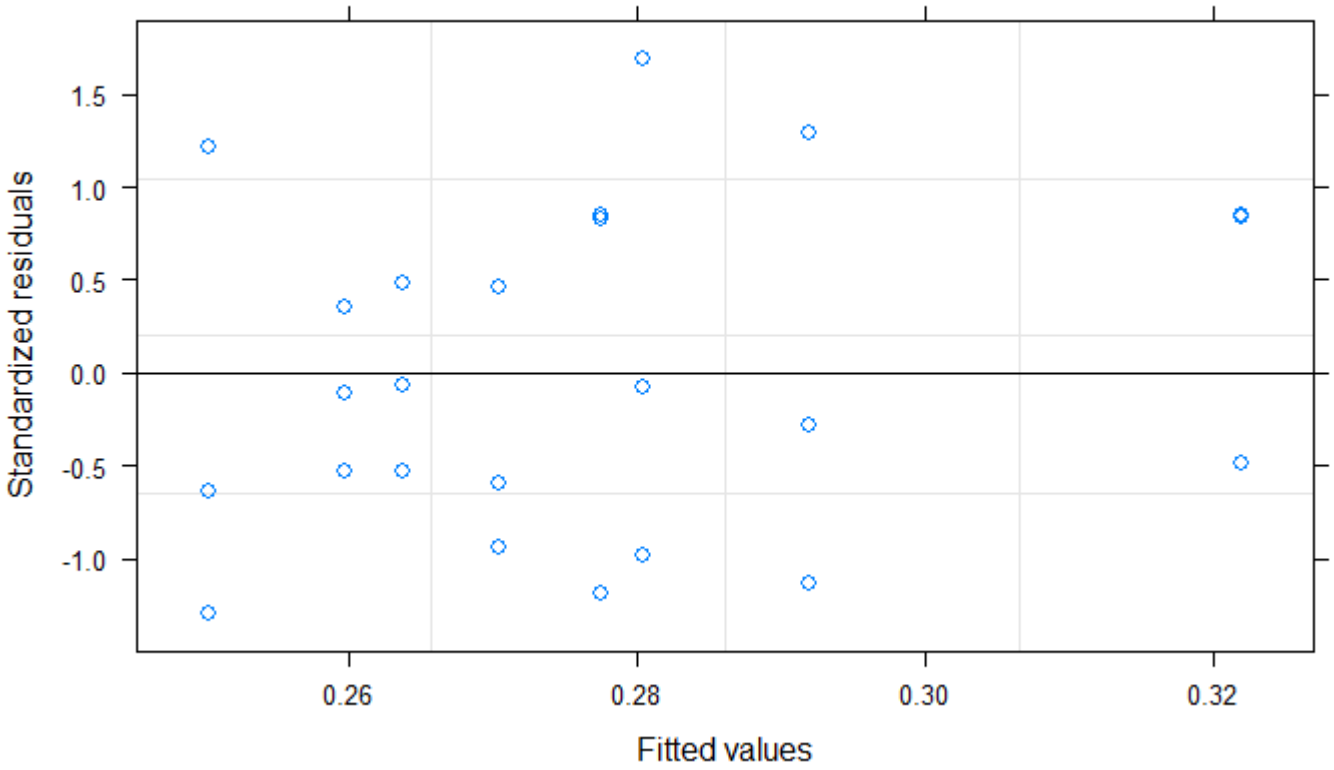
	Value	Std.Error	DF	t-value	p-value
	<chr>	<chr>	<chr>	<chr>	<chr>
(Intercept)	0.26633974	0.01028793	16	25.888572	0.0000
speciestrout	0.02841121	0.01680011	6	1.691132	0.1418

2 rows

```
 Correlation:
             (Intr)
speciestrout -0.612

Standardized Within-Group Residuals:
        Min          Q1         Med          Q3         Max
-1.29076505 -0.60701066 -0.09589237  0.82922658  1.68455778

Number of Observations: 24
Number of Groups: 8
```

Hide

```
plot(efficiency_model)
```


Standardized residuals
1.5
1.0
0.5
0.0
-0.5
-1.0
0.26
0.28
0.30
0.32
Fitted values