Statistics for the Sciences

Split-plot Designs

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Outline

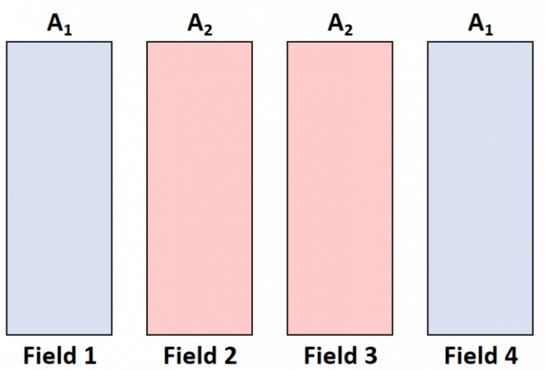
- Split-plot design
- Lab

Split-plot design

- A **split-plot design** is an experimental design in which researchers are interested in studying two factors in which:
  - One of the factors is 'easy' to change or vary.
  - One of the factors is 'hard' to change or vary.
- This type of design was developed in 1925 by mathematician Ronald Fisher for use in agricultural experiments.
- To illustrate the idea of the split-plot design, consider an example in which researchers want to study the effects of two irrigation methods (Factor A) and two fertilizers (Factor B) on crop yield.
  - There are four treatments: $A_1B_1, A_1B_2, A_2B_1, A_2B2$
  - Suppose there are only 4 fields (**experimental units**)
    - ⋆ A completely randomized design does not work

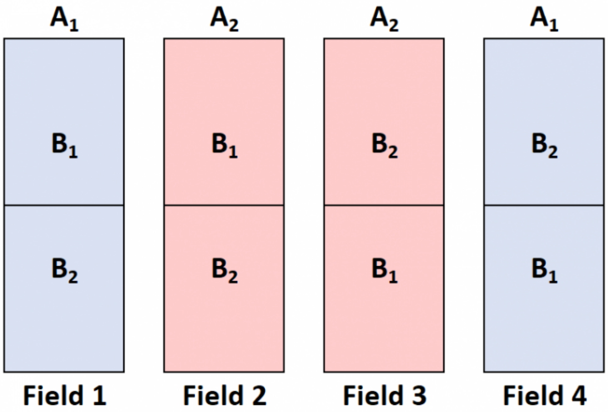
Split-plot design

- In this particular example, it's not possible to apply different irrigation methods to areas smaller than one field, but it is possible to apply different fertilizers to small areas.
  - We can randomly assign one of the irrigation methods (A_1 and A_2) to each field:



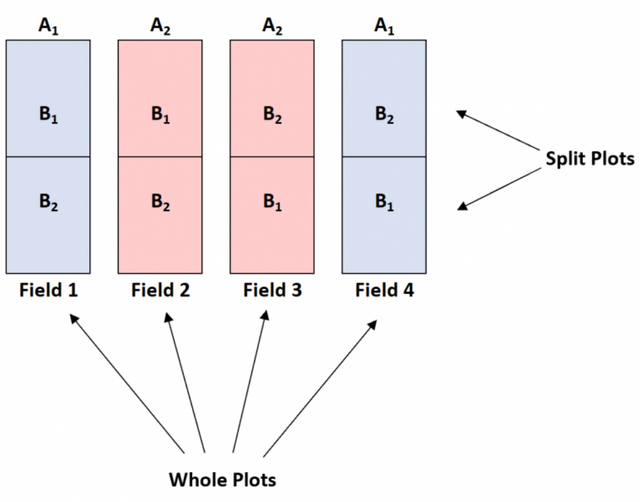
Split-plot design

- Then we can split each field in half and randomly assign one fertilizer (B_1 and B_2) to each half:



Split-plot design

- In this example, we have 4 "whole" plots and within each whole plot we have 2 "split" plots.



Split-plot design

Split-plot designs have two **advantages** over completely randomized designs:

- **Cost**: Since one of the factors in a split-plot design doesn't have to be changed for each split-plot, this means this type of design tends to be cheaper to carry out in practice.
- **Efficiency**: A split-plot design leads to an increase in precision in the estimates for all factor effects except for the whole-plot main effects.

Split-plot design

- Statistical model:

$$
\begin{aligned}
Y_{ijk} =& \mu + \tau_i + \eta_{k(i)} + \beta_j + (\tau\beta)_{ij} + \varepsilon_{ijk}, \\
& i = 1, \ldots, a; j = 1, \ldots, b; k = 1, \ldots, c
\end{aligned}
$$

- Whole plot effects:
  - τ_i: whole plot treatment effects (factor A)
  - $\eta_{k(i)}$: whole plot errors
- Split-plot effects
  - β_j: the split-plot treatment (factor B)
  - $(\tau\beta)_{ij}$: interaction effects
  - ε_{ijk}: subplot random error

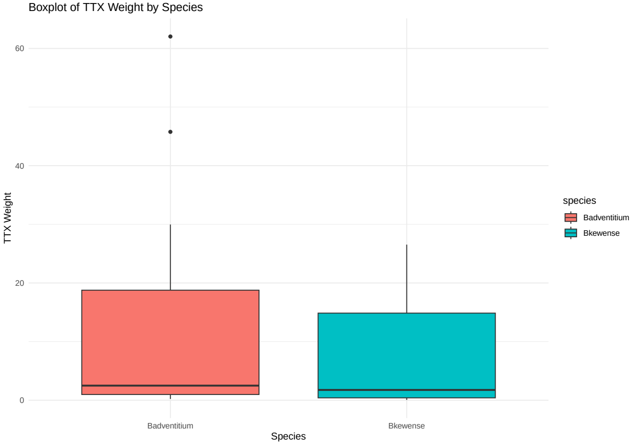
Split-plot design

- Example (`stokes.csv`): Stokes et al. (2014) studied the neurotoxin tetrodotoxin (TTX) in flatworms. The between-plots factor was flatworm species (fixed with two groups: Bipalium adventitium and Bipalium kewense) with individual flatworms (plots) nested within species. The within-plots factor was body segment (fixed with three groups: head, anterior body, posterior body) and each segment represented a "sub-plot". The response variable was the TTX concentration of tissue adjusted for weight.
  - The main research questions were about the fixed effects of **species**, body **segment** and their **interaction** on TTX concentration, but the analyses also provide information about the variances associated with the random effects of individual within species and the random interaction between individuals within species and body segment.
  - Response Variable: TTX concentration `ttxweight`
  - Main factor: flatworm `species` with two levels: `Badventitium` and `Bkewense`
  - Whole plots: Individual flatworms nested within each species, `indiv`.
  - Split Plot Factor: Body `segment` with three groups: `h`, `b`, and `p`

Split-plot design

```
##    indiv      species segment  finalttx   ttxweight      conc
## 1      1 Badventitium       h  59.942130 29.97106516  78.86305
## 2      1 Badventitium       p  18.330584  0.22354371  26.84862
## 3      1 Badventitium       b  36.837527  0.63512977  49.98230
## 4      2 Badventitium       h  62.033825 62.03382496  81.47767
## 5      2 Badventitium       p  46.976133  0.62634844  62.65555
## 6      2 Badventitium       b  61.316483  0.94333051  80.58099
## 7      3 Badventitium       h  29.104440 14.55221979  41.90968
## 8      3 Badventitium       p  50.882196  1.88452579  69.13188
## 9      3 Badventitium       b  66.454131  4.74672366  88.59680
## 10     4 Badventitium       h  46.064966 23.03248288  63.11034
## 11     4 Badventitium       p  55.289019  1.08409841  74.64041
## 12     4 Badventitium       b  64.832549  1.75223104  86.56982
## 13     5 Badventitium       h  40.353001 20.17650074  55.97038
## 14     5 Badventitium       p  42.508300  0.67473492  58.66451
## 15     5 Badventitium       b  83.629044  2.69771109 110.06544
## 16     6 Badventitium       h  45.773678 45.77367827  62.74623
## 17     6 Badventitium       p  75.437948  2.28599842  99.82657
## 18     6 Badventitium       b  66.198278  3.67768214  88.27698
## 19     7      Bkewense       h 108.396182 21.67923649 182.72076
## 20     7      Bkewense       p  58.131332  2.07611899  76.59955
## 21     7      Bkewense       b   6.653189  0.05544324  12.25188
## 22     8      Bkewense       h 100.120317 12.51503962 166.86719
## 23     8      Bkewense       p  26.944873  0.31699851  37.61648
## 24     8      Bkewense       b  50.761514  0.31925480  67.38728
## 25     9      Bkewense       h  78.199376 15.63987512 103.27835
## 26     9      Bkewense       p   9.360317  0.07091150  17.22953
## 27     9      Bkewense       b  49.695106  1.71362435  67.64801
## 28    10      Bkewense       h  51.972824 17.32427480  70.49516
## 29    10      Bkewense       p  49.734262  0.68129127  67.69696
## 30    10      Bkewense       b  50.483634  1.80298694  68.63367
## 31    11      Bkewense       h  75.669326 25.22310859 100.11579
## 32    11      Bkewense       p  19.082570  0.20518892  29.38234
## 33    11      Bkewense       b  76.367489  2.31416634 100.98849
## 34    12      Bkewense       h  53.084960 26.54247987  71.88533
## 35    12      Bkewense       p  49.266253  0.74645838  67.11195
## 36    12      Bkewense       b  44.945554  1.66465016  61.71107
```

Split-plot design



Split-plot design

- Consider log10 transformation of `ttxweight`

```
##    indiv      species segment   finalttx   ttxweight      conc
## 1      1 Badventitium       h  59.942130 29.97106516  78.86305
## 2      1 Badventitium       p  18.330584  0.22354371  26.84862
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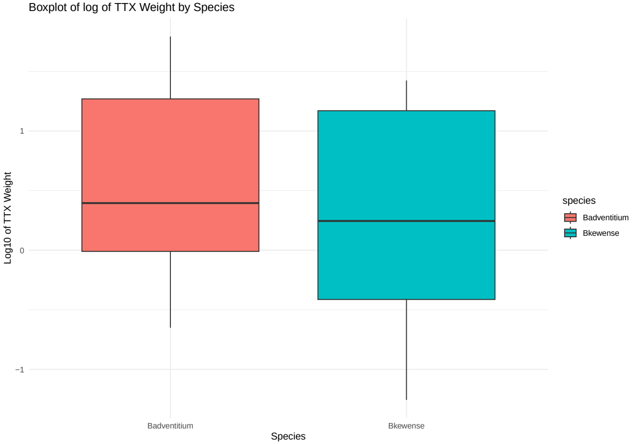
Split-plot design



Split-plot design

- LMER estimation with hypothesis testing

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: logttxweight ~ species + segment + species * segment + (1 | indiv)
##    Data: stokes
##
## REML criterion at convergence: 41.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.81144 -0.39960  0.08694  0.72676  1.72771
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  indiv    (Intercept) 0.0000   0.0000
##  Residual             0.1654   0.4067
## Number of obs: 36, groups:  indiv, 12
##
## Fixed effects:
##                          Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)                1.4600     0.1660 30.0000   8.793 8.36e-10 ***
## speciesBkewense           -0.1780     0.2348 30.0000  -0.758    0.454
## segmentb                  -1.1777     0.2348 30.0000  -5.015 2.23e-05 ***
## segmentp                  -1.5192     0.2348 30.0000  -6.470 3.78e-07 ***
## speciesBkewense:segmentb  -0.2171     0.3321 30.0000  -0.654    0.518
## speciesBkewense:segmentp  -0.1482     0.3321 30.0000  -0.446    0.659
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##                 (Intr) spcsBk sgmntb sgmntp spcsBkwns:sgmntb
## specisBkwns     -0.707
## segmentb        -0.707  0.500
## segmentp        -0.707  0.500  0.500
## spcsBkwns:sgmntb  0.500 -0.707 -0.707 -0.354
## spcsBkwns:sgmntp  0.500 -0.707 -0.354 -0.707  0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

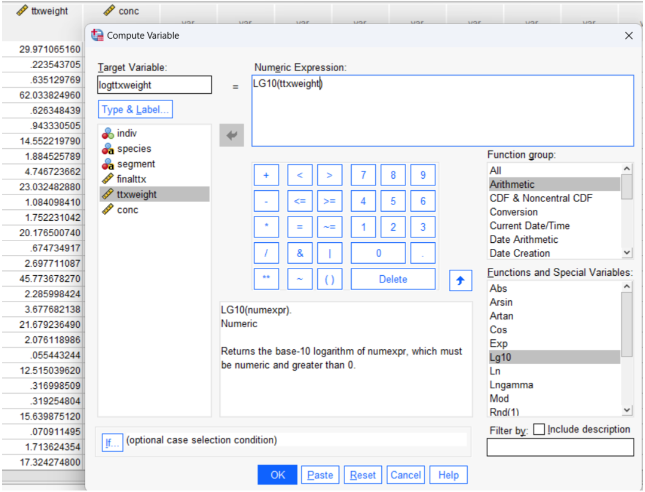
Lab

- ANOVA table

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## species          0.8087  0.8087     1    30  4.8890   0.03479 *
## segment         17.1494  8.5747     2    30 51.8402 1.844e-10 ***
## species:segment  0.0738  0.0369     2    30  0.2232   0.80128
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

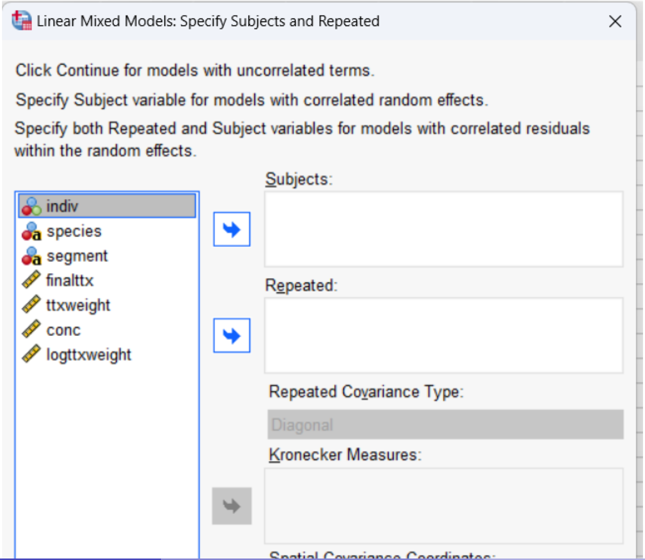
Lab

- After importing the data `stokes.csv`, add a variable of log10 transformation of `ttxweight`



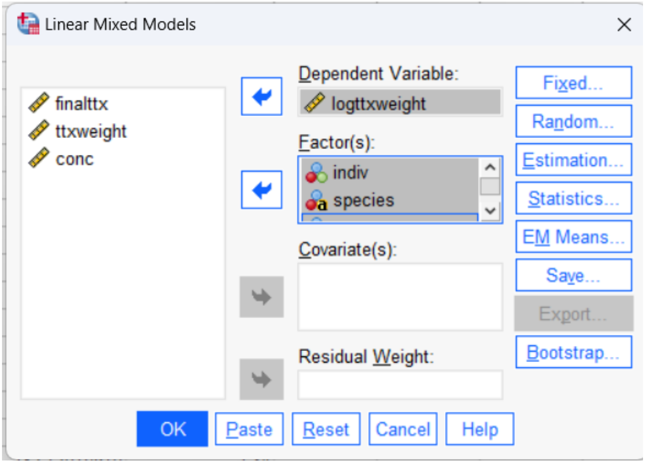
Lab

- Click on `Analyze` → `Mixed Models` → `Linear...` and
  - then click `Continue`



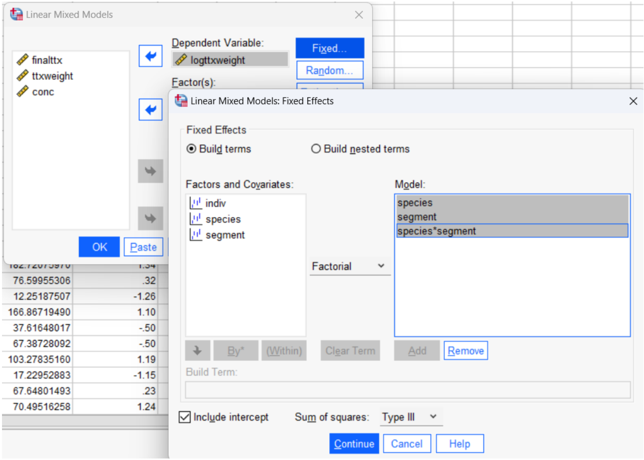
Lab

- Move the response variable to the `Dependent Variable` box and move the three factors `indiv`, `species` and `segment` to `Factor(s)` box.



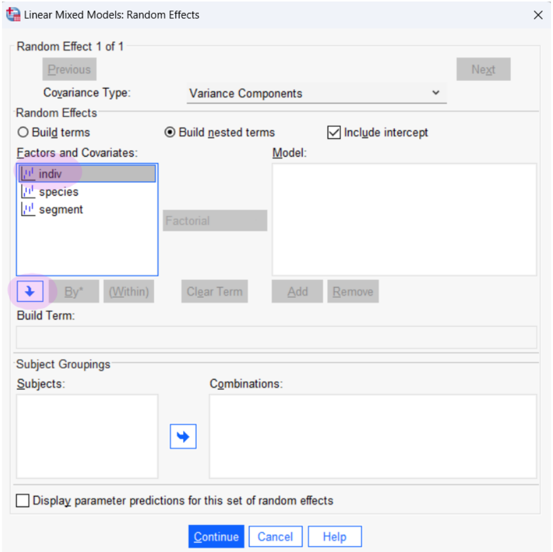
Lab

- Click on `Fixed Effects` to specify the interaction between `species` and `segment`



Lab

- Click on the `Random...` tab. We build the nested term `indiv(species)`: individuals nested in species



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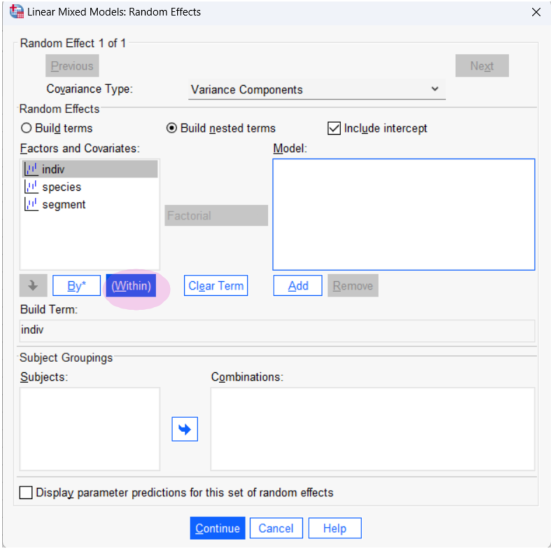

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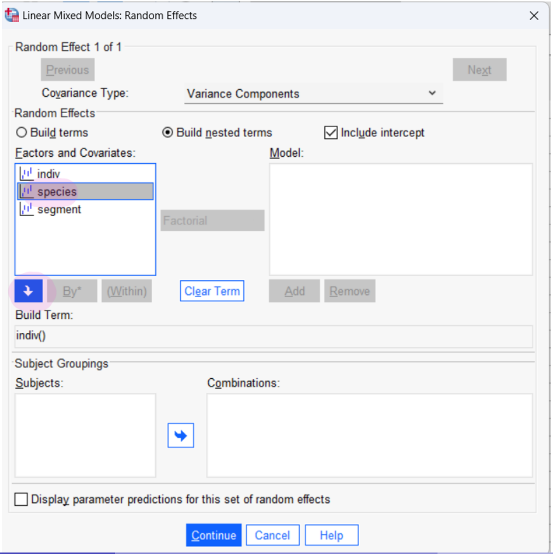

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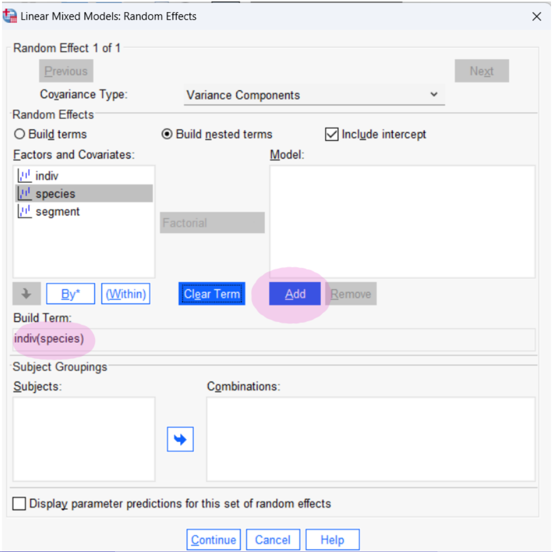

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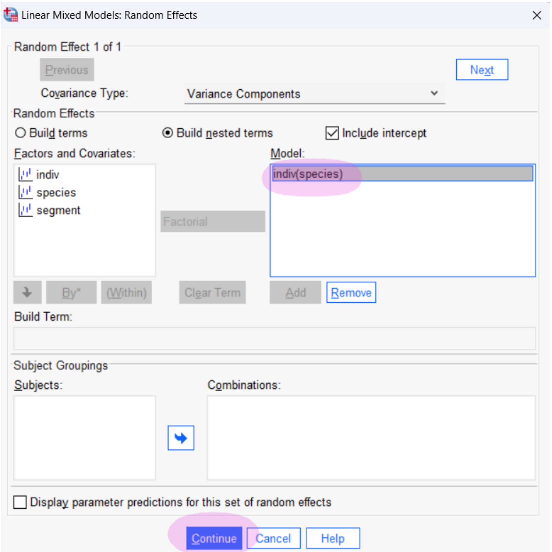
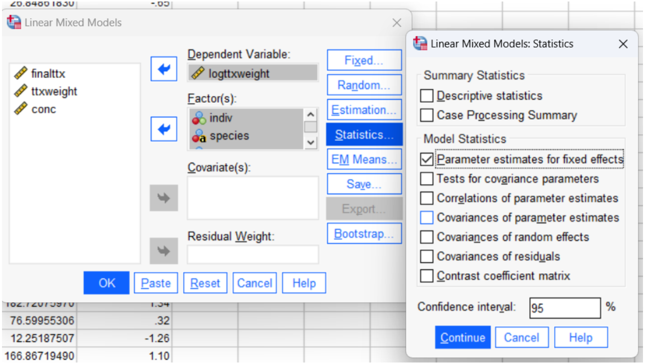
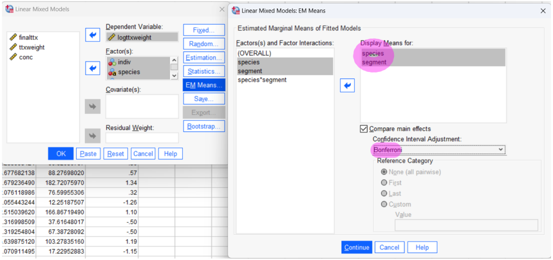


Lab


Linear Mixed Models
finalttx
ttxweight
conc
Dependent Variable:
logttxweight
Factor(s):
indiv
species
Covariate(s):
Residual Weight:
Fixed...
Random...
Estimation...
Statistics...
EM Means...
Save...
Export...
Bootstrap...
OK
Paste
Reset
Cancel
Help
76.59955306
.32
12.25187507
-1.26
166.86719490
1.10
Linear Mixed Models: Statistics
Summary Statistics
Descriptive statistics
Case Processing Summary
Model Statistics
Parameter estimates for fixed effects
Tests for covariance parameters
Correlations of parameter estimates
Covariances of parameter estimates
Covariances of random effects
Covariances of residuals
Contrast coefficient matrix
Confidence interval:
95
%
Continue
Cancel
Help

Lab

- We may want to compare the means of the fixed effects



Lab

Type III Tests of Fixed Effects[a]

Source	Numerator df	Denominator df	F	Sig.
Intercept	1	30	2.198	.149
species	1	30	4.889	.035
segment	2	30	51.840	<.001
species * segment	2	30	.223	.801

a. Dependent Variable: logttxweight.

Lab

Estimates of Fixed Effects[a]

Parameter	Estimate	Std. Error	df	t	Sig.	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
Intercept	-.385	.316	30	-1.219	.232	-1.031	.260
[species=Badventitium]	.326	.235	30	1.389	.175	-.153	.806
[species=Bkewense]	0[b]	0	.	.	.	.	.
[segment=b]	.273	.235	30	1.161	.255	-.207	.752
[segment=h]	1.667	.235	30	7.101	<.001	1.188	2.147
[segment=p]	0[b]	0	.	.	.	.	.
[species=Badventitium] * [segment=b]	.069	.332	30	.207	.837	-.609	.747
[species=Badventitium] * [segment=h]	-.148	.332	30	-.446	.659	-.826	.530
[species=Badventitium] * [segment=p]	0[b]	0	.	.	.	.	.
[species=Bkewense] * [segment=b]	0[b]	0	.	.	.	.	.
[species=Bkewense] * [segment=h]	0[b]	0	.	.	.	.	.
[species=Bkewense] * [segment=p]	0[b]	0	.	.	.	.	.

a. Dependent Variable: logttxweight.

b. This parameter is set to zero because it is redundant.

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