

Statistical modeling for phenotypic traits

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M3P_StatisticalAnalysis

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Statistical modeling for phenotypic traits

The explanatory variable (X) refers to the genotype, which is a categorical variable. The response variables (Y) are the phenotypic data of the variables dataframe.

In this case, the variables are:

And the genotypes are:

```
print(variables)
```

```
## [1] "DW_plant_g"
```

```
unique(endpoint$Genotype)
```

```
## [1] EPPN7_L EPPN10_L EPPN8_L EPPN3_L EPPN1_L EPPN2_L EPPN9_L EPPN14_L
## [9] EPPN4_L EPPN20_T EPPN13_L EPPN6_L EPPN11_L EPPN5_L EPPN12_L EPPN2_H
## [17] EPPN8_H EPPN10_H EPPN13_H EPPN7_H EPPN3_H EPPN4_H EPPN6_H EPPN14_H
## [25] EPPN1_H EPPN11_H EPPN15_H EPPN5_H EPPN9_H EPPN12_H
## 30 Levels: EPPN1_H EPPN1_L EPPN10_H EPPN10_L EPPN11_H EPPN11_L ... EPPN9_L
```

1. First linear models

Firstly, we model the $Y = X + r + c + e$ Where - Y is the phenotypic trait; - X the genotype (fixed effect); - r the row effect (fixed or random); - c the column effect (fixed or random);

```
fit_models_fixed <- function(data, trait_name) {  
  fixed_formula <- as.formula(paste(trait_name, "~ Genotype + Row + Column"))  
  fixed_model <- lm(fixed_formula, data)  
  print(paste("Summary for fixed effects model of", trait_name))  
  print(summary(fixed_model))  
  print(anova(fixed_model))  
}  
  
fit_models_random <- function(data, trait_name) {  
  random_formula <- as.formula(paste(trait_name, "~ Genotype + (1|Row) + (1|Column)"))  
  random_model <- lmer(random_formula, data)  
  print(paste("Summary for random effects model of", trait_name))  
  print(summary(random_model))  
  print(anova(random_model))  
  print(ranova(random_model))  
}  
  
for (trait in variables) {  
  fit_models_fixed(endpoint_clean, trait)  
}
```

```
## [1] "Summary for fixed effects model of DW_plant_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -155.848  -30.789   3.492   27.205  135.477
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    321.7517    27.7103   11.611 < 2e-16 ***
## GenotypeEPPN1_L -144.3868    23.1356   -6.241 1.47e-09 ***
## GenotypeEPPN10_H  60.7302    22.6345    2.683 0.00770 **
## GenotypeEPPN10_L -65.5556    21.8115   -3.006 0.00287 **
## GenotypeEPPN11_H  -7.6863    23.6958   -0.324 0.74588
## GenotypeEPPN11_L -168.5582    21.9979   -7.662 2.50e-13 ***
## GenotypeEPPN12_H  44.3697    22.0241    2.015 0.04483 *
## GenotypeEPPN12_L -155.6665    22.8783   -6.804 5.47e-11 ***
## GenotypeEPPN13_H -15.9995    21.7123   -0.737 0.46176
## GenotypeEPPN13_L -206.3777    22.3921   -9.217 < 2e-16 ***
## GenotypeEPPN14_H  74.4012    24.3876    3.051 0.00248 **
## GenotypeEPPN14_L -164.6728    22.3950   -7.353 1.83e-12 ***
## GenotypeEPPN15_H -17.2684    22.5998   -0.764 0.44541
## GenotypeEPPN2_H  -11.4513    21.7625   -0.526 0.59914
## GenotypeEPPN2_L -208.0948    22.5637   -9.223 < 2e-16 ***
## GenotypeEPPN20_T -139.0033    22.3591   -6.217 1.68e-09 ***
## GenotypeEPPN3_H    6.3053    22.6324    0.279 0.78075
## GenotypeEPPN3_L -122.9847    22.1383   -5.555 6.09e-08 ***
## GenotypeEPPN4_H  -21.8554    22.9550   -0.952 0.34181
## GenotypeEPPN4_L -228.5830    22.6232  -10.104 < 2e-16 ***
## GenotypeEPPN5_H   39.1054    22.1035    1.769 0.07787 .
## GenotypeEPPN5_L -151.0272    21.7886   -6.931 2.53e-11 ***
## GenotypeEPPN6_H   18.8878    22.9127    0.824 0.41040
## GenotypeEPPN6_L -154.7587    21.7482   -7.116 8.12e-12 ***
## GenotypeEPPN7_H  -9.8087    21.5785   -0.455 0.64975
## GenotypeEPPN7_L -174.8279    22.0282   -7.937 4.11e-14 ***
## GenotypeEPPN8_H   94.9134    23.9443    3.964 9.21e-05 ***
## GenotypeEPPN8_L -127.2823    21.8708   -5.820 1.50e-08 ***
## GenotypeEPPN9_H   62.6809    22.1101    2.835 0.00489 **
## GenotypeEPPN9_L -126.4491    22.6246   -5.589 5.11e-08 ***
## Row2            -12.7000     9.9030   -1.282 0.20067
## Row3            -39.9007    10.0145   -3.984 8.49e-05 ***
## Row4             -7.8409     9.9552   -0.788 0.43154
## Row5             48.3953    10.3889    4.658 4.78e-06 ***
## Row6             12.3630    10.2519    1.206 0.22879
## Row7             35.1240    11.5540    3.040 0.00257 **
## Row8             35.7974    16.0513    2.230 0.02647 *
## Column2         -32.4874    29.9402   -1.085 0.27875
## Column3          17.5388    31.1120    0.564 0.57336
## Column4           7.5881    30.3575    0.250 0.80279
## Column5           6.0557    31.6247    0.191 0.84827
## Column6         -12.1393    30.4287   -0.399 0.69022
## Column7          -4.1114    30.2742   -0.136 0.89207
## Column8           0.4091    31.9894    0.013 0.98980
```

```

## Column9      26.2091    33.2791    0.788    0.43158
## Column10     -23.3001    31.7652   -0.734    0.46382
## Column11      6.2927    33.4332    0.188    0.85083
## Column12      6.2432    30.7022    0.203    0.83900
## Column13     -31.3335    30.3762   -1.032    0.30312
## Column14     -26.9364    30.4247   -0.885    0.37667
## Column15     -12.8883    30.3658   -0.424    0.67155
## Column16     -54.1935    30.3781   -1.784    0.07543 .
## Column17     -32.9214    29.1327   -1.130    0.25935
## Column18     -60.1204    29.2875   -2.053    0.04096 *
## Column19      -6.5508    30.2812   -0.216    0.82887
## Column20     -10.9261    29.4512   -0.371    0.71090
## Column21     -26.5389    30.4212   -0.872    0.38369
## Column22     -52.7307    29.5123   -1.787    0.07498 .
## Column23     -34.2101    29.3368   -1.166    0.24449
## Column24     -24.2602    29.3469   -0.827    0.40908
## Column25     -29.5375    29.5156   -1.001    0.31775
## Column26      4.9037    30.6220    0.160    0.87288
## Column27     13.9644    29.3592    0.476    0.63468
## Column28     -42.3424    30.1109   -1.406    0.16069
## Column29     -22.3910    31.8174   -0.704    0.48214
## Column30     -26.9363    29.3862   -0.917    0.36007
## Column31     -37.8905    31.5848   -1.200    0.23122
## Column32      6.5468    31.1707    0.210    0.83379
## Column33     -8.8951    29.9488   -0.297    0.76666
## Column34     -7.4142    31.1910   -0.238    0.81227
## Column35      6.7492    31.3904    0.215    0.82991
## Column36     -9.9941    31.4332   -0.318    0.75075
## Column37     -39.2935    31.6738   -1.241    0.21573
## Column38     -48.6076    29.9460   -1.623    0.10560
## Column39     -38.1387    29.3170   -1.301    0.19428
## Column40     -45.4481    30.3817   -1.496    0.13572
## Column41     -45.3388    30.5431   -1.484    0.13874
## Column42      -4.7408    29.6675   -0.160    0.87315
## Column43     -40.8035    30.6718   -1.330    0.18441
## Column44     -78.3529    29.4821   -2.658    0.00829 **
## Column45     -80.4264    30.4917   -2.638    0.00878 **
## Column46    -106.9452    31.6716   -3.377    0.00083 ***
## Column47     -74.1330    33.5438   -2.210    0.02785 *
## Column48     -78.5066    31.1253   -2.522    0.01217 *
## Column49     -92.6116    33.1947   -2.790    0.00561 **
## Column50     -50.1852    31.5815   -1.589    0.11309
## Column51     -71.8097    33.2347   -2.161    0.03151 *
## Column52     -94.9064    31.8839   -2.977    0.00315 **
## Column53     -64.4735    31.8945   -2.021    0.04411 *
## Column54     -69.3765    31.3800   -2.211    0.02780 *
## Column55     -88.3983    31.6013   -2.797    0.00548 **
## Column56     -32.4037    33.5244   -0.967    0.33453
## Column57     -30.3266    31.6992   -0.957    0.33948
## Column58     -29.6844    31.4444   -0.944    0.34591
## Column59     -43.9694    31.4170   -1.400    0.16268
## Column60      6.1347    31.6186    0.194    0.84629
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.24 on 302 degrees of freedom

```

```
## (32 observations effacées parce que manquantes)
## Multiple R-squared: 0.8275, Adjusted R-squared: 0.7732
## F-statistic: 15.25 on 95 and 302 DF, p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_plant_g
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   29 3610982  124517   42.323 < 2.2e-16 ***
## Row         7  300670    42953   14.600 2.250e-16 ***
## Column     59  349775     5928    2.015 7.557e-05 ***
## Residuals 302  888503     2942
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
for (trait in variables) {
  fit_models_random(endpoint_clean, trait)
}
```

```
## [1] "Summary for random effects model of DW_plant_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
## Data: data
##
## REML criterion at convergence: 4121.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.89929 -0.57178 -0.04405  0.54199  2.86000
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## Column   (Intercept) 483.5    21.99
## Row      (Intercept) 826.5    28.75
## Residual                2949.8    54.31
## Number of obs: 398, groups: Column, 60; Row, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    297.0677    18.4157   58.8007  16.131 < 2e-16 ***
## GenotypeEPPN1_L -143.3686    22.2272  342.1834  -6.450 3.81e-10 ***
## GenotypeEPPN10_H  61.3637    21.7555  342.8670   2.821 0.005072 **
## GenotypeEPPN10_L -65.1141    21.1726  334.5289  -3.075 0.002275 **
## GenotypeEPPN11_H   0.4176    22.7405  342.5403   0.018 0.985360
## GenotypeEPPN11_L -166.7167    21.2474  338.3984  -7.846 5.67e-14 ***
## GenotypeEPPN12_H  45.4102    21.2640  339.4059   2.136 0.033432 *
## GenotypeEPPN12_L -157.0385    22.0928  338.2707  -7.108 7.02e-12 ***
## GenotypeEPPN13_H  -12.0599    21.0947  332.6908  -0.572 0.567908
## GenotypeEPPN13_L -209.9840    21.6864  336.3073  -9.683 < 2e-16 ***
## GenotypeEPPN14_H   78.2821    23.4009  343.6094   3.345 0.000913 ***
## GenotypeEPPN14_L -161.4972    21.4493  345.0776  -7.529 4.50e-13 ***
## GenotypeEPPN15_H  -16.9302    21.7041  342.0660  -0.780 0.435904
## GenotypeEPPN2_H   -5.7110    21.1393  333.9092  -0.270 0.787204
## GenotypeEPPN2_L  -208.2031    21.6990  341.4011  -9.595 < 2e-16 ***
## GenotypeEPPN20_T -135.2369    21.3931  345.1202  -6.322 8.01e-10 ***
## GenotypeEPPN3_H    5.2566    21.7119  342.5832   0.242 0.808843
## GenotypeEPPN3_L  -114.4274    21.3289  340.3499  -5.365 1.50e-07 ***
## GenotypeEPPN4_H   -26.4667    22.1431  339.6205  -1.195 0.232822
## GenotypeEPPN4_L  -219.4431    21.7336  342.1278 -10.097 < 2e-16 ***
## GenotypeEPPN5_H    41.2112    21.2817  340.8944   1.936 0.053637 .
## GenotypeEPPN5_L  -148.4151    21.1355  333.8320  -7.022 1.23e-11 ***
## GenotypeEPPN6_H    15.9671    21.8426  347.3298   0.731 0.465268
## GenotypeEPPN6_L  -152.1022    20.9535  340.0291  -7.259 2.67e-12 ***
## GenotypeEPPN7_H   -8.7589    21.0323  329.6501  -0.416 0.677353
## GenotypeEPPN7_L  -168.8436    21.2548  338.9720  -7.944 2.92e-14 ***
## GenotypeEPPN8_H   101.8070    22.8688  347.0299   4.452 1.15e-05 ***
## GenotypeEPPN8_L  -122.7911    21.0188  342.5604  -5.842 1.20e-08 ***
## GenotypeEPPN9_H    65.9135    21.2831  341.0133   3.097 0.002117 **
## GenotypeEPPN9_L  -130.3668    21.7507  342.6939  -5.994 5.20e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 30 > 12.
## Use print(summary(random_model), correlation=TRUE) or
##      vcov(summary(random_model))      if you need it

## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Genotype 3382286  116631    29 337.53  39.539 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_plant_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>         33 -2060.7 4187.4
## (1 | Row)       32 -2092.1 4248.3 62.834  1  2.248e-15 ***
## (1 | Column)   32 -2067.4 4198.9 13.446  1  0.0002455 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. Linear models with Plant_type

Model with X as Plant_type instead of Genotype, and row and column effects as random effects.
Plant_type is defined as H for Hybrid, L for pure Line and T for Tester.

```
endpoint_clean$Plant_type <- as.factor(endpoint_clean$Plant_type)
endpoint_clean$Plant_type <- relevel(endpoint_clean$Plant_type, ref = "T") # T as base
Level

fit_model_plant_type <- function(data, trait) {
  # Random effects model with Plant_type as a fixed effect
  model_formula <- as.formula(paste(trait, "~ Plant_type + (1|Row) + (1|Column)"))
  model <- lmer(model_formula, data)
  print(paste("Summary for mixed effects model of", trait))
  print(summary(model))
  print(anova(model))
  print(ranova(model))
}

for (trait in variables) {
  fit_model_plant_type(endpoint_clean, trait)
}
```

```
## [1] "Summary for mixed effects model of DW_plant_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
## Data: data
##
## REML criterion at convergence: 4474.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.69247 -0.61056 -0.01601  0.62670  2.84644
##
## Random effects:
## Groups   Name      Variance Std.Dev.
## Column   (Intercept) 611.2    24.72
## Row      (Intercept) 860.9    29.34
## Residual                4072.6   63.82
## Number of obs: 398, groups: Column, 60; Row, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)  159.06      20.76  80.69   7.662 3.54e-11 ***
## Plant_typeH  159.77      18.32 370.56   8.722 < 2e-16 ***
## Plant_typeL -15.95      18.35 372.70  -0.869   0.385
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.820
## Plant_typeL -0.823  0.933
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 2880418 1440209      2 355.05  353.63 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_plant_g ~ Plant_type + (1 | Row) + (1 | Column)
##              npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>          6 -2237.2 4486.5
## (1 | Row)        5 -2260.8 4531.7 47.238  1 6.287e-12 ***
## (1 | Column)     5 -2244.0 4498.0 13.486  1 0.0002403 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

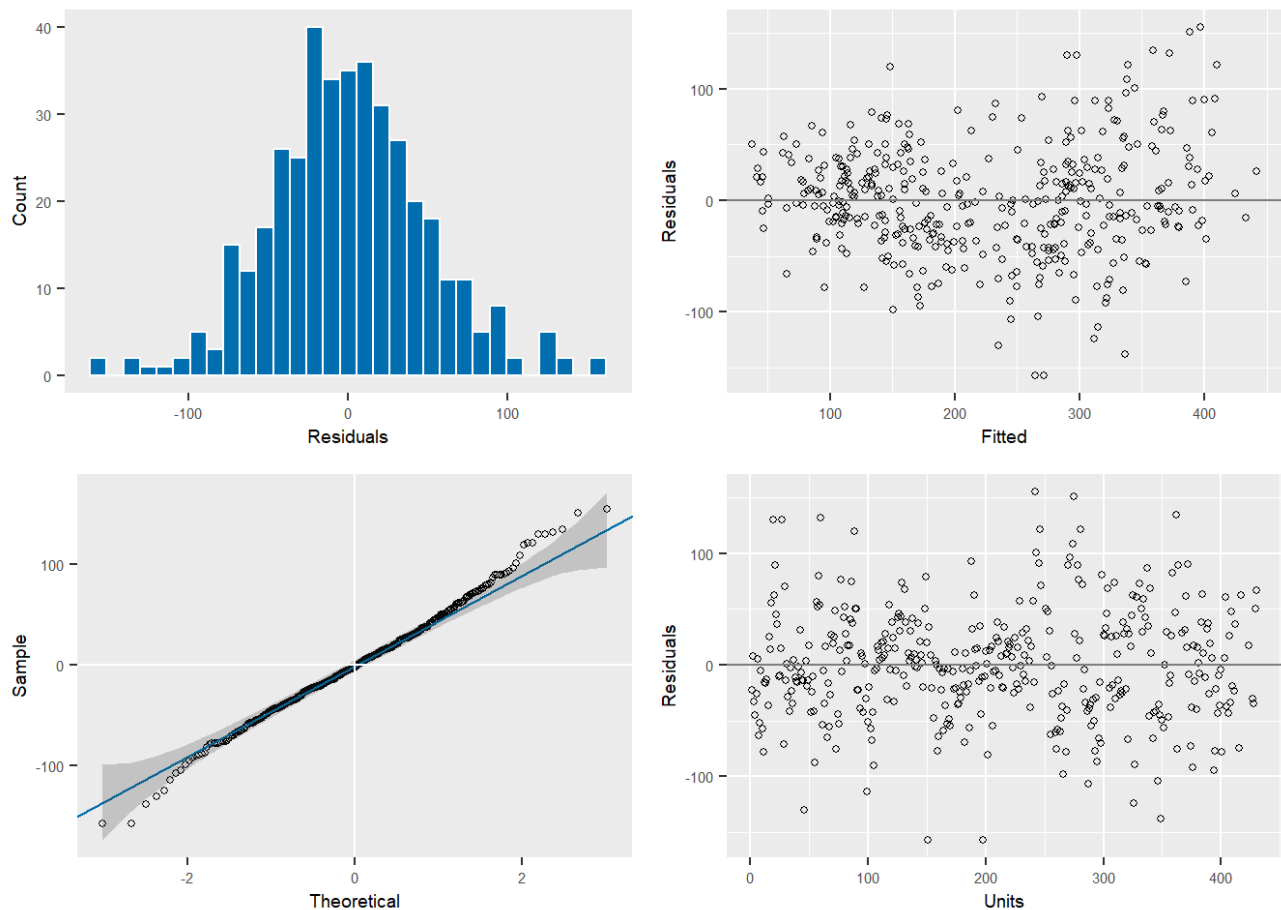
3. Linear models with asreml library

```
modasreml <- asreml(fixed = DW_plant_g ~ Genotype,
                    random = ~ Row + Column,
                    residual = ~ NULL,
                    data = endpoint_clean)
```



```
## ASReml Version 4.2 09/06/2024 16:52:50
##           LogLik       Sigma2      DF      wall
##  1      -1724.877      3146.414     368    16:52:50
##  2      -1723.898      3087.767     368    16:52:50
##  3      -1723.014      3018.866     368    16:52:50
##  4      -1722.585      2960.176     368    16:52:50
##  5      -1722.551      2950.647     368    16:52:50
##  6      -1722.551      2949.770     368    16:52:50
```

```
plot(modasrem1)
```



```
summary(modasrem1)$varcomp
```

```
##           component std.error  z.ratio bound %ch
## Row           826.4668  479.3949  1.723979    P    0
## Column          483.4594  183.1306  2.639971    P    0
## units!R        2949.7698  240.1935 12.280804    P    0
```

4. Linear models with Soil variable

Model with Soil as explicative variable.

5. Linear models with Soil variable with Plant_type

```
fit_models_for_soil_planttype <- function(data, trait) {
  # Base model with Soil as fixed effect and Row, Column as random effects
  mod0 <- lmer(as.formula(paste(trait, "~ Soil + (1|Row) + (1|Column)")), data = data)
  print(paste("Summary for base model of", trait))
  print(summary(mod0))
  print("Random effects ANOVA for base model:")
  print(ranova(mod0))

  # Model with Plant_type and Soil interaction
  mod1 <- lmer(as.formula(paste(trait, "~ Plant_type * Soil + (1|Row) + (1|Column)")),
data = data)
  print(paste("Summary for interaction model of", trait))
  print(summary(mod1))
  print("Random effects ANOVA for interaction model:")
  print(ranova(mod1))

  # Model with Plant_type and Soil without interaction
  mod2 <- lmer(as.formula(paste(trait, "~ Plant_type + Soil + (1|Row) + (1|Column)")),
data = data)
  print(paste("Summary for no interaction model of", trait))
  print(summary(mod2))
  print("Random effects ANOVA for no interaction model:")
  print(ranova(mod2))
}

# Iterate through each variable and fit models
for (trait in variables) {
  fit_models_for_soil_planttype(endpoint_clean, trait)
}
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## [1] "Summary for base model of DW_plant_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: as.formula(paste(trait, "~ Soil + (1|Row) + (1|Column)"))
## Data: data
##
## REML criterion at convergence: 4827.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.65278 -0.76888 -0.03531  0.77963  2.60128
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)          0.0      0.00
## Row      (Intercept)    923.5     30.39
## Residual                    11157.7  105.63
## Number of obs: 398, groups: Column, 60; Row, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   211.80      14.11  11.98  15.006 3.94e-09 ***
## SoilWD2       -18.48      14.34  338.59  -1.289   0.198
## SoilWW         68.50      13.59  393.34   5.042 7.04e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) SolWD2
## SoilWD2 -0.441
## SoilWW  -0.395  0.334
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## [1] "Random effects ANOVA for base model:"
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_plant_g ~ Soil + (1 | Row) + (1 | Column)
##           npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>         6 -2413.8 4839.6
## (1 | Row)       5 -2420.5 4851.0 13.345  1  0.0002591 ***
## (1 | Column)    5 -2413.8 4837.6  0.000  1  1.0000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for interaction model of DW_plant_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: as.formula(paste(trait, "~ Plant_type * Soil + (1|Row) + (1|Column)"))
##   Data: data
##
## REML criterion at convergence: 4342.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.4512 -0.5399 -0.0247  0.5090  2.7414
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Column   (Intercept)         753.8    27.45
##   Row      (Intercept)         637.8    25.25
##   Residual                    3204.3    56.61
## Number of obs: 398, groups:  Column, 60; Row, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)      140.71      28.61 238.79   4.919 1.62e-06 ***
## Plant_typeH       141.67      29.03 357.16   4.881 1.60e-06 ***
## Plant_typeL        -1.22      27.62 362.98  -0.044   0.965
## SoilWD2           12.14      38.25 367.80   0.317   0.751
## SoilWW            41.94      41.21 359.66   1.018   0.309
## Plant_typeH:SoilWD2 -4.71      40.17 366.15  -0.117   0.907
## Plant_typeL:SoilWD2 -18.71     39.17 366.11  -0.478   0.633
## Plant_typeH:SoilWW  60.37      45.79 316.77   1.318   0.188
## Plant_typeL:SoilWW -20.95      41.09 357.41  -0.510   0.610
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L SolWD2 SoilWW P_H:SWD P_L:SWD P_H:SWW
## Plant_typeH -0.901
## Plant_typeL -0.896  0.884
## SoilWD2     -0.673  0.682  0.678
## SoilWW      -0.631  0.670  0.614  0.469
## Plnt_H:SWD2  0.653 -0.720 -0.644 -0.955 -0.471
## Plnt_L:SWD2  0.640 -0.634 -0.713 -0.956 -0.437  0.910
## Plnt_tH:SWW  0.600 -0.702 -0.552 -0.446 -0.955  0.486   0.394
## Plnt_tL:SWW  0.592 -0.585 -0.661 -0.444 -0.927  0.421   0.467   0.834
## [1] "Random effects ANOVA for interaction model:"
## ANOVA-like table for random-effects: Single term deletions
```

```
##
## Model:
## DW_plant_g ~ Plant_type + Soil + (1 | Row) + (1 | Column) + Plant_type:Soil
##           npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>      12 -2171.3 4366.7
## (1 | Row)    11 -2189.1 4400.2 35.511  1  2.536e-09 ***
## (1 | Column) 11 -2184.0 4390.0 25.312  1  4.876e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for no interaction model of DW_plant_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: as.formula(paste(trait, "~ Plant_type + Soil + (1|Row) + (1|Column)"))
##   Data: data
##
## REML criterion at convergence: 4387.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3379 -0.5645 -0.0047  0.5625  2.8938
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   Column   (Intercept) 754.7    27.47
##   Row       (Intercept) 826.0    28.74
##   Residual                3259.6   57.09
## Number of obs: 398, groups:  Column, 60; Row, 8
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)  138.671    19.667   70.710   7.051 9.64e-10 ***
## Plant_typeH  159.456    16.521  361.137   9.652 < 2e-16 ***
## Plant_typeL  -14.207    16.562  363.203  -0.858   0.392
## SoilWD2       2.501     8.087  344.776   0.309   0.757
## SoilWW       65.697     7.464  337.715   8.802 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L SolWD2
## Plant_typeH -0.784
## Plant_typeL -0.783  0.934
## SoilWD2     -0.177  0.019 -0.012
## SoilWW     -0.152 -0.002  0.002  0.302
## [1] "Random effects ANOVA for no interaction model:"
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_plant_g ~ Plant_type + Soil + (1 | Row) + (1 | Column)
##           npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>       8 -2194.0 4403.9
## (1 | Row)     7 -2217.9 4449.7 47.793  1  4.737e-12 ***
## (1 | Column)  7 -2206.4 4426.9 24.991  1  5.759e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```