

Statistical modeling for phenotypic traits

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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_shoot_g" "FW_shoot_g" "DW_root_g"
```

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

```
## [1] EPPN2_H EPPN4_H EPPN2_L EPPN20_T EPPN1_L EPPN4_L EPPN1_H EPPN3_L  
## [9] EPPN3_H  
## 9 Levels: EPPN1_H EPPN1_L EPPN2_H EPPN2_L EPPN20_T EPPN3_H EPPN3_L ... EPPN4_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_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.12822 -0.02098  0.00000  0.02098  0.12822
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.767458   0.113894   6.738 1.48e-06 ***
## GenotypeEPPN1_L -0.189164   0.064118  -2.950 0.007912 **
## GenotypeEPPN2_H -0.216858   0.076730  -2.826 0.010433 *
## GenotypeEPPN2_L -0.361910   0.076394  -4.737 0.000126 ***
## GenotypeEPPN20_T -0.352060   0.075478  -4.664 0.000149 ***
## GenotypeEPPN3_H -0.020396   0.070912  -0.288 0.776596
## GenotypeEPPN3_L -0.260712   0.080673  -3.232 0.004182 **
## GenotypeEPPN4_H -0.008273   0.063898  -0.129 0.898276
## GenotypeEPPN4_L -0.486118   0.080919  -6.007 7.13e-06 ***
## Row2           -0.192377   0.108376  -1.775 0.091104 .
## Row3           -0.054708   0.115152  -0.475 0.639869
## Row4           -0.300415   0.116679  -2.575 0.018088 *
## Row5           -0.046516   0.139891  -0.333 0.742960
## Row6            0.124852   0.118917   1.050 0.306279
## Row7            0.064636   0.139054   0.465 0.647077
## Row8            0.030472   0.120957   0.252 0.803672
## Row9            0.011472   0.144233   0.080 0.937394
## Row10          -0.086495   0.122905  -0.704 0.489697
## Row11           0.099839   0.122579   0.814 0.424958
## Row12           0.057060   0.139035   0.410 0.685876
## Row13           0.046948   0.116754   0.402 0.691865
## Row14           0.031766   0.107089   0.297 0.769804
## Row15           0.055272   0.120957   0.457 0.652629
## Row16           0.040724   0.114991   0.354 0.726935
## Row17          -0.064059   0.108374  -0.591 0.561080
## Row18          -0.126213   0.120409  -1.048 0.307047
## Row19          -0.102589   0.119935  -0.855 0.402476
## Row20          -0.012161   0.122579  -0.099 0.921958
## Row21          -0.060382   0.118620  -0.509 0.616296
## Row22           0.131368   0.109171   1.203 0.242904
## Row23           0.104515   0.134770   0.776 0.447117
## Row24           0.013891   0.119435   0.116 0.908568
## Row25           0.001192   0.115152   0.010 0.991843
## Row26           0.192372   0.144233   1.334 0.197274
## Row27          -0.077784   0.107089  -0.726 0.476040
## Row28           0.029316   0.107089   0.274 0.787079
## Row29          -0.085307   0.121347  -0.703 0.490161
## Row30          -0.013607   0.121347  -0.112 0.911839
## Row31          -0.060708   0.109438  -0.555 0.585235
## Row32          -0.038182   0.118620  -0.322 0.750879
## Row33           0.103448   0.119828   0.863 0.398207
## Row34          -0.067256   0.117613  -0.572 0.573800
## Row35           0.010646   0.116605   0.091 0.928162
## Row36          -0.197047   0.126358  -1.559 0.134578
```

```
## Column2          -0.026331    0.022675   -1.161 0.259232
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08417 on 20 degrees of freedom
## (7 observations effacées parce que manquantes)
## Multiple R-squared:  0.9334, Adjusted R-squared:  0.787
## F-statistic: 6.375 on 44 and 20 DF,  p-value: 2.054e-05
##
## Analysis of Variance Table
##
## Response: DW_shoot_g
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   8 1.53177  0.191472  27.0273 4.258e-09 ***
## Row        35 0.44595  0.012741   1.7985  0.08317 .
## Column     1 0.00955  0.009552   1.3484  0.25923
## Residuals 20 0.14169  0.007084
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of FW_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8792 -0.2983  0.0000  0.2983  0.8792
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    9.4315     0.8786  10.735 5.42e-09 ***
## GenotypeEPPN1_L -2.2954     0.6115  -3.753 0.001583 **
## GenotypeEPPN2_H -3.0737     0.7248  -4.241 0.000551 ***
## GenotypeEPPN2_L -6.3665     0.7221  -8.816 9.49e-08 ***
## GenotypeEPPN20_T -5.2627     0.7339  -7.171 1.57e-06 ***
## GenotypeEPPN3_H -0.1240     0.6727  -0.184 0.855933
## GenotypeEPPN3_L -2.6685     0.7793  -3.424 0.003234 **
## GenotypeEPPN4_H -1.1562     0.6115  -1.891 0.075830 .
## GenotypeEPPN4_L -6.0556     1.0435  -5.803 2.12e-05 ***
## Row2            -1.1352     0.8524  -1.332 0.200506
## Row3             1.1495     0.8396   1.369 0.188803
## Row4            -2.3967     0.9134  -2.624 0.017780 *
## Row5             0.5619     0.9237   0.608 0.551028
## Row6             0.7041     1.3278   0.530 0.602778
## Row7             2.1868     1.1312   1.933 0.070046 .
## Row8             1.1319     1.0084   1.122 0.277271
## Row9             2.2413     1.1917   1.881 0.077244 .
## Row10            0.1569     0.9720   0.161 0.873666
## Row11            2.5376     0.9615   2.639 0.017217 *
## Row12            0.6841     1.3278   0.515 0.613038
## Row13            2.1312     0.8525   2.500 0.022951 *
## Row14            1.3481     0.8393   1.606 0.126630
## Row15            1.2269     1.3251   0.926 0.367451
## Row16            2.5043     0.8964   2.794 0.012469 *
## Row17            0.4350     0.7941   0.548 0.590979
## Row18           -0.7554     0.9433  -0.801 0.434326
```

```

## Row19      -0.3439      0.9410  -0.365  0.719315
## Row20      1.3776      0.9615   1.433  0.170034
## Row21      0.3824      0.8566   0.446  0.660927
## Row22      2.6145      0.8537   3.062  0.007049 **
## Row23      2.7146      1.1267   2.409  0.027602 *
## Row24      2.1800      0.9403   2.318  0.033150 *
## Row25      1.7495      0.8396   2.084  0.052598 .
## Row27     -2.2378      1.0173  -2.200  0.041943 *
## Row28      1.5231      0.8393   1.815  0.087243 .
## Row29      0.6230      0.9593   0.649  0.524736
## Row30      1.7430      0.9593   1.817  0.086888 .
## Row31      0.2110      0.8574   0.246  0.808580
## Row32     -0.1930      1.1471  -0.168  0.868364
## Row33      1.5439      1.1319   1.364  0.190333
## Row34      0.5159      0.8537   0.604  0.553610
## Row35      1.2391      0.9785   1.266  0.222477
## Row36     -1.3061      1.0161  -1.285  0.215870
## Column2    -0.8628      0.2244  -3.845  0.001298 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7941 on 17 degrees of freedom
## (11 observations effacées parce que manquantes)
## Multiple R-squared:  0.9722, Adjusted R-squared:  0.9018
## F-statistic: 13.81 on 43 and 17 DF,  p-value: 2.396e-07
##
## Analysis of Variance Table
##
## Response: FW_shoot_g
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   8 295.444  36.931 58.5574 7.354e-11 ***
## Row        34  69.787   2.053  3.2546 0.006025 **
## Column      1   9.324   9.324 14.7835 0.001298 **
## Residuals 17  10.721   0.631
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of DW_root_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.024348 -0.006685  0.000000  0.006685  0.024348
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.1012181  0.0187501   5.398 1.52e-05 ***
## GenotypeEPPN1_L -0.0178808  0.0142396  -1.256 0.221310
## GenotypeEPPN2_H -0.0273135  0.0152470  -1.791 0.085850 .
## GenotypeEPPN2_L -0.0446991  0.0151326  -2.954 0.006923 **
## GenotypeEPPN20_T -0.0572405  0.0150790  -3.796 0.000881 ***
## GenotypeEPPN3_H -0.0077210  0.0145120  -0.532 0.599589
## GenotypeEPPN3_L -0.0321970  0.0147364  -2.185 0.038897 *
## GenotypeEPPN4_H -0.0052103  0.0125302  -0.416 0.681239
## GenotypeEPPN4_L -0.0518541  0.0135730  -3.820 0.000829 ***

```

```

## Row2          -0.0248944  0.0184058 -1.353 0.188812
## Row3           0.0156635  0.0181173  0.865 0.395840
## Row4          -0.0283756  0.0196621 -1.443 0.161903
## Row5           0.0041326  0.0196608  0.210 0.835291
## Row6           0.0369759  0.0199434  1.854 0.076064 .
## Row7           0.0289863  0.0243794  1.189 0.246083
## Row8           0.0356692  0.0198877  1.794 0.085500 .
## Row9           0.0069055  0.0256678  0.269 0.790203
## Row10          0.0011042  0.0209384  0.053 0.958379
## Row11          0.0292055  0.0256678  1.138 0.266424
## Row12          0.0080692  0.0198877  0.406 0.688529
## Row13          0.0178984  0.0184138  0.972 0.340740
## Row14          0.0208707  0.0182127  1.146 0.263118
## Row15          0.0376692  0.0198877  1.894 0.070326 .
## Row16          0.0244191  0.0192120  1.271 0.215899
## Row17          0.0019000  0.0173294  0.110 0.913606
## Row18          0.0047946  0.0202960  0.236 0.815256
## Row19          -0.0032973  0.0200042 -0.165 0.870457
## Row20          0.0204341  0.0204776  0.998 0.328294
## Row21          0.0025917  0.0183970  0.141 0.889141
## Row22          0.0302408  0.0184942  1.635 0.115067
## Row23          0.0624759  0.0199434  3.133 0.004519 **
## Row24          -0.0084407  0.0202079 -0.418 0.679887
## Row25          0.0124635  0.0181173  0.688 0.498091
## Row26          0.0067208  0.0205585  0.327 0.746571
## Row27          0.0077207  0.0182127  0.424 0.675402
## Row28          0.0290207  0.0182127  1.593 0.124150
## Row29          -0.0009011  0.0205720 -0.044 0.965423
## Row30          0.0127989  0.0205720  0.622 0.539711
## Row31          0.0353989  0.0182690  1.938 0.064520 .
## Row32          0.0053917  0.0183970  0.293 0.771982
## Row33          0.0405111  0.0199336  2.032 0.053331 .
## Row34          0.0123337  0.0185301  0.666 0.512014
## Row35          0.0143910  0.0193038  0.746 0.463209
## Row36          -0.0111853  0.0219438 -0.510 0.614900
## Column2        -0.0110236  0.0042888 -2.570 0.016792 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01733 on 24 degrees of freedom
## (3 observations effacées parce que manquantes)
## Multiple R-squared:  0.8535, Adjusted R-squared:  0.585
## F-statistic: 3.178 on 44 and 24 DF, p-value: 0.001697
##
## Analysis of Variance Table
##
## Response: DW_root_g
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype   8 0.0225283 0.00281603  9.3772 8.764e-06 ***
## Row       35 0.0174824 0.00049950  1.6633  0.09764 .
## Column     1 0.0019840 0.00198400  6.6066  0.01679 *
## Residuals 24 0.0072074 0.00030031
## ---
## 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_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##   Data: data
##
## REML criterion at convergence: -79
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7007 -0.3612 -0.0930  0.4261  2.1097
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Row      (Intercept) 2.896e-03 0.053816
##   Column   (Intercept) 4.335e-05 0.006584
##   Residual                    7.800e-03 0.088320
## Number of obs: 65, groups: Row, 36; Column, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    0.76734    0.03858 40.54313  19.888 < 2e-16 ***
## GenotypeEPPN1_L -0.18528    0.05177 41.44873  -3.579 0.000896 ***
## GenotypeEPPN2_H -0.25391    0.05217 52.57898  -4.867 1.07e-05 ***
## GenotypeEPPN2_L -0.40255    0.05375 51.93073  -7.489 8.29e-10 ***
## GenotypeEPPN20_T -0.40088    0.05213 52.27958  -7.690 3.81e-10 ***
## GenotypeEPPN3_H -0.14943    0.05360 50.23468  -2.788 0.007468 **
## GenotypeEPPN3_L -0.29998    0.05399 53.61769  -5.556 8.84e-07 ***
## GenotypeEPPN4_H -0.02008    0.05026 42.41971  -0.400 0.691472
## GenotypeEPPN4_L -0.45416    0.05602 52.18692  -8.107 8.43e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) GEPPN1 GEPPN2_H GEPPN2_L GEPPN20 GEPPN3_H GEPPN3_L GEPPN4_H
## GntyEPPN1_L -0.675
## GntyEPPN2_H -0.724  0.516
## GntyEPPN2_L -0.703  0.503  0.541
## GntEPPN20_T -0.725  0.502  0.583  0.556
## GntyEPPN3_H -0.675  0.485  0.500  0.486  0.517
## GntyEPPN3_L -0.702  0.486  0.536  0.542  0.524  0.502
## GntyEPPN4_H -0.703  0.485  0.536  0.522  0.539  0.502  0.506
## GntyEPPN4_L -0.674  0.485  0.501  0.487  0.517  0.466  0.525  0.502
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Genotype  1.1449 0.14311      8 45.201  18.347 7.345e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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



```

## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>          12 39.510 -55.020
## (1 | Row)        11 38.804 -55.608 1.41206 1      0.2347
## (1 | Column)     11 39.504 -57.008 0.01261 1      0.9106
## [1] "Summary for random effects model of FW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##   Data: data
##
## REML criterion at convergence: 185.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.33508 -0.49096  0.03622  0.46413  2.04305
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   Row      (Intercept) 0.9824   0.9911
##   Column   (Intercept) 0.2453   0.4952
##   Residual                0.6989   0.8360
## Number of obs: 61, groups: Row, 35; Column, 2
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    10.2469     0.5823  6.0030  17.596 2.15e-06 ***
## GenotypeEPPN1_L -2.4515     0.5498 26.7933  -4.459 0.000132 ***
## GenotypeEPPN2_H -3.7752     0.5978 34.9967  -6.315 2.98e-07 ***
## GenotypeEPPN2_L -6.7439     0.6095 32.8869 -11.065 1.27e-12 ***
## GenotypeEPPN20_T -5.6357     0.6112 33.4766  -9.220 1.04e-10 ***
## GenotypeEPPN3_H -1.1749     0.5979 29.3524  -1.965 0.058952 .
## GenotypeEPPN3_L -3.4396     0.6381 34.7880  -5.390 5.01e-06 ***
## GenotypeEPPN4_H -1.1856     0.5586 25.2393  -2.122 0.043804 *
## GenotypeEPPN4_L -6.4067     0.7055 46.3418  -9.081 7.44e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) GEPPN1 GEPPN2_H GEPPN2_L GEPPN20 GEPPN3_H GEPPN3_L GEPPN4_H
## GntyEPPN1_L -0.552
## GntyEPPN2_H -0.592  0.569
## GntyEPPN2_L -0.577  0.559  0.640
## GntEPPN20_T -0.578  0.527  0.636  0.631
## GntyEPPN3_H -0.531  0.519  0.522  0.508  0.540
## GntyEPPN3_L -0.557  0.547  0.581  0.570  0.539  0.531
## GntyEPPN4_H -0.531  0.478  0.557  0.549  0.553  0.504  0.484
## GntyEPPN4_L -0.519  0.461  0.503  0.493  0.536  0.447  0.525  0.444
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Genotype 148.75  18.594      8 28.848  26.606 2.495e-11 ***
## ---

```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##               npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>         12 -92.958 209.92
## (1 | Row)       11 -95.985 213.97 6.0533  1   0.01388 *
## (1 | Column)   11 -95.295 212.59 4.6737  1   0.03063 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for random effects model of DW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##   Data: data
##
## REML criterion at convergence: -277.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6900 -0.4987 -0.0226  0.4568  2.0077
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Row      (Intercept) 1.048e-04 0.01024
##   Column   (Intercept) 4.121e-05 0.00642
##   Residual                    3.191e-04 0.01786
## Number of obs: 69, groups: Row, 36; Column, 2
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   0.107424   0.008890  9.050161  12.084 6.90e-07 ***
## GenotypeEPPN1_L -0.011087   0.010567  52.497669  -1.049 0.298885
## GenotypeEPPN2_H -0.026362   0.010419  56.940978  -2.530 0.014189 *
## GenotypeEPPN2_L -0.046476   0.010414  56.768034  -4.463 3.89e-05 ***
## GenotypeEPPN20_T -0.056975   0.010413  56.722828  -5.472 1.05e-06 ***
## GenotypeEPPN3_H -0.023500   0.010727  55.682921  -2.191 0.032670 *
## GenotypeEPPN3_L -0.028186   0.010405  56.403369  -2.709 0.008924 **
## GenotypeEPPN4_H -0.002301   0.010058  46.347461  -0.229 0.820075
## GenotypeEPPN4_L -0.037089   0.010232  52.027803  -3.625 0.000658 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) GEPPN1 GEPPN2_H GEPPN2_L GEPPN20 GEPPN3_H GEPPN3_L GEPPN4_H
## GntyEPPN1_L -0.597
## GntyEPPN2_H -0.628  0.526
## GntyEPPN2_L -0.628  0.527  0.568
## GntEPPN20_T -0.628  0.511  0.580  0.566
## GntyEPPN3_H -0.586  0.495  0.502  0.502  0.516
## GntyEPPN3_L -0.628  0.527  0.551  0.565  0.539  0.516
## GntyEPPN4_H -0.610  0.496  0.537  0.536  0.538  0.502  0.523
## GntyEPPN4_L -0.619  0.518  0.530  0.531  0.542  0.494  0.570  0.542
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq   Mean Sq NumDF   DenDF F value    Pr(>F)

```

```
## Genotype 0.017868 0.0022335      8 49.559 7.0004 3.862e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_root_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>         12 138.69 -253.37
## (1 | Row)       11 137.99 -253.97 1.3950  1    0.2376
## (1 | Column)   11 137.53 -253.07 2.3003  1    0.1293
```

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)
}
```

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

```
## [1] "Summary for mixed effects model of DW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
## Data: data
##
## REML criterion at convergence: -58.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.12320 -0.59604 -0.02325  0.58562  2.13101
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Row      (Intercept) 3.076e-03 5.546e-02
## Column   (Intercept) 7.633e-12 2.763e-06
## Residual                    1.684e-02 1.298e-01
## Number of obs: 65, groups: Row, 36; Column, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.37698    0.04940 60.99723   7.631 1.90e-10 ***
## Plant_typeH  0.27608    0.05476 54.20494   5.042 5.48e-06 ***
## Plant_typeL  0.06298    0.05587 58.31092   1.127  0.264
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.876
## Plant_typeL -0.867  0.772
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 0.74711 0.37355      2 59.683 22.176 6.286e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Plant_type + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>          6 29.421 -46.841
## (1 | Row)       5 29.149 -48.299 0.54202  1    0.4616
## (1 | Column)    5 29.421 -48.841 0.00000  1    1.0000
## [1] "Summary for mixed effects model of FW_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##   Data: data
##
## REML criterion at convergence: 255
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6206 -0.6481  0.1484  0.5771  1.5833
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
##   Row      (Intercept) 1.78927  1.3376
##   Column   (Intercept) 0.09104  0.3017
##   Residual                2.60285  1.6133
## Number of obs: 61, groups:  Row, 35; Column, 2
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   5.2070     0.7662 26.5879   6.796 2.9e-07 ***
## Plant_typeH    3.1742     0.7884 37.8544   4.026 0.000262 ***
## Plant_typeL    0.5227     0.8005 39.6711   0.653 0.517544
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.822
## Plant_typeL -0.820  0.775
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 81.934  40.967     2 42.836  15.739 7.507e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Plant_type + (1 | Row) + (1 | Column)
##           npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>         6 -127.51 267.03
## (1 | Row)       5 -129.16 268.33 3.2984  1    0.06935 .
## (1 | Column)    5 -127.65 265.30 0.2709  1    0.60271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for mixed effects model of DW_root_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##   Data: data
##
## REML criterion at convergence: -300.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7168 -0.7047  0.1348  0.5591  2.2471
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Row      (Intercept) 1.521e-04 0.01233
##   Column   (Intercept) 3.612e-05 0.00601
##   Residual                    3.949e-04 0.01987
## Number of obs: 69, groups:  Row, 36; Column, 2
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.053020   0.009057 10.824813   5.854 0.000118 ***
## Plant_typeH  0.041114   0.008730 52.575617   4.709 1.85e-05 ***
## Plant_typeL  0.022947   0.008861 57.740510   2.590 0.012136 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.763
## Plant_typeL -0.767  0.779
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq   Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 0.0099298 0.0049649     2 58.836 12.573 2.842e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_root_g ~ Plant_type + (1 | Row) + (1 | Column)
##           npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>         6 150.41 -288.83
## (1 | Row)       5 149.27 -288.54 2.2903  1    0.1302
## (1 | Column)    5 149.67 -289.34 1.4925  1    0.2218
```

3. Linear models with asreml library

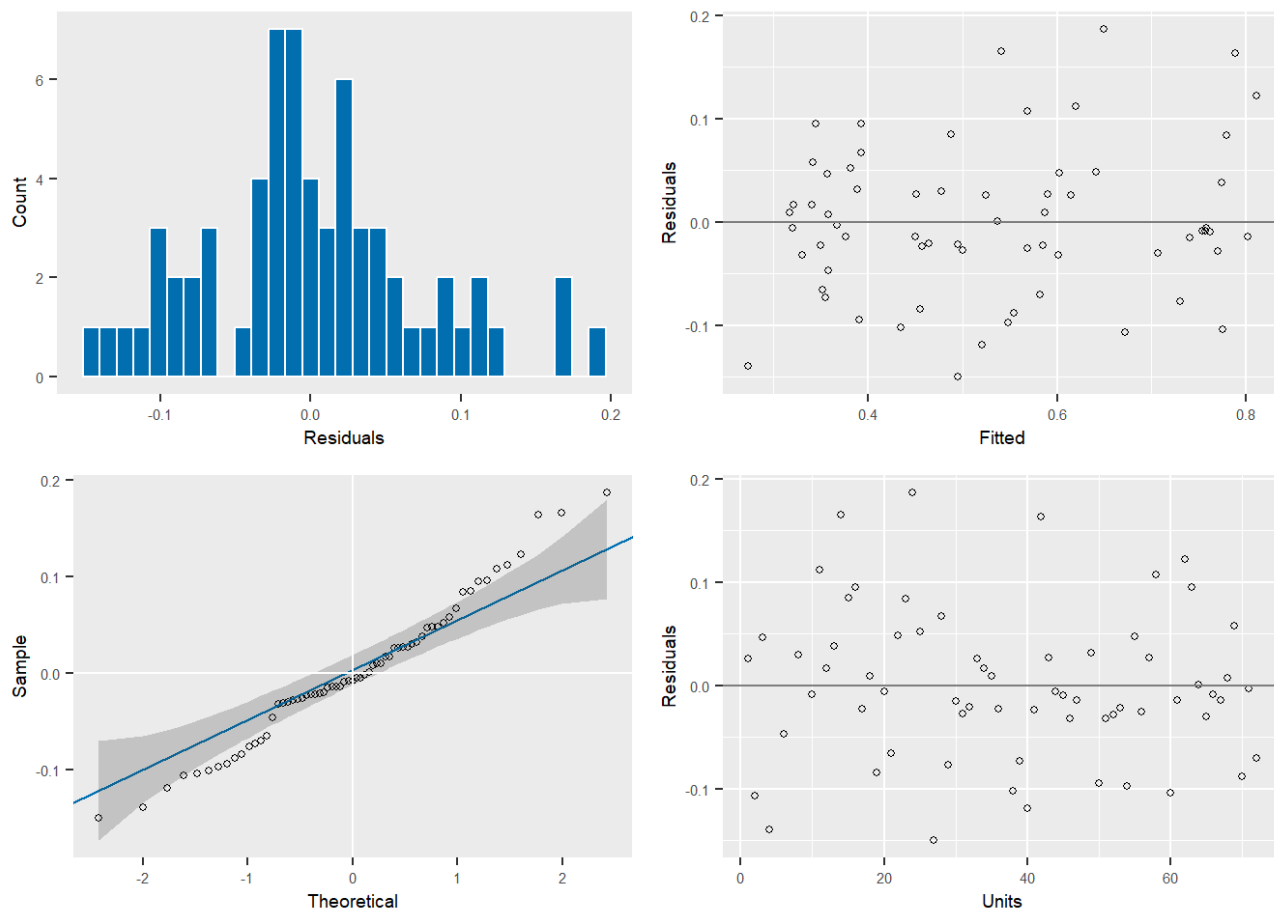
```
modasreml <- asreml(fixed = DW_shoot_g ~ Genotype,
  random = ~ Row + Column,
  residual = ~ NULL,
  data = endpoint_clean)
```

```
## ASReml Version 4.2 09/06/2024 17:09:05
```

```
##          LogLik      Sigma2    DF    wall
## 1      90.29639  0.009474445   56 17:09:05 ( 1 restrained)
## 2      90.81161  0.008973540   56 17:09:05
## 3      90.96622  0.007992394   56 17:09:05
## 4      90.97070  0.007820720   56 17:09:05
```

```
## Warning in asreml(fixed = DW_shoot_g ~ Genotype, random = ~Row + Column, : Some
## components changed by more than 1% on the last iteration
```

```
plot(modasreml)
```



```
summary(modasreml)$varcomp
```

```
##          component  std.error  z.ratio bound %ch
## Column  0.0000432757 0.0004212441 0.1027331    P 3.3
## Row      0.0029004850 0.0024077707 1.2046350    P 1.0
## units!R 0.0078207199 0.0024042357 3.2528923    P 0.0
```

4. Linear models with Soil variable

Model with Soil as explicative variable.

5. Linear models with Soil variable with Plant_type