

Statistical modeling for phenotypic traits

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4PMI_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_shoot_g" "DW_root_g" "Leaf_number" "DW_seed_g"
```

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

```
## [1] 4L 11H 7H 14H 12L 6L 12H 6H 23T 10L 9H 2L 1L 8H 10H 24T 11L 14L 13L
## [20] 3L 9L 7L 3H 1H 8L 15H 5L 15L 5H 4H 20T 13H 2H
## 33 Levels: 10H 10L 11H 11L 12H 12L 13H 13L 14H 14L 15H 15L 1H 1L 20T ... 9L
```

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
## -0.162622 -0.034347  0.002644  0.037865  0.232914
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.269506   0.029534   9.125 < 2e-16 ***
## Genotype10L -0.136411   0.028550  -4.778 3.07e-06 ***
## Genotype11H  0.050218   0.030363   1.654 0.099440 .
## Genotype11L -0.192004   0.028702  -6.690 1.53e-10 ***
## Genotype12H -0.101326   0.028824  -3.515 0.000524 ***
## Genotype12L -0.198454   0.030680  -6.468 5.40e-10 ***
## Genotype13H -0.020527   0.028957  -0.709 0.479079
## Genotype13L -0.232150   0.029445  -7.884 1.07e-13 ***
## Genotype14H -0.089527   0.028851  -3.103 0.002142 **
## Genotype14L -0.292603   0.031568  -9.269 < 2e-16 ***
## Genotype15H -0.095888   0.028445  -3.371 0.000871 ***
## Genotype15L -0.133000   0.029539  -4.503 1.04e-05 ***
## Genotype1H  -0.063350   0.028941  -2.189 0.029552 *
## Genotype1L  -0.161428   0.028671  -5.630 4.95e-08 ***
## Genotype20T -0.194854   0.028487  -6.840 6.37e-11 ***
## Genotype23T -0.007090   0.030543  -0.232 0.816627
## Genotype24T -0.183595   0.029621  -6.198 2.43e-09 ***
## Genotype2H  -0.121787   0.029464  -4.133 4.92e-05 ***
## Genotype2L  -0.163831   0.028231  -5.803 2.02e-08 ***
## Genotype3H  -0.089941   0.028539  -3.152 0.001828 **
## Genotype3L  -0.191364   0.028629  -6.684 1.58e-10 ***
## Genotype4H  -0.081549   0.029390  -2.775 0.005954 **
## Genotype4L  -0.256518   0.028691  -8.941 < 2e-16 ***
## Genotype5H   0.051377   0.028818   1.783 0.075868 .
## Genotype5L  -0.184727   0.028863  -6.400 7.93e-10 ***
## Genotype6H  -0.029144   0.028770  -1.013 0.312062
## Genotype6L  -0.155576   0.033486  -4.646 5.55e-06 ***
## Genotype7H  -0.082395   0.028802  -2.861 0.004594 **
## Genotype7L  -0.132776   0.028498  -4.659 5.24e-06 ***
## Genotype8H   0.001185   0.028884   0.041 0.967318
## Genotype8L  -0.178026   0.028821  -6.177 2.73e-09 ***
## Genotype9H  -0.060719   0.028772  -2.110 0.035851 *
## Genotype9L  -0.127632   0.029280  -4.359 1.93e-05 ***
## Row2        -0.006349   0.023505  -0.270 0.787310
## Row3         0.016484   0.024593   0.670 0.503318
## Row4         0.004183   0.023499   0.178 0.858857
## Row5         0.041688   0.023902   1.744 0.082401 .
## Row6         0.039503   0.023540   1.678 0.094606 .
## Row7         0.047998   0.023517   2.041 0.042334 *
## Row8         0.067030   0.023813   2.815 0.005280 **
## Row9         0.105297   0.024109   4.368 1.86e-05 ***
## Row10        0.079740   0.024013   3.321 0.001036 **
## Row11        0.135934   0.023346   5.822 1.83e-08 ***
## Row12        0.086423   0.024863   3.476 0.000603 ***
```

```

## Row13      0.094670    0.024366    3.885 0.000132 ***
## Row14      0.131585    0.023429    5.616 5.32e-08 ***
## Row15      0.124581    0.024376    5.111 6.50e-07 ***
## Row16      0.117617    0.023544    4.996 1.12e-06 ***
## Row17      0.086439    0.023962    3.607 0.000375 ***
## Row18      0.107576    0.024058    4.472 1.19e-05 ***
## Row19      0.103794    0.023305    4.454 1.29e-05 ***
## Row20      0.063386    0.024346    2.603 0.009796 **
## Row21      0.086759    0.023592    3.677 0.000290 ***
## Row22      0.052144    0.024438    2.134 0.033865 *
## Column9    -0.030783    0.019583   -1.572 0.117267
## Column10    0.002688    0.019827    0.136 0.892284
## Column11   -0.004443    0.019323   -0.230 0.818340
## Column12   -0.003037    0.019530   -0.156 0.876538
## Column13   -0.002699    0.019277   -0.140 0.888752
## Column14   -0.021874    0.019838   -1.103 0.271286
## Column15    0.011565    0.019900    0.581 0.561678
## Column16    0.069006    0.020185    3.419 0.000738 ***
## Column17    0.018203    0.020131    0.904 0.366789
## Column18    0.061631    0.019896    3.098 0.002180 **
## Column19    0.043543    0.020104    2.166 0.031292 *
## Column20    0.021774    0.019718    1.104 0.270566
## Column21    0.024601    0.019604    1.255 0.210727
## Column22    0.029276    0.019592    1.494 0.136397
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06214 on 243 degrees of freedom
## (19 observations effacées parce que manquantes)
## Multiple R-squared:  0.7621, Adjusted R-squared:  0.6965
## F-statistic: 11.62 on 67 and 243 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_shoot_g
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   32  2.25198  0.070374  18.2234 < 2.2e-16 ***
## Row         21  0.54159  0.025790   6.6783 6.245e-15 ***
## Column      14  0.21255  0.015182   3.9315 4.464e-06 ***
## Residuals  243  0.93841  0.003862
## ---
## 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
## -0.142177 -0.024704  0.002449  0.025230  0.103772
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.1723361  0.0226170   7.620 5.49e-13 ***
## Genotype10L -0.0904972  0.0219897  -4.115 5.28e-05 ***
## Genotype11H  0.0676554  0.0220671   3.066 0.002412 **

```

## Genotype11L	-0.0686613	0.0222012	-3.093	0.002212	**
## Genotype12H	-0.0274931	0.0234525	-1.172	0.242215	
## Genotype12L	-0.1235987	0.0220782	-5.598	5.77e-08	***
## Genotype13H	0.0522049	0.0223607	2.335	0.020366	*
## Genotype13L	-0.1191855	0.0226286	-5.267	3.03e-07	***
## Genotype14H	-0.0080967	0.0222443	-0.364	0.716177	
## Genotype14L	-0.1954490	0.0242773	-8.051	3.53e-14	***
## Genotype15H	-0.0324401	0.0219942	-1.475	0.141508	
## Genotype15L	-0.0621520	0.0227328	-2.734	0.006711	**
## Genotype1H	-0.0204312	0.0222874	-0.917	0.360189	
## Genotype1L	-0.0514409	0.0221020	-2.327	0.020754	*
## Genotype20T	-0.1212891	0.0219443	-5.527	8.29e-08	***
## Genotype23T	0.0327780	0.0220711	1.485	0.138796	
## Genotype24T	-0.0683418	0.0220759	-3.096	0.002190	**
## Genotype2H	-0.0407390	0.0221841	-1.836	0.067505	.
## Genotype2L	-0.0714928	0.0218201	-3.276	0.001203	**
## Genotype3H	-0.0522300	0.0220914	-2.364	0.018844	*
## Genotype3L	-0.0844624	0.0233503	-3.617	0.000361	***
## Genotype4H	-0.0267836	0.0225121	-1.190	0.235295	
## Genotype4L	-0.1507841	0.0231769	-6.506	4.29e-10	***
## Genotype5H	0.0612362	0.0222203	2.756	0.006292	**
## Genotype5L	-0.1100494	0.0223307	-4.928	1.53e-06	***
## Genotype6H	0.0414939	0.0221312	1.875	0.061991	.
## Genotype6L	-0.0554462	0.0244420	-2.268	0.024167	*
## Genotype7H	-0.0107304	0.0221130	-0.485	0.627929	
## Genotype7L	-0.0595267	0.0219285	-2.715	0.007106	**
## Genotype8H	0.0310646	0.0222349	1.397	0.163638	
## Genotype8L	-0.0828867	0.0221865	-3.736	0.000233	***
## Genotype9H	-0.0035485	0.0221505	-0.160	0.872856	
## Genotype9L	-0.0781718	0.0218862	-3.572	0.000426	***
## Row2	-0.0072173	0.0175855	-0.410	0.681861	
## Row3	-0.0014577	0.0180716	-0.081	0.935777	
## Row4	-0.0090984	0.0175843	-0.517	0.605330	
## Row5	0.0233261	0.0179139	1.302	0.194091	
## Row6	0.0268147	0.0182767	1.467	0.143613	
## Row7	0.0285806	0.0175908	1.625	0.105497	
## Row8	0.0539002	0.0175244	3.076	0.002337	**
## Row9	0.0888980	0.0180393	4.928	1.53e-06	***
## Row10	0.0583650	0.0179826	3.246	0.001335	**
## Row11	0.0914469	0.0174738	5.233	3.57e-07	***
## Row12	0.0691005	0.0177505	3.893	0.000128	***
## Row13	0.0480029	0.0178121	2.695	0.007525	**
## Row14	0.0902544	0.0182617	4.942	1.43e-06	***
## Row15	0.0908931	0.0179015	5.077	7.56e-07	***
## Row16	0.0800044	0.0176243	4.539	8.83e-06	***
## Row17	0.0624628	0.0179294	3.484	0.000585	***
## Row18	0.0935071	0.0184896	5.057	8.32e-07	***
## Row19	0.0795526	0.0174494	4.559	8.10e-06	***
## Row20	0.0470019	0.0177750	2.644	0.008713	**
## Row21	0.0591580	0.0176677	3.348	0.000940	***
## Row22	0.0260360	0.0178975	1.455	0.147021	
## Column9	-0.0243577	0.0146664	-1.661	0.098031	.
## Column10	-0.0048171	0.0146129	-0.330	0.741949	
## Column11	-0.0044733	0.0146732	-0.305	0.760731	
## Column12	-0.0162854	0.0146192	-1.114	0.266380	
## Column13	0.0016860	0.0146292	0.115	0.908341	

```

## Column14    -0.0199091  0.0150760  -1.321  0.187869
## Column15     0.0041022  0.0151546   0.271  0.786856
## Column16     0.0449397  0.0146688   3.064  0.002430 **
## Column17     0.0069440  0.0151038   0.460  0.646100
## Column18     0.0245436  0.0146648   1.674  0.095472 .
## Column19     0.0276490  0.0148459   1.862  0.063739 .
## Column20    -0.0035532  0.0145385  -0.244  0.807126
## Column21    -0.0002353  0.0146653  -0.016  0.987210
## Column22    -0.0015039  0.0144656  -0.104  0.917281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04653 on 246 degrees of freedom
## (16 observations effacées parce que manquantes)
## Multiple R-squared:  0.7597, Adjusted R-squared:  0.6942
## F-statistic: 11.6 on 67 and 246 DF,  p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_root_g
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype     32 1.25799  0.039312 18.1550 < 2.2e-16 ***
## Row           21 0.33250  0.015833  7.3120 < 2.2e-16 ***
## Column        14 0.09311  0.006651  3.0714 0.0002072 ***
## Residuals    246 0.53268  0.002165
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of Leaf_number"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.85344 -0.22412  0.01596  0.24867  1.18167
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  4.482052   0.246022  18.218 < 2e-16 ***
## Genotype10L  -0.656360   0.242859  -2.703  0.007388 **
## Genotype11H   0.061443   0.229060   0.268  0.788751
## Genotype11L  -0.685884   0.243237  -2.820  0.005221 **
## Genotype12H  -0.522630   0.237068  -2.205  0.028468 *
## Genotype12L  -0.291375   0.229893  -1.267  0.206271
## Genotype13H  -0.028109   0.237871  -0.118  0.906036
## Genotype13L  -0.693047   0.283866  -2.441  0.015377 *
## Genotype14H  -0.706678   0.238656  -2.961  0.003384 **
## Genotype14L  -1.670557   0.252732  -6.610  2.61e-10 ***
## Genotype15H  -0.005986   0.227284  -0.026  0.979010
## Genotype15L   0.383654   0.236182   1.624  0.105648
## Genotype1H    0.086528   0.231474   0.374  0.708885
## Genotype1L   -0.334872   0.229311  -1.460  0.145549
## Genotype20T  -0.367300   0.228023  -1.611  0.108583
## Genotype23T  -0.006378   0.236709  -0.027  0.978528
## Genotype24T  -0.706120   0.229357  -3.079  0.002329 **
## Genotype2H   -0.587398   0.235591  -2.493  0.013355 *

```

```

## Genotype2L -0.744553 0.240593 -3.095 0.002212 **
## Genotype3H -0.339334 0.235084 -1.443 0.150240
## Genotype3L -0.441150 0.228705 -1.929 0.054963 .
## Genotype4H 0.199108 0.251714 0.791 0.429747
## Genotype4L -0.920450 0.237222 -3.880 0.000136 ***
## Genotype5H 0.280968 0.236197 1.190 0.235441
## Genotype5L -0.323734 0.230794 -1.403 0.162044
## Genotype6H -0.015560 0.230220 -0.068 0.946173
## Genotype6L 0.034130 0.238106 0.143 0.886146
## Genotype7H -0.256630 0.230360 -1.114 0.266415
## Genotype7L -0.551878 0.244106 -2.261 0.024698 *
## Genotype8H 0.028667 0.230976 0.124 0.901335
## Genotype8L -0.155520 0.230724 -0.674 0.500950
## Genotype9H -0.206988 0.230178 -0.899 0.369450
## Genotype9L -0.643458 0.234128 -2.748 0.006461 **
## Row2 -0.171434 0.207444 -0.826 0.409421
## Row3 -0.128587 0.204123 -0.630 0.529349
## Row4 -0.024221 0.208524 -0.116 0.907632
## Row5 0.206979 0.212290 0.975 0.330585
## Row6 0.051172 0.205828 0.249 0.803880
## Row7 0.150289 0.203523 0.738 0.460996
## Row8 0.261880 0.206975 1.265 0.207044
## Row9 0.426955 0.200919 2.125 0.034643 *
## Row10 0.209563 0.204634 1.024 0.306860
## Row11 0.562539 0.203600 2.763 0.006187 **
## Row12 0.259178 0.202096 1.282 0.200964
## Row13 0.367318 0.206734 1.777 0.076917 .
## Row14 0.541595 0.202210 2.678 0.007927 **
## Row15 0.426665 0.202167 2.110 0.035890 *
## Row16 0.448643 0.207605 2.161 0.031715 *
## Row17 0.452506 0.204947 2.208 0.028229 *
## Row18 0.462366 0.206904 2.235 0.026391 *
## Row19 0.317096 0.203688 1.557 0.120886
## Row20 0.164522 0.202370 0.813 0.417066
## Row21 0.184950 0.201072 0.920 0.358620
## Row22 0.245119 0.204017 1.201 0.230798
## Column9 -0.079508 0.161433 -0.493 0.622823
## Column10 -0.295575 0.156255 -1.892 0.059787 .
## Column11 -0.225035 0.157042 -1.433 0.153216
## Column12 -0.023810 0.160115 -0.149 0.881916
## Column13 -0.162446 0.153994 -1.055 0.292575
## Column14 -0.237532 0.163151 -1.456 0.146773
## Column15 -0.233149 0.166118 -1.404 0.161800
## Column16 0.149282 0.159278 0.937 0.349608
## Column17 -0.170526 0.158115 -1.078 0.281935
## Column18 0.049746 0.161113 0.309 0.757777
## Column19 0.147685 0.161308 0.916 0.360858
## Column20 -0.049047 0.160079 -0.306 0.759580
## Column21 -0.082960 0.158806 -0.522 0.601890
## Column22 0.082774 0.159223 0.520 0.603654
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4964 on 232 degrees of freedom
## (30 observations effacées parce que manquantes)
## Multiple R-squared: 0.5246, Adjusted R-squared: 0.3873

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## F-statistic: 3.821 on 67 and 232 DF,  p-value: 2.202e-14
##
## Analysis of Variance Table
##
## Response: Leaf_number
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   32 46.428  1.45087   5.8881 < 2.2e-16 ***
## Row        21 11.347  0.54035   2.1929 0.002565 **
## Column     14  5.308  0.37914   1.5387 0.098475 .
## Residuals 232 57.167  0.24641
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for fixed effects model of DW_seed_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.038155 -0.007513 -0.000981  0.005777  0.068469
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0180881  0.0087069   2.077 0.038829 *
## Genotype10L  0.0101935  0.0077832   1.310 0.191564
## Genotype11H  0.0013712  0.0078996   0.174 0.862347
## Genotype11L  0.0456495  0.0080803   5.649 4.56e-08 ***
## Genotype12H  0.0029843  0.0079088   0.377 0.706256
## Genotype12L  0.0209513  0.0087016   2.408 0.016810 *
## Genotype13H  0.0112234  0.0081265   1.381 0.168541
## Genotype13L  0.0260373  0.0083124   3.132 0.001950 **
## Genotype14H  0.0252466  0.0081128   3.112 0.002085 **
## Genotype14L  0.0388422  0.0077217   5.030 9.62e-07 ***
## Genotype15H  0.0120990  0.0080597   1.501 0.134630
## Genotype15L  0.0139333  0.0080724   1.726 0.085634 .
## Genotype1H   0.0040293  0.0083041   0.485 0.627967
## Genotype1L   0.0112035  0.0078634   1.425 0.155529
## Genotype20T -0.0027261  0.0079619  -0.342 0.732351
## Genotype23T  0.0100183  0.0079303   1.263 0.207714
## Genotype24T  0.0079156  0.0081038   0.977 0.329663
## Genotype2H   0.0002131  0.0081021   0.026 0.979041
## Genotype2L   0.0361158  0.0077917   4.635 5.87e-06 ***
## Genotype3H   0.0095650  0.0080257   1.192 0.234526
## Genotype3L   0.0310987  0.0080119   3.882 0.000134 ***
## Genotype4H   0.0042275  0.0080132   0.528 0.598294
## Genotype4L   0.0211372  0.0078973   2.677 0.007954 **
## Genotype5H   0.0465367  0.0080950   5.749 2.73e-08 ***
## Genotype5L   0.0586537  0.0079040   7.421 2.03e-12 ***
## Genotype6H   0.0127101  0.0078354   1.622 0.106091
## Genotype6L   0.0295322  0.0078728   3.751 0.000221 ***
## Genotype7H   0.0255033  0.0079020   3.227 0.001424 **
## Genotype7L   0.0529000  0.0078417   6.746 1.14e-10 ***
## Genotype8H   0.0116346  0.0079353   1.466 0.143912
## Genotype8L   0.0279613  0.0081022   3.451 0.000660 ***
## Genotype9H   0.0211317  0.0079372   2.662 0.008286 **
## Genotype9L   0.0565798  0.0078347   7.222 6.82e-12 ***

```



```

## Row2      -0.0014757  0.0066379  -0.222  0.824260
## Row3      0.0024612  0.0062331   0.395  0.693297
## Row4      0.0102011  0.0065362   1.561  0.119914
## Row5      0.0016901  0.0063197   0.267  0.789367
## Row6     -0.0021374  0.0063747  -0.335  0.737697
## Row7     -0.0051920  0.0063795  -0.814  0.416536
## Row8     -0.0005846  0.0062047  -0.094  0.925009
## Row9      0.0085091  0.0062964   1.351  0.177833
## Row10     -0.0015306  0.0062128  -0.246  0.805613
## Row11     -0.0066624  0.0062934  -1.059  0.290834
## Row12     -0.0017793  0.0061921  -0.287  0.774088
## Row13      0.0027764  0.0061788   0.449  0.653586
## Row14     -0.0040112  0.0063419  -0.632  0.527672
## Row15     -0.0018846  0.0066015  -0.285  0.775528
## Row16      0.0027324  0.0063110   0.433  0.665437
## Row17     -0.0060340  0.0061552  -0.980  0.327926
## Row18     -0.0001328  0.0062746  -0.021  0.983128
## Row19     -0.0009553  0.0061563  -0.155  0.876811
## Row20      0.0071378  0.0062443   1.143  0.254146
## Row21     -0.0038659  0.0063873  -0.605  0.545588
## Row22     -0.0031865  0.0064125  -0.497  0.619696
## Column9    0.0071446  0.0050690   1.409  0.159996
## Column10   0.0005656  0.0051156   0.111  0.912049
## Column11   0.0068021  0.0050498   1.347  0.179250
## Column12  -0.0001833  0.0051398  -0.036  0.971587
## Column13   0.0042451  0.0049935   0.850  0.396110
## Column14   0.0063796  0.0049948   1.277  0.202755
## Column15   0.0025382  0.0051396   0.494  0.621866
## Column16  -0.0022655  0.0051605  -0.439  0.661052
## Column17   0.0016110  0.0048974   0.329  0.742473
## Column18  -0.0036885  0.0049387  -0.747  0.455890
## Column19   0.0007921  0.0051224   0.155  0.877236
## Column20  -0.0003963  0.0051639  -0.077  0.938895
## Column21   0.0040998  0.0049580   0.827  0.409118
## Column22   0.0015694  0.0049289   0.318  0.750448
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01539 on 239 degrees of freedom
## (23 observations effacées parce que manquantes)
## Multiple R-squared:  0.6421, Adjusted R-squared:  0.5418
## F-statistic: 6.4 on 67 and 239 DF, p-value: < 2.2e-16
##
## Analysis of Variance Table
##
## Response: DW_seed_g
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## Genotype   32  0.092957  0.00290491 12.2715 <2e-16 ***
## Row        21  0.005683  0.00027063  1.1433  0.3042
## Column     14  0.002858  0.00020417  0.8625  0.6005
## Residuals 239  0.056576  0.00023672
## ---
## 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: -623.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5144 -0.5478  0.0190  0.5546  3.8339
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Row      (Intercept) 0.0015943 0.03993
## Column   (Intercept) 0.0005848 0.02418
## Residual                    0.0038612 0.06214
## Number of obs: 311, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  3.572e-01  2.274e-02  2.309e+02  15.710 < 2e-16 ***
## Genotype10L -1.338e-01  2.839e-02  2.482e+02  -4.713 4.07e-06 ***
## Genotype11H  4.638e-02  3.018e-02  2.487e+02   1.537 0.125561
## Genotype11L -1.933e-01  2.853e-02  2.487e+02  -6.776 8.90e-11 ***
## Genotype12H -1.035e-01  2.862e-02  2.494e+02  -3.616 0.000362 ***
## Genotype12L -1.970e-01  3.044e-02  2.503e+02  -6.472 5.07e-10 ***
## Genotype13H -1.971e-02  2.872e-02  2.505e+02  -0.686 0.493296
## Genotype13L -2.384e-01  2.926e-02  2.489e+02  -8.146 1.83e-14 ***
## Genotype14H -8.710e-02  2.866e-02  2.492e+02  -3.039 0.002625 **
## Genotype14L -2.943e-01  3.137e-02  2.489e+02  -9.382 < 2e-16 ***
## Genotype15H -9.749e-02  2.832e-02  2.473e+02  -3.443 0.000676 ***
## Genotype15L -1.340e-01  2.935e-02  2.488e+02  -4.565 7.86e-06 ***
## Genotype1H   -6.318e-02  2.872e-02  2.500e+02  -2.200 0.028729 *
## Genotype1L   -1.602e-01  2.851e-02  2.484e+02  -5.621 5.09e-08 ***
## Genotype20T -1.943e-01  2.836e-02  2.473e+02  -6.853 5.73e-11 ***
## Genotype23T -1.130e-02  3.033e-02  2.496e+02  -0.373 0.709664
## Genotype24T -1.867e-01  2.941e-02  2.495e+02  -6.348 1.02e-09 ***
## Genotype2H   -1.230e-01  2.929e-02  2.486e+02  -4.199 3.73e-05 ***
## Genotype2L   -1.652e-01  2.814e-02  2.462e+02  -5.871 1.39e-08 ***
## Genotype3H   -9.137e-02  2.838e-02  2.481e+02  -3.219 0.001457 **
## Genotype3L   -1.899e-01  2.847e-02  2.481e+02  -6.671 1.64e-10 ***
## Genotype4H   -7.990e-02  2.924e-02  2.479e+02  -2.733 0.006728 **
## Genotype4L   -2.574e-01  2.852e-02  2.487e+02  -9.025 < 2e-16 ***
## Genotype5H    5.250e-02  2.862e-02  2.493e+02   1.834 0.067815 .
## Genotype5L   -1.874e-01  2.866e-02  2.497e+02  -6.541 3.44e-10 ***
## Genotype6H   -3.098e-02  2.857e-02  2.494e+02  -1.084 0.279257
## Genotype6L   -1.653e-01  3.321e-02  2.507e+02  -4.977 1.20e-06 ***
## Genotype7H   -8.033e-02  2.860e-02  2.497e+02  -2.809 0.005359 **
## Genotype7L   -1.377e-01  2.836e-02  2.477e+02  -4.855 2.13e-06 ***
## Genotype8H    8.725e-04  2.867e-02  2.499e+02   0.030 0.975748
## Genotype8L   -1.826e-01  2.862e-02  2.497e+02  -6.381 8.48e-10 ***
## Genotype9H   -6.402e-02  2.858e-02  2.494e+02  -2.240 0.025942 *
## Genotype9L   -1.308e-01  2.914e-02  2.475e+02  -4.487 1.11e-05 ***
```

```
## ---
```

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

```
##
```

```
## Correlation matrix not shown by default, as p = 33 > 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 2.0256  0.0633     32 248.66  16.394 < 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_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>          36 311.77 -551.54
## (1 | Row)       35 282.23 -494.47 59.073  1  1.520e-14 ***
## (1 | Column)    35 302.42 -534.84 18.696  1  1.533e-05 ***
## ---
## 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: -794.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.01162 -0.53624 -0.01182  0.55458  2.28260
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Row      (Intercept) 0.001026 0.03203
##  Column   (Intercept) 0.000223 0.01493
##  Residual                    0.002166 0.04654
## Number of obs: 314, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.226171  0.017763 239.787439  12.732 < 2e-16 ***
## Genotype10L -0.089257  0.021867 251.350641  -4.082 6.01e-05 ***
## Genotype11H  0.064460  0.021913 252.523636   2.942 0.003568 **
## Genotype11L -0.069982  0.022041 252.852647  -3.175 0.001684 **
## Genotype12H -0.032853  0.023280 252.899878  -1.411 0.159419
## Genotype12L -0.122508  0.021941 251.947766  -5.584 6.09e-08 ***
## Genotype13H  0.052435  0.022163 254.296390   2.366 0.018739 *
## Genotype13L -0.125153  0.022469 252.544506  -5.570 6.51e-08 ***
## Genotype14H -0.006456  0.022104 251.999526  -0.292 0.770476
## Genotype14L -0.197371  0.024090 253.166657  -8.193 1.27e-14 ***
## Genotype15H -0.034722  0.021867 251.513806  -1.588 0.113560
## Genotype15L -0.063827  0.022599 251.665588  -2.824 0.005118 **
## Genotype1H   -0.020791  0.022111 253.447471  -0.940 0.347952
## Genotype1L   -0.051145  0.021957 252.201459  -2.329 0.020635 *
## Genotype20T -0.121788  0.021853 250.057087  -5.573 6.46e-08 ***
## Genotype23T  0.031876  0.021937 251.848604   1.453 0.147441
## Genotype24T -0.070525  0.021939 251.935304  -3.215 0.001477 **
## Genotype2H   -0.041405  0.022026 252.744910  -1.880 0.061279 .
## Genotype2L   -0.073905  0.021720 250.393369  -3.403 0.000777 ***
```

```
## Genotype3H -0.053821 0.021929 252.830086 -2.454 0.014787 *
## Genotype3L -0.083919 0.023218 251.472276 -3.614 0.000364 ***
## Genotype4H -0.027291 0.022416 250.188991 -1.217 0.224573
## Genotype4L -0.153015 0.023081 250.017497 -6.629 2.06e-10 ***
## Genotype5H 0.061662 0.022072 252.352736 2.794 0.005612 **
## Genotype5L -0.112650 0.022143 253.950354 -5.087 7.06e-07 ***
## Genotype6H 0.038615 0.021974 252.702043 1.757 0.080074 .
## Genotype6L -0.062909 0.024241 253.737257 -2.595 0.010006 *
## Genotype7H -0.009490 0.021965 252.338338 -0.432 0.666087
## Genotype7L -0.064169 0.021809 251.231474 -2.942 0.003562 **
## Genotype8H 0.030330 0.022062 253.365722 1.375 0.170422
## Genotype8L -0.087281 0.022011 253.395051 -3.965 9.54e-05 ***
## Genotype9H -0.007272 0.021987 252.939650 -0.331 0.741113
## Genotype9L -0.081640 0.021779 250.707018 -3.749 0.000221 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 33 > 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 1.1001 0.034378    32 251.66   15.87 < 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_root_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>          36 397.41 -722.81
## (1 | Row)       35 364.33 -658.67 66.146  1 4.187e-16 ***
## (1 | Column)    35 391.58 -713.17 11.643  1 0.0006446 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for random effects model of Leaf_number"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
##      Data: data
##
## REML criterion at convergence: 478.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -5.5813 -0.4785  0.0247  0.5401  2.5941
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Row      (Intercept) 0.023284 0.15259
##  Column   (Intercept) 0.006526 0.08078
##  Residual                    0.246834 0.49682
## Number of obs: 300, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  4.683050   0.164093 266.001152  28.539 < 2e-16 ***
## Genotype10L -0.682838   0.238906 245.835923  -2.858 0.00463 **
## Genotype11H  0.015334   0.225415 245.858949   0.068 0.94582
## Genotype11L -0.692890   0.239280 246.027039  -2.896 0.00412 **
## Genotype12H -0.632845   0.232492 248.280092  -2.722 0.00695 **
## Genotype12L -0.305048   0.225894 247.174316  -1.350 0.17812
## Genotype13H -0.028015   0.232744 249.921358  -0.120 0.90429
## Genotype13L -0.717164   0.277269 250.632532  -2.587 0.01026 *
## Genotype14H -0.706996   0.233396 249.695386  -3.029 0.00271 **
## Genotype14L -1.694923   0.248290 246.773403  -6.826 6.71e-11 ***
## Genotype15H -0.055273   0.224689 242.517336  -0.246 0.80589
## Genotype15L  0.350932   0.232222 246.402041   1.511 0.13202
## Genotype1H   0.022959   0.226730 248.922993   0.101 0.91943
## Genotype1L  -0.330316   0.225721 245.729121  -1.463 0.14464
## Genotype20T -0.385352   0.225065 243.196272  -1.712 0.08814 .
## Genotype23T -0.023237   0.232179 248.241363  -0.100 0.92036
## Genotype24T -0.705011   0.225726 245.852120  -3.123 0.00200 **
## Genotype2H  -0.649948   0.231865 246.061501  -2.803 0.00546 **
## Genotype2L  -0.720354   0.237771 242.224904  -3.030 0.00271 **
```

```
## Genotype3H -0.364351 0.231454 245.368096 -1.574 0.11673
## Genotype3L -0.422280 0.225502 244.241286 -1.873 0.06232 .
## Genotype4H 0.252808 0.248268 244.300338 1.018 0.30955
## Genotype4L -0.989145 0.232524 248.504346 -4.254 2.98e-05 ***
## Genotype5H 0.296946 0.232240 246.369909 1.279 0.20224
## Genotype5L -0.366322 0.226385 248.501844 -1.618 0.10690
## Genotype6H -0.078345 0.225941 247.664394 -0.347 0.72907
## Genotype6L -0.074012 0.232756 250.253068 -0.318 0.75076
## Genotype7H -0.232772 0.225980 247.877747 -1.030 0.30399
## Genotype7L -0.628164 0.239541 247.777678 -2.622 0.00927 **
## Genotype8H 0.008677 0.226432 248.791328 0.038 0.96946
## Genotype8L -0.239840 0.226125 248.827395 -1.061 0.28988
## Genotype9H -0.268030 0.225937 247.597200 -1.186 0.23664
## Genotype9L -0.667602 0.231173 243.340322 -2.888 0.00423 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 33 > 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 44.839  1.4012    32 246.57  5.6768 3.869e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## Leaf_number ~ Genotype + (1 | Row) + (1 | Column)
##      npar logLik   AIC   LRT Df Pr(>Chisq)
## <none>    36 -239.46 550.91
## (1 | Row)    35 -243.17 556.34 7.4233 1 0.006439 **
## (1 | Column) 35 -240.06 550.13 1.2150 1 0.270352
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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



```
## [1] "Summary for random effects model of DW_seed_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: random_formula
## Data: data
##
## REML criterion at convergence: -1435.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.8203 -0.4478 -0.0405  0.2774  4.6956
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Row      (Intercept) 3.017e-06 1.737e-03
## Column   (Intercept) 2.942e-14 1.715e-07
## Residual                    2.346e-04 1.532e-02
## Number of obs: 307, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  1.854e-02  5.823e-03 2.740e+02  3.183 0.001625 **
## Genotype10L  1.126e-02  7.561e-03 2.623e+02  1.489 0.137591
## Genotype11H  2.599e-03  7.576e-03 2.699e+02  0.343 0.731785
## Genotype11L  4.697e-02  7.751e-03 2.713e+02  6.060 4.54e-09 ***
## Genotype12H  4.872e-03  7.581e-03 2.715e+02  0.643 0.520996
## Genotype12L  2.123e-02  8.233e-03 2.736e+02  2.579 0.010437 *
## Genotype13H  1.207e-02  7.751e-03 2.713e+02  1.557 0.120558
## Genotype13L  2.890e-02  7.960e-03 2.712e+02  3.630 0.000339 ***
## Genotype14H  2.602e-02  7.757e-03 2.727e+02  3.355 0.000908 ***
## Genotype14L  3.975e-02  7.556e-03 2.591e+02  5.261 3.00e-07 ***
## Genotype15H  1.299e-02  7.746e-03 2.694e+02  1.677 0.094719 .
## Genotype15L  1.408e-02  7.751e-03 2.713e+02  1.817 0.070322 .
## Genotype1H   5.487e-03  7.960e-03 2.710e+02  0.689 0.491232
## Genotype1L   1.276e-02  7.576e-03 2.698e+02  1.684 0.093295 .
## Genotype20T -2.640e-03  7.741e-03 2.671e+02 -0.341 0.733298
## Genotype23T  1.221e-02  7.581e-03 2.715e+02  1.611 0.108397
## Genotype24T  9.523e-03  7.752e-03 2.714e+02  1.229 0.220299
## Genotype2H   7.002e-04  7.746e-03 2.693e+02  0.090 0.928038
## Genotype2L   3.720e-02  7.566e-03 2.652e+02  4.917 1.54e-06 ***
## Genotype3H   1.049e-02  7.741e-03 2.671e+02  1.355 0.176621
## Genotype3L   3.213e-02  7.741e-03 2.670e+02  4.150 4.47e-05 ***
## Genotype4H   4.196e-03  7.741e-03 2.670e+02  0.542 0.588232
## Genotype4L   2.203e-02  7.576e-03 2.698e+02  2.909 0.003933 **
## Genotype5H   4.661e-02  7.751e-03 2.713e+02  6.013 5.86e-09 ***
## Genotype5L   5.967e-02  7.581e-03 2.715e+02  7.872 8.37e-14 ***
## Genotype6H   1.444e-02  7.571e-03 2.678e+02  1.908 0.057485 .
## Genotype6L   3.156e-02  7.576e-03 2.698e+02  4.166 4.18e-05 ***
## Genotype7H   2.741e-02  7.576e-03 2.699e+02  3.618 0.000354 ***
## Genotype7L   5.618e-02  7.571e-03 2.678e+02  7.421 1.55e-12 ***
## Genotype8H   1.303e-02  7.581e-03 2.715e+02  1.719 0.086687 .
## Genotype8L   3.259e-02  7.751e-03 2.712e+02  4.205 3.55e-05 ***
## Genotype9H   2.380e-02  7.581e-03 2.716e+02  3.140 0.001878 **
## Genotype9L   5.796e-02  7.571e-03 2.678e+02  7.656 3.49e-13 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 33 > 12.
## Use print(summary(random_model), correlation=TRUE) or
##      vcov(summary(random_model))      if you need it
```

```
## 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)
## Genotype 0.092344 0.0028857    32 268.37  12.299 < 2.2e-16 ***
## ---
## 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_seed_g ~ Genotype + (1 | Row) + (1 | Column)
##           npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>         36 717.83 -1363.7
## (1 | Row)       35 717.70 -1365.4 0.2541  1      0.6142
## (1 | Column)   35 717.83 -1365.7 0.0000  1      1.0000
```

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_shoot_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
## Data: data
##
## REML criterion at convergence: -626.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5893 -0.6216 -0.0308  0.5331  3.6832
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Row      (Intercept) 0.0014763 0.03842
## Column   (Intercept) 0.0005011 0.02238
## Residual                    0.0063638 0.07977
## Number of obs: 311, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.21705    0.01860 158.92165  11.670 < 2e-16 ***
## Plant_typeH  0.09091    0.01709 282.00599   5.321 2.11e-07 ***
## Plant_typeL -0.04329    0.01714 281.88497  -2.526  0.0121 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.775
## Plant_typeL -0.771  0.840
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type  1.2407 0.62033     2 281.88  97.478 < 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_shoot_g ~ Plant_type + (1 | Row) + (1 | Column)
##              npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>          6 313.20 -614.39
## (1 | Row)        5 297.17 -584.34 32.053  1  1.5e-08 ***
## (1 | Column)     5 309.15 -608.29  8.098  1  0.004431 **
## ---
## 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: -804.7
##
## Scaled residuals:
```

```

##      Min      1Q  Median      3Q      Max
## -2.4190 -0.6448 -0.0032  0.6292  3.2058
##
## Random effects:
## Groups   Name            Variance Std.Dev.
## Row      (Intercept) 0.0010376 0.03221
## Column   (Intercept) 0.0001539 0.01240
## Residual                    0.0036785 0.06065
## Number of obs: 314, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.17204    0.01360 138.31725  12.646 < 2e-16 ***
## Plant_typeH  0.05576    0.01245 286.27496   4.481 1.08e-05 ***
## Plant_typeL -0.03972    0.01246 285.01050  -3.188 0.00159 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.758
## Plant_typeL -0.754 0.826
## Type III Analysis of Variance Table with Satterthwaite's method
##              Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 0.62352 0.31176      2 285.64  84.751 < 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_root_g ~ Plant_type + (1 | Row) + (1 | Column)
##              npar logLik      AIC      LRT Df Pr(>Chisq)
## <none>          6 402.37 -792.75
## (1 | Row)        5 382.37 -754.73 40.017  1 2.517e-10 ***
## (1 | Column)     5 400.76 -791.52  3.224  1 0.07255 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Summary for mixed effects model of Leaf_number"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
##      Data: data
##
## REML criterion at convergence: 562.3
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -5.3198 -0.6316 -0.2129  0.7796  1.6142
##
## Random effects:
## Groups   Name            Variance Std.Dev.
## Row      (Intercept) 0.014671 0.12113
## Column   (Intercept) 0.008486 0.09212
## Residual                    0.353799 0.59481
## Number of obs: 300, groups: Row, 22; Column, 15
##

```

```
## Fixed effects:
##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  4.2921    0.1170 223.3396  36.669  <2e-16 ***
## Plant_typeH  0.2322    0.1229 284.0030   1.890   0.0598 .
## Plant_typeL -0.1208    0.1236 282.2206  -0.978   0.3292
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr) Plnt_H
## Plant_typeH -0.870
## Plant_typeL -0.864  0.824
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Plant_type 8.3606  4.1803     2 281.79  11.815 1.182e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## Leaf_number ~ Plant_type + (1 | Row) + (1 | Column)
##           npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>         6 -281.14 574.27
## (1 | Row)       5 -282.25 574.49 2.2190  1    0.1363
## (1 | Column)    5 -281.71 573.43 1.1531  1    0.2829
```

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

```
## [1] "Summary for mixed effects model of DW_seed_g"
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: model_formula
## Data: data
##
## REML criterion at convergence: -1501.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9135 -0.6364 -0.2418  0.3766  3.8634
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Row      (Intercept) 0.0000000 0.00000
## Column   (Intercept) 0.0000000 0.00000
## Residual                    0.0004018 0.02005
## Number of obs: 307, groups: Row, 22; Column, 15
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) 2.520e-02  3.788e-03 3.040e+02  6.651 1.35e-10 ***
## Plant_typeH 7.250e-03  4.155e-03 3.040e+02  1.745  0.082 .
## Plant_typeL 2.736e-02  4.147e-03 3.040e+02  6.597 1.86e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.912
## Plant_typeL -0.913  0.833
## 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 0.035924 0.017962     2    304 44.702 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_seed_g ~ Plant_type + (1 | Row) + (1 | Column)
##              npar logLik      AIC LRT Df Pr(>Chisq)
## <none>          6 750.61 -1489.2
## (1 | Row)        5 750.61 -1491.2   0  1          1
## (1 | Column)     5 750.61 -1491.2   0  1          1
```

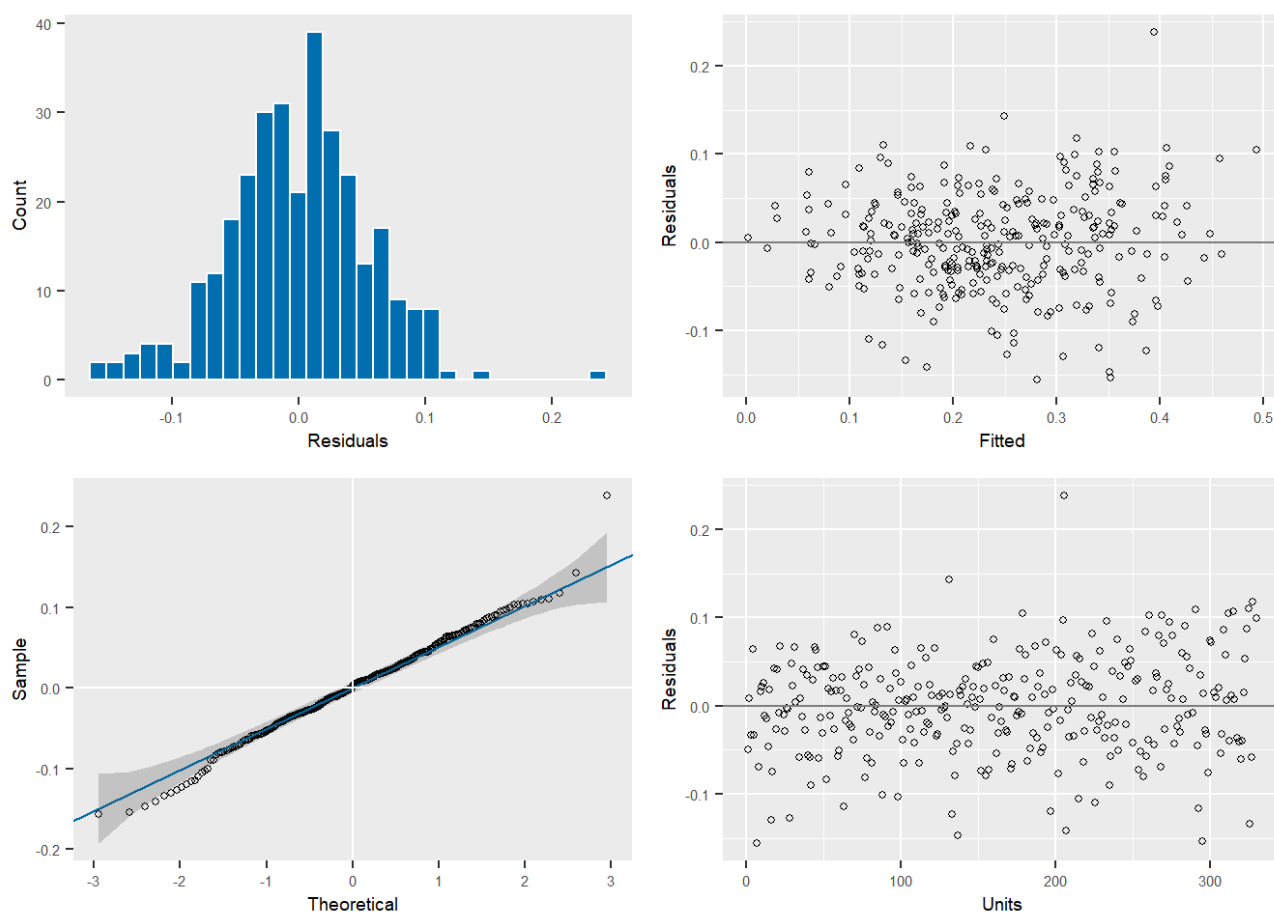
3. Linear models with asreml library

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

```
## ASReml Version 4.2 09/06/2024 17:07:13
```

##		LogLik	Sigma2	DF	wall
##	1	560.2162	0.004452107	278	17:07:13
##	2	563.0706	0.004274451	278	17:07:13
##	3	565.7086	0.004078695	278	17:07:13
##	4	566.9366	0.003944985	278	17:07:13
##	5	567.2268	0.003873483	278	17:07:13
##	6	567.2353	0.003861533	278	17:07:13

```
plot(modasreml)
```



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

##		component	std.error	z.ratio	bound	%ch
##	Column	0.0005848076	0.0002968696	1.969914	P	0.0
##	Row	0.0015944844	0.0005804261	2.747093	P	0.1
##	units!R	0.0038615329	0.0003503019	11.023442	P	0.0

4. Linear models with Soil variable

Model with Soil as explicative variable.

5. Linear models with Soil variable with Plant_type