

Statistical modeling for phenotypic traits

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NaPPI_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] "FW_shoot_g" "DW_shoot_g"
```

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

```
## [1] EPPN20_T EPPN06_H EPPN08_H EPPN10_L EPPN05_H EPPN11_H EPPN09_H EPPN04_H  
## [9] EPPN03_H EPPN12_H EPPN10_H EPPN01_H EPPN02_H EPPN11_L EPPN13_H EPPN07_L  
## 16 Levels: EPPN01_H EPPN02_H EPPN03_H EPPN04_H EPPN05_H EPPN06_H ... EPPN20_T
```

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 FW_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -132.841  -42.411   5.558   34.468  144.085
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    121.421     42.325   2.869  0.00525 **
## GenotypeEPPN02_H -26.071     34.005  -0.767  0.44549
## GenotypeEPPN03_H -41.632     32.190  -1.293  0.19957
## GenotypeEPPN04_H   8.961     35.474   0.253  0.80121
## GenotypeEPPN05_H  13.035     31.232   0.417  0.67751
## GenotypeEPPN06_H  20.704     29.515   0.701  0.48502
## GenotypeEPPN07_L  -2.406     56.457  -0.043  0.96612
## GenotypeEPPN08_H  63.552     37.624   1.689  0.09504 .
## GenotypeEPPN09_H  24.448     32.934   0.742  0.46004
## GenotypeEPPN10_H  39.966     35.985   1.111  0.27000
## GenotypeEPPN10_L  -3.939     58.815  -0.067  0.94677
## GenotypeEPPN11_H -11.086     32.908  -0.337  0.73709
## GenotypeEPPN11_L -71.586     47.719  -1.500  0.13746
## GenotypeEPPN12_H   8.923     33.808   0.264  0.79251
## GenotypeEPPN13_H  23.215     41.779   0.556  0.57996
## GenotypeEPPN20_T  11.062     48.423   0.228  0.81987
## Row2            21.522     24.636   0.874  0.38491
## Row3            19.819     22.967   0.863  0.39073
## Row4            -8.700     21.866  -0.398  0.69178
## Row5           -15.349     22.573  -0.680  0.49847
## Row6             3.404     23.148   0.147  0.88345
## Row7            15.735     23.701   0.664  0.50865
## Column2          85.025     40.191   2.116  0.03746 *
## Column3          86.058     39.228   2.194  0.03112 *
## Column4           6.984     37.956   0.184  0.85448
## Column5          36.771     40.748   0.902  0.36952
## Column6          50.714     40.848   1.242  0.21799
## Column7          37.374     42.573   0.878  0.38261
## Column8          82.538     39.397   2.095  0.03929 *
## Column9          35.682     41.341   0.863  0.39062
## Column10         58.783     44.304   1.327  0.18830
## Column11          2.926     42.563   0.069  0.94536
## Column12         52.258     42.306   1.235  0.22031
## Column13         40.871     40.068   1.020  0.31074
## Column14         51.866     43.194   1.201  0.23334
## Column15         14.202     39.507   0.359  0.72017
## Column16         20.758     42.212   0.492  0.62422
## Column17         14.416     39.665   0.363  0.71722
## Column18         63.216     39.798   1.588  0.11609
## Column19         58.316     39.491   1.477  0.14364
## Column20         65.693     39.929   1.645  0.10380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

## Residual standard error: 64.46 on 81 degrees of freedom
## (4 observations effacées parce que manquantes)
## Multiple R-squared: 0.3371, Adjusted R-squared: 0.009775
## F-statistic: 1.03 on 40 and 81 DF, p-value: 0.445
##
## Analysis of Variance Table
##
## Response: FW_shoot_g
##          Df Sum Sq Mean Sq F value Pr(>F)
## Genotype  15  83514   5567.6   1.3397 0.1987
## Row        6  17369   2894.9   0.6966 0.6530
## Column    19  70310   3700.5   0.8905 0.5953
## Residuals 81 336614   4155.7
## [1] "Summary for fixed effects model of DW_shoot_g"
##
## Call:
## lm(formula = fixed_formula, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.147  -4.099  -0.355   3.839  16.404
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    31.9559     5.2695   6.064 4.45e-08 ***
## GenotypeEPPN02_H -1.9572     4.1059  -0.477  0.6349
## GenotypeEPPN03_H -1.4156     3.9104  -0.362  0.7183
## GenotypeEPPN04_H  2.2071     4.3218   0.511  0.6110
## GenotypeEPPN05_H -0.3217     3.8513  -0.084  0.9337
## GenotypeEPPN06_H  0.1823     3.5197   0.052  0.9588
## GenotypeEPPN07_L -4.0275     7.0280  -0.573  0.5682
## GenotypeEPPN08_H  0.5698     4.5881   0.124  0.9015
## GenotypeEPPN09_H  8.9256     3.9632   2.252  0.0271 *
## GenotypeEPPN10_H -1.1883     4.6089  -0.258  0.7972
## GenotypeEPPN10_L  5.3203     7.2577   0.733  0.4657
## GenotypeEPPN11_H -1.1313     4.1230  -0.274  0.7845
## GenotypeEPPN11_L -7.2585     5.9282  -1.224  0.2245
## GenotypeEPPN12_H -1.6252     4.2461  -0.383  0.7029
## GenotypeEPPN13_H  9.2803     5.1219   1.812  0.0739 .
## GenotypeEPPN20_T -1.8217     5.9954  -0.304  0.7620
## Row2            -2.1680     2.9788  -0.728  0.4689
## Row3            -0.7290     2.9647  -0.246  0.8064
## Row4            -0.3930     2.8283  -0.139  0.8899
## Row5            -1.3462     2.9554  -0.456  0.6500
## Row6             3.1738     2.9612   1.072  0.2871
## Row7            -0.6065     3.2302  -0.188  0.8516
## Column2         10.0222     5.0395   1.989  0.0502 .
## Column3          6.6666     5.1875   1.285  0.2026
## Column4          0.3555     4.7515   0.075  0.9405
## Column5          0.4444     5.0969   0.087  0.9307
## Column6          3.5927     5.1358   0.700  0.4863
## Column7          3.0391     5.3609   0.567  0.5724
## Column8          4.9162     4.9245   0.998  0.3212
## Column9          2.5656     5.1722   0.496  0.6213
## Column10         0.5226     5.5674   0.094  0.9255
## Column11        -1.5940     5.3351  -0.299  0.7659

```

```
## Column12      1.0629      5.2939      0.201      0.8414
## Column13     -0.5705      5.0125     -0.114      0.9097
## Column14      2.6745      5.2336      0.511      0.6108
## Column15     -2.6535      5.3179     -0.499      0.6192
## Column16      1.3779      5.2886      0.261      0.7951
## Column17      2.1912      4.9742      0.441      0.6608
## Column18      1.5266      5.1404      0.297      0.7673
## Column19      0.7209      4.9400      0.146      0.8843
## Column20      1.5944      5.0072      0.318      0.7510
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.055 on 78 degrees of freedom
## (7 observations effacées parce que manquantes)
## Multiple R-squared:  0.3587, Adjusted R-squared:  0.0299
## F-statistic: 1.091 on 40 and 78 DF,  p-value: 0.3647
##
## Analysis of Variance Table
##
## Response: DW_shoot_g
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype  15 1747.2  116.483   1.7953 0.0502 .
## Row        6   248.5   41.423   0.6384 0.6991
## Column    19   835.5   43.974   0.6777 0.8295
## Residuals 78 5060.9   64.883
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

```
## [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: 1209.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.55797 -0.63370  0.01246  0.67486  2.50009
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)         0         0.00
## Row       (Intercept)         0         0.00
## Residual                    4003      63.27
## Number of obs: 122, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    168.826    22.368 106.000   7.548 1.62e-11 ***
## GenotypeEPPN02_H -23.891    30.742 106.000  -0.777   0.4388
## GenotypeEPPN03_H -25.425    30.010 106.000  -0.847   0.3988
## GenotypeEPPN04_H  11.864    32.744 106.000   0.362   0.7178
## GenotypeEPPN05_H  12.223    28.430 106.000   0.430   0.6681
## GenotypeEPPN06_H  19.900    26.884 106.000   0.740   0.4608
## GenotypeEPPN07_L  -3.606    50.017 106.000  -0.072   0.9427
## GenotypeEPPN08_H  66.407    34.168 106.000   1.944   0.0546 .
## GenotypeEPPN09_H  24.995    29.398 106.000   0.850   0.3971
## GenotypeEPPN10_H  41.125    32.744 106.000   1.256   0.2119
## GenotypeEPPN10_L -37.091    50.017 106.000  -0.742   0.4600
## GenotypeEPPN11_H  -4.483    30.742 106.000  -0.146   0.8843
## GenotypeEPPN11_L -35.830    42.832 106.000  -0.837   0.4047
## GenotypeEPPN12_H  -0.584    30.742 106.000  -0.019   0.9849
## GenotypeEPPN13_H  53.110    36.068 106.000   1.472   0.1439
## GenotypeEPPN20_T -37.226    42.832 106.000  -0.869   0.3867
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 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    83514   5567.6     15    106  1.3909 0.1651
```

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

```
## 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>      19 -604.88 1247.8
## (1 | Row)    18 -604.88 1245.8   0  1         1
## (1 | Column) 18 -604.88 1245.8   0  1         1
```

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

```
## [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: 742.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.22477 -0.59092 -0.01323  0.60512  2.55776
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)    0.00      0.000
## Row       (Intercept)    0.00      0.000
## Residual                    59.66      7.724
## Number of obs: 119, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   33.83556    2.57465 103.00000   13.142  <2e-16 ***
## GenotypeEPPN02_H -3.21333    3.64110 103.00000   -0.883   0.3796
## GenotypeEPPN03_H  0.05644    3.54891 103.00000    0.016   0.9873
## GenotypeEPPN04_H  0.86159    3.89250 103.00000    0.221   0.8253
## GenotypeEPPN05_H -1.13556    3.40594 103.00000   -0.333   0.7395
## GenotypeEPPN06_H  0.30889    3.15329 103.00000    0.098   0.9222
## GenotypeEPPN07_L -5.13056    6.03808 103.00000   -0.850   0.3975
## GenotypeEPPN08_H -0.45556    4.07088 103.00000   -0.112   0.9111
## GenotypeEPPN09_H  8.11444    3.47165 103.00000    2.337   0.0214 *
## GenotypeEPPN10_H -0.56722    4.07088 103.00000   -0.139   0.8895
## GenotypeEPPN10_L  2.53444    6.03808 103.00000    0.420   0.6755
## GenotypeEPPN11_H  0.66444    3.75316 103.00000    0.177   0.8598
## GenotypeEPPN11_L -5.20222    5.14929 103.00000   -1.010   0.3147
## GenotypeEPPN12_H -1.83431    3.75316 103.00000   -0.489   0.6261
## GenotypeEPPN13_H 12.13844    4.30821 103.00000    2.818   0.0058 **
## GenotypeEPPN20_T -3.43222    5.14929 103.00000   -0.667   0.5066
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 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 1747.2  116.48    15   103  1.9525 0.02603 *
## ---
## 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_shoot_g ~ Genotype + (1 | Row) + (1 | Column)
##      npar  logLik    AIC LRT Df Pr(>Chisq)
## <none>      19 -371.39 780.78
## (1 | Row)      18 -371.39 778.78  0  1          1
## (1 | Column)   18 -371.39 778.78  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)
}
```

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



```
## [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: 1336.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.39066 -0.65054  0.00325  0.62569  2.58837
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)          0        0.00
## Row      (Intercept)          0        0.00
## Residual                    4131     64.27
## Number of obs: 122, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   131.60      37.11 119.00   3.546 0.000559 ***
## Plant_typeH    48.94      37.60 119.00   1.302 0.195568
## Plant_typeL   10.24      44.35 119.00   0.231 0.817753
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.987
## Plant_typeL -0.837  0.826
## 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  16238  8119.3      2    119  1.9655 0.1446
```

```
## boundary (singular) fit: see help('isSingular')
## 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 -668.15 1348.3
## (1 | Row)        5 -668.15 1346.3  0  1          1
## (1 | Column)     5 -668.15 1346.3  0  1          1
```

```
## 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: 824.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8432 -0.6465 -0.1050  0.3915  3.7326
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)    0.000    0.0000
## Row       (Intercept)    0.624    0.7899
## Residual                    66.181    8.1352
## Number of obs: 119, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  30.4773      4.7172 115.8988   6.461 2.55e-09 ***
## Plant_typeH    4.2975      4.7722 115.0285   0.901   0.370
## Plant_typeL    0.4716      5.6268 114.9738   0.084   0.933
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H
## Plant_typeH -0.985
## Plant_typeL -0.835  0.825
## 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 143.83  71.913      2 115.23  1.0866 0.3408
```

```
## 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 -412.06 836.13
## (1 | Row)        5 -412.10 834.20 0.075423  1   0.7836
## (1 | Column)     5 -412.06 834.13 0.000000  1   1.0000
```

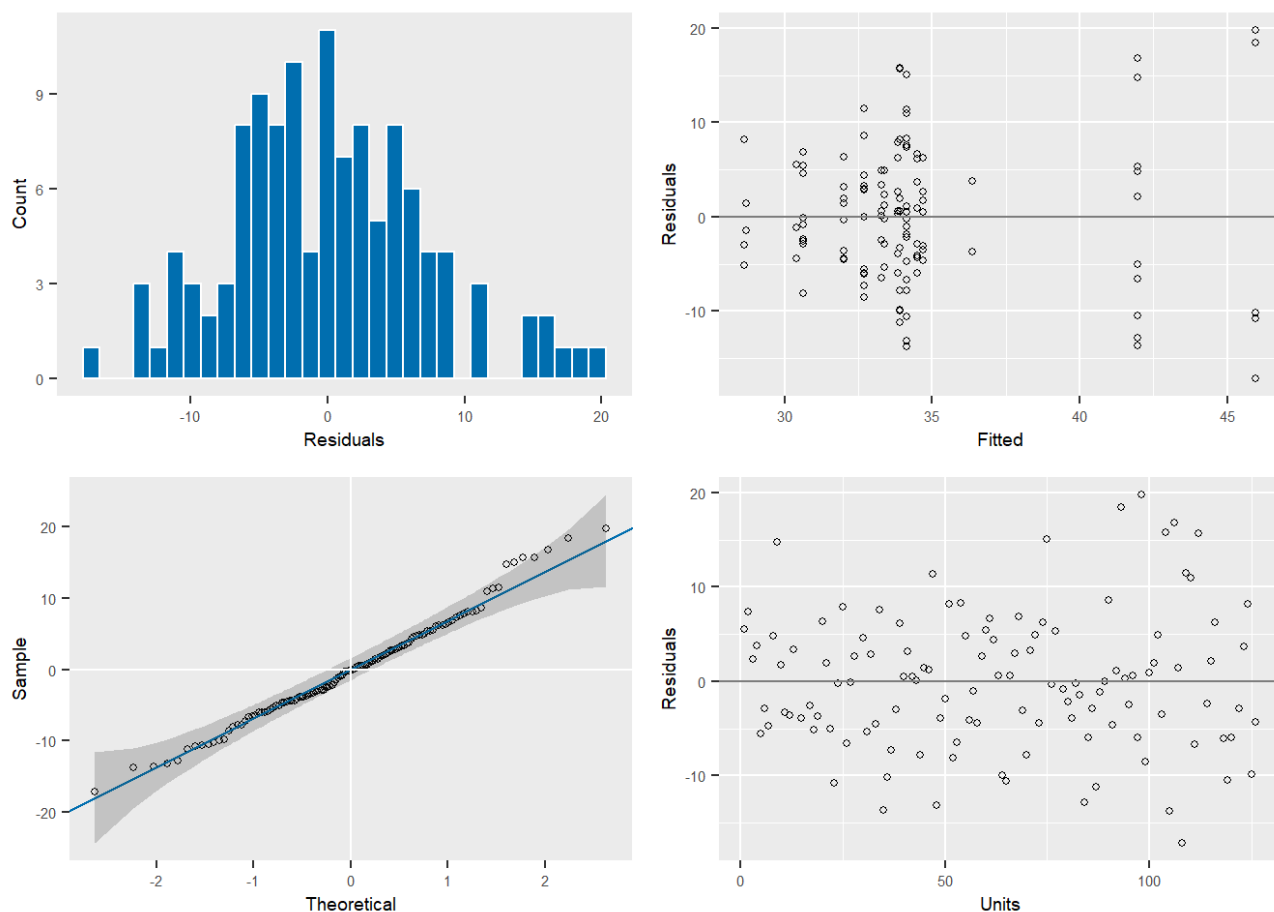
3. Linear models with asreml library

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

```
## ASReml Version 4.2 09/06/2024 16:46:39
```

##		LogLik	Sigma2	DF	wall	
##	1	-279.6868	55.29701	103	16:46:39	(2 restrained)
##	2	-276.9073	59.15946	103	16:46:39	(2 restrained)
##	3	-276.7513	59.62571	103	16:46:39	(2 restrained)
##	4	-276.7418	59.65716	103	16:46:39	(2 restrained)
##	5	-276.7412	59.65915	103	16:46:39	(2 restrained)

```
plot(modasreml)
```



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

##	component	std.error	z.ratio	bound	%ch
## Row	6.037082e-06	NA	NA	B	NA
## Column	6.037082e-06	NA	NA	B	NA
## units!R	5.965915e+01	9.123311	6.5392	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 FW_shoot_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: 1349.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.21212 -0.75218  0.03407  0.56962  2.51463
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)          0         0.00
## Row      (Intercept)          0         0.00
## Residual                    4179      64.64
## Number of obs: 122, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)  184.350      8.277 120.000  22.274  <2e-16 ***
## Soils2       -14.465     11.705 120.000  -1.236   0.219
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Soils2 -0.707
## 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')
## boundary (singular) fit: see help('isSingular')
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Soil + (1 | Row) + (1 | Column)
##      npar  logLik    AIC LRT Df Pr(>Chisq)
## <none>      5 -674.65 1359.3
## (1 | Row)      4 -674.65 1357.3  0  1          1
## (1 | Column)   4 -674.65 1357.3  0  1          1
```

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

```
## [1] "Summary for interaction model of FW_shoot_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: 1307.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.2698 -0.6942 -0.0029  0.5948  2.4666
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)          0         0.0
## Row      (Intercept)          0         0.0
## Residual                    4173      64.6
## Number of obs: 122, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    167.78     64.60 116.00   2.597   0.0106 *
## Plant_typeH     19.78     65.17 116.00   0.304   0.7620
## Plant_typeL    -24.29     72.22 116.00  -0.336   0.7372
## Soils2         -54.27     79.12 116.00  -0.686   0.4941
## Plant_typeH:Soils2  40.22     80.05 116.00   0.502   0.6163
## Plant_typeL:Soils2  50.44     93.24 116.00   0.541   0.5896
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L Soils2 P_H:SS
## Plant_typeH -0.991
## Plant_typeL -0.894  0.887
## Soils2      -0.816  0.809  0.730
## Plnt_tH:SS2  0.807 -0.814 -0.722 -0.988
## Plnt_tL:SS2  0.693 -0.687 -0.775 -0.849  0.839
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## [1] "Random effects ANOVA for interaction model:"
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Plant_type + Soil + (1 | Row) + (1 | Column) + Plant_type:Soil
##              npar logLik    AIC LRT Df Pr(>Chisq)
## <none>          9 -653.72 1325.4
## (1 | Row)        8 -653.72 1323.4   0  1         1
## (1 | Column)     8 -653.72 1323.4   0  1         1
```

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

```
## [1] "Summary for no interaction model of FW_shoot_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: 1328
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.28399 -0.70047 -0.00251  0.59674  2.48214
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)          0        0.00
## Row       (Intercept)          0        0.00
## Residual                    4113      64.13
## Number of obs: 122, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)  141.169     37.830 118.000   3.732 0.000294 ***
## Plant_typeH    46.549     37.569 118.000   1.239 0.217791
## Plant_typeL     6.825     44.341 118.000   0.154 0.877929
## Soils2        -14.353     11.635 118.000  -1.234 0.219792
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L
## Plant_typeH -0.975
## Plant_typeL -0.830  0.826
## Soils2      -0.205  0.052  0.062
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## [1] "Random effects ANOVA for no interaction model:"
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## FW_shoot_g ~ Plant_type + Soil + (1 | Row) + (1 | Column)
##              npar  logLik   AIC  LRT Df Pr(>Chisq)
## <none>           7 -664.01 1342
## (1 | Row)         6 -664.01 1340   0  1          1
## (1 | Column)      6 -664.01 1340   0  1          1
```

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

```
## [1] "Summary for base model of DW_shoot_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: 831.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7558 -0.7088 -0.0860  0.3933  3.6449
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept) 2.121e-15 4.606e-08
## Row       (Intercept) 1.044e+00 1.022e+00
## Residual                    6.595e+01 8.121e+00
## Number of obs: 119, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)   35.154      1.103  18.965  31.883 <2e-16 ***
## Soils2        -1.499      1.491  112.438  -1.006  0.317
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Soils2 -0.648
## 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_shoot_g ~ Soil + (1 | Row) + (1 | Column)
##      npar logLik   AIC    LRT Df Pr(>Chisq)
## <none>      5 -415.87 841.73
## (1 | Row)      4 -415.97 839.94 0.20373 1      0.6517
## (1 | Column)   4 -415.87 839.73 0.00000 1      1.0000
```

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



```
## [1] "Summary for interaction model of DW_shoot_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: 806.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7822 -0.6806 -0.0680  0.3428  3.6415
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)    0.0000   0.000
## Row      (Intercept)    0.4664   0.683
## Residual                    66.1835   8.135
## Number of obs: 119, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)      35.903      8.162 112.971   4.399 2.47e-05 ***
## Plant_typeH       -0.256      8.229 112.968  -0.031   0.975
## Plant_typeL      -7.867      9.116 112.597  -0.863   0.390
## Soils2            -8.143      9.995 112.993  -0.815   0.417
## Plant_typeH:Soils2  6.317     10.117 112.998   0.624   0.534
## Plant_typeL:Soils2 14.900     11.776 112.976   1.265   0.208
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L Soils2 P_H:SS
## Plant_typeH -0.991
## Plant_typeL -0.894  0.887
## Soils2      -0.816  0.810  0.730
## Plnt_tH:SS2  0.807 -0.814 -0.721 -0.988
## Plnt_tL:SS2  0.693 -0.688 -0.775 -0.848  0.838
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## [1] "Random effects ANOVA for interaction model:"
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Plant_type + Soil + (1 | Row) + (1 | Column) + Plant_type:Soil
##              npar  logLik    AIC      LRT Df Pr(>Chisq)
## <none>          9 -403.13 824.25
## (1 | Row)        8 -403.15 822.30 0.042487  1    0.8367
## (1 | Column)     8 -403.13 822.25 0.000000  1    1.0000
```

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

```
## [1] "Summary for no interaction model of DW_shoot_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: 820.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7487 -0.7008 -0.0778  0.3625  3.6480
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## Column   (Intercept)    0.0000   0.0000
## Row       (Intercept)    0.5961   0.7721
## Residual                    66.2212   8.1376
## Number of obs: 119, groups: Column, 20; Row, 7
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  31.4564     4.8224  114.9526   6.523 1.93e-09 ***
## Plant_typeH    4.0213     4.7817  114.0307   0.841   0.402
## Plant_typeL    0.1213     5.6392  113.9590   0.022   0.983
## Soils2        -1.4714     1.4968  110.5274  -0.983   0.328
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Plnt_H Plnt_L
## Plant_typeH -0.974
## Plant_typeL -0.828  0.826
## Soils2      -0.207  0.059  0.063
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
##
## [1] "Random effects ANOVA for no interaction model:"
```

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

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## DW_shoot_g ~ Plant_type + Soil + (1 | Row) + (1 | Column)
##              npar logLik   AIC    LRT Df Pr(>Chisq)
## <none>          7 -410.26 834.52
## (1 | Row)        6 -410.29 832.58 0.069286 1    0.7924
## (1 | Column)     6 -410.26 832.52 0.000000 1    1.0000
```