Genotype by Environment analysis using RAP

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Genotype by Environment Analysis using the RAP package

The RAP package is developed as an easy to use package for analysing data of plant breeding experiments with plenty of options for plotting and reporting the results of the analyses.

The package has 3 main components:

- Modeling trial data for single trials and extracting results
- Genotype by Environment (GxE) analysis
- QTL analysis

This vignette deals with the GxE part of the package and describes in detail how to perform the different types of analysis that are available in the package.

The following types of analysis can be done using RAP:

- Best variance-covariance model
- AMMI Analysis
- Finlay-Wilkinson Analysis
- Computation of mega environments
- Computation of stability measures

Data preparation

Just as for the analysis of single field trials the input for GxE analysis in the RAP package is an object of class TD. For a detailed description on how to construct such an object see the vignette Modeling field trials using RAP. For this vignette the TD object created in the final step of this vignette, `TDGxE`, will be used as analysis object.

Best variance-covariance model

The function gxeVarComp fits models with different variance-covariance structures to the GxE data and determines the best model for the data. With the default settings for the function lme4 is used for fitting the models and only a compound symmetry model is fitted. When changing the modeling engine to asreml 8 different models are fitted:

- identity
- compound symmetry
- diagonal
- heterogeneous compound symmetry
- outside
- factor analytic with one factor
- factor analytic with two factors
- unstructured

The best model for the data is selected based on either the Akaike Information Criterion (AIC) or the Baysian Information Criterion (BIC). Which criterion is used is determined by the parameter `criterion` in the function `gxeVarComp`.

Using the `TDGxE` TD object created in the RAP vignette the function can be used as follows:

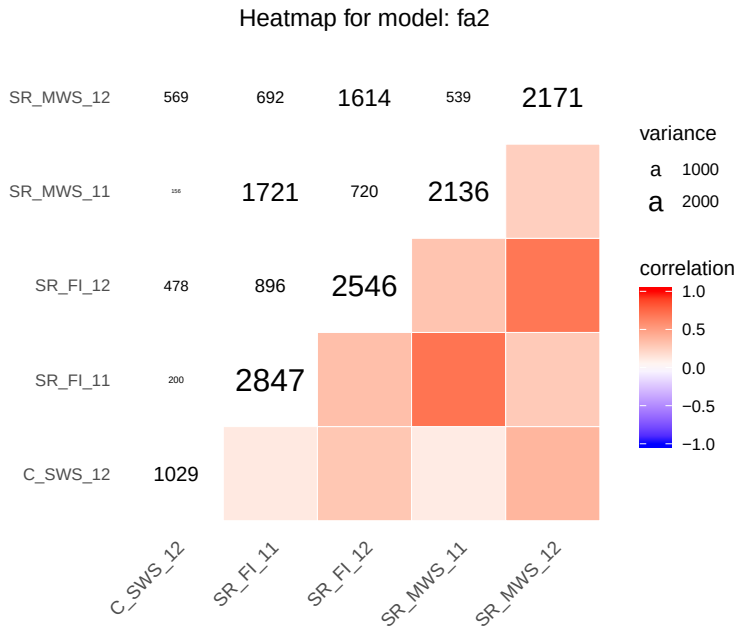
```
## Use lme4 for fitting the models - only compound symmetry
geVC <- gxeVarComp(TD = TDGxE, trait = "BLUEs_GY")
summary(geVC)
#> Best model: cs, based on BIC.
#>         AIC      BIC Deviance NParameters
#> cs 31188.53 31199.65 31184.53           2
```

```
## Use asreml for fitting the models - 8 models fitted.
## Use AIC as criterion for determining the best model.
if (requireNamespace("asreml")) {
  geVC2 <- gxeVarComp(TD = TDGxE, trait = "BLUEs_GY", engine = "asreml",
                      criterion = "AIC")
  summary(geVC2)
}
#> Best model: fa2, based on AIC.
#>                     AIC      BIC Deviance NParameters
#> fa2           27310.09 27384.80 27282.09          14
#> unstructured 27311.58 27391.63 27281.58          15
#> fa            27518.37 27571.74 27498.37          10
#> outside       27548.83 27580.86 27536.83           6
#> hcs           27639.91 27671.93 27627.91           6
#> cs            27672.67 27683.34 27668.67           2
#> diagonal      27904.72 27931.40 27894.72           5
#> identity      28001.40 28006.74 27999.40           1
```

As becomes clear from the summary the best model based on AIC is the model with a factor analytic variance-covariance structure with two factors. Note that for the both factor analytic models to be fitted a minimum of 5 environments are needed. If the data contains less environments those two models are skipped.

A heat map of the correlation between the environments based on the best fitted model can be plotted.

```
if (requireNamespace("asreml")) {
  plot(geVC2)
}
```



The upper left of the plot displays the variance between environments. Larger values are displayed in a bigger font. In the lower right of the plot correlations between environments are shown. A dark red color indicates a strong positive correlation between environments, a dark blue a strong negative correlation.

A report containing the most important results of the analysis can be made as well.

```
report(geVC2, outfile = "./myReports/varCompReport.pdf")
```

AMMI Analysis

The Additive Main Effects and Multiplicative Interaction (AMMI) model fits a model which involves the Additive Main effects (i.e. genotype and trial) along with the Multiplicative Interaction effects. Then a principal component analysis is done on the residuals (multiplicative interaction). This results in an interaction characterized by Interaction Principal Components (IPCA) enabling simultaneous plotting of genotypes and trials.

The ammi analysis can be performed with the RAP package using the function gxeAmmi.

```
## Run gxeAmmi with default settings.
geAm <- gxeAmmi(TD = TDGxE, trait = "BLUEs_GY")
summary(geAm)
#> Principal components
#> ====================
#>                              PC1       PC2
#> Standard deviation     1030.58353 715.42427
#> Proportion of Variance    0.49975   0.24083
#> Cumulative Proportion     0.49975   0.74058
#>
#> Anova
#> =====
#>                       Df     Sum Sq    Mean Sq   F value    Pr(>F)
#> Genotype             383  760625194    1985967    3.7378 < 2.2e-16 ***
#> Environment            4 8310680494 20776701235 3910.4240 < 2.2e-16 ***
```

```
#> Interactions       1532  813975825     531316
#> PC1                 386  406785224    1053848    3.8030 < 2.2e-16 ***
#> PC2                 384  196031610     510499    1.8422  6.41e-13 ***
#> Residuals           762  211158990     277112
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Environment scores
#> ==================
#>                   PC1         PC2
#> C_SWS_12    0.2278314 -0.81879355
#> SR_FI_11   -0.5946811  0.16138788
#> SR_FI_12    0.4069946  0.53407849
#> SR_MWS_11 -0.4826721 -0.01143373
#> SR_MWS_12  0.4425272  0.13476091
```

With the default settings in the principal components analysis a maximum of 2 principal components are used. This can be changed using the `nPC` parameter in the function. The number of principal components can never be larger than the number of environments and the number of genotypes in the data. By specifying `nPC = NULL` the algorithm will determine the number of principal components to use using a method of forward selection.

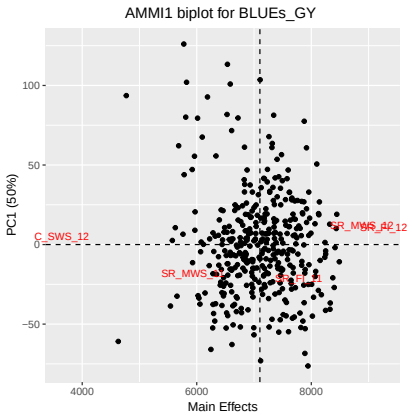
```
## Run gxeAmmi with 3 principal components.
geAm2 <- gxeAmmi(TD = TDGxE, trait = "BLUEs_GY", nPC = 3)
summary(geAm2)
#> Principal components
#> ====================
#>                              PC1       PC2       PC3
#> Standard deviation     1030.58353 715.42427 535.36893
#> Proportion of Variance    0.49975   0.24083   0.13486
#> Cumulative Proportion     0.49975   0.74058   0.87545
#>
#> Anova
#> =====
#>                     Df     Sum Sq    Mean Sq   F value    Pr(>F)
#> Genotype           383  760625194    1985967    3.7378 < 2.2e-16 ***
#> Environment          4 8310680494 20776701233 3910.4240 < 2.2e-16 ***
#> Interactions      1532  813975825     531316
#> PC1                386  406785224    1053848    3.9500 < 2.2e-16 ***
#> PC2                384  196031610     510499    1.9134 1.703e-10 ***
#> PC3                382  109775420     287370    1.0771    0.2345
#> Residuals          380  101383571     266799
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Environment scores
#> ==================
#>                   PC1         PC2         PC3
#> C_SWS_12    0.2278314 -0.81879355  0.06977221
#> SR_FI_11   -0.5946811  0.16138788  0.64279041
#> SR_FI_12    0.4069946  0.53407849 -0.14397531
#> SR_MWS_11 -0.4826721 -0.01143373 -0.73127110
#> SR_MWS_12  0.4425272  0.13476091  0.16268378
```

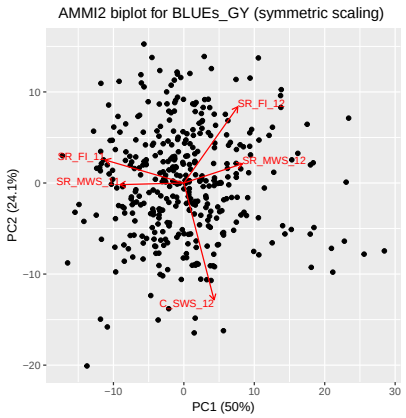
```
## Run gxeAmmi. Algorithm determines number of principal components.
geAm3 <- gxeAmmi(TD = TDGxE, trait = "BLUEs_GY", nPC = NULL)
summary(geAm3)
#> Principal components
#> ====================
#>                              PC1       PC2
#> Standard deviation     1030.58353 715.42427
#> Proportion of Variance    0.49975   0.24083
#> Cumulative Proportion     0.49975   0.74058
#>
#> Anova
#> =====
#>                       Df     Sum Sq    Mean Sq   F value    Pr(>F)
#> Genotype             383  760625194    1985967    3.7378 < 2.2e-16 ***
#> Environment            4 8310680494 20776701235 3910.4240 < 2.2e-16 ***
#> Interactions        1532  813975825     531316
#> PC1                  386  406785224    1053848    3.8030 < 2.2e-16 ***
#> PC2                  384  196031610     510499    1.8422  6.41e-13 ***
#> Residuals            762  211158990     277112
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Environment scores
#> ==================
#>                   PC1         PC2
#> C_SWS_12    0.2278314 -0.81879355
#> SR_FI_11   -0.5946811  0.16138788
#> SR_FI_12    0.4069946  0.53407849
#> SR_MWS_11 -0.4826721 -0.01143373
#> SR_MWS_12  0.4425272  0.13476091
```

If the data contains a column year it is possible to perform the AMMI analysis per year in the data. This can be done by specifying the parameter `byYear = TRUE`.

The results of an AMMI analysis can be displayed in a biplot. Two types of biplot are available. "AMMI1" plots the main effects against the first principal component. "AMMI2" plots the first against the second principal component.

```
## Create an AMMI1 and AMMI2 biplot.
plot(geAm, scale = 0.5, plotType = "AMMI1")
plot(geAm, scale = 0.5, plotType = "AMMI2")
```





The

AMMI plot function has many options to customize the plot. It is possible to plot different principal components on the axis, group and color genotypes by a variable in the data and use a different scaling factor. Run `help(plot.AMMI)` for more details.

For the AMMI analysis a report can be made as well.

```
report(geAm, outfile = "./myReports/AMMIReport.pdf")
```

Finlay-Wilkinson Analysis

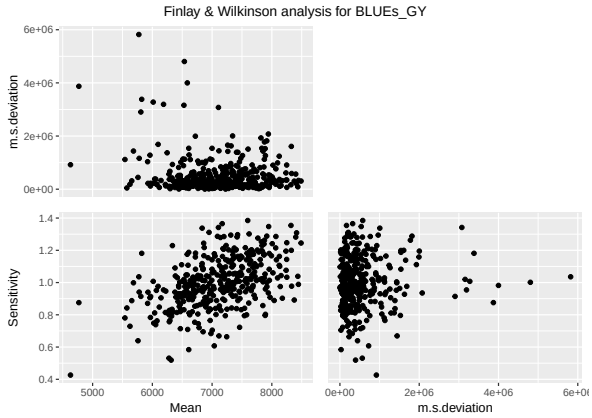
With the Finlay-Wilkinson Analysis (Finlay and Wilkinson 1963) a modified joint regression analysis is used to rank germplasm based on phenotypic stability for each individual trait.

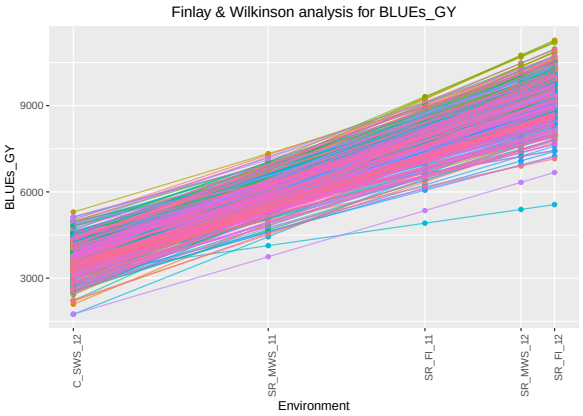
In the RAP package this analysis can be done using the gxeFW function.

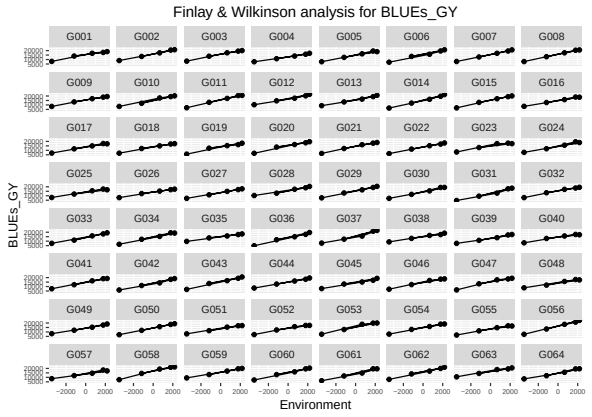
```
geFW <- gxeFw(TD = TDGxE, trait = "BLUEs_GY")
summary(geFW)
#> Environmental effects
#> ====================
#>       trial     effect       SE     mean rank
#> 1  C_SWS_12 -3450.6949 56.48279 3651.430    5
#> 2  SR_FI_11   661.1322 56.58694 7762.838    3
#> 3  SR_FI_12  2176.7587 56.48279 9279.343    1
#> 4 SR_MWS_11 -1171.7041 56.58694 5930.812    4
#> 5 SR_MWS_12  1784.5081 56.48279 8887.059    2
#>
#> Anova
#> =====
#>                       Df     Sum Sq    Mean Sq   F value Pr(>F)
#> genotype             383  760927259    1986755    3.7129 <2e-16 ***
#> trial                  4 8308722428 2077180607 3881.8460 <2e-16 ***
#> Sensitivities        383  200189459     522688    0.9768 0.6051
#> Residual            1147  613761116     535101
#> Total               1917 9883600263    5155764
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Most sensitive genotypes
#> =========
#>  genotype      sens   sigmaE  genMean    sigma       mse
#>      G202 0.4261900 0.157044 4630.041 326.7125 920155.42
#>      G229 0.5190070 0.157044 6314.679 326.7125 394503.53
#>      G338 0.5311154 0.157044 6278.680 326.7125 564566.01
#>      G330 0.5840103 0.157044 6609.668 326.7125  29086.74
#>      G285 0.6073710 0.157044 7036.768 326.7125 724189.99
```

Several plots can be made to investigate the output of the analysis.

```
plot(geFW, plotType = "scatter")
plot(geFW, plotType = "line")
plot(geFW, plotType = "trellis")
```







A report can be made as well.

```
report(geFW, outfile = "./myReports/FWReport.pdf")
```

Computation of mega environments

For the computation of mega environments an AMMI model is fitted and then using the fitted values of this model the environments are clustered
Mega environments can be created by two methods. The first method groups environments based on their best performing genotype; i.e. environments that share the same best genotype belong to the same mega environment, regardless whether environments correspond to years or locations.
In the second method genotypes that are above a certain quantile are used to classify locations into mega environments that are consistent across years. In this method, genotypes are scored according to whether they are above the `cutOff` threshold for the genotypic ranking within each location (1 if a genotype is above the cutOff and 0 if below). This genotype by location matrix with 1's and 0's is used to calculate the correlation between locations. Then, correlations across years are combined using the method by Charter and Alexander (Charter and Alexander 1993). The combined correlations are used to calculate Euclidean distances for hierarchical clustering. The number of mega environments obtained with the hierarchical clustering procedure is chosen to maximize the correlated response to selection within mega environments, as proposed in Atlin et al (Atlin et al. 2000).
Since the test data doesn't contain information about the year only the first method is available for this data. This is the default setting for the gxeMegaEnv function.

```
geMegaEnv <- gxeMegaEnv(TD = TDGxE, trait = "BLUEs_GY")
#>  Mega factor     Trial Winning genotype AMMI estimates
#>            1 SR_MWS_12             G037      10863.969
#>            2  SR_FI_12             G056      11528.407
```

```
#>            3  C_SWS_12            G188       5423.140
#>            4  SR_FI_11            G276      10137.297
#>            4 SR_MWS_11            G276       7953.709
```

As can be seen in the column Mega Factor in the output 4 mega environments have been created. In the environments SR_FI_11 and SR_MWS_11 G276 is the best genotype so those two environments have been clustered together. The other three environments have different winning genotypes and therefore are in their own mega environment.

Computation of stability measures

Different measures of stability can be calculated using the RAP package, the cultivar-superiority measure of Lin & Binns (LIN and BINNS 1988), Shukla's (Shukla 1972) stability variance and Wricke's (Wricke 1962) ecovalence.

The cultivar-superiority measure is the sum of the squares of the difference between genotypic mean in each environment and the mean of the best genotype, divided by twice the number of environments. Genotypes with the smallest values of the superiority tend to be more stable, and closer to the best genotype in each environment.

Shukla's stability variance (static stability) is defined as the variance around the germplasm's phenotypic mean across all environments. This provides a measure of the consistency of the genotype, without accounting for performance.

Wricke's Ecovalence Stability Coefficient is the contribution of each genotype to the GxE sum of squares, in an unweighted analysis of the GxE means. A low value indicates that the genotype responds in a consistent manner to changes in environment; i.e. stable from a dynamic point of view. Like static stability, the Wricke's Ecovalence does not account for genotype performance.

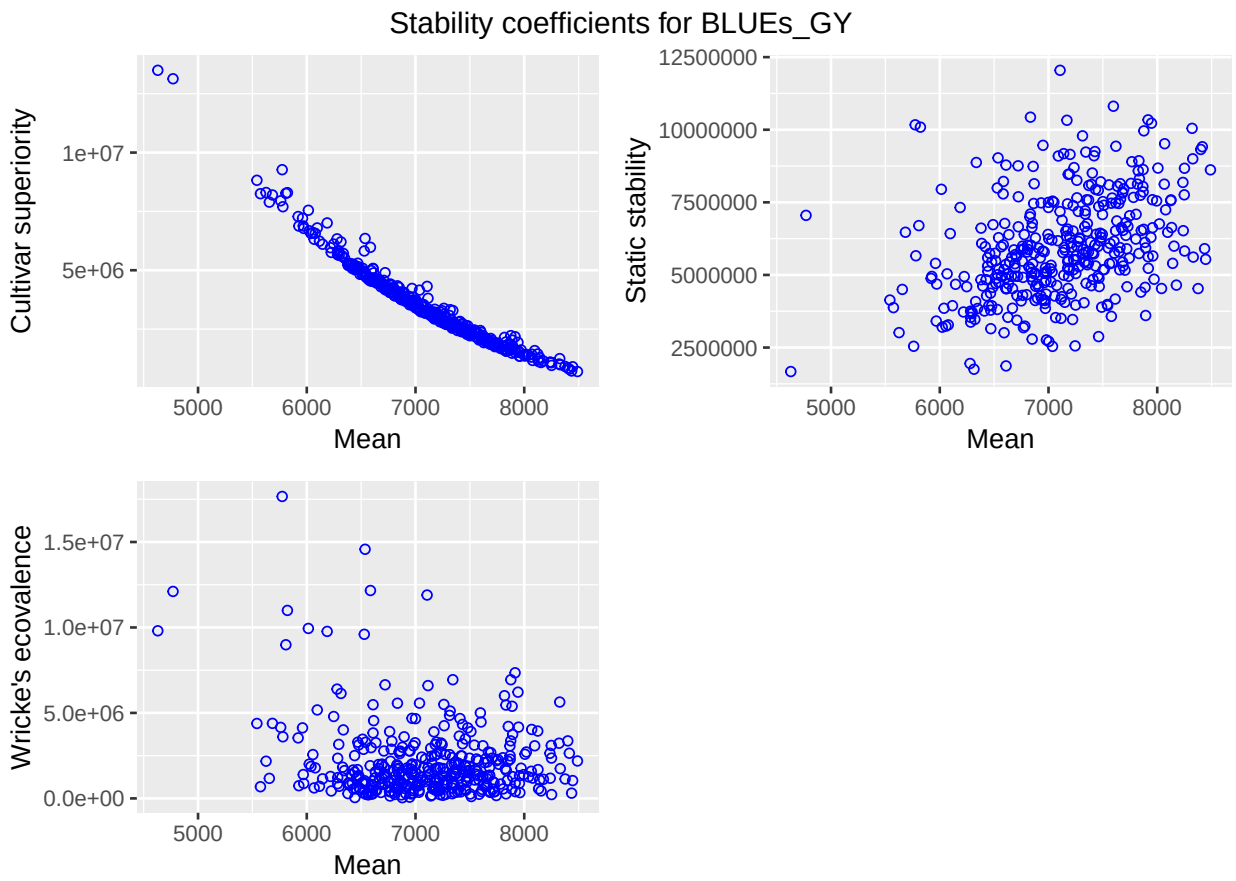
```
geStab <- gxeStability(TD = TDGxE, trait = "BLUEs_GY")
summary(geStab)
#>
#> Cultivar-superiority measure (Top 10% genotypes)
#>  genotype superiority     mean
#>      G202    13494769 4630.041
#>      G288    13135607 4770.062
#>      G384     9272209 5774.064
#>      G249     8821607 5541.442
#>      G316     8303387 5625.830
#>      G208     8296293 5822.169
#>      G260     8266599 5807.864
#>      G248     8251252 5573.973
#>      G378     8197606 5684.175
#>      G383     7950219 5760.066
#>      G250     7893958 5655.763
#>      G136     7698152 5780.283
#>      G360     7549292 6014.688
#>      G295     7282660 5920.772
#>      G257     7210056 5960.757
#>      G205     7009958 6187.658
#>      G161     6882322 5967.887
#>      G165     6877280 5927.171
#>      G254     6797544 6096.553
#>      G324     6778109 5971.614
#>      G315     6676581 6022.966
```

```
#>      G326     6599884 6056.449
#>      G356     6568367 6078.123
#>      G219     6563032 6038.901
#>      G381     6350470 6536.117
#>      G338     6334648 6278.680
#>      G321     6316695 6067.733
#>      G096     6234851 6116.712
#>      G229     6204870 6314.679
#>      G251     6112043 6247.754
#>      G199     6105092 6145.454
#>      G157     5976124 6585.634
#>      G333     5959314 6218.026
#>      G357     5829326 6294.176
#>      G283     5818191 6528.855
#>      G223     5814390 6284.350
#>      G361     5757641 6225.296
#>      G127     5733376 6284.475
#>      G031     5715564 6336.111
#>
#> Static stability (Top 10% genotypes)
#>  genotype   static     mean
#>      G286 12046595 7106.561
#>      G077 10809302 7596.784
#>      G181 10433051 6833.935
#>      G197 10340757 7915.891
#>      G358 10325838 7169.372
#>      G073 10225251 7947.329
#>      G384 10169164 5774.064
#>      G208 10089354 5822.169
#>      G056 10048045 8320.500
#>      G037  9961493 7876.846
#>      G120  9789337 7312.918
#>      G084  9518877 8068.285
#>      G099  9463566 6949.386
#>      G014  9431445 7619.940
#>      G100  9414558 8414.758
#>      G058  9320748 8400.497
#>      G093  9249250 7427.062
#>      G194  9231666 7343.354
#>      G131  9177058 7139.452
#>      G179  9150819 7198.045
#>      G212  9103521 7418.642
#>      G371  9094483 7090.381
#>      G381  9031031 6536.117
#>      G369  8998574 8326.462
#>      G297  8931974 7831.617
#>      G103  8898290 7766.727
#>      G031  8872464 6336.111
#>      G141  8783816 6609.460
#>      G259  8758228 6720.370
#>      G036  8737823 6859.104
#>      G195  8697237 7234.842
#>      G075  8679875 8006.810
```

```
#>      G142  8673762 8250.561
#>      G262  8627998 7870.004
#>      G101  8618730 8489.525
#>      G011  8583549 7825.607
#>      G156  8510243 7402.909
#>      G143  8477603 7192.949
#>      G061  8463380 7181.751
#>
#> Wricke's ecovalence (Top 10% genotypes)
#>  genotype   wricke     mean
#>      G384 17665165 5774.064
#>      G381 14574450 6536.117
#>      G157 12162796 6585.634
#>      G288 12107556 4770.062
#>      G286 11896559 7106.561
#>      G208 10997293 5822.169
#>      G360  9942805 6014.688
#>      G202  9805416 4630.041
#>      G205  9769627 6187.658
#>      G283  9600957 6528.855
#>      G260  8988071 5807.864
#>      G197  7349575 7915.891
#>      G194  6944368 7343.354
#>      G037  6943038 7876.846
#>      G259  6646124 6720.370
#>      G353  6599333 7115.091
#>      G338  6394171 6278.680
#>      G276  6214758 7942.348
#>      G229  6139238 6314.679
#>      G071  6008682 7818.405
#>      G369  5636616 8326.462
#>      G285  5571807 7036.768
#>      G181  5569426 6833.935
#>      G167  5497294 7260.758
#>      G141  5481074 6609.460
#>      G297  5462534 7831.617
#>      G291  5389608 7888.538
#>      G254  5175351 6096.553
#>      G175  5110657 7319.000
#>      G077  5003208 7596.784
#>      G120  4857177 7312.918
#>      G251  4791634 6247.754
#>      G169  4684561 6967.923
#>      G080  4672020 7409.070
#>      G089  4664193 6999.729
#>      G334  4547866 6615.061
#>      G166  4467591 7602.611
#>      G378  4389954 5684.175
#>      G249  4382411 5541.442
```

Plotting the results yields a scatter plot for each stability measure.

```
plot(geStab)
```



For the computation of stability measures a report can be made.

```
report(geStab, outfile = "./myReports/stabReport.pdf")
```

It is possible to calculate the stability measures based on mega environments instead of regular environments. To do so the parameter `useMegaEnv` has to be set to `TRUE`.

```
## Compute stabilities measures based on mega environments computed in
## previous paragraph.
geStabME <- gxeStability(TD = geMegaEnv, trait = "BLUEs_GY", useMegaEnv = TRUE)
summary(geStabME)
#>
#> Cultivar-superiority measure (Top 10% genotypes)
#>  genotype superiority     mean
#>      G202    16062254 4630.041
#>      G288    12951183 4770.062
#>      G249    10485808 5541.442
#>      G250     9531106 5655.763
#>      G248     9465304 5573.973
#>      G316     9317957 5625.830
#>      G383     9113378 5760.066
#>      G384     8779234 5774.064
#>      G378     8629384 5684.175
#>      G260     8434024 5807.864
#>      G136     8397868 5780.283
```

```
#>      G208     8206311 5822.169
#>      G315     8167359 6022.966
#>      G326     8146785 6056.449
#>      G165     8128119 5927.171
#>      G219     8070708 6038.901
#>      G161     7945952 5967.887
#>      G338     7865491 6278.680
#>      G295     7800827 5920.772
#>      G251     7798687 6247.754
#>      G229     7735152 6314.679
#>      G257     7705611 5960.757
#>      G360     7683005 6014.688
#>      G324     7662296 5971.614
#>      G356     7640894 6078.123
#>      G199     7521240 6145.454
#>      G321     7450241 6067.733
#>      G357     7325598 6294.176
#>      G096     7297447 6116.712
#>      G223     7204198 6284.350
#>      G254     7155783 6096.553
#>      G333     7072766 6218.026
#>      G205     6983714 6187.658
#>      G329     6980348 6329.899
#>      G299     6920678 6283.417
#>      G361     6806109 6225.296
#>      G127     6753023 6284.475
#>      G323     6744943 6297.963
#>      G216     6675019 6346.940
#>
#> Static stability (Top 10% genotypes)
#>  genotype   static     mean
#>      G286 13999250 7106.561
#>      G077 13531672 7596.784
#>      G197 13367454 7915.891
#>      G073 12691302 7947.329
#>      G181 12527941 6833.935
#>      G084 12483187 8068.285
#>      G358 12390526 7169.372
#>      G037 12314466 7876.846
#>      G120 12157644 7312.918
#>      G056 12087526 8320.500
#>      G100 11859049 8414.758
#>      G014 11846648 7619.940
#>      G208 11835917 5822.169
#>      G099 11713861 6949.386
#>      G036 11445637 6859.104
#>      G212 11399241 7418.642
#>      G058 11343973 8400.497
#>      G142 11259150 8250.561
#>      G262 11234646 7870.004
#>      G031 11190122 6336.111
#>      G143 11079405 7192.949
#>      G101 10973261 8489.525
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#>      G093 10905123 7427.062
#>      G297 10889964 7831.617
#>      G061 10850468 7181.751
#>      G194 10823502 7343.354
#>      G156 10741754 7402.909
#>      G141 10692245 6609.460
#>      G011 10690663 7825.607
#>      G075 10685906 8006.810
#>      G103 10671127 7766.727
#>      G384 10632688 5774.064
#>      G371 10582157 7090.381
#>      G006 10556652 7691.924
#>      G259 10552739 6720.370
#>      G375 10506227 7634.404
#>      G131 10502525 7139.452
#>      G198 10434018 7556.159
#>      G167 10359247 7260.758
#>
#> Wricke's ecovalence (Top 10% genotypes)
#>  genotype   wricke     mean
#>      G384 12366447 5774.064
#>      G381 10236181 6536.117
#>      G202  9024066 4630.041
#>      G288  8961553 4770.062
#>      G286  8802312 7106.561
#>      G208  7854699 5822.169
#>      G157  7377751 6585.634
#>      G205  6494081 6187.658
#>      G260  6334611 5807.864
#>      G283  6327283 6528.855
#>      G360  6279887 6014.688
#>      G229  5407739 6314.679
#>      G338  5228157 6278.680
#>      G297  5206988 7831.617
#>      G353  5197017 7115.091
#>      G285  5127803 7036.768
#>      G037  5105810 7876.846
#>      G071  5034271 7818.405
#>      G194  5008186 7343.354
#>      G259  4665244 6720.370
#>      G197  4561397 7915.891
#>      G077  4517946 7596.784
#>      G181  4478829 6833.935
#>      G276  4373825 7942.348
#>      G383  3987184 5760.066
#>      G141  3951390 6609.460
#>      G120  3885420 7312.918
#>      G291  3713240 7888.538
#>      G073  3710574 7947.329
#>      G254  3643464 6096.553
#>      G080  3551743 7409.070
#>      G251  3531617 6247.754
#>      G169  3466748 6967.923
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#>      G084  3425281 8068.285
#>      G167  3397592 7260.758
#>      G369  3387634 8326.462
#>      G334  3376417 6615.061
#>      G330  3235845 6609.668
#>      G187  3216586 7480.441
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References

Atlin, G.N., R.J. Baker, K.B. McRae, and X. Lu. 2000. "Selection Response in Subdivided Target Regions." *Crop Science* 40 (1): 7. https://doi.org/10.2135/cropsci2000.4017.

Charter, Richard A., and Ralph A. Alexander. 1993. "A Note on Combining Correlations." *Bulletin of the Psychonomic Society* 31 (2): 123–24. https://doi.org/10.3758/bf03334158.

Finlay, KW, and GN Wilkinson. 1963. "The Analysis of Adaptation in a Plant-Breeding Programme." *Australian Journal of Agricultural Research* 14 (6): 742. https://doi.org/10.1071/ar9630742.

LIN, C. S., and M. R. BINNS. 1988. "A SUPERIORITY MEASURE OF CULTIVAR PERFORMANCE FOR CULTIVAR LOCATION DATA." *Canadian Journal of Plant Science* 68 (1): 193–98. https://doi.org/10.4141/cjps88-018.

Shukla, G K. 1972. "Some Statistical Aspects of Partitioning Genotype-Environmental Components of Variability." *Heredity* 29 (2): 237–45. https://doi.org/10.1038/hdy.1972.87.

Wricke, G. 1962. "Evaluation Method for Recording Ecological Differences in Field Trials." *Z Pflanzenzücht* 47: 92–96.