Extending the package

Muhammad Yaseen

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1 Abstract

How a new analysis is added to DiallelAnalysisR so that it fits the rest of the package: a computational core, an exported function, a result with methods, a help page, tests and a vignette section.

2 The parts of an analysis

1. **Core**: an internal function `.da_<analysis>_core()` that takes the table of cell means (or the plot data) and returns the named list of results; no printing, no options.
2. **Exported function**: checks the arguments (`.da_check_data()`, `.da_column()` for column arguments, `.da_check_number()` for codes), calls the core, and wraps the result with `.da_result()`, which adds the class `c("da_<analysis>", "da_result", "list")`.
3. **Plot**: an internal `.da_plot_<analysis>()`; `plot()` finds it by the class.
4. **Help page**: the model and every formula in LaTeX, every argument, every component of the result, references, examples with every argument written out.
5. **Tests**: closed forms against an independent calculation; input errors; methods.

6. **Vignette**: a section or a vignette in this series.

3 Building blocks available

```
cd <- DiallelAnalysisR:::.da_cell_data(
    y      = GriffingData1$Yield
  , p1     = GriffingData1$Cross1
  , p2     = GriffingData1$Cross2
  , rep    = GriffingData1$Rep
  , method = 1L
  , fn     = "example"
  )
names(cd)
```

```
 [1] "M"        "parents"  "R"        "mse"      "df_e"     "ss_e"
 [7] "anova"    "n_plots"  "cells"    "balanced" "plots"
```

```
round(x = cd$M[1:3, 1:3], digits = 2)
```

```
       1      2      3
1  85.65  87.01  90.46
2  80.69  98.26 111.58
3 102.23 104.56  74.07
```

```
cd$anova
```

```
           Df     Sum Sq   Mean Sq
Rep         3   1036.192  345.3972
Crosses    63 104923.873 1665.4583
Residuals 189  21755.963  115.1109
```

`.da_cell_data()` gives the table of cell means, the error mean square and its degrees of freedom for any of Griffing's layouts; a new analysis starts from it.

4 Example: heterosis over the mid-parent

The heterosis of `Heterosis()` was built from these blocks. Its first step, by hand:

```
cd2 <- DiallelAnalysisR:::.da_cell_data(
    y      = GriffingData2$Yield
  , p1     = GriffingData2$Cross1
  , p2     = GriffingData2$Cross2
  , rep    = GriffingData2$Rep
  , method = 2L
  , fn     = "example"
  )
```

```
M <- cd2$M
mid <- outer(X = diag(M), Y = diag(M), FUN = "+") / 2
het <- 100 * (M - mid) / mid
diag(het) <- NA
round(x = het[1:4, 1:4], digits = 1)
```

```
   1    2    3    4
1 NA -5.4 13.3 29.7
2 NA   NA 29.5 -7.1
3 NA   NA   NA 21.5
4 NA   NA   NA   NA
```

The exported function adds the argument checks, the better-parent and standard heterosis, the t tests with the standard error of each difference from MS_E, a classed result, a plot method, tables for `da_export()` and tests:

```
h <-
  Heterosis(
      y      = Yield
    , Rep    = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data   = GriffingData2
    , Check  = NULL
    , Better = c("higher", "lower")[1]
    )
all.equal(target = h$Heterosis$MP[1:3], current = het[1, 2:4],
 ↪  check.attributes = FALSE)
```

```
[1] TRUE
```

5 Summary

Every analysis of the package follows the same pattern; a new one reuses the cell-means table, the error mean square, the result class, the plot theme and the test helpers.