

Package ‘rhoneycmb’

February 11, 2023

Title Analysis of Honeycomb Selection Designs

Version 2.0.0

Description A useful statistical tool for the construction and analysis of Honeycomb Selection Designs. More information about this type of designs: Fasoula V. (2013) <[doi:10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)> Fasoula V.A., and Tokatlidis I.S. (2012) <[doi:10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0)> Fasoulas A.C., and Fasoula V.A. (1995) <[doi:10.1002/9780470650059.ch3](https://doi.org/10.1002/9780470650059.ch3)> Tokatlidis I. (2016) <[doi:10.1017/S0014479715000150](https://doi.org/10.1017/S0014479715000150)> Tokatlidis I., and Vlachostergios D. (2016) <[doi:10.3390/d8040029](https://doi.org/10.3390/d8040029)>.

Depends R (>= 4.2)

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 7.2.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

LazyData true

Imports stats, utils, graphics

NeedsCompilation no

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Repository CRAN

Date/Publication 2023-02-11 14:40:02 UTC

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analysis	<i>Analysis of the honeycomb selection design.</i>
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Description

This function analyzes the response variable of the data frame.

Usage

```
analysis(
  Main_Data_Frame = NULL,
  Response_Vector = NULL,
  ring = 6,
  blocks = FALSE,
  row_element = NULL,
  plant_element = NULL,
  CRS = 5
)
```

Arguments

Main_Data_Frame	A data frame generated by one of the functions HSD(), HSD0(), HSD01() and HSD03().
Response_Vector	A vector containing the response variable data.
ring	The number of plants per moving ring.
blocks	The moving circular block.
row_element	The position of the plant (number of row) in the center of a moving ring/circular block.
plant_element	The position of the plant (number of plant) in the center of a moving ring/circular block.
CRS	The number of selected plants used for the CRS index.

Value

A list.

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. [10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6). doi:[10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)
- Fasoula V.A., and Tokatlidis I.S. (2012). Development of crop cultivars by honeycomb breeding. *Agronomy for Sustainable Development* 32:161–180. [10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0) doi:[10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0)
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- Tokatlidis I. (2016). Sampling the spatial heterogeneity of the honeycomb model in maize and wheat breeding trials: Analysis of secondary data compared to popular classical designs. *Experimental Agriculture*, 52(3), 371-390. doi:[10.1017/S0014479715000150](https://doi.org/10.1017/S0014479715000150)
- Tokatlidis I., and Vlachostergios D. (2016). Sustainable Stewardship of the Landrace Diversity. *Diversity* 8(4):29. doi:[10.3390/d8040029](https://doi.org/10.3390/d8040029)

Examples

```
main_data<-HSD(7,2,10,10,1)
main_data$Data<-wheat_data$total_yield

analysis(main_data,"Data",6)
```

generate

Available honeycomb selection designs.

Description

This function is used to generate the available honeycomb selection designs including k parameters.

Usage

```
generate(E_gen = NULL)
```

Arguments

E_gen A single number or a vector of entries.

Value

A dataframe.

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. [10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6). doi:[10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)
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Examples

```
generate(1:50)
```

HSD	<i>Construction of the honeycomb selection design.</i>
-----	--

Description

This function creates a data frame of a honeycomb selection design.

Usage

```
HSD(E, K, rows, plpr, distance, poly = TRUE)
```

Arguments

E	The number of entries.
K	The k parameter.
rows	The number of rows.
plpr	The number of plants per row.
distance	The plant-to-plant distance in meters.
poly	If TRUE the polygon pattern is displayed.

Value

A dataframe.

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. 10.1002/9781118497869.ch6. doi:10.1002/9781118497869.ch6
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Examples

```
HSD(7,2,10,10,1)
```

HSD0

Construction of the honeycomb selection design without control.

Description

This function creates a data frame of an honeycomb selection design (one entry, without control).

Usage

```
HSD0(rows, plpr, distance, poly = TRUE)
```

Arguments

rows	The number of rows.
plpr	The number of plants per row.
distance	The plant-to-plant distance in meters.
poly	If TRUE set polygon pattern is displayed.

Value

A dataframe.

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. [10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6). doi:[10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)
- Fasoula V.A., and Tokatlidis I.S. (2012). Development of crop cultivars by honeycomb breeding. *Agronomy for Sustainable Development* 32:161–180. [10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0) doi:[10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0)
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Examples

```
HSD0(10,10,1)
```

HSD01

Construction of the honeycomb selection design with one control.

Description

This function creates a data frame of an honeycomb selection design (one entry, one control).

Usage

```
HSD01(K, rows, plpr, distance, poly = TRUE)
```

Arguments

K	The K parameter.
rows	The number of rows.
plpr	The number of plants per row.
distance	Distance between plants in meters.
poly	If TRUE the polygon pattern is displayed.

Value

A dataframe.

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. [10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6). doi:[10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)
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Examples

```
HSD01(1, 10, 10, 1)
```

HSD03

Construction of the honeycomb selection design with three controls.

Description

This function creates a data frame of a honeycomb selection design (one entry, three controls).

Usage

```
HSD03(K, rows, plpr, distance, poly = TRUE)
```

Arguments

K	The k parameter.
rows	The number of rows.
plpr	The number of plants per row.
distance	Distance between plants in meters.
poly	If TRUE the polygon pattern is displayed.

Value

A dataframe

References

- Fasoula V. (2013). Prognostic Breeding: A New Paradigm for Crop Improvement. *Plant Breeding Reviews* 37: 297-347. [10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6). doi:[10.1002/9781118497869.ch6](https://doi.org/10.1002/9781118497869.ch6)
- Fasoula V.A., and Tokatlidis I.S. (2012). Development of crop cultivars by honeycomb breeding. *Agronomy for Sustainable Development* 32:161–180. [10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0) doi:[10.1007/s13593-011-0034-0](https://doi.org/10.1007/s13593-011-0034-0)
- Fasoulas A.C., and Fasoula V.A. (1995). Honeycomb selection designs. In J. Janick (ed.). *Plant Breeding Reviews* 13: 87-139. doi:[10.1002/9780470650059.ch3](https://doi.org/10.1002/9780470650059.ch3)
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Examples

HSD03(1,10,10,1)

wheat_data

A dataset

Description

A dataset containing observations from an R7 honeycomb selection design.

Usage

wheat_data

Format

wheat_data\$main_spike_weight The weight (g) of the main spike of a single plant.

wheat_data\$tillers_spike_weight The weight (g) of tillers' spikes of a single plant.

wheat_data\$total_yield The total yield (g) of a single plant.

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