

Package ‘BKBreed’

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Type Package

Title Colourful Biometrical Analysis for Plant Breeding and Genetics

Version 0.3.2

Description A compact, colour-first toolkit for the analysis of plant breeding and genetics field experiments. It provides analysis of variance for the randomised block design (RBD) and factorial RBD, a check-anchored intra-block analysis for augmented alpha-lattice designs, and the core biometrical-genetics workflow used in crop improvement: estimation of genetic variability (genotypic and phenotypic coefficients of variation, broad-sense heritability, expected genetic advance), genotypic and phenotypic correlation, path-coefficient analysis, line x tester and Griffing diallel combining-ability analysis (general combining ability and specific combining ability), Mahalanobis D-square genetic-divergence analysis with Tocher and hierarchical clustering, and genotype-by-environment stability analysis (Eberhart-Russell regression and the additive main effects and multiplicative interaction (AMMI) model). Methods follow Griffing (1956) <doi:10.1071/BI9560463> and Eberhart and Russell (1966) <doi:10.2135/cropsci1966.0011183X000600010011x>. Every analysis returns a tidy result object and a publication-ready 'ggplot2' figure using a bespoke high-contrast colour system.

License GPL-3

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Imports stats, utils, grDevices, ggplot2

Suggests ggrepel, patchwork, knitr, rmarkdown, testthat (>= 3.0.0)

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BugReports <https://github.com/bkpraveenars-del/BKBreed/issues>

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Contents

BKBreed-package	2
bk_augmented	3
bk_correlation	4
bk_data	4
bk_diallel	5
bk_diversity	6
bk_frbd	6
bk_lxt	7
bk_palette	8
bk_path	9
bk_plot	9
bk_rbd	10
bk_stability	11
bk_variability	11
scale_colour_bk	12
theme_bk	13
Index	14

BKBreed-package	<i>BKBreed: Colourful Biometrical Analysis for Plant Breeding and Genetics</i>
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Description

A compact, colour-first toolkit for analysing plant-breeding and genetics field experiments: RBD, Factorial RBD and Augmented Alpha-Lattice designs; genetic variability, correlation and path analysis; Mahalanobis D-square divergence; and Eberhart-Russell / AMMI stability. Every analysis returns a tidy object and a publication-ready ggplot2 figure via [bk_plot](#).

Author(s)

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See Also

[bk_rbd](#), [bk_frbd](#), [bk_augmented](#), [bk_variability](#), [bk_correlation](#), [bk_path](#), [bk_diversity](#), [bk_stability](#), [bk_plot](#).

bk_augmented	<i>Augmented Alpha-Lattice / Augmented RCBD analysis</i>
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Description

Analysis of augmented designs. Block effects are estimated by intra-block least squares from replicated checks; every genotype mean is adjusted and classical Federer standard errors are reported.

Usage

```
bk_augmented(data, trait, gen, block, rep = NULL, checks = NULL, alpha = 0.05)
```

Arguments

data	A data frame in long format.
trait	Character; response column.
gen	Character; genotype column (checks and test entries).
block	Character; (incomplete) block column.
rep	Character or NULL; replication column for the alpha-lattice layout.
checks	Character vector of check names; if NULL, genotypes occurring more than once are treated as checks.
alpha	Significance level (default 0.05).

Value

An object of class `bk_augmented` with adjusted means, block effects, error MS and Federer critical differences.

Examples

```
d <- bk_data("augmented")
res <- bk_augmented(d, "grain_yield", "genotype", "block", "rep",
  checks = c("CHK-1", "CHK-2", "CHK-3", "CHK-4"))
res
bk_plot(res)
```

bk_correlation	<i>Genotypic and phenotypic correlation</i>
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Description

Genotypic and phenotypic correlation coefficients among traits, via analysis of covariance.

Usage

```
bk_correlation(data, traits, gen, rep)
```

Arguments

data	A data frame in long format.
traits	Character vector of trait columns (≥ 2).
gen	Character; genotype column.
rep	Character; replication column.

Value

An object of class `bk_correlation` with matrices `rg` and `rp`.

Examples

```
cr <- bk_correlation(bk_data("rbd"),
  c("grain_yield", "plant_height", "tillers", "test_weight"),
  "genotype", "rep")
cr
bk_plot(cr)
```

bk_data	<i>Load a bundled BKBreed example dataset</i>
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Description

Convenience loader for the demonstration datasets shipped with the package.

Usage

```
bk_data(name = c("rbd", "frbd", "augmented", "mlt", "lxt", "diallel"))
```

Arguments

name	One of "rbd", "frbd", "augmented", "mlt", "lxt", "diallel".
------	---

Value

A data frame.

Examples

```
head(bk_data("rbd"))
```

bk_diallel

Griffing diallel combining-ability analysis (Method 2, Model I)

Description

Griffing's (1956) diallel analysis for a half diallel of parents plus one set of F1 crosses without reciprocals (Method 2), with genotypes as fixed effects (Model I). Standard errors are computed exactly by propagating the per-entry error variance through the linear GCA/SCA estimators.

Usage

```
bk_diallel(data, trait, parent1, parent2, rep, alpha = 0.05)
```

Arguments

data	A data frame in long format with one row per plot.
trait	Character; response column.
parent1, parent2	Character; the two parent columns of each entry. Diagonal entries (parent1 == parent2) are the parents/selfs.
rep	Character; replication column.
alpha	Significance level for testing effects (default 0.05).

Value

An object of class `bk_diallel` with the combining-ability ANOVA, parental GCA effects, the SCA matrix, exact standard errors, Baker's predictability ratio and variance components.

See Also

[bk_lxt](#), [bk_plot](#)

Examples

```
res <- bk_diallel(bk_data("diallel"), trait = "grain_yield",
                  parent1 = "parent1", parent2 = "parent2", rep = "rep")
res
bk_plot(res)
bk_plot(res, type = "sca")
```

bk_diversity	<i>Mahalanobis D-square genetic divergence</i>
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Description

Computes Mahalanobis D-square distances among genotypes using the pooled error covariance, then groups them by Tocher and Ward clustering.

Usage

```
bk_diversity(data, traits, gen, rep,
             method = c("tocher", "hierarchical"), clusters = NULL)
```

Arguments

data	A data frame in long format.
traits	Character vector of trait columns.
gen	Character; genotype column.
rep	Character; replication column.
method	Clustering for the default figure: tocher (default) or hierarchical.
clusters	Number of hierarchical clusters; if NULL, matches the Tocher count.

Value

An object of class bk_diversity with the D2 matrix, cluster memberships and cluster means.

Examples

```
dv <- bk_diversity(bk_data("rbd"),
                  c("grain_yield", "plant_height", "tillers", "test_weight"),
                  "genotype", "rep")
dv
bk_plot(dv)
```

bk_frbd	<i>Two-factor Factorial RBD analysis</i>
---------	--

Description

ANOVA for a two-factor factorial in a randomised block design, with main-effect and interaction means and factor-specific critical differences.

Usage

```
bk_frbd(data, trait, factorA, factorB, rep, alpha = 0.05)
```

Arguments

data	A data frame in long format.
trait	Character; response column.
factorA, factorB	Character; the two treatment factor columns.
rep	Character; replication/block column.
alpha	Significance level (default 0.05).

Value

An object of class `bk_frbd`.

Examples

```
res <- bk_frbd(bk_data("frbd"), "grain_yield", "nitrogen", "variety", "rep")
res
bk_plot(res)
```

bk_lxt

Line x Tester combining-ability analysis

Description

Kempthorne's Line x Tester analysis for $l \times t$ crosses in a randomised block design. Partitions crosses into lines, testers and line x tester; estimates GCA and SCA effects; and derives additive and dominance variances (assuming inbred parents, $F = 1$).

Usage

```
bk_lxt(data, trait, line, tester, rep, alpha = 0.05)
```

Arguments

data	A data frame of the crosses in long format.
trait	Character; response column.
line	Character; line (female) column.
tester	Character; tester (male) column.
rep	Character; replication column.
alpha	Significance level for testing GCA/SCA effects (default 0.05).

Value

An object of class `bk_lxt` with the combining-ability ANOVA, GCA effects for lines and testers, SCA effects, proportional contributions and variance components.

See Also

[bk_plot](#)

Examples

```
res <- bk_lxt(bk_data("lxt"), trait = "grain_yield",
              line = "line", tester = "tester", rep = "rep")
res
bk_plot(res)
bk_plot(res, type = "sca")
```

bk_palette	<i>BKBreed colour palettes</i>
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Description

A curated set of high-contrast palettes used across all BKBreed figures.

Usage

```
bk_palette(name = c("field", "spectrum", "canopy", "sunrise", "earth"),
           n = NULL, reverse = FALSE)
```

Arguments

name	Palette name.
n	Number of colours to return (interpolated if needed).
reverse	Logical; reverse the palette order.

Value

A character vector of hex colours.

Examples

```
bk_palette("sunrise", 5)
bk_palette("spectrum", 11)
```

bk_path	<i>Path-coefficient analysis</i>
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Description

Partitions the correlation of each causal trait with a target trait into direct and indirect effects (Wright's path analysis).

Usage

```
bk_path(data, traits, dependent, gen, rep, type = c("genotypic", "phenotypic"))
```

Arguments

data	A data frame in long format.
traits	Character vector of causal (independent) traits.
dependent	Character; the target/effect trait.
gen	Character; genotype column.
rep	Character; replication column.
type	Correlation basis: genotypic (default) or phenotypic.

Value

An object of class `bk_path` with direct/indirect effects and the residual.

Examples

```
pa <- bk_path(bk_data("rbd"),
  c("plant_height", "tillers", "panicle_len", "test_weight"),
  "grain_yield", "genotype", "rep")
pa
bk_plot(pa)
```

bk_plot	<i>Draw the signature figure for a BKBreed result</i>
---------	---

Description

Generic entry point returning the publication-ready figure for whichever analysis produced x.

Usage

```
bk_plot(x, ...)
```

Arguments

x A BKBreed result object.
 ... Passed to the specific method (e.g. type for stability and correlation).

Value

A ggplot2 object.

Examples

```
bk_plot(bk_rbd(bk_data("rbd"), "grain_yield", "genotype", "rep"))
```

bk_rbd	<i>Randomised Block Design (RBD) analysis</i>
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Description

One-call ANOVA for a randomised complete block design with SE, critical difference, CV and compact-letter groupings.

Usage

```
bk_rbd(data, trait, gen, rep, alpha = 0.05)
```

Arguments

data A data frame in long format.
 trait Character; response column.
 gen Character; genotype/treatment column.
 rep Character; replication/block column.
 alpha Significance level for the critical difference (default 0.05).

Value

An object of class bk_rbd with elements anova, means, cv, sem, sed and cd.

See Also

[bk_plot](#), [bk_frbd](#)

Examples

```
res <- bk_rbd(bk_data("rbd"), "grain_yield", "genotype", "rep")
res
bk_plot(res)
```

bk_stability	<i>GxE stability analysis (Eberhart-Russell + AMMI)</i>
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Description

Multi-location trial analysis: combined ANOVA, Eberhart-Russell regression (bi, S2di) and an AMMI decomposition with IPCA scores for biplots.

Usage

```
bk_stability(data, trait, gen, env, rep)
```

Arguments

data	A data frame in long format.
trait	Character; response column.
gen	Character; genotype column.
env	Character; environment/location column.
rep	Character; replication column.

Value

An object of class `bk_stability` with combined ANOVA, Eberhart-Russell parameters and AMMI scores.

Examples

```
st <- bk_stability(bk_data("mlt"), "grain_yield",
                  "genotype", "environment", "rep")
st
bk_plot(st)
bk_plot(st, type = "er")
```

bk_variability	<i>Genetic variability parameters</i>
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Description

Estimates GCV, PCV, ECV, broad-sense heritability, genetic advance and genetic advance as percent of mean for one or more traits.

Usage

```
bk_variability(data, traits, gen, rep, k = 2.063)
```

Arguments

data	A data frame in long format.
traits	Character vector of trait columns.
gen	Character; genotype column.
rep	Character; replication column.
k	Selection differential (default 2.063 for 5 percent intensity).

Value

An object of class `bk_variability` (a data frame with metadata).

Examples

```
v <- bk_variability(bk_data("rbd"),
  c("grain_yield", "plant_height", "tillers", "test_weight"),
  "genotype", "rep")
v
bk_plot(v)
```

scale_colour_bk

Discrete BKBreed colour and fill scales

Description

Discrete colour and fill scales built on the BKBreed palettes.

Usage

```
scale_colour_bk(pal_name = "sunrise", reverse = FALSE, ...)
scale_color_bk(pal_name = "sunrise", reverse = FALSE, ...)
scale_fill_bk(pal_name = "sunrise", reverse = FALSE, ...)
```

Arguments

pal_name	BKBreed palette name (see bk_palette).
reverse	Logical; reverse the palette.
...	Passed to <code>ggplot2::discrete_scale</code> (e.g. name for the legend title).

Value

A `ggplot2` scale.

Examples

```
library(ggplot2)
ggplot(iris, aes(Sepal.Length, Sepal.Width, colour = Species)) +
  geom_point() + scale_colour_bk("sunrise")
```

theme_bk

A clean, high-contrast ggplot2 theme

Description

The BKBreed figure theme.

Usage

```
theme_bk(base_size = 12, base_family = "", grid = TRUE)
```

Arguments

base_size	Base font size in points.
base_family	Font family.
grid	Logical; draw light major grid lines.

Value

A ggplot2 theme object.

Examples

```
library(ggplot2)
ggplot(mtcars, aes(wt, mpg)) + geom_point() + theme_bk()
```

Index

bk_augmented, [2](#), [3](#)
bk_correlation, [2](#), [4](#)
bk_data, [4](#)
bk_diallel, [5](#)
bk_diversity, [2](#), [6](#)
bk_frbd, [2](#), [6](#), [10](#)
bk_lxt, [5](#), [7](#)
bk_palette, [8](#), [12](#)
bk_path, [2](#), [9](#)
bk_plot, [2](#), [5](#), [8](#), [9](#), [10](#)
bk_rbd, [2](#), [10](#)
bk_stability, [2](#), [11](#)
bk_variability, [2](#), [11](#)
BKBreed (BKBreed-package), [2](#)
BKBreed-package, [2](#)

scale_color_bk (scale_colour_bk), [12](#)
scale_colour_bk, [12](#)
scale_fill_bk (scale_colour_bk), [12](#)

theme_bk, [13](#)