

Package ‘FnR’

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Title Inbreeding and Numerator Relationship Coefficients

Version 0.0.0.1

Description Compute inbreeding coefficients using the method of Meuwissen and Luo (1992) <[doi:10.1186/1297-9686-24-4-305](https://doi.org/10.1186/1297-9686-24-4-305)>, and numerator relationship coefficients between individuals using the method of Van Vleck (2007) <<https://pubmed.ncbi.nlm.nih.gov/18050089/>>.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Imports gggroups

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://github.com/nilforooshan/FnR>

BugReports <https://github.com/nilforooshan/FnR/issues>

NeedsCompilation no

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FnR-package

*FnR: Inbreeding and Numerator Relationship Coefficients***Description**

Compute inbreeding coefficients using the method of Meuwissen and Luo (1992) doi: [10.1186/12979686244305](https://doi.org/10.1186/12979686244305), and numerator relationship coefficients between individuals using the method of Van Vleck (2007) <https://pubmed.ncbi.nlm.nih.gov/18050089/>.

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See Also

Useful links:

- <https://github.com/nilforooshan/FnR>
- Report bugs at <https://github.com/nilforooshan/FnR/issues>

calcR

*Compute numerator relationship coefficients between two distinct groups of individuals***Description**

Compute numerator relationship coefficients between two distinct groups of individuals

Usage

```
calcR(ped, set1, set2, type = "notdam-notsire")
```

Arguments

ped : A data frame with integer columns corresponding to ID, SIRE, and DAM. IDs should be sequential, starting from 1. Missing parents (SIRE and DAM) are denoted as 0.

set1 : A set of individual IDs.

set2 : A set of individual IDs, distinct from set1.

type : "notdam-notsire" (default), "sire-sire", or "dam-dam" relationships
 "notdam-notsire" requires set1 and set2 individuals not to be members of ped\$DAM and ped\$SIRE, respectively.
 "sire-sire" requires set1 and set2 individuals to be members of ped\$SIRE.
 "dam-dam" requires set1 and set2 individuals to be members of ped\$DAM.

Value

: Numerator relationship coefficients between set1 and set2 individuals in the form of a matrix (a partition of the numerator relationship matrix **A**).

Examples

```
# A sample pedigree data frame:
ped <- data.frame(
  ID = 1:12,
  SIRE = c(0, 0, 0, 2, 2, 0, 4, 6, 0, 6, 10, 10),
  DAM = c(0, 0, 0, 1, 1, 0, 3, 5, 7, 8, 9, 0)
)

# Example 1: Calculate inbreeding coefficients.
ggroups::inbreed(ped)

# Example 2: Calculate relationship coefficients between two groups of animals,
# one's members not among dams, and the members of the other not among sires.
calcR(ped, set1 = c(12, 6), set2 = c(11, 8), type = "notdam-notsire")
# Since `"notdam-notsire"` is the default type, `type = "notdam-notsire"` might be omitted.

# Example 3: Calculate relationship coefficients between dam 7 and dams 8 and 9.
calcR(ped, set1 = 7, set2 = 8:9, type = "dam-dam")

# Example 4: Calculate relationship coefficients between sires 2 & 6 and sires 4 & 10.
calcR(ped, set1 = c(2, 6), set2 = c(4, 10), type = "sire-sire")
```

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