

Package ‘AlleloBin’

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Type Package

Title A Shiny Application for Allele Binning in Microsatellite Markers

Version 1.0.0

Description Provides allele binning functionality for SSR/microsatellite markers using least-squares minimization (Idury & Cardon (1997) <doi:10.1101/gr.7.11.1104>).
Includes a 'Shiny' application for interactive use, summary statistics, and visualization.

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Encoding UTF-8

Imports shiny, readxl, stats, utils, openxlsx

Suggests testthat (>= 3.0.0), roxygen2

Config/roxygen2/version 8.0.0

Config/testthat/edition 3

URL <https://github.com/vpprasanth/AlleloBin>

BugReports <https://github.com/vpprasanth/AlleloBin/issues>

NeedsCompilation no

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Repository CRAN

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Contents

allele_binning	2
AlleloBin	2
example_data	3
save_results	3

Index	5
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allele_binning	<i>Allele Binning Function</i>
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Description

This function bins observed SSR allele sizes into discrete allele classes using repeat length information (Idury & Cardon, 1997).

Usage

```
allele_binning(data, repeat_lengths, ploidy = 2, progress = FALSE)
```

Arguments

data	A data.frame with columns: Marker, Genotype, Allele1...AlleleN
repeat_lengths	A numeric vector of repeat lengths (same order as markers)
ploidy	Integer, number of alleles per genotype (default = 2)
progress	Logical, whether to update a Shiny progress bar

Value

A list of results per marker: min/max allele, bins, frequencies

AlleloBin	<i>Run AlleloBin Shiny App</i>
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Description

Launches the Shiny application for allele binning.

Usage

```
AlleloBin()
```

Value

No return value, launches 'Shiny' app

example_data

*Example Data***Description**

Example SSR allele dataset ('data.txt') and repeat length file ('info.txt') included with the package.

Details

References Idury, R.M. & Cardon, L.R. (1997). A Simple Method for Automated Allele Binning in Microsatellite Markers. Genome Research, 11:1104–1109.

Value

A data.frame with example SSR allele data

Examples

```
datafile <- system.file("extdata", "data.txt", package = "AlleloBin")
infofile <- system.file("extdata", "repeat_length.txt", package = "AlleloBin")
data <- read.table(datafile, header = FALSE)
info <- read.table(infofile, header = FALSE)
repeat_lens <- as.numeric(info[[1]])
allele_binning(data, repeat_lens, ploidy = 2)
```

save_results

*Save AlleloBin results to Excel***Description**

Utility function to export allele binning results into an Excel workbook. Each marker gets its own worksheet containing bin summary, allele calls, and marker summary with strict decimal formatting.

Usage

```
save_results(results, file)
```

Arguments

results	List of marker results from allele_binning()
file	Output Excel file path

Value

None (writes Excel file to disk)

Examples

```
xlsx_file <- system.file("extdata", "data.xlsx", package = "AlleloBin")
repeat_file <- system.file("extdata", "repeat_length.xlsx", package = "AlleloBin")

data_xlsx <- openxlsx::read.xlsx(xlsx_file)

# Ensure repeat_length is numeric vector, not data frame
repeat_length <- as.numeric(openxlsx::read.xlsx(repeat_file)[[1]])

results <- allele_binning(data_xlsx, repeat_length, ploidy = 2)
save_results(results, file.path(tempdir(), "AlleloBin_Output.xlsx"))
```

Index

allele_binning, [2](#)

AlleloBin, [2](#)

example_data, [3](#)

save_results, [3](#)