

Package ‘CloneVerify’

December 13, 2021

Title This will classify Criollo_22, Matina_1_6, Pound_7 clones using
SNP data

Version 0.0.0.9000

Description This package will take SNP genotypic data and be able to match it to the most commonly used clones that are used for trials and los theier labels (Criollo_22, Matina_1_6, and Pound_7). In the end we will have a file with verified clonal names associated with the unique identifiers of the sample/tree name so we can back-track and relabel them physcially.Lazydata=True

License use_mit_license()

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Depends R (>= 2.10)

Imports tidyverse

LazyData true

Suggests rmarkdown, knitr, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

Author Dayana Rodezno [aut, cre]

Maintainer Dayana Rodezno <drodezno@ufl.edu>

R topics documented:

demo	2
dend	2
na	3
uni_gt	3
Verify	3
Index	5

demo

A standard data set of SNP data of 3 clonal references and 65 Unknown samples that need to be identified as one of the three clones.

Description

I have included an example of our data called "DemoData.csv". The 3 clones in this data set are (Criollo_22, Matina_1_6, Pound_7). Each row in the data set represents an individual tree. The columns are:

Usage

demo

Format

An object of class `data.frame` with 68 rows and 10 columns.

Details

Chip.BC = The chip barcode the genotyping was done on.

Well = The location of the sample on the chip

ID = The status of the tree. Whether it is a clonal reference (Criollo_22, Matina_1_6, Pound_7) or if it the sample/tree that is an unknown(we do not know what it is a clone of). Unknowns can happen for a lot of reasons such as loss of tag information, or poorly kept maps.

DC= A unique identifier given to each sample/tree

Columns 5-10: Are 10 SNP marker names that are used for "offtyping" the trees. These specific markers are used for these three clones because they result in 1 = homozygote_1, 2= homozygote_2, 3= Heterozygote. So they make it really easy to tell these three clones apart.

dend

: *Dendogram*

Description

Groups the samples in a dendogram This function will group samples in a dendogram so that we can verify how many clonal groups are present in the data.

Usage

dend(x)

Arguments

x data frame

Author(s)

Dayana

na	: <i>NA remove</i>
----	--------------------

Description

Removes missing data This function will remove sample rows that have any missing SNP data (NA)

Usage

```
na(data)
```

Arguments

data	data frame
------	------------

Author(s)

Dayana

uni_gt	: <i>Unique clone</i>
--------	-----------------------

Description

Find the unique genotypes in the data set This function will condense the unique data rows to see how many clones we have

Usage

```
uni_gt(data)
```

Arguments

data	data frame
------	------------

Verify	: <i>Verify clones</i>
--------	------------------------

Description

Identifies unknown clones Verifies the unknown clones and identifies the clone in a new column

Usage

```
Verify(data)
```

Arguments

data	data frame
------	------------

Author(s)

Dayana

Dayana

Index

- * **datasets**
 - demo, [2](#)
- demo, [2](#)
- dend, [2](#)
- na, [3](#)
- uni_gt, [3](#)
- Verify, [3](#)