Package 'lievens'

May 3, 2024

Title Real-Time PCR Data Sets by Lievens et al. (2012)

Version 0.0.1

Description Real-time quantitative polymerase chain reaction (qPCR) data sets by Lievens et al. (2012) <doi:10.1093/nar/gkr775>. Provides one single tabular tidy data set in long format, encompassing three dilution series, targeted against the soybean Lectin endogene. Each dilution series was assayed in one of the following PCR-efficiency-modifying conditions: no PCR inhibition, inhibition by isopropanol and inhibition by tannic acid. The inhibitors were co-diluted along with the dilution series. The co-dilution series consists of a five-point, five-fold serial dilution. For each concentration there are 18 replicates. Each amplification curve is 60 cycles long. Original raw data file is available at the Supplementary Data section at Nucleic Acids Research Online <doi:10.1093/nar/gkr775>.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports tibble

Depends R (>= 2.10)

LazyData true

URL https://rmagno.eu/lievens/, https://github.com/ramiromagno/lievens

BugReports https://github.com/ramiromagno/lievens/issues

NeedsCompilation no

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R topics documented:

`lievens` *qPCR data sets by Lievens et al. (2012)*

Description

One single tabular tidy data set in long format, encompassing three data sets of five-point, five-fold dilution series: (i) without any inhibitor, (ii) with isopropanol inhibition and (iii) with tannic acid inhibition. The target amplicon consisted of a sequence within the soybean Lectin endogene. Please read the Methods section of Lievens et al. (2012) for more experimental details.

Each data set consists of a five-point, five-fold dilution series spanning an amplicon copy number range from $100,000$ down to 160. Each concentration is replicated 18 times. Each reaction has been amplified through 60 cycles.

Dilution series:

```
dplyr::filter(lievens, inhibitor == "none")
#> # A tibble: 5,400 x 13
#>    plate well  target dye   inhibitor inhibitor_conc sample sample_type
#>    <fct> <fct> <fct>  <fct> <fct>              <dbl> <fct>  <fct>
#>  1 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  2 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  3 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  4 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  5 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  6 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  7 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  8 soy   <NA>  Le1    SYBR  none                   0 S1     std
#>  9 soy   <NA>  Le1    SYBR  none                   0 S1     std
#> 10 soy   <NA>  Le1    SYBR  none                   0 S1     std
#> # i 5,390 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Isopropanol inhibition:

A series of reactions subjected to inhibition by isopropanol with concentrations: 2.5, 0.5, 0.1, 0.02, and 0.004 % (v/v). Because samples have been co-diluted, the initial copy numbers of the target amplicon also follow the same five-fold progression in tandem: $100,000$, $20,000$, $4,000$, 800 and 160 copies.

```
dplyr::filter(lievens, inhibitor == "isopropanol")
#> # A tibble: 5,400 x 13
#>   plate        well  target dye   inhibitor inhibitor_conc sample sample_type
#>    <fct>          <fct> <fct>  <fct> <fct>              <dbl> <fct>  <fct>
#>  1 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  2 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  3 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
```

```
#>  4 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  5 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  6 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  7 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  8 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#>  9 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#> 10 soy+isopropan~ <NA>  Le1    SYBR  isopropa~            2.5 S1     std
#> # i 5,390 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Tannic acid inhibition:

A series of reactions subjected to inhibition by tannic acid with concentrations: 0.2, 0.04, 0.008, 0.0016 and 0.0032 ul/mL. Because samples have been co-diluted, the initial copy numbers of the target amplicon also follow the same five-fold progression in tandem: 100,000, 20,000, 4,000, 800 and 160.

```
dplyr::filter(lievens, inhibitor == "tannic acid")
#> # A tibble: 5,400 x 13
#>   plate       well  target dye   inhibitor inhibitor_conc sample sample_type
#>    <fct>          <fct> <fct>  <fct> <fct>              <dbl> <fct>  <fct>
#>  1 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  2 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  3 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  4 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  5 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  6 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  7 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  8 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#>  9 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#> 10 soy+tannic ac~ <NA>  Le1    SYBR  tannic a~            0.2 S1     std
#> # i 5,390 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Format

A tibble providing amplification curve data in long format. Each row is for an amplification curve point.

`plate` Plate identifier. There is one identifier for each of the four data sets.

`well` Well identifier, i.e. the position within a PCR plate. This information was not available from the original publication, thus all values are `NA`.

`target` Target identifier. In all data sets the target is an amplicon consisting of soybean Lectin endogene `"Le1"`.

`dye` Type of fluorescence dye, in this data set it is always SYBR Green I master mix (Roche) (`"SYBR"`).

`inhibitor` Name of the molecule used as PCR inhibitor. In the case of the dilution series the value is `"none"`.

`inhibitor_conc` Inhibitor concentration. Units are % (v/v) for isopropanol, and ug/mL for tannic acid.

`sample` Name of the biological sample. Samples have a simple consecutive identifier: S1, S2, ..., S5.

`sample_type` Sample type. All reactions are standard curves, i.e. `"std"`.

`replicate` Replicate identifier.

`copies` Standard copy number of the amplicon.

`dilution` Dilution factor. Higher number means greater dilution, e.g. `5` means a 1:5 (five-fold) dilution relative to most concentrated standard.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

Source

doi:10.1093/nar/gkr775

Examples

```
lievens
```

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