Package 'sisti'

April 28, 2024

Title Real-Time PCR Data Sets by Sisti et al. (2010)

Version 0.0.1

Description This data package contains four datasets of quantitative PCR (qPCR) amplification curves that were used as supplementary data in the research article by Sisti et al. (2010), <doi:10.1186/1471-2105-11-186>. The primary dataset comprises a ten-fold dilution series spanning copy numbers from 3.14 × 10^7 to 3.14 × 10^2, with twelve replicates per concentration. These samples are based on a pGEM-T Promega plasmid containing a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1), amplified using the ND1/ND2 primer pair. The remaining three datasets contain qPCR results in the presence of specific PCR inhibitors: tannic acid, immunoglobulin G (IgG), and quercetin, respectively, to assess their effects on the amplification process. These datasets are useful for researchers interested in PCR kinetics. The original raw data file is available as Additional File 1: <https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-11-186/MediaObjects/12859_2009_3643_MOESM1_ESM.XLS>.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports tibble

Depends R (>= 2.10)

LazyData true

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

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

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-04-28 11:00:02 UTC

R topics documented:

`sisti` *qPCR data sets by Sisti et al. (2010)*

Description

One single tabular tidy data set in long format, encompassing four data sets of amplification curves: (i) six-point, ten-fold dilution series, (ii) tannic acid inhibition, (iii) IgG inhibition and (iv) quercitin inhibition. The target amplicon consisted of a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1). Please read the Methods section of Sisti et al. (2010) for more experimental details.

Dilution series:

A six-point, ten-fold dilution series spanning an amplicon copy number range 3.14×10^7 thru 3.14×10^2. Each concentration is replicated twelve times. Each reaction has been amplified through 50 cycles.

```
dplyr::filter(sisti, plate == "calibration")
#> # A tibble: 3,600 x 13
#>    plate       well  target dye   sample sample_type inhibitor inhibitor_conc
#>    <fct>       <fct> <fct>  <fct> <fct>  <fct>       <fct>             <dbl>
#>  1 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  2 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  3 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  4 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  5 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  6 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  7 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  8 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#>  9 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#> 10 calibration <NA>  MT-ND1 SYBR  pGEM-T std         none                  0
#> # i 3,590 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: 0.000391, 0.000781, 0.00156, 0.00312, 0.00625, 0.0125, 0.025, 0.05 and 0.1 mg/mL. Each tannic acid concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "tannic acid")
#> # A tibble: 2,160 x 13
#>    plate       well  target dye   sample sample_type inhibitor   inhibitor_conc
#>    <fct>       <fct> <fct>  <fct> <fct>  <fct>       <fct>               <dbl>
```

```
#>  1 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  2 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  3 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  4 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  5 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  6 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  7 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  8 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#>  9 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#> 10 tannic acid <NA>  MT-ND1 SYBR  pGEM-T std        tannic acid          0.1
#> # i 2,150 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Immunoglobulin G (IgG) inhibition:

A series of reactions subjected to inhibition by IgG with concentrations: 0.00781, 0.0156, 0.0312, 0.0625, 0.125, 0.25, 0.5, 1 and 2 mg/mL. Each IgG concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "IgG")
#> # A tibble: 2,160 x 13
#>    plate well  target dye   sample sample_type inhibitor inhibitor_conc
#>    <fct> <fct> <fct>  <fct> <fct>  <fct>       <fct>              <dbl>
#>  1 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  2 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  3 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  4 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  5 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  6 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  7 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  8 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#>  9 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#> 10 IgG   <NA>  MT-ND1 SYBR  pGEM-T std         IgG                    2
#> # i 2,150 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Quercitin inhibition:

A series of reactions subjected to inhibition by quercitin with concentrations: 0.000312, 0.000625, 0.00125, 0.0025, 0.005, 0.01, 0.02, and 0.04 mg/mL. Each quercitin concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "quercitin")
#> # A tibble: 1,920 x 13
#>    plate     well  target dye   sample sample_type inhibitor inhibitor_conc
#>    <fct>     <fct> <fct>  <fct> <fct>  <fct>       <fct>             <dbl>
#>  1 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin          0.04
#>  2 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin          0.04
#>  3 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin          0.04
```

```
#>  4 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#>  5 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#>  6 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#>  7 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#>  8 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#>  9 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#> 10 quercitin <NA>  MT-ND1 SYBR  pGEM-T std         quercitin           0.04
#> # i 1,910 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 a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1), thus the values are all `"MT-ND1"`.

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

`sample` Name of the biological sample. All samples are based on a pGEM-T Promega plasmid, so all values are `"pGEM-T"`.

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

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

`inhibitor_conc` Inhibitor concentration in mg/mL.

`replicate` Replicate identifier.

`copies` Standard copy number of the amplicon.

`dilution` Dilution factor. Higher number means greater dilution, e.g. `10` means a 1:10 (ten-fold) dilution.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

Source

doi:10.1186/1471210511186

Examples

```
sisti
```

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