Package: guescini (via r-universe)

September 18, 2024

Type Package

Title Real-Time PCR Data Sets by Guescini et al. (2008)

Version 0.1.0

Description Real-time quantitative polymerase chain reaction (qPCR) data by Guescini et al. (2008) <doi:10.1186/1471-2105-9-326> in tidy format. This package provides two data sets where the amplification efficiency has been modulated: either by changing the amplification mix concentration, or by increasing the concentration of IgG, a PCR inhibitor. Original raw data files: <https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-9-326/MediaObjects/12859_2008_2311_MOESM1_ESM.xls> and <https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-9-326/MediaObjects/12859_2008_2311_MOESM5_ESM.xls>.

License CC BY 4.0

Encoding UTF-8

LazyData true

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

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

RoxygenNote 7.3.1

Roxygen list(markdown = TRUE)

Depends R (>= 2.10)

Imports tibble

Repository https://patterninstitute.r-universe.dev

RemoteUrl https://github.com/ramiromagno/guescini

RemoteRef HEAD

RemoteSha 6c90277eb10da8617223af52fc005aee9c8f1ee4

Contents

`amp_mix_perc` *Amplification mix percentage*

Description

This data set is for a set of quantitative real-time PCR runs that targets the amplification of a sequence of the MT-ND1 gene, for a seven-point, ten-fold a serial dilution starting at 3.14 x 10^7 copies of DNA molecules. In addition, a range of amplification mix quantities ranging from 60% to 100% are also performed. This results in 5 serial dilutions, one for each amplification mix quantity (0.6, 0.7, 0.8, 0.9 and 1.0). Please read the Methods section of Guescini et al. (2008) for more details.

Each data set comprises a seven-point, ten-fold dilution series, repeated in 12 independent runs targeting an amplicon for the MT-ND1 gene. A slight amplification inhibition in the quantitative real-time PCR experiments was obtained by using two systems: decreasing the amplification mix (`amp_mix_perc`) used in the reaction and adding varying amounts of IgG, a known PCR inhibitor. Please read the Methods section of Guescini et al. (2008) for more details.

Format

A tibble with 21,000 rows and 12 variables:

`plate` Plate identifier.

`well` Well identifier. Values are always `NA` (not available). This variable is kept nevertheless to be coherent with other data sets from other similar R data packages.

`dye` The type of dye used. In this data set the values are always `"SYBR"`, meaning SYBR Green I master mix (Roche).

`target` Target identifier: the amplicon used, `"MT_ND1"`.

`sample_type` Sample type (all curves are standards, i.e. `"std"`).

`run` This variable discriminates amplification curves within the group defined by `amp_mix_perc` and `copies`. Range: 1 thru 12.

`replicate` Replicate identifier: 1 thru 3.

`amp_mix_perc` Amplification mix percentage.

`copies` Standard copy number.

`dilution` Dilution factor. Higher number means greater dilution.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

A tibble with 21,000 rows and 11 variables:

`plate` Plate identifier.

`well` Well identifier. Values are always `NA` (not available). This variable is kept nevertheless to be coherent with other data sets from other similar R data packages.

`dye` The type of dye used. In this data set the values are always `"SYBR"`, meaning SYBR Green I master mix (Roche).

`target` Target identifier: the amplicon used, `"MT_ND1"`.

`sample_type` Sample type (all curves are standards, i.e. `"std"`).

`replicate` Replicate identifier: 1 thru 3.

`amp_mix_perc` Amplification mix percentage.

`copies` Standard copy number.

`dilution` Dilution factor. Higher number means greater dilution.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

Source

doi:10.1186/147121059326

doi:10.1186/147121059326

Examples

```
amp_mix_perc
```

```
amp_mix_perc
```

`IgG_inhibition` *IgG inhibition*

Description

This data set is for a set of quantitative real-time PCR runs that were performed in the presence of an optimal amplification reaction mix added with serial dilutions of IgG (0.0, 0.25, 0.50, 1.0, and 2.0 $\mu g/ml$) thus acting as the inhibitory agent. There are two replicates for each concentration of IgG. The concentration of the amplicon ND1/ND2 is 41,700,000 copies. Please read the Methods section of Guescini et al. (2008) for more details.

Format

A tibble with 400 rows and 10 variables:

`plate` Plate identifier.

`well` Well identifier. Values are always `NA` (not available). This variable is kept nevertheless to be coherent with other data sets from other similar R data packages.

`dye` The type of dye used. In this data set the values are always `"SYBR"`, meaning SYBR Green I master mix (Roche).

`target` Target identifier: the amplicon used, `"MT_ND1"`.

`sample_type` Sample type (all curves are standards, i.e. `"std"`).

`replicate` Replicate identifier: 1 thru 3.

`IgG_conc` IgG concentration in $\mu g/ml$.

`copies` Standard copy number.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

Source

doi:10.1186/147121059326

Examples

```
IgG_inhibition
```

Index