

Package ‘micturate’

June 1, 2022

Type Package

Title Tools for urine samples

Version 0.1.0

Description Simple tools for helping with various aspects of urinary analysis.

License GPL (>= 3)

Encoding UTF-8

LazyData true

Depends R (>= 2.10),
magrittr

Imports dplyr,
tidyr,
tibble,
gaml2r

Suggests testthat,
covr,
readr

URL <https://github.com/wilsontom/micturate>

BugReports <https://github.com/wilsontom/micturate/issues>

RoxygenNote 7.1.2

Roxygen list(markdown = TRUE)

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correction_factor	<i>Correction Factor</i>
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Description

Calculate the normalisation correction factor

Usage

```
correction_factor(x, norm_value = 1.006)
```

Arguments

x	a numeric vector of refractive index values
norm_value	a numeric value specifying the target value to normalise to

Value

a numeric vector of correction factors

creatinine_plate_index	<i>96 Well Plate Map for Total Creatinine Assay</i>
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Description

96 Well Plate Map for Total Creatinine Assay

Usage

```
creatinine_plate_index
```

Format

A tbl_df

WELL well position

NAME sample name

CLASS sample class

CONC concentration

nacl_sg_standards	<i>Specific Gravity Values for NaCl Standards</i>
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Description

Specific Gravity Values for NaCl Standards

Usage

nacl_sg_standards

Format

A tbl_df

sample_name sample name

specific_gravity specific gravity

normalisation_volumes	<i>Normalisation Volumes</i>
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Description

Calculate the required volumes based on normalisation correction factors

Usage

normalisation_volumes(x, total_volume = 500)

Arguments

x a numeric vector of correction factors

total_volume a numeric value specifying the total required volume (urine + water)

Value

a tbl_df of required urine and water volumes

pooling_sheet	<i>Urine Pooling Sheet</i>
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Description

Urine Pooling Sheet

Usage

```
pooling_sheet(ri_data, norm_value, volume)
```

Arguments

ri_data	a tbl_df of sample_name , value and group
norm_value	a numeric value to normalise to
volume	a numeric value for the total volume per sample

Value

a tbl_df of pooling volumes for each **sample_name**

refractive_index_prediction	<i>Predict RI values from HPLC-RI</i>
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Description

Predict RI values from HPLC-RI

Usage

```
refractive_index_prediction(gaml_file)
```

Arguments

gaml_file	a GAML file containing HPLC-RI data. See <code>micturate::plate_maps('urine_ri')</code> for more details
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Value

a tbl_df of predicted refractive index values

urea_plate_index	<i>96 Well Plate Map for Total Urea Assay</i>
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Description

96 Well Plate Map for Total Urea Assay

Usage

urea_plate_index

Format

A tbl_df

WELL well position

NAME sample name

CLASS sample class

CONC concentration

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