

# Package: micturate (via r-universe)

June 6, 2026

**Type** Package

**Title** Tools for urine samples

**Version** 0.1.2

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

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5), magrittr

**Imports** base64enc, dplyr, tidyr, tibble, xml2

**Suggests** testthat, covr, readr

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

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

**RoxygenNote** 7.3.2

**Roxygen** list(markdown = TRUE)

**Config/pak/sysreqs** libicu-dev libxml2-dev

**Repository** <https://wilsontom.r-universe.dev>

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**RemoteUrl** <https://github.com/wilsontom/micturate>

**RemoteRef** HEAD

**RemoteSha** 964a84544f78b674814ad6af9525f5fc09b6956c

## Contents

correction_factor . . . . .	2
creatinine_plate_index . . . . .	2
normalisation_volumes . . . . .	3
pooling_sheet . . . . .	3
refractive_index_prediction . . . . .	4
sampel_adjustments . . . . .	4
urea_plate_index . . . . .	5

**Index****6**


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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

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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

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normalisation\_volumes *Normalisation Volumes*

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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

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pooling\_sheet        *Urine Pooling Sheet*

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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**

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refractive\_index\_prediction  
*Predict RI values from HPLC-RI*

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**Description**

Predict RI values from HPLC-RI

**Usage**

```
refractive_index_prediction(gaml_file, standards)
```

**Arguments**

gaml_file	a GAML file containing HPLC-RI data.
standards	a two column tbl_df of external calibration standards. Columns must be named sample_name and specific_gravity. sample_name should use the format S01, S02, S03, etc... If NULL then a set of package calibration standards will be used instead.

**Value**

a tbl\_df of predicted refractive index values

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samel\_adjustments     *Urine Sample Adjustments*

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**Description**

Urine Sample Adjustments

**Usage**

```
samel_adjustments(ri_data, norm_value, volume)
```

**Arguments**

ri_data	a tbl_df of <b>sample_name, value</b>
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**

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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

# Index

## \* datasets

- creatinine\_plate\_index, [2](#)
- urea\_plate\_index, [5](#)

correction\_factor, [2](#)  
creatinine\_plate\_index, [2](#)

normalisation\_volumes, [3](#)

pooling\_sheet, [3](#)

refractive\_index\_prediction, [4](#)

sampel\_adjustments, [4](#)

urea\_plate\_index, [5](#)