

Package ‘tikatuwq’

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Type Package

Title Water Quality Analysis Tools for the Brazilian Context

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Maintainer Vinicius Saraiva Santos <vinisaraiva@gmail.com>

Description Tools to import, clean, validate, and analyze freshwater quality data in Brazil. Implements water quality indices including the Water Quality Index (WQI/IQA), the Trophic State Index (TSI/IET) after Carlson (1977) <[doi:10.4319/lo.1977.22.2.0361](https://doi.org/10.4319/lo.1977.22.2.0361)> and Lamparelli (2004) <<https://www.teses.usp.br/teses/disponiveis/41/41134/tde-20032006-075813/publico/TeseLamparelli2004.pdf>>, and the National Sanitation Foundation Water Quality Index (NSF WQI) <[doi:10.1007/s11157-023-09650-7](https://doi.org/10.1007/s11157-023-09650-7)>. The package also checks compliance with Brazilian standard CONAMA Resolution 357/2005 <https://conama.mma.gov.br/?id=450&option=com_sisconama&task=arquivo.download> and generates reproducible reports for routine monitoring workflows.

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URL <https://github.com/tikatuwq/tikatuwq>,
<https://tikatuwq.github.io/tikatuwq/>

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Author Vinicius Saraiva Santos [aut, cre] (ORCID:
 <<https://orcid.org/0009-0007-1387-7927>>)
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clean_units	<i>Normalize/standardize units (placeholder)</i>
-------------	--

Description

Extension point to normalize units (e.g., mg/L, uS/cm). Currently returns df unchanged.

Usage

```
clean_units(df, units_map = NULL)
```

Arguments

- df Input data frame / tibble.
- units_map Optional mapping of units.

Value

The input df unchanged (placeholder).

See Also

[read_wq\(\)](#)

Examples

```
clean_units(data.frame(ph = c(7, 7.2), od = c(6.5, 7.0)))
```

conama_check	<i>CONAMA conformity check (detailed; default class = "2")</i>
--------------	--

Description

For each parameter present in df, adds columns:

- *_ok (logical),
- *_status one of "ok", "acima_do_maximo", "abaixo_do_minimo",
- *__lim_min and *__lim_max (thresholds used),
- *__delta (difference to the relevant limit; >0 above max, <0 below min, 0 if ok).

If multiple limit rows exist for the same parameter, *_ok is TRUE if any row is satisfied; for status/lim_min/lim_max/delta, the first satisfied row is chosen; if none satisfy, the row with the smallest absolute violation (min |delta|) is used.

Usage

```
conama_check(df, classe = "2")
```

Arguments

df	A tibble/data.frame with parameter columns (e.g., ph, turbidez, od, dbo).
classe	Character class label (e.g., "especial", "1", "2", "3", "4").

Value

The input df with additional columns per parameter as described.

See Also

[conama_limits\(\)](#), [conama_summary\(\)](#), [conama_report\(\)](#), [conama_text\(\)](#)

Examples

```
## Not run:
data("wq_demo", package = "tikatuwq")
head(conama_check(wq_demo, classe = "2"))

## End(Not run)
```

conama_limits

Limits for Brazilian CONAMA 357/2005

Description

Returns the parameter limits defined by CONAMA Resolution 357/2005 for a given water-use class.

Usage

```
conama_limits(class)
```

Arguments

class	Integer or character. Target class (e.g., 1, 2, 3, 4 or "special"), according to CONAMA 357/2005.
-------	---

Value

A tibble/data frame with one row per parameter and regulatory thresholds. Typical columns:

- parametro: parameter name (character, normalized to snake_case)
- classe: class label (character)
- min/max (or equivalents): numeric thresholds (may be NA)
- other metadata columns if present (e.g., unit, criterion)

Examples

```
# Class 2 thresholds (first rows)
head(conama_limits(2))
```

conama_report	<i>CONAMA conformity report (table)</i>
---------------	---

Description

CONAMA conformity report (table)

Usage

```
conama_report(  
  df,  
  classe = "2",  
  only_violations = TRUE,  
  pretty = FALSE,  
  decimal_mark = ",",  
  big_mark = "."  
)
```

Arguments

df	Input data
classe	CONAMA class label (e.g., "2")
only_violations	If TRUE, returns only rows with status != "ok"
pretty	If TRUE, returns formatted numeric columns for display
decimal_mark	Decimal separator (default ",")
big_mark	Thousands separator (default ".")

Value

A tibble. When pretty = FALSE: parametro, valor, lim_min, lim_max, status, delta. When pretty = TRUE, numeric columns are formatted as character with "natural" decimals.

See Also

[conama_summary\(\)](#), [conama_text\(\)](#)

Examples

```
## Not run:  
data("wq_demo", package = "tikatuwq")  
conama_report(wq_demo, classe = "2", only_violations = TRUE)  
conama_report(wq_demo, classe = "2", only_violations = TRUE, pretty = TRUE)  
  
## End(Not run)
```

conama_summary	<i>CONAMA conformity summary (long format)</i>
----------------	--

Description

CONAMA conformity summary (long format)

Usage

```
conama_summary(df, classe = "2")
```

Arguments

df	Input data
classe	CONAMA class label

Value

A tibble with columns: parametro, valor, lim_min, lim_max, status, ok, delta.

See Also

[conama_check\(\)](#), [conama_report\(\)](#), [conama_text\(\)](#)

Examples

```
## Not run:
data("wq_demo", package = "tikatuwq")
head(conama_summary(wq_demo, classe = "2"))

## End(Not run)
```

conama_text	<i>Text summary of conformity (bulleted, formatted)</i>
-------------	---

Description

Text summary of conformity (bulleted, formatted)

Usage

```
conama_text(
  df,
  classe = "2",
  only_violations = FALSE,
  decimal_mark = ",",
  big_mark = "."
)
```

Arguments

df	Input data
classe	CONAMA class label
only_violations	If TRUE, list only parameters with violation
decimal_mark	Decimal separator (default ",")
big_mark	Thousands separator (default ".")

Value

Character vector of lines (first line is a header, the rest are bullets).

See Also

[conama_summary\(\)](#), [conama_report\(\)](#)

Examples

```
## Not run:
data("wq_demo", package = "tikatuwq")
cat(conama_text(wq_demo, classe = "2"), sep = "\n")

## End(Not run)
```

generate_analysis	<i>Generate analytical paragraphs (rule-based)</i>
-------------------	--

Description

Produces 3–5 short, human-readable paragraphs summarizing water quality, using IQA/WQI, CONAMA-357 compliance and (optionally) simple time trends. It is **rule-based** (não usa IA) e aceita metadados opcionais para compor o texto.

Usage

```
generate_analysis(
  df,
  classe_conama = "2",
  incluir_tendencia = TRUE,
  parametros_tendencia = c("turbidez", "od", "pH"),
  contexto = list(rio = NA, periodo = NA, cidade = NA)
)
```

Arguments

<code>df</code>	Data frame contendo ao menos a coluna ponto. Recomenda-se também as colunas necessárias para checagens CONAMA e para o cálculo do IQA.
<code>classe_conama</code>	Character (ex. "2"). Classe-alvo para a checagem da Resolução CONAMA 357/2005.
<code>incluir_tendencia</code>	Logical; se TRUE, calcula tendências lineares simples ao longo do tempo.
<code>parametros_tendencia</code>	Character vector; nomes dos parâmetros para testar tendência temporal.
<code>contexto</code>	Lista com metadados opcionais (PT/EN), por exemplo <code>list(rio = "Rio Pardo", periodo = "jan-jun/2025", cidade = "Lençóis")</code> . As chaves aceitas são rio/river, periodo/period, cidade.

Value

Vetor de character com 3 a 5 parágrafos analíticos prontos para relatório.

See Also

[iqa\(\)](#), [conama_check\(\)](#)

Examples

```
## Not run:
library(tikatuwq)
data("wq_demo")
txt <- generate_analysis(
  df = wq_demo,
  classe_conama = "2",
  incluir_tendencia = TRUE,
  parametros_tendencia = c("turbidez", "od", "pH"),
  contexto = list(rio = "Rio Azul", periodo = "jan-jun/2025")
)
cat(paste(txt, collapse = "\n\n"))

## End(Not run)
```

iet_carlson

Trophic State Index (Carlson)

Description

Computes Carlson's Trophic State Index (TSI/IET) from Secchi depth, chlorophyll-a, and total phosphorus. Returns component scores and the overall IET as the row-wise mean of available components.

Usage

```
iet_carlson(secchi = NULL, clorofila = NULL, tp = NULL)
```

Arguments

secchi	Numeric vector with Secchi depth (m).
clorofila	Numeric vector with chlorophyll-a (ug/L).
tp	Numeric vector with total phosphorus (ug/L).

Details

Implemented component formulas (Carlson 1977):

- $TSI_Secchi = 60 - 14.41 * \log_{10}(secchi)$
- $TSI_Chla = 9.81 * \log_{10}(clorofila) + 30.6$
- $TSI_TP = 14.42 * \log_{10}(tp) + 4.15$

Inputs may contain NA and are recycled according to R rules. The overall index IET is the row mean of the available components (`na.rm = TRUE`).

Value

A data frame with columns (when applicable):

- `TSI_Secchi` — component from Secchi depth.
- `TSI_Chla` — component from chlorophyll-a.
- `TSI_TP` — component from total phosphorus.
- `IET` — overall Carlson index (row mean).

References

Carlson, R. E. (1977). *A trophic state index for lakes*. Limnology and Oceanography, 22(2), 361–369. doi:10.4319/lo.1977.22.2.0361

See Also

[iet_lamparelli\(\)](#), [iqa\(\)](#), [conama_check\(\)](#)

Examples

```
# Example data
secchi <- c(1.2, 0.8, 0.4)      # m
clorofila <- c(5, 12, 30)      # ug/L
tp <- c(20, 40, 70)           # ug/L

iet_carlson(secchi = secchi, clorofila = clorofila, tp = tp)

# With only one component
iet_carlson(secchi = secchi)
```

iet_lamparelli	<i>Trophic State Index (Lamparelli)</i>
----------------	---

Description

Computes components of the Lamparelli trophic state index (TSI/IET) from total phosphorus, chlorophyll-a, and Secchi depth, and returns the overall Lamparelli index as the row-wise mean of available components.

Usage

```
iet_lamparelli(
  tp = NULL,
  chla = NULL,
  sd = NULL,
  ambiente = c("rio", "reservatorio")
)
```

Arguments

tp	Numeric total phosphorus (mg/L).
chla	Numeric chlorophyll-a (ug/L).
sd	Numeric Secchi disk depth (m).
ambiente	Character, environment type: 'rio' or 'reservatorio'.

Details

Implemented component formulas (simple skeleton):

- $IET_TP = 10 + 10 * \log_{10}(\max(tp, 0.001))$
- $IET_Chla = 10 + 10 * \log_{10}(\max(chla, 0.001))$
- $IET_Secchi = 60 - 14.41 * \log_{10}(\max(sd, 0.001))$

The overall IET_Lamp is the row mean of available components (`na.rm = TRUE`). Inputs are recycled by standard R vector recycling rules and can contain NA.

This is a minimal, pragmatic implementation intended for quick summaries; practitioners should confirm the most appropriate equations/coefficients for the specific waterbody type and region before regulatory use.

Value

A data frame with columns (when applicable):

- IET_TP — component from total phosphorus.
- IET_Chla — component from chlorophyll-a.
- IET_Secchi — component from Secchi depth.
- IET_Lamp — overall Lamparelli index (row mean).
- ambiente — the informed environment label.

References

- Carlson, R. E. (1977). *A trophic state index for lakes*. Limnology and Oceanography, 22(2), 361–369. doi:10.4319/lo.1977.22.2.0361
- Lamparelli, M. C. (2004). *Graus de trofia em corpos d'água do Estado de São Paulo*. (Tese de Doutorado). Instituto de Biociências, USP.

See Also

`iet_carlson()`, `iqa()`, `conama_check()`

Examples

```
# Vectors (can include NA)
tp  <- c(0.02, 0.05, 0.10)      # mg/L
chla <- c(5, 12, 30)            # ug/L
sd  <- c(1.2, 0.8, 0.4)         # m

iet_lamparelli(tp = tp, chla = chla, sd = sd, ambiente = "reservatorio")

# With a single component:
iet_lamparelli(tp = tp, ambiente = "rio")
```

iqa	<i>Water Quality Index (WQI / IQA)</i>
-----	--

Description

Computes IQA/WQI by combining parameter-specific sub-scores (Q_i) via a **weighted mean**. Sub-scores are obtained by piecewise-linear interpolation over approximate curves (CETESB/NSF-like).

Usage

```
iqa(
  df,
  pesos = c(od = 0.17, coliformes = 0.15, dbo = 0.1, nt_total = 0.1, p_total = 0.1,
    turbidez = 0.08, tds = 0.08, pH = 0.12, temperatura = 0.1),
  method = c("CETESB_approx"),
  na_rm = FALSE
)
```

Arguments

df	Data frame (or tibble) with required parameter columns. Expected defaults (Portuguese names): od, coliformes, dbo, nt_total, p_total, turbidez, tds, pH (or pH), temperatura.
pesos	Named numeric weights for each parameter (sum not required). Defaults follow CETESB/NSF practice:

	• <code>od = 0.17</code> • <code>coliformes = 0.15</code> • <code>dbo = 0.10</code> • <code>nt_total = 0.10</code> • <code>p_total = 0.10</code> • <code>turbidez = 0.08</code> • <code>tds = 0.08</code> • <code>pH = 0.12</code> (mapped to column <code>ph</code> if needed) • <code>temperatura = 0.10</code>
<code>method</code>	Character scalar; interpolation table set. Currently only "CETESB_approx".
<code>na_rm</code>	Logical; if FALSE (default), rows containing missing <code>Qi</code> values will trigger an error. If TRUE, the IQA is computed using only available parameters, with the denominator adjusted to the sum of the weights of present parameters.

Details

Column name compatibility:

- The interpolation table uses the key "pH". If your data uses a `ph` column (lowercase), it is automatically mapped to the "pH" curve.
- All other parameter names are used as-is.

Values are clipped into $[0, 100]$ after aggregation.

Value

The input `df` with an added numeric column `IQA`. The attribute "iqa_method" is set on the returned `data.frame/tibble`.

Examples

```
# Minimal example using the demo data:
d <- wq_demo
d2 <- iqa(d, na_rm = TRUE)
head(d2$IQA)
```

 nsfwqi

NSF Water Quality Index (NSF WQI, prototype)

Description

Computes a **prototype** NSF WQI as a weighted arithmetic mean of parameter sub-scores (`Qi`) using simple piecewise rules. This is intended for quick demonstrations and is **not** a full replication of the original NSF curves.

Usage

```
nsfwqi(
  df,
  pesos = c(do = 0.17, fc = 0.16, ph = 0.11, bod = 0.11, temp_change = 0.1, po4 = 0.1,
    no3 = 0.1, turbidez = 0.08, sst = 0.07),
  na_rm = FALSE
)
```

Arguments

<code>df</code>	Data frame containing columns compatible with the mapping above.
<code>pesos</code>	Named numeric vector with parameter weights. Defaults follow a common NSF WQI variant: <code>do=.17, fc=.16, ph=.11, bod=.11, temp_change=.10, po4=.10, no3=.10, turbidez=.08, sst=.07</code> .
<code>na_rm</code>	Logical; allow NA per row and rescale weights to available parameters (TRUE) or error on missing inputs (FALSE).

Details

The function accepts both NSF-style column names and common Brazilian aliases. The mapping tried (if present) is:

- `do` <- `od`
- `fc` <- `coliiformes`
- `ph` <- `pH` or `ph`
- `bod` <- `dbo`
- `turbidez` stays `turbidez`
- `sst` <- `solidos_suspensos`
- `po4` <- `po4` or `p_ortofosfato`
- `no3` <- `no3` or `n_nitrato`
- `temp_change` must be supplied as-is (delta T to reference)

If `na_rm = TRUE`, weights are rescaled **per row** to the parameters available in that row. If `na_rm = FALSE` (default), any missing required input leads to an error.

Value

The input `df` with an added numeric column `NSFWQI`.

Examples

```
d <- wq_demo
# create minimal aliases so the prototype can run
d$do <- d$od
d$fc <- d$coliiformes
d$ph <- d$ph
d$bod <- d$dbod
```

```
# others are missing; use na_rm = TRUE to rescale weights by row
out <- nsfwqi(d, na_rm = TRUE)
head(out$NSFWQI)
```

plot_box	<i>Boxplots by site/parameter</i>
----------	-----------------------------------

Description

Boxplots of one numeric parameter grouped by a categorical column.

Usage

```
plot_box(df, parametro, by = "ponto")
```

Arguments

df	Data frame with water quality data.
parametro	Character; name of the numeric parameter column.
by	Character; grouping column (e.g., "ponto").

Value

A ggplot object.

See Also

[plot_series\(\)](#), [plot_heatmap\(\)](#), [iqa\(\)](#)

Examples

```
data(wq_demo)
plot_box(wq_demo, "turbidez", by = "ponto")
```

plot_heatmap	<i>Heatmap of parameters vs. sites</i>
--------------	--

Description

Heatmap for long-format data (date x parameter).

Usage

```
plot_heatmap(df_long)
```

Arguments

df_long Long-format data frame with columns data, parametro, valor.

Value

A ggplot object.

Examples

```
# Example: reshape wq_demo to long and plot
data(wq_demo)
library(tidyr)
df_long <- tidyr::pivot_longer(
  wq_demo,
  cols = c("ph", "od", "turbidez", "dbo"),
  names_to = "parametro",
  values_to = "valor"
)
plot_heatmap(df_long)
```

plot_iqa	<i>Plot IQA by site/date</i>
----------	------------------------------

Description

Bar plot of IQA values per site/date. Requires an IQA column.

Usage

```
plot_iqa(df)
```

Arguments

df Data frame returned by iqa() (or with equivalent columns).

Value

A ggplot object.

See Also

[iqa\(\)](#), [plot_series\(\)](#), [plot_box\(\)](#)

Examples

```
data(wq_demo)
d <- iqa(wq_demo, na_rm = TRUE)
plot_iqa(d)
```

plot_map

Mapa interativo de pontos de coleta

Description

Gera um mapa Leaflet com os pontos de coleta que possuam coordenadas de latitude e longitude validas. Mostra informacoes adicionais no popup.

Usage

```
plot_map(
  data,
  popup_cols = NULL,
  cluster = TRUE,
  color_by = NULL,
  tiles = "OpenStreetMap"
)
```

Arguments

data	Um data.frame contendo as colunas de coordenadas. Sao aceitos nomes "latitude"/"longitude" ou "lat"/"lon".
popup_cols	Vetor de colunas a exibir no popup (ex.: c("rio","ponto","data","iqa")). Se NULL, usa colunas comuns se existirem.
cluster	Agrupar marcadores proximos (TRUE/FALSE). Default = TRUE.
color_by	Nome de coluna para colorir os pontos (opcional). Se for "iqa", aplica classes de qualidade da agua.
tiles	Provedor de tiles (default = "OpenStreetMap").

Value

Objeto htmlwidget (mapa Leaflet).

Examples

```
df <- data.frame(
  rio = c("Buranhem", "Chamagunga"),
  ponto = c("P1", "P2"),
  data = as.Date(c("2025-09-20", "2025-09-21")),
  latitude = c(-16.435, -16.498),
  longitude = c(-39.062, -39.080),
  iqa = c(72, 58)
)
plot_map(df, popup_cols = c("rio", "ponto", "data", "iqa"), color_by = "iqa")
```

plot_series	<i>Time series by parameter</i>
-------------	---------------------------------

Description

Plot a time series for one numeric parameter, optionally colored/faceted by a grouping column.

Usage

```
plot_series(df, parametro, facet = NULL)
```

Arguments

df	Data frame with a data column (Date/POSIXct) and the parameter column.
parametro	Character; name of the numeric column to plot on Y.
facet	Character or NULL; optional grouping column name to color/facet.

Value

A ggplot object.

See Also

[plot_box\(\)](#), [plot_heatmap\(\)](#), [iqa\(\)](#)

Examples

```
data(wq_demo)
# Basic: time series of turbidity
p <- plot_series(wq_demo, "turbidez")
# With color/facet by sampling point
p2 <- plot_series(wq_demo, "turbidez", facet = "ponto")
```

read_wq	<i>Read water-quality CSV (robust parsing)</i>
---------	--

Description

Reads a CSV file with **comma or semicolon delimiter** and **comma or dot** as decimal mark, ignoring unit suffixes (e.g., "0,04 mg/L"). Everything is read as text first, column names are normalized, and likely numeric columns are parsed robustly. A conservative safeguard adjusts obviously out-of-range pH values (e.g., 72 -> 7.2).

Usage

```
read_wq(path, tz = "America/Bahia")
```

Arguments

path	Path to the CSV file.
tz	Time zone for dates (kept for compatibility; dates are Date).

Value

A tibble with:

- normalized, lowercase column names (spaces to _, non-alnum removed);
- numeric columns parsed ignoring unit strings;
- data parsed to Date (tries ymd then dmy);
- ponto coerced to character (if present).

Parsed numeric candidates

```
c("ph", "od", "turbidez", "dbo", "coliformes", "p_total", "ptotal", "fosforo_total", "temperatura", "ec", "co
```

See Also

```
clean\_units\(\), validate\_wq\(\), conama\_check\(\), iqa\(\)
```

Examples

```
## Not run:
# Minimal example (write a small CSV and read it):
tmp <- tempfile(fileext = ".csv")
writeLines(
  c("ponto;data;ph;od;turbidez",
    "R1_01;2025-01-20;7,2;6,8;5,1",
    "R1_01;21/01/2025;7.1;7.0;4.8 mg/L"),
  tmp
)
x <- read_wq(tmp)
```

```
str(x)

## End(Not run)
```

render_report	<i>Render a water-quality report from the internal R Markdown template</i>
---------------	--

Description

Renders an HTML report using the package's internal R Markdown template. By default, the output is written to a **temporary directory** to comply with CRAN policies. The function returns (invisibly) the full path to the generated file.

Usage

```
render_report(
  df,
  meta = list(river = NA, period = NA),
  output_file = "wq_report.html",
  output_dir = tempdir(),
  template = system.file("templates", "report_rmd.Rmd", package = "tikatuwq")
)
```

Arguments

df	Data frame with the input data used by the template.
meta	Named list with contextual metadata (e.g., river, period).
output_file	File name for the report (default "wq_report.html").
output_dir	Directory where the file will be written (default tempdir()). It will be created if it does not exist.
template	Path to the internal template file. Defaults to the package Rmd template shipped under inst/templates/report_rmd.Rmd.

Details

The template expects a data frame with columns compatible with the package (e.g., ponto, data, parameters used by IQA/CONAMA checks). You can pass optional metadata via meta, such as river and period.

This function relies on **rmarkdown** (listed in Suggests). If the package is not available, an informative error is thrown.

Value

Invisible character string: the absolute path to the generated report.

Notes

- The default output directory is `tempdir()` to avoid writing into the user's project folder during examples or automated checks.
- The template is an **Rmd** (R Markdown). If you prefer Quarto, provide a custom template path to a `.qmd` and ensure your environment supports it.

See Also

`rmarkdown::render()`

Examples

```
# Minimal example (writes to a temporary directory)
d <- wq_demo
path <- render_report(d, meta = list(river = "Example River", period = "Jan-Feb"))
file.exists(path)
```

resume_wq

Descriptive summaries by group

Description

Computes basic descriptive statistics (mean, median, sd) for all **numeric** columns in `df`, grouped by one or more keys.

Usage

```
resume_wq(df, by = c("ponto", "mes"), funs = c("mean", "median", "sd"))
```

Arguments

<code>df</code>	A data frame or tibble.
<code>by</code>	Character vector with grouping column names (default <code>c("ponto", "mes")</code>). Any names not present in <code>df</code> are ignored.
<code>funs</code>	Deprecated (kept for compatibility; ignored). The function always computes mean, median and sd with <code>na.rm = TRUE</code> .

Details

- Grouping columns not found in `df` are silently dropped.
- If no grouping columns remain, an error is thrown.
- Only numeric columns are summarized; if none exist, an error is thrown.
- Missing values are ignored (`na.rm = TRUE`).

Value

A tibble with the grouping keys and one column per statistic/variable, named as {var}_{stat} (e.g., od_mean, od_median, od_sd).

See Also

[dplyr::summarise\(\)](#), [dplyr::across\(\)](#)

Examples

```
# Using the demo dataset shipped with the package
d <- wq_demo
# Example: group by point (ponto)
s1 <- resume_wq(d, by = "ponto")
head(s1)

# Example: group by point and month (if 'mes' exists in your data)
# s2 <- resume_wq(d, by = c("ponto", "mes"))
```

 validate_wq

Validate presence of required columns

Description

Ensures a minimal set of columns exists in the dataset; otherwise throws an error listing the missing names.

Usage

```
validate_wq(
  df,
  required = c("ph", "turbidez", "od", "dbo", "nt_total", "p_total", "tds",
    "temperatura", "coliiformes")
)
```

Arguments

df Input data frame / tibble.

required Character vector of required column names.

Value

The input df if valid; otherwise, an error is thrown.

See Also

[read_wq\(\)](#), [conama_check\(\)](#)

Examples

```
df_ex <- data.frame(
  ph = 7, turbidez = 2, od = 7, dbo = 3,
  nt_total = 0.8, p_total = 0.05, tds = 150,
  temperatura = 24, coliformes = 200
)
validate_wq(df_ex)
```

wq_demo

Demo water quality dataset

Description

A tiny example dataset used in examples and vignettes. Column names follow the package's Portuguese conventions (e.g., ponto, data, turbidez).

Usage

```
data(wq_demo)
```

Format

A data frame (tibble) with 20 rows and 11 columns:

ponto character, monitoring point id
data Date, sampling date
ph numeric, pH
od numeric, dissolved oxygen (mg/L)
turbidez numeric, NTU
dbo numeric, mg/L
coliformes integer, MPN/100 mL
p_total numeric, total phosphorus (mg/L)
nt_total numeric, total nitrogen (mg/L)
temperatura numeric, degrees Celsius
tds numeric, total dissolved solids (mg/L)

Details

The dataset is simulated for illustrative purposes and is suitable for quick examples of `iqa()`, `conama_check()`, and plotting helpers.

Source

Simulated for package examples.

See Also

[iqa\(\)](#), [conama_check\(\)](#), [plot_series\(\)](#), [plot_box\(\)](#), [plot_iqa\(\)](#), [plot_heatmap\(\)](#)

Examples

```
data("wq_demo", package = "tikatuwq")
head(wq_demo)
# quick IQA example:
# iqa(wq_demo, na_rm = TRUE)
```

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