Package ‘admiralneuro’

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Type Package

Title Neuroscience Extension Package for ADaM in 'R' Asset Library

Version 0.2.1

Description Programming neuroscience specific Clinical Data Standards Interchange Consortium (CDISC) compliant Analysis Data Model (ADaM) datasets in 'R'. ADaM datasets are a mandatory part of any New Drug or Biologics License Application submitted to the United States Food and Drug Administration (FDA). Analysis derivations are implemented in accordance with the ``Analysis Data Model Implementation Guide'' (CDISC Analysis Data Model Team, 2021, <https://www.cdisc.org/standards/foundational/adam>). This package extends the 'admiral' package.

License Apache License (>= 2)

BugReports https://github.com/pharmaverse/admiralneuro/issues

URL https://pharmaverse.github.io/admiralneuro/, https://github.com/pharmaverse/admiralneuro

Depends R (>= 4.1)

Imports admiral (>= 1.4.1), admiraldev (>= 1.4.0), cli (>= 3.6.2), dplyr (>= 1.1.1), hms (>= 0.5.3), lifecycle (>= 0.1.0), lubridate (>= 1.7.4), magrittr (>= 1.5), purrr (>= 0.3.3), rlang (>= 0.4.4), stringr (>= 1.4.0), tibble (>= 3.2.1), tidyr (>= 1.0.2), tidyselect (>= 1.1.0)

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Repository CRAN

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`admiralneuro_adapet` *Amyloid PET Scan Analysis Dataset - Neuro*

Description

An updated ADaM ADAPET dataset using NV, AG, SUPPNV, ADSL

Usage

```
admiralneuro_adapet
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 83 rows and 50 columns.

See Also

Other datasets: `admiralneuro_adtpet`, `adsl_neuro`

`admiralneuro_adtpet` *Tau PET Scan Analysis Dataset - Neuro*

Description

An updated ADaM ADTPET dataset using NV, AG, SUPPNV, ADSL

Usage

`admiralneuro_adtpet`

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 34 rows and 47 columns.

See Also

Other datasets: `admiralneuro_adapet`, `adsl_neuro`

`adsl_neuro` *Subject Level Analysis Dataset-updated*

Description

An updated ADaM ADSL dataset with Alzheimer's Disease patients

Usage

`adsl_neuro`

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 15 rows and 36 columns.

See Also

Other datasets: `admiralneuro_adapet`, `admiralneuro_adtpet`

`compute_centiloid` *Compute Centiloid Value*

Description

Computes the Centiloid value based on an amyloid Positron Emission Tomography (PET) scan radioactive tracer, Standardized Uptake Value Ratio (SUVR) value, pipeline, and reference region. Also allows for custom formula parameters.

Usage

```
compute_centiloid(
  tracer,
  pipeline,
  ref_region,
  suvr,
  custom_slope = NULL,
  custom_intercept = NULL
)
```

Arguments

`tracer`	Amyloid PET tracer A character string is expected. If `custom_slope` and `custom_intercept` are specified, this parameter is ignored. See Details section for accepted values in combination with `pipeline` and `ref_region`. **Permitted values** a character scalar, i.e., a character vector of length one **Default value** none
`pipeline`	SUVR pipeline A character string is expected. If `custom_slope` and `custom_intercept` are specified, this parameter is ignored. See Details section for accepted values in combination with `tracer` and `ref_region`. **Permitted values** a character scalar, i.e., a character vector of length one **Default value** none
`ref_region`	Reference region A character string is expected. If `custom_slope` and `custom_intercept` are specified, this parameter is ignored. See Details section for accepted values in combination with `tracer` and `ref_region`. **Permitted values** a character scalar, i.e., a character vector of length one **Default value** none
`suvr`	SUVR value A positive numeric value is expected. **Permitted values** a numeric scalar, i.e., a numeric vector of length one

Default value none

`custom_slope` Optional slope parameter for custom Centiloid calculation formula

A numeric value is expected when provided. When `custom_slope` is specified (along with `custom_intercept`), this overrides the standard formula parameters `tracer`, `pipeline`, and `ref_region`. Default is `NULL`.

Permitted values a numeric scalar, i.e., a numeric vector of length one

Default value `NULL`

`custom_intercept`

Optional intercept parameter for custom centiloid calculation formula

A numeric value is expected when provided. When `custom_intercept` is specified (along with `custom_slope`), this overrides the standard formula parameters `tracer`, `pipeline`, and `ref_region`. Default is `NULL`.

Permitted values a numeric scalar, i.e., a numeric vector of length one

Default value `NULL`

Details

The Centiloid scale is a standardized quantitative measure for amyloid PET imaging that allows comparison between different tracers and analysis methods. This function converts SUVR values to the Centiloid scale based on published conversion equations for specific tracer, pipeline, and reference region combinations.

Centiloid is calculated as:

$$Centiloid = slope \times SUVR + intercept$$

where slope and intercept are formula parameters. If `custom_slope` and `custom_intercept` are not specified, this function uses pre-defined slope and intercept based on the user's selections of tracer, pipeline, and reference region.

The combinations of tracer, pipeline and reference region in the table below are supported. The columns "slope" and "intercept" then show the values of the slope and intercept that `compute_centiloid()` will use to calculate the centiloid value in each case.

tracer	pipeline	ref_region	slope	intercept
18F-Florbetapir	AVID FBP SUVR PIPELINE¹	Whole Cerebellum	183.07	-177.26
18F-Florbetaben	AVID FBB SUVR PIPELINE²	Whole Cerebellum	156.06	-148.13
18F-Florbetapir	BERKELEY FBP SUVR PIPELINE³	Whole Cerebellum	188.22	-189.16
18F-Florbetaben	BERKELEY FBB SUVR PIPELINE³	Whole Cerebellum	157.15	-151.87

The equations used for the conversions are based on the following references:

¹ Navitsky, et al. (2018). doi:10.1016/j.jalz.2018.06.1353 ² Sims, et al. (2024). doi:10.1001/jama.2023.13239 ³ Royse, et al. (2021). doi:10.1186/s13195021008361

Alternatively, the user can override the pre-selection by specifying both `custom_slope` and `custom_intercept` instead. When `custom_slope` and `custom_intercept` are specified, the function ignores `tracer`, `pipeline` and `ref_region` for calculation purposes. However, this function **always requires** specification of `tracer`, `pipeline`, and `ref_region` parameters, even when using custom slope and intercept values. This design choice ensures that users remain cognizant of the imaging context and analysis methodology when computing Centiloid values.

For additional Centiloid transformation formulas, see: Iaccarino, L. et al. (2025). doi:10.1016/j.nicl.2025.103765

If a matching combination of tracer, pipeline, and reference region is not specified and both `custom_slope` and `custom_intercept` are not specified, the function aborts with an error.

Value

A numeric Centiloid value.

Examples

Using standard parameters:

Computes Centiloid with predefined slope/intercept for supported tracer/pipeline/ref_region combinations:

```
compute_centiloid(
  tracer = "18F-Florbetapir",
  pipeline = "AVID FBP SUVR PIPELINE",
  ref_region = "Whole Cerebellum",
  suvr = 1.25
)
#> [1] 51.5775
```

Using custom parameters:

Computes Centiloid by overriding slope/intercept using custom values:

```
compute_centiloid(
  tracer = "MyTracer",
  pipeline = "MyPipeline",
  ref_region = "MyRegion",
  suvr = 1.25,
  custom_slope = 193,
  custom_intercept = -187
)
#> [1] 54.25
```

See Also

Other com_bds_findings: `compute_upsit_percentile()`

`compute_upsit_percentile`

Compute UPSIT Percentile Based on Age, Sex, and Score

Description

This function computes the UPSIT (University of Pennsylvania Smell Identification Test) percentile for a given subject based on their age, sex, and UPSIT raw score. The percentile is determined by looking up the corresponding value in a normative reference table.

Usage

```
compute_upsit_percentile(sex, age, upsit_score)
```

Arguments

`sex`	Sex of the subject. Must be either "M" or "F" A character string of either "M" or "F" is expected **Permitted values** a character scalar, i.e., a character vector of length one **Default value** none
`age`	Age of the subject in years. **Permitted values** a numeric scalar, i.e., a numeric vector of length one **Default value** none
`upsit_score`	The UPSIT ranging from 0 to 40. Higher scores indicate better olfactory function. **Permitted values** a numeric scalar, i.e., a numeric vector of length one **Default value** none

Details

The function uses an internal lookup table (`upsit_lookup`) that contains normative percentile data stratified by sex, age range, and UPSIT score. The lookup table is based on published normative data.

Age ranges in the lookup table include:

- 50-54 years
- 55-59 years
- 60-64 years
- 65-69 years
- 70-74 years
- 75-79 years
- 80+ years (no upper limit)

The function is designed to work efficiently in vectorized operations within data processing pipelines (e.g., with `dplyr::mutate()`)

Value

A numeric percentile value. The UPSIT percentile value corresponding to the input parameters. Returns `NA_real_` if no matching entry is found in the lookup table.

Examples

Look up for male percentile:
A 52 years old male with upsit raw score of 25

```
compute_upsit_percentile(sex = "M", age = 52, upsit_score = 25)
#> [1] 5
```

Look up for female percentile:
A 81 years old female with upsit raw score of 30

```
compute_upsit_percentile(sex = "F", age = 81, upsit_score = 30)
#> [1] 39
```

Returns NA:
Minimal age is 50 and score of 0 and 40, return NA if no match found

```
compute_upsit_percentile(sex = "M", age = 45, upsit_score = 25)
#> [1] NA
```

References

Brumm MC, et. al., Updated Percentiles for the University of Pennsylvania Smell Identification Test in Adults 50 Years of Age and Older. doi:10.1212/WNL.0000000000201463

See Also

Other com_bds_findings: `compute_centiloid()`

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