Package 'admiralneuro'

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Type Package

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

Version 0.1.0

Description Programming neuroscience Clinical Data Standards Interchange Consortium (CDISC) compliant Analysis Data Model (ADaM) datasets. 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)

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

Depends R (>= 4.1)

Imports admiral (>= 1.2.0), admiraldev (>= 1.2.0), cli (>= 3.6.2), dplyr (>= 1.0.5), 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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Contents

`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, ag_neuro, dm_neuro, nv_neuro, suppnv_neuro

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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, ag_neuro, dm_neuro, nv_neuro, suppnv_neuro

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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, ag_neuro, dm_neuro, nv_neuro, suppnv_neuro

ag_neuro *Procedure Agents for Nervous System Dataset*

Description

A SDTM AG domain dataset containing procedure agents for nervous system

Usage

```
ag_neuro
```

Format

A data frame with 12 columns:

STUDYID Study Identifier

DOMAIN Domain Abbreviation

USUBJID Unique Subject Identifier

AGSEQ Sequence Number

AGTRT Reported Agent Name

AGCAT Category for Category

AGDOSE Dose per Administration

AGDOSEU Dose Units

AGROUTE Route of Administration

AGLNKID Link ID

VISITNUM Visit Number

VISIT Visit Name

AGSTDTC Start Date/Time of Agent

Details

Procedure Agents for Nervous System Dataset

A SDTM AG domain dataset

Source

Constructed using nv_neuro from {admiralneuro} package

See Also

Other datasets: admiralneuro_adapet, admiralneuro_adtpet, adsl_neuro, dm_neuro, nv_neuro, suppnv_neuro

`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`.
`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`.
`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`.
`suvr`	SUVR value A numeric value is expected.
`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`.
`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`.

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 PIPELINE[1]	Whole Cerebellum	183.07	-177.26
18F-Florbetaben	AVID FBB SUVR PIPELINE[2]	Whole Cerebellum	156.06	-148.13
18F-Florbetapir	BERKELEY FBP SUVR PIPELINE[3]	Whole Cerebellum	188.22	-189.16
18F-Florbetaben	BERKELEY FBB SUVR PIPELINE[3]	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
compute_centiloid(
  tracer = "18F-Florbetapir",
```

```
  pipeline = "AVID FBP SUVR PIPELINE",
  ref_region = "Whole Cerebellum",
  suvr = 1.25
)

# Using custom parameters
compute_centiloid(
  tracer = "MyTracer",
  pipeline = "MyPipeline",
  ref_region = "MyRegion",
  suvr = 1.25,
  custom_slope = 193,
  custom_intercept = -187
)
```

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dm_neuro *Demographic Dataset - Neuro*

Description

An updated SDTM DM dataset subset with age appropriate Alzheimer's Disease patients

Usage

```
dm_neuro
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 15 rows and 26 columns.

See Also

Other datasets: `admiralneuro_adapet`, `admiralneuro_adtpet`, `adsl_neuro`, `ag_neuro`, `nv_neuro`, `suppnv_neuro`

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nv_neuro *Nervous System Findings Dataset*

Description

A SDTM NV domain dataset containing nervous system findings and measurements

Usage

```
nv_neuro
```

Format

A data frame with 20 columns:

STUDYID Study Identifier

DOMAIN Domain Abbreviation

USUBJID Unique Subject Identifier

NVSEQ Sequence Number

NVLNKID Link ID

NVTESTCD Short Name of Nervous System Test

NVTEST Name of Nervous System Test

NVCAT Category for Nervous System Test

NVLOC Location Used for the Measurement

NVMETHOD Method of Test or Examination

NVNAM Vendor Name

NVORRES Result or Finding in Original Units

NVORRESU Original Units

NVSTRESC Character Result/Finding in Std Format

NVSTRESN Numeric Result/Finding in Standard Units

NVSTRESU Standard Units

VISITNUM Visit Number

VISIT Visit Name

NVDTC Date/Time of Collection

NVDY Study Day of Collection

NVLOBXFL Last Observation Before Exposure Flag

Details

Nervous System Findings Dataset

A SDTM NV domain dataset for Alzheimer's disease observational and interventional studies, including amyloid and tau PET data at baseline and two follow-up visits reflect levels of pathology appropriate for disease or treatment course

Source

Constructed using `dm_neuro` from `{admiralneuro}` package for USUBJID and cohort information, `vs` from `{pharmaversesdtm}` for visit schedule such as VISIT, NVDTC, NVDY

See Also

Other datasets: `admiralneuro_adapet`, `admiralneuro_adtpet`, `adsl_neuro`, `ag_neuro`, `dm_neuro`, `suppnv_neuro`

suppnv_neuro *Supplemental Nervous System Findings Dataset*

Description

A SDTM SUPPNV domain dataset containing reference regions used for SUVR calculation

Usage

```
suppnv_neuro
```

Format

A data frame with 8 columns:

STUDYID Study Identifier

RDOMAIN Related Domain Abbreviation

USUBJID Unique Subject Identifier

IDVAR Identifying Variable

IDVARVAL Identifying Variable Value

QNAM Qualifier Variable Name

QLABEL Qualifier Variable Label

QVAL Data Value

QORIG Origin

QEVAL Evaluator

Details

Supplemental Nervous System Findings Dataset

A SDTM SUPPNV domain dataset

Source

Constructed using `nv_neuro` from `{admiralneuro}` package

See Also

Other datasets: `admiralneuro_adapet`, `admiralneuro_adtpet`, `adsl_neuro`, `ag_neuro`, `dm_neuro`, `nv_neuro`

Index