

# Package ‘admiralneuro’

February 5, 2026

**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)

**Suggests** diffdf, DT, htmltools, knitr, metatools, methods,  
pharmaversesdtm (>= 1.0.0), reactable, readxl, rmarkdown,  
testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**RoxygenNote** 7.3.3**NeedsCompilation** no

**Author** Jian Wang [aut, cre] (ORCID: <<https://orcid.org/0009-0002-4677-3781>>),  
 Miles Almond [aut] (ORCID: <<https://orcid.org/0009-0007-1784-0355>>),  
 Xiao Chen [aut] (ORCID: <<https://orcid.org/0009-0000-6959-5151>>),  
 Fanny Gautier [aut] (ORCID: <<https://orcid.org/0009-0004-3581-0131>>),  
 Gayatri G. [aut],  
 Meilin Jiang [aut] (ORCID: <<https://orcid.org/0000-0003-4515-4567>>),  
 Leena Khatri [aut] (ORCID: <<https://orcid.org/0000-0002-2268-4023>>),  
 Edoardo Mancini [aut] (ORCID: <<https://orcid.org/0009-0006-4899-8641>>),  
 Eric Nantz [aut],  
 Lina Patil [aut],  
 Chris Peletrides [aut],  
 Eli Lilly and Company [cph, fnd],  
 Cytel Inc. [cph, fnd],  
 F. Hoffmann-La Roche AG [cph, fnd]

**Maintainer** Jian Wang <wang\_jian\_wj@lilly.com>**Repository** CRAN**Date/Publication** 2026-02-04 23:20:02 UTC**Contents**

admiralneuro_adapet . . . . .	2
admiralneuro_adtpet . . . . .	3
adsl_neuro . . . . .	3
compute_centiloid . . . . .	4
compute_upsit_percentile . . . . .	7

**Index** **9**


---

 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	<i>Tau PET Scan Analysis Dataset - Neuro</i>
---------------------	--

---

**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	<i>Subject Level Analysis Dataset-updated</i>
------------	---

---

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

	<b>Default value</b> 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. <b>Permitted values</b> a numeric scalar, i.e., a numeric vector of length one <b>Default value</b> 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. <b>Permitted values</b> a numeric scalar, i.e., a numeric vector of length one <b>Default value</b> 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:

$$\text{Centiloid} = \text{slope} \times \text{SUVR} + \text{intercept}$$

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 <sup>1</sup>	Whole Cerebellum	183.07	-177.26
18F-Florbetaben	AVID FBB SUVR PIPELINE <sup>2</sup>	Whole Cerebellum	156.06	-148.13
18F-Florbetapir	BERKELEY FBP SUVR PIPELINE <sup>3</sup>	Whole Cerebellum	188.22	-189.16
18F-Florbetaben	BERKELEY FBB SUVR PIPELINE <sup>3</sup>	Whole Cerebellum	157.15	-151.87

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

<sup>1</sup> Navitsky, et al. (2018). doi:10.1016/j.jalz.2018.06.1353 <sup>2</sup> Sims, et al. (2024). doi:10.1001/jama.2023.13239 <sup>3</sup> 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](https://doi.org/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

<code>sex</code>	Sex of the subject. Must be either "M" or "F". A character string of either "M" or "F" is expected. <b>Permitted values</b> a character scalar, i.e., a character vector of length one <b>Default value</b> none
<code>age</code>	Age of the subject in years. <b>Permitted values</b> a numeric scalar, i.e., a numeric vector of length one <b>Default value</b> none
<code>upsit_score</code>	The UPSIT ranging from 0 to 40. Higher scores indicate better olfactory function. <b>Permitted values</b> a numeric scalar, i.e., a numeric vector of length one <b>Default value</b> 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](https://doi.org/10.1212/WNL.0000000000201463)

**See Also**

Other com\_bds\_findings: [compute\\_centiloid\(\)](#)



# Index

## \* **com\_bds\_findings**

compute\_cenitloid, 4  
compute\_upsit\_percentile, 7

## \* **datasets**

admiralneuro\_adapet, 2  
admiralneuro\_adtpet, 3  
adsl\_neuro, 3

admiralneuro\_adapet, 2, 3  
admiralneuro\_adtpet, 3, 3  
adsl\_neuro, 3, 3

compute\_cenitloid, 4, 8  
compute\_upsit\_percentile, 6, 7