

# Package ‘ProAE’

June 30, 2022

**Type** Package

**Title** PRO-CTCAE Scoring, Analysis, and Graphical Tools

**Version** 0.2.10

**Author** Blake Langlais [aut, cre],  
Brie Noble [ctb],  
Molly Klanderma [ctb],  
Amylou Dueck [aut]

**Maintainer** Blake Langlais <langlais.blake@mayo.edu>

**Description** A collection of tools to facilitate standardized analysis and graphical procedures when using the National Cancer Institute’s Patient-Reported Outcomes version of the Common Terminology Criteria for Adverse Events (PRO-CTCAE).

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** ggplot2, ggnewscale, ggtext, dplyr, Hmisc, magrittr,  
ggpattern, DescTools, gridExtra

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**Depends** R (>= 4.0.0)

**RoxygenNote** 7.1.2

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2022-06-30 19:40:02 UTC

## R topics documented:

ProAE . . . . .	2
PROCTCAE_table . . . . .	2
toxAUC . . . . .	3

toxFigures . . . . .	4
toxScores . . . . .	7
toxSummary . . . . .	8
toxTables . . . . .	9
tox_acute . . . . .	11
tox_chronic . . . . .	11
tox_cumulative . . . . .	12
tox_cyclic . . . . .	12
tox_late . . . . .	13

<b>Index</b>	<b>14</b>
--------------	-----------

---

ProAE	<i>ProAE.</i>
-------	---------------

---

### Description

This package is a collection of tools for analyzing and plotting PRO-CTCAE data

---

PROCTCAE_table	<i>PRO-CTCAE variable / label crosswalk</i>
----------------	---

---

### Description

A crosswalk / look-up table of expected variable names for associated PRO-CTCAE symptom items.

### Format

A data frame with 124 rows and 2 variables

### Details

- name. Expected variable name - item number/letter corresponds to the NCI-PRO-CTCAE (English) Item Library Version 1.0
- short\_label. Item label including the item symptom group and frequency, severity, interference, or presence component

### Author(s)

Blake Langlais

### References

<https://healthcaredelivery.cancer.gov/pro-ctcae/instrument-pro.html>

---

toxAUC	<i>Create longitudinal mean score line plots for PRO-CTCAE data with modified Area Under the Curve (AUC) estimates showing descriptive symptomatic adverse event burden worsening and improvement from baseline.</i>
--------	--

---

### Description

Data format should be in 'long' format, where each PRO-CTCAE item is a variable/column.

### Usage

```
toxAUC(
  dsn,
  id_var,
  cycle_var,
  baseline_val,
  arm_var = NA,
  cycle_limit = NA,
  y_limit = 4,
  tab_ymin = NA,
  tab_ymax = NA,
  round_dec = 2,
  overwrite_title = NA,
  permute_tests = FALSE,
  permute_n = 2000,
  bootstrap_ci = FALSE,
  bootstrap_ci_alpha = 0.05,
  bootstrap_n = 2000
)
```

### Arguments

dsn	A data.frame object with PRO-CTCAE data
id_var	A character string. Name of ID variable differentiating each unique patient.
cycle_var	A character string. Name of variable differentiating one longitudinal/repeated PRO-CTCAE survey from another, within an individual ID.
baseline_val	A number indicating the expected baseline cycle/time point.
arm_var	A character string. Name of arm variable differentiating treatment groups. Must be character or factor class. Overall frequencies will be reported if no arm/grouping variable is provided. Defaults to NA.
cycle_limit	A number. Limit the number of cycles to be use to calculate the AUC metrics up to and including a given cycle number. All available cycle time points are used if no cycle number is provided. Defaults to NA.
y_limit	A number. Y axis limit for plots. Defaults to 4.

tab_ymin	A number. Y axis coordinate for adjusting the vertical placement of the AUC table within the figure. Defaults to NA.
tab_ymax	A number. Y axis coordinate for adjusting the vertical placement of the AUC table within the figure. Defaults to NA.
round_dec	A number. Number of decimal places to be shown within the AUC table. Defaults to 2.
overwrite_title	A character string. Add main title to plots. Defaults to NA.
permute_tests	Logical. Calls to calculate p values comparing the difference in AUC between two arms using a permutation test. Typical two- sided null hypothesis for a permutation test is applied. That is, assigning subjects to groups is interchangeable when calculating AUC. Computation time may be extensive depending on data size, number of PRO-CTCAE items, and number of permutations called. Consider staring out an open window or crafting a haiku during this time. Defaults to FALSE.
permute_n	A number. The number of permutations to be used for permutation tests. Defaults to 2000.
bootstrap_ci	Logical. Calls to construct alpha-level confidence intervals for the difference in AUC between arms. Similar considerations for computation time as permute_tests are recommended here. Defaults to FALSE.
bootstrap_ci_alpha	A number. Specifies the alpha level for bootstrap confidence intervals. Must be between 0 and 1. Defaults to 0.05.
bootstrap_n	A number. The number of bootstrap iterations to be used for bootstrap confidence intervals. Defaults to 2000.

### Examples

```
## Not run:
AUC=toxAUC(dsn = ProAE::tox_acute,
id_var = "id",
cycle_var = "Cycle",
baseline_val = 1)
AUC[[1]]

## End(Not run)
```

---

toxFigures

*Create PRO-CTCAE severity frequency distribution figures for individual survey items and composite scores*

---

### Description

Data format should be in 'long' format, where each PRO-CTCAE item is a variable/column.

**Usage**

```

toxFigures(
  dsn,
  id_var,
  cycle_var,
  baseline_val,
  arm_var = NA,
  plot_limit = NA,
  colors = 1,
  bar_label = 0,
  cycle_label = FALSE,
  cycle_vals = NA,
  cycle_labs = NA,
  summary_only = FALSE,
  cycles_only = FALSE,
  x_lab_angle = 0,
  x_lab_vjust = 1,
  x_lab_hjust = 0,
  x_label = "Randomized Treatment Assignment",
  footnote_break = FALSE
)

```

**Arguments**

dsn	A data.frame object with PRO-CTCAE data
id_var	A character string. Name of ID variable differentiating each PRO-CTCAE survey/participant entered as a quoted string.
cycle_var	A character string. Name of variable differentiating one longitudinal/repeated PRO-CTCAE survey from another, within an individual ID.
baseline_val	A number indicating the expected baseline cycle/time point.
arm_var	A character string. Name of arm variable differentiating treatment groups. Must be character or factor class. Overall AUC will be reported if no arm/grouping variable is provided. Defaults to NA.
plot_limit	A number. Limit the number of cycles to be plotted up to and including a given cycle number. All available cycle time points are plotted if no cycle number is provided. Defaults to NA.
colors	A number. Specify the coloring scheme of symptom grades within frequency bars. Options include: 1 = Blue and red color shading, 2 = qualitative color shades (color blind friendly), 3 = black and white. Defaults to 1.
bar_label	A number. Label frequency bars with sample size (n) or percent shown on the y-axis. Label options include: 1 = sample size (n) within each cycle (symptom grade 0 or higher), 2 = sample size (n) within each cycle with present symptoms (symptom grade > 0), 3 = sample size (n) within each cycle with severe symptoms (symptom grade >= 3), 4 = percent of subjects within each cycle with present symptoms (symptom grade > 0), 5 = percent of subjects within each cycle with severe symptoms (symptom grade >= 3). No labels will be applied if not specified. Defaults to NA.

cycle_label	Logical. Assign custom labels to cycles/time point. If TRUE, the cycle_vals and cycle_labs must also be specified.
cycle_vals	Numeric column vector. Vector of values seen within the cycle_var variable. Must be same length of cycle_labs. Defaults to NA.
cycle_labs	Character column vector. Vector of labels to be mapped to the associated cycle_vals. Must be same length of cycle_vals. Defaults to NA.
summary_only	Logical. Only display the summary measures in figures / Suppress the individual time points from plotting. Defaults to FALSE.
cycles_only	Logical. Only display the longitudinal time points in figures / Suppress the summary measures from plotting. Defaults to FALSE.
x_lab_angle	A integer between 0 and 360. Allows the user to rotate the x axis labels in order to fit long arm names (0 or 45 recommended). Defaults to 0.
x_lab_vjust	A number. A ggplot2 object option. Allows the user to vertically adjusts the x axis labels in order to fit arm names. Defaults to 1.
x_lab_hjust	A number. A ggplot2 object option. Allows the user to horizontally adjusts the x axis labels in order to fit arm names. Defaults to 0.
x_label	A character string. Label for the x axis of the plot. Defaults to "Randomized Treatment Assignment" if arm_var is specified, defaults to "Overall" if not arm_var is specified.
footnote_break	Logical. Add a line break to the footnote Defaults to FALSE.

### Value

A list object. The returned object is a (k X 2) or (k x 3) nested list. Where k is the number of PRO-CTCAE item groups (e.g. pain, fatigue, nausea); list[[1 ... i ... k]]. For each list item there are 2 or 3 elements. The 1st element of each list item is the name of the PRO-CTCAE item group returned as a string. The 2nd element is the PRO-CTCAE figure as a ggplot object.

### Examples

```
fig_acute = toxFigures(dsn = ProAE::tox_acute,
  cycle_var = "Cycle",
  baseline_val = 1,
  arm_var = "arm",
  id_var = "id",
  x_lab_angle = -45,
  x_lab_vjust = .3,
  x_lab_hjust = .2,
  colors = 2)
fig_acute[[1]]
```

---

toxScores	<i>Re-code PRO-CTCAE text responses, apply a zero-imputation procedure, and construct PRO-CTCAE composite grades.</i>
-----------	---

---

## Description

This function takes in a data frame set with PRO-CTCAE survey text fields/responses and returns a data frame with appropriate numerical re-coding. This function will accept 1 or up to all 124 PRO-CTCAE survey fields. All PRO-CTCAE variable names MUST conform to a pre-specified naming structure. PRO-CTCAE variable names are made up of FOUR components: 1) 'PROCTCAE', 2) number [1,2,3, ..., i, ..., 80], 3) 'A', 'B', or 'C' component of the i-th PRO-CTCAE field, 4) and 'SCL' (if severity, interference, or frequency) or 'IND' (if yes/no variable). Each component must be delimited by an underscore (\_)

## Usage

```
toxScores(
  dsn,
  reformat = FALSE,
  impute = FALSE,
  composites = FALSE,
  short_labels = FALSE
)
```

## Arguments

dsn	A data.frame object with PRO-CTCAE data
reformat	Reformat PRO-CTCAE text responses to numeric scores. Defaults to FALSE.
impute	Apply zero-imputation where appropriate. Defaults to FALSE.
composites	Construct composite grade using available PRO-CTCAE variables within dsn. Defaults to FALSE.
short_labels	Add PRO-CTCAE short labels to available PRO-CTCAE variables within returned object

## Details

- [EX1] Question 1 of PRO-CTCAE should be: PROCTCAE\_1A\_SCL
- [EX2] Question 48 of PRO-CTCAE should be: PROCTCAE\_48A\_SCL, PROCTCAE\_48B\_SCL, PROCTCAE\_48C\_SCL
- [EX3] Question 73 of PRO-CTCAE should be: PROCTCAE\_73A\_IND

This function also constructs PRO-CTCAE composite grades. Composite grade variables for respective PRO-CTCAE item groups are created and named as PROCTCAE\_##\_COMP.

1. [https://healthcaresdelivery.cancer.gov/pro-ctcae/pro-ctcae\\_english.pdf](https://healthcaresdelivery.cancer.gov/pro-ctcae/pro-ctcae_english.pdf)

2. Ethan Basch, et al. Development of a Composite Scoring Algorithm for the National Cancer Institute's Patient-Reported Outcomes version of the Common Terminology Criteria for Adverse Events (PRO-CTCAE). ISOQOL 2019
3. Basch E, et al. Composite Grading Algorithm for the National Cancer Institute's Patient-Reported Outcomes version of the Common Terminology Criteria for Adverse Events (PRO-CTCAE). Clinical Trials 2020.

Data format should be in 'long' format, where each PRO-CTCAE item is a variable/column.

### Value

A data.frame object.

### Examples

```
tox_acute_comp = toxScores(dsn = ProAE::tox_acute, composites = TRUE)
```

---

toxSummary

*Create patient-level and group-level summary statistics.*

---

### Description

Data format should be in 'long' format, where each PRO-CTCAE item is a variable/column.

### Usage

```
toxSummary(
  dsn,
  id_var,
  cycle_var,
  summary_measure,
  baseline_val = NA,
  arm_var = NA
)
```

### Arguments

dsn	A data.frame object with PRO-CTCAE data.
id_var	A character string. Name of ID variable differentiating each PRO-CTCAE survey/participant entered as a quoted string.
cycle_var	A character string. Name of variable differentiating one longitudinal/repeated PRO-CTCAE survey from another, within an individual ID.
summary_measure	A character string. Type of summary statistic to be used. Please consult current literature for appropriate interpretations of the summary measure selected and suitable analysis procedures for comparing groups. Options include: "max" = Use subjects' maximum score. "max_post_bl" = Use subjects' maximum score



post-baseline visit. "bl\_adjusted" = Use subjects' baseline adjusted score over the study period. The baseline adjusted score is derived by the following: If the maximum score post-baseline is more severe than the baseline score, then the use maximum score post-baseline is used as the adjusted score. Otherwise, if the maximum score post-baseline is the same or less severe than the baseline score, then zero (0) is used as the adjusted score. "toxicity\_idx" = Construct patient-level toxicity index. "AUC\_worsening" = Calculate group-level AUC describing

baseline\_val A number indicating the expected baseline cycle/time point.  
 arm\_var A character string. Name of arm variable differentiating treatment arms or other grouping factor. Required for group-level summary measures.

### Value

A data.frame with only the id and PRO-CTCAE variables being summarized. Each subject will now only have 1 observation (PRO-CTCAE variables are now the summary measure value).

### Examples

```
toxSummary(dsn=ProAE::tox_acute,
  id_var="id",
  cycle_var="Cycle",
  baseline_val=1,
  summary_measure = "max")
```

---

toxTables	<i>Create toxicity tables for individual and composite PRO-CTCAE survey items.</i>
-----------	--

---

### Description

Data format should be in 'long' format, where each PRO-CTCAE item is a variable/column.

### Usage

```
toxTables(
  dsn,
  id_var,
  cycle_var,
  baseline_val,
  type = "bl_adjusted",
  test = "c",
  riskdiff = FALSE,
  risk_ci = "wald",
  risk_ci_alpha = 0.05,
  arm_var = NA,
  cycle_limit = NA
)
```

**Arguments**

<code>dsn</code>	A data.frame object with PRO-CTCAE data.
<code>id_var</code>	A character string. Name of ID variable differentiating each PRO-CTCAE survey/participant entered as a quoted string.
<code>cycle_var</code>	A character string. Name of variable differentiating one longitudinal/repeated PRO-CTCAE survey from another, within an individual ID.
<code>baseline_val</code>	A number indicating the expected baseline cycle/time point.
<code>type</code>	A character string. Type of summary measure to be used. Options include: "max_post_bl" = Use subjects' maximum score post-baseline visit. "bl_adjusted" = Use subjects' baseline adjusted score over the study period. The baseline adjusted score is derived by the following: If the maximum score post-baseline is more severe than the baseline score, then the use maximum score post-baseline is used as the adjusted score. Otherwise, if the maximum score post-baseline is the same or less severe than the baseline score, then zero (0) is used as the adjusted score. Defaults to "bl_adjusted".
<code>test</code>	A character string. Specify the statistical test to apply where comparing rates among arms. Options include: "c" = chi square, "f" = fisher's exact. Defaults to "c".
<code>riskdiff</code>	Logical. Calculates risk differences between two arms. Valid if there are only two arms in the data.frame specified. This option will countermand options called with the test parameter. Defaults to FALSE.
<code>risk_ci</code>	A character string. Specify the confidence interval type to be constructed for risk differences. Options include: "wald", and "agresti-caffo". Defaults to "wald".
<code>risk_ci_alpha</code>	A number between 0 and 1. Specify the alpha level of the risk difference confidence intervals. Defaults to 0.05.
<code>arm_var</code>	A character string. Name of arm variable differentiating treatment groups. Must be character or factor class. Overall frequencies will be reported if no arm/grouping variable is provided. Defaults to NA.
<code>cycle_limit</code>	A number. Limit the data to be analyzed up to and including a given cycle number or time point. Defaults to NA.

**Value**

A list object with data.frame elements for individual items and composite grades.

**Examples**

```
toxTables(dsn=ProAE::tox_acute, id_var="id", cycle_var="Cycle", baseline_val=1)
```

---

tox_acute	<i>PRO-CTCAE data reflecting acute drug toxicity</i>
-----------	--

---

**Description**

Simulated example data where the drug group experiences acute toxicity followed by symptom abatement over the course of treatment.

**Format**

A data frame with 1400 rows and 5 variables

**Details**

- id. Subject identifier
- Cycle. Time variable denoting visits/cycles (1-10)
- arm. Treatment groups include drug and placebo
- PROCTCAE\_78A\_SC. PRO-CTCAE frequency item for nosebleeds
- PROCTCAE\_78B\_SC. PRO-CTCAE severity item for nosebleeds

**Author(s)**

Blake Langlais

---

tox_chronic	<i>PRO-CTCAE data reflecting chronic drug toxicity</i>
-------------	--

---

**Description**

Simulated example data where the drug group experiences chronic toxicity over the course of treatment.

**Format**

A data frame with 1400 rows and 5 variables

**Details**

- id. Subject identifier
- Cycle. Time variable denoting visits/cycles (1-10)
- arm. Treatment groups include drug and placebo
- PROCTCAE\_78A\_SC. PRO-CTCAE frequency item for nosebleeds
- PROCTCAE\_78B\_SC. PRO-CTCAE severity item for nosebleeds

**Author(s)**

Blake Langlais

---

tox\_cumulative      *PRO-CTCAE data reflecting cumulative drug toxicity*

---

**Description**

Simulated example data where drug toxicity is cumulative over the course of treatment.

**Format**

A data frame with 1400 rows and 5 variables

**Details**

- id. Subject identifier
- Cycle. Time variable denoting visits/cycles (1-10)
- arm. Treatment groups include drug and placebo
- PROCTCAE\_78A\_SC. PRO-CTCAE frequency item for nosebleeds
- PROCTCAE\_78B\_SC. PRO-CTCAE severity item for nosebleeds

**Author(s)**

Blake Langlais

---

tox\_cyclic      *PRO-CTCAE data reflecting cyclical drug toxicity*

---

**Description**

Simulated example data where the drug group experiences cyclicly toxicity post-treatment administration

**Format**

A data frame with 1400 rows and 5 variables

**Details**

- id. Subject identifier
- Cycle. Time variable denoting visits/cycles (1-10)
- arm. Treatment groups include drug and placebo0
- PROCTCAE\_78A\_SC. PRO-CTCAE frequency item for nosebleeds
- PROCTCAE\_78B\_SC. PRO-CTCAE severity item for nosebleeds

**Author(s)**

Blake Langlais

---

`tox_late`*PRO-CTCAE data reflecting late incipient drug toxicity*

---

**Description**

Simulated example data where the drug group experiences late incipient toxicity towards the end of the treatment period.

**Format**

A data frame with 1400 rows and 5 variables

**Details**

- `id`. Subject identifier
- `Cycle`. Time variable denoting visits/cycles (1-10)
- `arm`. Treatment groups include drug and placebo
- `PROCTCAE_78A_SC`. PRO-CTCAE frequency item for nosebleeds
- `PROCTCAE_78B_SC`. PRO-CTCAE severity item for nosebleeds

**Author(s)**

Blake Langlais

# Index

## \* data

- PROCTCAE\_table, 2
- tox\_acute, 11
- tox\_chronic, 11
- tox\_cumulative, 12
- tox\_cyclic, 12
- tox\_late, 13

ProAE, 2

PROCTCAE\_table, 2

tox\_acute, 11

tox\_chronic, 11

tox\_cumulative, 12

tox\_cyclic, 12

tox\_late, 13

toxAUC, 3

toxFigures, 4

toxScores, 7

toxSummary, 8

toxTables, 9