Package: TwoDcDAPSA (via r-universe)

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Type Package

Title Calculate TwoDcDAPSA: PROs-Joint Contrast (PJC) and Swollen–Tender Joints Contrast (STC) Scores and Quartiles

Version 0.1.1

Description Provides a calculator for the two-dimensional clinical Disease Activity index for Psoriatic Arthritis (TwoDcDAPSA), a principal component-derived measure that complements the conventional clinical DAPSA score. TwoDcDAPSA captures residual variation in patient-reported outcomes (pain and patient global assessment) and joint counts (swollen and tender) after adjusting for standardized cDAPSA using natural spline coefficients derived from published models. Residuals are standardized and combined with fixed principal component loadings to yield two continuous component scores: the PROs-Joint Contrast (PJC) and the Swollen–Tender joints Contrast (STC), along with quartile-based groupings (including optional combined quartile groupings). The package applies pre-specified coefficients, residual standardization, and loadings to new datasets but does not estimate spline models or principal components itself.

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`calculate_PJC` *Calculate TwoDcDAPSA: PROs-Joint Contrast (PJC) Score and Quartile Groups*

Description

Computes PJC as a loading-weighted combination of standardized residuals for Pain, Patient Global, SJC, and TJC after adjusting each for cDAPSA via a natural spline model. Includes input "tuning": coerces character columns to numeric (warning if NAs introduced) and checks for out-of-range values (SJC 0-66, TJC 0-68, Pain/Patient Global 0-10) with configurable handling. If `cDAPSA` is not provided, it is computed as `SJC + TJC + Pain + Patient_Global`. If `cDAPSA` is provided, it is verified against this sum (within `cdapsa_tolerance`); any discrepancy results in an error.

Usage

```
calculate_PJC(
  data,
  cohort_id = "cohort_id",
  cDAPSA = NULL,
  Pain = "Pain",
  Patient_Global = "Patient_Global",
  SJC = "SJC",
  TJC = "TJC",
  oob_action = c("stop", "na", "drop"),
  cdapsa_tolerance = 1e-08,
  center_scale = list(Pain = c(center = 4.303191, scale = 2.798819), Patient_Global =
   c(center = 4.795213, scale = 2.791098), SJC = c(center = 3.783245, scale = 4.707089),
   TJC = c(center = 5.194149, scale = 7.371234), cDAPSA = c(center = 18.0758, scale =
    14.03964)),
  ns_knots = c(-0.7176679, -0.2190796, 0.4219626),
  ns_boundary_knots = c(-1.287483, 5.265392),
  coef_list = list(Pain = c(-1.48889, 1.93539, 2.25211, 3.35687, 2.68578), Patient_Global
   = c(-1.7289, 2.1364, 2.35881, 3.95251, 2.66605), SJC = c(-0.76905, 0.47397, 1.9502,
    4.45945, 5.98404), TJC = c(-0.74115, 0.27891, 2.50892, 4.68559, 6.15326)),
  loadings = c(0.598197, 0.5960272, -0.330572, -0.4214665),
  pjc_cutoffs = c(-Inf, -0.79954204, 0.07402262, 0.88778526, Inf),
```

```
  resid_center_scale = list(center = c(Pain = 1.155879e-15, `Patient Global` =
    9.679019e-16, `Swollen Joint Count` = -2.764596e-15, `Tender Joint Count` =
    -3.534933e-15), scale = c(Pain = 0.6478511, `Patient Global` = 0.6282206,
    `Swollen Joint Count` = 0.589554, `Tender Joint Count` = 0.3902453))
)
```

Arguments

`data`	A data.frame/tibble with the required columns.
`cohort_id`	Name of the cohort id column.
`cDAPSA`	Optional. Name of the cDAPSA column. If `NULL` (default), cDAPSA is computed as `SJC` + `TJC` + `Pain` + `Patient_Global`. If non-`NULL`, the provided column is verified to equal that sum within `cdapsa_tolerance`; otherwise an error is thrown.
`Pain`	Name of the Pain column (0-10).
`Patient_Global`	Name of the Patient Global column (0-10).
`SJC`	Name of the Swollen Joint Count column (0-66).
`TJC`	Name of the Tender Joint Count column (0-68).
`oob_action`	What to do when an input is out of its valid range (SJC 0-66, TJC 0-68, Pain/Patient Global 0-10). One of: `"stop"` (error), `"na"` (keep rows but set PJC/Quartile to NA), or `"drop"` (remove rows). Default is `"stop"`.
`cdapsa_tolerance`	Numeric tolerance for comparing provided cDAPSA to the computed sum; default `1e-8`.
`center_scale`	List of centers/scales used to standardize inputs.
`ns_knots`	Numeric vector of interior knots for the spline on standardized cDAPSA.
`ns_boundary_knots`	Numeric vector of boundary knots for the spline on standardized cDAPSA.
`coef_list`	Named list of regression coefficients (intercept + 4 spline basis) for each component.
`loadings`	Numeric loadings (length 4) for Pain, Patient Global, SJC, TJC residuals.
`pjc_cutoffs`	Numeric vector of 5 cut points to define 4 quartile bins (include.lowest=TRUE).
`resid_center_scale`	List with `center` and `scale` vectors for standardizing residuals.

Details

The function returns both 4-level quartiles (`PJC_quartile`: Q1–Q4) and a 3-level grouped factor (`PJC_quartile_combine`) that combines Q2 and Q3 (levels: `Q1`, `Q2&3`, `Q4`).

Value

A tibble with `cohort_id`, `PJC`, `PJC_quartile`, and `PJC_quartile_combine`.

See Also

`calculate_STC` for the Swelling–Tenderness Contrast (STC; PC2).

Examples

```
# Minimal example WITHOUT a cDAPSA column (it will be computed as SJC+TJC+Pain+PG)
df1 <- data.frame(
  id = 1:3,
  pain = c(4, 6, 8),
  pg   = c(3, 7, 9),
  sjc  = c(1, 3, 5),
  tjc  = c(0, 2, 4)
)
calculate_PJC(
  df1,
  cohort_id = "id",
  cDAPSA = NULL,
  Pain = "pain",
  Patient_Global = "pg",
  SJC = "sjc",
  TJC = "tjc",
  oob_action = "na"
)

# Example WITH a consistent cDAPSA column (verified against the sum)
df2 <- transform(df1, cdapsa = pain + pg + sjc + tjc)
calculate_PJC(
  df2,
  cohort_id = "id",
  cDAPSA = "cdapsa",
  Pain = "pain",
  Patient_Global = "pg",
  SJC = "sjc",
  TJC = "tjc"
)
```

`calculate_STC` *Calculate TwoDcDAPSA: Swelling–Tenderness Contrast (STC) Score and Quartile Groups*

Description

Computes STC (PC2) as a loading-weighted combination of standardized residuals for Pain, Patient Global, SJC, and TJC after adjusting each for cDAPSA via a natural spline model. STC emphasizes swelling relative to tenderness under the default PC2 loadings.

Usage

```
calculate_STC(
  data,
  cohort_id = "cohort_id",
  cDAPSA = NULL,
  Pain = "Pain",
  Patient_Global = "Patient_Global",
  SJC = "SJC",
  TJC = "TJC",
  oob_action = c("stop", "na", "drop"),
  cdapsa_tolerance = 1e-08,
 center_scale = list(Pain = c(center = 4.303191, scale = 2.798819), Patient_Global =
  c(center = 4.795213, scale = 2.791098), SJC = c(center = 3.783245, scale = 4.707089),
  TJC = c(center = 5.194149, scale = 7.371234), cDAPSA = c(center = 18.0758, scale =
    14.03964)),
  ns_knots = c(-0.7176679, -0.2190796, 0.4219626),
  ns_boundary_knots = c(-1.287483, 5.265392),
 coef_list = list(Pain = c(-1.48889, 1.93539, 2.25211, 3.35687, 2.68578), Patient_Global
  = c(-1.7289, 2.1364, 2.35881, 3.95251, 2.66605), SJC = c(-0.76905, 0.47397, 1.9502,
    4.45945, 5.98404), TJC = c(-0.74115, 0.27891, 2.50892, 4.68559, 6.15326)),
  stc_loadings = c(-0.05043539, -0.01476495, 0.73876801, -0.6719078),
  stc_cutoffs = c(-Inf, -0.3881481, -0.1027692, 0.4411657, Inf),
  resid_center_scale = list(center = c(Pain = 1.155879e-15, `Patient Global` =
    9.679019e-16, `Swollen Joint Count` = -2.764596e-15, `Tender Joint Count` =
    -3.534933e-15), scale = c(Pain = 0.6478511, `Patient Global` = 0.6282206,
    `Swollen Joint Count` = 0.589554, `Tender Joint Count` = 0.3902453))
)
```

Arguments

`data`	A data.frame/tibble with the required columns.
`cohort_id`	Name of the cohort id column.
`cDAPSA`	Optional. Name of the cDAPSA column. If `NULL` (default), cDAPSA is computed as `SJC` + `TJC` + `Pain` + `Patient_Global`. If non-`NULL`, the provided column is verified to equal that sum within `cdapsa_tolerance`; otherwise an error is thrown.
`Pain`	Name of the Pain column (0-10).
`Patient_Global`	Name of the Patient Global column (0-10).
`SJC`	Name of the Swollen Joint Count column (0-66).
`TJC`	Name of the Tender Joint Count column (0-68).
`oob_action`	What to do when an input is out of its valid range (SJC 0-66, TJC 0-68, Pain/Patient Global 0-10). One of: `"stop"` (error), `"na"` (keep rows but set STC/Quartile to NA), or `"drop"` (remove rows). Default is `"stop"`.
`cdapsa_tolerance`	Numeric tolerance for comparing provided cDAPSA to the computed sum; default `1e-8`.

`center_scale`	List of centers/scales used to standardize inputs.
`ns_knots`	Numeric vector of interior knots for the spline on standardized cDAPSA.
`ns_boundary_knots`	Numeric vector of boundary knots for the spline on standardized cDAPSA.
`coef_list`	Named list of regression coefficients (intercept + 4 spline basis) for each component.
`stc_loadings`	Numeric loadings (length 4) for Pain, Patient Global, SJC, TJC residuals.
`stc_cutoffs`	Numeric vector of 5 cut points to define 4 quartile bins (include.lowest=TRUE).
`resid_center_scale`	List with `center` and `scale` vectors for standardizing residuals.

Details

Includes input "tuning": coerces character columns to numeric (warning if NAs introduced) and checks for out-of-range values (SJC 0-66, TJC 0-68, Pain/Patient Global 0-10) with configurable handling. If `cDAPSA` is not provided, it is computed as `SJC` + `TJC` + `Pain` + `Patient_Global`. If `cDAPSA` is provided, it is verified against this sum (within `cdapsa_tolerance`); any discrepancy results in an error.

The function returns both 4-level quartiles (`STC_quartile`: Q1–Q4) and a 3-level grouped factor (`STC_quartile_combine`) that combines Q1 and Q4 (levels: `Q1&4`, `Q2`, `Q3`).

Value

A tibble with `cohort_id`, `STC`, `STC_quartile`, and `STC_quartile_combine`.

See Also

`calculate_PJC` for the PROs-Joint Contrast (PJC; PC1).

Examples

```
# Minimal example WITHOUT a cDAPSA column (it will be computed as SJC+TJC+Pain+PG)
df1 <- data.frame(
  id = 1:3,
  pain = c(4, 6, 8),
  pg   = c(3, 7, 9),
  sjc  = c(1, 3, 5),
  tjc  = c(0, 2, 4)
)
calculate_STC(
  df1,
  cohort_id = "id",
  cDAPSA = NULL,
  Pain = "pain",
  Patient_Global = "pg",
  SJC = "sjc",
  TJC = "tjc",
  oob_action = "na"
)
```

```
# Example WITH a consistent cDAPSA column (verified against the sum)
df2 <- transform(df1, cdapsa = pain + pg + sjc + tjc)
calculate_STC(
  df2,
  cohort_id = "id",
  cDAPSA = "cdapsa",
  Pain = "pain",
  Patient_Global = "pg",
  SJC = "sjc",
  TJC = "tjc"
)
```

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