

# Package ‘QoLR’

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**Title** Analysis of Health-Related Quality of Life in oncology

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**Depends** R (>= 2.10.0), survival, zoo

**Description** To generate the scores of the EORTC QLQ-C30 questionnaire and supplementary modules and to determine the time to quality of life score deterioration in longitudinal analysis.

**License** GPL (>= 2.0)

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

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|              |   |
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| QoLR-package | <i>Analysis of Health-Related Quality of Life in oncology</i> |
|--------------|---|

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## Description

A set of functions to generate the scores of the EORTC QLQ-C30 questionnaire and supplementary modules. Two other programs to determine the time to deterioration in a Quality of Life score in longitudinal analysis with different definitions of deterioration explored.

## Details

Package: QoLR  
 Type: Package  
 Version: 1.0  
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 License: GPL (>=2.0)

A set of functions to generate the scores of the EORTC QLQ-C30 questionnaire, for example function 'scoring.QLQC30', and supplementary modules. Function 'TTD' to determine the time to deterioration in a Quality of Life score in longitudinal analysis and function 'TUDD' to determine the time until definitive deterioration

## Author(s)

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## References

Anota A. et al. Time to Health-related Quality of Life score deterioration as a modality of longitudinal analysis for health-related quality of life studies in oncology: do we need RECIST for quality

of life to achieve standardization? Qual Life Res. 2013 Nov 26.

Bonnetain F. et al. Time until definitive deterioration as a means of longitudinal analysis for treatment trials in patients with metastatic pancreatic adenocarcinoma. Eur J Cancer 2010, 46(5): 2753-2762.

Fayers PM. et al. The EORTC QLQ-C30 scoring manual. 3rd ed. Brussels: EORTC, 2001.

Hamidou Z. et al. Time to deterioration in quality of life score as a modality of longitudinal analysis in patients with breast cancer. The Oncologist 2011, 16(10):1458-1468.

## Examples

```
# To generate the scores of the EORTC QLQ-C30 for the data frame dataqol1:
data(dataqol1)
scoring.QLQC30(dataqol1, items = 2:31)

# To determine the time to deterioration of 5 points at least as compared to
# the baseline score for the score "QoL" and the score "pain".
# For score "QoL", a deterioration is observed if the score decreases,
# thus, order equals to 1 for this score.
# For score "pain", a deterioration is observed if the score increases,
# thus, order equals to 2 for this score.
data(dataqol2)
ttd=TTD(dataqol2,score=c("QoL","pain"),order=c(1,2),MCID=5)
head(ttd)

# To determine the time until definitive deterioration of 5 points at least
# of the score "QoL" as compared to the baseline score with no further
# improvement of more than 5 points:
data(dataqol2)
ttd=TUDD(dataqol2,score="QoL",order=1,MCID=5)
head(ttd)
```

---

dataqol1

*QLQ-C30 dataset*

---

## Description

A data frame with the responses to the 30 items of the EORTC QLQ-C30 questionnaire for 20 patients

## Usage

```
data(dataqol1)
```

**Format**

id subject identification number  
q1 item 1  
q2 item 2  
q3 item 3  
q4 item 4  
q5 item 5  
q6 item 6  
q7 item 7  
q8 item 8  
q9 item 9  
q10 item 10  
q11 item 11  
q12 item 12  
q13 item 13  
q14 item 14  
q15 item 15  
q16 item 16  
q17 item 17  
q18 item 18  
q19 item 19  
q20 item 20  
q21 item 21  
q22 item 22  
q23 item 23  
q24 item 24  
q25 item 25  
q26 item 26  
q27 item 27  
q28 item 28  
q29 item 29  
q30 item 30

**See Also**

[scoring.QLQC30](#)

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|          |  |
|----------|--|
| dataqol2 | <i>Longitudinal quality of life data</i> |
|----------|--|

---

**Description**

A data frame with 6 quality of life measures for 60 patients. The dataset is in long format.

**Usage**

```
data(dataqol2)
```

**Format**

id subject identification number  
time visit number for quality of life assessment  
date date of quality of life measurement  
QoL score of global quality of life  
pain score of pain  
arm treatment arm  
death date of death

---

|           |   |
|-----------|---|
| first_pos | <i>First positive element of a vector</i> |
|-----------|---|

---

**Description**

A function to obtain the first positive element of a vector

**Usage**

```
first_pos(X)
```

**Arguments**

X a vector

`maxi.false`*Last element of a boolean vector equals to FALSE*

---

**Description**

Report the position of the last element of a boolean vector equals to FALSE

**Usage**`maxi.false(vector)`**Arguments**

`vector`            a boolean vector

---

`maxi.time`*Report the highest score at each measurement time point*

---

**Description**

A function to report the highest score at each measurement time point taking into account all previous scores

**Usage**`maxi.time(vector)`**Arguments**

`vector`            A vector with quality of life scores

**Value**

a vector which the i-th value is equals to the maximum of the first values of the given vector until to the i-th position

**Examples**

```
vect=c(10,20,30,10,2,0,4,50,20)
maxi.time(vect)
```

---

|           |   |
|-----------|---|
| mini.time | <i>Report the lowest score at each measurement time point</i> |
|-----------|---|

---

**Description**

A function to report the lowest score at each measurement time point taking into account all previous scores

**Usage**

```
mini.time(vector)
```

**Arguments**

vector            A vector with quality of life scores

**Value**

a vector which the i-th value is equals to the minimum of the first values of the given vector until to the i-th position

**Examples**

```
vect=c(10,20,30,10,2,0,4,50,20)
mini.time(vect)
```

---

|         |   |
|---------|---|
| plotTTD | <i>Plot the Kaplan-Meier curve of the TTD or TUDD</i> |
|---------|---|

---

**Description**

A program that plot the time to deterioration curves according to the Kaplan-Meier estimation method for all patients or according to treatment arm. Additional information can be added such as the number of patients at risk and the number of the cumulative events

**Usage**

```
plotTTD(time, event, group = NULL, nrisk = FALSE, nevent = FALSE, group.names = NULL,
t = NULL, info = FALSE, pos.info = NULL, xlab, ylab)
```

**Arguments**

|             |   |
|-------------|---|
| time        | vector equals to the time to deterioration or the time to censor  |
| event       | a dummy vector equals to 1 if the patient is deteriorated and 0 if not  |
| group       | the name of the variable corresponding to the treatment arm, only if you want survival curves according to treatment arm. Only two groups are allowed                                     |
| nrisk       | Boolean equals to FALSE by default. If nrisk is TRUE, then the number of patients at risk is printed under the curve at each t time point.  |
| nevent      | Boolean equals to FALSE by default. If event is TRUE, then the number of cumulative events is printed under the curve at each t time point. In that case, you must also fix nrisk to TRUE |
| group.names | if you want survival curves according to treatment arm, you must give the name of the treatment arms in the group.names vector  |
| t           | if nrisk is TRUE, you must give the time points to print the number of patients at risk in vector t   |
| info        | Boolean equals to FALSE by default. If two groups are given in the group vector, then the result of the Log-rank test and the Hazard ratio are added to the graph if info is TRUE         |
| pos.info    | the position of the Log-rank test and the Hazard ratio on the graph   |
| xlab        | a title for x axis  |
| ylab        | a title for y axis  |

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**Examples**

```
# Kaplan-Meier survival curve of the Time until definitive deterioration
# of the score "QoL" with a minimal clinically important difference of 5 points
# as compared to the baseline score
#tudd1=TUDD(dataqol2, score="QoL", MCID=5,ref.init="baseline",ref.def="def1")
#ttd_1=merge(tudd1,unique(dataqol2[,c("id","arm")]))
## In the next graph, we added the number of patients at risk at time t
## and the result of the Log Rank Test and the Univariate Hazard Ratio
## of arm 2 vs. arm 1
#plotTTD(ttd_1$time.5.QoL,ttd_1$event.5.QoL,ttd_1$arm,nrisk=T,nevent=F,
#group.names=c("arm 1","arm 2"),t=seq(0,8,2),info=T,pos.info=c(6,0.8),
#xlab="time (months)",ylab="probability (%)")
```



**Description**

A program that computes the scores of the module QLQ-BN20 specific to brain cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQBN20(X, id="", items = 1:20)
```

**Arguments**

|       |  |
|-------|--|
| X     | input data matrix or data frame with items of the EORTC QLQ-BN20 in columns. Missing values are inserted as NA.        |
| id    | name of the variable in the dataframe X corresponding to the patient identification number                             |
| items | a vector which indicates the positions of the 20 items, in the correct order. By default items are column 1 to 20 of X |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|   |   |
|---|---|
| Y | a data frame with the id variable and the score obtained for each dimension. Each score is represented by one column of Y. The names of the scores are those proposed in the scoring manual. If there is no id variable in the dataframe X, then Y only contains the scores |
|---|---|

**Author(s)**

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**References**

Taphoorn, M.J., et al. (2010). An international validation study of the EORTC brain cancer module (EORTC QLQ-BN20) for assessing health-related quality of life and symptoms in brain cancer patients. *European Journal of Cancer*, 46(6), 1033-1040.

---

`scoring.QLQBR23`*Scoring of the module EORTC QLQ-BR23*

---

**Description**

A program that computes the scores of the module QLQ-BR23 specific to breast cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQBR23(X, id="", items = 1:23)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-BR23 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 23 items, in the correct order. By default items columns 1 to 23 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

**References**

Sprangers MA, et al. (1996). The European Organization for Research and Treatment of Cancer breast cancer-specific quality-of-life questionnaire module: first results from a three-country field study. *J Clin Oncol* 14:2756-68.

---

|                |   |
|----------------|---|
| scoring.QLQC30 | <i>Scoring of the health-related quality of life questionnaire EORTC QLQ-C30 for cancer</i> |
|----------------|---|

---

### Description

A program that computes the scores of the core questionnaire QLQ-C30 according to the EORTC scoring manual.

### Usage

```
scoring.QLQC30(X, id="", items = 1:30)
```

### Arguments

|       |   |
|-------|---|
| X     | input data matrix or data frame with items of the EORTC QLQ-C30 in columns. Missing values are inserted as NA.          |
| id    | name of the variable in the dataframe X corresponding to the patient identification number                              |
| items | a vector which indicates the positions of the 30 items, in the correct order. By default items are columns 1 to 30 of X |

### Details

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

### Value

|   |   |
|---|---|
| Y | a data frame with the id variable and the score obtained for each dimension. Each score is represented by one column of Y. The names of the scores are those proposed in the scoring manual. If there is no id variable in the dataframe X, then Y only contains the scores |
|---|---|

### Author(s)

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### References

Aaronson N.K., et al. (1993). The European Organization for Research and Treatment of Cancer QLQ-C30: A quality-of-life instrument for use in international clinical trials in oncology. *Journal of the National Cancer Institute*, 85(5), 365-376.

Fayers PM. et al. *The EORTC QLQC30 scoring manual*. 3rd ed. Brussels: EORTC, 2001.

## Examples

```
# scoring of the data frame dataqol1:  
data(dataqol1)  
scoring.QLQC30(dataqol1, id="id", items = 2:31)
```

---

scoring.QLQCR29

*Scoring of the module EORTC QLQ-CR29 for colorectal cancer*

---

## Description

A program that computes the scores of the module QLQ-CR29 according to the EORTC scoring manual.

## Usage

```
scoring.QLQCR29(X, id="", items = 1:29)
```

## Arguments

|       |   |
|-------|---|
| X     | input data matrix or data frame with items of the EORTC QLQ-CR29 in columns. Missing values are inserted as NA.         |
| id    | name of the variable in the dataframe X corresponding to the patient identification number                              |
| items | a vector which indicates the positions of the 29 items, in the correct order. By default items are columns 1 to 29 of X |

## Details

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

## Value

|   |   |
|---|---|
| Y | a data frame with the id variable and the score obtained for each dimension. Each score is represented by one column of Y. The names of the scores are those proposed in the scoring manual. If there is no id variable in the dataframe X, then Y only contains the scores |
|---|---|

## Author(s)

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

**References**

Whistance RN, et al. Clinical and psychometric validation of the EORTC QLQ-CR29 questionnaire module to assess health-related quality of life in patients with colorectal cancer. *European journal of cancer*. 2009 Nov;45(17):3017-26.

---

 scoring.QLQCX24

*Scoring of the module EORTC QLQ-CX24 for cervical cancer*


---

**Description**

A program that computes the scores of the module QLQ-CX24 according to the EORTC scoring manual.

**Usage**

```
scoring.QLQCX24(X, id="", items = 1:24)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-CX24 in columns. Missing values are inserted as NA.                      |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                              |
| <code>items</code> | a vector which indicates the positions of the 24 items, in the correct order. By default items are columns 1 to 24 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

Amelie Anota

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**References**

Greimel ER, et al. (2006). The European Organization for Research and Treatment of Cancer (EORTC) Quality-of-Life questionnaire cervical cancer module. *Cancer*, 107(8), 1812-1822.

---

`scoring.QLQEN24`*Scoring of the module EORTC QLQ-EN24 for endometrial cancer*

---

**Description**

A program that computes the scores of the module QLQ-EN24 according to the EORTC scoring manual.

**Usage**

```
scoring.QLQEN24(X, id="", items = 1:24)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-EN24 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 24 items, in the correct order. By default items columns 1 to 24 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

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**References**

Greimel E., et al. (2011). Psychometric validation of the European organisation for research and treatment of cancer quality of life questionnaire-endometrial cancer module (EORTC QLQ-EN24). *European Journal of Cancer*, 47(2), 183-190.

**Description**

A program that computes the scores of the module QLQ-H&N35 for head and neck cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQHN35(X, id="", items = 1:35)
```

**Arguments**

|       |   |
|-------|---|
| X     | input data matrix or data frame with items of the EORTC QLQ-H&N35 in columns. Missing values are inserted as NA.    |
| id    | name of the variable in the dataframe X corresponding to the patient identification number                          |
| items | a vector which indicates the positions of the 35 items, in the correct order. By default items columns 1 to 35 of X |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|   |   |
|---|---|
| Y | a data frame with the id variable and the score obtained for each dimension. Each score is represented by one column of Y. The names of the scores are those proposed in the scoring manual. If there is no id variable in the dataframe X, then Y only contains the scores |
|---|---|

**Author(s)**

Amelie Anota

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**References**

Bjordal, K., et al.(1999). Quality of life in head and neck cancer patients: validation of the European Organization for Research and Treatment of Cancer Quality of Life Questionnaire-H&N35. *Journal of Clinical Oncology*, 17(3), 1008-1008

---

`scoring.QLQLC13`*Scoring of the module EORTC QLQ-LC13*

---

**Description**

A program that computes the scores of the module QLQ-LC13 for lung cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQLC13(X, id="", items = 1:13)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-LC13 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 13 items, in the correct order. By default items columns 1 to 13 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

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**References**

Bergman B, et al. (1994). The EORTC QLQ-LC13: a modular supplement to the EORTC Core Quality of Life Questionnaire (QLQ-C30) for use in lung cancer clinical trials. EORTC Study Group on Quality of Life. Eur J Cancer 30A:635-42.



---

`scoring.QLQMY20`*Scoring of the module EORTC QLQ-MY20*

---

**Description**

A program that computes the scores of the module QLQ-MY20 for myeloma according to the EORTC scoring manual.

**Usage**

```
scoring.QLQMY20(X, id="", items = 1:20)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-MY20 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 20 items, in the correct order. By default items columns 1 to 20 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

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**References**

Cocks, K., et al. (2007). An international field study of the reliability and validity of a disease-specific questionnaire module (the QLQ-MY20) in assessing the quality of life of patients with multiple myeloma. *European Journal of Cancer*, 43(11), 1670-1678.

---

`scoring.QLQOES18`*Scoring of the module EORTC QLQ-OES18*

---

**Description**

A program that computes the scores of the module QLQ-OES18 for oesophageal cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQOES18(X, id="", items = 1:18)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-OES18 in columns. Missing values are inserted as NA.                 |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 18 items, in the correct order. By default items columns 1 to 18 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

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**References**

Blazeby, J. M., et al. (2003). Clinical and psychometric validation of an EORTC questionnaire module, the EORTC QLQ-OES18, to assess quality of life in patients with oesophageal cancer. *European Journal of Cancer*, 39(10), 1384-1394.

---

`scoring.QLQOG25`*Scoring of the module EORTC QLQ-OG25*

---

**Description**

A program that computes the scores of the module QLQ-OG25 for oesophago-gastric cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQOG25(X, id="", items = 1:25)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-OG25 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 25 items, in the correct order. By default items columns 1 to 25 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

**References**

Lagergren, P., et al.(2007). Clinical and psychometric validation of a questionnaire module, the EORTC QLQ-OG25, to assess health-related quality of life in patients with cancer of the oesophagus, the oesophago-gastric junction and the stomach. *European Journal of Cancer*, 43(14), 2066-2073.

---

`scoring.QLQPR25`*Scoring of the module EORTC QLQ-PR25*

---

**Description**

A program that computes the scores of the module QLQ-PR25 for prostate cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQPR25(X, id="", items = 1:25)
```

**Arguments**

|                    |  |
|--------------------|--|
| <code>X</code>     | input data matrix or data frame with items of the EORTC QLQ-PR25 in columns. Missing values are inserted as NA.                  |
| <code>id</code>    | name of the variable in the dataframe <code>X</code> corresponding to the patient identification number                          |
| <code>items</code> | a vector which indicates the positions of the 25 items, in the correct order. By default items columns 1 to 25 of <code>X</code> |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|                |  |
|----------------|--|
| <code>Y</code> | a data frame with the <code>id</code> variable and the score obtained for each dimension. Each score is represented by one column of <code>Y</code> . The names of the scores are those proposed in the scoring manual. If there is no <code>id</code> variable in the dataframe <code>X</code> , then <code>Y</code> only contains the scores |
|----------------|--|

**Author(s)**

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

**References**

van Andel G, et al. An international field study of the EORTC QLQ-PR25: a questionnaire for assessing the health-related quality of life of patients with prostate cancer. *European journal of cancer*. 2008 Nov;44(16):2418-24.

**Description**

A program that computes the scores of the module QLQ-STO22 for gastric cancer according to the EORTC scoring manual.

**Usage**

```
scoring.QLQSTO22(X, id="", items = 1:22)
```

**Arguments**

|       |   |
|-------|---|
| X     | input data matrix or data frame with items of the EORTC QLQ-STO22 in columns. Missing values are inserted as NA.    |
| id    | name of the variable in the dataframe X corresponding to the patient identification number                          |
| items | a vector which indicates the positions of the 22 items, in the correct order. By default items columns 1 to 22 of X |

**Details**

A score is generated if the patient answered to at least half of the corresponding items. The scores are generated according to the EORTC scoring guidelines. Simple imputation by the personal mean is retained. In this way, missing items are ignored.

**Value**

|   |   |
|---|---|
| Y | a data frame with the id variable and the score obtained for each dimension. Each score is represented by one column of Y. The names of the scores are those proposed in the scoring manual. If there is no id variable in the dataframe X, then Y only contains the scores |
|---|---|

**Author(s)**

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

**References**

Blazeby, J.M., et al. (2004). Clinical and psychometric validation of a questionnaire module, the EORTC QLQ-STO 22, to assess quality of life in patients with gastric cancer. *European Journal of Cancer*, 40(15), 2260-2268.

---

TTD *Time to Quality of Life score deterioration*

---

### Description

A program that computes the time to deterioration in a quality of life score.

### Usage

```
TTD(X, score = "", MCID, ref.init = "baseline", order = 1,
no_baseline = "censure", no_follow = "censure", death = NA, sensitivity = FALSE)
```

### Arguments

|             |   |
|-------------|---|
| X           | input data matrix or data frame with at least one quality of life score. Missing values are inserted as NA.   |
| score       | vector with the name of the quality of life scores of interest  |
| MCID        | the minimal clinically important difference   |
| ref.init    | the reference score to qualify the deterioration. By default, ref.init is "baseline", i.e. the reference score is the baseline score. If ref.init is "best", the best previous quality of life score is the reference score. If ref.init is "previous", the last previous score is the reference score. |
| order       | a vector equals to 1 if the deterioration corresponds to a decrease of the score, 2 otherwise   |
| no_baseline | By default, no_baseline equals to "censure" to indicate that patients with no baseline score are censored at baseline (Day 0). If no_baseline equals "event", these patients are deteriorated since baseline  |
| no_follow   | By default, no_follow equals to "censure" to indicate that patients with no follow-up score are censored just after baseline (Day 1). If no_follow equals to "event", these patients are deteriorated just after baseline   |
| death       | missing if patients who died without experienced a deterioration are censored at the time of the last quality of life assessment, equals to the name of the death date in the dataframe X otherwise   |
| sensitivity | Boolean equals to FALSE by default. If sensitivity is TRUE, then all sensitivity analyses are performed, integrating patients with no baseline or with no follow up as event (SA1), death as event (SA2) and simultaneously no baseline, no follow and death (SA3)                                      |

### Details

To apply this function, the dataset must respect a general structure. The dataset X must be in long format with the following variables in this order:

1. Patient's identification number
2. Variable identify the number of the quality of life assessment, i.e. the visit number

3. Date of quality of life measures
4. quality of life scores
5. Other variables as the date of death or the treatment arm.

The dataset must also be sorted by patient's identification number and quality of life measurement time. Dates must be in Julian format (i.e. number of days since a reference time point).

All these definitions are extensively described in the referenced papers below.

### Value

The result is a dataframe with the `id` variable of the dataframe `X` and the results of the time to deterioration analyses performed.

For each score and each time to deterioration analysis, two variables are created called `event` and `time` with the name of the corresponding score as a suffix.

Moreover, if `sensitivity` is `TRUE`, a suffix is added to each result of this function reflecting the sensitivity analysis corresponding (SA1, SA2 or SA3).

The first variable `event` is a dummy vector equals to 1 if the patient is deteriorated and 0 if not. The second variable `time` equals to the time in months to deterioration since baseline if the patient is deteriorated or the time to censor.

As example, for a given score "qol" and one analyse performed (i.e. `sensitivity` is `FALSE`), then two variables are created called `event.qol` and `time.qol`.

### Author(s)

Amelie Anota

Maintainer: Amelie Anota <aanota@chu-besancon.fr>

### References

Anota A., et al. Time to Health-related Quality of Life score deterioration as a modality of longitudinal analysis for health-related quality of life studies in oncology: do we need RECIST for quality of life to achieve standardization? *Qual Life Res.* 2013 Nov 26.

Hamidou Z., et al. Time to deterioration in quality of life score as a modality of longitudinal analysis in patients with breast cancer. *The Oncologist* 2011, 16(10):1458-1468.

### See Also

[TUDD](#)

### Examples

```
data(dataqol2)
# deterioration of 5 points at least as compared to the baseline score for
# the score "QoL" and the score "pain"
TTD(dataqol2,score=c("QoL","pain"),order=1:2,MCID=5)
```

---

TUDD *Time until definitive deterioration in a quality of life score*

---

### Description

A program that computes the time until definitive deterioration in quality of score.

### Usage

```
TUDD(X, score = "", MCID, ref.init = "baseline", ref.def = "def1", order = 1,
     no_baseline = "censure", no_follow = "censure", death = NA, sensitivity = FALSE)
```

### Arguments

|             |   |
|-------------|---|
| X           | input data matrix or data frame with a quality of life score. Missing values are inserted as NA.  |
| score       | vector with the name of the quality of life scores of interest  |
| MCID        | a vector equals to the minimal clinically important difference (MCID). Several MCID can be specified  |
| ref.init    | the reference score to qualify the deterioration. By default, ref.init is "baseline", i.e. the reference score is the baseline score. If ref.init is "best", the best previous quality of life score is the reference score. If ref.init is "previous", the last previous score is the reference score.   |
| ref.def     | the deterioration is definitive 1: if there is no clinically significant improvement as compared to the reference score ("def1"); 2: if the deterioration is also observed at all times following the deterioration ("def2"); 3: or there is no clinically significant improvement as compared to the score qualifying the deterioration ("def3") |
| order       | a vector equals to 1 if the deterioration corresponds to a decrease of the score, 2 otherwise   |
| no_baseline | By default, no_baseline equals to "censure" to indicate that patients with no baseline score are censored at baseline (Day 0). If no_baseline equals "event", these patients are deteriorated since baseline  |
| no_follow   | By default, no_follow equals to "censure" to indicate that patients with no follow-up score are censored just after baseline (Day 1). If no_follow equals to "event", these patients are deteriorated just after baseline   |
| death       | missing if patients who died without experienced a deterioration are censored at the time of the last quality of life assessment, equals to the name of the death date in the dataframe X otherwise   |
| sensitivity | Boolean equals to FALSE by default. If sensitivity is TRUE, then all sensitivity analyses are performed, integrating patients with no baseline or with no follow up as event (SA1), death as event (SA2) and simultaneously no baseline, no follow and death (SA3)  |



**Details**

To apply this function, the dataset must respect a general structure. The dataset X must be in long format with the following variables in this order:

1. Patient's identification number
2. Variable identify the quality of life assessment, i.e. the visit number
3. Date of quality of life measure
4. quality of life scores
5. Other variables as the date of death or the treatment arm.

The dataset must also be sorted by patient's identification number and quality of life measurement time.

Dates must be in Julian format (i.e. number of days since a reference time point).

All these definitions are extensively described in the referenced papers below.

**Value**

The result is a dataframe with the `id` variable of the dataframe X and the results of the time to deterioration analyses performed.

For each score and each time to deterioration analysis, two variables are created called `event` and `time` with the value of the MCID and the name of the corresponding score as a suffix.

Moreover, if `sensitivity` is TRUE, a suffix is added to each result of this function reflecting the sensitivity analysis corresponding (SA1, SA2 or SA3).

The first variable `event` is a dummy vector equals to 1 if the patient is deteriorated and 0 if not. The second variable `time` equals to the time in months to deterioration since baseline if the patient is deteriorated or the time to censor.

As example, for a given score "qol", `MCID = 5` and one analyse performed (i.e. `sensitivity` is FALSE), then two variables are created called `event.5.qol` and `time.5.qol`.

**Author(s)**

Amelie Anota

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**References**

Anota A., et al. Time to Health-related Quality of Life score deterioration as a modality of longitudinal analysis for health-related quality of life studies in oncology: do we need RECIST for quality of life to achieve standardization? *Qual Life Res.* 2013 Nov 26.

Bonnetain F., et al. Time until definitive deterioration as a means of longitudinal analysis for treatment trials in patients with metastatic pancreatic adenocarcinoma. *Eur J Cancer* 2010, 46(5): 2753-2762.

**See Also**

[TTD](#)

**Examples**

```

data(dataqol2)
# Time to definitive deterioration of 5 points at least of the "QoL" score
# as compared to the best previous score with no further improvement of more
# than 5 points :
ttd=TUDD(dataqol2,score=c("QoL","pain"),ref.init="best",order=1,MCID=5)
head(ttd)

```

---

|        |                             |
|--------|-----------------------------|
| whicha | <i>To check a condition</i> |
|--------|-----------------------------|

---

**Description**

A function to check a condition

**Usage**

```
whicha(condition)
```

**Arguments**

condition      a logical vector

**Value**

0 if the logical vector does not contain the value TRUE. Otherwise give the TRUE indices

---

|           |  |
|-----------|--|
| write.TTD | <i>Write in a csv file the results of the time to deterioration analysis</i> |
|-----------|--|

---

**Description**

A program that computes the time to deterioration in a quality of life score and print the results in a csv file according to treatment arm

**Usage**

```

write.TTD(X, score = "", order = 1, ref.init = "baseline", MCID, death = NA,
group = NULL, names.group, sensitivity = TRUE, file = "")

```

**Arguments**

|             |   |
|-------------|---|
| X           | input data matrix or data frame with a quality of life score. Missing values are inserted as NA   |
| score       | vector with the name of the quality of life scores of interest  |
| order       | a vector equals to 1 if the deterioration corresponds to a decrease of the score, 2 otherwise   |
| ref.init    | the reference score to qualify the deterioration. By default, ref.init is "baseline", i.e. the reference score is the baseline score. If ref.init is "best", the best previous quality of life score is the reference score. If ref.init is "previous", the last previous score is the reference score. |
| MCID        | vector equals to the minimal clinically important difference (MCID). Several MCID can be specified  |
| death       | missing if patients who died without experienced a deterioration are censored at the time of the last quality of life assessment, equals to the name of the death date in the dataframe X otherwise   |
| group       | the name of the variable in X corresponding to the treatment arm. Only two groups are allowed   |
| names.group | the name of each treatment group to print   |
| sensitivity | Boolean equals to TRUE by default. If sensitivity is TRUE, then all sensitivity analyses are performed, integrating patients with no baseline or with no follow up as event, death as event and simultaneously no baseline, no follow and death   |
| file        | the name of the csv file to create with the results of the time to deterioration analysis   |

**Value**

this function does not return value in R console but create a csv file with the results of the time to deterioration analysis

**Author(s)**

Amelie ANOTA

Maintainer: Amelie ANOTA <aanota@chu-besancon.fr>

**See Also**

[TTD](#)

**Examples**

```
### The time to deterioration of scores "QoL" and "pain" of the dataqol2 data
### set as compared to the baseline score
### with two MCID (5 points and 10 points)
### and according to the treatment arm called "arm"
### all sensitivity analyses are performed simultaneously to the main definition
### the created file is named "file_TTD_baseline.csv" and is located
```

```
### in the current directory

data(dataqol2)
write.TTD(dataqol2,score=c("QoL","pain"),order=c(1,2),MCID=c(5,10),
group="arm",names.group=c("arm 1","arm 2"),sensitivity=FALSE,
file="file_TTD_baseline")
```

---

|            |  |
|------------|--|
| write.TUDD | <i>Write in a csv file the results of the time until definitive deterioration analysis</i> |
|------------|--|

---

### Description

A program that computes the time until definitive deterioration in a quality of life score and print the results in a csv file according treatment arm

### Usage

```
write.TUDD(X, score = "", order = 1, ref.init = "baseline", MCID, ref.def = "def1",
death = NA, group = NULL, names.group, sensitivity = TRUE, file = "")
```

### Arguments

|             |   |
|-------------|---|
| X           | input data matrix or data frame with a quality of life score. Missing values are inserted as NA   |
| score       | vector with the name of the quality of life scores of interest  |
| order       | a vector equals to 1 if the deterioration corresponds to a decrease of the score, 2 otherwise   |
| ref.init    | the reference score to qualify the deterioration. By default, ref.init is "baseline", i.e. the reference score is the baseline score. If ref.init is "best", the best previous quality of life score is the reference score. If ref.init is "previous", the last previous score is the reference score.   |
| MCID        | vector equals to the minimal clinically important difference (MCID). Several MCIDs can be specified   |
| ref.def     | the deterioration is definitive 1: if there is no clinically significant improvement as compared to the reference score ("def1"); 2: if the deterioration is also observed at all times following the deterioration ("def1"); 3: or there is no clinically significant improvement as compared to the score qualifying the deterioration ("def3") |
| death       | missing if patients who died without experienced a deterioration are censored at the time of the last QoL score, equals to the name of the death date in the dataframe X otherwise  |
| group       | the name of the variable in X corresponding to the treatment arm. Only two groups are allowed.  |
| names.group | the name of each treatment group to print   |

|             |   |
|-------------|---|
| sensitivity | Boolean equals to TRUE by default. If sensitivity is TRUE, then all sensitivity analyses are performed, integrating patients with no baseline or with no follow up as event, death as event and simultaneously no baseline, no follow and death |
| file        | the name of the csv file to create with the results of the time to deterioration analysis   |

**Value**

this function does not return value in R console but create a csv file with the results of the time to deterioration analysis

**Author(s)**

Amelie ANOTA

Maintainer: Amelie ANOTA <aanota@chu-besancon.fr>

**See Also**

[TUDD](#)

**Examples**

```
### The time until definitive deterioration of scores "QoL" and "pain" of the
### dataqol2 data set as compared to the baseline score
### with two MCID (5 points and 10 points)
### and according to the treatment arm called "arm"
### all sensitivity analyses are performed simultaneously to the main definition
### the created file is named "file_TTD_baseline.csv" and is located
### in the current directory

data(dataqol2)
write.TUDD(dataqol2,score=c("QoL","pain"),order=c(1,2),MCID=c(5,10),
group="arm",names.group=c("arm 1","arm 2"),sensitivity=FALSE,
file="file_TTD_baseline")
```

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