

# Package ‘QRIPkg’

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**Title** Quantile Regression Index Score

**Version** 0.2.0

**Description** The `QRI_func()` function performs quantile regression analysis using age and sex as predictors to calculate the Quantile Regression Index (QRI) score for each individual’s regional brain imaging metrics and then averages across the regional scores to generate an average tissue specific score for each subject. The `QRI_plot()` is used to plot QRI and generate the normative curves for individual measurements.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Depends** R (>= 2.10)

**Imports** ggplot2, quantreg, stats

**NeedsCompilation** no

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 QRI\_func

*Quantile Regression Index Score*


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### Description

The QRI\_func() performs quantile regression analysis using age and sex as predictors to calculate the Quantile Regression Index (QRI) score for each individual's regional brain imaging metrics and then averages across the regional scores to generate an average tissue specific score for each subject. The QRI indicates individual deviations from the expected aging trajectory. Positive QRI indicates accelerated vs. expected aging trajectory while negative QRI indicates delayed aging. The expected aging trajectory is modeled based on sample of controls.

### Usage

```
QRI_func(ID, DXcontrol, predictors, resp.range, data)
```

### Arguments

ID	a column name of subject ID in data
DXcontrol	The expected aging trajectory should only be calculated from the controls(i.e. DXcontrol='control==0'). If DXcontrol=NULL, the expected aging trajectory will be calculated from the full data.
predictors	column names of predictors (i.e. age, sex)
resp.range	a column range of responses
data	a data frame contains predictors and responses in the quantile regression model.

### Details

The QRI score can be used as an alternative to BrainAge to assess accelerated brain aging by determining an individuals' placement on the expected aging trajectory. A study by Ryan et al (2020) demonstrated that QRI and BrainAge share up to 80% of the variance in both patients and controls. The typical function usage involves calling the QRI function with the following parameters (age, sex) on a list of tissue-specific neuroimaging traits such as regional white matter fractional anisotropy, regional gray matter cortical thickness, or gray matter subcortical volumes. Quantile regression is performed using the controls (DXcontrol='control==0') to generate the normative curves for the 5th, 50th, and 95th percentiles. Then each patient (DXcontrol='control==1') and control's individual (DXcontrol='control==0') data is compared to the expected aging trajectory. Each regional measure is assigned a score based upon its location: values > 95% of the expected age data are assigned a value of "-1"; values < 5% receive a value of "1"; all others are assigned "0". The function then averages across the regional data to generate a tissue-specific QRI score (i.e. white matter QRI).

### Value

This function returns the average tissue-specific QRI scores for all subjects.

**Note**

The `QRI_func()` function is developed at the Maryland Psychiatric Research Center, Department of Psychiatry, University of Maryland School of Medicine. This project is supported by NIH R01 EB015611 grant. Please cite our funding if you use this software.

Meghann C. Ryan, L. Elliot Hong, Kathryn S. Hatch, Shuo Chen, Krystl Haerian, Jingtao Wang, Eric L. Goldwaser, Xiaoming Du, Bhim M. Adhikari, Heather Bruce, Stephanie Hare, Mark D. Kvarda, Neda Jahanshad, Thomas E. Nichols, Paul M. Thompson, Peter Kochunov. The Additive Impact of Metabolic Disorders and Psychiatric Illnesses on Accelerated Brain Aging. In Review

**References**

Roger Koenker (2020). `quantreg`: Quantile Regression. R package version 5.61. <https://CRAN.R-project.org/package=quantreg>

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

**Examples**

```
QRI <- QRI_func(ID='ID', DXcontrol='Control==0', predictors=c('Age', 'Sex'), resp.range=c(5:6),
data=QRIpkg::subcortical)
```

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QRI\_plot

*Quantile Regression Index plot*

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**Description**

The `QRI_plot()` is used to plot Quantile Regression Index (QRI) and generate the normative curves for individual's regional brain imaging metrics.

**Usage**

```
QRI_plot(x, y, xlab, ylab, DXcontrol, data)
```

**Arguments**

<code>x</code>	the x coordinate for the QRI plot
<code>y</code>	the y coordinate for the QRI plot
<code>xlab</code>	the label for the x coordinate
<code>ylab</code>	the label for the y coordinate
<code>DXcontrol</code>	the expected aging trajectory. It should only be calculated from the controls(i.e. <code>DXcontrol='control==0'</code> ). If <code>DXcontrol=NULL</code> , the expected aging trajectory will be calculated from the full data.
<code>data</code>	a data frame contains the predictor(x coordinate), response(y coordinate) and control( <code>DXcontrol</code> ) in the quantile regression model.

## Details

The QRI score can be used as an alternative to BrainAge to assess accelerated brain aging by determining an individuals' placement on the expected aging trajectory. A study by Ryan et al (2020) demonstrated that QRI and BrainAge share up to 80% of the variance in both patients and controls. The typical function usage involves calling the QRI function with the following parameters (age, sex) on a list of tissue-specific neuroimaging traits such as regional white matter fractional anisotropy, regional gray matter cortical thickness, or gray matter subcortical volumes. Quantile regression is performed using the controls (DXcontrol='control==0') to generate the normative curves for the 5th, 50th, and 95th percentiles. Then each patient (DXcontrol='control==1') and control's individual (DXcontrol='control==0') data is compared to the expected aging trajectory. Each regional measure is assigned a score based upon its location: values > 95% of the expected age data are assigned a value of "-1"; values < 5% receive a value of "1"; all others are assigned "0". The function then averages across the regional data to generate a tissue-specific QRI score (i.e. white matter QRI).

## Value

This function returns a plot for individual measurements.

## Note

The QRI\_plot() function is developed at the Maryland Psychiatric Research Center, Department of Psychiatry, University of Maryland School of Medicine. This project is supported by NIH R01 EB015611 grant. Please cite our funding if you use this software.

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## References

H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016.

Roger Koenker (2020). quantreg: Quantile Regression. R package version 5.61. <https://CRAN.R-project.org/package=quantreg>

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

## Examples

```
QRIplot <- QRI_plot(x='Age',y='Ventricle', xlab='Age', ylab='Ventricle', DXcontrol='Control==0',  
data=QRIpkg::subcortical)
```

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subcortical

*Subcortical*

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### Description

Simulated volumes of subcortical structures are used as an example for this function. You can calculate QRI for this dataset"

### Usage

```
subcortical
```

### Format

A data frame with 8000 rows and 12 variables:

**ID** subjects' ID

**Age** subjects' age

**Control** indicators of control group

**Sex** subjects' gender

**Ventricle** Simulated volumes of Ventricle

**Thalamus** Simulated volumes of Thalamus

**Caudate** Simulated volumes of Caudate

**Putamen** Simulated volumes of Putamen

**Palladium** Simulated volumes of Palladium

**Hippocampus** Simulated volumes of Hippocampus

**Amygdala** Simulated volumes of Amygdala

**Accumbens** Simulated volumes of Accumbens

### Source

subcortical is from Maryland Psychiatric Research Center, Department of Psychiatry, University of Maryland School of Medicine.

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