

# Package ‘BayesGWQS’

October 12, 2022

**Type** Package

**Title** Bayesian Grouped Weighted Quantile Sum Regression

**Version** 0.1.1

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**Description**

Fits Bayesian grouped weighted quantile sum (BGWQS) regressions for one or more chemical groups with binary outcomes. Wheeler DC et al. (2019) <[doi:10.1016/j.sste.2019.100286](https://doi.org/10.1016/j.sste.2019.100286)>.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Depends** R (>= 4.0.0)

**SystemRequirements** JAGS

**Imports** coda, stats, rjags, stringr, plyr

**Suggests** testthat

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2022-01-20 22:42:54 UTC

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`bgwqs.fit`*Bayesian Grouped WQS Regression*

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**Description**

This function fits a Bayesian grouped weighted quantile sum (BGWQS) regression model.

**Usage**

```
bgwqs.fit(  
  y,  
  x,  
  z,  
  x.s,  
  n.quantiles = 4,  
  working.dir,  
  n.chains = 1,  
  n.iter = 10000,  
  n.burnin = 5000,  
  n.thin = 1,  
  n.adapt = 500,  
  DIC = FALSE  
)
```

**Arguments**

<code>y</code>	A vector containing outcomes.
<code>x</code>	A matrix of component data.
<code>z</code>	A vector or matrix of controlling covariates.
<code>x.s</code>	A vector of the number of components in each index.
<code>n.quantiles</code>	The number of quantiles to apply to the component data.
<code>working.dir</code>	A file path to the directory.
<code>n.chains</code>	The number of Markov chains; must be a positive integer.
<code>n.iter</code>	The number of total iterations per chain, including burn in.
<code>n.burnin</code>	The number of iterations to discard at the beginning.
<code>n.thin</code>	The thinning rate; must be a positive integer.
<code>n.adapt</code>	The number of adaption iterations.
<code>DIC</code>	Logical; whether or not the user desires the function to return DIC.

**Value**

A list which includes BUGS output, sample chains post-burnin, and convergence test results.

**Examples**

```
## Not run:
data("simdata")
group_list <- list(c("pcb_118", "pcb_138", "pcb_153", "pcb_180", "pcb_192"),
                  c("as", "cu", "pb", "sn"),
                  c("carbaryl", "propoxur", "methoxychlor", "diazinon", "chlorpyrifos"))
x.s <- make.x.s(simdata, 3, group_list)
X <- make.X(simdata, 3, group_list)
Y <- simdata$Y
work_dir <- tempdir()
results <- bgwqs.fit(y = Y, x = X, x.s = x.s, n.quantiles=4,
                    working.dir = work_dir,
                    n.chains = 1, n.iter = 10000, n.burnin = 5000, n.thin = 1, n.adapt = 500)

## End(Not run)
```

make.X

*Forms matrix of components***Description**

This function returns a matrix of component variables, X. The user can specify the desired chemicals and order by creating a list of string vectors, each vector containing the variable names of all desired elements of that group.

**Usage**

```
make.X(df, num.groups, groups)
```

**Arguments**

df	A dataframe containing named component variables
num.groups	An integer representing the number of component groups desired
groups	A list, each item in the list being a string vector of variable names for one component group

**Value**

A matrix of component variables

**Examples**

```
data("simdata")
group_list <- list(c("pcb_118", "pcb_138", "pcb_153", "pcb_180", "pcb_192"),
                  c("as", "cu", "pb", "sn"),
                  c("carbaryl", "propoxur", "methoxychlor", "diazinon", "chlorpyrifos"))
X <- make.X(simdata, 3, group_list)
X
```

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make.x.s	<i>Forms component group ID vector of X</i>
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**Description**

This function returns a vector which lets WQS.fit know the size and order of groups in X

**Usage**

```
make.x.s(df, num.groups, groups)
```

**Arguments**

df	A dataframe containing named component variables
num.groups	An integer representing the number of component groups desired
groups	A list, each item in the list being a string vector of variable names for one component group

**Value**

A vector of integers, each integer relating how many columns are in each group

**Examples**

```
data("simdata")
group_list <- list(c("pcb_118", "pcb_138", "pcb_153", "pcb_180", "pcb_192"),
                  c("as", "cu", "pb", "sn"),
                  c("carbaryl", "propoxur", "methoxychlor", "diazinon", "chlorpyrifos"))
x.s <- make.x.s(simdata, 3, group_list)
x.s
```

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simdata	<i>Simulated data of chemical concentrations and one binary outcome variable</i>
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**Description**

Data were simulated to have 0.7 in-group correlation and 0.3 between-group correlation. There are three groups, with the third being significantly correlated to the outcome variable.

**Usage**

```
simdata
```

**Format**

A data frame with 1000 rows and 15 variables:

**pcb\_118** a numeric vector; part of group 1  
**pcb\_138** a numeric vector; part of group 1  
**pcb\_153** a numeric vector; part of group 1  
**pcb\_180** a numeric vector; part of group 1  
**pcb\_192** a numeric vector; part of group 1  
**as** a numeric vector; part of group 2  
**cu** a numeric vector; part of group 2  
**pb** a numeric vector; part of group 2  
**sn** a numeric vector; part of group 2  
**carbaryl** a numeric vector; part of group 3  
**propoxur** a numeric vector; part of group 3  
**methoxychlor** a numeric vector; part of group 3  
**diazinon** a numeric vector; part of group 3  
**chlorpyrifos** a numeric vector; part of group 3  
**Y** a numeric vector; the outcome variable

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weight.plot

*Generates Plots of weights by group*


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**Description**

This function takes the object created by the bgwqs.fit function and a vector of group names and generates a random forest variable importance plot for each group. The weights in each group are listed in descending order.

**Usage**

```
weight.plot(fit.object, group.names, group.list, x.s)
```

**Arguments**

<code>fit.object</code>	The object that is returned by the bgwqs.fit function
<code>group.names</code>	A string vector containing the name of each group included in the BGWQS regression. Will be used for plot titles.
<code>group.list</code>	A list, each item in the list being a string vector of variable names for one component group.
<code>x.s</code>	A vector of the number of components in each index.

**Value**

A plot for each group of the BGWQS regression

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