

# Package ‘SAGA’

December 3, 2015

**Type** Package

**Title** Software for the Analysis of Genetic Architecture

**Version** 2.0.0

**Date** 2015-12-01

**Author** Heath Blackmon and Jeffery P. Demuth

**Maintainer** Heath Blackmon <coleoguy@gmail.com>

**Description** Implements an information theory approach to the analysis of line cross data providing model averaged results of parameter estimates and unconditional standard errors. Also includes functions to provide a visualization of models space, custom plots of multi-model inference results, and traditional line cross analysis plots.

**License** GPL (>= 2)

**URL** <https://github.com/coleoguy/SAGA>

**Imports** plotrix, viridis

**Suggests** knitr

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2015-12-03 13:05:04

## R topics documented:

SAGA-package . . . . .	2
AICtoMW . . . . .	2
AnalyzeCrossesMM . . . . .	3
cohortID . . . . .	5
data . . . . .	5
DisplayCmatrix . . . . .	6
EvaluateModel . . . . .	8
plot . . . . .	8
plotObserved . . . . .	9
VisModelSpace . . . . .	10

**Index****11**

SAGA-package

*Software for the Analysis of Genetic Architecture SAGA***Description**

Provides multimodel parameter estimates of genetic architecture. Uses weighted least squares to solve all possible models. Chooses the model or models that are most appropriate based on AICc weights and produces model weighted parameter estimates and unconditional standard errors. A function to visualize the distribution of model fits across model space allows users to graphically see how well defined the "true" model is with their dataset.

**Details**

Package: SAGA

Version: 2.0.0

**Author(s)**

Heath Blackmon and Jeffery P. Demuth  
 coleoguy@gmail.com

**References**

Lynch, M. and B. Walsh. 1998. Genetics and analysis of quantitative traits. Sinauer Associates, Inc., Sunderland, Massachusetts.

Burnham, K. P. and D. R. Anderson. 2002. Model selection and multimodel inference: a practical information-theoretic approach. Springer Science & Business Media.

AICtoMW

*converts AIC or AICc to model weights***Description**

This function generates model weights based on either delta AIC scores or delta AICc scores.

**Usage**

AICtoMW(x)

**Arguments**

x a numeric vector containing delta AIC or delta AICc scores

**Details**

This function returns a numeric vector containing model weights

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
# load data
data(PH)
# analyze it
results <- AnalyzeCrossesMM(PH)
# calculate model weights
AICtoMW(results[[3]])
```

---

AnalyzeCrossesMM

*Multimodel Analysis of Line Cross Data*


---

**Description**

Analyze all possible genetic architecture models based on mean phenotypes from line cross data.

**Usage**

```
AnalyzeCrossesMM(data, Cmatrix = "XY", model.sum = .95,
  max.models = 300000, even.sex = F, graph=F,
  cex.axis=1, cex.names=1, cex.main=1, max.pars = NULL)
```

**Arguments**

data	a data frame with the first three columns: 1) id of the cohort this must mach the coefficient row of the c-matrix 2) mean phenotype measure of the cohort 3) Standard error of the cohort's mean phenotype
Cmatrix	A text string used to select the mid-parent scaled c-matrix to be used in the analysis. Included options are "XY", "XO", "ZW", "ZO", or "esd". If you need a different matrix you can supply it here as well.
model.sum	This is the sum of the probability of the models to be included
max.models	The maximum number of fitted models to return from the function. This is included as an option to allow analysis of large model space on computers with limited RAM.

<code>even.sex</code>	A logical by default it is false. It should be set as true if either sexed cohorts are included or if mixed sex cohorts are included but have equal numbers of males and females.
<code>max.pars</code>	Optional parameter limiting the size of the equations evaluated.
<code>graph</code>	Logical indicating whether a plot of results should be produced
<code>cex.axis</code>	expansion factor for numeric axis labels.
<code>cex.names</code>	expansion factor for CGE labels.
<code>cex.main</code>	expansion factor for main title.

**Details**

Provides model averaged estimates of the contribution of composite genetic effects to the line means in line cross analysis experiments. Using AICc models are given weights and these are used to construct a confidence model set that allows for parameter estimates and errors to include model selection uncertainty. (see Burnham and Anderson 2002). The vignette contains a lengthy discussion of

**Value**

Returns a "genarch" object which is a list with the following elements:

<code>models:</code>	a list containing the weighted least squares solution for all models tested.
<code>estimates:</code>	a data frame containing Model Weighted Average for each parameter and its unconditional standard error.
<code>daicc:</code>	a vector of the delta AICc scores for all models tested.
<code>varimp:</code>	a data frame containing the variable importance scores for composite effects.

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**References**

Burnham, K. P., & Anderson, D. R. (2002). Model selection and multimodel inference: a practical information-theoretic approach. Springer.

**See Also**

[VisModelSpace](#)

**Examples**

```
data(PH)
results <- AnalyzeCrossesMM(PH)
```

---

`cohortID`*Display a lookup table for cohort IDs*

---

**Description**

A data frame allowing the user to lookup ID numbers for each cohort. Parents are listed in parentheses and sire x dam.

**Usage**

```
cohortID(sexed=T)
```

**Arguments**

`sexed` if True then will return all available cohorts if False then returns only mixed sex cohorts

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
IDs <- cohortID()
```

---

`data`*empirical datasets*

---

**Description**

ban.osa: Productivity of crosses involving *Tribolium castaneum* from Ecuador and Japan [1]

dar.bho: Productivity of crosses involving *Tribolium castaneum* from Tanzania and India [1]

per.inf: Productivity of crosses involving *Tribolium castaneum* from Peru and Portugal [1]

sin.cro: Productivity of crosses involving *Tribolium castaneum* from Malaysia and Croatia [1]

PH: Plant height data for *Nicotiana rustica* [2]

SL: Sperm length data for male *Drosophila mojavensis* line cross analysis [3]

SR: Sperm receptacle length data for female *Drosophila mojavensis* line cross analysis [3]

**Usage**

```
data(ban.osa)
```

**Value**

A data frame with rows for each cohort and 3 columns:

id	a numeric vector
mean	a numeric vector
SE	a numeric vector

**Source**

- [1] Demuth, J.P., Evolution of Hybrid Incompatibility in the beetle *Tribolium Castaneum*, in *Biology*. 2004, Indiana University: Bloomington. p. 152.
- [2] Lynch, M., and B. Walsh, 1998 Lynch, M., & Walsh, B. (1998). *Genetics and analysis of quantitative traits*. Sinauer Associates, Inc., Sunderland, Massachusetts.
- [3] Miller, G. T., Starmer, W. T., & S. Pitnick 2003. Quantitative genetic analysis of among-population variation in sperm and female sperm-storage organ length in *Drosophila mojavensis*. *Genetical research*, 81(03), 213-220.

**Examples**

```
data(ban.osa)
data(dar.bho)
data(per.inf)
data(sin.cro)
data(PH)
data(SL)
data(SR)
```

---

DisplayCmatrix

*Display a matrix of composite genetic effects*

---

**Description**

A data frame representing the c-matrix scaled to the midparent. Column names describe the composite effects. The argument "esd" should be used for species that do not have sex chromosomes.

**Usage**

```
DisplayCmatrix(table = "XY")
```

**Arguments**

table	a character string specifying the sex determination system. Current options are "XY", "ZW", "esd"
-------	---

**Value**

M	mean
Aa	autosomal additive
Ad	autosomal dominance
Xa	X chromosome additive
Xd	X chromosome dominance
Ya	Y chromosome additive
Ca	cytotype additive
Mea	maternal effect additive
Med	maternal effect dominance
AaAa	autosomal additive by additive epistasis
AaAd	autosomal additive by dominance epistasis
AdAd	autosomal dominance by dominance epistasis
XaAa	X chromosome additive by autosomal additive epistasis
XaAd	X chromosome additive by autosomal dominance epistasis
XdAa	X chromosome dominance by autosomal additive epistasis
XdAd	X chromosome dominance by autosomal dominance epistasis
YaAa	Y chromosome additive by autosomal additive epistasis
YaAd	Y chromosome additive by autosomal dominance epistasis
YaXa	Y chromosome additive by X additive epistasis
CaAa	cytotype additive by autosomal additive epistasis
CaAd	cytotype additive by autosomal dominance epistasis
CaXa	cytotype additive by X chromosome additive epistasis
CaXd	cytotype additive by X chromosome dominance epistasis
CaYa	cytotype additive by Y chromosome additive epistasis

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
cmat <- DisplayCmatrix("XY")
```

---

EvaluateModel	<i>Evaluate Single Model</i>
---------------	------------------------------

---

### Description

This function allows the user to explore a specific model in a "genarch" object

### Usage

```
EvaluateModel(data, model, cex.axis=1, cex.names=1, cex.main=1)
```

### Arguments

data	This is a "genarch" object returned by the function AnalyzeCrossesMM
model	This is the number corresponding to the model the user wishes to investigate.
cex.axis	expansion factor for numeric axis labels.
cex.names	expansion factor for name labels.
cex.main	expansion factor for main title.

### Author(s)

Heath Blackmon and Jeffery P. Demuth

### Examples

```
data(PH)
results <- AnalyzeCrossesMM(PH)
EvaluateModel(results, model=11)
```

---

plot	<i>provides a custom plot of a genarch object</i>
------	---

---

### Description

Plot a publication quality figure of a genarch object with many built-in customization such as only a subset with variable importances over a chosen cut-off. If a cut-off is chosen that would make it so only a single bar would be plotted the min.vi argument will be automatically reduced to include at least the two CGEs with the highest variable importance.

### Usage

```
## S3 method for class 'genarch'
plot(x, min.vi = .5, main=NULL,
      cex.axis=1, cex.names=1, cex.main=1,
      maxval=NULL, minval=NULL, viridis=F, ...)
```



**Arguments**

x	This is the observed data used in the function AnalyzeCrossesMM
min.vi	This is a "genarch" object returned by the function AnalyzeCrossesMM
main	title for the Y axis
cex.axis	expansion factor for Y axis
cex.names	expansion factor for CGE names on x axis
cex.main	expansion factor for main title
maxval	custom maximum value for a plot
minval	custom minimum value for a plot
viridis	logical indicating if the viridis color palette should be used
...	further arguments passed to plot

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
data(PH)
results <- AnalyzeCrossesMM(PH)
plot(results)
```

---

plotObserved                      *provides the traditional line cross analysis plot.*

---

**Description**

plot the observed results from a line cross analysis experiment as well as expectation from a simple additive model.

**Usage**

```
plotObserved(data, results, pch, col, xlab, ylab, main, SE)
```

**Arguments**

data	This is the observed data used in the function AnalyzeCrossesMM
results	This is a "genarch" object returned by the function AnalyzeCrossesMM
pch	optional - a vector to specify the symbol to be used for observed line means if the vector is shorter than the number of lines it will be recycled.
col	optional - a vector to specify the color of symbol to be used for observed line means if the vector is shorter than the number of lines it will be recycled.
xlab	optional - title for the X axis
ylab	optional - title for the Y axis
main	optional - main title for the graph
SE	include standard error bars; default is TRUE

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
data(PH)
plotObserved(data=PH)
```

---

VisModelSpace

*Visualize Model Space*

---

**Description**

This function plots squares for every model evaluated. The color of the square is a function of the AICc weight of that model. Model numbers are printed on top of each square allowing the user to investigate any models of interest using the function EvaluateModel

**Usage**

```
VisModelSpace(data, cex.u = 3, cex.mtext = 1, cex.leg = 0.8)
```

**Arguments**

data	This is a "genarch" object returned by the function AnalyzeCrossesMM
cex.u	expansion factor for the boxes representing the models
cex.mtext	expansion factor for the x and y axis labels
cex.leg	expansion factor for the legend

**Author(s)**

Heath Blackmon and Jeffery P. Demuth

**Examples**

```
data(PH)
results <- AnalyzeCrossesMM(PH)
VisModelSpace(results, cex.u=3)
```

# Index

\*Topic **\textasciitildekwd1**

EvaluateModel, 8

\*Topic **\textasciitildekwd2**

EvaluateModel, 8

\*Topic **datasets**

data, 5

AICtoMW, 2

AnalyzeCrossesMM, 3

ban.osa (data), 5

cohortID, 5

dar.bho (data), 5

data, 5

DisplayCmatrix, 6

EvaluateModel, 8

per.inf (data), 5

PH (data), 5

plot, 8

plotObserved, 9

SAGA (SAGA-package), 2

SAGA-package, 2

sin.cro (data), 5

SL (data), 5

SR (data), 5

VisModelSpace, 4, 10