

The `gamlss` packages

Mikis Stasinopoulos¹ Bob Rigby¹

¹STORM, London Metropolitan University

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The R packages

- `gamlss` the original package
- `gamlss.dist` all `gamlss.family` distributions
- `gamlss.data` different sets of data
- `gamlss.demo` demos for distributions and smoothing
- `gamlss.nl` non-linear term fitting
- `gamlss.tr` generating truncated distributions
- `gamlss.cens` for censored (left, right or interval) response variables
- `gamlss.mx` finite mixtures distributions and random effects
- `gamlss.add` for extra additive terms
- `gamlss.util` for extra utilities

The GAMLSS framework packages can be downloaded and installed from CRAN, the R library at <http://www.r-project.org/>. Test versions may be found at the GAMLSS web site at <http://www.gamlss.com/>.

Demonstration

```
library(gamlss)
data(abdom)
plot(y~x, col="blue", xlab="age", ylab="circumference",
      data=abdom)
.....
SEE FILE chaper-3-rscript.r
.....
AIC(abd1,abd2,abd3, abd5, abd6,abd7)
GAIC(abd1,abd2,abd3, abd5, abd6,abd7)
GAIC(abd1,abd2,abd3, abd5, abd6,abd7, k=log(length(abdom$y)))
```

The gamlss package

Classification of the available functions

- Fitting or Updating a Model
- Extracting Information from the Fitted Model
- Selecting a Model
- Plotting and Diagnostics
- Centile Estimation

Fitting or Updating a Model

`gamlss()` for fitting and creating a `gamlss` object

`refit()` to refit a `gamlss` object (i.e. continue iterations)

`update()` to update a given `gamlss` model object

`gamlssML()` fitting a parametric distribution to a single (response) variable

`histDist()` to fit and plot a parametric distribution

`fitDist()` select a parametric distribution from an appropriate list

Extracting Information from the Fitted Model

- `GAIC()` generalised Akaike information criterion (or AIC)
- `coef()` the linear coefficients
- `deviance()` the global deviance $-2 \log L$
- `fitted()` the fitted values for a distribution parameter
- `predict()` to predict from new data individual distribution parameter values
- `predictAll()` to predict from new data all the distribution parameter values
- `print()` : to print a gamlss object
- `residuals()` to extract the normalised (randomised) quantile residuals
- `summary()` to summarise the fit in a gamlss object
- `vcov()` to extract the variance-covariance matrix of the ^{beta} estimates.

Selecting a Model

`add1()` `drop1()` to add or drop a single term

`find.hyper()` to find the hyper-parameters

`stepGAIC()` to select explanatory terms in one parameter

`stepGAICAll.A()` to select explanatory terms in all the parameters (strategy A)

`stepGAICAll.B()` to select explanatory terms in all the parameters (strategy B)

`stepTGD()` selecting variables using a test set the global deviance for new (test) data set given a fitted gamlss model.

Diagnostics

`plot()` a plot of four graphs for the normalized (randomized) quantile residuals

`pdf.plot()` for plotting the pdf functions for a given fitted gamlss object or a given gamlss.family distribution

`Q.stats()` for printing and plotting the Q statistics of Royston and Wright (2000).

`rqres.plot()` for plotting QQ-plots of different realisations of randomised residuals (for discrete distributions)

`wp()` worm plot of the residuals from a fitted gamlss object

`dtop()` detrended Own's plot of the residuals

Centile estimation

`centiles()` to plot centile curves against an x-variable.

`centiles.com()` to compare centiles curves for more than one object.

`centiles.split()` as for `centiles()`, but splits the plot at specified values of x.

`centiles.pred()` to predict and plot centile curves for new x-values.

`centiles.fan()` fan plot of centile curves

`fitted.plot()` to plot fitted values for all the parameters against an x-variable

`lms()` a function trying to automate the process of fitting growth curves

Other useful functions

`prof.dev()` the profile global deviance of one of the distribution parameters

`prof.term()` for plotting the profile global deviance of one of the model (beta) parameters

`show.link()` for showing available link functions

`term.plot()` for plotting additive (smoothing) terms

`gen.likelihood()` generates the likelihood from a GAMLSS fitted model [used in `vcov()`]

The gamlss() function

```
gamlss( formula = ~1, sigma.formula}= ~1,  
        nu.formula = ~1, tau.formula = ~1,  
        family = NO(),  
        data = sys.parent(), weights = NULL,  
        contrasts = NULL, method = RS(), start.from = NULL,  
        mu.start = NULL, sigma.start = NULL,  
        nu.start = NULL, tau.start = NULL,  
        mu.fix = FALSE, sigma.fix = FALSE, nu.fix = FALSE,  
        tau.fix = FALSE, control = gamlss.control(...),  
        i.control = glim.control(...), ...)
```

Arguments of the gamlss() function

formula = $y \sim x1 + x3$

sigma.fo = $\sim x1$

nu.fo = $\sim x2$

tau.fo = ~ 1

data = abdom

family = LO

weights = freq

method = mixed(10,50)

control = gamlss.control(trace=FALSE)

Starting values

Generally are not needed:

```
start.mu= 2 or start.mu=fitted(m1, "mu")
```

The same applies for other parameters

```
start.sigma , start.nu, start.tau
```

[Starting from a previous model](#)

```
start.from= model1
```

END

for more information see

www.gamlss.org