



GenStat – Progress towards Release 10

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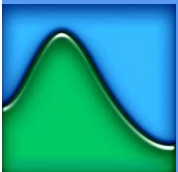
Victor Harbour 6th December 2006

Server enhancements

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- programming
 - CALLS – lists external calls within a procedure
- enhanced text handling
 - TXBREAK – breaks up a text into words
 - TXPOSITION – finds strings within the lines of a text (forwards or backwards, allowing skips, ignoring/respecting case)
 - TXCONSTRUCT – constructs texts from scalars, variates, factors, texts or pointers (append/concatenate, change/respect case, reverse &c)
 - TXFIND – finds a subtext within a text (forwards or backwards, allowing skips, ignoring/respecting case or multi-spaces &c)
 - TXCLEAN, TXREPLACE..?
- ANOVA
 - no restriction now on number of comparisons
- regression
 - PARALLEL parameter for PREDICT
 - symmetric weight matrices allowed (within-group) in FITCURVE

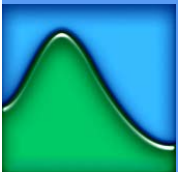
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Procedures accepted for PL18

- BGXGENSTAT runs WinBUGS from GenStat in batch mode using scripts
- BXPLOT produces plots for output and diagnostics from MCMC simulations
- DOTHISTOGRAM plots dot histograms
- FACSTANDARDIZE standardizes the levels or labels of a list of factors
- FCORRELATION forms the correlation matrix for a list of variates
- FFREERESPONSEFACTOR forms multiple-response factors from free-response data
- MIN1DIMENSION finds the minimum of a function in one dimension
- NLAR1 fits curves with an AR1 or a power-distance correlation model
- PDUPLICATE duplicates a pointer, with all its components
- RAR1 fits regressions with an AR1 or a power-distance correlation model
- RQUADRATIC fit a quadratic surface and estimates its stationary point
- VGRAPH plots one- or two-way tables of means from REML
- WSTATISTIC calculates the Shapiro-Wilk test for Normality

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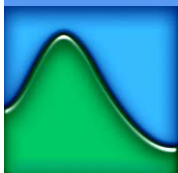


Further procedures

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- anticipated
 - analysis of distance
 - beta-binomial distribution
 - distance sampling
 - genetic algorithm
 - Mantel-Haenszel statistic
 - plotting of large data sets
 - redundancy analysis
 - simulated annealing
 - survey enhancements
 - MCMC analysis of GLMMs
- suggested
 - bag and boost, random forests &c
 - Gauss-Newton & Newton Raphson
 - informative drop out (Diggle & Kenward 1994)
 - meta analysis (results e.g. from clinical trials)
- welcomed
 - your contributions

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Wish list?

- data mining
- mathematical modelling
- capture/recapture
- design algorithms
- GARCH
- genetics – QTLs, *omics &c
- lasso
- multivariate time series (VARMA)
- multiple imputation
- nonlinear mixed models
- quantile regression
- surface fitting
- wavelets
- your suggestions...?

Questions

- what new facilities would you like?
 - how would you use them?
- what might tempt your non-GenStat colleagues?
 - who are they and what are they using now!
- what new products would be attractive?
 - data mining
 - modelling
 - Visualist 2 (ADVISE)
- how should VSNi support GenStat in Australasia?
 - are current support times (and quality) OK?
 - courses, visits, workshops?
 - local representation?
- what questions should I have asked!

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