



Hierarchical Generalized Linear Models in Practice

Roger Payne

VSN International, 5 The Waterhouse,
Waterhouse Street, Hemel Hempstead, UK
and Rothamsted Research, Harpenden, UK

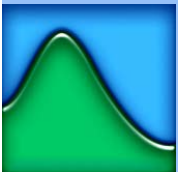
email: Roger.Payne@vsni.co.uk

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HGLMs – introduction

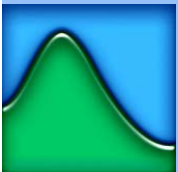
- Hierarchical generalized linear models
 - extend generalized linear models to >1 source of error
 - include generalized linear mixed models as a special case
 - but the additional random terms are not constrained to follow a Normal distribution, nor to have an identity link
 - allow for modelling of the dispersion of the error terms
 - extending quasi-likelihood methods of Nelder & Pregibon (1987)
 - have an efficient fitting algorithm
 - no numerical integration is required
 - are explained in the book *Generalized Linear Models with Random Effects: Unified Analysis via H-likelihood* by Lee, Nelder & Pawitan (2006)
 - examples available in GenStat *for Windows* 9th Edition onwards
- Hierarchical generalized nonlinear models
 - include nonlinear parameters in the HGLM fixed model
 - in GenStat *for Windows* 10th Edition



HGLMs – definition

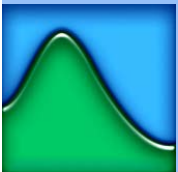
- expected value $E(y) = \mu$
link $\eta = g(\mu)$
distribution – Normal, Binomial, Poisson or Gamma (from *exponential family*)
- but linear predictor $\eta = X\beta + \sum_i Z_i v_i$
now contains additional vectors of random effects v_i with Normal, beta, gamma or inverse gamma distributions and with their own link functions
 - Normal-identity gives a GLMM but HGLM algorithms use much improved Laplace approximations in their use of adjusted profile likelihood
- inference by *h-likelihood*

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H-likelihood (LNP §4.5)

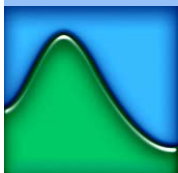
- is an extended likelihood $L(\theta, v; y, v) \equiv L(\theta; y) \times L(\theta, v; v|y)$ where the random parameters v are on the *canonical scale*
 - i.e. $L(\theta_1, v^{\wedge}_{\theta_1}; y, v) / L(\theta_2, v^{\wedge}_{\theta_2}; y, v) = L(\theta_1; y) / L(\theta_2; y)$
 - where $v^{\wedge}_{\theta_1}$ and $v^{\wedge}_{\theta_2}$ are estimates of v for θ at θ_1 and θ_2
 - can treat like an ordinary log-likelihood
 - estimates and information matrices from joint maximization of h-likelihood are identical to those from maximizing the marginal likelihood
 - requires profile likelihood of θ from the extended likelihood to be proportional to the marginal likelihood $L(\theta)$
- minor extension: canonical scale may not be available for all parameters – e.g. (say) for v but not for φ
 - then make joint inferences for (θ, v) , but estimation of φ needs marginal likelihood, approximated by adjusted profile likelihood
- if no canonical scale
 - use extended likelihood to estimate random parameters
 - use adjusted profile likelihood to estimate fixed parameters (but enhanced Laplace approximations available)



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E.g. Normal-Normal HGGLM

- $y = X\beta + Zv + \varepsilon$
 - ε follows multivariate Normal(0, Σ), v follows multivariate Normal(0, D)
 - Σ and D parameterized by variance-component parameters $\tau = (\sigma^2, \sigma_v^2)$
- so (LNP Example 6.1) we have linear predictor
 - $\eta = g(\mu) = X\beta + Zv$
 - where $g(\cdot)$ is the identity function, and $u = v$
- and GLMs
 - $y|u$ follows a GLM distribution with
 - $E(y|u) = \mu$
 - $\text{var}(y|u) = \phi V(\mu)$ where $\phi = \sigma^2$, $V(\mu) = 1$
 - u is distributed as Normal(0, λ), with $\lambda = \sigma_v^2$
- constraint is $E(u) = 0$
- extended likelihood (LNP §5.4) is
 - $\log L(\theta, v; y, v) = \log f(y, v) = \log f(y|v) + \log f(v)$
 $= \frac{1}{2} \log |2\pi\Sigma| - \frac{1}{2} (y - X\beta - Zv)^t \Sigma^{-1} (y - X\beta - Zv) - \frac{1}{2} \log |2\pi D| - v^t D^{-1} v$

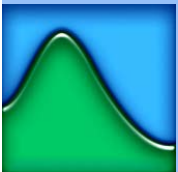


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E.g. Normal-Normal HGGLM

- extended likelihood (LNP §5.4)
 - $\log L(\theta, v; y, v) = \log f(y, v) = \log f(y|v) + \log f(v)$
 $= \frac{1}{2} \log |2\pi\Sigma| - \frac{1}{2}(y - X\beta - Zv)^t \Sigma^{-1} (y - X\beta - Zv) - \frac{1}{2} \log |2\pi D| - v^t D^{-1} v$
 - note: $\tau = (\sigma^2, \sigma_v^2)$ appears only in Σ and D
- Fisher information
 - $I(v^\wedge) = Z^t \Sigma^{-1} Z + D^{-1}$
 - depends on τ but not on β
- so scale v is canonical for β (but not for τ , which must be estimated by a marginal likelihood)
- i.e. the extended likelihood is an h-likelihood
 - joint estimation is possible for β and v
 - but dispersion parameters τ estimated by adjusted profile likelihood

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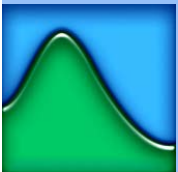


E.g. Normal-Normal HGMLM

- extended likelihood (LNP §5.4)
 - $\log L(\theta, v; y, v) = \log f(y, v) = \log f(y|v) + \log f(v)$
 $= \frac{1}{2} \log |2\pi\Sigma| - \frac{1}{2}(y - X\beta - Zv)^t \Sigma^{-1} (y - X\beta - Zv) - \frac{1}{2} \log |2\pi D| - \frac{1}{2} v^t D^{-1} v$
- differentiate with respect to β and v
 - $\partial L(\beta, \tau, v; y, \tau, v) / \partial \beta = X^t \Sigma^{-1} (y - X^t \beta - Z^t v)$
 - $\partial L(\beta, \tau, v; y, \tau, v) / \partial v = Z^t \Sigma^{-1} (y - X^t \beta - Z^t v)$
- normal equations

$$\begin{pmatrix} X^t \Sigma^{-1} X & X^t \Sigma^{-1} Z \\ Z^t \Sigma^{-1} X & Z^t \Sigma^{-1} Z + D^{-1} \end{pmatrix} \begin{pmatrix} \hat{\beta} \\ \hat{v} \end{pmatrix} = \begin{pmatrix} X^t \Sigma^{-1} y \\ Z^t \Sigma^{-1} y \end{pmatrix}$$

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Augmented mean model

- normal equations

$$\begin{pmatrix} X^t \Sigma^{-1} X & X^t \Sigma^{-1} Z \\ Z^t \Sigma^{-1} X & Z^t \Sigma^{-1} Z + D^{-1} \end{pmatrix} \begin{pmatrix} \hat{\beta} \\ \hat{v} \end{pmatrix} = \begin{pmatrix} X^t \Sigma^{-1} y \\ Z^t \Sigma^{-1} y \end{pmatrix}$$

- same equations are given by an *augmented* mean model

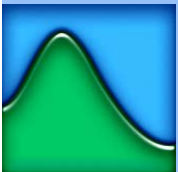
$$\begin{pmatrix} y \\ \psi_M \end{pmatrix} = \begin{pmatrix} X & Z \\ 0 & I \end{pmatrix} \begin{pmatrix} \beta \\ v \end{pmatrix} + e^*,$$

where the error term e^* is normal with mean zero and variance matrix

$$\Sigma_a \equiv \begin{pmatrix} \Sigma & 0 \\ 0 & D \end{pmatrix},$$

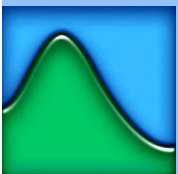
- $\psi_M \equiv E(u) = 0$
- write as $y_a = T\delta + \varepsilon^*$
- normal equations are $(T^t \Sigma_a^{-1} T)^{-1} \delta^{\wedge} = T^t \Sigma_a^{-1} y$ (as above)
- can fit as an ordinary weighted regression
- see LNP §5.3.5

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Dispersion model (LNP §5.4.2)

- marginal likelihood $L(\beta, \tau) =$
 - $|2\pi\Sigma|^{-1/2} \int \exp\{-1/2(y-X\beta-Zv)^t\Sigma^{-1}(y-X\beta-Zv)\}$
 $\times |2\pi D|^{-1/2} \exp\{-1/2v^t D^{-1}v\} dv$
 - $|2\pi\Sigma|^{-1/2} \exp\{-1/2(y-X\beta-Zv)^t\Sigma^{-1}(y-X\beta-Zv)\}$
 $\times |2\pi D|^{-1/2} \exp\{-1/2v^{\wedge}_{\beta\tau}{}^t D^{-1}v^{\wedge}_{\beta\tau}\} \times \int \exp\{-1/2(v-v^{\wedge}_{\beta\tau})^t I(v^{\wedge}_{\beta\tau})(v-v^{\wedge}_{\beta\tau})\} dv$
 - $|2\pi\Sigma|^{-1/2} \exp\{-1/2(y-X\beta-Zv)^t\Sigma^{-1}(y-X\beta-Zv)\}$
 $\times |2\pi D|^{-1/2} \exp\{-1/2v^{\wedge}_{\beta\tau}{}^t D^{-1}v^{\wedge}_{\beta\tau}\} \times |I(v^{\wedge}_{\beta\tau})/(2\pi)|^{-1/2}$
- marginal log-likelihood =
 - $h(\beta, \tau, v^{\wedge}_{\beta\tau}) - 1/2 \log\{|I(v^{\wedge}_{\beta\tau})/(2\pi)|\}$
 - and can show that $I(v^{\wedge}_{\beta\tau}) = Z^t\Sigma^{-1}Z + D^{-1}$
- profile likelihood of variance components is
 - $h(\beta^{\wedge}_{\tau}, \tau, v^{\wedge}_{\tau}) - 1/2 \log\{|I(v^{\wedge}_{\tau})/(2\pi)|\}$
 - with $I(v^{\wedge}_{\tau}) = Z^t\Sigma^{-1}Z + D^{-1}$
- with REML adjustment this becomes
 - $h(\beta^{\wedge}_{\tau}, \tau, v^{\wedge}_{\tau}) - 1/2 \log\{|I(v^{\wedge}_{\tau})/(2\pi)|\} - 1/2 \log\{|X^t V^{-1}X/(2\pi)|\}$
- fit by Extended Quasi Likelihood i.e. by gamma GLM
 - (Nelder & Pregibon 1974, Lee & Nelder 1998)



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Fitting algorithm

- interconnected Normal and Gamma GLMs (§5.4.4)

Component	β (fixed)	σ^2 (fixed)
Response	y	d^*
Mean	μ	σ^2
Variance	σ^2	$2(\sigma^2)^2$
Link	$\eta = \mu$	$\xi = h(\sigma^2)$
Linear Pred.	$X\beta + Zv$	γ
Dev. Comp.	d	$\text{gamma}(d^*, \sigma^2)$
Prior Weight	$1/\sigma^2$	$(1 - q)/2$

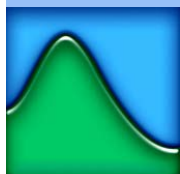
Component	v (random)	σ_v^2 (fixed)
Response	ψ_M	d_M^*
Mean	u	σ_v^2
Variance	σ_v^2	$2(\sigma_v^2)^2$
Link	$\eta_M = g_M(u)$	$\xi_M = h_M(\sigma_v^2)$
Linear Pred.	v	γ_m
Deviance	d_M	$\text{gamma}(d_M^*, \sigma_v^2)$
Prior Weight	$1/\sigma_v^2$	$(1 - q_M)/2$

$$d_i = (y_i - X_i\hat{\beta} - Z_i\hat{v})^2,$$

$$d_{Mi} = \hat{v}_i^2,$$

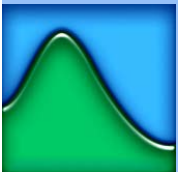
$$\text{gamma}(d^*, \phi) = 2\{-\log(d^*/\phi) + (d^* - \phi)/\phi\} \text{ and}$$

(q, q_M) are leverages, given by the diagonal elements of $T(T^t\Sigma_a^{-1}T)^{-1}T^t\Sigma_a^{-1}$.

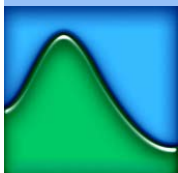
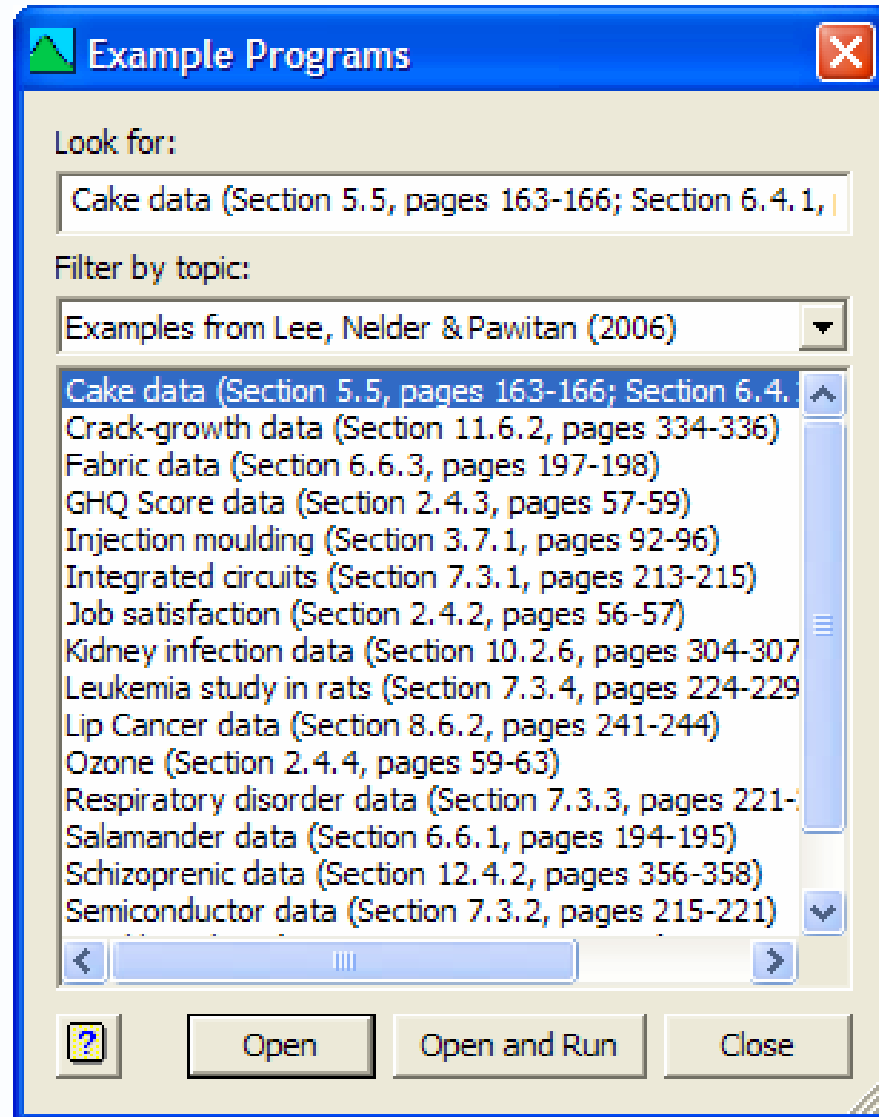
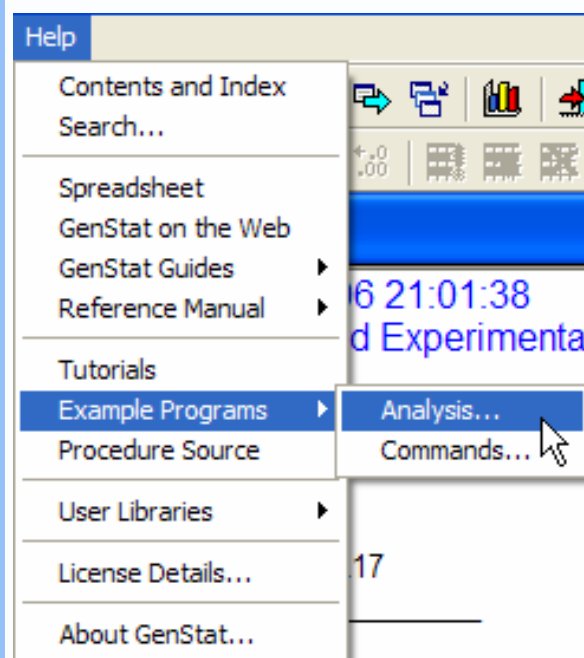


HGLMs in GenStat

- procedures (Payne, Lee, Nelder & Noh 2008)
 - HGFIXEDMODEL – defines the fixed model for an HGLM or DHGLM
 - HGRANDOMMODEL – defines the random model for an HGLM
 - HGDRANDOMMODEL – adds random terms into the dispersion models of an HGLM, so that the whole model becomes a DHGLM
 - HGNONLINEAR – defines nonlinear parameters for the fixed model
 - HGANALYSE – fits a hierarchical generalized linear model (HGLM) or a double hierarchical generalized linear model (DHGLM)
 - HGDISPLAY – displays results from an HGLM or DHGLM
 - HG PLOT – produces model-checking plots for an HGLM or DHGLM
 - HGPREDICT – forms predictions from an HGLM or DHGLM analysis
 - HGKEEP – saves information from an HGLM or DHGLM analysis
 - HGGRAPH – plots predictions from an HGLM or DHGLM analysis
 - HGWALD – gives Wald tests for fixed terms that can be dropped
- menus
 - Stats | Regression Analysis | Mixed Models | Hierarchical Generalized Linear Models
 - cover the standard situations, but not dispersion modelling nor DHGLMs
 - ..



GenStat HGLM examples

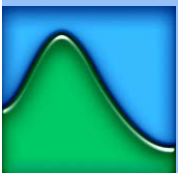


Example – chocolate cakes

Row	Replicate	Batch	Recipe	Temperature	Angle
1	1	1	1	175	42
2	1	1	1	185	46
3	1	1	1	195	47
4	1	1	1	205	39
5	1	1	1	215	53
6	1	1	1	225	42
7	1	2	2	175	39
8	1	2	2	185	46
9	1	2	2	195	51
10	1	2	2	205	49
11	1	2	2	215	55
12	1	2	2	225	42
13	1	3	3	175	46
14	1	3	3	185	44
15	1	3	3	195	45
16	1	3	3	205	46
17	1	3	3	215	48
18	1	3	3	225	63

- LNP §5.5
- breaking angle of chocolate cakes
- split plot:
Replicate/Batch/Cake
- treatment factors:
Recipe (whole-plot factor, between Batches),
Temperature (sub-plot factor, within Batches)
- analyse as a Normal-Normal HGLM to compare with familiar REML

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HGLM menu – for cakes

Available Data:

- Angle
- Batch
- Recipe
- Replicate
- Temperature

Response Variate: Angle

Fixed Model

Model: Recipe * Temperature

Distribution: Normal

Link Function: Identity

Binomial Totals:

Operators:

Random Model

Model: Replicate / Batch

Distribution: Normal

Link Function: Identity

Run Options... Save... Further Output...
Cancel Defaults Predict...

Stats Tools Window Help

- Summary Statistics
- Statistical Tests
- Distributions
- Regression Analysis
- Design
- Analysis of Variance
- Mixed Models (REML)
- Multivariate Analysis
- Six Sigma
- Survey Analysis
- Time Series
- Spatial Analysis
- Survival Analysis
- Repeated Measurements
- Multiple Experiments
- Microarrays
- Sample Size

- Linear Models...
- Generalized Linear Models...
- Logistic Models...
- Log-linear Models...
- Probit Models...
- Ordinal Models...
- All-Effects Models...
- Screening Models...
- Split-Plot Models...
- Standard Curves...
- Nonlinear Models...
- Mixed Models
 - Generalized Linear Mixed Models...
 - Hierarchical Generalized Linear Models...
- Regression Trees...

- find menu in Mixed models section of Regression Analysis on Stats menu

Output: Normal-Normal HGLM

Hierarchical generalized linear model

Response variate: Angle

Mean model

Fixed terms: Recipe*Temperature
Distribution: normal
Link: identity
Random terms: Replicate/Batch
Distribution: normal
Link: identity
Dispersion: free

← mean model

Dispersion model

Distribution: gamma
Link: logarithm

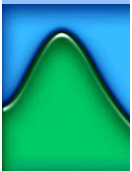
← dispersion model here
just fits variance
components

Estimates from the mean model

	estimate	s.e.	t(252)
constant	29.133	2.038	14.294
Recipe 2	-2.267	1.796	-1.262
Recipe 3	-1.200	1.796	-0.668
Temperature 185	2.400	1.652	1.453
Temperature 195	1.667	1.652	1.009
Temperature 205	4.400	1.652	2.663
Temperature 215	9.533	1.652	5.771
Temperature 225	5.933	1.652	3.591
Recipe 2 .Temperature 185	0.133	2.336	0.057
Recipe 2 .Temperature 195	3.200	2.336	1.370
Recipe 2 .Temperature 205	0.867	2.336	0.371
Recipe 2 .Temperature 215	-1.933	2.336	-0.827

← estimates of parameters
in the mean model

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Output: Normal-Normal HGLM

Recipe 3 .Temperature 195	2.133	2.336	0.913
Recipe 3 .Temperature 205	-1.467	2.336	-0.628
Recipe 3 .Temperature 215	-3.067	2.336	-1.313
Recipe 3 .Temperature 225	1.867	2.336	0.799

← estimated parameters in mean model (continued)
fixed terms only by default

Estimates from the dispersion model

Estimates of parameters

Parameter	estimate	s.e.	t(**)	antilog of estimate
phi	3.0190	0.0945	31.93	20.47
lambda Replicate	3.641	0.390	9.35	38.12
lambda Replicate.Batch	1.315	0.365	3.61	3.723

← parameters in dispersion models (logged variance components)

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	1535.137
-2 × h	1787.389
-2 × P _v (h)	1639.073
-2 × P _{β,v} (h)	1595.346
-2 × EQD(y v)	1535.137
-2 × EQD	1787.389
-2 × P _v (EQD)	1639.073
-2 × P _{β,v} (EQD)	1595.346

← assess random & dispersion models by $-2 \times P_{\beta,v}(h)$

← fixed model by $-2 \times P_v(h)$

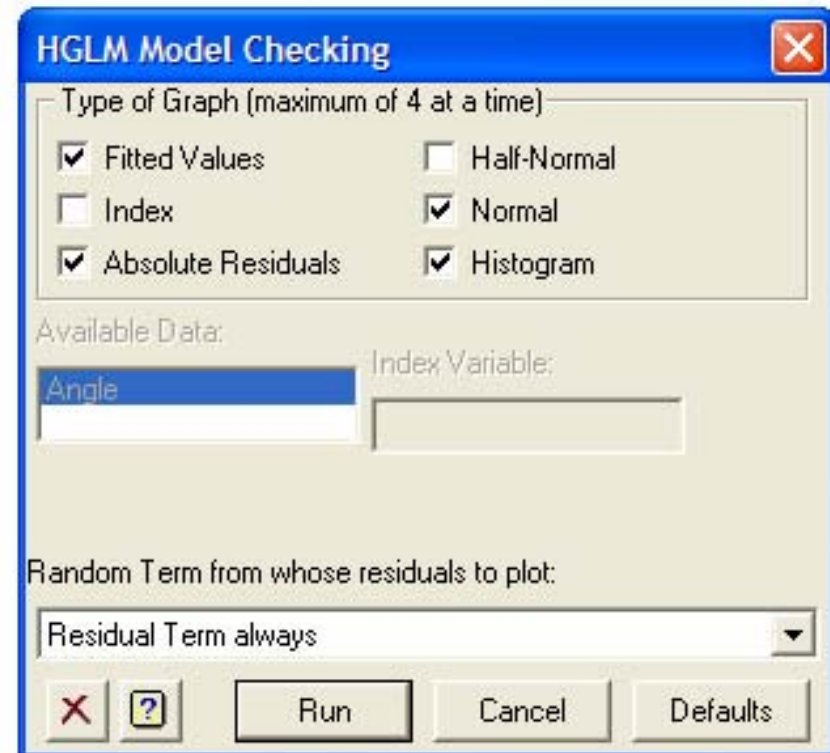
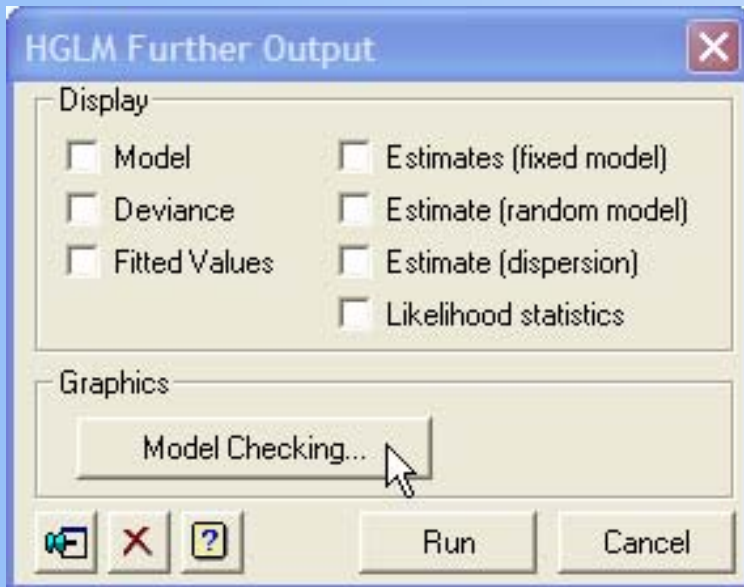
← for DIC use $-2 \times (h/v)$

← h-likelihood of mean model is $-2 \times (h)$

← EQD's are approximations to profile likelihoods ..

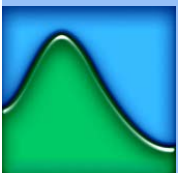
Fixed parameters in mean model	18
Random parameters in mean model	60
Fixed dispersion parameters	3
Random dispersion parameters	0

Further output and model checking

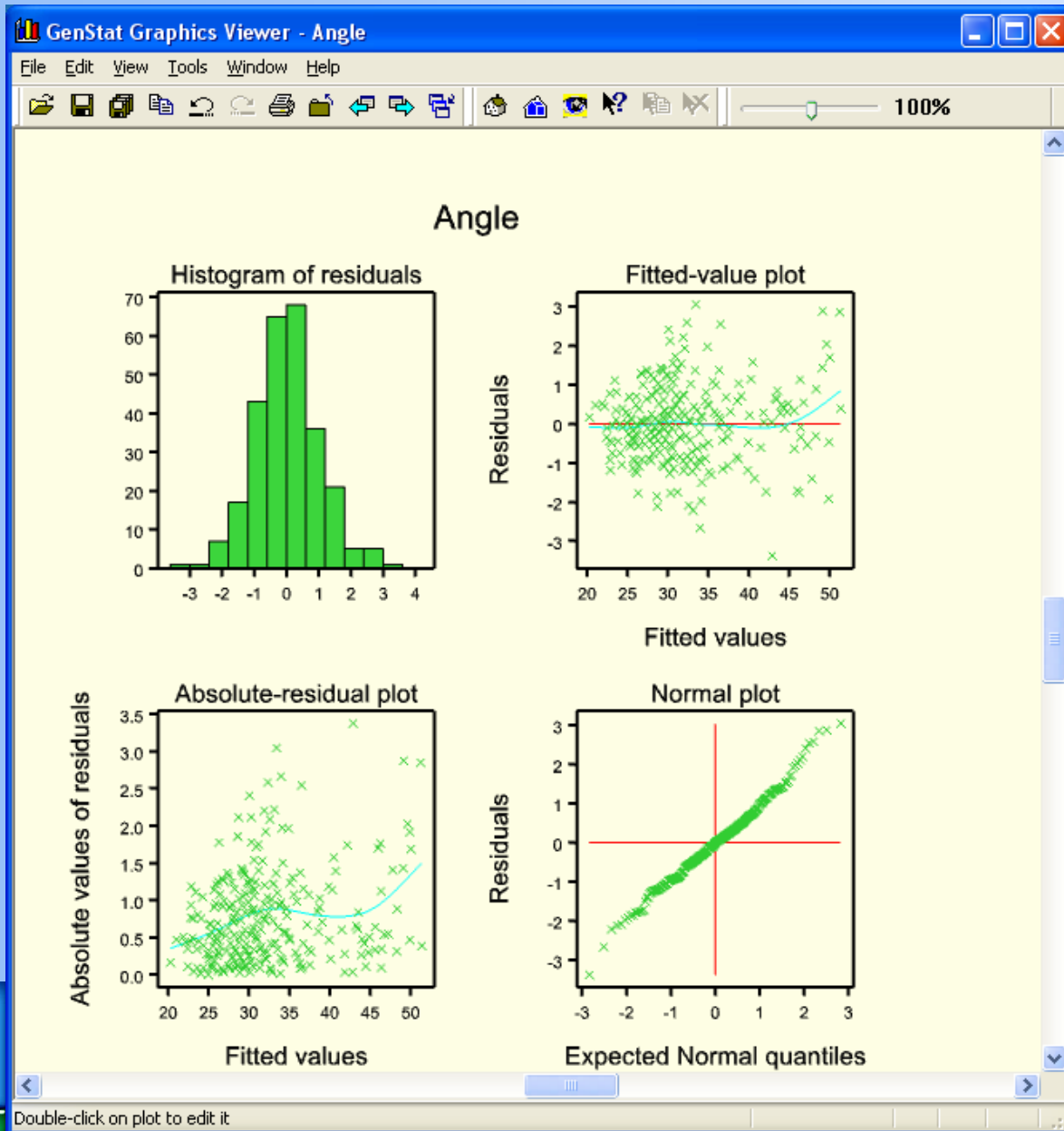


- click on *Further Output* button in *HGLM* menu
- click on *Model Checking* button in *HGLM Further Output* menu to obtain *HGLM Model Checking* menu

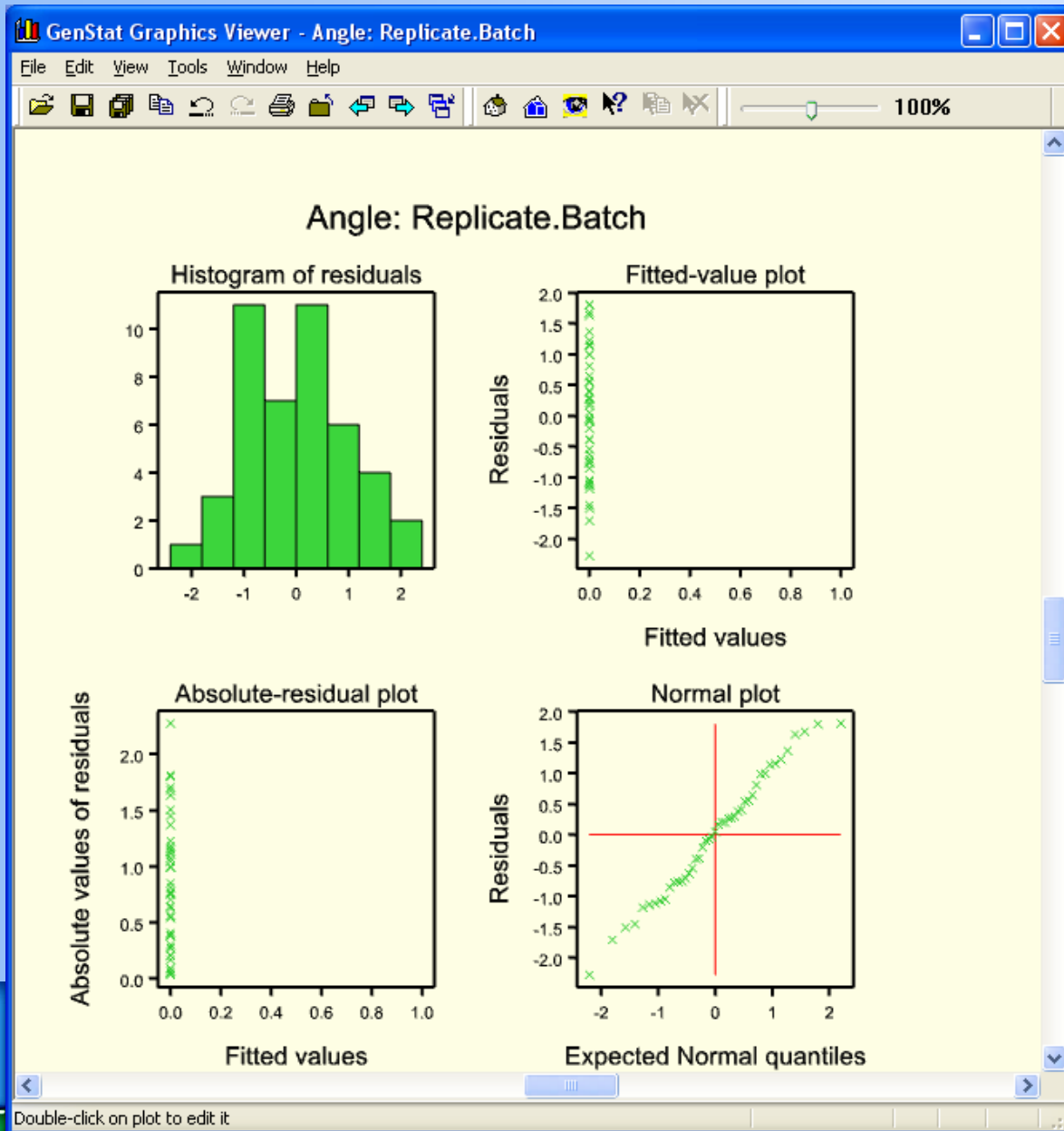
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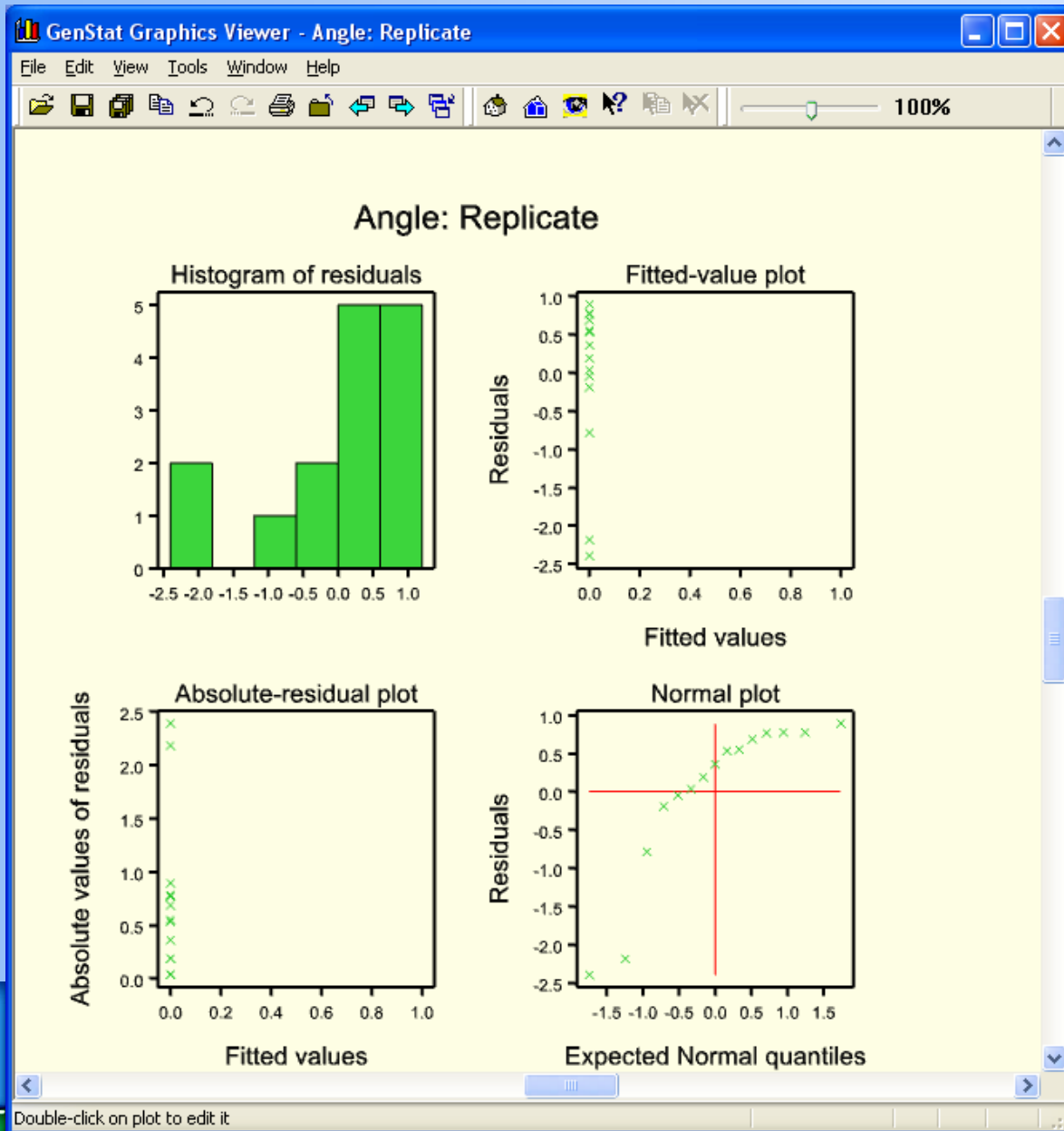
Residual plots for cakes



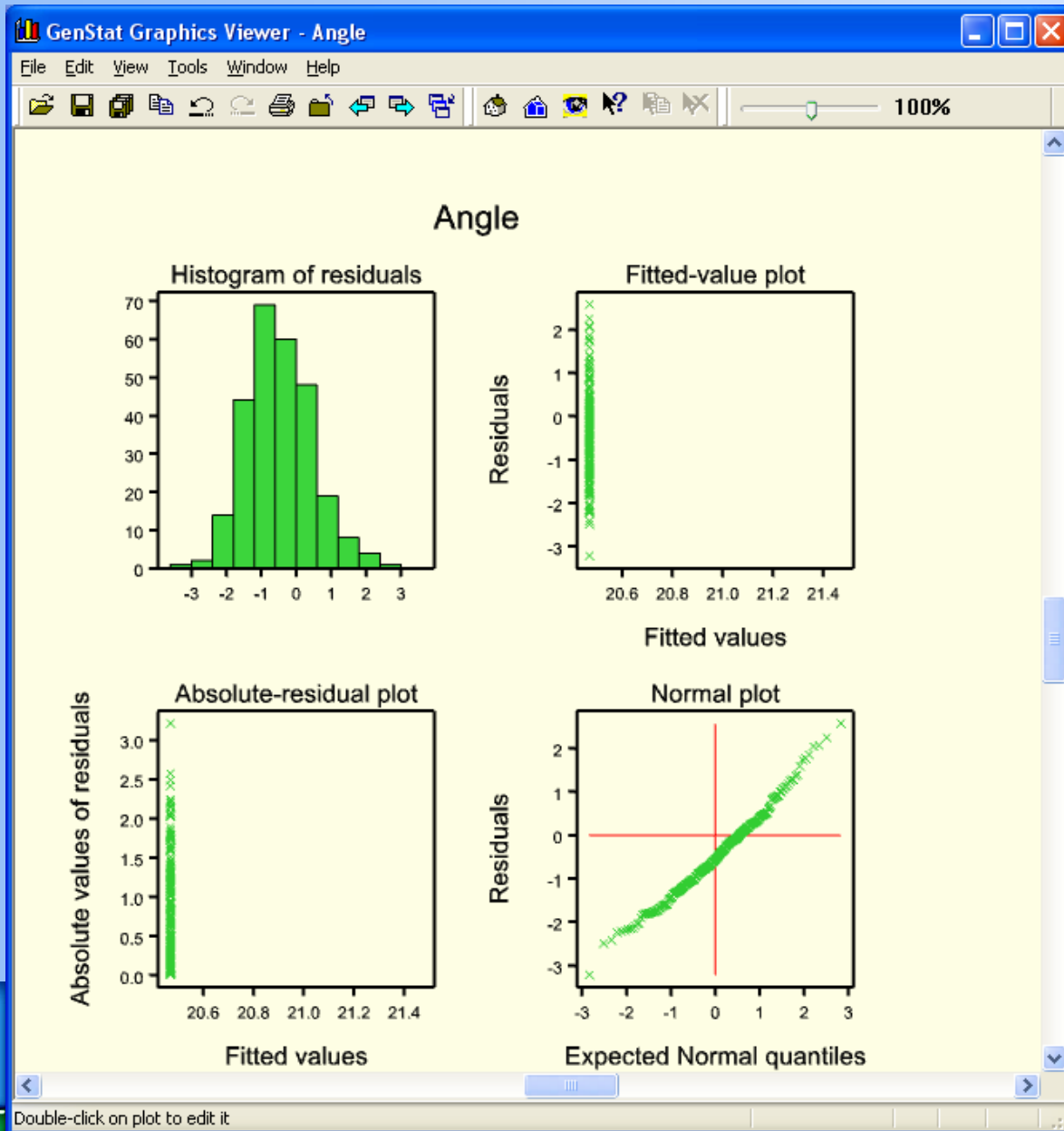
Residual plots for batches



Residual plots for replicates



Residual plots for dispersion model



Compare to REML

```
14  " Compare with REML "  
15  VCOMPONENTS  [FIXED=Recipe*Temperature] Replicate/Batch/Cake  
16  REML          [PRINT=* "components,effects"] Angle  
17  VKEEP        Replicate/Batch/Cake; COMPONENTS=gamma_r,gamma_b,sigma  
18  PRINT        LOG(sigma,gamma_r,gamma_b)
```

```
LOG(sigma) LOG(gamma_r) LOG(gamma_b)  
3.019      3.641        1.314
```

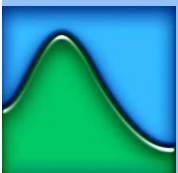
```
19  HGDISPLAY   [PRINT=dispersion]
```

Hierarchical generalized linear model

Estimates from the dispersion model

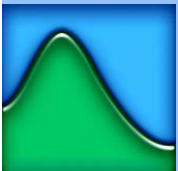
Estimates of parameters

Parameter	estimate	s.e.	t(*)	antilog of estimate
phi	3.0190	0.0945	31.93	20.47
lambda Replicate	3.641	0.390	9.35	38.12
lambda Replicate.Batch	1.315	0.365	3.61	3.723



Assess fixed model using $-2 p_v(h)$

```
" assess the fixed model - drop terms one at a time "  
VARIATE      [NVALUES=3; IPRINT=extra] Change;\br/>EXTRA='Change in -2 ~{times} P~_v(h) '  
TEXT         [VALUES='Temperature','Recipe','Recipe.Temperature'] Drop  
HGDISPLAY   [PRINT=likelihood]  
HGKEEP      LIKELIHOOD=L1  
  
HGFIXEDMODEL Recipe+Temperature  
HGANALYSE   [PRINT=likelihood] Angle  
HGKEEP      LIKELIHOOD=L2  
CALCULATE   Change$[3] = L2$[3] - L1$[3]  
  
HGFIXEDMODEL Temperature  
HGANALYSE   [PRINT=likelihood] Angle  
HGKEEP      LIKELIHOOD=L3  
CALCULATE   Change$[2] = L3$[3] - L2$[3]  
  
HGFIXEDMODEL  
HGANALYSE   [PRINT=likelihood] Angle  
HGKEEP      LIKELIHOOD=L4  
CALCULATE   Change$[1] = L4$[3] - L3$[3]  
PRINT       Drop,Change; FIELD=24  
  
" compare with REML Wald statistics "  
VDISPLAY    [PRINT=wald]
```



Assess fixed model using $-2 p_v(h)$

```
47 " Compare with REML - Wald and likelihood statistics "  
48 PRINT Drop,Change; FIELD=24
```

Drop	Change in $-2 \times P_v(h)$
Temperature	86.05
Recipe	3.13
Recipe.Temperature	10.06

```
49 VDISPLAY [PRINT=wald]
```

Tests for fixed effects

Sequentially adding terms to fixed model

Fixed term	Wald statistic	n.d.f.	F statistic	d.d.f.	F pr
Recipe	3.16	2	1.58	28.0	0.224
Temperature	102.60	5	20.52	210.0	<0.001
Recipe.Temperature	10.06	10	1.01	210.0	0.439

Dropping individual terms from full fixed model

Fixed term	Wald statistic	n.d.f.	F statistic	d.d.f.	F pr
Recipe.Temperature	10.06	10	1.01	210.0	0.439

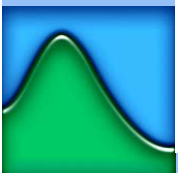
Message: denominator degrees of freedom for approximate F-tests are calculated using algebraic derivatives ignoring fixed/boundary/singular variance parameters.

```
50 HGDISPLAY [PRINT=wald; SAVE=nnhglm]
```

Hierarchical generalized linear model

Wald tests for dropping HGLM fixed terms

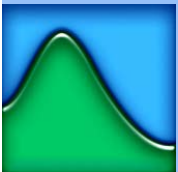
Term	Wald statistic	d.f.	approx. pr.
Recipe.Temperature	10.06	10	0.435



Conjugate HGLMs

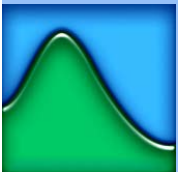
- random parameters are on the *canonical scale*
- the contribution of the random parameters to the extended likelihood (Ξ the h-likelihood) has the same form as the likelihood of the base GLM
- so it can easily be fitted together with the base GLM in the augmented mean model (same variance function, same iterative reweighting scheme etc...)
- examples
 - Normal – Normal most obvious
 - Poisson – Gamma most useful?
 - Binomial – Beta next most useful?
 - Gamma – Inverse Gamma
- algorithmically and intuitively appealing

..



Conjugate HGLM e.g. Poisson-Gamma

- Poisson-gamma HGLM (LNP Ex. 6.2 & 6.3): linear predictor
 - $\eta = \log(\mu) = X\beta + Zv$
 - where $v = \log(u)$
- Poisson-gamma HGLM: distributions
 - $y|u$ follows a Poisson distribution with $E(y|u) = \mu$
 - log-likelihood is $\sum\{y \log(\mu) - \mu\}$
 - u has a Gamma distribution
 - log-likelihood is $\sum\{(\psi_M \log(u) - u - \log(\lambda)/\lambda - \log\Gamma(1/\lambda))\}$
 - $\psi_M = E(u) = 1$
 - this is the conjugate distribution for the Poisson (so this is a *conjugate* HGLM)
 - note: gamma distribution for random effects has $V_M(u) = u$ and log canonical link, but standard gamma GLM has $V(\mu) = \mu^2$ and reciprocal canonical link
- kernel of h-loglikelihood (LNP §6.3) is
 - $\sum\{y \log(\mu) - \mu\} + \sum\{(\psi_M \log(u) - u - \log(\lambda)/\lambda - \log\Gamma(1/\lambda))\}$
 - v is canonical for β (but not λ)
 - estimate λ by profile lhd (c.f. variance components in normal-normal)

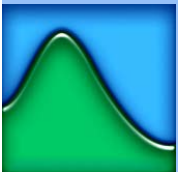


..

Non-conjugate HGLMs

- random parameters no longer on the canonical scale
 - use extended likelihood to estimate random parameters
 - use adjusted profile likelihood to estimate fixed parameters
 - but enhanced Laplace approximations available (Noh & Lee 06)
- augmented mean model now has a different GLM for the base GLM from the augmented units
- examples
 - Poisson – Normal Poisson GLMM
 - Binomial – Normal Binomial GLMM
 - Gamma – Normal Gamma GLMM
- algorithmically more difficult, but can still be fitted within the GLM framework

..



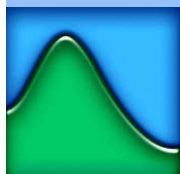
HGLMs

- examples of HGLMs (LNP Table 6.2)

$y u$ dist.	$g(\mu)^*$	u dist.	$v(u)$	Model
Normal	id	Normal	id	Conjugate HGLM Linear mixed model
Binomial	logit	Beta	logit	Conjugate HGLM beta-binomial model
Binomial	logit	Normal	id	Binomial GLMM
Binomial	comp	Gamma	log	HGLM
Gamma	recip	Inverse-gamma	recip	Conjugate HGLM
Gamma	log	Inverse-gamma	recip	Conjugate HGLM with non-canonical link
Gamma	log	Gamma	log	HGLM
Poisson	log	Normal	id	Poisson GLMM**
Poisson	log	Gamma	log	Conjugate HGLM

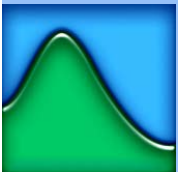
* id= identity, recip= reciprocal, comp= complementary-log-log

** In GLMMs, we take $v = v(u) = u$



Birds in Tasmania

- HGLM
 - base GLM – Poisson distribution, Log link
 - random terms – Gamma distribution, Log link
 - i.e. Poisson-Gamma conjugate HGLM
- random terms
 - site (*Site*)
 - treatment locations within site (*SiteTreat*)
 - sample plots within treatment locations (*Plot*)
- fixed terms
 - connected by habitat strips (*Treatment*)
 - vegetation type (*Vegetation*)
 - time of day (*AM_vs_PM*)
- data set used by Steve Candy, Forestry Tasmania, at the Workshop *Extensions of Generalized Linear Models* (Nelder, Payne & Candy) before the Australasian Genstat Conference, Surfers Paradise, 30 January 2001



..

Vegetation * Treatment * AM_vs_PM

Hierarchical generalized linear model

Response variate: TotalNo

Mean model

Fixed terms: Vegetation*Treatment*AM_vs_PM
Distribution: poisson
Link: logarithm
Random terms: Site + SiteTreat + Plot
Distribution: gamma
Link: logarithm
Dispersion: fixed

← mean model

Dispersion model

Distribution: gamma
Link: logarithm

← dispersion model

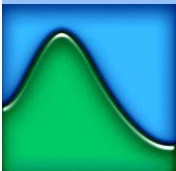
Likelihood statistics

-2 × h(y v)	2017.896
-2 × h	1867.242
-2 × P _v (h)	2173.327
-2 × P _{ρ,v} (h)	2200.500
-2 × EQD(y v)	2018.567
-2 × EQD	1866.832
-2 × P _v (EQD)	2172.917
-2 × P _{ρ,v} (EQD)	2200.089

← likelihood statistics

Fixed parameters in mean model	12
Random parameters in mean model	132
Fixed dispersion parameters	3
Random dispersion parameters	0

← d.f.



Wald tests

```
11  HGWALD
```

Wald tests for dropping HGLM fixed terms

Term	Wald statistic	d.f.	approx. pr.
Vegetation.Treatment.AM_vs_PM	2.576	2	0.276

```
12  HGKEEP      LIKELIHOOD=L1; LDF=D1
```

```
13  CALCULATE   T1 = CPUTIME(0)
```

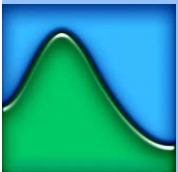
```
14  PRINT       T1 - TO; DECIMALS=2; HEADING='Time taken (seconds)'
```

```
Time taken (seconds)
```

```
4.58
```

- no evidence of a 3-factor interaction

..



Omit Vegetation.Treatment.AM_vs_PM

Hierarchical generalized linear model

Response variate: TotalNo

Mean model

Fixed terms: Vegetation*Treatment*AM_vs_PM - (Vegetation.Treatment.AM_vs_PM)

Distribution: poisson

Link: logarithm

Random terms: Site + SiteTreat + Plot

Distribution: gamma

Link: logarithm

Dispersion: fixed

Dispersion model

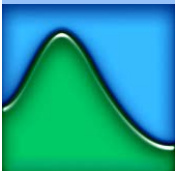
Distribution: gamma

Link: logarithm

Likelihood statistics

$-2 \times h(y v)$	2019.526
$-2 \times h$	1871.466
$-2 \times P_v(h)$	2175.924
$-2 \times P_{\beta,v}(h)$	2200.036
$-2 \times EQD(y v)$	2020.197
$-2 \times EQD$	1871.047
$-2 \times P_v(EQD)$	2175.504
$-2 \times P_{\beta,v}(EQD)$	2199.617

Fixed parameters in mean model	10
Random parameters in mean model	132
Fixed dispersion parameters	3
Random dispersion parameters	0



Wald tests and Change

Wald tests for dropping HGLM fixed terms

Term	Wald statistic	d.f.	approx. pr.
Vegetation.Treatment	4.489	2	0.106
Vegetation.AM_vs_PM	4.951	2	0.084
Treatment.AM_vs_PM	5.471	1	0.019

```
20  HGKEEP      LIKELIHOOD=L2; LDF=D2
21  CALCULATE   Lchange,Dchange = L2$(3),D2$(1) - L1$(3),D1$(1)
22  PRINT       Lchange,Dchange; HEAD='Change','d.f.'; DECIMALS=2,0
```

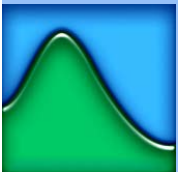
```
Change      d.f.
 2.60        -2
```

```
23  CALCULATE   T2 = CPUTIME(0)
24  PRINT       T2 - T1; DECIMALS=2; HEADING='Time taken (seconds)'
```

```
Time taken (seconds)
      4.27
```

- change deviance 2.60 on 2 d.f. for omitting Vegetation.Treatment.AM_vs_PM (c.f. Wald 2.58)
- next omit Vegetation.Treatment

..



Omit Vegetation.Treatment

Hierarchical generalized linear model

Response variate: TotalNo

Mean model

Fixed terms: Vegetation*Treatment*AM_vs_PM - (Vegetation.Treatment.AM_vs_PM) - (Vegetation.Treatment)

Distribution: poisson

Link: logarithm

Random terms: Site + SiteTreat + Plot

Distribution: gamma

Link: logarithm

Dispersion: fixed

Dispersion model

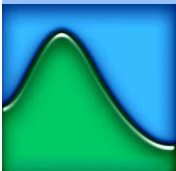
Distribution: gamma

Link: logarithm

Likelihood statistics

$-2 \times h(y v)$	2018.510
$-2 \times h$	1881.726
$-2 \times P_v(h)$	2180.339
$-2 \times P_{\beta,v}(h)$	2201.810
$-2 \times EQD(y v)$	2019.181
$-2 \times EQD$	1881.270
$-2 \times P_v(EQD)$	2179.883
$-2 \times P_{\beta,v}(EQD)$	2201.354

Fixed parameters in mean model	8
Random parameters in mean model	132
Fixed dispersion parameters	3
Random dispersion parameters	0



Wald tests and Change

Wald tests for dropping HGLM fixed terms

Term	Wald statistic	d.f.	approx. pr.
Vegetation.AM_vs_PM	4.996	2	0.082
Treatment.AM_vs_PM	5.183	1	0.023

```
31  HGKEEP      LIKELIHOOD=L3; LDF=D3
32  CALCULATE   Lchange,Dchange = L3$(3),D3$(1) - L2$(3),D2$(1)
33  PRINT       Lchange,Dchange; HEAD='Change','d.f.'; DECIMALS=2,0
```

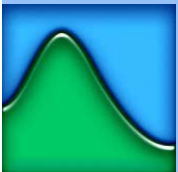
Change	d.f.
4.42	-2

```
34  CALCULATE   T3 = CPUTIME(0)
35  PRINT       T3 - T2; DECIMALS=2; HEADING='Time taken (seconds)'
```

Time taken (seconds)
4.19

- change deviance 4.42 on 2 d.f. for omitting Vegetation.Treatment (c.f. Wald 4.49)
- next omit Vegetation.AM_PM

..



Omit Vegetation.AM_PM

Hierarchical generalized linear model

Response variate: TotalNo

Mean model

Fixed terms: Vegetation*Treatment*AM_vs_PM - (Vegetation.Treatment.AM_vs_PM) - (Vegetation.Treatment) - (Vegetation.AM_vs_PM)

Distribution: poisson

Link: logarithm

Random terms: Site + SiteTreat + Plot

Distribution: gamma

Link: logarithm

Dispersion: fixed

Dispersion model

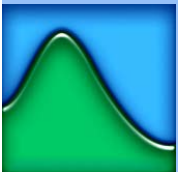
Distribution: gamma

Link: logarithm

Likelihood statistics

$-2 \times h(y v)$	2024.828
$-2 \times h$	1884.965
$-2 \times P_v(h)$	2185.312
$-2 \times P_{\beta,v}(h)$	2200.958
$-2 \times EQD(y v)$	2025.499
$-2 \times EQD$	1884.525
$-2 \times P_v(EQD)$	2184.872
$-2 \times P_{\beta,v}(EQD)$	2200.517

Fixed parameters in mean model	6
Random parameters in mean model	132
Fixed dispersion parameters	3
Random dispersion parameters	0



Wald tests and Change

Wald tests for dropping HGLM fixed terms

Term	Wald statistic	d.f.	approx. pr.
Vegetation	21.71	2	0.000
Treatment.AM_vs_PM	5.48	1	0.019

```
42  HGKEEP      LIKELIHOOD=L4; LDF=D4
43  CALCULATE   Lchange,Dchange = L4$(3),D4$(1) - L3$(3),D3$(1)
44  PRINT       Lchange,Dchange; HEAD='Change','d.f.'; DECIMALS=2,0
```

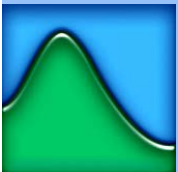
Change	d.f.
4.97	-2

```
45  CALCULATE   T4 = CPUTIME(0)
46  PRINT       T4 - T3; DECIMALS=2; HEADING='Time taken (seconds)'
```

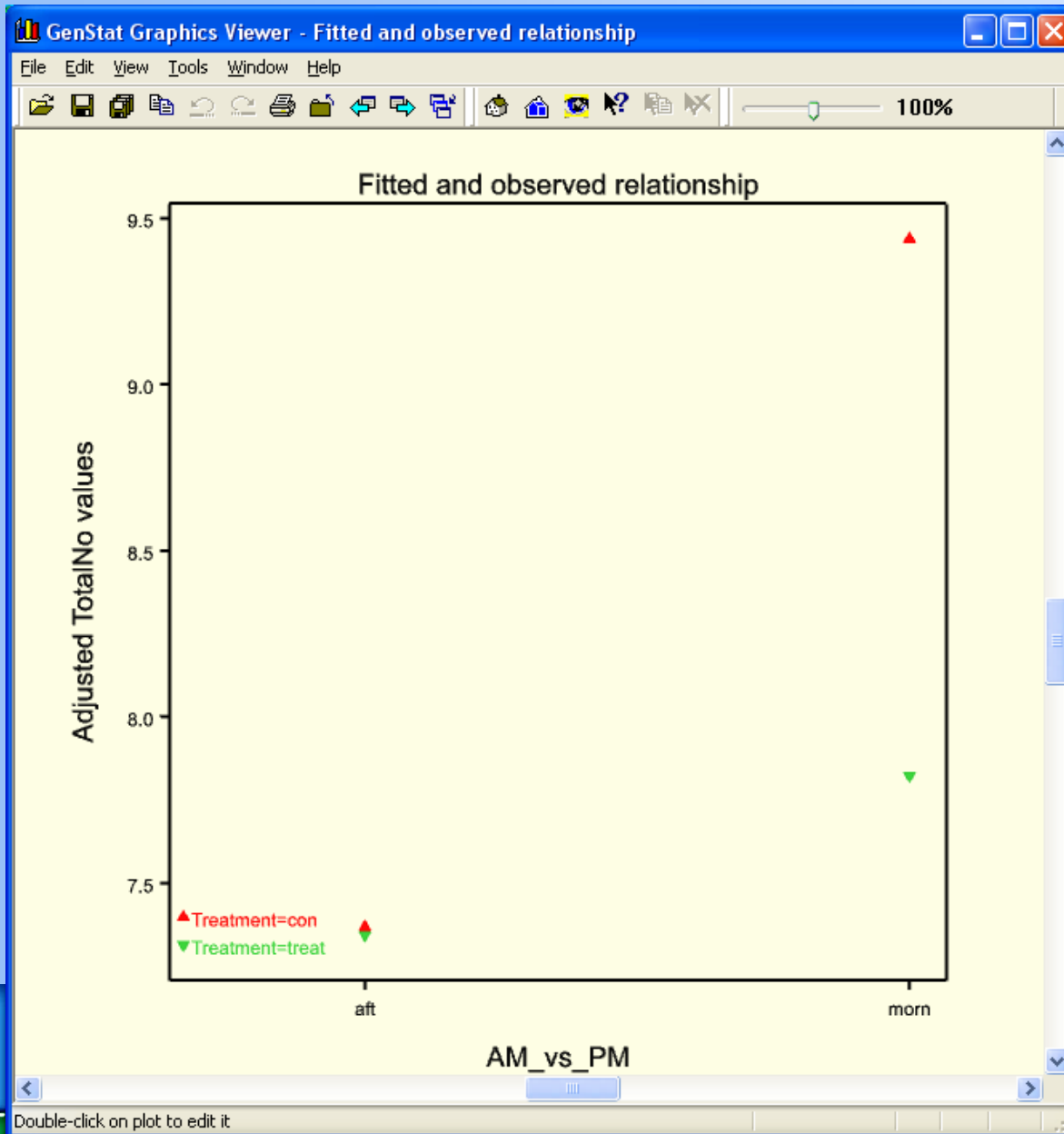
Time taken (seconds)
4.11

- change deviance 4.97 on 2 d.f. for omitting Vegetation.AM_PM (c.f. Wald 5.00)
- now study results

..



Predicted means: treatment x time of day

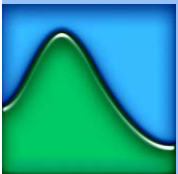


Total time taken (seconds)
17.28

Hierarchical generalized nonlinear models

- expected value $E(y) = \mu$
link $\eta = g(\mu)$
distribution – Normal, Binomial, Poisson or Gamma (from *exponential family*)
linear predictor $\eta = X\beta + \sum_i Z_i \gamma_i$
random effects γ_i with either beta, Normal, gamma or inverse gamma distributions, and their own link functions
- nonlinear parameters in fixed terms in the linear predictor
 - $X\beta = \sum x_i \beta_i$
 - but now some x_i 's are nonlinear functions of explanatory variables and parameters that are to be estimated
- extension of generalized nonlinear models of Lane (1996)
- constraint – available only for conjugate HGLM's

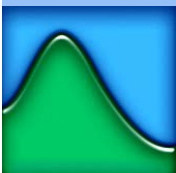
..



Implementation – interlinked GLMs

- fit nonlinear parameters by maximizing h-likelihood of augmented mean model

Components	β (fixed)		γ (fixed)
Response	y		d^*
Mean	μ		ϕ
Variance	$\phi V(\mu)$		$2\phi^2$
Link	$\eta = g(\mu)$		$\xi = h(\phi)$
Linear Pred.	$X\beta + Zv$		$G\gamma$
Dev. Comp.	d	→	$\text{gamma}(d^*, \phi)$
Prior Weight	$1/\phi$	←	$(1 - q)/2$
Components	u (random)		λ (fixed)
Response	ψ_M		d_M^*
Mean	u		λ
Variance	$\lambda V_M(u)$		$2\lambda^2$
Link	$\eta_M = g_M(u)$		$\xi_M = h_M(\lambda)$
Linear Pred.	v		$G_M \gamma_M$
Deviance	d_M	→	$\text{gamma}(d_M^*, \lambda)$
Prior Weight	$1/\lambda$	←	$(1 - q_M)/2$

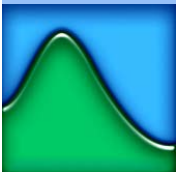


Growth of Hooded Parrot nestlings

- Hooded Parrot (*Psephotus dissimilis*)
- grass parrot in Northern Territory of Australia
- nests in termite mounds
- nests also inhabited by moth larvae that feed on nestling waste

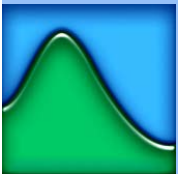


Acknowledgement: S Cooney
Australian National University, Canberra
<http://www.anu.edu.au/BoZo/stuart/HPP.htm>



Growth of Hooded Parrot nestlings

- investigate relationship between parrot and moth
 - beneficial, commensal or parasitic
- 41 nests located and monitored
- each brood had between 1-7 chicks
- treatments randomized to nests
 - moth larvae left or experimentally removed from nest
- weight of chicks measured over time
- growth modelled over time by logistic curve
 - $weight = a + c / (1 + \exp\{-b \times (age - m)\})$
 - model linear in a and c , nonlinear in b and m
- fit as HGGLM because
 - brood is a random effect
 - treatments are applied to complete broods



..

Initial values from logistic curve

```
3 " fit logistic standard curve (ignoring Brood) to get initial values "  
4 MODEL      Weight  
5 FITCURVE   [CURVE=logistic; NOMESSAGE=residual] Age * Treat
```

Nonlinear regression analysis

Response variate: Weight
Explanatory: Age
Grouping factor: Treat, all linear parameters separate
Fitted Curve: $A + C/(1 + \text{EXP}(-B*(X - M)))$

Summary of analysis

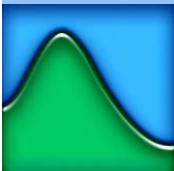
Source	d.f.	s.s.	m.s.	v.r.
Regression	5	133643.	26728.51	899.02
Residual	516	15341.	29.73	
Total	521	148984.	285.96	

Percentage variance accounted for 89.6
Standard error of observations is estimated to be 5.45.

Estimates of parameters

Parameter	estimate	s.e.
B	0.2647	0.0132
M	9.909	0.236
C Treat N	47.81	
A Treat N	0.1966	
C Treat Y	48.68	
A Treat Y	0.5423	

```
6 RKEEP      ESTIMATES=Estcurve
```



HGNLM, common A, B, C and M

```
9 HGRANDOMMODEL [DISTRIBUTION=normal; LINK=identity] Brood
10 HGFIXEDMODEL [DISTRIBUTION=normal; LINK=identity] ExpBM
11 " define nonlinear parameters and expression; initialize derived x-variate "
12 SCALAR B,M; VALUE=Estcurve$['B','M']
13 EXPRESSION [VALUE=( ExpBM = (1/(1 + EXP(-B*(Age-M)))) )] CalcExpBM
14 CALCULATE #CalcExpBM
15 " define nonlinear fixed term "
16 HGNONLINEAR [CALCULATION=CalcExpBM; VECTORS=ExpBM, Age]\
17 B,M; INITIAL=Estcurve$['B','M']
18 HGANALYSE [PRINT=model,fixed,dispersion,likelihood] Weight
```

Hierarchical generalized linear model

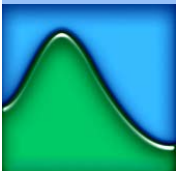
Response variate: Weight

Mean model

Fixed terms: ExpBM
Distribution: normal
Link: identity
Random terms: Brood
Distribution: normal
Link: identity
Dispersion: free

Dispersion model

Distribution: gamma
Link: logarithm



HGNLM, common A, B, C and M

Estimates from the mean model

	estimate	s.e.	t(518)
B	0.26	0.0172	14.89
M	10.04	0.2897	34.66
constant	0.19	1.4896	0.13
ExpBM	48.87	1.8512	26.40

Estimates from the dispersion model

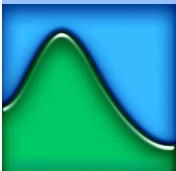
Estimates of parameters

Parameter	estimate	s.e.	t(*)	antilog of estimate
phi	3.0239	0.0640	47.23	20.57
lambda Brood	2.155	0.258	8.36	8.629

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	3025.719
-2 × h	3211.537
-2 × P _v (h)	3124.117
-2 × P _{β,v} (h)	3122.544
-2 × EQD(y v)	3025.719
-2 × EQD	3211.537
-2 × P _v (EQD)	3124.117
-2 × P _{β,v} (EQD)	3122.544



HGNLM, common B, C and M

```
21 " HGNLM with Brood as random effect: different A, common C, B and M "  
22 HGRANDOMMODEL [DISTRIBUTION=normal; LINK=identity] Brood  
23 HGFIXEDMODEL [DISTRIBUTION=normal; LINK=identity] ExpBM + Treat  
24 " define nonlinear fixed term "  
25 HGNONLINEAR [CALCULATION=CalcExpBM; VECTORS=ExpBM, Age]\  
26 B,M; INITIAL=Estcurve$['B','M']  
27 HGANALYSE [PRINT=model,fixed,dispersion,likelihood] Weight
```

Hierarchical generalized linear model

Response variate: Weight

Mean model

Fixed terms: ExpBM + Treat

Distribution: normal

Link: identity

Random terms: Brood

Distribution: normal

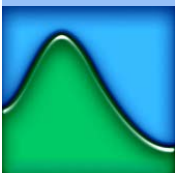
Link: identity

Dispersion: free

Dispersion model

Distribution: gamma

Link: logarithm



HGNLM, common B, C and M

Estimates from the mean model

	estimate	s.e.	t(517)
B	0.26	0.0172	14.89
M	10.05	0.2896	34.70
constant	-0.01	1.5176	-0.01
ExpBM	48.82	1.8493	26.40
Treat Y	0.77	1.1578	0.67

Estimates from the dispersion model

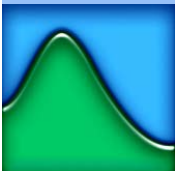
Estimates of parameters

Parameter	estimate	s.e.	t(**)	antilog of estimate
phi	3.0239	0.0640	47.22	20.57
lambda Brood	2.174	0.261	8.33	8.790

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	3025.460
-2 × h	3211.257
-2 × P _v (h)	3123.691
-2 × P _{β,v} (h)	3119.973
-2 × EQD(y v)	3025.460
-2 × EQD	3211.257
-2 × P _v (EQD)	3123.691
-2 × P _{β,v} (EQD)	3119.973



HGNLM, common B and M

```
30 " HGNLM: different A and C, common nonlinear B and M "  
31 HGRANDOMMODEL [DISTRIBUTION=normal; LINK=identity] Brood  
32 HGFIXEDMODEL [DISTRIBUTION=normal; LINK=identity] ExpBM * Treat  
33 " define nonlinear fixed term "  
34 HGNONLINEAR [CALCULATION=CalcExpBM; VECTORS=ExpBM, Age]\  
35 B,M; INITIAL=Estcurve$['B','M']  
36 HGANALYSE [PRINT=model,fixed,dispersion,likelihood] Weight
```

Hierarchical generalized linear model

Response variate: Weight

Mean model

Fixed terms: ExpBM*Treat

Distribution: normal

Link: identity

Random terms: Brood

Distribution: normal

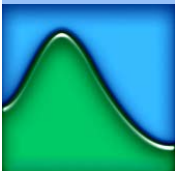
Link: identity

Dispersion: free

Dispersion model

Distribution: gamma

Link: logarithm



HGNLM, common B and M

Estimates from the mean model

	estimate	s.e.	t(516)
B	0.26	0.017	14.86
M	10.05	0.291	34.54
constant	0.25	1.529	0.17
ExpBM	48.30	1.897	25.46
Treat Y	-0.11	1.411	-0.08
ExpBM.Treat Y	1.53	1.379	1.11

Estimates from the dispersion model

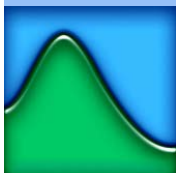
Estimates of parameters

Parameter	estimate	s.e.	t(**)	antilog of estimate
phi	3.0228	0.0641	47.15	20.55
lambda Brood	2.183	0.261	8.37	8.875

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	3023.883
-2 × h	3210.079
-2 × P _v (h)	3122.471
-2 × P _{β,v} (h)	3116.258
-2 × EQD(y v)	3023.883
-2 × EQD	3210.079
-2 × P _v (EQD)	3122.471
-2 × P _{β,v} (EQD)	3116.258



HGNLM, common M

```
39 " HGNLM: different A, B and C, common M "  
40 HGRANDOMMODEL [DISTRIBUTION=normal; LINK=identity] Brood  
41 HGFIXEDMODEL [DISTRIBUTION=normal; LINK=identity] ExpBM * Treat  
42 VARIATE [NVALUES=2] B12  
43 EXPRESSION [VALUE=( ELEMENTS(2(B12);1,2) = B1,B2 )] ExpB2M[1]  
44 EXPRESSION [VALUE=( ExpBM=(1/(1 + EXP(-NEWLEVELS(Treat;B12)*(Age-M)))) )]\  
45 ExpB2M[2]  
46 SCALAR B1,B2,M; VALUE=Estcurve$['B','B','M']  
47 CALCULATE #ExpB2M[1]  
48 CALCULATE #ExpB2M[2]  
49 HGNONLINEAR [CALCULATION=ExpB2M[1,2]; VECTORS=ExpBM, Age]\  
50 B1,B2,M; INITIAL=Estcurve$['B','B','M']  
51 HGANALYSE [PRINT=model,fixed,dispersion,likelihood] Weight
```

Hierarchical generalized linear model

Response variate: Weight

Mean model

Fixed terms: ExpBM*Treat

Distribution: normal

Link: identity

Random terms: Brood

Distribution: normal

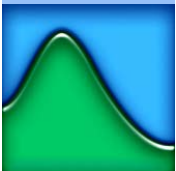
Link: identity

Dispersion: free

Dispersion model

Distribution: gamma

Link: logarithm



HGNLM, common M

Estimates from the mean model

	estimate	s.e.	t(515)
B1	0.266	0.021	12.57
B2	0.237	0.024	9.99
M	10.035	0.289	34.78
constant	0.706	1.562	0.45
ExpBM	47.464	2.010	23.61
Treat Y	-1.555	2.074	-0.75
ExpBM.Treat Y	4.124	3.068	1.34

Estimates from the dispersion model

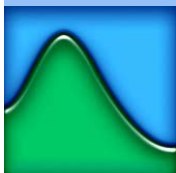
Estimates of parameters

Parameter	estimate	s.e.	t(**)	antilog of estimate
phi	3.0230	0.0642	47.11	20.55
lambda Brood	2.176	0.261	8.33	8.807

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	3023.039
-2 × h	3208.880
-2 × P _v (h)	3121.326
-2 × P _{β,v} (h)	3115.093
-2 × EQD(y v)	3023.039
-2 × EQD	3208.880
-2 × P _v (EQD)	3121.326
-2 × P _{β,v} (EQD)	3115.093



HGNLM, different A, B, C and M

```
54 " HGNLM: different A, B, C and M "  
55 HGRANDOMMODEL [DISTRIBUTION=normal; LINK=identity] Brood  
56 HGFIXEDMODEL [DISTRIBUTION=normal; LINK=identity] ExpBM * Treat  
57 VARIATE [NVALUES=2] B12,M12  
58 EXPRESSION [VALUE=( ELEMENTS(2(B12),2(M12);1,2) = B1,B2,M1,M2 )] ExpB2M2[1]  
59 EXPRESSION [VALUE=( ExpBM=\  
60 (1/(1 + EXP(-NEWLEVELS(Treat;B12) * (Age-NEWLEVELS(Treat;M12)))))) ] ExpB2M2[2]  
61 SCALAR B1,B2,M1,M2; VALUE=Estcurve$['B','B','M','M']  
62 CALCULATE #ExpB2M2[1]  
63 CALCULATE #ExpB2M2[2]  
64 HGNONLINEAR [CALCULATION=ExpB2M2[1,2]; VECTORS=ExpBM, Age]\  
65 B1,B2,M1,M2; INITIAL=Estcurve$['B','B','M','M']  
66 HGANALYSE [PRINT=model,fixed,dispersion,likelihood] Weight
```

Hierarchical generalized linear model

Response variate: Weight

Mean model

Fixed terms: ExpBM*Treat

Distribution: normal

Link: identity

Random terms: Brood

Distribution: normal

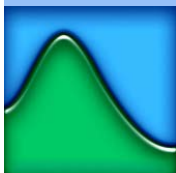
Link: identity

Dispersion: free

Dispersion model

Distribution: gamma

Link: logarithm



HGNLM, different A, B, C and M

Estimates from the mean model

	estimate	s. e.	t(514)
B1	0.263	0.022	12.05
B2	0.243	0.028	8.66
M1	9.958	0.344	28.97
M2	10.243	0.528	19.40
constant	0.415	1.740	0.24
ExpBM	47.764	2.177	21.94
Treat Y	-0.385	3.304	-0.12
ExpBM.Treat Y	2.900	4.070	0.71

Estimates from the dispersion model

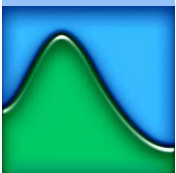
Estimates of parameters

Parameter	estimate	s. e.	t(*)	antilog of estimate
phi	3.0245	0.0642	47.08	20.58
lambda Brood	2.179	0.261	8.34	8.836

Message: s.e.s are based on dispersion parameter with value 1.

Likelihood statistics

-2 × h(y v)	3022.818
-2 × h	3208.781
-2 × P _v (h)	3121.155
-2 × P _{β,v} (h)	3114.936
-2 × EQD(y v)	3022.818
-2 × EQD	3208.781
-2 × P _v (EQD)	3121.155
-2 × P _{β,v} (EQD)	3114.936



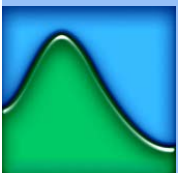
Likelihood statistics

```
69  " compare likelihoods "  
70  PRINT          L,LA,LAC,LABC,LABCM; DECIMALS=2; FIELD=10
```

	L	LA	LAC	LABC	LABCM
-2 * h(y v)	3025.72	3025.46	3023.88	3023.04	3022.82
-2 * h	3211.54	3211.26	3210.08	3208.88	3208.78
-2 * P_v(h)	3124.12	3123.69	3122.47	3121.33	3121.15
-2 * P_beta,v(h)	3122.54	3119.97	3116.26	3115.09	3114.94
-2 * EQD(y v)	3025.72	3025.46	3023.88	3023.04	3022.82
-2 * EQD	3211.54	3211.26	3210.08	3208.88	3208.78
-2 * P_v(EQD)	3124.12	3123.69	3122.47	3121.33	3121.15
-2 * P_beta,v(EQD)	3122.54	3119.97	3116.26	3115.09	3114.94

- no evidence of any treatment effects

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Standard curve (ignoring brood)

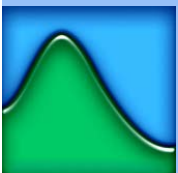
```
72 " compare to logistic standard curve (ignoring Brood) "  
73 MODEL      Weight  
74 TERMS      Age * Treat  
75 FITCURVE   [PRINT=*; CURVE=logistic] Age  
76 ADD        [PRINT=*] Treat  
77 ADD        [PRINT=*] Age.Treat  
78 ADD        [PRINT=*; NONLINEAR=separate]  
79 RDISPLAY   [PRINT=accumulated; FPROBABILITY=yes]
```

Nonlinear regression analysis

Accumulated analysis of variance

Change	d.f.	s.s.	m.s.	v.r.	F pr.
+ Age	3	133539.09	44513.03	1498.57	<.001
+ Treat	1	93.51	93.51	3.15	0.077
+ Age.Treat	1	9.93	9.93	0.33	0.563
+ Separate nonlinear	2	73.31	36.66	1.23	0.292
Residual	514	15267.69	29.70		
Total	521	148983.54	285.96		

- an inappropriate analysis for people without GenStat & HGNLMs
- suggestion of a treatment effect



GNLM with Brood as a fixed term

```
81 " compare to generalized nonlinear model (treating Brood as fixed) "  
82 MODEL      Weight  
83 TERMS      ExpBM * Treat + Brood  
84 EXPRESSION [VALUE=( ExpBM = (1/(1 + EXP(-B*(Age-M)))) )] CalcExpBM  
85 RCYCLE     B,M; INITIAL=Estcurve$['B','M']  
86 FIT        [PRINT=*; NOMESS=alias; CONSTANT=estimate; CALC=CalcExpBM] ExpBM  
87 ADD        [PRINT=*; NOMESS=alias] Treat  
88 ADD        [PRINT=*; NOMESS=alias] Brood  
89 ADD        [PRINT=*; NOMESS=alias] ExpBM.Treat  
90 RDISPLAY   [PRINT=accumulated; FPROBABILITY=yes]
```

Nonlinear regression analysis

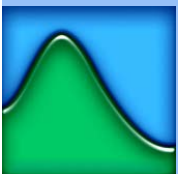
Accumulated analysis of variance

Change	d.f.	s.s.	m.s.	v.r.	F pr.
+ ExpBM	3	133539.09	44513.03	2157.86	<.001
+ Treat	1	93.94	93.94	4.55	0.033
+ Brood	37	5437.11	146.95	7.12	<.001
+ ExpBM.Treat	1	32.42	32.42	1.57	0.211
Residual	479	9880.98	20.63		
Total	521	148983.54	285.96		

```
91  
92 CALCULATE T1 = CPUTIME(0)  
93 PRINT      T1 - T0; DECIMALS=2; HEADING='Time taken (seconds)'
```

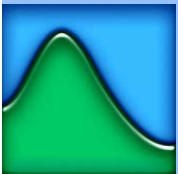
Time taken (seconds)
18.52

- an alternative inappropriate analysis
- significant (but misleading) treatment effects



Conclusions

- the HGLM menus & procedures provide very useful extensions to the standard Generalized linear Models
- represent the current state of the ongoing research by Lee, Nelder *et al.* on extensions to generalized linear models
- GenStat is providing a flexible and convenient framework for the collaboration – to try out, and then distribute, our ideas
- the methodology is described in the book
 - Lee, Y., Nelder, J.A. & Pawitan, Y. (2006). *Generalized Linear Models with Random Effects: Unified Analysis via H-likelihood*. CRC Press.
- there are many extensions (+ corrections) since then
 - including HGNLMS, in *GenStat for Windows 10th Edition*
 - Wald tests and plots of predicted means to come in the 11th Edition
- for further information, see vsni.co.uk or email roger.payne@vsni.co.uk



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