Linear Threshold Models

- With the notable exception of the normal distribution, few distributions have "nice" multivariate analogs.

- Multiple trait models for non-normal data are typically built in one of two ways.

  1. Using one of the variables as a covariate in the other's linear predictor.
  2. Using an over-dispersion covariance structure

- In `ASReml` the second dependent variable is assumed to normal random variable.

Covariate Approach

- Normal random variable

$$\boldsymbol{y}_2|\boldsymbol{u}_2 \sim \mathrm{N}(\boldsymbol{X}\boldsymbol{\beta}_2 + \boldsymbol{Z}\boldsymbol{u_2}, \boldsymbol{I}\sigma^2_{e1})$$

- GLM variate (Conditional on the Normal Variate)

$$\begin{aligned}
\boldsymbol{y}_1|\boldsymbol{y}_2, \boldsymbol{u} &\sim f(\boldsymbol{X}\boldsymbol{\beta}_1 + \boldsymbol{Z}\boldsymbol{u_1} + b\boldsymbol{y}_2) \\
\boldsymbol{\eta}_1 &= \boldsymbol{X}[\boldsymbol{\beta}_1 + b\boldsymbol{\beta}_2] + \boldsymbol{Z}[\boldsymbol{u_1} + b\boldsymbol{u}_2] + b\boldsymbol{e}_2 \\
\boldsymbol{\beta}^*_1 &= \boldsymbol{\beta}_1 + b\boldsymbol{\beta}_2 \\
\boldsymbol{u}^*_1 &= \boldsymbol{u_1} + b\boldsymbol{u}_2
\end{aligned}$$

- Dependency between the two traits are modeled through the linear predictor

- Reasonable if all the effects for trait 2 are included in the model for trait 1.

- Need to adjust the estimated effects for trait 1.

Adjusted Covariance Matrix

$$\begin{aligned}\boldsymbol{G} &= \begin{pmatrix} 1 & b \\ 0 & 1 \end{pmatrix} \begin{pmatrix} \sigma_{g1}^2 & \sigma_{g12} \\ \sigma_{g21} & \sigma_{g2}^2 \end{pmatrix} \begin{pmatrix} 1 & 0 \\ b & 1 \end{pmatrix} \\ &= \begin{pmatrix} \sigma_{g11}^2 + 2b\sigma_{g12} + b^2\sigma_{g2}^2 & \sigma_{g12} + b\sigma_{g2}^2 \\ \sigma_{g21} + b\sigma_{g2}^2 & \sigma_{g2}^2 \end{pmatrix}\end{aligned}$$

Residual Covariance Matrix

$$
\begin{aligned}
\operatorname{var}(\boldsymbol{y}_{1i}|\boldsymbol{u}) &\simeq \phi^2\nu(\mu_{1i}) + b^2 \operatorname{var}\left(\frac{\partial\mu_{1i}}{\partial\eta_{1i}}\right) \\
&\simeq \phi^2\nu(\mu_{1i}) + b^2\left[\frac{\partial\mu_{1i}}{\partial\eta_{1i}}\right]^2\sigma^2_{e2} \\
&= \nu(\mu_{1i})\left[\phi^2 + b^2\left[\frac{\partial\mu_{1i}}{\partial\eta_{1i}}\right]^2\frac{\sigma^2_{e2}}{\nu(\mu_{1i})}\right] \\
\operatorname{cov}(\boldsymbol{y}_{1i}|\boldsymbol{u}) &\simeq b\frac{\partial\mu_{1i}}{\partial\eta_{1i}}\sigma^2_{e2} \\
&= b\frac{\partial\mu_{1i}}{\partial\eta_{1i}}\sigma^2_{e2}\frac{1}{\sqrt{\nu(\mu_{1i})}}\sqrt{\nu(\mu_{1i})}
\end{aligned}
$$

ASREML:

```
Linear Threshold Covariate Example
  Origin 2 !I
  Sire 6 !I
  Season 2 !I
  Pelvic_Opening
  Sex 2 !A
  Birth_Weight
  Diff 2 !A
  Score
linthresh.dat !ASUV !MAXIT 100
```

```
Score Pelvic_Opening !BINOMIAL !LOGIT  ~ Trait Trait.Origin,
Trait.Season Trait.Sex at(Trait,1).Pelvic_Opening !r Trait.Sire
1 2 1
0 0 I
2 0 US 1 0 1100 !GPZP
Trait.Sire 2
2 0 US .4   -.1 100 !GP
6 0 I
```

Results:

```
Source                Model  terms     Gamma     Component    Comp/SE   % C
Residual        UnStructured  1   1  0.970365      0.970365       4.27   0 P
Residual        UnStructured  2   1   0.00000       0.00000       0.00   0 F
Residual        UnStructured  2   2   1101.77       1101.77       4.41   0 P
Trait.Sire        UnStructured 1  1  0.420309      0.420309       0.44   0 P
Trait.Sire        UnStructured 2  1   1.37408       1.37408       0.16   0 P
Trait.Sire        UnStructured 2  2   117.850       117.850       0.72   0 P
Covariance/Variance/Correlation Matrix UnStructured Residual
 0.9704       0.000
  0.000       1102.
Covariance/Variance/Correlation Matrix UnStructured Trait.Sire
 0.4203      0.1952
  1.374       117.8
```

Solutions

```
 at(Trait,1).Pelvic_O       1.001              -0.1369E-01  0.1202E-01
 Trait.Sex                  1.M                  0.000       0.000
 Trait.Sex                  1.F                 -1.764      0.9054
```

Over dispersion Model

- Use a scaled covariance matrix

$$\boldsymbol{R}_i = \begin{pmatrix} \sigma_{e1}^2 \nu(\mu 1i) & \sigma_{e12}\sqrt{\nu(\mu_{1i})} \\ \sigma_{e12}\sqrt{\nu(\mu_{1i})} & \sigma_{e2}^2 \end{pmatrix}$$

- Has the advantage of simplicity

ASREML:

```
Linear Threshold Example
  Origin 2 !I
  Sire 6 !I
  Season 2 !I
  Pelvic_Opening
  Sex 2 !A
  Birth_Weight
  Diff 2 !A
  Score
linthresh.dat !ASUV !MAXIT 100
```

```
Score Pelvic_Opening !BINOMIAL !LOGIT  ~ Trait Trait.Origin,
Trait.Season Trait.Sex !r Trait.Sire
1 2 1
0 0 I
2 0 US 1 -1 1100 !GP
Trait.Sire 2
2 0 US .4   -.1 100 !GP
6 0 I
```

Results:

```
Source                Model  terms     Gamma     Component    Comp/SE   % C
Residual        UnStructured  1  1  0.907744      0.907744       4.35   0 P
Residual        UnStructured  2  1  -3.96929      -3.96929      -1.33   0 P
Residual        UnStructured  2  2   1104.54       1104.54       4.41   0 P
Trait.Sire        UnStructured 1  1  0.392674      0.392674       0.44   0 P
Trait.Sire        UnStructured 2  1 -0.610015     -0.610015      -0.08   0 P
Trait.Sire        UnStructured 2  2   114.874       114.874       0.70   0 P
Covariance/Variance/Correlation Matrix UnStructured Residual
 0.9077     -0.1254
 -3.969       1105.
Covariance/Variance/Correlation Matrix UnStructured Trait.Sire
 0.3927     -0.9083E-01
-0.6100       114.9
```

Comparing Results:

$$\widehat{b} = -.01369$$

Source	Covariate	Adjusted	Over Dispersion
σ^2_{e1}	0.9704	1.0783	0.9077
σ_{e12}	0.000	-10.897	-3.9693
σ^2_{e2}	1101.77		1104.54
σ^2_{g1}	0.42030	0.4048	.3927
σ_{g12}	1.3741	-0.2393	-0.6100
σ^2_{g2}	117.85		114.87

Sire Effects

- Covariate Model

$$S_{1i}^{a} = S_{1i}^{u} + bS_{2i}$$