

# Multinomial Regression Models

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## Objectives:

- Multinomial distribution and likelihood
- Ordinal data: Cumulative link models (POM).
- Ordinal data: Continuation models (CRM).

## Models for Multinomial Data

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### Example Data:

- Wisconsin Study of Diabetic Retinopathy (WESDR).
- Diabetic retinopathy is one of the leading causes of blindness in people aged 20-75 years in the US.
- Disease characterized by appearance of small hemorrhages in the retina which progress and lead to severe visual loss.

- **Disease severity:**

None

Mild

Moderate

Proliferative

- **Covariates:**

duration of diabetes

glycosolated hemoglobin

diastolic blood pressure

age at diagnosis

## Models for Ordinal Data

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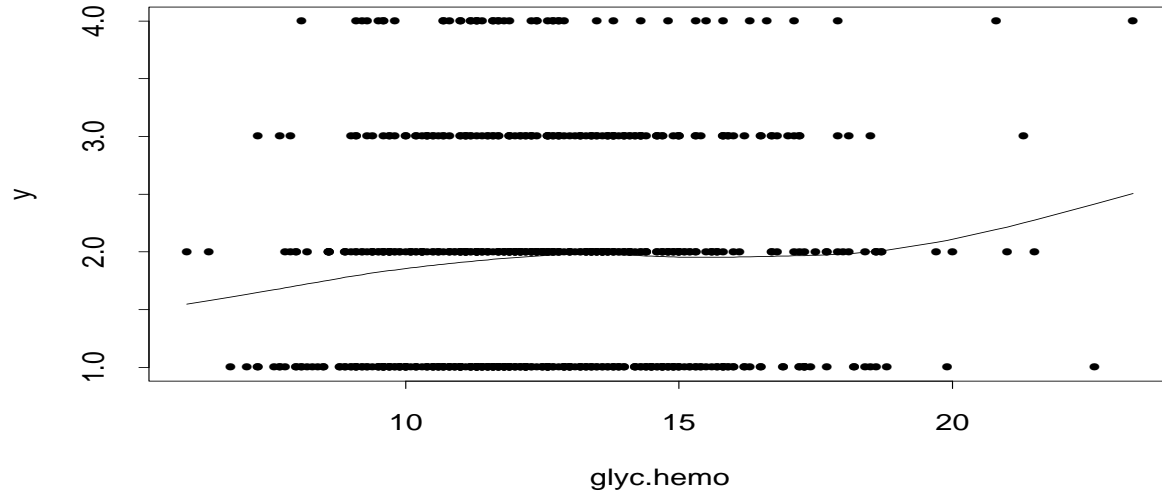
Example Data:

**Q:** How does the distribution of disease severity vary as a function of covariates?

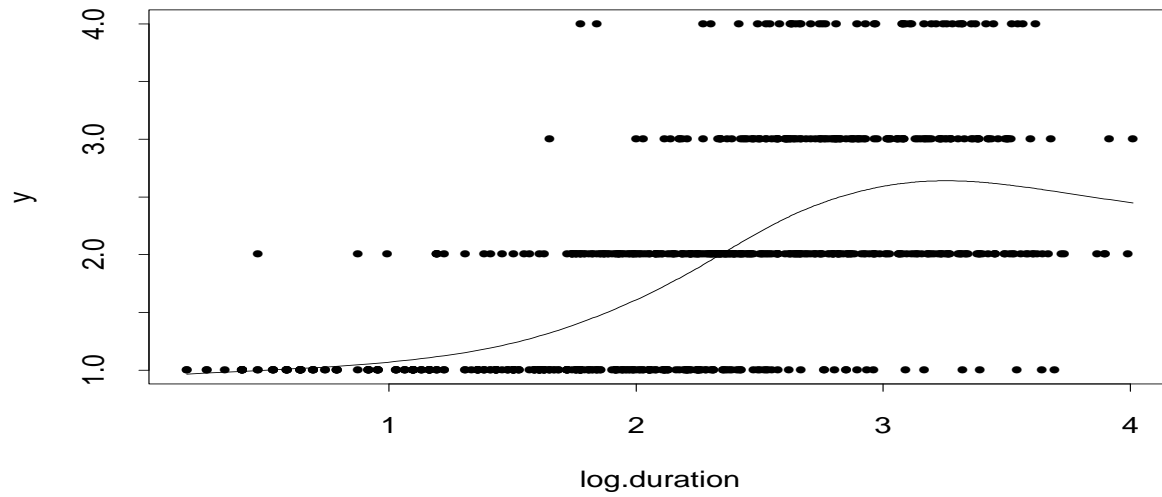
**Q:** Possible approaches to analysis?

Ideas?

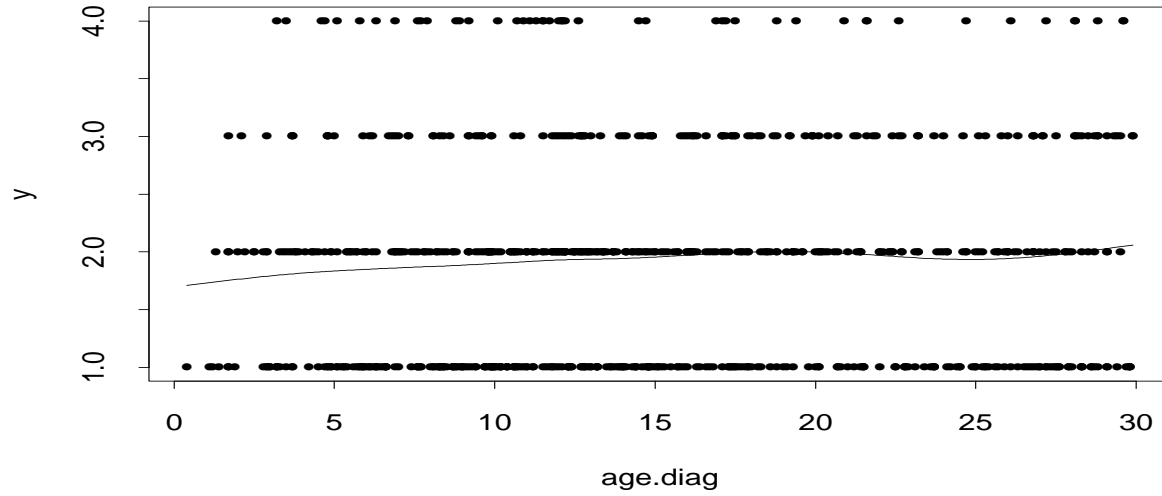
Score versus GlycHemo



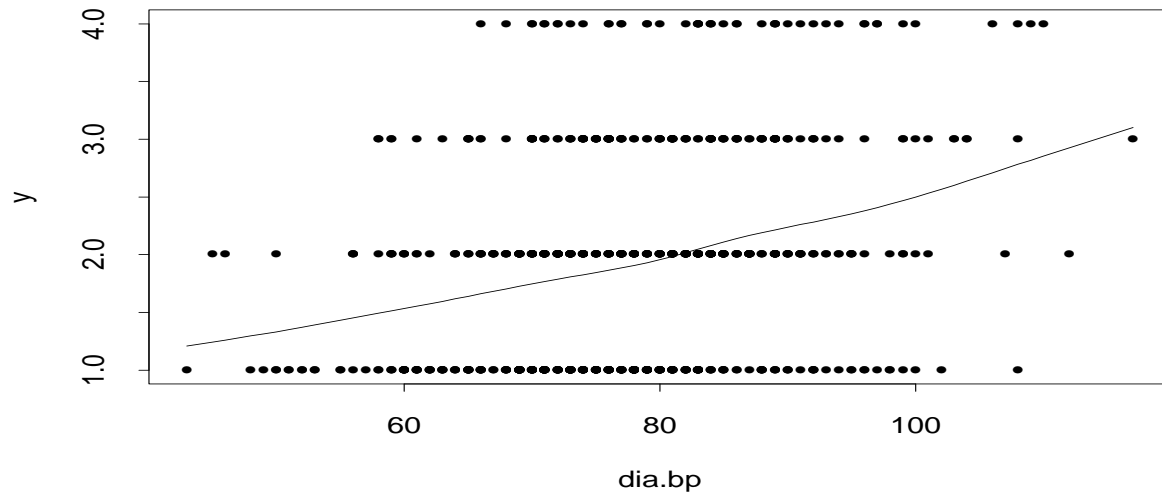
Score versus logDuration



Score versus AgeDiag



Score versus DiaBP



## Multinomial Response Models

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- Common categorical outcomes take more than two levels:
  - Pain severity = low, medium, high
  - Conception trials = 1, 2 if not 1, 3 if not 1-2
- The basic probability model is the multi-category extension of the Bernoulli (Binomial) distribution – multinomial.
- Univariate outcome with multivariate representation:
  - Let  $O_i \in [1, 2, 3, \dots, C]$  be a categorical outcome.
  - Let  $Y_{ij}$  be the indicator  $Y_{ij} = \mathbf{1}(O_i = j)$ ,  
 $j = 1, 2, \dots, (C - 1)$ .

$$O_i = j \Leftrightarrow Y_{ij} = 1 \text{ and } Y_{ik} = 0 \quad \forall k \neq j$$

$$O_i \Leftrightarrow \mathbf{Y}_i = \begin{pmatrix} Y_{i1} \\ Y_{i2} \\ \vdots \\ Y_{iC} \end{pmatrix}$$



○ Probability given by

$$P(O_i) = P(\mathbf{Y}_i) = \pi_{i1}^{Y_{i1}} \pi_{i2}^{Y_{i2}} \dots \left(1 - \sum_{k=1}^{C-1} \pi_{ik}\right)^{(1 - \sum_{k=1}^{C-1} Y_{ik})}$$

$$E[Y_{ij}] = \pi_{ij}$$

$$\text{cov}[Y_{ij}, Y_{ik}] = \begin{cases} -\pi_{ij}\pi_{ik} & j \neq k \\ \pi_{ij}(1 - \pi_{ij}) & j = k \end{cases}$$

## What is Ordinal Data?

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- Categories (fixed number) that are ordered much like the *ordinal* numbers:

*first, second, ...*

- It doesn't make sense to talk about a distance between the categories:

- ★ HIGH, MEDIUM, LOW

- ★ NEVER, RARELY, SOMETIMES, ALWAYS

- e.g. "Drachman Class"

## Ordinal Data

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**Q:** Is this type of data really that common?

**A:** Lincoln Moses (Stanford) surveyed vol. 306 of NEJM and found that 32/168 articles contained ordered categorical data!

“We found no indication that any of the authors in vol. 306 used an analysis that takes account of the ordering.” (p. 447)

## Ordinal? Binary? Continuous?

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**Q:** Do we lose much information by GROUPING (categorizing) a measurement?

**Example:** rather than analysis of BMI as a continuous measurement we recode into: non-obese; obese; severely obese.

**Q:** Do we gain much information by using the ordered categories over just DICHOTOMIZING?

**Example:** rather than analysis of BMI **categories** we use the indicator of severely obese.

## Ordinal? Binary? Continuous?

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Evaluation:

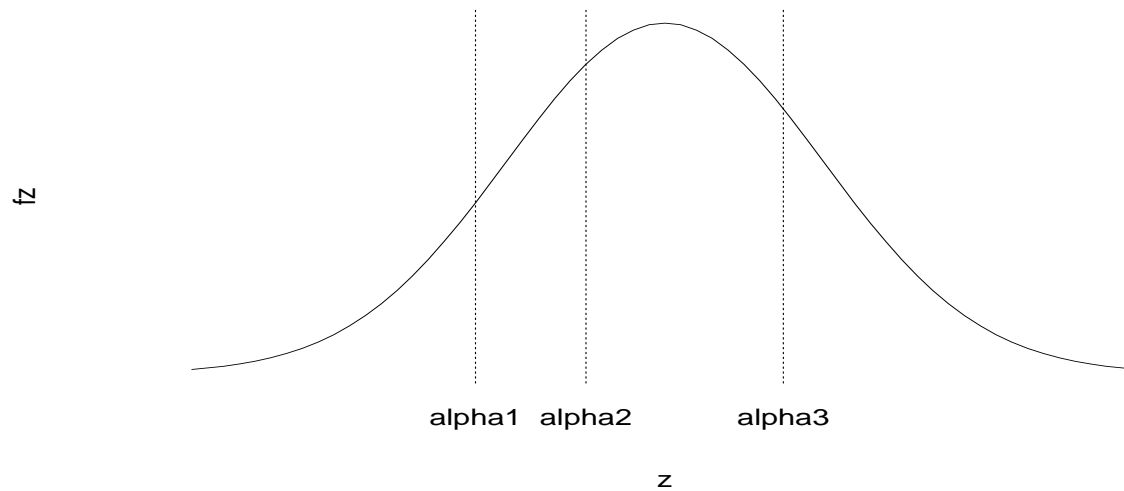
- 1) Assume an underlying Gaussian:  $O_i \sim \mathcal{N}(\mu, 1)$ .
- 2) Define CUTPOINTS  $\alpha \in \mathcal{R}^C$ .

Define:  $Y_{ij} = \mathbf{1}(O_i \in (\alpha_{j-1}, \alpha_j])$

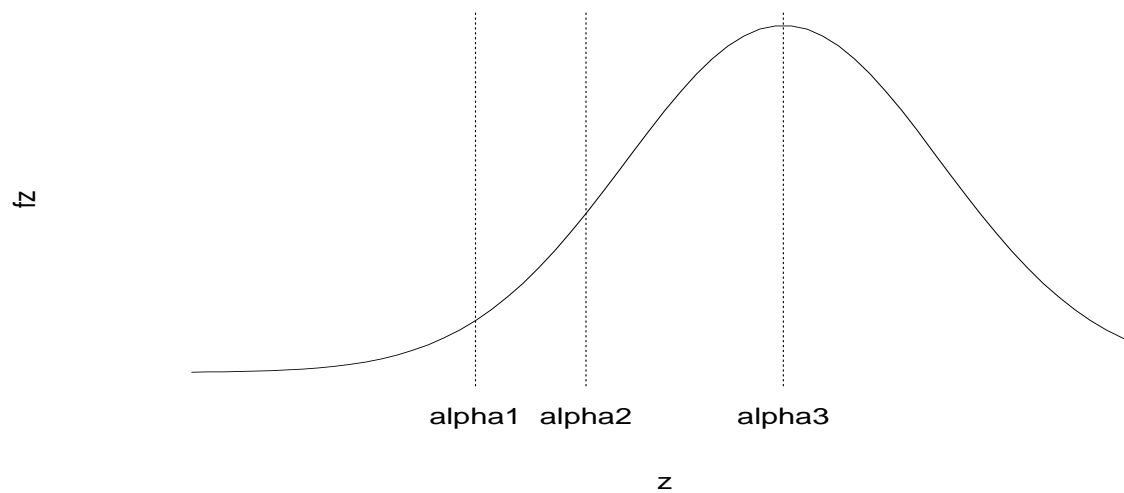
$$\begin{aligned} E(Y_{ij}) &= P(O_i \in (\alpha_{j-1}, \alpha_j]) \\ &= P(O_i \leq \alpha_j) - P(O_i \leq \alpha_{j-1}) \\ \pi_{ij} &= \Phi(\alpha_j - \mu) - \Phi(\alpha_{j-1} - \mu) \end{aligned}$$

$\mathbf{Y}_i$  represents a multinomial random variable with  $m = 1$ ,  $\boldsymbol{\pi}_i$ .

Gaussian with cut-points ( $\mu=0$ )



Gaussian with cut-points ( $\mu=3/4$ )



## Ordinal versus Continuous?

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Given a sample of  $\mathbf{Y}_1, \mathbf{Y}_2, \dots, \mathbf{Y}_n$  we can obtain the MLE for  $\mu$  (and we'll just assume  $\alpha$  is known).

We obtain (derive this yourself!):

$$\mathcal{I}_n = \sum_i \sum_j \frac{\partial \pi_{ij}}{\partial \mu} \frac{1}{\pi_{ij}} \frac{\partial \pi_{ij}}{\partial \mu}$$

If we assume that the  $\mathbf{Y}_i$ 's are i.i.d then we can drop the subscript  $i$  and we can compare the information from the categorized, or grouped, data  $Y_i$  to the information in the continuous  $O_i$ :

Asymptotic relative efficiency:

$$\frac{\text{var}(\hat{\mu}_O)}{\text{var}(\hat{\mu}_Y)} = \frac{1/n}{\left[ n \sum_j \frac{\partial \pi_j}{\partial \mu} \frac{1}{\pi_j} \frac{\partial \pi_j}{\partial \mu} \right]^{-1}} = \mathcal{I}_1$$

**Q:** How does the efficiency depend on  $C$ , the number of categories?

**Q:** How does the efficiency depend on the locations  $\alpha_j$ ?



## Efficiency versus C

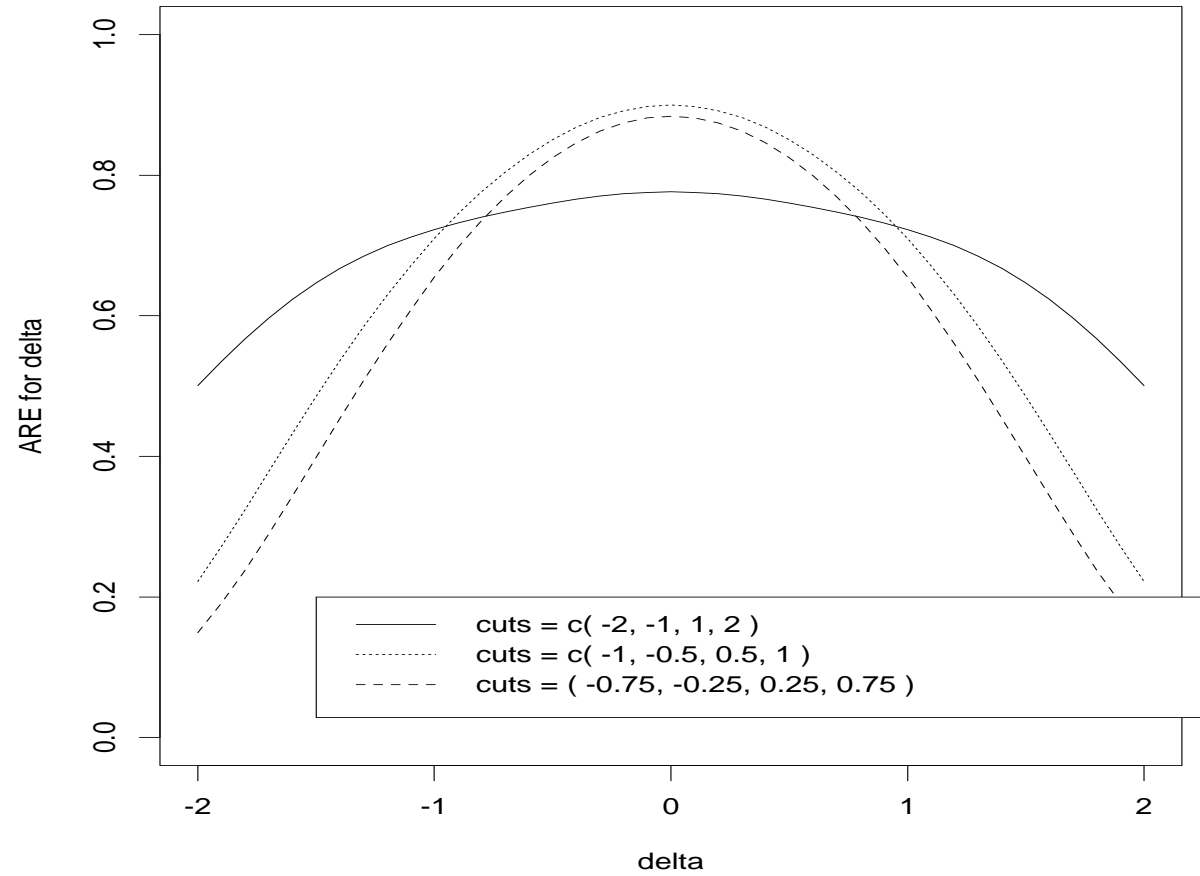
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For this I actually used the MLE's variance based on estimating the location difference  $\mu_1 - \mu_2 = \Delta$  and the cut-point parameters.

For the cutpoints I used the  $1/(C + 1)$ -tiles of  $\mathcal{N}(0, 1)$  shifted by  $\Delta/2$  (ie. cut-points are between the two locations).

$C$	ARE
1	0.565
2	0.727
3	0.800
4	0.841
5	0.867
6	0.884
7	0.897
8	0.907
9	0.914
10	0.920

ARE using different thresholds, C=5



Some references on grouping data :

Connor R.J. (1972), "Grouping for testing trends in categorical data", *Journal of the American Statistical Association*, 67: 601-604.

- binary & continuous  $\Rightarrow 2 \times k$
- Efficiency from 65% - 97% for testing ( $k=2, \dots, 6$ )

Armstrong B.G. and Sloan M. (1989), "Ordinal regression models for epidemiologic data", *American Journal of Epidemiology*, 129: 191-204.

- POM versus logistic regression.
- A smart dichotomization yields 75-80% efficiency.

Sankey S.S and Weissfeld L.A. (1998), "A study of the effect of dichotomizing ordinal data upon modeling", *Communications in Statistics, Part B – Sim & Comp*, 27: 871-887.

## Probability Model = Multinomial

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- Fixed number of categories ( $C$ ).
- Fixed sample size ( $m$ ).

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Insect species  $1, 2, \dots, C$ .

Sites  $s_1, s_2, \dots, s_m$ .

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Scheme 1

When first insect enters trap it shuts.

All traps left until catch 1.

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Scheme 2

If insect enters it can't get out.

All traps left for 24 hours.

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$\mathbf{Y}_{1,i} = (0, 0, 0, 1, 0)$      $\mathbf{Y}_{2,i} = (0, 4, 1, 0, 2)$

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## Probability Model = Multinomial

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Given  $Y_{ij}$  = number of type  $j$  out of  $m_i$ ;  $\sum_j Y_{ij} = m_i$

$$P(Y_{i1} = y_{i1}, Y_{i2} = y_{i2}, \dots, Y_{iC} = y_{iC}) = \frac{m_i!}{y_{i1}! y_{i2}! \dots y_{iC}!} \prod_{j=1}^C \pi_{ij}^{y_{ij}}$$

In this representation the parameter  $\pi_{ij}$  can be defined via:

- Given  $m_i = 1$ :
- Given  $m_i > 1$ :

## Some properties of multinomial

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1)  $w_1, w_2, \dots, w_C$  independent  $w_i \sim \mathcal{P}(\lambda_i)$ .

Then  $(w_1, w_2, \dots, w_C \mid \sum_j w_j = m) \sim$

$$\text{mult}\left(m, \frac{\lambda_1}{\sum_j \lambda_j}, \frac{\lambda_2}{\sum_j \lambda_j}, \dots, \frac{\lambda_C}{\sum_j \lambda_j}\right)$$

2) If  $\mathbf{Y} \sim \text{mult}(m, \boldsymbol{\pi})$

$$\implies Y_j \sim \text{binomial}(m, \pi_j)$$

3)  $\text{cov}(Y_j, Y_k) = -m\pi_j\pi_k$  for  $j \neq k$ .

4) REPRODUCIBLE: Let  $\mathbf{Y} = (\mathbf{Y}_1, \mathbf{Y}_2)$  then

$$(\mathbf{Y}_1, \text{sum}(\mathbf{Y}_2)) \sim \text{mult}(m, \boldsymbol{\pi}_1, \text{sum}(\boldsymbol{\pi}_2))$$

5) REPRODUCIBLE for CONDITIONALS:

Condition on  $Y_j$ :  $(Y_1, Y_2, \dots, (-j), \dots, Y_C \mid Y_j = t) \sim$

$$\text{mult}(m - t, \frac{\pi_1}{1 - \pi_j}, \frac{\pi_2}{1 - \pi_j}, \dots, (-j), \dots, \frac{\pi_C}{1 - \pi_j})$$

6) Define cumulative totals  $Z_j = \sum_{k=1}^j Y_k$ ,  $\gamma_j = \sum_{k=1}^j \pi_k$ :

$$Z_j \sim \text{binomial}(m, \gamma_j)$$

$$Z_i \mid Z_j = z_j, i < j \sim \text{binomial}(z_j, \frac{\gamma_i}{\gamma_j})$$



## Multinomial as Vector Exponential Family

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$$\begin{aligned} P(\mathbf{Y}_i) &= \left[ \prod_{j=1}^{C-1} \pi_{ij}^{Y_{ij}} \right] \left( 1 - \sum_k \pi_{ik} \right)^{\left( 1 - \sum_k^{C-1} Y_{ik} \right)} \\ &= \exp \left[ \sum_j^{C-1} Y_{ij} \cdot \log(\pi_{ij}) + \right. \\ &\quad \left. \left( 1 - \sum_k^{C-1} Y_{ik} \right) \cdot \log \left( 1 - \sum_k^{C-1} \pi_{ik} \right) \right] \end{aligned}$$

## Multinomial as Vector Exponential Family

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$$\begin{aligned} P(\mathbf{Y}_i) &= \exp \left[ \sum_j^{C-1} Y_{ij} \cdot \log(\pi_{ij}/\pi_{iC}) + \log(\pi_{iC}) \right] \\ &= \exp \left[ \mathbf{Y}_i^T \boldsymbol{\theta}_i - b(\boldsymbol{\theta}_i) \right] \end{aligned}$$

**Note:** we have “dropped” the last category.

where

$$\theta_{ij} = \log(\pi_{ij}/\pi_{iC})$$

$$b(\boldsymbol{\theta}_i) = -\log(\pi_{iC}) = \log\left[1 + \sum_k^{C-1} \exp(\theta_{ik})\right] \quad (\text{verify!})$$

$$\frac{\partial}{\partial \theta_{ij}} b(\boldsymbol{\theta}_i) = \pi_{ij} \quad (\text{verify!})$$

$$\frac{\partial^2}{\partial \theta_{ij} \partial \theta_{ik}} b(\boldsymbol{\theta}_i) = \begin{cases} -\pi_{ij}\pi_{ik} & k \neq j \\ \pi_{ij}(1 - \pi_{ij}) & k = j \end{cases}$$

## Models for Ordinal Data

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```

dia.bp80|y
      |1      |2      |3      |4      |RowTot1|
-----+-----+-----+-----+-----+
0      |200     |144     | 59     | 16     |419     |
      |0.477   |0.344   |0.141   |0.038   |0.58    |
-----+-----+-----+-----+
1      | 75     |126     | 69     | 31     |301     |
      |0.249   |0.419   |0.229   |0.103   |0.42    |
-----+-----+-----+-----+
ColTot1|275     |270     |128     |47      |720     |
      |0.382   |0.375   |0.178   |0.065   |        |
-----+-----+-----+-----+

```

Test for independence of all factors  
 $\text{Chi}^2 = 45.46906$  d.f.= 3 (p=7.354828e-10)

```
Call:  crosstabs( ~ dia.bp80 + (y > 1))
dia.bp80|(y > 1)
```

	FALSE	TRUE	RowTot1	
0	200	219	419	
	0.48	0.52	0.58	
1	75	226	301	
	0.25	0.75	0.42	
ColTot1	275	445	720	

Test for independence of all factors

Chi<sup>2</sup> = 38.62691 d.f.= 1 (p=5.130671e-10)

odds ratio = 2.74 , ( 1.983 , 3.786 )

log-odds ratio = 1.008 , s.e.= 0.165

```
Call:  crosstabs( ~ dia.bp80 + (y > 2))
dia.bp80|(y > 2)
```

	FALSE	TRUE	RowTot1
0	344	75	419
	0.82	0.18	0.58
1	201	100	301
	0.67	0.33	0.42
ColTot1	545	175	720

Test for independence of all factors

Chi^2 = 22.35406 d.f.= 1 (p=2.267331e-06)

Yates' correction not used

odds ratio = 2.276 , ( 1.611 , 3.215 )

log-odds ratio = 0.822 , s.e.= 0.176

```
Call:  crosstabs( ~ dia.bp80 + (y > 3))
dia.bp80|(y > 3)
```

	FALSE	TRUE	RowTot1	
0	403	16	419	
	0.962	0.038	0.58	
1	270	31	301	
	0.897	0.103	0.42	
ColTot1	673	47	720	

Test for independence of all factors

Chi^2 = 12.05597 d.f.= 1 (p=0.0005162686)

odds ratio = 2.848 , ( 1.539 , 5.269 )

log-odds ratio = 1.047 , s.e.= 0.314

## Proportional Odds Model

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- model the cumulative indicators:  $Z_{ij} = \mathbf{1}(O_i \leq j)$

$$\begin{aligned}\text{Define } \gamma_{ij} &= P(O_i \leq j) \\ &= E(Z_{ij})\end{aligned}$$

$$\boxed{\text{GLM}} \quad g(\gamma_{ij}) = \beta_{(0,j)} - \mathbf{X}_i \boldsymbol{\beta}$$

- For a single  $j$  this is equivalent to logistic regression when we use a logit link.



- The model with the logit link is called the **Proportional odds model**.
- Another common link is the complementary log-log link,  $g(\gamma) = \log(-\log(1 - \gamma))$ , which is the discrete time proportional hazards model. (more on this later)
- There is an ordering constraint:

$$\beta_{(0,1)} \leq \beta_{(0,2)} \cdots \leq \beta_{(0,C-1)}$$

## Score equations

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The underlying model is the multinomial which yields

$$\frac{\partial \log \mathcal{L}}{\partial \boldsymbol{\beta}} = \sum_i \left( \frac{\partial \boldsymbol{\pi}_i}{\partial \boldsymbol{\beta}} \right)^T \boldsymbol{\Sigma}_i^{-1} (\mathbf{Y}_i - \boldsymbol{\pi}_i)$$

Note:  $\mathbf{L} =$

$$\begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 1 & 1 & 0 & \dots & 0 \\ 1 & 1 & 1 & \dots & 0 \\ \vdots & & & & \\ 1 & 1 & 1 & \dots & 1 \end{bmatrix}$$

## Score equations

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Properties of  $\mathbf{L}$ :

$$\mathbf{L}\mathbf{Y}_i = \mathbf{Z}_i$$

$$\mathbf{L}\boldsymbol{\pi}_i = \boldsymbol{\gamma}_i$$

$$\frac{\partial \log \mathcal{L}}{\partial \boldsymbol{\beta}} = \sum_i \left( \frac{\partial \mathbf{L}\boldsymbol{\pi}_i}{\partial \boldsymbol{\beta}} \right)^T (\mathbf{L}\boldsymbol{\Sigma}_i\mathbf{L}^T)^{-1} \mathbf{L} (\mathbf{Y}_i - \boldsymbol{\pi}_i)$$

$$\frac{\partial \log \mathcal{L}}{\partial \boldsymbol{\beta}} = \sum_i \left( \frac{\partial \boldsymbol{\gamma}_i}{\partial \boldsymbol{\beta}} \right)^T [\text{cov}(\mathbf{Z}_i)]^{-1} (\mathbf{Z}_i - \boldsymbol{\gamma}_i)$$

## Reparameterization of POM

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- There are several ways this model can be parameterized.
- We have used indicators for  $O_{ij} \leq j$  and:

$$\text{logit}(\gamma_{ij}) = \beta_{(0,j)} - \mathbf{X}_i \boldsymbol{\beta}$$

- Alternatively we may model  $Z_{ij}^* = 1(O_{ij} > j)$  and:

$$E(Z_{ij}^*) = 1 - \gamma_{ij} = \mu_{ij}^*$$

$$\begin{aligned} \text{logit}(\mu_{ij}^*) &= -\beta_{(0,j)} + \mathbf{X}_i \boldsymbol{\beta} \\ &= \beta_{(0,j)}^* + \mathbf{X}_i \boldsymbol{\beta} \end{aligned}$$

Ordinal Regression  
Cumulative Link GLM

link = logit

-2\*maxL = 1712.95

Regression Coefficients and S.E.'s

	estimate	S.E.	z
c1	0.1102717	0.09516786	1.158707
c2	-1.5880006	0.11420678	-13.904609
c3	-3.1492179	0.17159607	-18.352506
dia.bp80	0.9425179	0.14279883	6.600319

Ordinal Regression  
Cumulative Link GLM

link = logit

-2\*maxL = 1694.77

Regression Coefficients and S.E.'s

	estimate	S.E.	z
c1	0.64781282	0.081852364	7.914406
c2	-1.07600308	0.088720335	-12.128032
c3	-2.66667489	0.152165220	-17.524865
dia.bp	0.05209068	0.006700984	7.773586

Ordinal Regression  
Cumulative Link GLM

link = logit

-2\*maxL = 1337.79

Regression Coefficients and S.E.'s

	estimate	S.E.	z
c1	0.179575318	0.106663795	1.6835639
c2	-2.374525515	0.142756804	-16.6333614
c3	-4.245398609	0.204729189	-20.7366552
glyc.hemo	0.095083429	0.029752798	3.1957810
log.duration	2.126978406	0.135675906	15.6769058
age.diag	0.009541847	0.010055159	0.9489504
dia.bp	0.045025747	0.007348497	6.1272053

## Ordinal Data Regression

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- Models for ordinal data can be viewed as “simultaneous regressions” for the cumulative indicators  $Z_{ij} = \mathbf{1}(O_i \leq j)$ .
- Probability model is the multinomial.
- Models for ordinal data use the order information but do not assign numbers to the outcome levels. Models are also invariant to collapsing the categories (ie. combine 4th and 5th levels).



## Ordinal Data Regression

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- Models for ordinal data are useful as something intermediate to just dichotomizing the data, or to assigning scores and using linear regression.
- **Fact** For a single binary covariate  $X = 0/1$  the score test using the POM model is the Wilcoxon! (see MN exercise 5.10). Thus, these models can be thought of as models for the rank of the data.

## Models for Multinomial Data

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- Another approach to the analysis of ordered categorical data is to model **conditional** expectations.



Infection in 0-6 months.

Infection in 6-12 months **given** uninfected at 6.

Infection in 12-18 months **given** uninfected at 12.



Salmon dies before point #1.

Salmon dies before point #2 **given** past #1.

Salmon dies before point #3 **given** past #2.

## Multinomial Framework

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Define:

- $Y_{ij} = \mathbf{1}(O_i = j)$
- $\mathbf{Y}_i = \text{vec}(Y_{ij})$
- $H_{ij} = 1 - \sum_{k=1}^{j-1} Y_{ik} \quad H_{i1} = 1$

## Multinomial Framework

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Model:

$$\begin{aligned} E[Y_{ij} | H_{ij} = 1] &= \mu_{ij} \\ &= \frac{\pi_{ij}}{1 - \gamma_{i(j-1)}} \end{aligned}$$

$$\begin{aligned} g(\mu_{ij}) &= \alpha_j + \mathbf{X}_{ij}\boldsymbol{\beta}_j \\ & \quad j = 1, 2, \dots, C - 1 \end{aligned}$$

Note :  $E[Y_{ij} | H_{ij}] = \mu_{ij} \cdot H_{ij}$

**Example:**

	$j = 1, 2, \dots, 5$				
	1	2	3	4	5
$Y_{ij}$	0	0	1	0	0
$H_{ij}$	1	1	1	0	0
$\mu_{ij}$	$\mu_{i1}$	$\mu_{i2}$	$\mu_{i3}$	$\mu_{i4}$	$\mu_{i5}$
$E[Y_{ij}   H_{ij}]$	$\mu_{i1}$	$\mu_{i2}$	$\mu_{i3}$	0	0

## Multinomial – CRM Models

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- Models for  $E(Y_{ij} | H_{ij})$  are sometimes called “continuation ratio models” (Agresti 1990).
- These conditional models are also known as discrete-time survival models, in particular, if we assume that the ordered categories are time intervals,  $\mathcal{G}_j = (t_{j-1}, t_j]$ , and  $O_i$  records the interval that the time,  $T_i$  falls in:

$$O_i = j \Leftrightarrow T_i \in \mathcal{G}_j$$

## Multinomial – CRM Models

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$$\boxed{\text{PH Assumption}} : P(T_i > t) = \exp[-\Lambda(t)] \\ = \exp[-\Lambda_0(t) \exp(\mathbf{X}_i \boldsymbol{\beta})]$$

then

$$E(Y_{ij} | H_{ij} = 1) = \mu_{ij}$$

$$\log(-\log(1 - \mu_{ij})) = \alpha_j + \mathbf{X}_i \boldsymbol{\beta}$$

$$\alpha_j = \log[\Lambda_0(t_j) - \Lambda_0(t_{j-1})]$$

**Note:** The PH model uses a common  $\boldsymbol{\beta}$  rather than a coefficient specific to each time interval,  $\boldsymbol{\beta}_j$ .

## CRM Model

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- The multinomial probability factors:

$$\begin{aligned} P(\mathbf{Y}_i = \mathbf{y}_i) &= \prod_{j=1}^C \pi_{ij}^{y_{ij}} \\ &= P(y_{i1})P(y_{i2} \mid y_{i1})P(y_{i3} \mid y_{i1}, y_{i2}) \dots \\ &\quad \dots P(y_{iC} \mid y_{ik} \ k < C) \end{aligned}$$



## CRM Model

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$$\begin{aligned} P(\mathbf{Y}_i = \mathbf{y}_i) &= \prod_{j=1}^{C-1} \left( \frac{\pi_{ij}}{1 - \gamma_{i(j-1)}} \right)^{y_{ij}} \left( 1 - \frac{\pi_{ij}}{1 - \gamma_{i(j-1)}} \right)^{h_{ij} - y_{ij}} \\ &= \prod_{j=1}^{C-1} \left( \frac{\pi_{ij}}{1 - \gamma_{i(j-1)}} \right)^{y_{ij}} \left( \frac{1 - \gamma_{ij}}{1 - \gamma_{i(j-1)}} \right)^{h_{ij} - y_{ij}} \end{aligned}$$

Note:

$$\text{logit}\left(\frac{\pi_{ij}}{1 - \gamma_{i(j-1)}}\right) = \log\left(\frac{\pi_{ij}}{1 - \gamma_{ij}}\right)$$

Comments:

- This likelihood factorization implies that we obtain the MLE for this model using the pairs  $(Y_{ij}, H_{ij} = 1)$  and treating them as independent Bernoulli random variables.
- For any  $(j, k)$

$$E [(Y_{ij} - \mu_{ij}H_{ij})(Y_{ik} - \mu_{ik}H_{ik})] = 0$$

**Q:** justification for this?

## WESDR Example:

```
#
nsubjects <- nrow( data )
#
wisc.data <- data.frame(
  y = wisc.all.data[, "r.level"],
  glyc.hemo = wisc.all.data[, "glyc.hemo"],
  log.duration = log( wisc.all.data[, "duration" ] ),
  age.diag = wisc.all.data[, "age.diag"],
  dia.bp = wisc.all.data[, "dia.bp"]
)
print( wisc.data[1:5,] )
#
###
### Construct CRM data...
###
#
##### (1) construct the pairs (Y,H)
#
```

```
ncuts <- max(wisc.data$y) - 1
print( paste("ncuts =", ncuts, "\n\n") )
y.crm <- NULL
h.crm <- NULL
id <- NULL
for( j in 1:nsubjects ){
  yj <- rep( 0, ncuts )
  if( wisc.data$y[j] <= ncuts ) yj[ wisc.data$y[j] ] <- 1
  hj <- 1 - c(0,cumsum(yj)[1:(ncuts-1)])
  y.crm <- c( y.crm, yj )
  h.crm <- c( h.crm, hj )
  id <- c( id, rep(j,ncuts) )
}
```

```

##### (2) construct the intercepts
#
level <- factor( rep(1:ncuts, nsubjects ) )
int.mat <- NULL
for( j in 1:ncuts ){
  intj <- rep( 0, ncuts )
  intj[ j ] <- 1
  int.mat <- cbind( int.mat, rep( intj, nsubjects) )
}
dimnames(int.mat) <- list( NULL, paste("Int",c(1:ncuts),sep="") )
#
##### (3) expand the X's
#
glyc.hemo <- rep( wisc.data$glyc.hemo , rep(ncuts,nsubjects) )
log.duration <- rep( wisc.data$log.duration , rep(ncuts,nsubjects) )
age.diag <- rep( wisc.data$age.diag , rep(ncuts,nsubjects) )
dia.bp <- rep( wisc.data$dia.bp , rep(ncuts,nsubjects) )
#
print( cbind( y.crm, h.crm, level, int.mat, glyc.hemo, log.duration,
              age.diag, dia.bp)[1:15,] )
#

```

```
##### (4) drop the H=0 and build dataframe
#
keep <- h.crm==1
wisc.crm.data <- data.frame(
    id = id[keep],
    y = y.crm[keep],
    level = level[keep],
    glyc.hemo = glyc.hemo[keep],
    log.duration = log.duration[keep],
    age.diag = age.diag[keep],
    dia.bp = dia.bp[keep] )
#
print( wisc.crm.data[1:15,] )
```

## Original Data:

	y	glyc.hemo	log.duration	age.diag	dia.bp
1	3	13.7	2.332144	29.9	89
2	2	13.5	2.292535	18.6	90
3	3	13.8	2.747271	28.7	85
4	1	8.4	3.540959	20.1	99
5	3	12.8	3.131137	29.3	84

## Expanded Data:

	id	y.crm	h.crm	level	Int1	Int2	Int3	glyc.hemo
[1,]	1	0	1	1	1	0	0	13.7
[2,]	1	0	1	2	0	1	0	13.7
[3,]	1	1	1	3	0	0	1	13.7
[4,]	2	0	1	1	1	0	0	13.5
[5,]	2	1	1	2	0	1	0	13.5
[6,]	2	0	0	3	0	0	1	13.5
[7,]	3	0	1	1	1	0	0	13.8
[8,]	3	0	1	2	0	1	0	13.8
[9,]	3	1	1	3	0	0	1	13.8
[10,]	4	1	1	1	1	0	0	8.4
[11,]	4	0	0	2	0	1	0	8.4
[12,]	4	0	0	3	0	0	1	8.4
[13,]	5	0	1	1	1	0	0	12.8
[14,]	5	0	1	2	0	1	0	12.8
[15,]	5	1	1	3	0	0	1	12.8



	id	y	level	glyc.hemo	log.duration	age.diag	dia.bp	
	1	1	0	1	13.7	2.332144	29.9	89
	2	1	0	2	13.7	2.332144	29.9	89
	3	1	1	3	13.7	2.332144	29.9	89
	4	2	0	1	13.5	2.292535	18.6	90
	5	2	1	2	13.5	2.292535	18.6	90
	6	3	0	1	13.8	2.747271	28.7	85
	7	3	0	2	13.8	2.747271	28.7	85
	8	3	1	3	13.8	2.747271	28.7	85
	9	4	1	1	8.4	3.540959	20.1	99
	10	5	0	1	12.8	3.131137	29.3	84
	11	5	0	2	12.8	3.131137	29.3	84
	12	5	1	3	12.8	3.131137	29.3	84
	13	6	0	1	13.0	3.258097	21.8	70
	14	6	0	2	13.0	3.258097	21.8	70
	15	6	1	3	13.0	3.258097	21.8	70

## WESDR Models

---

```
#####  
##### Model fitting...  
#####  
#  
options( contrasts="contr.treatment" )  
#  
table( wisc.crm.data$level )  
#  
fit1 <- glm( y ~ glyc.hemo, family=binomial,  
            subset=(as.integer(level)==1), data = wisc.crm.data )  
summary( fit1, cor=F )  
fit2 <- glm( y ~ glyc.hemo, family=binomial,  
            subset=(as.integer(level)==2), data = wisc.crm.data )  
summary(fit2, cor=F )  
fit3 <- glm( y ~ glyc.hemo, family=binomial,
```

```
subset=(as.integer(level)==3), data = wisc.crm.data )
summary(fit3, cor=F )
#
fit4 <- glm( y ~ level + glyc.hemo, family=binomial,
            data = wisc.crm.data )
summary( fit4, cor=F )
fit5 <- glm( y ~ level * glyc.hemo, family=binomial,
            data = wisc.crm.data )

#
anova( fit4, fit5 )
#
```

## Separate fits:

```
table(level)
:  1 :  2 :  3
 720 445 175
```

```
***LEVEL=1
```

```
Coefficients:
```

	Value	Std. Error	t value
(Intercept)	0.22510208	0.38001813	0.5923456
glyc.hemo	-0.05627671	0.02974703	-1.8918429

---

\*\*\*LEVEL=2

Coefficients:

	Value	Std. Error	t value
(Intercept)	1.01503739	0.48744691	2.082355
glyc.hemo	-0.04551101	0.03731596	-1.219613

---

\*\*\*LEVEL=3

	Value	Std. Error	t value
(Intercept)	0.27807196	0.87839180	0.3165694
glyc.hemo	0.05636293	0.06755021	0.8343856

---

**CRM fits:**

	Value	Std. Error	t value
(Intercept)	0.02245317	0.28434528	0.07896444
level: 2	0.92319834	0.12399549	7.44541891
level: 3	1.50031056	0.18751941	8.00082817
glyc.hemo	-0.04008980	0.02184728	-1.83500205

(Dispersion Parameter for Binomial family taken to be 1 )

Null Deviance: 1857.608 on 1339 degrees of freedom

Residual Deviance: 1754.334 on 1336 degrees of freedom

Number of Fisher Scoring Iterations: 3

**CRM fits:**

Analysis of Deviance Table

Response: y

	Terms	Resid.	Df	Resid.	Dev	Test	Df	Deviance
1	level + glyc.hemo		1336	1754.334				
2	level * glyc.hemo		1334	1751.906	+level:glyc.hemo	2	2.428885	

## Summary

---

- Multinomial models use a multivariate response vector to represent the outcome.
- For these models the **mean** ( $\pi_i$ ) determines the **covariance**.
- Proportional odds models consider all possible dichotomizations.
- Continuation ratio models consider an ordered sequence of **conditional** expectations.



References :

McCullagh & Nelder, Chapter 5 *Polytomous Regression*

Ananth C.V. and Kleinbaum D.G. (1997), "Regression models for ordinal responses: A review of methods and applications", *Int J of Epi*, 26: 1323-1333.

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Agresti A. (1999), "Modelling ordered categorical data: recent advances and future challenges", *Statistics in Medicine*, 18: 2191-2207.