What to do today (Mar 29)?

1. *Introduction and Preparation*
2. *Analysis with Binary Variables (Chp 1-2)*
3. *Analysis with Multicategory Variables (Chp 3)*
4. *Analysis with Count Variables (Chp 4)*
5. *Model Selection and Evaluation (Chp 5)*

6. **Additional Topics (Chp 6)**
   - *6.1 Exact inference (Chp 6.2)*
   - *6.2 Revisit to Loglinear and Logistic Models for Contingency Tables: the Loglinear-Logit Connection* (Supplementary)
   - **6.3 Revisit III to GLM and Some Advanced Topics (Chp 5.3, Chp 6.5)**
     - **6.3.1 Revisit III to GLM**
     - **6.3.2 Marginal Modeling**
     - *6.3.3 Mixed Ect Models for Correlated Data*

6.3.1 Revisit III to GLM

GOAL: to study how $Y \leftarrow X_1, \ldots, X_K$?

Generalized Linear Models:

- **Random Component.** response r.v. Y follows a distn with $\mu(x_1, \ldots, x_k) = E(Y|x_1, \ldots, x_k)$ to be examined

- **Systematic Component.** $\alpha + \beta_1 x_1 + \ldots + \beta_K x_K$

  Some x_k can be based on others: e.g. $x_3 = x_1 x_2$.

- **Link Function.** $g(\mu) = \alpha + \beta_1 x_1 + \ldots + \beta_K x_K$

  The link function $g(\cdot)$ links the *random componet* through its mean and the *systematic component*.

Recall the *glm* function in R to conduct a GLM analysis:

$$R\text{: } tmp.out < -glm(Y \sim X*Z, family)$$

family(object,...) in *R* for function *glm*, for example

- binomial(link = "logit")
- poisson(link = "log")
- gaussian(link = "identity") $\Longrightarrow$ *R: e.g. lm(Y∼X*Z)*
- and some others, such as quasipoisson(link = "log") to be studied

6.3.1B Revisit III to GLM: Additional Examples

Probit Regression Model.

To study $Y \leftarrow X, Z$? with binary response $Y = 1$, or 0 and explanatory variables X, Z:

- the *Probit Regression Model (Probit)*:
  - *Randome Component.* r.v. $Y \sim Bernoulli(\pi)$ with $\mu(x,z) = E(Y|X=x, Z=z) = P(Y=1|X=x, Z=z) = \pi(x,z)$ and $V(Y|X=x, Z=z) = \pi(x,z)[1-\pi(x,z)]$
  - *Systematic Component.* $h(x,z) = \alpha + \beta x + \gamma z + \eta xz$, a linear function of x, z, xz
  - *Link Function.* $g : \mu \to probit(\mu)$:
    $probit\big[\mu(x,z)\big] = probit\big[\pi(x,z)\big] = h(x,z)$
    $\Leftrightarrow \pi(x,z) = \Phi(h(x,z))$

$\Phi(\cdot)$ the cumulative distn of $N(0,1)$: e.g. $\Phi(-1.645) = 0.05$ and $\Phi(1.96) = 1 - 0.025$

6.3.1B Revisit III to GLM: Additional Examples

Quasi-Poisson Regression:

- *Randome Component.* r.v. Y with
  $\mu(x,z) = E(Y|X=x, Z=z)$ and
  $V(Y|X=x, Z=z) = \rho\mu(x,z)$
- *Systematic Component.* $h(x,z) = \alpha + \beta x + \gamma z + \eta xz$, a linear function of x, z, xz
- *Link Function.* $g : \mu \to \log(\mu)$:
  $\log\left[\mu(x,z)\right] = h(x,z)$
  $\Leftrightarrow \mu(x,z) = \exp(h(x,z))$

6.3.1C Revisit III to GLM: Final visit to the Horseshoe Crab Study

Data Description.

Obstn	C	S	W	Wt	Sa
1	2	3	28.3	3.05	8
2	3	3	22.5	1.55	0
3	1	1	26.0	2.30	9

- who? $n = 173$ female horseshoe crabs selected by a study
- what?
  - C=color: 1,2,3,4 for light med, medium, dark med and dark (with the distn: 12, 95, 44, 22)
  - S=spine: 1, 2,3 for both good, one or both worn/broken (with the distn: 37, 15, 121)
  - W=width: ranging 21.0 to 33.5cm (with mean, sd: 26.4, 2.1)
  - Wt=weight: ranging 1.2kg to 5.2kg (with mean, sd: 2.44, 0.58)
  - Sa=number of satellites (ranging from 0 to 19)
- why? to explore the association of Sa with other variables
- when and where?

Conduct Regression Analyses

A. Regression with Binary Response

Preparation ... ...

$C <- as.factor(ex.crab[,1]); S <- as.factor(ex.crab[,2]);$
$W <- ex.crab[,3]; Wt <- ex.crab[,4];$
$tmpyA <- ifelse(Sa > 0, 1, 0)$

- **A.1 Logistic Regression**
- **A.2 Probit Regression**
- **A.3 Comparisons**

R : $tmp.outA1a < -glm(tmpyA \sim C + S + W + Wt, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-8.06501	3.92855	-2.053	0.0401	*
C2	-0.10290	0.78259	-0.131	0.8954	
C3	-0.48886	0.85312	-0.573	0.5666	
C4	-1.60867	0.93553	-1.720	0.0855	.
S2	-0.09598	0.70337	-0.136	0.8915	
S3	0.40029	0.50270	0.796	0.4259	
W	0.26313	0.19530	1.347	0.1779	
Wt	0.82578	0.70383	1.173	0.2407	

Null deviance: 225.76 on 172 degrees of freedom
Residual deviance: 185.20 on 165 degrees of freedom

AIC: 201.2

surprising analysis results about the effects of the predictors!

$\Longrightarrow$ the investigation on the possible collinearity ...

Are W and Wt closely correlated?

$\Longrightarrow$ removing Wt from the list of predictors ...

$R : tmp.outA1b < -glm(tmpyA \sim C + S + W, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-11.09953	2.97706	-3.728	0.000193	***
C2	-0.14340	0.77838	-0.184	0.853830	
C3	-0.52405	0.84685	-0.619	0.536030	
C4	-1.66833	0.93285	-1.788	0.073706	.
S2	-0.05782	0.70308	-0.082	0.934453	
S3	0.37703	0.50191	0.751	0.452540	
W	0.45624	0.10779	4.233	2.31e-05	***

Null deviance: 225.76 on 172 degrees of freedom
Residual deviance: 186.61 on 166 degrees of freedom
AIC: 200.61

Is it the model to use?

Model Selection (Variable Selection):

$tmp.outA1c < -glm(tmpyA \sim C * S * W, family = binomial)$
$step(tmp.outA1c)$
Start: AIC=212.44
$tmpyA \sim C * S * W$

	Df	Deviance	AIC
- C:S:W	3	173.67	209.67
$< none >$		170.44	212.44

Step: AIC=209.67
$tmpyA \sim C + S + W + C : S + C : W + S : W$

⋮	⋮	⋮	⋮

$Call : glm(formula = tmpyA \sim C + W, family = binomial(link = \text{“}logit\text{”}))$
Coefficients:

(Intercept)	C2	C3	C4	W
-11.38519	0.07242	-0.22380	-1.32992	0.46796

Degrees of Freedom: 172 Total (i.e. Null); 168 Residual
Null Deviance: 225.8
Residual Deviance: 187.5 AIC: 197.5

Alternative ways of using the color variable?

- C=1,2,3,4 as an ordinal variable?

$glm(formula = tmpyA \sim tmpC + W, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-10.0708	2.8068	-3.588	0.000333	***
tmpC	-0.5090	0.2237	-2.276	0.022860	*
W	0.4583	0.1040	4.406	1.05e-05	***

Null deviance: 225.76 on 172 degrees of freedom
Residual deviance: 189.12 on 170 degrees of freedom
AIC: 195.12

- Group the categories of color into two: dark vs lighter color?

$glm(formula = tmpyA \sim tmpCb + W, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-11.6790	2.6925	-4.338	1.44e-05	***
tmpCb2	-1.3005	0.5259	-2.473	0.0134	*
W	0.4782	0.1041	4.592	4.39e-06	***

Null deviance: 225.76 on 172 degrees of freedom
Residual deviance: 187.96 on 170 degrees of freedom
AIC: 193.96

Report the Regression with $logit\left[\pi(i,w)\right] = \alpha + \beta_i^C + \gamma w$: $i = 1, 2$ for lighter, dark color.

- The fitted model:

$$logit\left[\hat{\pi}(i,w)\right] = \begin{cases} -11.68 + 0.48w & \text{for i=1 (lighter color)} \\ -11.68 - 1.30 + 0.48w & \text{for i=2 (dark color)} \end{cases}$$

or $logit\left[\hat{\pi}(x,w)\right] = -11.68 - 1.30x + 0.48w$ if using the dummy variable $x = 0, 1$ for lighter, dark color.

- Is YesSa positively associated with W in the presence of C?

To conduct a test on $H_0 : \gamma = 0$ vs $H_1 : \gamma > 0$:
$Z = \frac{\hat{\gamma}}{SE_{\hat{\gamma}}}$; $Z_{obs} = 4.59$; $p = 4.39e - 06/2$

An alternative: to compare $M_0 : tmpA \sim Logit(tmpCb)$ vs
$M_1 : tmpA \sim Logit(tmpCb, W)$

This can only test on $H_0 : \gamma = 0$ vs $H_1 : \gamma \neq 0$: (i) fit both M_0 and M_1, (ii) obtain their $G(M_0|M_s) = 214.79$ with df=171, $G(M_1|M_s) = 187.96$ with df=170 $\Rightarrow$ $G(M0|M1) = 214.79 - 187.96$; $df = 1$; $p = 1 - pchisq(26.83, 1) < 0.001$

Report the Regression with $logit\left[\pi(i,w)\right] = \alpha + \beta_i^C + \gamma w$: $i = 1, 2$ for lighter, dark color.

- What is the OR of YesSa comparing ligther vs dark color crab adjusting for W? Give its MLE and an 95% CI.

  $\log OR = \beta_1^C - \beta_2^C$: its MLE is $0 - \hat{\beta}_2^C = 1.30$ with $SE_{\hat{\beta}_2^C} = 0.526$

  $\Longrightarrow$ OR's MLE 3.67 and 95% CI $(1.31, 10.29)$

- Give estimates of the probability of YesSa with lighter and dark colored crabs if their width= 26.3cm (the mean width of the observed crabs') and width=35cm: $\pi(i,w) = \frac{exp(\alpha+\beta_i^C+\gamma w)}{1+exp(\alpha+\beta_i^C+\gamma w)}$

	width=26.3cm		width=35.0cm	
Estimates	lighter (i=1)	dark (i=2)	lighter (i=1)	dark (i=2)
$\hat{\alpha} + \hat{\beta}_i^C + \hat{\gamma} w$	0.90	-0.40	5.06	3.76
(SE)	(0.20)	(0.49)	(0.98)	(1.08)
95% CI	(0.51,1.29)	(-1.37,1.86)	(3.14,6.98)	(1.64,7.18)
$\hat{\pi}(i,w)$	0.71	0.40	0.99	0.98
95% CI	(0.62,0.78)	(0.20, 0.87)	(0.96,1.00)	(0.84,1.00)

$R: tmp.outA2 < -glm(tmpyA \sim tmpCb + W, family = binomial(link = \text{“}probit\text{”}))$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-6.98838	1.54195	-4.532	5.84e-06	***
tmpCb2	-0.76494	0.31341	-2.441	0.0147	*
W	0.28637	0.05924	4.834	1.34e-06	***

Null deviance: 225.76 on 172 degrees of freedom
Residual deviance: 187.72 on 170 degrees of freedom

AIC: 193.72

MLE and 95% CI for the prob of YesSa with lighter colored crabs and width=26.3cm:

- $\hat{\pi}(1, 26.3) = pnorm(\hat{\alpha} + \hat{\beta}_1^C + \hat{\gamma}26.3) = 0.706$
- CI: (0.624, 0.779)

B. Regression with Count Response

- **B.1 Poisson Regression**
- **B.2 Quasi-Poisson Regression**
- **B.3 Comparisons**

Preparation ... ...

$C < -as.factor(ex.crab[, 1]); S < -as.factor(ex.crab[, 2]);$
$W < -ex.crab[, 3]; Wt < -ex.crab[, 4];$
$Sa < -round(ex.crab[, 5]);\ tmpyB < -Sa$

$R : tmp.outB1a < -glm(tmpyB \sim C + S + W, family = poisson)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-2.54385	0.62426	-4.075	4.60e-05	***
C2	-0.22158	0.16789	-1.320	0.1869	
C3	-0.46036	0.19554	-2.354	0.0186	*
C4	-0.48544	0.22824	-2.127	0.0334	*
S2	-0.13879	0.21269	-0.653	0.5141	
S3	0.02363	0.11729	0.201	0.8403	
W	0.14596	0.02189	6.669	2.58e-11	***

Null deviance: 632.79 on 172 degrees of freedom
Residual deviance: 558.63 on 166 degrees of freedom
AIC: 927.93

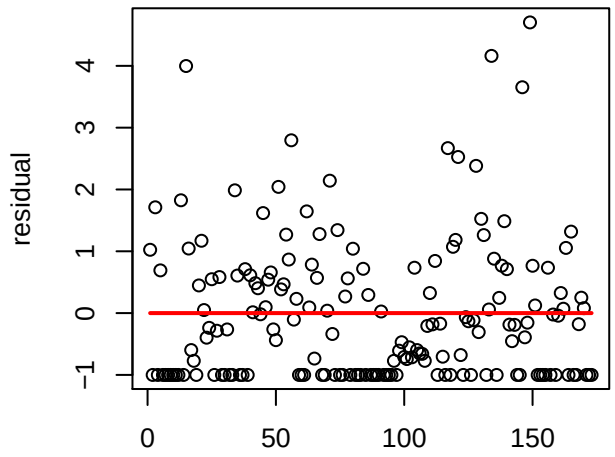
Alternative ways of using the color variable?

$R : tmp.outB1c < -glm(tmpyB \sim tmpC + W, family = poisson)$

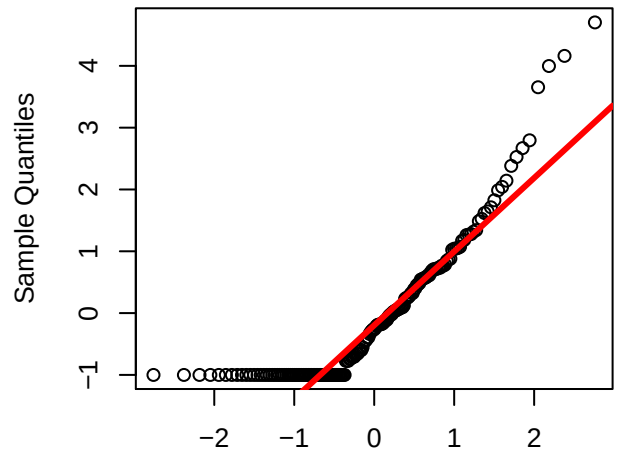
	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-2.51998	0.61063	-4.127	3.68e-05	***
tmpC	-0.16940	0.06184	-2.739	0.00616	**
W	0.14957	0.02068	7.233	4.72e-13	***

Null deviance: 632.79 on 172 degrees of freedom
Residual deviance: 560.20 on 170 degrees of freedom
AIC: 921.5

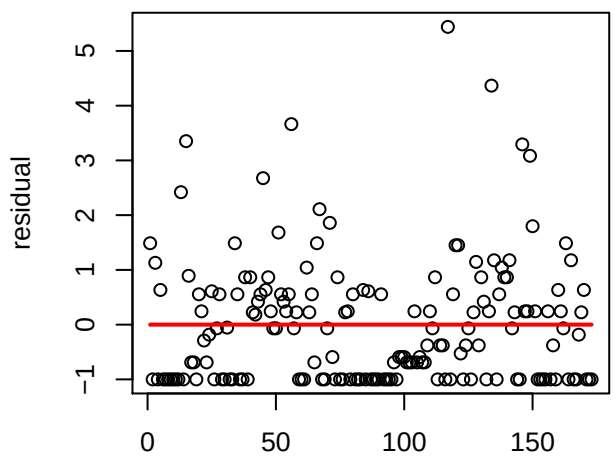
Model Checking: Residual Plots:



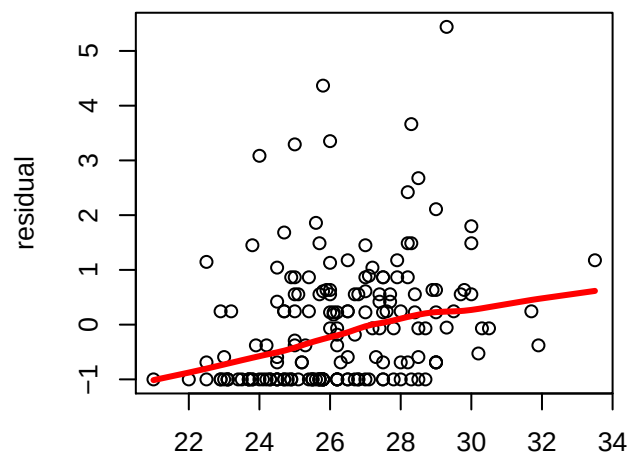
(1) Residuals with outB1c



(2) outB1c residual qqnorm



(3) Residuals with outB1c−W



(4) Residuals with outB1c−W vs W

What if the Poisson assumption is not appropriate?

R : $tmp.outB2a < -glm(tmpyB \sim tmpC + W, family = quasipoisson(link = \text{“}log\text{”}))$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-2.51998	1.09722	-2.297	0.0229	*
tmpC	-0.16940	0.11112	-1.524	0.1292	
W	0.14957	0.03716	4.025	8.55e-05	***

(Dispersion parameter for quasipoisson family taken to be 3.228764)

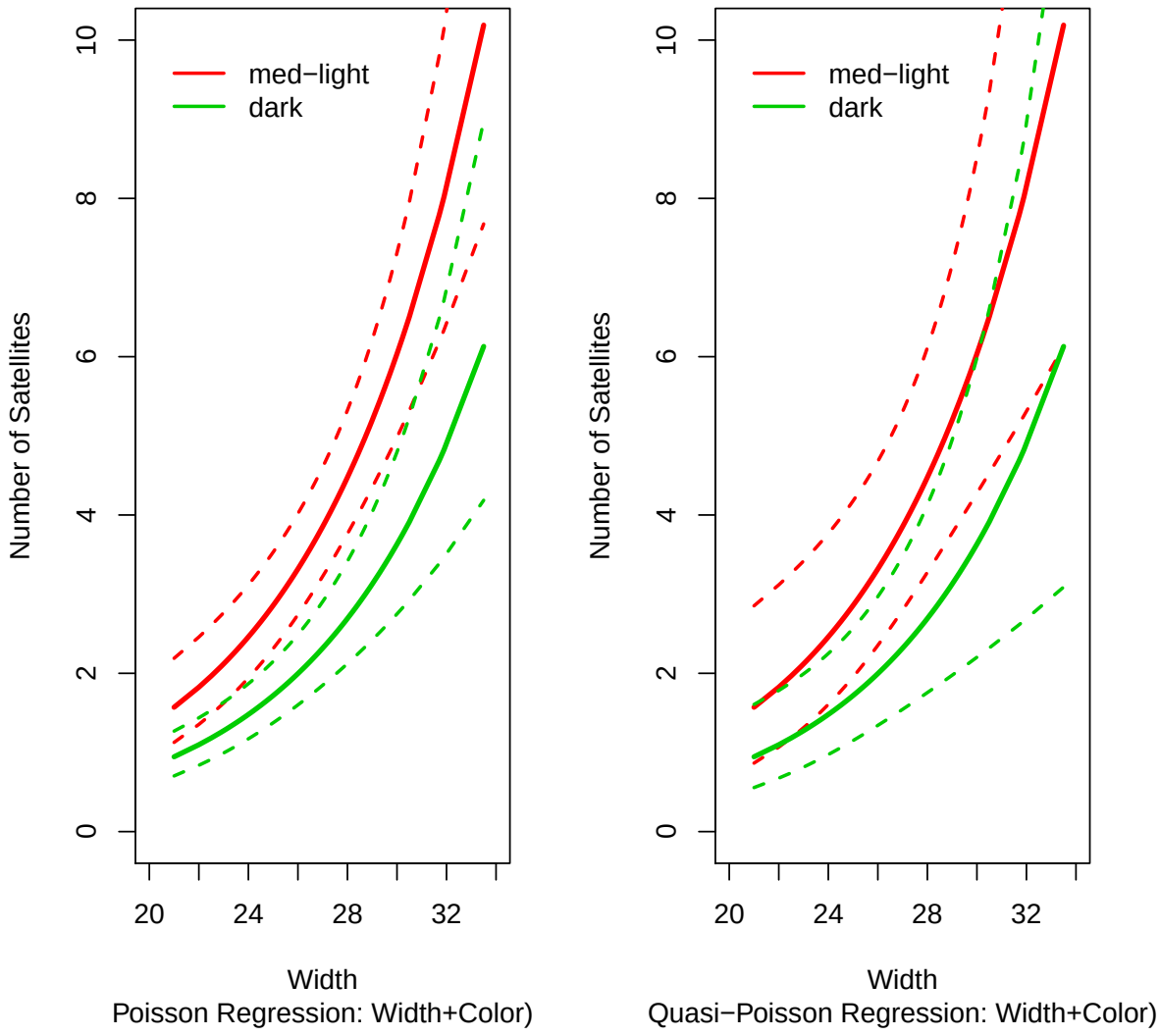
Null deviance: 632.79 on 172 degrees of freedom

Residual deviance: 560.20 on 170 degrees of freedom

AIC: NA

Comparisons between Poisson vs Quasi-Poisson:

- estm for the parameters: the same
- estm for the SE of the parameter estimators: different when the counts are overdispersed
  - Poisson Regression: under-estm the SE



6.3.2A Marginal Modeling: Quasi-Score

Recall *inference with GLM* ...

A. Modelling:

- Assume a GLM model,
  - **Random Component.** response r.v. $Y|X = x, Z = z \sim f(y|x, z)$ with $\mu(x, z) = E(Y|X = x, Z = z)$
  - **Systematic Component.** $h(x, z) = \beta_0 + \beta_1 x + \beta_2 z$
  - **Link Function.** $g(\mu) = h(x, z)$
- That is, assume $Y|X = x, Z = z \sim f(y|\mu) = f(y|x, z; \beta_0, \beta_1, \beta_2)$

B. Data: $\{(y_i, x_i, z_i) : i = 1, \ldots, n\}$ from n indpt individuals

C. Statistical Inference with GLM: the likelihood-based methods

What if we can't confidently specify response r.v.

$Y|X = x, Z = z \sim f(y|x, z)$**?**

If, instead, we'd like to assume $Var(Y|X = x, Z = z) = l(\mu(x, z))$, such as $\phi\mu(x, z)$ in the Quasi-Poisson case. $\Longrightarrow$ **Moment (Marginal) Modeling**

What if the observations are not indpt?

6.3.2B Marginal Modeling: GEE Approach

A. Modelling: Assume r.v. Y with $\mu(x,z) = E(Y|X=x, Z=z)$

B. Data: $\{(y_{ij}, x_{ij}, z_{ij}) : j = 1, \ldots, J_i; i = 1, \ldots, n\}$ from n indpt individuals: n indpt clusters of observations

C. GEE approach:

- R : $gee(formula, id, data, family, corstr)$:
  - id: identifies the clusters
  - family=gaussian, binomial, poisson, Gamma, and quasi
  - corstr: the covariance structure of the response observations within a cluster, such"independence", "fixed", "stat_M_dep", "non_stat_M_dep", "exchangeable", "AR-M" and "unstructured"
- An alternative function R : $geeglm()$

Example. Alcohol, Cigarette, and Marijuana Use for High School Seniors, by Gender (G) and Race (R)

		Marijuana Use (M)							
		White				Other			
		Female		Male		Female		Male	
Alcohol Use (A)	Cigarette Use (C)	Yes	No	Yes	No	Yes	No	Yes	No
Yes	Yes	405	268	453	228	23	23	30	19
	No	13	218	28	201	2	19	1	18
No	Yes	1	17	1	17	0	1	1	8
	No	1	117	1	133	0	12	0	17

the total number of subjects: n=2276

- How are A, C, M associated?
  previous example with a partial table
- How are A,C,M associated, adjusting for R (race) and G (gender)? See the following ...

Step 1. Preliminary Analysis

- 1.1. Loglinear analysis:

- variable selection
  - starting with $(ACGMR)$; variable selection using $R : step()$ $\Longrightarrow$ (ACGR, AM,CM,GM,MR)
  - further variable selection with (ACG,ACR, AGR, CGR, AM,CM,GM,RM)? $\Longrightarrow$ (ACR, AG, AM,CM,GM,MR)
- analysis outcome with the selected model

$R : tmp.out1 < -glm(counts \sim (AUse * CUse * Race + AUse * Gender + AUse * MUse + CUse * MUse + MUse * Gender), data = Table713, family = poisson)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	5.97802	0.04847	123.323	$<$ 2e-16	***
AUseno	-5.87657	0.46542	-12.626	$<$ 2e-16	***
CUseno	-3.03133	0.15235	-19.898	$<$ 2e-16	***
Raceother	-2.65694	0.10614	-25.033	$<$ 2e-16	***
Gendermale	0.14457	0.06473	2.233	0.025522	*
MUseno	-0.38955	0.07089	-5.495	3.9e-08	***
AUseno:CUseno	2.20630	0.19227	11.475	$<$ 2e-16	***
AUseno:Raceother	1.37601	0.37288	3.690	0.000224	***
CUseno:Raceother	0.21459	0.19606	1.095	0.273716	
AUseno:Gendermale	0.29852	0.12743	2.343	0.019147	*
AUseno:MUseno	3.00592	0.46484	6.467	1.0e-10	***
CUseno:MUseno	2.84789	0.16384	17.382	$<$ 2e-16	***
Gendermale:MUseno	-0.26929	0.09039	-2.979	0.002891	**
AUseno:CUseno:Raceother	-1.09579	0.45240	-2.422	0.015428	*

Null deviance: 4818.051 on 31 degrees of freedom
Residual deviance: 15.154 on 18 degrees of freedom

AIC: 179.39

$R : tmp.out1b < -glm(counts \sim (AUse * CUse * Race + AUse * Gender + AUse * MUse + CUse * MUse + MUse * Gender), data = Table713, family = quasipoisson)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	5.97802	0.04266	140.130	$<$ 2e-16	***
AUseno	-5.87657	0.40960	-14.347	2.71e-11	***
CUseno	-3.03133	0.13407	-22.609	1.15e-14	***
Raceother	-2.65694	0.09341	-28.445	$<$ 2e-16	***
Gendermale	0.14457	0.05697	2.538	0.020619	*
MUseno	-0.38955	0.06238	-6.244	6.86e-06	***
AUseno:CUseno	2.20630	0.16921	13.039	1.31e-10	***
AUseno:Raceother	1.37601	0.32816	4.193	0.000547	***
CUseno:Raceother	0.21459	0.17254	1.244	0.229558	
AUseno:Gendermale	0.29852	0.11214	2.662	0.015883	*
AUseno:MUseno	3.00592	0.40909	7.348	8.05e-07	***
CUseno:MUseno	2.84789	0.14419	19.751	1.20e-13	***
Gendermale:MUseno	-0.26929	0.07955	-3.385	0.003298	**
AUseno:CUseno:Raceother	-1.09579	0.39814	-2.752	0.013108	*

(Dispersion parameter for quasipoisson family taken to be 0.7745045)

AIC: NA

- 1.2. Logistic analysis: using $A \sim logit(CR, G, M)$

$R : tmp.out12 < -glm(AUse \sim CUse * Race + Gender + MUse,$
$weight = counts, data = Table713, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-5.8248	0.4659	-12.501	$<$ 2e-16	***
CUseno	2.1937	0.1928	11.377	$<$ 2e-16	***
Raceother	1.2046	0.3884	3.102	0.00192	**
Gendermale	0.2677	0.1364	1.963	0.04967	*
MUseno	2.9831	0.4651	6.414	1.42e-10	***
CUseno:Raceother	-0.9500	0.4675	-2.032	0.04217	*

the estimated log(OR) of using A comparing using M vs not:

- from tmp.out12: $\hat{\beta}_2^M - \hat{\beta}_1^M = 2.98$
- from tmp.out1: $\hat{\lambda}_{22}^{AM} + \hat{\lambda}_{11}^{AM} - \hat{\lambda}_{21}^{AM} - \hat{\lambda}_{21}^{AM} = 3.01$

Step 2. Marginal analysis with a newly defined response

- Defintion.
  - "Response"=using substance ###yes=1; no=0
  - "Type"=the type of substance ###1,2,3 for A,C,M

    alternatively, using two dummy variables S1=1,0 for using A or not, and S2=1,0 for using C or not (as in Agresti, 1996)
- Logistic Regression: viewing all observations indpt
  - variable selection from $Response \sim logit(G * R * Type)$ to $Response \sim logit(G * Type, R)$
  - analysis outcome ... ...

$R : tmp.out2 < -glm(Response \sim Gender * Type + Race,$
$data = Table713dataC, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	1.90766	0.08854	21.545	$<$ 2e-16	***
Gender2	-0.16643	0.12004	-1.386	0.1656	
Type2	-1.21857	0.10835	-11.247	$<$ 2e-16	***
Type3	-2.29661	0.10724	-21.416	$<$ 2e-16	***
Race2	-0.40701	0.10010	-4.066	4.78e-05	***
Gender2:Type2	0.15247	0.14910	1.023	0.3065	
Gender2:Type3	0.36862	0.14716	2.505	0.0123	*
	Null deviance: 8883.1 on 6827 degrees of freedom				
	Residual deviance: 7876.4 on 6821 degrees of freedom				
AIC: 7890.4					

$R : tmp.out2b < -glm(Response \sim Gender * S1 + Gender * S2 + Race, data = Table713dataC, family = binomial)$

	Estimate	Std. Error	z value	$Pr(>\|z\|)$	
(Intercept)	-0.38895	0.06147	-6.327	2.49e-10	***
Gender2	0.20219	0.08515	2.374	0.0176	*
S1	2.29661	0.10724	21.416	< 2e-16	***
S2	1.07804	0.08788	12.267	< 2e-16	***
Race2	-0.40701	0.10010	-4.066	4.78e-05	***
Gender2:S1	-0.36862	0.14716	-2.505	0.0123	*
Gender2:S2	-0.21614	0.12277	-1.761	0.0783	.

Null deviance: 8883.1 on 6827 degrees of freedom

Residual deviance: 7876.4 on 6821 degrees of freedom

AIC: 7890.4

Step 3. GEE analysis with the newly defined response

- Logistic Regression, adjusting for the possible correlation among observations from the same student
  - $n = 2276$ students (clusters): ID used for diff students
  - each student has 3 response obstns:
    working correlation: "exchangable"
    $cor(Y_{iA}, Y_{iC}) = cor(Y_{iA}, Y_{iM}) = cor(Y_{iC}, Y_{iM}) = \rho$
- R : library(gee) $\rightarrow$ gee; library(geepack) $\rightarrow$ geeglm

$R : tmp.out3 < -gee(Response \sim Race + Gender * Type, id = ID,$
$data = Table713dataC, family = binomial, corstr = \text{“}exchangeable\text{”})$

	Estimate	Naive S.E	Naive z	Robust S.E.	Robust z
(Intercept)	1.9059457	0.08876452	21.471931	0.08892841	21.432360
Race2	-0.3826952	0.13561541	-2.821915	0.13545120	-2.825336
Gender2	-0.1686674	0.11996805	-1.405936	0.11988703	-1.406886
Type2	-1.2181782	0.08290443	-14.693765	0.08289060	-14.696216
Type3	-2.2956989	0.08237034	-27.870457	0.09056542	-25.348515
Gender2:Type2	0.1523329	0.11372451	1.339490	0.11309395	1.346958
Gender2:Type3	0.3679203	0.11273372	3.263622	0.12163124	3.024883
Working Correlation					
1.0000000	0.4376341	0.4376341			
0.4376341	1.0000000	0.4376341			
0.4376341	0.4376341	1.0000000			

$R : tmp.out3b < -geeglm(Response \sim Race + Gender * Type, id = ID,$
$data = Table713dataC, family = binomial, corstr = \text{“}exchangeable\text{”})$

	Estimate	Std.err	Wald	$Pr(>\|W\|)$	
(Intercept)	1.90594	0.08893	459.346	< 2e-16	***
Race2	-0.38269	0.13545	7.982	0.00472	**
Gender2	-0.16867	0.11989	1.979	0.15947	
Type2	-1.21818	0.08289	215.979	< 2e-16	***
Type3	-2.29570	0.09057	642.548	< 2e-16	***
Gender2:Type2	0.15233	0.11309	1.814	0.17799	
Gender2:Type3	0.36792	0.12163	9.150	0.00249	**

Estimated Scale Parameters:

	Estimate	Std.err
(Intercept)	0.9988	0.02859

Correlation: Structure = exchangeable Link = identity

Estimated Correlation Parameters:

	Estimate	Std.err
alpha	0.4376	0.02072

Number of clusters: 2276 Maximum cluster size: 3

$R : tmp.out32 < -gee(Response \sim Race + Gender * S1 + Gender * S2, id = ID,$
$data = Table713dataC, family = binomial, corstr = \text{“}exchangeable\text{”})$

	Estimate	Naive S.E	Naive z	Robust S.E.	Robust z
(Intercept)	-0.3898	0.06179	-6.308	0.06186	-6.300
Race2	-0.3827	0.13562	-2.822	0.13545	-2.825
Gender2	0.1993	0.08512	2.341	0.08511	2.341
S1	2.2957	0.08237	27.870	0.09057	25.349
S2	1.0775	0.06591	16.349	0.06080	17.723
Gender2:S1	-0.3679	0.11273	-3.264	0.12163	-3.025
Gender2:S2	-0.2156	0.09207	-2.342	0.08416	-2.562
Working Correlation					
1.0000000	0.4376341	0.4376341			
0.4376341	1.0000000	0.4376341			
0.4376341	0.4376341	1.0000000			

What will we study next?

1. *Introduction and Preparation*
2. *Analysis with Binary Variables (Chp 1-2)*
3. *Analysis with Multicategory Variables (Chp 3)*
4. *Analsyis with Count Response (Chp 4)*
5. *Model Selection and Evaluation (Chp 5)*
6. **Additional Topics (Chp 6)**
   - *6.1 Exact Inference (Chp 6.2)*
   - *6.2 Revisit to Loglinear and Logistic Models for Contingency Tables: the Loglinear-Logit Connection*
   - **6.3 Revisit III to GLM and Advanced Topics (Chp 5.3, Chp 6.5)**
     - *6.3.1 Revisit III to GLM*
     - *6.3.2 Marginal Modeling: Quasi-Score, Generalized Estimating Equation (GEE)*
     - **6.3.3 Mixed Effect Models for Correlated Data**