#### **Epidemiology Models**

- i. General:  $E[\#events] = Rate \times PT$
- ii. Specific way that rates are interrelated (form of 'rate model')
  - (a) (Additive, Rate Difference):  $Rate = Rate_0 + \beta_1 X_1 + \beta_2 X_2 \dots$
  - (b) (Multiplicative, Rate Ratio):  $Rate = Rate_0 \times \exp\{\beta_1 X_1 + \beta_2 X_2 \dots\}$ 
    - (or, equivalently, .....):  $\log(Rate) = \log(Rate_0) + \beta_1 X_1 + \beta_2 X_2 \dots$

#### Statistical Fitting of these Models

- i. General:  $E[\#events] = Rate \times PT$
- ii. Specifically, how model is implemented in statistical packages: In both instances, expand the  $Rate \times PT$  product
  - (a) (Add.):  $E[\#events] = \{Rate_0 + \beta_1 X_1 + \beta_2 X_2 \dots\} \times PT$

 $E[\#events] = Rate_0 \times \underline{PT} + \beta_1 \times X_1 \times PT + \beta_2 \times X_2 \times PT \dots$ 

(specify 'no-intercept'; in  $\mathbb{R}$ ,  $\#events \sim -1 + ...,$ )

(b) (Mult):  $E[\#events] = Rate_0 \times \exp\{\beta_1 X_1 + \beta_2 X_2 \dots\} \times PT$ 

 $\log\{E[\#events]\} = \log(Rate_0) + \beta_1 \times X_1 + \beta_2 \times X_2 \dots + \log(PT)$ 

(use log(PT) as 'offset'; cf worked e.g.'s for R / SAS code)

1 Rate : no. of cases / {amount of experience (P-T)}

- Inference Model: Poisson distribution for numerator.
- Déjà: Exact (discrete distrn.) & Gaussian approximations
- New: Regression Approach:

"Usual" Linear model : (*not appropriate*) E[cases] = rate  $\times$  Denominator × Denominator = "No-intercept" model (Gaussian variation around line) # Ayas et al data on PI's in Residents ## Incidence, Overall cases=c(498); InternMonths=c(17003); ## regression through origin, Gaussian variation around mean [true line] summary( lm(cases ~ -1+InternMonths) ) Residuals: ALL 1 residuals are 0: no residual degrees of freedom! Coefficients: Estimate Std. Error t value Pr(>|t|)InternMonths 0.02929 NA NA NA Residual standard error: NaN on 0 degrees of freedom Multiple R-Squared: 1, Adjusted R-squared: NaN F-statistic: NaN on 1 and 0 DF, p-value: NA

Estimate, namely 0.02929 cases/InternMonth is sensible. But : no df with which to calculate SE or CI • New: Regression Approach: "Generalized" Linear model : (Poisson variation) = rate × Denominator E[cases] \_ × Denominator same "no-intercept" model, but Poisson variation summary(qlm(cases ~ -1 + InternMonths))family = poisson(link=identity))) Deviance Residuals: [1] 0 Coefficients: Estimate Std. Error z value Pr(>|z|)InternMonths 0.029289 0.001312 22.32 <2e-16 --rate--(Dispersion parameter for poisson family taken to be 1) Null deviance: Inf on 1 df Residual deviance: 3.1086e-15 on 0 df AIC: 10.049 Check: SE[rate] = sqrt[#cases) / Denominator = sgrt[498] / 17003 = 0.001312

## • Since rates > 0; safer to model (natural) log of the rate

E[cases]	= rate	<del>)</del>	×	Denominator
log [ E[cases] ]	= log{ı	rate}	+	log[ Denominator ]
log [ µ     ]	=		+	log[ Denominator ]
log [ µ     ]	=	0	+	1 × log[ Denominator ]
	=	0	+	1 × log[ Denominator ]

(no need to estimate  $_1$ ; already know  $_1 == 1$ )

in this instance, log[ Denominator ] is an "offset"

To model log [ $\mu$ | x], use log "*link*" (default link for Poisson)

<u>Canonical links</u> (Binomial : logit; Poisson: log) ensure that whatever the value of the linear predictor, any fitted proportion will be between 0 and 1, and any rate (no. cases) between 0 and infinity.

# "Generalized" Linear model : (Poisson variation, log link)

```
summary( glm(cases ~ 1, family=poisson,
             offset=log(InternMonths) ) )
Deviance Residuals: [1] 0
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) <u>-3.53055</u>
                      0.04481* -78.79
                                           <2e-16
             log[ rate ]
        log[498/17003]
    i.e.,
(Dispersion parameter for poisson family taken to be 1)
    Null deviance: 1.0747e-13 on 0 df
Residual deviance: 1.0747e-13 on 0 df
                                           AIC: 10.049
*Check: SE[log rate] = sqrt[ 1 / #cases ]
                    = sqrt[ 1 / 498 ] = 0.04481
```

Note that we are able to calculate an SE for the estimate of the rate (previous page] and for the estimate of the log rate, even though we have no df with which to estimate the residual variation around he line (the line goes through our one data point). We are able to do this because the variance of a Poisson random variable is equal to the mean of the random variable. So, since the fitted mean no. of cases is 498, the model is able to provide an estimate of how much variation there would be if the mean were indeed 498, ie SD = sqrt[498]. The SE 'borrowed from' the model' is called a "model-based" SE.

In the usual regression with Gaussian variation, (i) the variance is estimated separately, using the mean of the squared residuals and (ii) the variance about the (true) line of means is assumed to be the same at all values of x. The Poisson model better reflects the variability of counts: the variation is higher when the expected (or average) count is higher (but the <u>cv</u> is smaller, the larger the count ie  $cv = /\mu = sqrt[\mu]/\mu = 1/sqrt[\mu]$ .

### **Comparison of 2 Rates**

```
• Rate difference / Ratio•

<u>Example</u>

Extended Periods (coded 'X' = 1)

35 percutaneous injuries in 26667 opportunities

vs.

Non-Extended Periods (coded 'X' = 0)
```

```
46 percutaneous injuries in 60763 opportunities Regression framework for rate difference (RD)
```

```
observed rate when X = 0 (reference category)
```

 $b_0 = rate[0] = 46 / 60763 = 0.0007570$ 

observed rate difference, rd

$$rd = 35/26667 - 46 / 60763 = 0.0005554$$

In general (single, binary x)

RATE 
$$\mid X = RATE_0 + RD \times X$$

= B<sub>0</sub> + B<sub>1</sub>  $\times$  X

So...

$$E[ \#CASES | X ] = RATE_{x} \times PT$$
$$= ( B_{0} + B_{1} \times X) \times PT$$
$$= B_{0} \times PT + B_{1} \times X \times PT$$
$$= B_{0} \times Z_{0} + B_{1} \times Z_{1}$$

This is a regression with 2 terms ( $z_0 \& z_1$ ), and no intercept

# cases=c(35,46); PT=c(26667,60763); e=c(1,0); ePT = e\*PT; ds <- data.frame(cases=cases, opps=PT, extended=e,</pre> (same

Rate difference (rd), and CI for RD, via regression framework

extended.opps = ePT);

ds

cases	aqqo	extended	extended.opps
-------	------	----------	---------------

1	35 26667	1	26667
2	46 60763	0	0

attach(ds)

# regression to obtain rate difference

#### 

Deviance Residuals: [1] 0 0

#### Coefficients:

Estimate Std. Error z value Pr(>|z|) opps 0.0007570 0.0001116 6.782 1.18e-11 \*\*\* extended.opps 0.0005554 0.0002483 2.237 0.0253 \* ---Signif. codes: 0 `\*\*\*' 0.001 `\*\*' 0.01 `\*' 0.05 `.' 0.1 ` ' 1 (Dispersion parameter for poisson family taken to be 1)

Null deviance: Inf on 2 df Residual deviance: 1.3323e-15 on 0 df AIC: 15.068

\*Check: SE[rate difference] , as in Rothman,

= sqrt[ Var[rate<sub>1</sub>] + Var[rate<sub>0</sub>] ] = 0.0002483

# Regression framework for rate ratio (RR) [2 Rates]

(same, e.g., ignoring, for now, the self-paired structure)

```
observed rate when X = 0 (reference category)
```

 $b_0 = rate[0] = 46 / 60763 = 0.0007570$ 

observed rate ratio, rr

$$rr = (35/26667) / (46/60763) = 1.73$$

In general

RATE | 
$$X = RATE_0 \times RR$$
 if  $X=1$   
RR if  $X=1$ 

=  $RATE_0 \times exp[log[RR] \times X]$ 

$$log[RATE | X] = log[RATE_0] + log[RR] \times X$$
$$= B_0 + B_1 \times X$$

So...

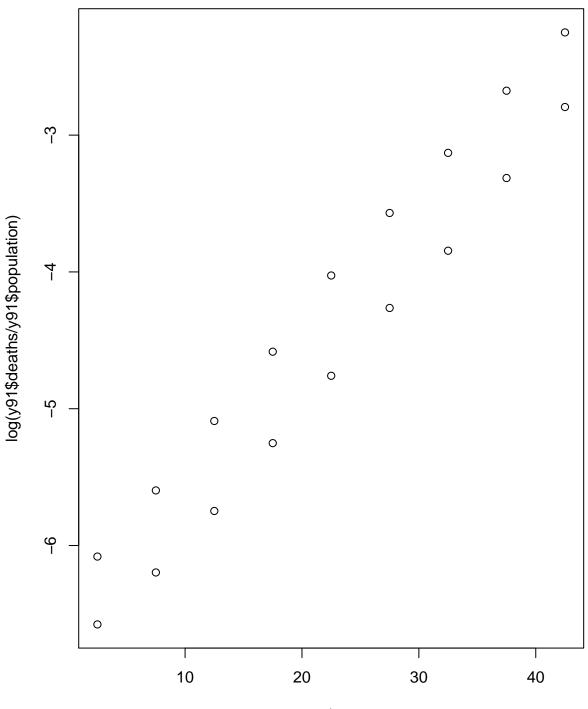
 $E[ \#CASES | X ] = RATE_{x} \times PT$   $log[ E[ \#CASES | X ] ] = log[RATE_{x}] + log[PT]$   $= B_{0} + B_{1} \times X + log[PT]$   $= B_{0} + B_{1} \times X + 1 \times log[PT]$ "offset"

(an "offset" is a term whose coefficient is KNOWN to be 1)

regression models for 'event rate' data

```
Rate ratio (rr), and CI for RR, via regression framework
                                                             Rates & Rate ratios: multiple regression [Many Rates]
                                                             Example: age-specific death rates, male/female 1991, Québec.
# to obtain rate ratio [ log.opps = log(opps) ]
                                                             ds=read.table("quedata.txt",header=T)
summary(glm(cases ~ extended,
                                                             ds7191=ds[(ds$age > 40) & (ds$age < 85) & (
    family=poisson(link=log*),offset=log.opps))
                                                             (ds$year==1971) | (ds$year==1991)),] ;attach(ds7191)
Deviance Residuals:
                                                             # age and sex specific death rates '91
[1] 0 0
                                                             y91=ds[(ds$age > 40) & (ds$age < 85 ) & (ds$year==1991) ,]</pre>
Coefficients:
                                                             y91$age=y91$age - 40
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -7.1861
                         0.1474 -48.739
                                          <2e-16 ***
                                                             (y91m$deaths/y91m$population) / (y91f$deaths/y91f$population)
extended
              0.5503
                         0.2243
                                  2.453
                                          0.0142 *
                                                             1.64 1.82 1.93 1.95 2.08 2.00 2.04 1.89 1.72
_ _ _
                                                             mean 1.90
Signif. codes: 0 `***' 0.001 `**' 0.01 `*' 0.05 `.' 0.1 ` ' 1
                                                             plot(y91$age, log(y91$deaths / y91$population)) next page
(Dispersion parameter for poisson family taken to be 1)
                                                             summary( glm(deaths ~ age + male, family=poisson,
                                                                            offset=log(population),data=y91) )
    Null deviance: 5.8023e+00 on 1 df
Residual deviance: -3.7748e-15 on 0 df AIC: 15.068
                                                             Coefficients:
                                                                           Estimate Std. Error z value Pr(>|z|)
                                                             (Intercept) -6.9030313 0.0172228 -400.81
                                                                                                         <2e-16 ***
                                                                                                         <2e-16 ***
                                                             age
                                                                          0.0956970 0.0004896 195.47
                                                                          0.6506765 0.0106740
                                                                                                 60.96
                                                                                                         <2e-16 ***
*Check:
                                                             male
                                                             rr = exp[0.0956970] = 1.10 rr = exp[0.6506765] = 1.91
            = \log[rate_0] = \log[46/60763]
 -7.1861
                                                                 Null deviance: 47005.299 on 17 df
                                                             Residual deviance:
                                                                                   63.095 on 15 df AIC: 234.73
 0.5503
            = log[rateRatio]
                                                             summary( glm(deaths ~ age + male + age*male,
                                                                family=poisson, offset=log(population),data=y91)
            = \log[(35/26667) / (46/60763)]
                                                             )
 So, rateratio = \exp[\log \operatorname{rateRatio}] = \exp[0.5503] = 1.73
                                                             Coefficients:
                                                                           Estimate Std. Error z value Pr(>|z|)
                                                                                                          <2e-16 ***
      SE[log of rate ratio], as in Rothman,
                                                             (Intercept) -6.9308474 0.0256471 -270.239
                                                                          0.0965921 0.0007816 123.579
                                                                                                          <2e-16 ***
                                                             aqe
            = sqrt[1/35 + 1/46] = 0.2243
                                                                                                          <2e-16 ***
                                                             male
                                                                          0.6952540 0.0321127
                                                                                                 21.650
                                                                         -0.0014773 0.0010029 -1.473
                                                             age:male
                                                                                                           0.141
95% Cl for log[RateRatio]: 0.5503 +/- 1.96 × 0.2243
                                                             Residual deviance:
                                                                                   60.923 on 14 df AIC: 234.56
95% Cl for RateRatio: exp[ 0.5503 +/- 1.96 × 0.2243 ]
                                                             Male and female death rates are 'close to proportional'
                                                             [see 'multiplicative' model of Clayton & Hills, Table 22.5 Ch 22 ]
* no need to specify, as Log is default link for Poisson
```

upper=male; age=age-40





# Male circumcision for HIV prevention in men in Rakai, Uganda: a randomised trial: The Lancet Feb 25 2007

Ronald H Gray, Godfrey Kigozi, David Serwadda, Frederick Makumbi, Stephen Watya, Fred Nalugoda, Noah Kiwanuka, Lawrence H Moulton, Mohammad A Chaudhary, Michael Z Chen, Nelson K Sewankambo, Fred Wabwire-Mangen, Melanie C Bacon, Carolyn F M Williams, Pius Opendi, Steven J Reynolds, Oliver Laeyendecker, Thomas C Quinn, Maria J Wawer

#### Summary

<u>Background</u> Ecological and observational studies suggest that male circumcision reduces the risk of HIV acquisition in men. Our aim was to investigate the effect of male circumcision on HIV incidence in men.

<u>Methods:</u> 4996 uncircumcised, HIV-negative men aged 15–49 years who agreed to HIV testing and counselling were enrolled in this randomised trial in rural Rakai district, Uganda. Men were randomly assigned to receive immediate circumcision (n=2474) or circumcision delayed for 24 months (2522). HIV testing, physical examination, and interviews were repeated at 6, 12, and 24 month follow-up visits. The primary outcome was HIV incidence. Analyses were done on a modified intention-to-treat basis. This trial is registered with ClinicalTrials.gov, with the number NCT00425984.

<u>Findings</u>: Baseline characteristics of the men in the intervention and control groups were much the same at enrolment. Retention rates were much the same in the two groups, with 90–92% of participants retained at all time points. In the modified intention-to-treat analysis, HIV incidence over 24 months was 0.66 cases per 100 person-years in the intervention group and 1.33 cases per 100 person-years in the control group (estimated efficacy of intervention 51%, 95% CI 16–72; p=0.006). The as-treated efficacy was 55% (95% CI 22–75; p=0.002); efficacy from the Kaplan-Meier time-to-HIV-detection as-treated analysis was 60% (30–77; p=0.003). HIV incidence was lower in the intervention group than it was in the control group in all sociodemographic, behavioural, and sexually transmitted disease symptom subgroups. Moderate or severe adverse events occurred in 84 (3.6%) circumcisions; all resolved with treatment. Behaviours were much the same in both groups during follow-up.

<u>Interpretation</u> Male circumcision reduced HIV incidence in men without behavioural disinhibition. Circumcision can be recommended for HIV prevention in men.

From Table 3 of article...

<pre>&gt; ds=read.table("UgandaTrial.txt",header=T); ds</pre>							
t.from t.to intervention	partic						
1 0 6 1		2263		1172.1	.76		
2 0 6 0		2319	19	1206.7			
3 6 12 1		2235	5	1190.7	.35		
4 6 12 0		2229	14	1176.3			
5 12 24 1		964	: 3	989.7	.25		
6 12 24 0		980	12	1008.7			
> fit= glm(events ~ interv	ention	, famil	y=poiss	on,			
offset=log(py),			1 1				
<pre>&gt; summary(fit)</pre>		-, .					
Deviance Residuals:							
1 2 3		4	5	6			
2.0379 0.7256 -1.0784		-	-	-			
2.0379 0.7230 1.0701	0.11	10 1.	5510	0.3015			
Coefficients:							
Estimate Std.	Error	z valu	Pr(>	z   )			
(Intercept) -4.3224							
intervention -0.7040							
	0.2001	2.70	0.00	001			
Mull device at 16 2106 and 5 df							
Null deviance: 16.3106 on 5 df							
Residual deviance: 8.5173 on 4 df AIC: 37.095							
<pre>&gt; 0.01*round(100*exp(fit\$coefficients))</pre>							
> 0.01 IOUNG(IOO EXD(IICACOETICIENCE))							
(Theorem ) intermention							
(Intercept) intervention							
0.01 0.	.49						
ch zowach i on i	1	2	<b>→</b>	-	C		
observation:	1	2	3 4	5	6		

observation:	1	2	3	4	5	6
0.1*round(10*fit\$fit)	7.7	16.0	7.8	15.6	6.5	13.4
ds\$events	14	19	5	14	3	12

#### \* Proportional hazards?

Cumulative no.	of participants	2387	2430
Cumulative inci	dent events	22	45
Cumulative pers	son-years	3352.4	3391.8 i.r.r.
Cumulative inci	dence per 100 p-y	<u>??</u> 0.66	1.33 <u>0.49</u>
			( <u>0.28 to 0.84</u> )