

R Script for Poisson Regression Model (Count Data)

```
MyModel=glm(Infections ~ Swimmer + Location + Sex + Age,  
poisson (link = log), data = earinfection)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2645	-1.5740	-1.1165	0.5223	6.5151

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	2.39806	0.32369	7.409	1.28e-13	***
Swimmer	-0.60863	0.10502	-5.795	6.82e-09	***
Location	-0.48960	0.10483	-4.670	3.01e-06	***
Sex	0.02938	0.10916	0.269	0.788	
Age	-0.02606	0.01222	-2.132	0.033	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 824.51 on 286 degrees of freedom
Residual deviance: 760.01 on 282 degrees of freedom
AIC: 1142.4

Number of Fisher Scoring iterations: 6

```
Library(LOGIT)  
toOR(model)
```

	or	delta	zscore	pvalue	exp.loci.	exp.upci.
(Intercept)	11.0019	3.5612	7.4086	0.0000	5.8337	20.7486
Swimmer	0.5441	0.0571	-5.7953	0.0000	0.4429	0.6685
Location	0.6129	0.0642	-4.6703	0.0000	0.4990	0.7527
Sex	1.0298	0.1124	0.2692	0.7878	0.8315	1.2755
Age	0.9743	0.0119	-2.1323	0.0330	0.9512	0.9979

Note: In R there are several options for changing the reference cell. The simplest of these may be the `relevel()` function. The two arguments are the factor name and the desired reference category. The `as.factor()` function can be nested within `relevel()` if necessary.