

Arthritis - Cumulative Logit Model

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A simple data frame for the arthritis data is created with the numbers given for the individual cells.

```
> arthritis <- data.frame(drug=c(rep("new agent", 24+37+21+19+6), rep("active control", 11  
+ assessment=c(rep(1,24), rep(2,37), rep(3,21), rep(4,19), rep(5,6), rep(1,11), rep(2,51),  
> library(VGAM)
```

Now a cumulative model is fitted.

```
> cumart <- vglm(assessment ~ drug, family=cumulative(parallel=TRUE, link="logit"), data=a  
> summary(cumart)
```

Call:

```
vglm(formula = assessment ~ drug, family = cumulative(parallel = TRUE,  
link = "logit"), data = arthritis)
```

Pearson Residuals:

	Min	1Q	Median	3Q	Max
logit(P[Y<=1])	-0.7	-0.6	-0.3	-0.2	2.4
logit(P[Y<=2])	-1.7	-0.6	0.3	0.9	1.0
logit(P[Y<=3])	-2.1	0.2	0.3	0.4	1.1
logit(P[Y<=4])	-4.2	0.1	0.2	0.2	0.6

Coefficients:

	Value	Std. Error	t value
(Intercept):1	-1.8	0.2	-8.0
(Intercept):2	0.1	0.2	0.6
(Intercept):3	1.0	0.2	5.2
(Intercept):4	2.6	0.3	8.6
drugnew agent	0.3	0.2	1.2

Number of linear predictors: 4

Names of linear predictors:

```
logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3]), logit(P[Y<=4])
```

Dispersion Parameter for cumulative family: 1

Residual Deviance: 637 on 871 degrees of freedom

Log-likelihood: -318 on 871 degrees of freedom

Number of Iterations: 3