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+51+22+21+7)),
+ assessment=c(rep(1,24), rep(2,37), rep(3,21), rep(4,19), rep(5,6), rep(1,11),
+ rep(2,51), rep(3,22), rep(4,21), rep(5,7)))

> library(VGAM)
```

Now a cumulative model is fitted.

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

> 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