Binary Logistic Regression

Conway

Warning: package 'knitr' was built under R version 3.5.3

Prompt

The data are based on a mock jury study conducted by Shari Diamond and Jonathan Casper. Subjects (N = 100) watched a videotaped sentencing phase trial in which the defendant had already been found guilty. The issue for the jurors to decide was whether the defendant deserved the death penalty. These data were collected "pre-deliberation" (i.e., each juror was asked to provide his/her vote on the death penalty verdict, then the jurors met as a group to decide the overall jury verdict). The initial individual verdicts are given in this data set. Verdict is dummy coded: 0 = life sentence, 1 = death penalty.

Load packages and import data

```
# Load packages
library(pacman)

## Warning: package 'pacman' was built under R version 3.5.3

p_load(psych, jmv, aod, QuantPsyc, ggeffects, ggplot2)

# Import data
BL <- read.csv("https://www.dropbox.com/s/hd43va8a7hjfj27/Diamond.csv?dl=1")</pre>
```

Descriptive statistics

DESCRIPTIVES

##

##

Descriptives

##								
##		verdict	danger	rehab	punish	gendet	specdet	incap
##								
##	N	100	100	100	100	100	100	100
##	Missing	0	0	0	0	0	0	0
##	Mean	0.480	4.16	4.89	4.94	5.17	4.76	4.92
##	Median	0.00	4.00	5.00	4.00	5.00	4.00	5.00
##	Standard deviation	0.502	2.70	2.91	3.30	3.10	3.01	3.13
##	Minimum	0	0	0	0	0	0	0

##	Maximum	1	10	10	10	10	10	10
##	Skewness	0.0813	0.360	0.191	0.195	0.00548	0.113	0.0856
##	Std. error skewness	0.241	0.241	0.241	0.241	0.241	0.241	0.241
##	Kurtosis	-2.03	-0.690	-1.25	-1.33	-1.33	-1.19	-1.03
##	Std. error kurtosis	0.478	0.478	0.478	0.478	0.478	0.478	0.478

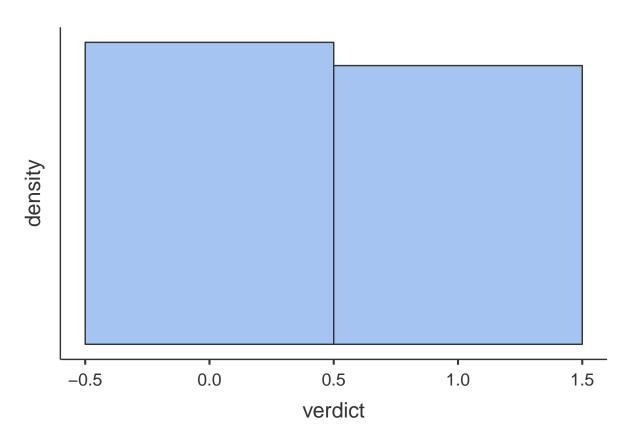
##

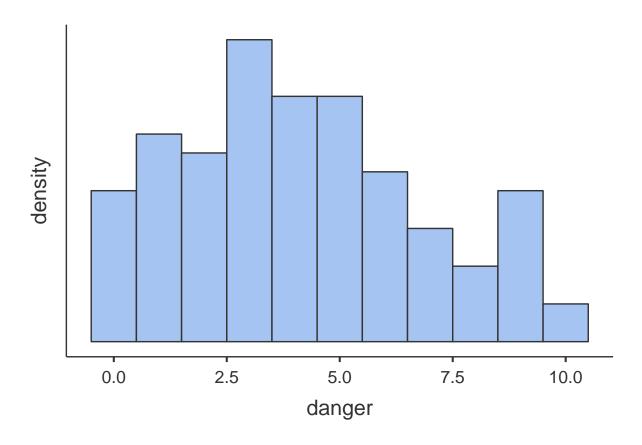
##

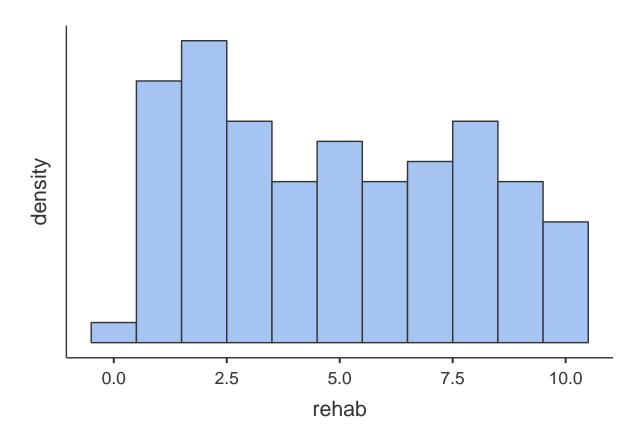
FREQUENCIES

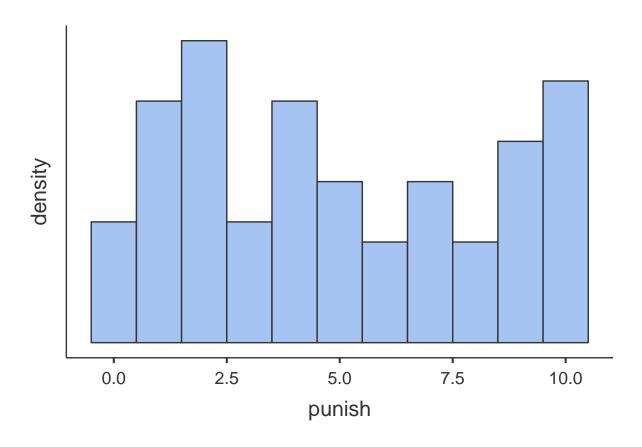
Frequencies of verdict

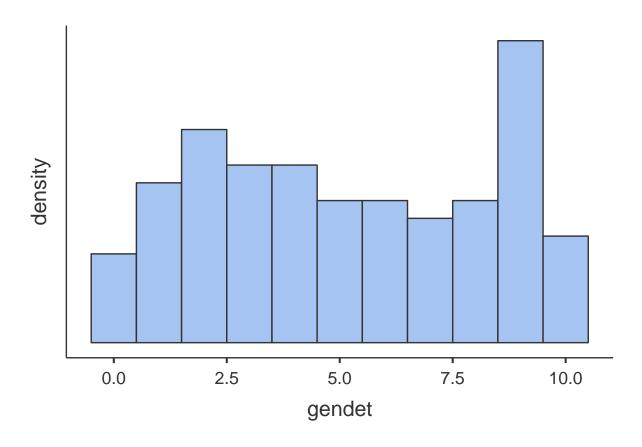
## ## ##	Levels	Counts	% of Total	Cumulative %
## ##	0	52	52.0	52.0
##	1	48	48.0	100.0
##				

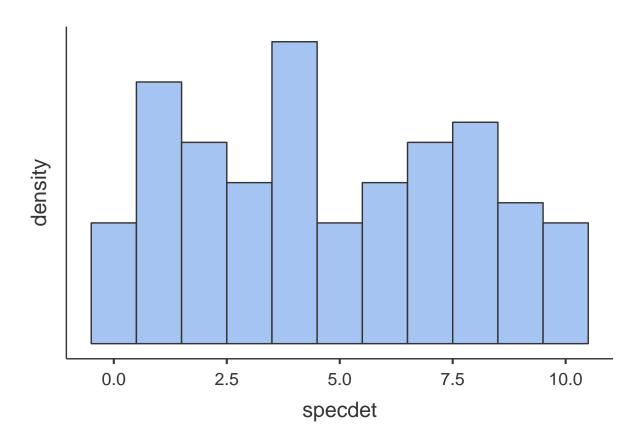


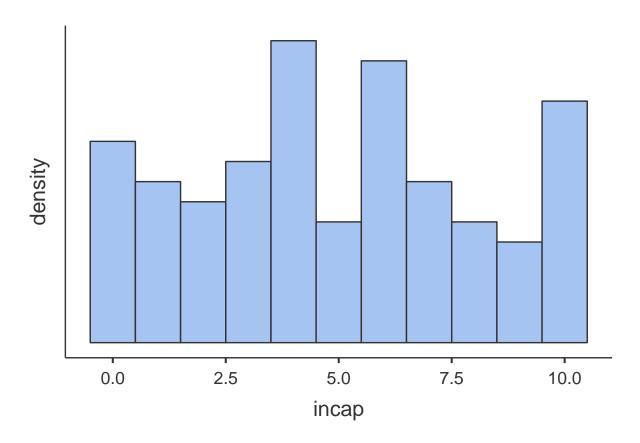












 $Assumptions \ 1. \ Independence \ of \ Observations \ 2. \ Predictor \ Variables \ Normally \ Distributed \ 3. \ Multicollinearity$

Correlations

##

##

punish

p-value

Pearson's r

```
# Correlation
cortable <- corrMatrix(data = BL,</pre>
                        vars = c('verdict', 'danger', 'rehab', 'punish', 'gendet', 'specdet', 'incap'),
                        flag = TRUE)
cortable
##
    CORRELATION MATRIX
##
##
##
    Correlation Matrix
##
##
                                 verdict
                                            danger
                                                       rehab
                                                                  punish
                                                                            gendet
                                                                                       specdet
                                                                                                   incap
##
##
      verdict
                                             0.346
                                                       -0.226
                                                                  0.042
                                                                             0.232
                                                                                         0.057
                                                                                                   0.070
                 Pearson's r
##
                 p-value
                                             < .001
                                                        0.024
                                                                  0.679
                                                                             0.020
                                                                                         0.574
                                                                                                   0.491
##
                                                       -0.087
##
      danger
                 Pearson's r
                                                                 -0.101
                                                                             0.038
                                                                                         0.083
                                                                                                   0.124
##
                 p-value
                                                        0.392
                                                                  0.317
                                                                             0.709
                                                                                         0.411
                                                                                                   0.221
##
                 Pearson's r
                                                                  0.073
                                                                             0.091
                                                                                         0.002
                                                                                                  -0.014
##
      rehab
```

0.472

0.365

0.023

0.988

0.016

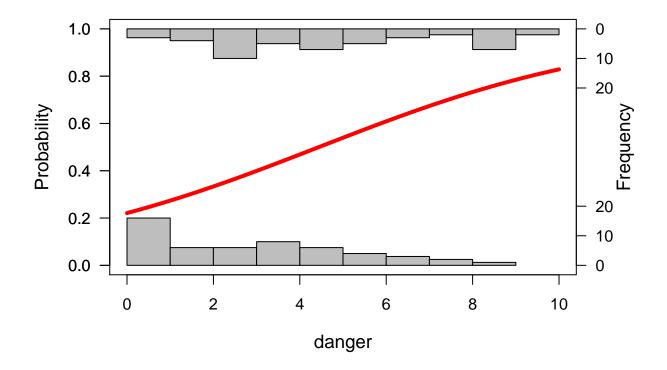
0.888

-0.107

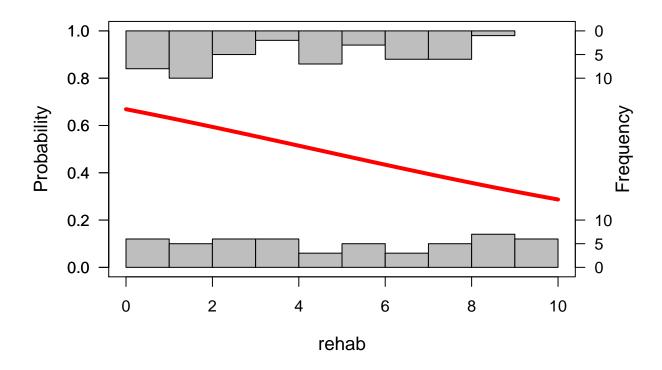
```
##
                  p-value
                                                                              0.823
                                                                                          0.876
                                                                                                     0.290
##
                                                                                          0.094
##
      gendet
                  Pearson's r
                                                                                                     0.112
##
                  p-value
                                                                                          0.352
                                                                                                     0.269
##
                  Pearson's r
                                                                                                    -0.064
##
      specdet
                  p-value
                                                                                                     0.526
##
##
                  Pearson's r
##
      incap
##
                  p-value
##
##
      Note. * p < .05, ** p < .01, *** p < .001
```

Logistic Plots

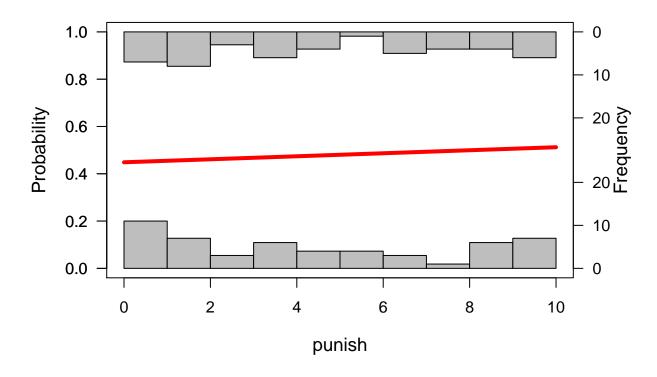
```
p_load(popbio)
logi.hist.plot(BL$danger, BL$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "danger")
```



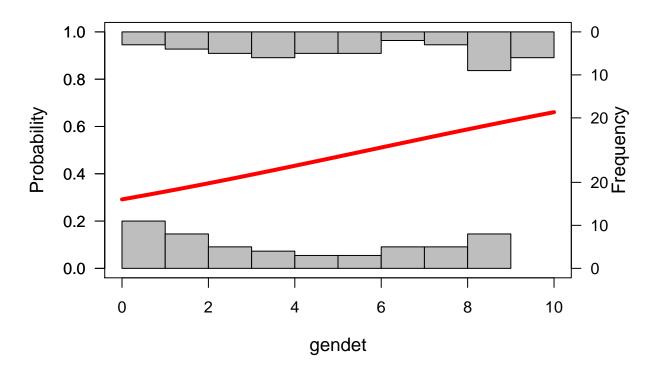
logi.hist.plot(BL\$rehab, BL\$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "rehab")



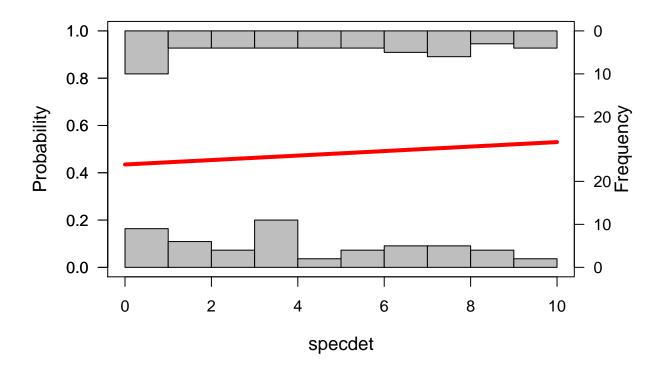
logi.hist.plot(BL\$punish, BL\$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "punish")



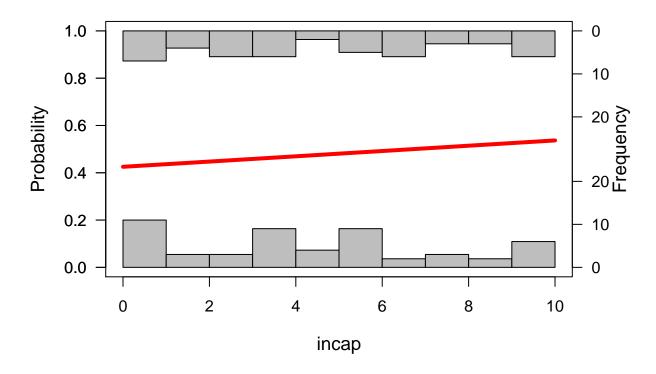
logi.hist.plot(BL\$gendet, BL\$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "gendet")



logi.hist.plot(BL\$specdet, BL\$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "specdet")



logi.hist.plot(BL\$incap, BL\$verdict, boxp=FALSE, type="hist", col="gray", xlabel = "incap")



BiLoRe Models

```
# Null model
# Null deviance = Chi squared for the model
\# df = N - (\# of parameters)
model0 <- glm(BL$verdict ~ 1, family = binomial)</pre>
summary(model0)
##
## Call:
## glm(formula = BL$verdict ~ 1, family = binomial)
##
## Deviance Residuals:
     Min
               1Q Median
##
                               ЗQ
                                      Max
## -1.144 -1.144
                            1.212
                                    1.212
##
## Coefficients:
##
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.08004
                           0.20016
                                      -0.4
                                              0.689
##
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 138.47 on 99 degrees of freedom
## Residual deviance: 138.47 on 99 degrees of freedom
## AIC: 140.47
##
## Number of Fisher Scoring iterations: 3
```

```
print("Logit")
## [1] "Logit"
coef(model0)
## (Intercept)
## -0.08004271
print("Odds")
## [1] "Odds"
model0.odds
## (Intercept)
    0.9230769
model0.probs <- model0.odds / (1 + model0.odds) #</pre>
print("Probabilities")
## [1] "Probabilities"
model0.probs
## (Intercept)
         0.48
print("Columns = Observed, Rows = Predicted")
## [1] "Columns = Observed, Rows = Predicted"
print("Null model")
## [1] "Null model"
ClassLog(model0, BL$verdict) # classification success under the null model (baseline)
## $rawtab
##
         resp
##
           0 1
##
    FALSE 52 48
##
## $classtab
##
         resp
##
          0 1
##
    FALSE 1 1
##
## $overall
## [1] 0.52
##
## $mcFadden
## [1] 2.220446e-16
# Model with predictors specific to the defendent.
# when odds ratio < 1 just flip (invert) the result(in relation to "no" instead of in relation to "yes"
# AIC is used to compare non-nested models for fit (lower means better fit)
# top chi-squared indicates the change of chi-squared vs the null model (Deviance + chi squared)
```

```
model1.jmv <- jmv::logRegBin(</pre>
 data = BL,
 dep = verdict,
 covs = vars(danger, specdet, incap, rehab, punish, gendet),
 blocks = list(
  list(
    'danger',
    'specdet',
    'incap')),
 refLevels = list(
  list(
    var = 'verdict',
    ref = '0')),
 modelTest = TRUE,
 OR = TRUE,
 class = TRUE,
 acc = TRUE,
 collin = TRUE)
model1.jmv
##
## BINOMIAL LOGISTIC REGRESSION
##
## Model Fit Measures
##
  ______
##
   Model Deviance AIC R<sup>2</sup>-McF <U+03C7><sup>2</sup> df p
##
##
              126
                   134
                        0.0916
                               12.7
                                     3
##
  ______
##
##
##
  MODEL SPECIFIC RESULTS
##
## MODEL 1
##
##
  Model Coefficients
##
  ______
    Predictor Estimate SE Z
                                   p
##
                                         Odds ratio
  ______
##
##
    Intercept -1.4592 0.6289 -2.320 0.020
                                              0.232
             0.2786 0.0868 3.208 0.001
##
    danger
                                              1.321
##
    specdet
             0.0228 0.0719 0.316 0.752
                                              1.023
            0.0220
                            0.316
                    0.0696
##
    incap
                                   0.752
##
  ______
##
    Note. Estimates represent the log odds of "verdict = 1" vs.
    "verdict = 0"
##
##
##
##
  ASSUMPTION CHECKS
##
## Collinearity Statistics
##
##
            VIF Tolerance
```

```
##
##
     danger 1.01 0.986
##
     specdet 1.01
                         0.988
      incap 1.02
                         0.984
##
##
##
##
   PREDICTION
##
##
  Classification Table verdict
##
     Observed 0 1 % Correct
##
##
##
                                 65.4
          0
                 34 18
##
          1
                 21 27
                               56.2
##
##
     Note. The cut-off value is set
##
     to 0.5
##
##
## Predictive Measures
##
    Accuracy
##
##
        0.610
##
   _____
##
     Note. The
     cut-off value
     is set to 0.5
##
# Model with predictors about the criminal justice system.
#Multicollinearity
#Tolerance = 1 - R squared --> for our purpose < .4 is bad
#VIF = 1/Tolerance
# Small VIF values indicates low correlation among variables under ideal conditions
#Multicollinearity occurs when two or more predictors in the model are correlated and provide redundant
model2.jmv <- jmv::logRegBin(</pre>
 data = BL,
 dep = verdict,
  covs = vars(danger, specdet, incap, rehab, punish, gendet),
  blocks = list(
   list(
     'rehab',
     'punish',
     'gendet')),
  refLevels = list(
   list(
     var = 'verdict',
     ref = '0')),
  modelTest = TRUE,
  OR = TRUE,
```

```
class = TRUE,
 acc = TRUE,
 collin = TRUE)
model2.jmv
##
##
  BINOMIAL LOGISTIC REGRESSION
##
## Model Fit Measures
##
   Model Deviance AIC R<sup>2</sup>-McF <U+03C7><sup>2</sup> df p
     1
            126 134 0.0901 12.5 3 0.006
##
##
##
##
##
   MODEL SPECIFIC RESULTS
##
   MODEL 1
##
##
##
   Model Coefficients
##
##
     Predictor
               Estimate
                                          p
                                                  Odds ratio
   _____
##
    Intercept -0.2619 0.5875 -0.446 0.656 rehab -0.1946 0.0770 -2.527 0.011
##
                                                       0.770
##
    rehab
                                                      0.823
##
    punish
                0.0373 0.0650 0.575 0.566
                                                      1.038
             0.1830 0.0720 2.540 0.011
##
     gendet
##
##
     Note. Estimates represent the log odds of "verdict = 1" vs.
##
     "verdict = 0"
##
##
##
   ASSUMPTION CHECKS
##
##
   Collinearity Statistics
##
##
             VIF
                   Tolerance
##
##
    rehab
            1.06
##
   punish 1.01
                      0.991
    gendet 1.05 0.952
##
##
##
##
  PREDICTION
##
   Classification Table verdict
##
##
   Observed 0 1 % Correct
##
##
                            75.0
##
          0
               39 13
```

54.2

1 22

##

26

```
##
##
     Note. The cut-off value is set
##
     to 0.5
##
##
## Predictive Measures
  -----
##
     Accuracy
##
   _____
##
       0.650
   _____
     Note. The
##
##
     cut-off value
##
     is set to 0.5
# Model with all predictors
model3.jmv <- jmv::logRegBin(</pre>
 data = BL,
 dep = verdict,
 covs = vars(danger, specdet, incap, rehab, punish, gendet),
 blocks = list(
   list(
     'danger',
     'specdet',
     'incap',
     'rehab',
     'punish',
     'gendet')),
 refLevels = list(
   list(
     var = 'verdict',
     ref = '0')),
 modelTest = TRUE,
 OR = TRUE,
 class = TRUE,
 acc = TRUE,
 collin = TRUE)
model3.jmv
##
## BINOMIAL LOGISTIC REGRESSION
##
## Model Fit Measures
##
    Model Deviance AIC R<sup>2</sup>-McF <U+03C7><sup>2</sup> df p
##
   ______
                114 128
                                      24.4
        1
                              0.176
                                             6
##
##
##
##
## MODEL SPECIFIC RESULTS
##
## MODEL 1
```

Model Coefficients

##						
##	Predictor	Estimate	SE	Z	p	Odds ratio
## ##	Intercept	-1.74758	0.9173	-1.9052	0.057	0.174
##	danger	0.29339	0.0929	3.1575	0.002	1.341
##	specdet	0.00590	0.0786	0.0751	0.940	1.006
##	incap	0.00353	0.0759	0.0465	0.963	1.004
##	rehab	-0.18784	0.0814	-2.3077	0.021	0.829
##	punish	0.07012	0.0711	0.9861	0.324	1.073
##	gendet	0.18574	0.0773	2.4019	0.016	1.204
##						

Note. Estimates represent the log odds of "verdict = 1" vs.

"verdict = 0"

##

##

##

ASSUMPTION CHECKS

##

Collinearity Statistics

##			
##		VIF	Tolerance
##			
##	danger	1.07	0.933
##	specdet	1.02	0.977
##	incap	1.05	0.955
##	rehab	1.04	0.957
##	punish	1.06	0.941
##	gendet	1.06	0.948
##			

##

##

##

PREDICTION

Classification Table verdict

Observed	0	1	% Correct
0 1	39	13	75.0
	16	32	66.7

Note. The cut-off value is set to 0.5

##

##

Predictive Measures

Accuracy

0.710

-----## Note. The

cut-off value

is set to 0.5

```
Model Comparison
# Model1 vs. Model3
# This is a similar set up to multiple regression in terms of the code, so if you know you will be runn
modelcomp.jmv <- jmv::logRegBin(</pre>
  data = BL,
  dep = verdict,
  covs = vars(danger, specdet, incap, rehab, punish, gendet),
  blocks = list(
   list(
      'danger',
     'specdet',
      'incap'),
    list(
      'rehab',
     'punish',
     'gendet')),
  refLevels = list(
   list(
     var = 'verdict',
     ref = '0')),
  modelTest = TRUE,
  OR = TRUE,
  class = TRUE,
  acc = TRUE,
  collin = TRUE)
modelcomp.jmv
##
## BINOMIAL LOGISTIC REGRESSION
##
## Model Fit Measures
##
   Model Deviance AIC R<sup>2</sup>-McF <U+03C7><sup>2</sup> df p
##
##
        1
##
                                                          0.005
```

```
126 134 0.0916 12.7 3
114 128 0.1763 24.4 6
##
      2
                                   6 < .001
##
##
##
## Model Comparisons
##
  Model Model <U+03C7>2 df p
##
  -----
##
   1 - 2 11.7
##
                         3 0.008
##
##
##
##
 MODEL SPECIFIC RESULTS
##
##
 MODEL 1
##
```

Model Coefficients

```
SE Z p
##
     Predictor Estimate
                                                    Odds ratio
  ______
##
##
                                   -2.320 0.020
                  -1.4592
                           0.6289
     Intercept

      danger
      0.2786
      0.0868
      3.208
      0.001

      specdet
      0.0228
      0.0719
      0.316
      0.752

      incap
      0.0220
      0.0696
      0.316
      0.752

##
##
                                                          1.023
##
     Note. Estimates represent the log odds of "verdict = 1" vs.
##
##
     "verdict = 0"
##
##
   ASSUMPTION CHECKS
##
##
##
  Collinearity Statistics
##
               VIF
##
                      Tolerance
##
    danger
##
             1.01
                         0.986
     specdet 1.01
     specdet 1.01 0.988 incap 1.02 0.984
##
##
##
##
##
##
  PREDICTION
## Classification Table verdict
    Observed 0 1 % Correct
          0
                34 18
                              65.4
##
          1 21 27
##
                              56.2
##
##
     Note. The cut-off value is set
##
     to 0.5
##
##
## Predictive Measures
##
   _____
##
     Accuracy
   -----
##
       0.610
   _____
##
##
    Note. The
##
    cut-off value
##
     is set to 0.5
##
##
## MODEL 2
##
## Model Coefficients
## ------
   Predictor Estimate SE Z p Odds ratio
##
```

```
-1.9052
             -1.74758
##
    Intercept
                       0.9173
                                         0.057
                                                    0.174
                                        0.002
##
    danger
              0.29339 0.0929
                               3.1575
                                                    1.341
##
    specdet
              0.00590 0.0786
                                0.0751 0.940
                                                    1.006
##
               0.00353 0.0759
                                0.0465
    incap
                                        0.963
                                                    1.004
              -0.18784 0.0814
##
    rehab
                               -2.3077 0.021
                                                    0.829
##
    punish
              0.07012 0.0711 0.9861 0.324
                                                    1.073
              0.18574 0.0773 2.4019 0.016
##
    gendet
                                                   1.204
##
##
    Note. Estimates represent the log odds of "verdict = 1" vs.
##
    "verdict = 0"
##
##
   ASSUMPTION CHECKS
##
##
##
   Collinearity Statistics
##
             VIF
##
                   Tolerance
##
    danger
##
            1.07
                      0.933
    specdet 1.02
##
                     0.977
    incap 1.05 rehab 1.04
                     0.955
##
##
  rehab
                     0.957
    punish
##
            1.06
                      0.941
    gendet 1.06
##
                     0.948
##
   -----
##
##
##
  PREDICTION
##
## Classification Table verdict
##
   _____
##
    Observed 0 1
                       % Correct
##
   _____
##
         0 39 13
                           75.0
         1 16 32 66.7
##
##
##
   Note. The cut-off value is set
##
    to 0.5
##
##
## Predictive Measures
##
  -----
    Accuracy
##
##
##
      0.710
  _____
##
   Note. The
##
##
    cut-off value
##
    is set to 0.5
Center Predictors
BL$dangerC <- BL$danger - mean(BL$danger)</pre>
BL$rehabC <- BL$rehab - mean(BL$rehab)</pre>
BL$punishC <- BL$punish - mean(BL$punish)</pre>
```

```
BL$gendetC <- BL$gendet - mean(BL$gendet)
BL$specdetC <- BL$specdet - mean(BL$specdet)
BL$incapC <- BL$incap - mean(BL$incap)</pre>
```

Re-run model with all predictors and run parsimonious model.

```
#remove not significant predictors
finalmodel.jmv <- logRegBin(</pre>
  data = BL,
  dep = verdict,
  covs = vars(dangerC, specdetC, incapC, rehabC, punishC, gendetC),
  blocks = list(
    list(
      'dangerC', # significant predictors only
      'rehabC',
      'gendetC'),
    list(
      'specdetC', # full model
      'incapC',
      'punishC')),
  refLevels = list(
   list(
      var = 'verdict',
     ref = '0')),
  modelTest = TRUE,
  OR = TRUE,
  class = TRUE,
  acc = TRUE,
  collin = TRUE)
finalmodel.jmv
```

```
##
 BINOMIAL LOGISTIC REGRESSION
##
##
## Model Fit Measures
##
 ______
  Model Deviance AIC R2-McF <U+03C7>2
##
 ______
##
##
   1
        115 123 0.169 23.4 3 < .001
   2 114 128 0.176 24.4 6 < .001
##
 ______
##
##
##
## Model Comparisons
 -----
##
  Model Model <U+03C7>2 df p
##
## -----
##
   1 - 2 1.00 3 0.801
 _____
##
##
##
## MODEL SPECIFIC RESULTS
```

```
##
## MODEL 1
##
## Model Coefficients
##
  ______
##
    Predictor Estimate SE Z p Odds ratio
            -0.0955 0.2263 -0.422 0.673
    Intercept
##
                                             0.909
##
    dangerC
             0.2797 0.0888 3.151 0.002
                                            1.323
##
    rehabC
             -0.1807 0.0806 -2.242 0.025
                                            0.835
##
    gendetC
             0.1881 0.0765 2.460 0.014
                                            1.207
  ______
##
##
    Note. Estimates represent the log odds of "verdict = 1" vs.
##
    "verdict = 0"
##
##
##
  ASSUMPTION CHECKS
##
## Collinearity Statistics
  _____
##
##
           VIF Tolerance
##
  -----
  dangerC 1.01
##
                  0.992
                   0.972
##
   rehabC 1.03
##
  gendetC 1.04
                  0.964
##
##
##
  PREDICTION
##
##
  Classification Table verdict
##
   Observed 0 1 % Correct
##
##
            37 15
                        71.2
##
        0
                       66.7
##
        1 16 32
##
  _____
##
   Note. The cut-off value is set
##
   to 0.5
##
##
## Predictive Measures
  _____
##
##
   Accuracy
     0.690
##
##
##
   Note. The
##
   cut-off value
##
    is set to 0.5
##
##
## MODEL 2
```

##

Model Coefficients

## ## ##	Predictor	Estimate	SE	Z	р	Odds ratio
##	Intercept	-0.09352	0.2277	-0.4108	0.681	0.911
##	$\mathtt{dangerC}$	0.29339	0.0929	3.1575	0.002	1.341
##	rehabC	-0.18784	0.0814	-2.3077	0.021	0.829
##	${\tt gendetC}$	0.18574	0.0773	2.4019	0.016	1.204
##	${ t specdetC}$	0.00590	0.0786	0.0751	0.940	1.006
##	incapC	0.00353	0.0759	0.0465	0.963	1.004
##	punishC	0.07012	0.0711	0.9861	0.324	1.073
##						

Note. Estimates represent the log odds of "verdict = 1" vs.

"verdict = 0"

##

##

##

##

##

##

##

##

##

ASSUMPTION CHECKS

Collinearity Statistics

	VIF	Tolerance
dangerC rehabC	1.07 1.04	0.933 0.957
${\tt gendetC}$	1.06	0.948
${ t specdetC}$	1.02	0.977
${\tt incapC}$	1.05	0.955
punishC	1.06	0.941

PREDICTION

Classification Table verdict

Observed	0	1	% Correct
0	39	13	75.0
1	16	32	66.7

Note. The cut-off value is set to 0.5

##

Predictive Measures

Accuracy

0.710

-----## Note. The

Note. The
cut-off value
is set to 0.5

Use regression equation to calculate predicted logit, odds, and probability

```
# Let D = danger, R = rehab, G = gendet
D = 10
R = 0
G = 10

predlogit <- -.096 + (.278*D) + (-.181*R) + (.188*G)
predodds <- exp(predlogit)
predprob <- predodds / (1 + predodds)

predlogit
## [1] 4.564
predodds
## [1] 95.96658
predprob</pre>
## [1] 0.9896872
```