```
> setwd("C:\\Users\\Aasthaa\\Documents\\RA_Hutch\\2009_11_13_fromDaryl")
> source("rocreg.R")
> source("hidden.R")
>
> ### Documentation examples
> nnhs2 <- read.csv("http://labs.fhcrc.org/pepe/book/data/nnhs2.csv",header = TRUE, sep = ",")
>
> rocreg(dataset="nnhs2", d="d", markers="y1", cluster="id", noccsamp=T)
ROC regression for markers: y1
```

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status

bootstrap samples: 1000

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                        Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.452   0.0998   0.27   0.672
 alpha_1 0.9   0.0744   0.779   1.07


```
> rocreg(dataset="nnhs2", d="d", markers="y1", adjcov="gender", regcov="gender", cluster="id",
noccsamp=T, level=90)
ROC regression for markers: y1
Model intercept term covariates: gender
```

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum d=0 d=1 Total
 1   2170 64 2234
 2   2739 85 2824
 Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status
 and from within covariate strata

bootstrap samples: 1000

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                    Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [90% Conf. Interval]
 alpha_0 0.495   0.315   -0.0607   0.989
 alpha_1 0.914   0.0727   0.809   1.05
 gender -0.0285   0.193   -0.331   0.317

> rocreg(dataset="nnhs2", d="d", markers="y1", adjcov="gender", regcov="gender", pvcmeth="normal",
cluster="id", noccsamp=T)
ROC regression for markers: y1
Model intercept term covariates: gender

Percentile value calculation
method: normal

Covariate adjustment

method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum d=0 d=1 Total
 1   2170 64 2234
 2   2739 85 2824
 Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status
 and from within covariate strata

bootstrap samples: 1000

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                    Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.48   0.314   -0.112   1.12
 alpha_1 1.04   0.0836   0.895   1.23
 gender -0.00853   0.192   -0.382   0.374

> rocreg(dataset="nnhs2", d="d", markers=c("y1","y2"), adjcov=c("currage","gender"),
adjmodel="linear", regcov="currage", cluster="id", noccsamp=T)
ROC regression for markers: y1, y2
Model intercept term covariates: currage

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: linear model

covariates: currage, gender

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status

bootstrap samples: 1000

****
Model results for marker: y1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
   Min   1Q Median   3Q   Max
-27.356 -5.132   1.104   4.804 48.274

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.48666   1.28861 -1.154   0.249
currage   -0.20325   0.03239 -6.275 3.8e-10 ***
gender   0.24717   0.22291   1.109   0.268

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

(Dispersion parameter for gaussian family taken to be 60.08613)

   Null deviance: 297081 on 4906 degrees of freedom
Residual deviance: 294662 on 4904 degrees of freedom
AIC: 34028

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results

Number of strata = 1   Number of obs   = 5056
                     Replications   = 1000

       Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 -1.27   1.14   -3.51   0.884
alpha_1 0.937   0.0776   0.796   1.11
currage 0.0448   0.0298   -0.0101   0.104

****
Model results for marker: y2

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-24.8469 -4.4290 -0.1300   4.2539 35.4476

Coefficients:
         Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.3488   1.1617 -5.465 4.86e-08 ***
currage   -0.1694   0.0292 -5.802 6.98e-09 ***
gender   0.7014   0.2010   3.490 0.000487 ***

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

(Dispersion parameter for gaussian family taken to be 48.83636)

   Null deviance: 241680 on 4906 degrees of freedom
Residual deviance: 239494 on 4904 degrees of freedom
AIC: 33011

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5056
                     Replications   = 1000

       Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]

alpha_0 -1.52   1.05   -3.48   0.592
alpha_1 0.915   0.0689   0.791   1.06
currage 0.0483   0.0274   -0.00582 0.0996

> rocreg(dataset="nnhs2", d="d", markers="y1", adjcov="gender", regcov="gender", sregcov="gender", link="logit", cluster="id", noccsamp=T)
ROC regression for markers: y1
Model intercept term covariates: gender
Model slope term covariates: gender

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum d=0 d=1 Total
 1   2170 64 2234
 2   2739 85 2824
 Total   4909 149 5058

GLM fit
link function: logit - bilogistic ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status
 and from within covariate strata

bootstrap samples: 1000

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                     Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]

```
alpha_0  0.793      0.539           -0.299    1.88
alpha_1  0.841      0.246           0.371     1.34
gender   -0.0258    0.335           -0.663    0.689
s_gender 0.0436     0.159           -0.245    0.378
```

> ### Covariate adjustment
> dis <- nnhs2$d
> m1 <- nnhs2$y1
> m2 <- nnhs2$y2
> m3 <- nnhs2$y3
>
> # One marker
> test <-
rocreg(d="dis",markers="m1",adjcov=c("nnhs2$gender"),adjmodel="stratified",pvcmeth="empirical")
ROC regression for markers: m1

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: gender
# of case-containing strata: 2

```
 Stratum dis=0 dis=1 Total
 1     2170 64   2234
 2     2739 85   2824
 Total  4909 149  5058
```

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 1000

****
Model results for marker: m1

ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                          Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 0.451   0.0881   0.283   0.628
alpha_1 0.914   0.0683   0.799   1.06

> test
$rocreg_m1
$rocreg_m1$fit

Call: glm(formula = as.formula(formulaStr), family = binomial(probit),   data = reg)

Coefficients:
(Intercept)   x
   0.4507   0.9139

Degrees of Freedom: 1489 Total (i.e. Null); 1488 Residual
Null Deviance: 1948
Residual Deviance: 1580   AIC: 1584

$rocreg_m1$V
        alpha_0   alpha_1
alpha_0 0.007767241   NA
alpha_1 0.001070052 0.004666298

$GLMparm
  alpha_0 alpha_1
m1   0.451   0.914

> rocreg(d="dis",markers="m1",adjcov="nnhs2$gender",adjmodel="stratified",pvcmeth="normal",
nsamp=100)
ROC regression for markers: m1

Percentile value calculation
method: normal

Covariate adjustment

method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum dis=0 dis=1 Total
 1   2170 64   2234
 2   2739 85   2824
 Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100

****
Model results for marker: m1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                    Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.467   0.0941   0.306   0.642
 alpha_1 1.04   0.0855   0.888   1.21

> rocreg(d="dis",markers="m1",adjcov="nnhs2$y2",adjmodel="linear",pvcmeth="normal", nsamp=100)
ROC regression for markers: m1

Percentile value calculation
method: normal

Covariate adjustment
method: linear model
covariates: y2

GLM fit
link function: probit - binormal ROC

number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: m1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-22.6108 -4.3916   0.5024   4.2454   43.6259

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.20880   0.18605 -11.87   <2e-16 ***
y2   0.56972   0.01357   41.98   <2e-16 ***

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

(Dispersion parameter for gaussian family taken to be 44.55492)

   Null deviance: 297140 on 4908 degrees of freedom
Residual deviance: 218631 on 4907 degrees of freedom
AIC: 32573

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                   Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.285   0.0901   0.129   0.479
 alpha_1 1.36   0.105   1.17   1.53

> rocreg(d="dis",markers="m1",adjcov="nnhs2$y2",adjmodel="linear",pvcmeth="empirical",
nsamp=100)
ROC regression for markers: m1

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: linear model
covariates: y2

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: m1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-22.6108 -4.3916   0.5024   4.2454   43.6259

Coefficients:
         Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.20880   0.18605 -11.87   <2e-16 ***
y2   0.56972   0.01357   41.98   <2e-16 ***

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

(Dispersion parameter for gaussian family taken to be 44.55492)

   Null deviance: 297140 on 4908 degrees of freedom
Residual deviance: 218631 on 4907 degrees of freedom
AIC: 32573

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                        Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.274   0.0912   0.116   0.482
 alpha_1 1.11   0.0805   0.966   1.24
>

> # Multiple markers
> test <- rocreg(d="dis", markers=c("nnhs2$y1","nnhs2$y2"),
adjcov="nnhs2$gender",adjmodel="stratified",pvcmeth="empirical",nsamp=100)
ROC regression for markers: y1, y2

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum dis=0 dis=1 Total
 1   2170 64   2234
 2   2739 85   2824
 Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

and from within covariate strata

bootstrap samples: 100

****

Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                    Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 0.451   0.092   0.286   0.628
alpha_1 0.914   0.075   0.78   1.07

****

Model results for marker: y2

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                    Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 0.329   0.0923   0.167   0.496
alpha_1 0.891   0.0711   0.782   1.05

> test
$rocreg_m1
$rocreg_m1$fit

Call: glm(formula = as.formula(formulaStr), family = binomial(probit),   data = reg)

Coefficients:
(Intercept)   x
   0.4507   0.9139

Degrees of Freedom: 1489 Total (i.e. Null); 1488 Residual
Null Deviance: 1948
Residual Deviance: 1580   AIC: 1584

$rocreg_m1$V
         alpha_0   alpha_1
alpha_0 0.008463501   NA
alpha_1 0.001983079 0.005620647

$rocreg_m2
$rocreg_m2$fit

Call: glm(formula = as.formula(formulaStr), family = binomial(probit),   data = reg)

Coefficients:
(Intercept)   x
    0.3286   0.8914

Degrees of Freedom: 1489 Total (i.e. Null); 1488 Residual
Null Deviance: 2001
Residual Deviance: 1637   AIC: 1641

$rocreg_m2$V
         alpha_0   alpha_1
alpha_0 0.008515064   NA
alpha_1 0.001549163 0.005051124

$GLMparm
   alpha_0 alpha_1
y1   0.451   0.914
y2   0.329   0.891

> rocreg(d="dis", markers=c("nnhs2$y1","nnhs2$y2"),
adjcov="nnhs2$gender",adjmodel="stratified",pvcmeth="normal",nsamp=100)
ROC regression for markers: y1, y2

Percentile value calculation
method: normal

Covariate adjustment
method: stratified
covariates: gender
# of case-containing strata: 2

 Stratum dis=0 dis=1 Total
 1   2170 64   2234
 2   2739 85   2824

Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                   Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.467   0.0941   0.306   0.642
 alpha_1 1.04   0.0855   0.888   1.21

****
Model results for marker: y2

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 5058
                   Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.309   0.0882   0.173   0.479
 alpha_1 0.961   0.0757   0.834   1.13

> rocreg(d="dis", markers=c("nnhs2$y1","nnhs2$y2"),
adjcov="m3",adjmodel="linear",pvcmeth="empirical",nsamp=100)
ROC regression for markers: y1, y2

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: linear model
covariates: m3

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
   Min   1Q Median   3Q   Max
-28.588 -5.099   1.110   4.861   46.663

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -7.41363   0.27780 -26.69 < 2e-16 ***
m3   0.38715   0.06562   5.90 3.88e-09 ***

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

(Dispersion parameter for gaussian family taken to be 60.12773)

   Null deviance: 297140 on 4908 degrees of freedom
Residual deviance: 295047 on 4907 degrees of freedom
AIC: 34045

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                    Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.43   0.1   0.206   0.595
 alpha_1 0.902   0.0716   0.793   1.07

****
Model results for marker: y2

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-25.47259 -4.45726 -0.09874   4.37939   34.03224

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -10.7817   0.2510 -42.946 < 2e-16 ***
m3   0.2557   0.0593   4.312 1.65e-05 ***

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

(Dispersion parameter for gaussian family taken to be 49.10665)

   Null deviance: 241879 on 4908 degrees of freedom
Residual deviance: 240966 on 4907 degrees of freedom
AIC: 33051

Number of Fisher Scoring iterations: 2

****

ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                      Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.33   0.101   0.12   0.527
 alpha_1 0.87   0.0644   0.752   1.02

> rocreg(d="dis", markers=c("nnhs2$y1","nnhs2$y2"),
adjcov="m3",adjmodel="linear",pvcmeth="normal",nsamp=100)
ROC regression for markers: y1, y2

Percentile value calculation
method: normal

Covariate adjustment
method: linear model
covariates: m3

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
   Min   1Q Median   3Q   Max
-28.588 -5.099   1.110   4.861 46.663

Coefficients:
       Estimate Std. Error t value Pr(>|t|)

(Intercept) -7.41363   0.27780 -26.69 < 2e-16 ***
m3   0.38715   0.06562   5.90 3.88e-09 ***

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

(Dispersion parameter for gaussian family taken to be 60.12773)

    Null deviance: 297140 on 4908 degrees of freedom
Residual deviance: 295047 on 4907 degrees of freedom
AIC: 34045

Number of Fisher Scoring iterations: 2

****

   ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                    Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.45   0.0999   0.223   0.617
 alpha_1 1.02   0.08   0.875   1.22

****
Model results for marker: y2

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
    Min   1Q   Median   3Q   Max
-25.47259 -4.45726 -0.09874   4.37939   34.03224

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
(Intercept) -10.7817   0.2510 -42.946 < 2e-16 ***
m3   0.2557   0.0593   4.312 1.65e-05 ***

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

(Dispersion parameter for gaussian family taken to be 49.10665)

Null deviance: 241879 on 4908 degrees of freedom
Residual deviance: 240966 on 4907 degrees of freedom
AIC: 33051

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5058
                        Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.309   0.101   0.103   0.511
 alpha_1 0.969   0.0669   0.854   1.11

>
> # Multiple adjcov variables
> test <- rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("sitenum","gender"),adjmodel="stratified",pvcmeth="empirical",nsamp=100)
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: sitenum, gender
# of case-containing strata: 12

 Stratum d=0 d=1 Total
 1   575 9 584
 2   101 4 105
 3   98 7 105
 4   876 26 902
 5   313 7 320
 6   207 11 218
 7   768 11 779
 8   164 4 168
 9   117 5 122

```
10    942  40  982
11    478  21  499
12    270  4   274
Total  4909 149 5058
```

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 12   Number of obs   = 5058
                      Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.446   0.0916   0.289   0.626
 alpha_1 0.941   0.0673   0.804   1.04

> test
$rocreg_m1
$rocreg_m1$fit

Call: glm(formula = as.formula(formulaStr), family = binomial(probit),   data = reg)

Coefficients:
(Intercept)   x
   0.4460   0.9405

Degrees of Freedom: 1489 Total (i.e. Null); 1488 Residual
Null Deviance: 1952
Residual Deviance: 1566   AIC: 1570

$rocreg_m1$V
      alpha_0   alpha_1

alpha_0 0.008386143   NA
alpha_1 0.001446344 0.004534165

$GLMparm
  alpha_0 alpha_1
y1   0.446   0.941

> rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("sitenum","gender"),adjmodel="stratified",pvcmeth="normal",nsamp=100)
ROC regression for markers: y1

Percentile value calculation
method: normal

Covariate adjustment
method: stratified
covariates: sitenum, gender
# of case-containing strata: 12

 Stratum d=0 d=1 Total
 1   575 9 584
 2   101 4 105
 3   98 7 105
 4   876 26 902
 5   313 7 320
 6   207 11 218
 7   768 11 779
 8   164 4 168
 9   117 5 122
 10   942 40 982
 11   478 21 499
 12   270 4 274
 Total   4909 149 5058

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100

```
****************************
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata =  12          Number of obs  =  5058
                    Replications   =  100

    Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.463      0.0934          0.306    0.646
 alpha_1 1.02       0.0765          0.863    1.15



> rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("currage","y3"),adjmodel="linear",pvcmeth="empirical",nsamp=100)
ROC regression for markers: y1

Percentile value calculation
method:       empirical
tie correction: no

Covariate adjustment
method:    linear model
covariates: currage, y3

GLM fit
link function:    probit - binormal ROC
number of points: 10
on FPR interval:  (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100



****************************
Model results for marker: y1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)
```

Deviance Residuals:
   Min   1Q   Median   3Q   Max
-27.665 -5.085   1.100   4.749 48.281

Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.39416   1.27232   0.310   0.757
currage   -0.20302   0.03227 -6.292 3.41e-10 ***
y3   0.38749   0.06543   5.922 3.39e-09 ***

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

(Dispersion parameter for gaussian family taken to be 59.67438)

    Null deviance: 297081 on 4906 degrees of freedom
Residual deviance: 292643 on 4904 degrees of freedom
AIC: 33995

Number of Fisher Scoring iterations: 2

****

   ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 5056
                      Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.447   0.0948   0.253   0.607
 alpha_1 0.951   0.0744   0.822   1.08

> rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("currage","y3"),adjmodel="linear",pvcmeth="normal",nsamp=100)
ROC regression for markers: y1

Percentile value calculation
method: normal

Covariate adjustment
method: linear model
covariates: currage, y3

GLM fit

link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  Covariate adjustment - linear model, controls only

Call:
glm(formula = as.formula(formulaStr), data = ctrlsData)

Deviance Residuals:
   Min   1Q   Median   3Q   Max
-27.665 -5.085   1.100   4.749   48.281

Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.39416   1.27232   0.310   0.757
currage   -0.20302   0.03227 -6.292 3.41e-10 ***
y3   0.38749   0.06543   5.922 3.39e-09 ***

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

(Dispersion parameter for gaussian family taken to be 59.67438)

   Null deviance: 297081 on 4906 degrees of freedom
Residual deviance: 292643 on 4904 degrees of freedom
AIC: 33995

Number of Fisher Scoring iterations: 2

****

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs = 5056
                   Replications   = 100

```
      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 0.443      0.0964           0.272    0.625
alpha_1 1.05       0.0771           0.931    1.18




> #nostsamp
> rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("sitenum","gender"),adjmodel="stratified",pvcmeth="empirical",nsamp=100,nostsamp=T)
ROC regression for markers: y1

Percentile value calculation
method:      empirical
tie correction: no

Covariate adjustment
method:    stratified
covariates: sitenum, gender
# of case-containing strata: 12

 Stratum d=0  d=1 Total
 1     575 9  584
 2     101 4  105
 3      98  7  105
 4     876 26 902
 5     313 7  320
 6     207 11 218
 7     768 11 779
 8     164 4  168
 9     117 5  122
 10    942 40 982
 11    478 21 499
 12    270 4  274
 Total  4909 149 5058

GLM fit
link function:    probit - binormal ROC
number of points: 10
on FPR interval:  (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100
```

```
*****************************
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata =  12            Number of obs   = 5058
                      Replications    = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.446        0.0933           0.239    0.589
 alpha_1 0.941        0.0715           0.803    1.09
> rocreg(dataset="nnhs2", d="d", markers=c("y1"),
adjcov=c("sitenum","gender"),adjmodel="stratified",pvcmeth="normal",nsamp=100,nostsamp=T)
ROC regression for markers: y1

Percentile value calculation
method: normal

Covariate adjustment
method:    stratified
covariates: sitenum, gender
# of case-containing strata: 12
```

Stratum	d=0	d=1	Total
1	575	9	584
2	101	4	105
3	98	7	105
4	876	26	902
5	313	7	320
6	207	11	218
7	768	11	779
8	164	4	168
9	117	5	122
10	942	40	982
11	478	21	499
12	270	4	274
Total	4909	149	5058

```
GLM fit
link function:    probit - binormal ROC
number of points: 10
on FPR interval:  (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata
```

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 12   Number of obs   = 5058
                        Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.463   0.0968   0.268   0.635
 alpha_1 1.02   0.0778   0.89   1.18

> ### Pancreatic cancer data set, more options
> panCan <- read.csv("http://www.fhcrc.org/science/labs/pepe/book/data/wiedat2b.csv", header =
TRUE, sep = ",")
> rocreg(dataset="panCan",d="d",markers="y1", nsamp=100, tiecorr=T)
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: yes

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                    Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.19   0.15   0.963   1.54
alpha_1 0.478   0.114   0.283   0.712

> rocreg(dataset="panCan",d="d",markers="y1", regcov="y2", nsamp=100)
ROC regression for markers: y1
Model intercept term covariates: y2

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                    Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.14   0.167   0.87   1.46
alpha_1 0.48   0.116   0.287   0.728
y2   0.00128   0.00289   -0.00267 0.00798
Warning messages:

1: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred
2: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred
3: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred
4: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred
5: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred
6: In glm.fit(x = X, y = Y, weights = weights, start = start, etastart = etastart, :
  fitted probabilities numerically 0 or 1 occurred

> rocreg(dataset="panCan",d="d",markers="y1", regcov="y2", sregcov="y2", nsamp=100)
ROC regression for markers: y1
Model intercept term covariates: y2
Model slope term covariates: y2

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                  Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.14   0.168   0.853   1.44
alpha_1 0.49   0.12   0.256   0.67
y2   0.00118   0.00434   -0.00236 0.0148

s_y2   -0.000263   0.00299   -0.00218   0.00759
There were 13 warnings (use warnings() to see them)

> rocreg(dataset="panCan", d="d", markers="y1", pvcmeth="normal",nsamp=100)
ROC regression for markers: y1

Percentile value calculation
method: normal

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                      Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.14   0.121   0.928   1.4
 alpha_1 0.607   0.0784   0.399   0.7

>
> #Link function and interval
> rocreg(dataset="panCan", d="d", markers="y1", interval=c(0, 0.1, 10), link="probit")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC

number of points: 10
on FPR interval: (0,0.1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

   ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                     Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.13   0.354   0.37   1.72
 alpha_1 0.404   0.161   0.0349   0.661

> rocreg(dataset="panCan", d="d", markers="y1", link="logit")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: logit - bilogistic ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

   ROC-GLM model

Bootstrap results

Number of strata = 1   Number of obs   = 141
                    Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 2.05   0.337   1.57   2.81
alpha_1 0.522   0.133   0.315   0.829

> rocreg(dataset="panCan", d="d", markers="y1", interval=c(0, 0.1, 10), link="logit")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: logit - bilogistic ROC
number of points: 10
on FPR interval: (0,0.1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

   ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                    Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.57   0.505   0.517   2.45
alpha_1 0.279   0.114   0.0236   0.453

>
> #Bootstrap options
> rocreg(dataset="panCan", d="d", markers="y1", noccsamp=T, nsamp=500)
ROC regression for markers: y1

Percentile value calculation

method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 w/o respect to case/control status

bootstrap samples: 500

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                        Replications   = 500

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.19   0.177   0.883   1.58
 alpha_1 0.478   0.114   0.287   0.714

>
> #resfile
> dis <- panCan$d
> panCan <- cbind(panCan, dis)
> panCan <- panCan[,-which(names(panCan)=="d")]
> #1 marker - create file
> rocreg(dataset="panCan",d="dis",markers="y1", nsamp=100, resfile="testResfileRocreg")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling

separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                    Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.19   0.15   0.963   1.54
alpha_1 0.478   0.114   0.284   0.71

> #1 marker - Try to overwrite existing file
> rocreg(dataset="panCan",d="dis",markers="y2", nsamp=100, resfile="testResfileRocreg")
Error in rocreg(dataset = "panCan", d = "dis", markers = "y2", nsamp = 100, :
  file specified by resfile already exists, use 'replace' option to replace existing file

> #Multiple markers
> rocreg(dataset="panCan",d="dis",markers=c("y1","y2"), nsamp=100, resfile="testResfileRocreg",
replace=T)
ROC regression for markers: y1, y2

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                        Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.19   0.15   0.963   1.54
 alpha_1 0.478   0.114   0.284   0.71

****
Model results for marker: y2

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 141
                        Replications   = 100

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 0.789   0.181   0.356   1.06
 alpha_1 1   0.184   0.667   1.33

> #Multiple markers - Try to overwrite existing file
> rocreg(dataset="panCan",d="dis",markers=c("y1","y2"), nsamp=100, resfile="testResfileRocreg")
Error in rocreg(dataset = "panCan", d = "dis", markers = c("y1", "y2"), :
  file specified by resfile already exists, use 'replace' option to replace existing file

> ### Ovarian Cancer dataset
> ovCan <- read.csv("http://www.fhcrc.org/science/labs/pepe/book/data/ocdata_b.csv", header =
TRUE, sep = ",")
> rocreg(dataset="ovCan", d="d", markers=c("y1","y2"))
ROC regression for markers: y1, y2

Percentile value calculation
method: empirical
tie correction: no

GLM fit

link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 1200
                      Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.02   0.092   0.864   1.22
alpha_1 0.953   0.0808   0.813   1.13

****
Model results for marker: y2

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 1200
                      Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 2.17   0.19   1.93   2.66
alpha_1 1.19   0.154   0.99   1.58

> rocreg(dataset="ovCan", d="d", markers="y1", tiecorr=T, pvcmeth="empirical")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: yes

GLM fit
link function: probit - binormal ROC

number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

   ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 1200
                        Replications   = 1000

      Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.02   0.092   0.864   1.22
 alpha_1 0.953   0.0808   0.813   1.13

> rocreg(dataset="ovCan", d="d", markers="y1", link="logit")
ROC regression for markers: y1

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: logit - bilogistic ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 1000

****
Model results for marker: y1

   ROC-GLM model

Bootstrap results

Number of strata = 1   Number of obs   = 1200
                    Replications   = 1000

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.78   0.173   1.49   2.15
alpha_1 1.01   0.088   0.859   1.19

> ### Daryl error - CIs don't contain estimate
> adjCovDat <- read.csv("http://labs.fhcrc.org/pepe/dabs/sj_ms2_fig1_scen1b.csv",header = TRUE, sep
= ",")
> rocreg(dataset="adjCovDat", d="d", markers="y",level=95, nsamp=100)
ROC regression for markers: y

Percentile value calculation
method: empirical
tie correction: no

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls

bootstrap samples: 100

****
Model results for marker: y

  ROC-GLM model

Bootstrap results
Number of strata = 1   Number of obs   = 20000
                    Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
alpha_0 1.55   0.0208   1.51   1.59
alpha_1 0.9   0.0158   0.867   0.928

> rocreg(dataset="adjCovDat", d="d", markers="y",level=95, nsamp=100, adjcov = "z", adjmodel = "stratified")
ROC regression for markers: y

Percentile value calculation
method: empirical
tie correction: no

Covariate adjustment
method: stratified
covariates: z
# of case-containing strata: 2

 Stratum d=0   d=1   Total
 1   8991 5096 14087
 2   1009 4904 5913
 Total   10000 10000 20000

GLM fit
link function: probit - binormal ROC
number of points: 10
on FPR interval: (0,1)

 model coefficient bootstrap se's and CI's based on sampling
 separately from cases and controls
 and from within covariate strata

bootstrap samples: 100

****
Model results for marker: y

  ROC-GLM model

Bootstrap results
Number of strata = 2   Number of obs   = 20000
                   Replications   = 100

     Observed Coef. Bootstrap Std. Err. [95% Conf. Interval]
 alpha_0 1.31   0.0219   1.27   1.35
 alpha_1 0.99   0.0197   0.95   1.03