432 Class 09

https://thomaselove.github.io/432-2023/

2023-02-14

Today's Agenda

- A New NHANES Example
- Logistic Regression Analyses in Project A
  - Establishing a Research Question
  - Identifying / Tidying Outcome and Candidate Predictors
  - Dealing with Missing Data
  - Building a "Main Effects" Model and Plotting Effects
  - Considering Non-Linear Terms
  - Fitting an "Augmented" Model and Plotting Effects
  - Summarizing/Presenting a Final Model
    - In-Sample and Validated Model Summaries
    - Selecting Model Y or Model Z
    - Describing a Meaningful Effect (see Notes, Chapter 22)
    - ROC curve for the Final Model
    - Nomogram for the Final Model

Today's R Setup

```
knitr::opts_chunk$set(comment = NA)

library(nhanesA)
library(broom)
library(caret)
library(janitor)
library(knitr)
library(mosaic)
library(naniar)
library(pROC)
library(rms)
library(simputation)
library(tidyverse)

theme_set(theme_bw())
```

Section 1

The Data

NHANES Data

We'll use data from the 2011-2012 administration of NHANES here, just because I don't want to overlap with any studies people might be thinking about for Project B.

Data bases we'll use are:

- **DEMO_G** for Demographic Variables
- **CDQ_G** for Cardiovascular Health Questionnaire
- **HSQ_G** for Current Health Status Questionnaire
- **BPX_G** for Blood Pressure Examination Results
- **BMX_G** for Body Measures Examination Results
- **MCQ_G** for Medical Conditions Questionnaire

Pulling the Data, I

```
demo_g <- nhanes("DEMO_G") |> tibble(); dim(demo_g)
```

```
[1] 9756   48
```

```
cdq_g <- nhanes("CDQ_G") |> tibble(); dim(cdq_g)
```

```
[1] 3603   17
```

```
hsq_g <- nhanes("HSQ_G") |> tibble(); dim(hsq_g)
```

```
[1] 8956   14
```

Pulling the Data, II

```
bpx_g <- nhanes("BPX_G") |> tibble(); dim(bpx_g)
```

```
[1] 9338   27
```

```
bmx_g <- nhanes("BMX_G") |> tibble(); dim(bmx_g)
```

```
[1] 9338   26
```

```
mcq_g <- nhanes("MCQ_G") |> tibble(); dim(mcq_g)
```

```
[1] 9364   92
```

Merging the Tibbles

```
df_mlist <- list(demo_g, cdq_g, hsq_g, bpx_g, bmx_g, mcq_g)

nh_merge <- df_mlist |>
  reduce(left_join, by = "SEQN") # reduce is from purrr

dim(nh_merge)
```

```
[1] 9756  219
```

We had 224 variables in our original six tibbles, but that counts the SEQN variable six times, and we only have it once in our `nh_merge` tibble.

Now, which of these 219 variables are we actually going to use?

The 7 Variables We'll Use Today

NHANES	Description	Source
SEQN	Identifying code	All 6 files
CDQ010	Shortness of breath on stairs/inclines?	CDQ_G
RIDAGEYR	Age in years at screening	DEMO_G
HSD010	General health condition (E/VG/G/F/P)	HSQ_G
BPXDI1	Diastolic BP (first reading, in mm Hg)	BPX_G
BMXBMI	Body Mass Index (kg/m^2)	BMX_G
MCQ010	Ever been told you have asthma	MCQ_G

Selecting Today's Variables

```
nh_today <- nh_merge |>
  select(SEQN, CDQ010, age = RIDAGEYR, sroh = HSD010,
         dbp = BPXDI1, bmi = BMXBMI,
         asthma = MCQ010) |>
  filter(CDQ010 < 3) |>
  filter(age < 80)

dim(nh_today)
```

```
[1] 3234    7
```

Check the variables, 1

1. SEQN should be unique for each row in the data.

```
identical(nrow(nh_today), n_distinct(nh_today$SEQN))
```

```
[1] TRUE
```

Check the variables, 2

2. CDQ010 was 1 for Yes, 2 for No. We want 1 for Yes, 0 for No.

```
nh_today <- nh_today |> mutate(sbreath = 2 - CDQ010)

nh_today |> count(CDQ010, sbreath) # sanity check
```

```
# A tibble: 2 x 3
  CDQ010 sbreath     n
   <dbl>   <dbl> <int>
1      1       1  1015
2      2       0  2219
```

```
nh_today <- nh_today |> select(-CDQ010) |>
  relocate(sbreath, .after = "SEQN")
```

Check the variables, 3

3. Age should be between 40 and 79 years
4. Body mass index should be between 12.4 and 82.1 kg/m^2
5. Diastolic BP should be between 30 and 120 mm Hg (treat values below 30 as NA)

```
df_stats(~ age + bmi + dbp, data = nh_today) |>
  rename(var = response) |> kable(digits = 1)
```

var	min	Q1	median	Q3	max	mean	sd	n	missing
age	40.0	48.0	57.0	65.0	79.0	57.3	10.7	3234	0
bmi	13.6	24.7	28.3	32.9	82.1	29.5	6.9	3062	172
dbp	0.0	66.0	74.0	80.0	120.0	73.1	12.4	2854	380

Replace dbp values below 30 with NA

```
nh_today |> count(dbp < 30)
```

```
# A tibble: 3 x 2
  `dbp < 30`     n
  <lgl>      <int>
1 FALSE       2842
2 TRUE          12
3 NA           380
```

```
nh_today <- replace_with_na_at(nh_today, "dbp", ~ .x < 30)

favstats(~ dbp, data = nh_today) |> kable(digits = 1)
```

min	Q1	median	Q3	max	mean	sd	n	missing
30	66	74	80	120	73.4	11.6	2842	392

Check the variables, 4

6. `asthma` should be a two-level factor (currently 1 = Yes, 2 = No, 9 = Don't Know, which we'll treat as missing)

```
nh_today |> count(asthma)
```

```
# A tibble: 3 x 2
  asthma     n
   <dbl> <int>
1      1   452
2      2  2779
3      9     3
```

Recoding Asthma as a factor with 3 missing values

```
nh_today <- nh_today |>
  mutate(asthma = fct_recode(
    factor(asthma), "Yes" = "1", "No" = "2", NULL = "9"),
    asthma = fct_relevel(asthma, "No"))

nh_today |> tabyl(asthma) |> adorn_pct_formatting()
```

```
 asthma    n percent valid_percent
     No 2779   85.9%         86.0%
    Yes  452   14.0%         14.0%
   <NA>    3    0.1%             -
```

Check the variables, 5

7. Self-reported overall health should be a five-level factor

```
nh_today <- nh_today |>
  mutate(sroh = fct_recode(factor(sroh), "E" = "1", "VG" = "2"
                                         "F" = "4", "P" = "5"))

nh_today |> tabyl(sroh) |> adorn_pct_formatting() |> kable()
```

sroh	n	percent	valid_percent
E	238	7.4%	8.5%
VG	684	21.2%	24.5%
G	1119	34.6%	40.1%
F	612	18.9%	21.9%
P	136	4.2%	4.9%
NA	445	13.8%	-

Which Variables are Missing?

```
miss_var_summary(nh_today)
```

```
# A tibble: 7 x 3
  variable n_miss pct_miss
  <chr>     <int>    <dbl>
1 sroh        445  13.8
2 dbp         392  12.1
3 bmi         172   5.32
4 asthma        3   0.0928
5 SEQN          0   0
6 sbreath       0   0
7 age           0   0
```

How Many Missing Values?

```
miss_case_table(nh_today)
```

```
# A tibble: 4 x 3
  n_miss_in_case n_cases pct_cases
           <int>   <int>     <dbl>
1              0    2555      79.0
2              1     475      14.7
3              2      75       2.32
4              3     129       3.99
```

Updated Codebook

We have 3234 rows and 7 in the `nh_today` data now. 2555, or 79% of the rows have complete data on these 7 variables.

Name	Description	NHANES Source
SEQN	Identifying code	All 6 files
sbreath	Shortness of breath on stairs/inclines?	CDQ_G (CDQ010)
age	Age in years at screening	DEMO_G (RIDAGEYR)
sroh	Self-reported health (E/VG/G/F/P)	HSQ_G (HSD010)
dbp	Diastolic BP (1st reading, in mm Hg)	BPX_G (BPXDI1)
bmi	Body Mass Index (kg/m^2)	BMX_G (BMXBMI)
asthma	Ever been told you have asthma?	MCQ_G (MCQ010)

- Inclusions/Exclusions: Valid (1 or 0) response to sbreath, age between 40 and 79 years, inclusive.

Section 2

Project A Tasks

Establishing a Research Question

How effectively can we predict whether or not an adult subject has experienced "shortness of breath when hurrying on the level or walking up a slight hill" on the basis of their age, self-reported overall health, diastolic blood pressure, body mass index and whether or not they have been told they have asthma?

- Our data come from NHANES 2011-12, and describe a total of 3234 (unweighted) adult (ages 40-79) subjects.
- We will not use survey weights in this work.

Identifying / Tidying Outcome

Our outcome is the subject's response to the following question:

Have you had shortness of breath either when hurrying on the level or walking up a slight hill?

This was asked of adults ages 40 years and up, as question `CDQ010` on the `CDQ_G` questionnaire in NHANEZS 2011-12, and we've included subjects who gave either a Yes or No response.

```
nh_today |> tabyl(sbreath) |> adorn_totals() |>
  adorn_pct_formatting()
```

```
 sbreath    n percent
       0 2219   68.6%
       1 1015   31.4%
   Total 3234  100.0%
```

Identifying Candidate Predictors

The five predictors we will examine for this outcome are `age`, `sroh`, `dbp`, `bmi` and `asthma`.

Name	Description	Missing?
SEQN	Identifying code	None
sbreath	Shortness of breath on stairs/inclines?	None
age	Age in years at screening	None
sroh	Self-reported health (E/VG/G/F/P)	445
dbp	Diastolic BP (1st reading, in mm Hg)	392
bmi	Body Mass Index (kg/m^2)	172
asthma	Ever been told you have asthma?	3

Dealing with Missing Data

We have excluded all cases with missing `sbreath` so our outcome is complete.

We will assume MAR for the remaining missing values and then use single imputation both to:

- build a Spearman ρ^2 plot
- fit our models Y and Z

If you wanted to use multiple imputation in the project, I would do that at the end, by refitting the "winning" model and summarizing those results (after imputation) only as part of your **Final Model** materials. I might also use `aregImpute()` to get my single imputation, although I won't here.

Single Imputation via simputation

```
set.seed(43212345)
nh_today_i <- nh_today |> data.frame() |>
  impute_rhd(asthma ~ age) |>
  impute_rlm(dbp ~ age + asthma) |>
  impute_rlm(bmi ~ dbp + age + asthma) |>
  impute_cart(sroh ~ age + bmi) |>
  as_tibble()

n_miss(nh_today_i) # should now have no missing data
```

```
[1] 0
```

Resulting nh_today_i tibble

```
nh_today_i
```

```
# A tibble: 3,234 x 7
    SEQN sbreath   age sroh    dbp   bmi asthma
   <dbl>   <dbl> <dbl> <fct> <dbl> <dbl> <fct>
 1 62164       0    44 G        56  23.2 No
 2 62172       0    43 G        70  33.3 No
 3 62177       0    51 G        68  20.1 No
 4 62179       0    55 VG       78  27.6 No
 5 62182       1    75 G        69.6 28.5 No
 6 62191       0    70 G        68  28.5 No
 7 62199       1    57 VG       70  28   No
 8 62200       0    42 VG       88  27.6 No
 9 62201       0    58 G        73.3 28.6 No
10 62209       1    62 F        60  26   No
# ... with 3,224 more rows
```

Section 3

Model Y: The "Main Effects"

Building a "Main Effects" Model and Plotting Effects

First, we'll assume MAR and do our analysis on the (singly) imputed data `nh_today_i`)

```
d <- datadist(nh_today_i)
options(datadist = "d")

modY_si <- lrm(sbreath ~ age + sroh + dbp + bmi + asthma,
               data = nh_today_i, x = TRUE, y = TRUE)
```

modY_si results (from lrm fit)

```
> modY_si
Logistic Regression Model

 lrm(formula = sbreath ~ age + sroh + dbp + bmi + asthma, data = nh_today_i,
     x = TRUE, y = TRUE)

                       Model Likelihood      Discrimination    Rank Discrim.
                             Ratio Test             Indexes          Indexes
 Obs           3234    LR chi2     426.39      R2       0.174    C       0.718
  0            2219    d.f.             8      R2(8,3234)0.121    Dxy     0.436
  1            1015    Pr(> chi2) <0.0001    R2(8,2089.3)0.181    gamma   0.436
 max |deriv| 2e-10                            Brier    0.187    tau-a   0.188

            Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept -4.1132 0.4878 -8.43  <0.0001
 age        0.0149 0.0039  3.79  0.0002
 sroh=VG    0.4849 0.2337  2.07  0.0380
 sroh=G     1.1641 0.2179  5.34  <0.0001
 sroh=F     1.8890 0.2269  8.33  <0.0001
 sroh=P     1.9771 0.2780  7.11  <0.0001
 dbp       -0.0062 0.0038 -1.63  0.1033
 bmi        0.0544 0.0062  8.79  <0.0001
 asthma=Yes 0.7981 0.1111  7.18  <0.0001
```

Key Fit Summary Statistics for Model Y (modY_si)

```
temp <- modY_si$stats
temp["C"]
```

```
        C
0.7181358
```

```
temp["R2"]
```

```
       R2
0.1735251
```

The Nagelkerke R^2 for this model is 0.174 and the C statistic is 0.718.

glm version of this same fit

```
modY_si_g <- glm(sbreath ~ age + sroh + dbp + bmi + asthma,
                 data = nh_today_i,
                 family = binomial(link = logit))
```

```
> modY_si_g

Call:  glm(formula = sbreath ~ age + sroh + dbp + bmi + asthma, family = binomial(link = logit),
    data = nh_today_i)

Coefficients:
(Intercept)          age       srohVG        srohG        srohF        srohP          dbp
  -4.113185     0.014921     0.484919     1.164107     1.888952     1.977082    -0.006171
        bmi    asthmaYes
   0.054416     0.798134

Degrees of Freedom: 3233 Total (i.e. Null);  3225 Residual
Null Deviance:      4024
Residual Deviance: 3598         AIC: 3616
```

```
glance(modY_si_g) |> select(AIC, BIC) |> kable(dig = 1)
```

AIC	BIC
3615.7	3670.4

Tidied Table of Model Y (Exponentiated) Coefficients

Here's the code: result is on next slide.

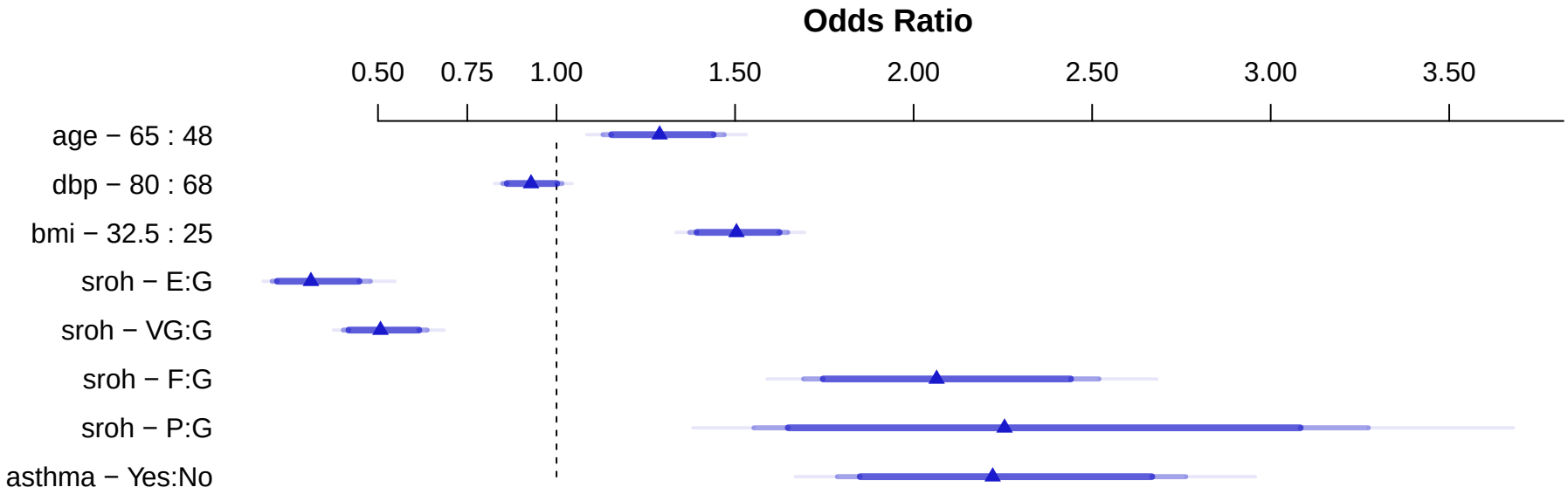
```
tidy(modY_si_g, exponentiate = TRUE,
     conf.int = TRUE, conf.level = 0.90) |>
  select(term, estimate, std.error,
         low90 = conf.low, high90 = conf.high,
         p = p.value) |> kable(digits = 3)
```

Tidied Table of Model Y (Exponentiated) Coefficients

term	estimate	std.error	low90	high90	p
(Intercept)	0.016	0.488	0.007	0.036	0.000
age	1.015	0.004	1.008	1.022	0.000
srohVG	1.624	0.234	1.117	2.415	0.038
srohG	3.203	0.218	2.267	4.652	0.000
srohF	6.612	0.227	4.607	9.737	0.000
srohP	7.222	0.278	4.609	11.519	0.000
dbp	0.994	0.004	0.988	1.000	0.103
bmi	1.056	0.006	1.045	1.067	0.000
asthmaYes	2.221	0.111	1.850	2.667	0.000

Model Y Effects Plot on Odds Ratio Scale

```
plot(summary(modY_si))
```

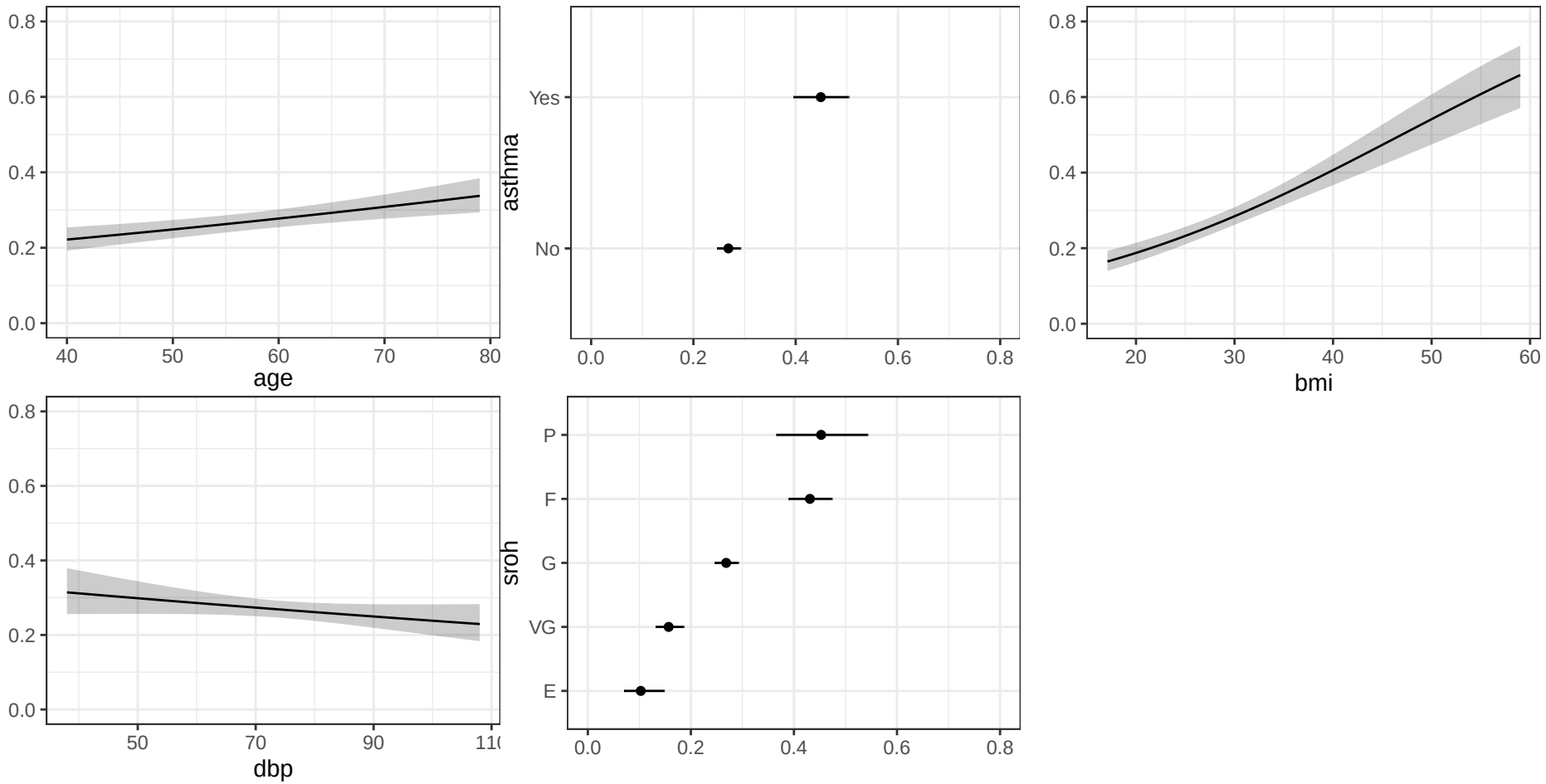


Details of Effects Plot (Model Y)

```
> summary(modY_si)
            Effects                  Response : sbreath

 Factor           Low High Diff. Effect    S.E.      Lower 0.95 Upper 0.95
 age              48  65.0 17.0   0.253660 0.066962  0.12242    0.384900
  Odds Ratio      48  65.0 17.0   1.288700       NA  1.13020    1.469500
 dbp              68  80.0 12.0  -0.074048 0.045455 -0.16314    0.015043
  Odds Ratio      68  80.0 12.0   0.928630       NA  0.84947    1.015200
 bmi              25  32.5  7.5   0.408120 0.046411  0.31716    0.499080
  Odds Ratio      25  32.5  7.5   1.504000       NA  1.37320    1.647200
 sroh - E:G        3   1.0   NA  -1.164100 0.217900 -1.59120   -0.737040
  Odds Ratio       3   1.0   NA   0.312200       NA  0.20369    0.478530
 sroh - VG:G       3   2.0   NA  -0.679190 0.116900 -0.90831   -0.450060
  Odds Ratio       3   2.0   NA   0.507030       NA  0.40320    0.637590
 sroh - F:G        3   4.0   NA   0.724850 0.101520  0.52588    0.923810
  Odds Ratio       3   4.0   NA   2.064400       NA  1.69190    2.518900
 sroh - P:G        3   5.0   NA   0.812980 0.190200  0.44019    1.185800
  Odds Ratio       3   5.0   NA   2.254600       NA  1.55300    3.273200
 asthma - Yes:No   1   2.0   NA   0.798130 0.111120  0.58035    1.015900
  Odds Ratio       1   2.0   NA   2.221400       NA  1.78670    2.761900
```

Prediction Plot for Model Y

```
ggplot(Predict(modY_si, fun = plogis))
```



Confusion Matrix for Model Y

How well does our Model Y classify subjects using a decision rule at 0.5?

```
modY_aug <- augment(modY_si_g, type.predict = "response")

modY_aug <- modY_aug |>
  mutate(pred = ifelse(.fitted >= 0.5,
                       "Predict SB", "Predict No SB"))

modY_aug |> tabyl(pred, sbreath) |>
  adorn_totals(where = c("row", "col")) |> adorn_title()
```

	sbreath		
pred	0	1	Total
Predict No SB	2040	726	2766
Predict SB	179	289	468
Total	2219	1015	3234

- What fraction of our predictions are correct with this decision rule?

Summaries of Classification Accuracy, 1

	sbreath		
pred	0	1	Total
Predict No SB	2040	726	2766
Predict SB	179	289	468
Total	2219	1015	3234

- **Accuracy** is (2040 + 289) / 3234 = 0.720
  - 72.0% of this model's predictions were accurate.
- **Sensitivity** is 289 / 1015 = 0.285
  - 28.5% of those who actually were short of breath are predicted to be short of breath.
- **Specificity** is 2040 / 2219 = 0.919
  - 91.9% of those who actually weren't short of breath were predicted not to be short of breath.

Summaries of Classification Accuracy, 2

	sbreath		
pred	0	1	Total
Predict No SB	2040	726	2766
Predict SB	179	289	468
Total	2219	1015	3234

- **Positive Predictive Value (PPV)** is 289 / 468 = 0.618
  - 61.8% of those predicted to be short of breath actually were short of breath.
- **Negative Predictive Value (NPV)** is 2040 / 2766 = 0.738
  - 73.8% of those predicted to not be short of breath actually were not short of breath.

Using the caret package to get a confusion matrix

```
cmY <- confusionMatrix(
  data = factor(modY_aug$.fitted >= 0.5),
  reference = factor(modY_aug$sbreath == 1),
  positive = "TRUE")
```

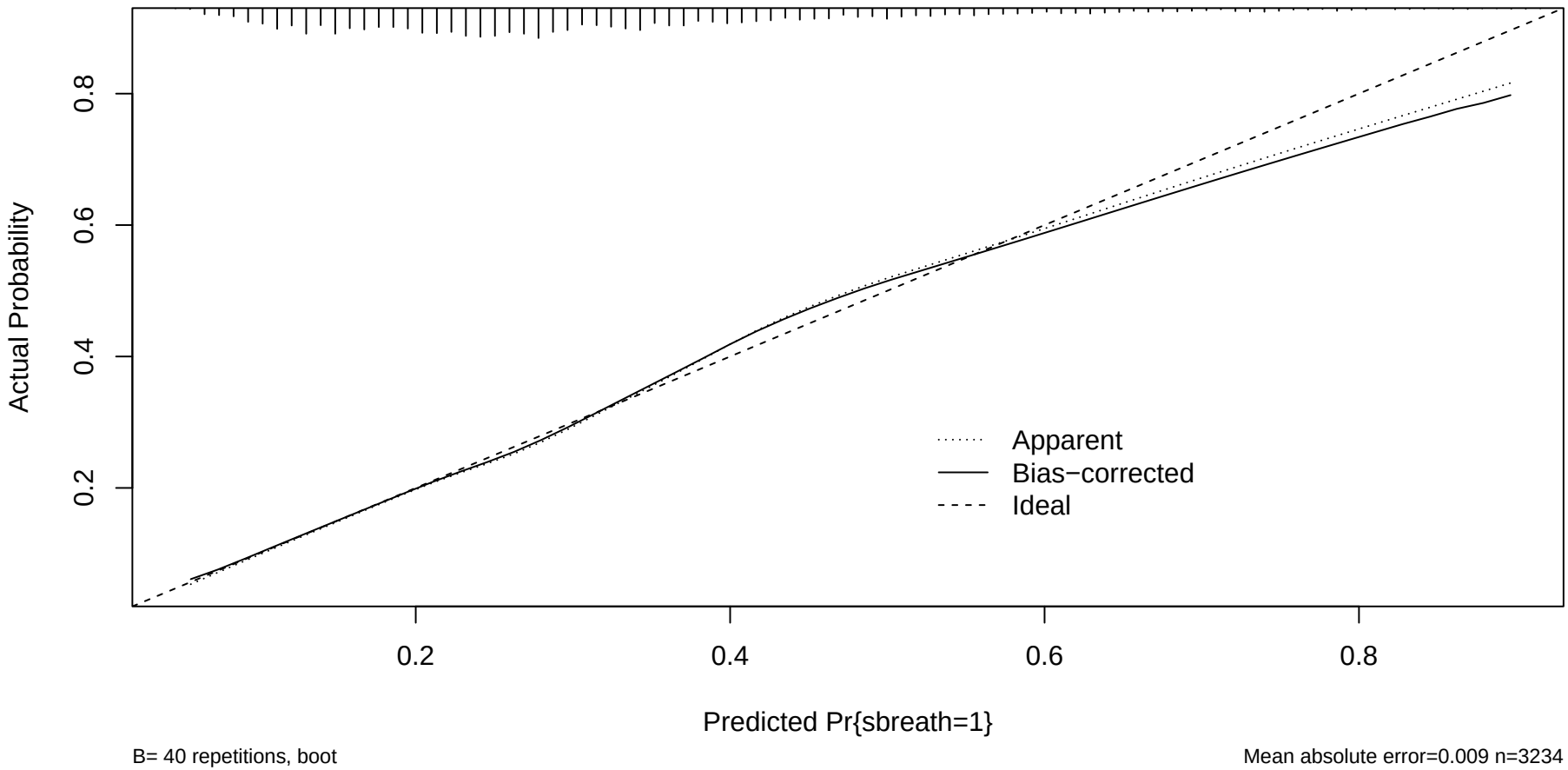
Result on the next slide.

Confusion Matrix Output (from caret) for Model Y

```
> cmY
Confusion Matrix and Statistics

          Reference
Prediction FALSE TRUE
     FALSE  2040  726
     TRUE    179  289

               Accuracy : 0.7202
                 95% CI : (0.7043, 0.7356)
    No Information Rate : 0.6861
    P-Value [Acc > NIR] : 1.393e-05

                  Kappa : 0.239

 Mcnemar's Test P-Value : < 2.2e-16

            Sensitivity : 0.28473
            Specificity : 0.91933
         Pos Pred Value : 0.61752
         Neg Pred Value : 0.73753
             Prevalence : 0.31385
         Detection Rate : 0.08936
   Detection Prevalence : 0.14471
      Balanced Accuracy : 0.60203

       'Positive' Class : TRUE
```

Calibration Plot for Model Y

```
plot(calibrate(modY_si))
```



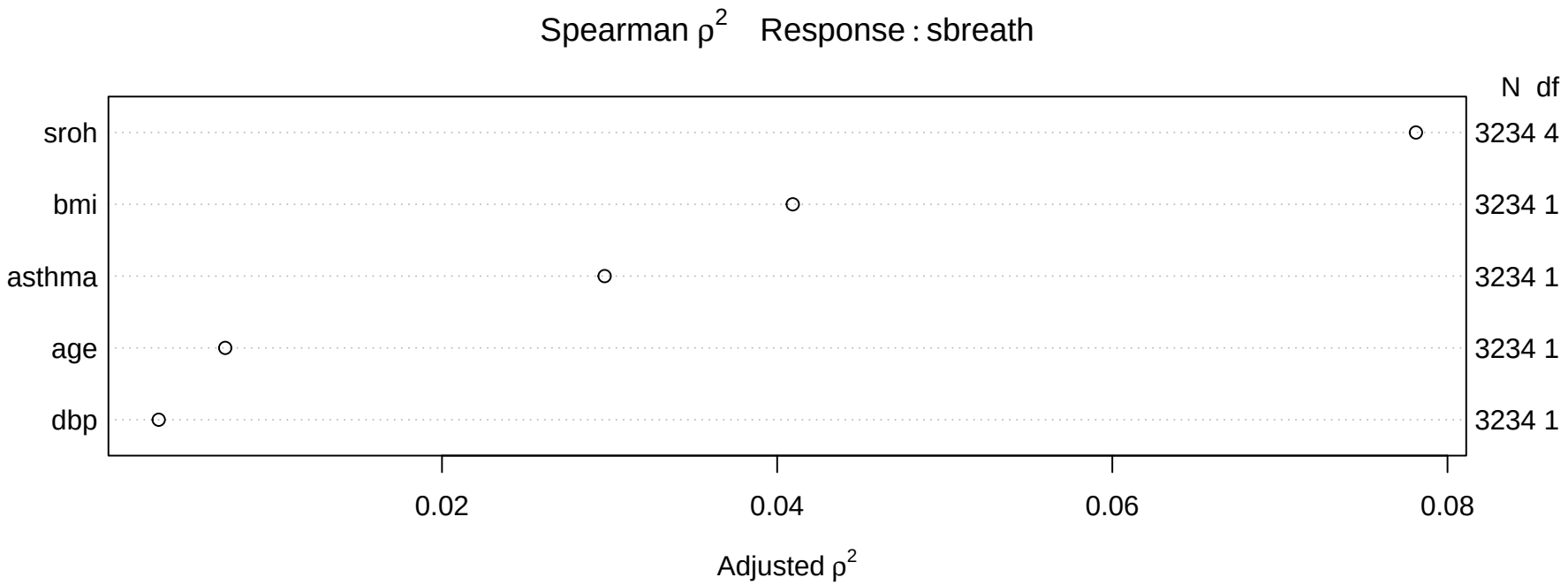
Section 4

Model Z: The "Augmented" model

Considering Non-Linear Terms

- Use 3-6 additional degrees of freedom to account for non-linearity, and add 1-3 non-linear terms.
- We'll start with the Spearman ρ^2 plot...

```
plot(spearman2(sbreath ~ age + sroh + dbp + bmi + asthma,
               data = nh_today_i))
```



Fitting an "Augmented" Model

We'll include the interaction of `sroh` and `bmi`, which will add 4 df, and a restricted cubic spline with three knots in `bmi` (which will add one more), and stop there.

```
## note: datadist has already been set up

modZ_si <- lrm(sbreath ~ age + sroh + rcs(bmi,3) +
                    sroh %ia% bmi + dbp + asthma,
               data = nh_today_i, x = TRUE, y = TRUE)
```

modZ_si results (from lrm fit)

```
> modZ_si
Logistic Regression Model

 lrm(formula = sbreath ~ age + sroh + rcs(bmi, 3) + sroh %ia%
     bmi + dbp + asthma, data = nh_today_i, x = TRUE, y = TRUE)

                       Model Likelihood        Discrimination    Rank Discrim.
                             Ratio Test              Indexes          Indexes
 Obs           3234    LR chi2     428.25       R2       0.174    C       0.719
  0            2219    d.f.            13      R2(13,3234)0.120    Dxy     0.438
  1            1015    Pr(> chi2) <0.0001    R2(13,2089.3)0.180    gamma   0.438
 max |deriv| 4e-09                           Brier    0.187    tau-a   0.189

              Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept    -4.2765 1.1558 -3.70  0.0002
 age           0.0148 0.0039  3.75  0.0002
 sroh=VG       0.4052 1.1722  0.35  0.7295
 sroh=G        1.5974 1.0686  1.49  0.1350
 sroh=F        2.1630 1.0985  1.97  0.0489
 sroh=P        2.9370 1.2318  2.38  0.0171
 bmi           0.0596 0.0387  1.54  0.1235
 bmi'          0.0095 0.0207  0.46  0.6461
 sroh=VG * bmi 0.0023 0.0402  0.06  0.9539
 sroh=G * bmi -0.0151 0.0368 -0.41  0.6811
 sroh=F * bmi -0.0100 0.0376 -0.27  0.7907
 sroh=P * bmi -0.0323 0.0414 -0.78  0.4352
 dbp          -0.0061 0.0038 -1.62  0.1047
 asthma=Yes    0.8017 0.1111  7.21  <0.0001
```

glm version of Model Z

```
modZ_si_g <- glm(sbreath ~ age + sroh + rcs(bmi, 3) +
                   sroh %ia% bmi + dbp + asthma,
                 data =nh_today_i,
                 family =binomial(link =logit))
```

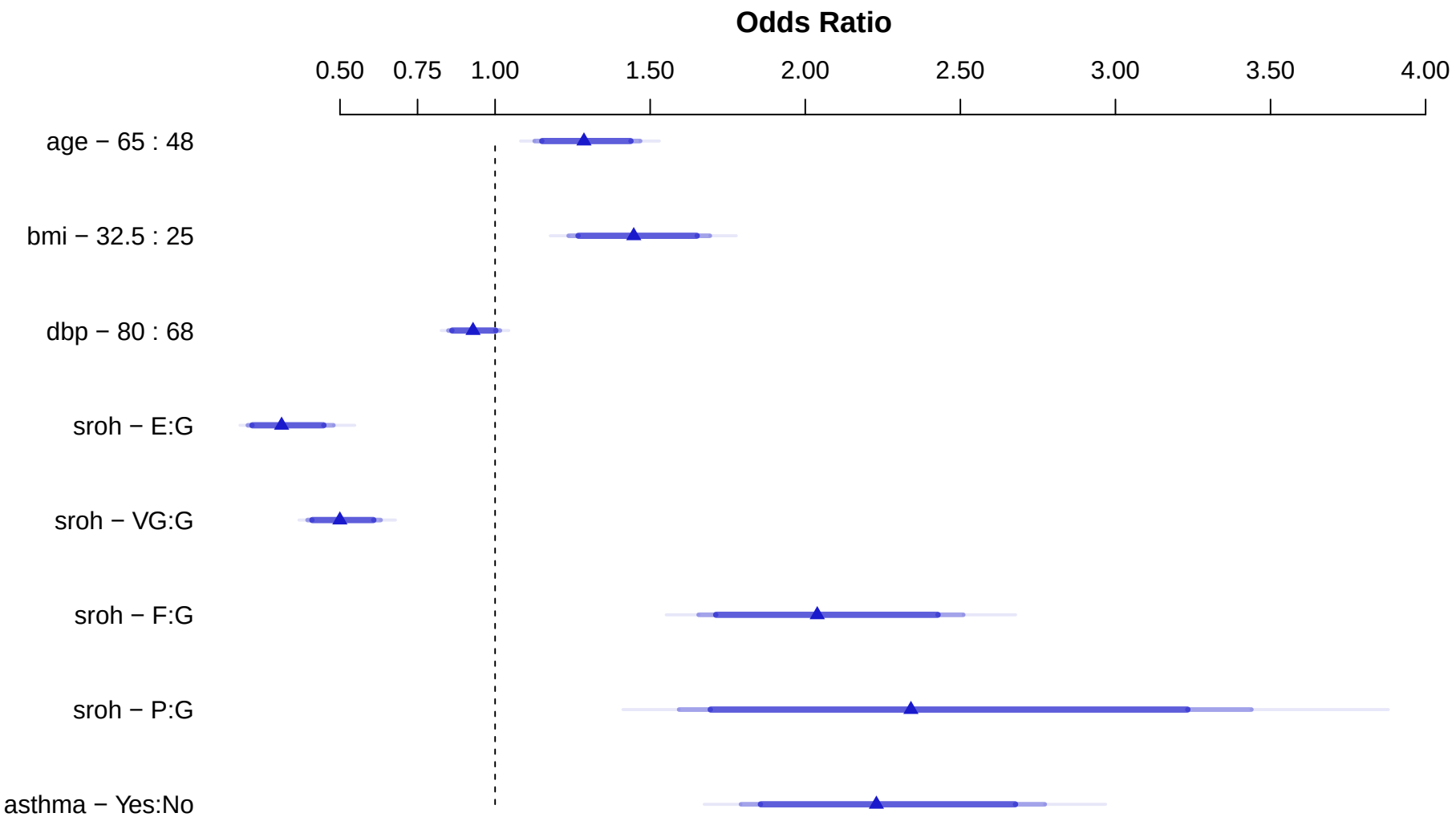
```
> modZ_si_g

Call:  glm(formula = sbreath ~ age + sroh + rcs(bmi, 3) + sroh %ia%
    bmi + dbp + asthma, family = binomial(link = logit), data = nh_today_i)

Coefficients:
                (Intercept)                          age                        srohVG                         srohG
                  -4.276453                     0.014819                     0.405248                     1.597374
                      srohF                        srohP              rcs(bmi, 3)bmi             rcs(bmi, 3)bmi'
                   2.163030                     2.937031                     0.059582                     0.009525
sroh %ia% bmisroh=VG * bmi   sroh %ia% bmisroh=G * bmi   sroh %ia% bmisroh=F * bmi   sroh %ia% bmisroh=P * bmi
                   0.002326                    -0.015125                    -0.009987                    -0.032268
                       dbp                   asthmaYes
                  -0.006146                     0.801692

Degrees of Freedom: 3233 Total (i.e. Null);  3220 Residual
Null Deviance:      4024
Residual Deviance: 3596         AIC: 3624
```

Tidied Table of Model Z (Exponentiated) Coefficients

term	estimate	std.error	low90	high90
(Intercept)	0.014	1.156	0.002	0.092
age	1.015	0.004	1.008	1.022
srohVG	1.500	1.172	0.215	10.758
srohG	4.940	1.068	0.836	30.246
srohF	8.697	1.098	1.402	55.705
srohP	18.860	1.232	2.436	147.704
rcs(bmi, 3)bmi	1.061	0.039	0.995	1.132
rcs(bmi, 3)bmi'	1.010	0.021	0.976	1.045
sroh %ia% bmisroh=VG * bmi	1.002	0.040	0.937	1.072
sroh %ia% bmisroh=G * bmi	0.985	0.037	0.926	1.049
sroh %ia% bmisroh=F * bmi	0.990	0.038	0.930	1.055
sroh %ia% bmisroh=P * bmi	0.968	0.041	0.904	1.038
dbp	0.994	0.004	0.988	1.000
asthmaYes	2.229	0.111	1.857	2.677

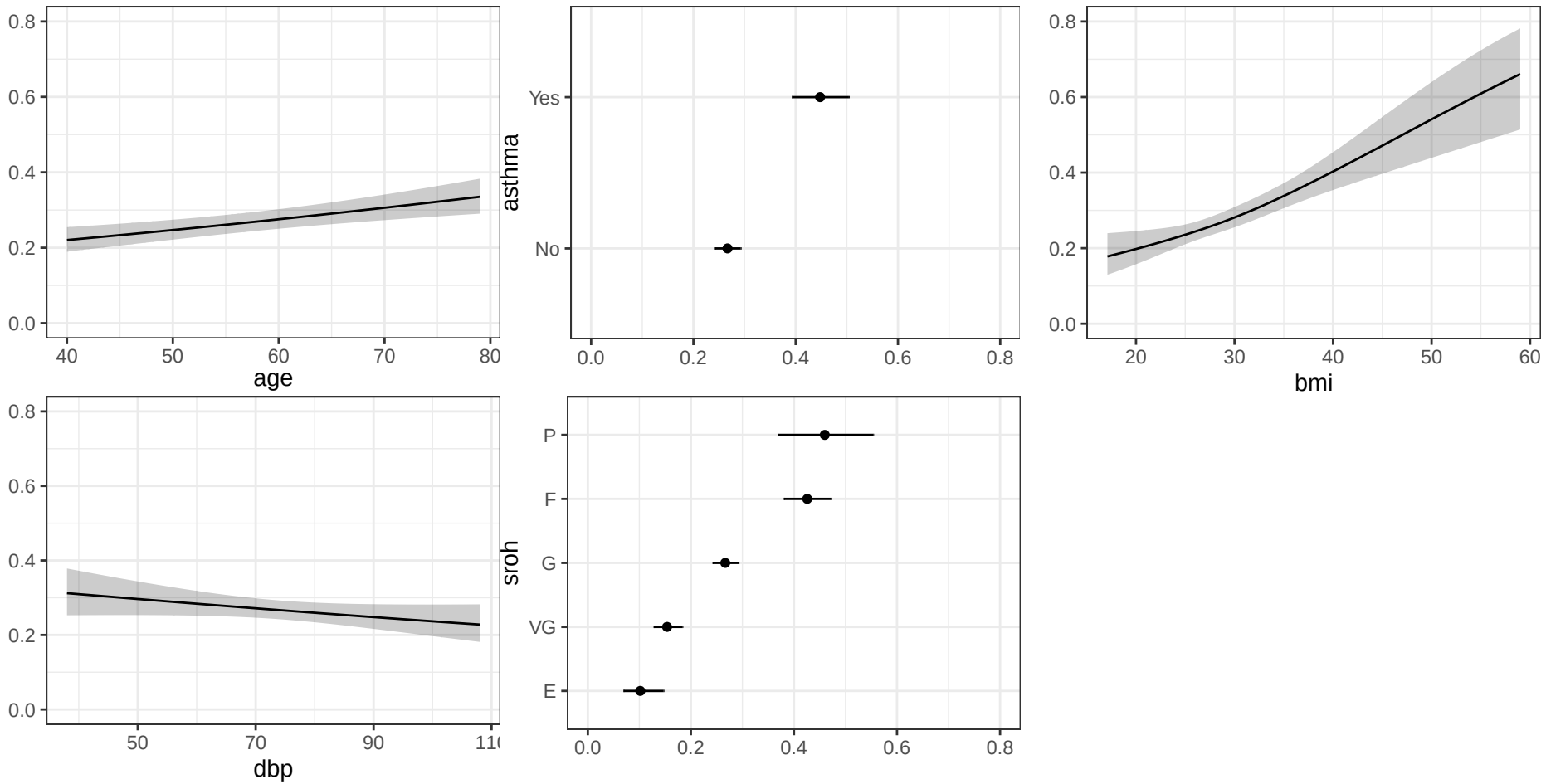
Model Z Effects Plot on Odds Ratio Scale

```
plot(summary(modZ_si))
```



Prediction Plot for Model Z

```
ggplot(Predict(modZ_si, fun = plogis))
```



Confusion Matrix for Model Z

How well does our Model Z classify subjects using a decision rule at 0.5?

```
modZ_aug <- augment(modZ_si_g, type.predict = "response")

modZ_aug <- modZ_aug |>
  mutate(pred = ifelse(.fitted >= 0.5,
                       "Predict SB", "Predict No SB"))

modZ_aug |> tabyl(pred, sbreath) |>
  adorn_totals(where = c("row", "col")) |> adorn_title()
```

	sbreath		
pred	0	1	Total
Predict No SB	2040	725	2765
Predict SB	179	290	469
Total	2219	1015	3234

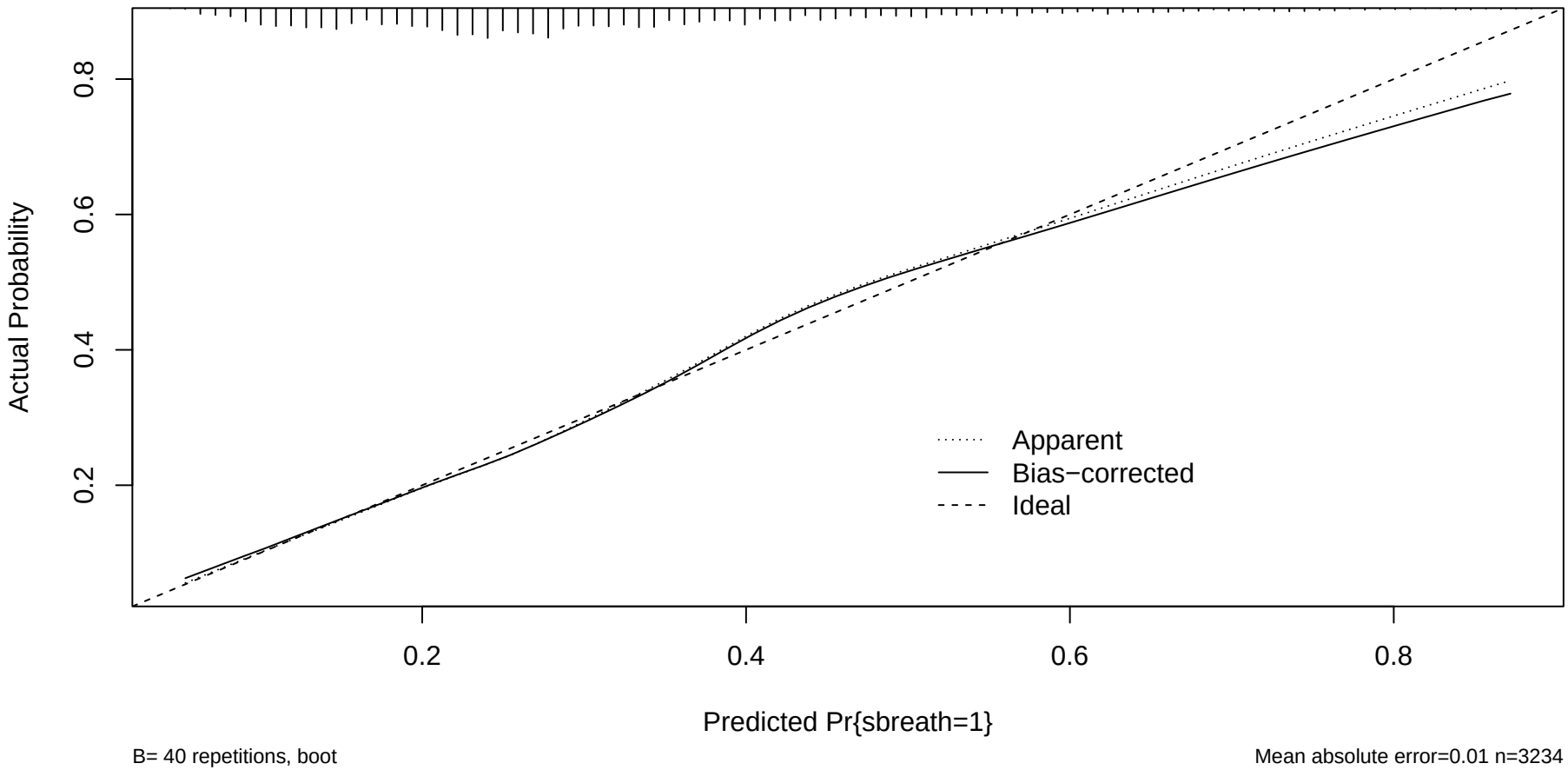
Key Summaries of Classification Accuracy

	sbreath		
pred	0	1	Total
Predict No SB	2040	725	2765
Predict SB	179	290	469
Total	2219	1015	3234

- **Sensitivity** is only slightly changed, to 290 / 1015 = 0.286
  - 28.6% of those who actually were short of breath are predicted to be short of breath.
- **Specificity** is still 2040 / 2219 = 0.919
  - 91.9% of those who actually weren't short of breath were predicted not to be short of breath.
- **Positive Predictive Value (PPV)** is 290 / 469 = 0.618
  - Again, 61.8% of those predicted to be short of breath actually were short of breath.

Calibration Plot for Model Z

```
plot(calibrate(modZ_si))
```



Section 5

Summarizing/Presenting a Final Model

Compare Models Y and Z on Key Summaries

```
temp1 <- bind_rows(glance(modY_si_g), glance(modZ_si_g)) |>
  mutate(model = c("Y", "Z")) |>
  select(model, AIC, BIC)

temp2 <- tibble(model = c("Y", "Z"),
  auc = c(modY_si$stats["C"], modZ_si$stats["C"]),
  r2_nag = c(modY_si$stats["R2"], modZ_si$stats["R2"]))

left_join(temp1, temp2, by = "model") |> kable()
```

model	AIC	BIC	auc	r2_nag
Y	3615.664	3670.398	0.7181358	0.1735251
Z	3623.808	3708.949	0.7188002	0.1742317

ANOVA comparing Model Y to Z

```
> anova(modZ_si)
                Wald Statistics          Response: sbreath

 Factor                                     Chi-Square d.f. P
 age                                         14.08      1   0.0002
 sroh  (Factor+Higher Order Factors)        165.26      8   <.0001
  All Interactions                            1.79      4   0.7745
 bmi  (Factor+Higher Order Factors)          79.65      6   <.0001
  All Interactions                            1.79      4   0.7745
  Nonlinear                                   0.21      1   0.6461
 sroh * bmi  (Factor+Higher Order Factors)    1.79      4   0.7745
 dbp                                         2.63      1   0.1047
 asthma                                     52.03      1   <.0001
 TOTAL NONLINEAR + INTERACTION               1.89      5   0.8642
 TOTAL                                     352.90     13   <.0001
>
```

Validating Model Summaries (code)

```
set.seed(432123)
valY <- validate(modY_si, B = 40)
valZ <- validate(modZ_si, B = 40)

val_1 <- bind_rows(valY[1,], valZ[1,]) |>
  mutate(model = c("Y", "Z"),
         AUC_nominal = 0.5 + (index.orig/2),
         AUC_validated = 0.5 + (index.corrected/2)) |>
  select(model, AUC_nominal, AUC_validated)

val_2 <- bind_rows(valY[2,], valZ[2,]) |>
  mutate(model = c("Y", "Z"),
         R2_nominal = index.orig,
         R2_validated = index.corrected) |>
  select(model, R2_nominal, R2_validated)
```

See next slide for the result.

Validating Model Summaries

```
val <- left_join(val_1, val_2, by = "model")

val |> kable()
```

model	AUC_nominal	AUC_validated	R2_nominal	R2_validated
Y	0.7181438	0.7163131	0.1735251	0.1692934
Z	0.7187991	0.7132489	0.1742317	0.1632280

Which model should we choose?

Describing a Meaningful Effect

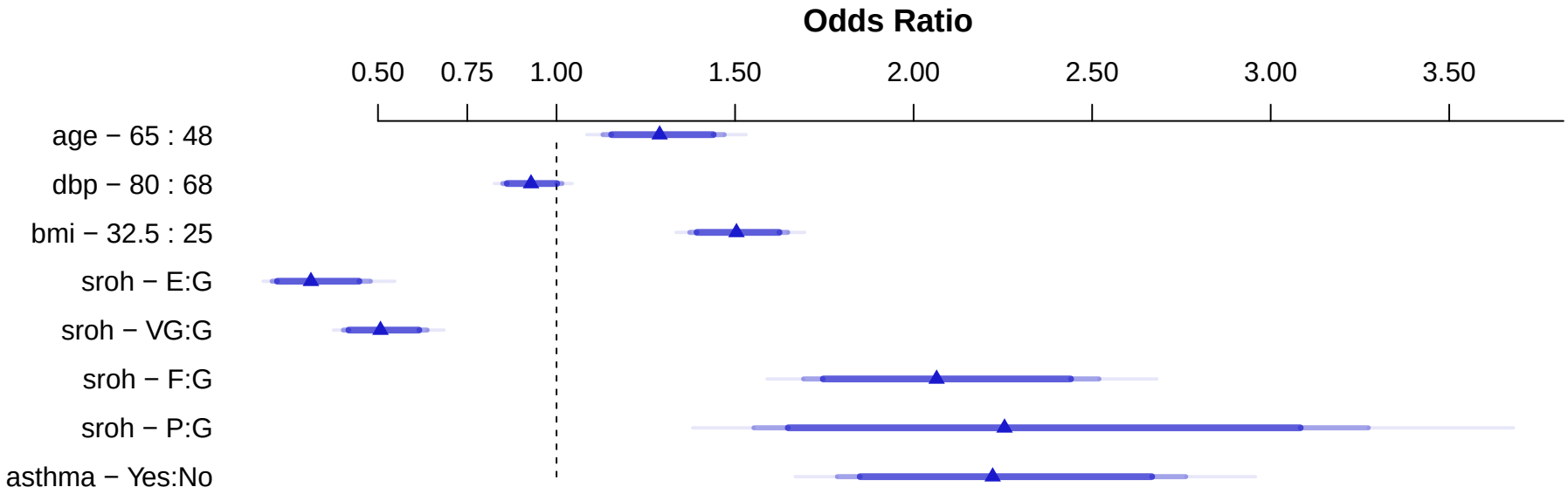
This is for you to do.

> *[W]rite a detailed and correct description of the effect of at least one predictor on your outcome for your chosen logistic regression model, providing all necessary elements of such a description, and link this directly to what the (effects) plot is telling you.*

See Chapter 22 of the Notes for more details, and this is also the major task in several questions within Lab 4. The effects plot for Model Y is repeated in the next slide, and you'll want the actual summary as well as the plot so you can specify the numbers. We prefer you discuss a meaningful effect, should one exist. Pick an effect to describe that is interesting to you.

Model Y Effects Plot on Odds Ratio Scale

```
plot(summary(modY_si))
```



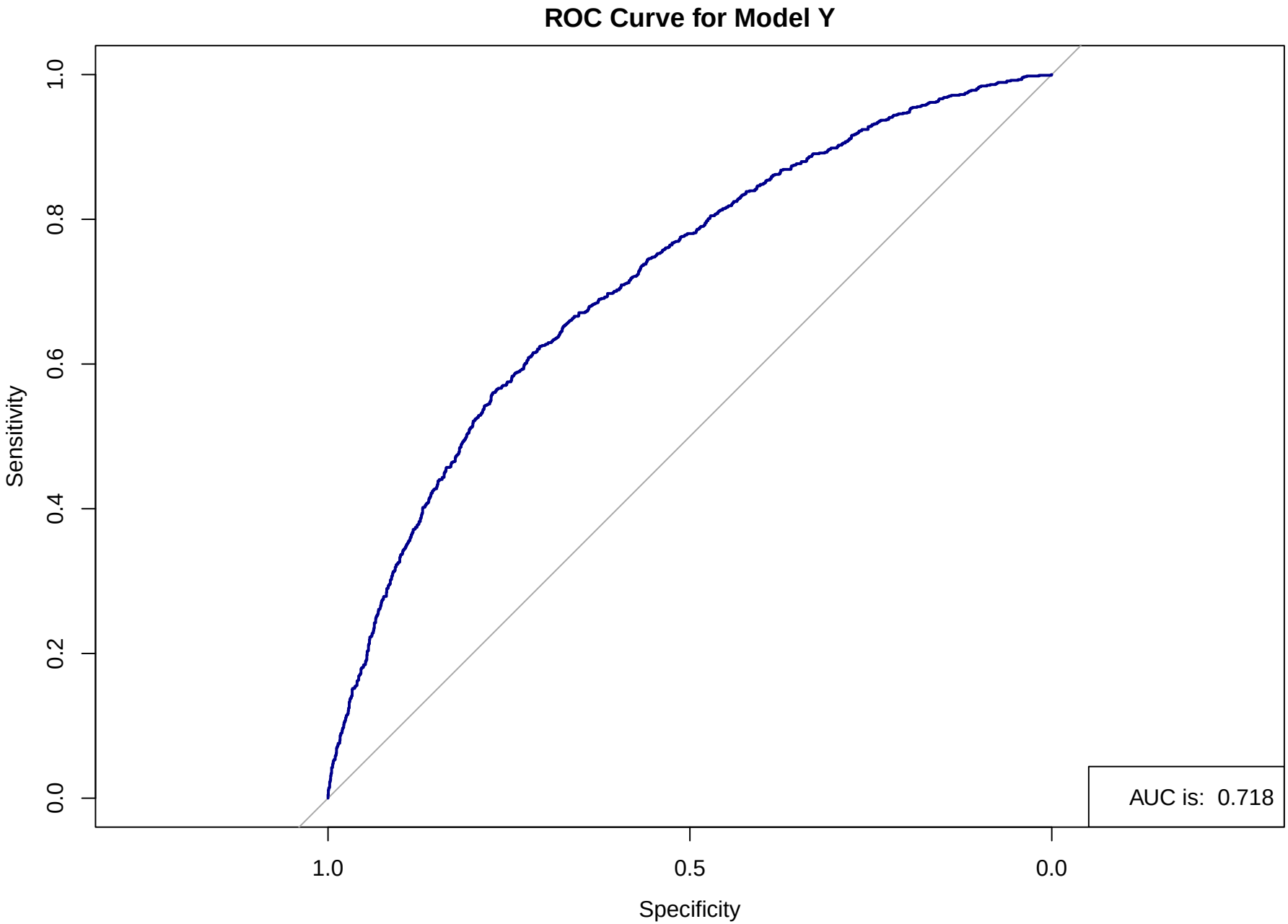
ROC Calculations for Model Y

```
roc_modY <- roc(nh_today_i$sbreath ~
    predict(modY_si_g, type="response"), ci = TRUE)

roc_modY
```

```
Call:
roc.formula(formula = nh_today_i$sbreath ~ predict(modY_si_g,

Data: predict(modY_si_g, type = "response") in 2219 controls (
Area under the curve: 0.7181
95% CI: 0.6992-0.7371 (DeLong)
```

```
plot(roc_modY, main = "ROC Curve for Model Y",
     lwd = 2, col = "salmon")
legend('bottomright',
   legend = paste("AUC is: ",round_half_up(auc(roc_modY),3)))
```

ROC plot for Model Y



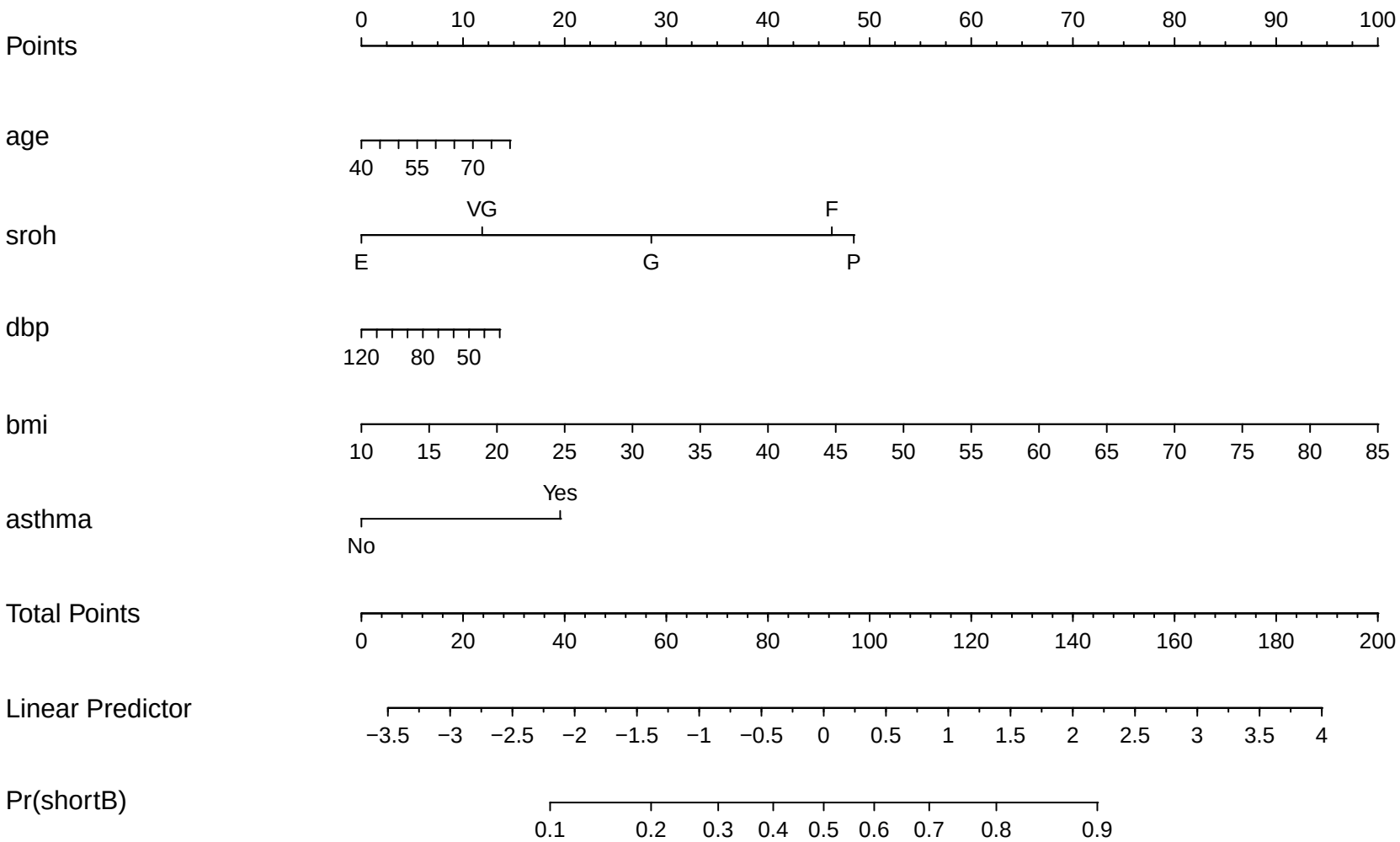
Nomogram for the Final Model (Model Y)

```
plot(nomogram(modY_si, fun = plogis,
              fun.at=c(seq(0.1, 0.9, by = 0.1)),
              funlabel = "Pr(shortB)"))
```

Result on next slide.

- The final part of your summary of the final model should be a nomogram **with a demonstration of a predicted probability associated with two new subjects of interest** that differ in terms of some of the parameters in your model.
- Your predictions should describe two different subjects. You don't have to call them Harry and Sally, but it is helpful to give them actual names.

Nomogram for Model Y



Next Time

More on Logistic Regression

- See section 20 for more on confusion matrices and ROC curves and some material on assessing assumptions through residual plots, all of which are in the context of logistic models fit with `glm()`.
- See section 21 for more on using Spearman's ρ^2 plot, Nagelkerke R^2, the C statistic, its relationship to Somers' d, validation and plotting the results, along with some thoughts on identifying influential points, mostly in the context of logistic models fit with `lrm()`.
- See section 22 for some thoughts on estimating and interpreting effect sizes in logistic and in linear models. Some really useful tips to be found here.