Working with linear and logistics regression models

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Further remarks on logistic regression

- **Diagnostics**: residuals and leverages
- **Test of fit**: The Hosmer-Lemeshow test
- **Enough data?**

General things for regression models:

- **The `lincom` commando**
- **Co-linearity** - correlated explanatory variables
- **What model should I use?**
- **Automatic model selection**
- **The consequences of model selection**

Logistic regression models: Diagnostics

In the linear regression we saw some example of statistics:

residuals, **standardized residuals** and **leverage**

which can be used in the **model checking** and search for strange or **influential** data points.

Such statistics can also be defined for the logistic regression model.

But they are much more **difficult to interpret** and **cannot** in general be **recommended**.

Checking the validity of a logistic regression model will mainly based on **comparing** it with other **models**.

We will return to this later!

Logistic regression models: Test of fit

A common and to some extend informative test of fit is the **Hosmer-Lemeshow** test.

Consider the model for obesity from yesterday

$$\text{logit}\left(\Pr(\text{obese})\right) = \beta_0 + \beta_1 \cdot woman + \beta_2 \cdot (age - 45)$$

```
Logit estimates                                   Number of obs   =       4690
                                                  LR chi2(2)      =      55.68
                                                  Prob > chi2     =     0.0000
Log likelihood = -1767.7019                       Pseudo R2       =     0.0155
------------------------------------------------------------------------------
       obese |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      _Isex_2 |   .2743977   .0903385     3.04   0.002      .0973375    .451458
       age45 |   .0344723   .0051354     6.71   0.000      .0244072    .0445374
       _cons |  -2.147056   .0721981   -29.74   0.000     -2.288561   -2.00555
------------------------------------------------------------------------------
```

Significantly better than nothing - but is it good?

Logistic regression models: Test of fit

What about comparing the **estimated prevalence** with the **observed prevalence**?

In the Hosmer-Lemeshow test the data is **divided** into groups (traditionally 10) according to the **estimated** probabilities

and the **observed** and **expected** counts are compared in these groups by a chi-square test.

Most programs that can fit a logistic regression model can calculate this test.

In STATA it is done by (**after fitting the model**):

`lfit, group(10) table`

The data is divided into **deciles** after the estimated probabilities.

Logistic regression models: Test of fit

OUTPUT

Logistic model for obese, goodness-of-fit test
(Table collapsed on quantiles of estimated probabilities)

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.0841	64	40.9	462	485.1	526
2	0.0953	43	45.5	453	450.5	496
3	0.1045	44	44.6	398	397.4	442
4	0.1112	42	50.3	422	413.7	464
5	0.1217	44	51.4	394	386.6	438
6	0.1332	52	63.0	441	430.0	493
7	0.1456	53	61.7	389	380.3	442
8	0.1592	62	69.8	392	384.2	454
9	0.1834	98	89.9	424	432.1	522
10	0.2407	99	83.8	314	329.2	413

number of observations = 4690
number of groups = 10
Hosmer-Lemeshow chi2(8) = 26.01
Prob > chi2 = 0.0010

One problem: Too many in the tails

Significant difference between observed and expected!

Logistic regression models: Test of fit

```
xi: logit obese i.sex*age45
lfit, group(10) table
Logistic model for obese, goodness-of-fit test
  (Table collapsed on quantiles of estimated probabilities)
```

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.0796	36	35.9	466	466.1	502
2	0.1011	42	41.1	406	406.9	448
3	0.1053	49	49.6	429	428.4	478
4	0.1096	50	54.8	458	453.2	508
5	0.1124	52	54.2	436	433.8	488
6	0.1153	51	46.4	355	359.6	406
7	0.1182	52	53.9	410	408.1	462
8	0.1590	76	70.3	428	433.7	504
9	0.2133	96	91.8	391	395.2	487
10	0.3310	97	103.0	310	304.0	407

number of observations = 4690
number of groups = 10
Hosmer-Lemeshow chi2(8) = 2.43
Prob > chi2 = 0.9650

The models 'fit' - when we look at in this way !!!!!!!

Logistic regression models: Do you have enough data?

All inference in logistic regression models are based on asymptotics , i.e. **assuming that you have a lot of data** !

Rule of thumb:
You should have at least **10 events** per variable (parameter) in the model.

Large standard errors typical indicate that you have to little information concerning the variable and that the **estimate and standard error are not valid.**

Lower your **ambitions** or get **more data** !

Exact methods exist, but only one (**expensive**) program can do it.

And it will give also wide confidence intervals.

The `lincom` command after `logit` or `regress`

Consider the model:

$$\text{logit}\big(\Pr(\text{obese})\big) = \beta_0 + \beta_1 \cdot \text{woman} + \beta_2 \cdot (\text{age} - 45)$$

```
  obese |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
--------+----------------------------------------------------------------
_Isex_2 |   .2743977   .0903385     3.04   0.002     .0973375     .451458
    age |   .0344723   .0051354     6.71   0.000     .0244072    .0445374
  _cons |  -3.698309   .2550901   -14.50   0.000    -4.198277   -3.198342
------------------------------------------------------------------------------
```

Here men are reference.

If we want to find the log odds for a 45 year old women we can calculate by hand -3.698+0.274=-3.424

But what about confidence interval.

We could change the reference to women and fit the model once more.

The `lincom` command after `logit` or `regress`

$$\text{logit}\big(\Pr(\text{obese})\big) = \beta_0 + \beta_1 \cdot \text{woman} + \beta_2 \cdot (\text{age} - 45)$$

STATA has a command that can be used for this: "lincom"

```
lincom _cons+_Isex

 ( 1)  _Isex_2 + _cons = 0
------------------------------------------------------------------------------
obese |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
------+-----------------------------------------------------------------------
  (1) |  -3.423912   .2528214   -13.54   0.000    -3.919432   -2.92839
------------------------------------------------------------------------------
```

You can add , `or` to get odds/odds ratios.

```
 lincom _cons+_Isex,or
 ( 1)  _Isex_2 + _cons = 0
------------------------------------------------------------------------------
  obese | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
--------+---------------------------------------------------------------------
    (1) |   .0325847   .0082381   -13.54   0.000     .0198524     .053483
------------------------------------------------------------------------------
```


The `lincom` command after `logit` or `regress`

$$\text{logit}\big(\Pr(\text{obese})\big) = \beta_0 + \beta_1 \cdot \text{woman} + \beta_2 \cdot (\text{age} - 45)$$

Some examples:

Odds for a 42 year old woman:

```
lincom _cons+_Isex-age45*3,or
 ( 1)  _Isex_2 - 3 age45 + _cons = 0
------------------------------------------------------------------------------
  obese | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
--------+---------------------------------------------------------------------
    (1) |   .1386122   .0088678   -30.89   0.000     .1222772    .1571295
------------------------------------------------------------------------------
```

Odds ratio for 4.5 age difference:

```
lincom age45*4.5,or
 ( 1)  4.5 age45 = 0
------------------------------------------------------------------------------
  obese | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
--------+---------------------------------------------------------------------
    (1) |   1.167804   .0269869     6.71   0.000     1.116091    1.221914
------------------------------------------------------------------------------
```


Colinearity

Consider a subsample of the serum cholesterol data set and the **three** models:

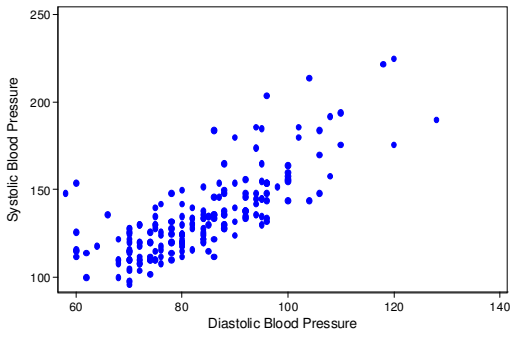
model 0: `regress logscl sex sbp dbp`
model 1: `regress logscl sex dbp`
model 2: `regress logscl sex sbp`

```
    Variable |      model0      model1      model2
-------------+----------------------------------------
         sbp |    .00126448                .0014988
             |    .00087992                .0005548
             |       0.1524                  0.0075
         dbp |    .00056517    .00239702
             |    .00164485     .0010424
             |       0.7315      0.0226
         sex |    .02080574    .02446746    .0197773
             |    .02636149    .02631111    .02613048
             |       0.4310        0.3536       0.4501
       _cons |    5.1444085    5.1555212    5.1615877
             |    .09912234    .09909537    .08539118
             |       0.0000        0.0000       0.0000
-------------+----------------------------------------
           N |         194          194          194
----------------------------------------------------------
                                legend: b/se/p
```

Estimate
Se
p

Each BP-measure is statistical significant, when the other is removed!

Colinearity



SBP and DBP are **highly positively correlated** that will lead to **highly negatively correlated estimates**!!!

Colinearity

This can be seen by listing the **correlation between the estimates.**
In STATA by the command: `vce, cor`

```
regress logscl sbp dbp sex
vce,cor
             |      sbp      dbp      sex    _cons
-------------+------------------------------------
         sbp |   1.0000
         dbp |  -0.7750   1.0000
         sex |  -0.0967   0.1135   1.0000
       _cons |  -0.0780  -0.5044  -0.4665   1.0000
```

If two estimates are highly correlated, it indicates that it is very difficult to estimate the **"independent effect"** of the each of the two variables.

Often it is even **nonsense** to try to do it!

Often it see better to try to **reformulate the problem**.

Colinearity

One way to work around the problem of colinearity is to '**ortogonalize**' it:

Create two new variable:

one measures the **blood pressure**

and another that measure the **difference** in systolic and diastolic blood pressure.

Some **candidates**:

`(sbp+dbp)/2` and `(sbp-dbp)`

`(sbp+dbp)/2` and `(sbp/dbp)`

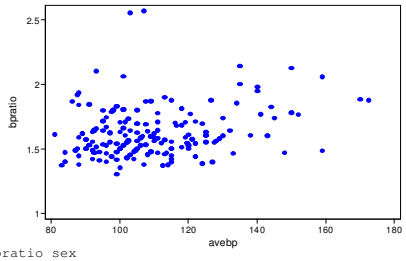
`ln(sbp*dbp)/2` and `ln(sbp/dbp)`

We will here consider the second pair.

Colinearity

`avebp=(sbp+dbp)/2` and `bpratio=(sbp/dbp)`

Only weakly associated




```
regress logscl avebp bpratio sex
vce,cor
             |    avebp  bpratio      sex    _cons
-------------+------------------------------------
       avebp |   1.0000
     bpratio |  -0.2456   1.0000
         sex |   0.0382  -0.1041   1.0000
       _cons |  -0.4542  -0.6874  -0.2585   1.0000
```


Colinearity

The serum cholesterol data set and the **three** models:

model 0: `regress logscl sex avebp bpratio`
model 1: `regress logscl sex avebp`
model 2: `regress logscl sex bpratio`

Variable	model0	model1	model2
avebp	.00198973	.00206564	
	.0007887	.00076285	
	0.0125	0.0074	
bpratio	.02769662		.07148118
	.07067134		.06946246
	0.6956		0.3048
sex	.02060675	.02168128	.01806662
	.02632924	.026128	.02667689
	0.4348	0.4077	0.4991
_cons	5.1003417	5.1351912	5.2485724
	.12936418	.09374803	.11685799
	0.0000	0.0000	0.0000
N	194	194	194

legend: b/se/p

Blood pressure seems to play a role,

The ratio between SBP and DBP might not.

Colinearity

Look out for it:

- systolic and diastolic blood pressure
- 24 hour blood pressure and 'clinical' blood pressure
- weight and height
- age and parity
- age and time since menopause
- BMI and skinfold measure
- age , birth cohort and calendar time
- volume and concentration
- ……

Remember you will need **a huge amount** of data to disentangle the effect for correlated explanatory variables

Which model should I use?

This a hard question!

The first thing to remember is that all models are **approximations**!

The "true" , the "best" or the "correct" model **does not exist!**

The **quality** of a model depends on what you want to use it for.

So the first thing to clarify is:
What is the **purpose** of your analysis – what is the **aim** of your data collection?

Different purposes – different models!!!!!

When found out what you want you still have an **infinity** of models to chose between.

Which model should I use?

The choice is always a choice between **complicated** and **less complicated** models.

Complicated models are often better models, in the sense that they are **better approximation** to the truth.

But complicated models can be:

Very hard to **estimate** – many parameters.

Very hard to **understand**

Very hard to **communicate**

So in these senses they are **not so good** models.

Which model should I use?

Less complicated models are often not as good models, in the sense that they are **not so good approximations** to the truth.

But less complicated models can be:

Easy to **estimate** – few parameters.

Easy to **understand**

Easy to **communicate**

So in these senses they are **better** models.

The first thing to remember is that all models are **approximations**!

Statistics significance has nothing to do with the quality of the model!

Which model should I use?

You can often divide the explanatory variables **into groups**:

Variables of **primary interest- main exposure**

Variables of **less interest** – variables you want to **adjust** for.

A good model will try to introduce the **first** group in an **interpretable** way into model.

- You want to **known** "how they work"

E.g. if you specifically are interested on the "effect" of age you should model age in a **understandable** way.

Still you have to look out for colinearity.

Which model should I use?

The second type of variables can be introduce any way you like.

It can be very complicated – you do not care- as long as they do the job that is **adjust sufficiently**.

If you are not interested in age in itself – you just want to adjust – then age can be introduce in a complicated/weird way, e.g. a fourth order polynomial.

In **general**:

Models with many parameters need more data to obtain precise estimate.

Again few data – lower the ambition !

Automatic model selection

Some programs (even STATA) have programmed algorithms for **automatic model selection**!

That is, procedures that will find the 'best' model to answer you question with out knowing what **you want**, **know** or anything else about the **problem**!

It is very rarely of any interest, especially if you have **little data**.

There are in general three types of such algorithms:

Backward selection : You specify a **start model** and the procedure will reduce the model by **removing** variable from the model until nothing can be removed.

The **criteria** for removing variables are typically **low p-values**.

Automatic model selection

Forward selection : You specify a **start model** together with a **list** of variable that might be included in a model. The procedure will build the model by **adding variable** from the list to the model until nothing can be added.

The **criteria** for removing variables is typically **high p-values**.

Best subset selection: You specify a **list** of variable that might be included in a model and **number** of variables you want in the model. The procedure will then search among the possible models and find the best.

The **criteria** is the typically the **highest likelihood** or related statistics.

Automatic model selection

Some comments:

- These procedures **do not know anything about the subject**.
- They will not consider **transformation** of the variables.
- or **interaction**.
- They will chose **arbitrarily** between explanatory variables that are highly correlated.

Model selection and some implications

Even when you do not use automatic model selection procedures :The **final** model is selected!

That is, you have spend some time **working** with the model you present!

You might choose only to include **statistical significant** variables in the model.

You might group **two levels** of a covariate **into one level** if there is no statistical significant difference between the two groups.

The implications of this selection:

- The **estimates** tend to be to far **away from null**.
- The **standard errors** are to **small**.
- The **CI's** are to **narrow** and the **p-values** to **small**.