# WS #9 - Drop-in-deviance Test

### Math 150, Jo Hardin

Monday, February 23, 2026

Your Name: ______________________________________________

Names of people you worked with: ______________________________________________

Cat or Dog?

**Task:** HERS is a clinical trial to test the efficacy and safety of estrogen + progestin therapy. The logistic model aims to predict whether the individuals had a pre-existing medical condition, `medcond`, using `age`, `drinkany`, and `diabetes`.

```
glm(medcond ~ age + diabetes + drinkany, data = HERS, family="binomial") |> tidy()
```

```
# A tibble: 4 x 5
  term        estimate std.error statistic     p.value
  <chr>          <dbl>     <dbl>     <dbl>       <dbl>
1 (Intercept)  -1.72     0.413       -4.17 0.0000300
2 age           0.0176   0.00605      2.90 0.00369
3 diabetes      0.442    0.0895       4.94 0.000000786
4 drinkany     -0.252    0.0834      -3.01 0.00257
```

```
glm(medcond ~ (age + diabetes + drinkany)^2, data = HERS, family="binomial") |> tidy()
```

```
# A tibble: 7 x 5
  term              estimate std.error statistic  p.value
  <chr>                <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)       -2.14      0.616      -3.47  0.000515
2 age                0.0235    0.00905     2.60  0.00941
3 diabetes           2.65      0.940       2.82  0.00481
4 drinkany          -0.714     0.864      -0.827 0.408
5 age:diabetes      -0.0326    0.0140     -2.33  0.0201
6 age:drinkany       0.00757   0.0128      0.593 0.553
7 diabetes:drinkany -0.153     0.198      -0.770 0.441
```

```r
glm(medcond ~ age + diabetes + drinkany, data = HERS, family="binomial") |> glance()
```

```
# A tibble: 1 x 8
  null.deviance df.null logLik   AIC   BIC deviance df.residual  nobs
          <dbl>   <int>  <dbl> <dbl> <dbl>    <dbl>       <int> <int>
1         3644.    2760 -1799. 3605. 3629.    3597.        2757  2761
```

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```

A likelihood ratio test (LRT) is calculated using the deviances arrived at from `glance()`. The LRT is also called the "drop-in-deviance" test (because the deviance gets smaller, it *drops*).

$$2 * ln(L(null)) = constant - null.deviance$$

$$2 * ln(L(MLE)) = constant - deviance$$

Therefore:

$$-2[ln(L(null)) - ln(L(MLE))] = null.deviance - deviance$$

Conduct a drop in deviance test (also called a likelihood ratio test) to evaluate whether any interaction at all is warranted in the model.

1. Write down the null hypothesis in terms of the relevant $\beta$ values.
2. Find the deviance for the model under the null hypothesis and the deviance for the model under the alternative hypothesis.
3. Using the test statistic (difference in deviances) and the Chi-squared distribution with the appropriate degrees of freedom, calculate the p-value (you'll likely need `pchisq()`).
4. From the p-value, what is the conclusion with respect to the model? That is, which model do you put forward to your client?

**Solution:**

1. Using the second model (the one with interaction terms), $H_0 : \beta_4 = \beta_5 = \beta_6 = 0$
2. null deviance = 3597.325; full model deviance = 3590.151
3. The p-value is computed using the chi-square distribution.

```r
1 - pchisq(3597 - 3590, 3)
```

```
[1] 0.07189777
```

4. Although borderline, the p-value is greater than 0.05 indicating that we can't reject $H_0$. Here that means we don't have evidence to believe that the coefficients are non-zero. In addition to the p-value, we can also use Occam's Razor as a strategy: simple models are often better. So we will not move forward with any interaction terms in the model.