EBM with Doctor Subtypes

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Doctor variation

Now let's take a doctor-centric view. Suppose that doctors (indexed by j) diagnose with a probability that depends on (1) the representativeness of the patient's symptoms, R_i (2) the patients demographics X_i, and (3) the parameters of their own diagnostic habits, $\boldsymbol{\theta}_j = (\beta_{0j}, \beta_{1j}, \beta_{2j})$. Explicitly, for patient i seeing doctor j,

$$D_i \sim_{iid} \text{Bernoulli}\left(\phi(R_i, X_i, \boldsymbol{\theta}_j)\right)$$

where,

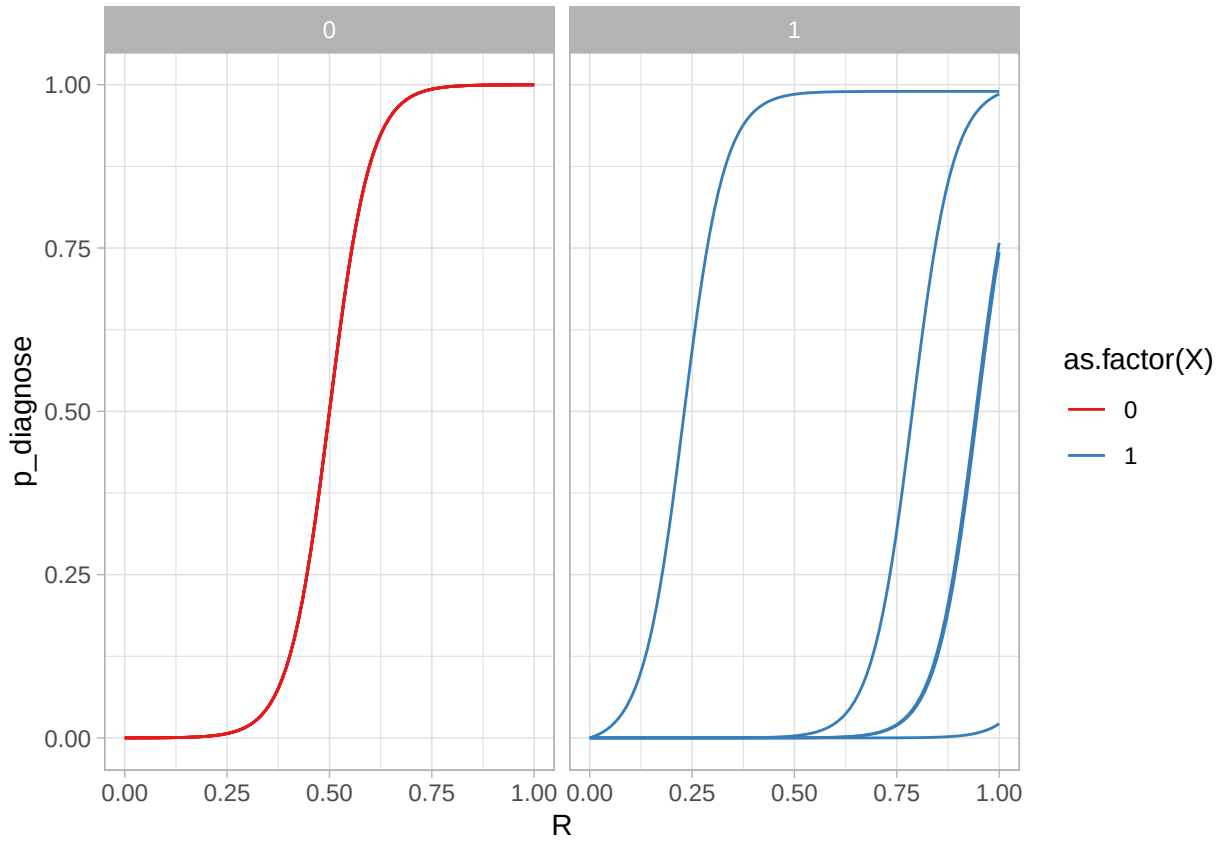
$$\phi(R_i, X_i) = \frac{1}{1 + exp(-(\beta_{0j} + \beta_{1j} R_i + \beta_{2j} X_i))} - c_{x_i \boldsymbol{\theta_j}}.$$

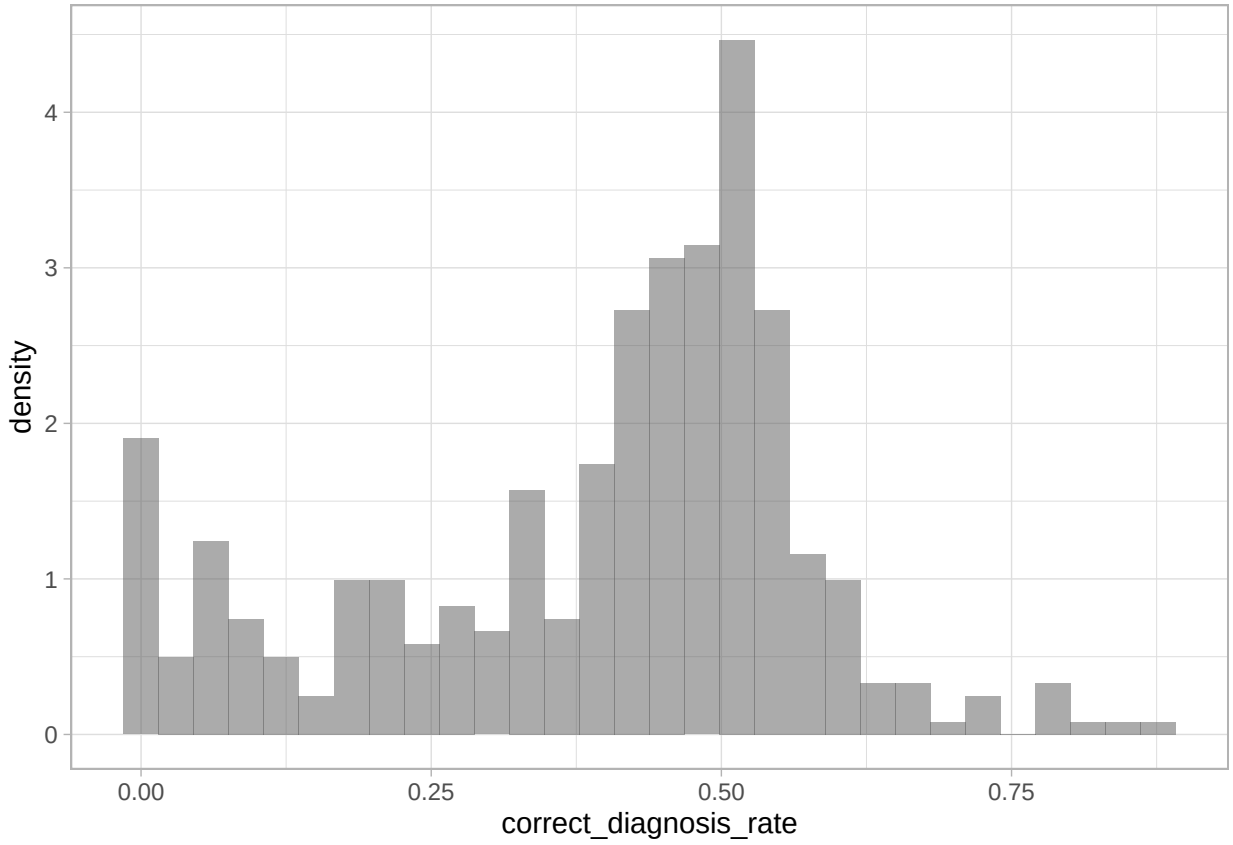
Doctors vary:

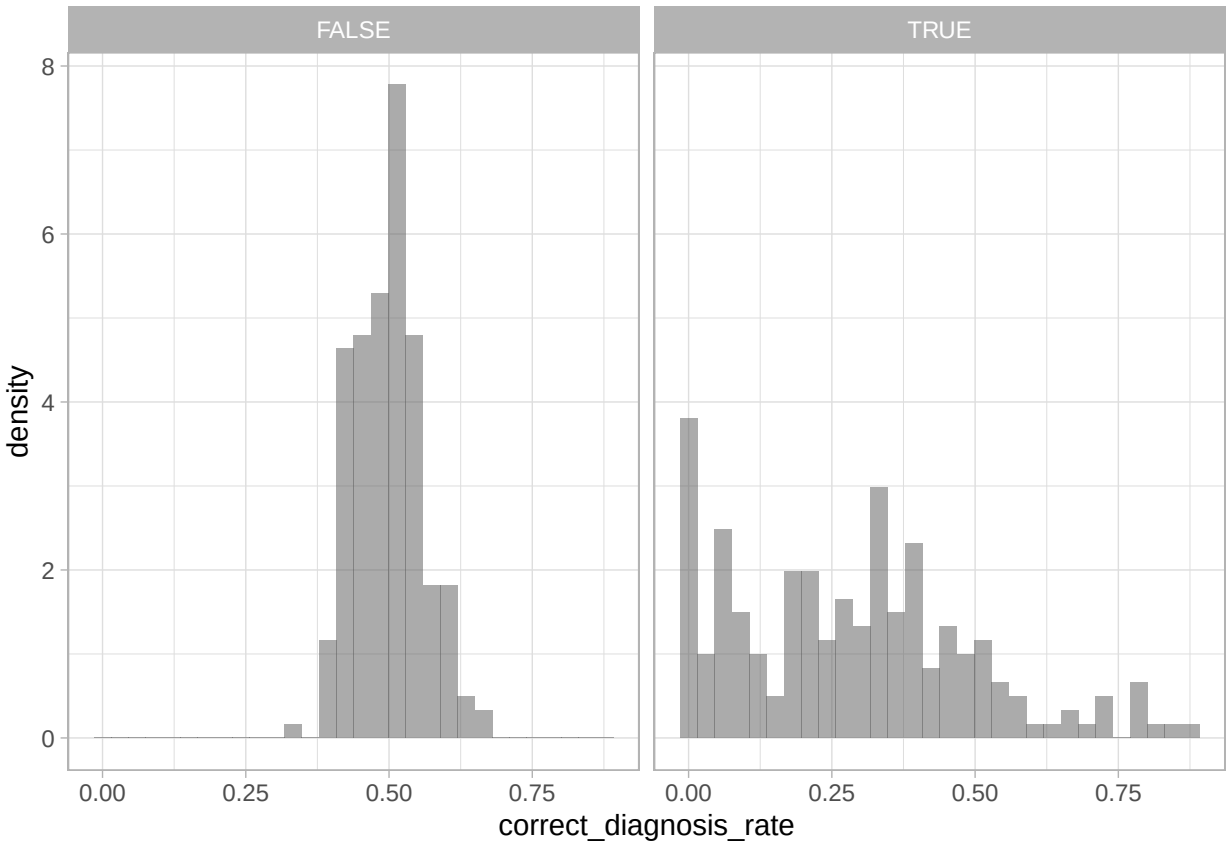
Recall that an ideal diagnostic model would have $\beta_1 = \infty$ and $\beta_2 = 0$, since the only feature that really matters is the symptoms, and in this world the symptoms only emerge when the disease is present. However, doctors aren't perfect at recognizing the symptoms of this disease. Instead, our doctors have their own diagnostic preferences. Some weight the symptoms more heavily and largely ignore demographics; others weight the demographics heavily and are unlikely to diagnose most cases with the disease in the underdiagnosed demographic group.

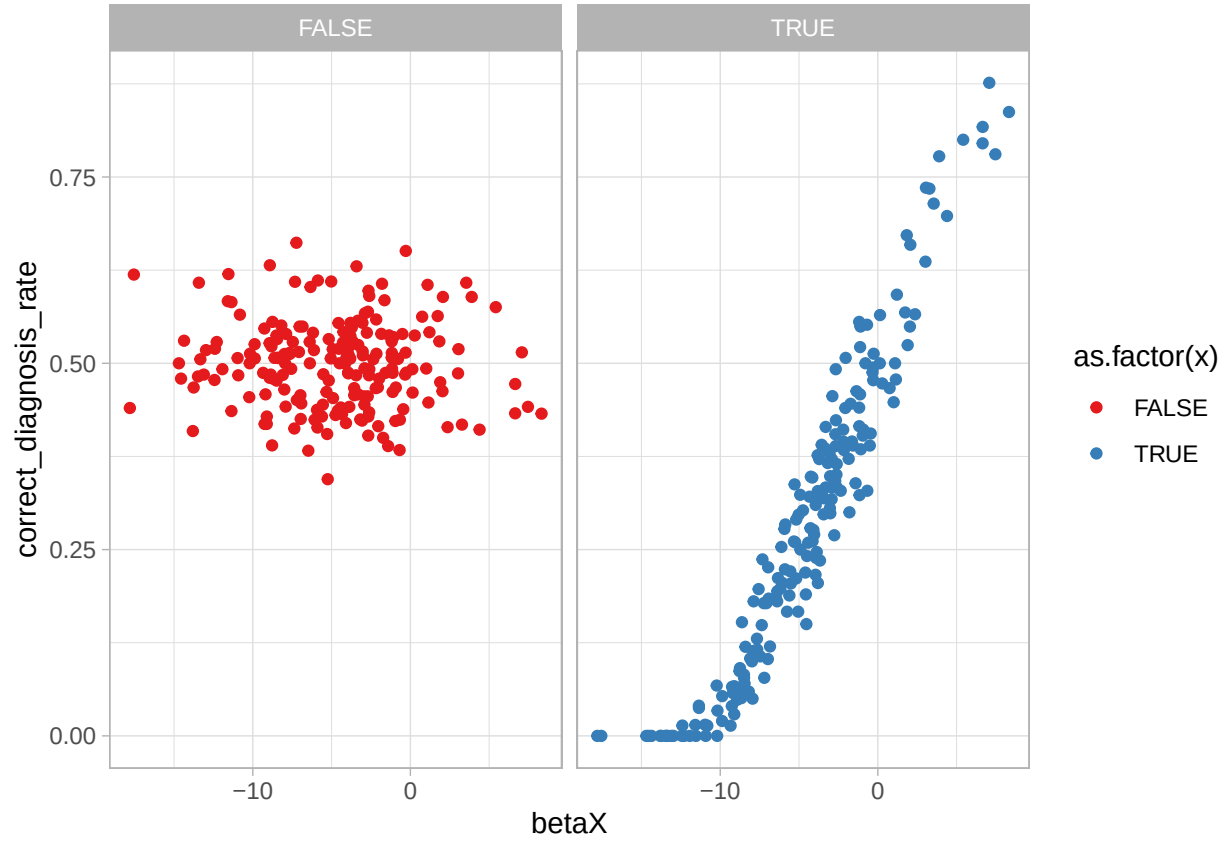
A simple doctor population

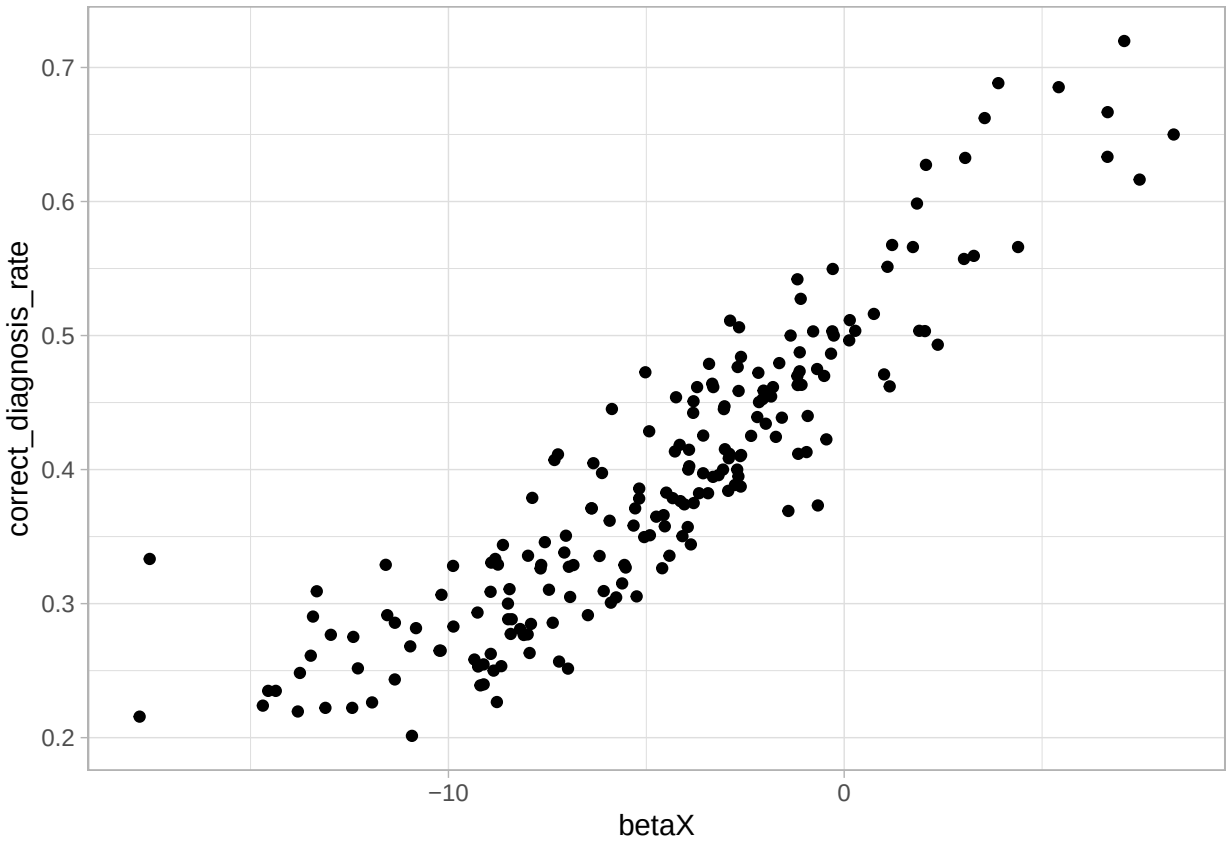
Now let's imagine we have a population of 200 doctors with their own diagnostic practices. Each doctor sees 200 patients a year. A histogram rates of correct diagnosis of disease patients for each doctor is shown below, first as an aggregate, then subsetted by X.


0
1
1.00
0.75
0.50
0.25
0.00
p_diagnose
0.00
0.25
0.50
0.75
1.00
R
as.factor(X)
0
1


4
3
2
1
0
density
0.00
0.25
0.50
0.75
correct_diagnosis_rate


FALSE
TRUE
density
correct_diagnosis_rate
0
2
4
6
8
0.00
0.25
0.50
0.75


FALSE
TRUE
correct_diagnosis_rate
betaX
0.00
0.25
0.50
0.75
−10
0
as.factor(x)
FALSE
TRUE



As expected, the doctors have similar diagnosis patterns when $X = 0$, but type B doctors perform much more poorly when patients with $X = 1$ are considered.

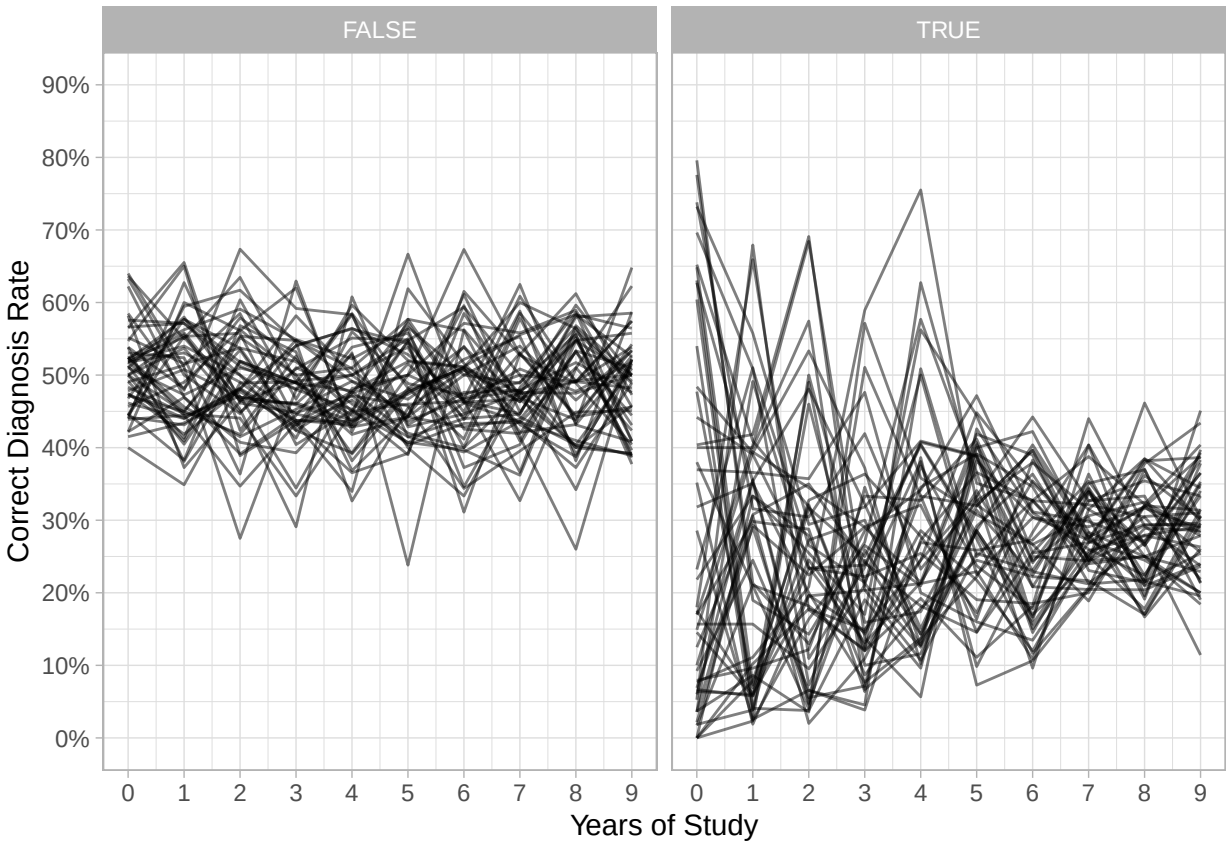
A data-driven diagnostic model

```
##
## Call:  glm(formula = diagnosed ~ x + representativeness, family = "binomial",
##     data = df)
##
## Coefficients:
##        (Intercept)               xTRUE  representativeness
##             -6.078              -2.439              11.831
##
## Degrees of Freedom: 199999 Total (i.e. Null);  199997 Residual
## Null Deviance:       89290
## Residual Deviance: 19080     AIC: 19090
```

What happens over time

Homogenous Doctors

First, let's suppose all doctors have the same diagnostic habits. Let $\theta_A = \theta_B = (-10, 20, -5)$


FALSE
TRUE
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
Correct Diagnosis Rate
0 1 2 3 4 5 6 7 8 9
0 1 2 3 4 5 6 7 8 9
Years of Study