Post test probability of disease in sympomatic and asymptomatic adult after negative BinaxNOW rapid antigen coronavirus test under varying pre-test probabilities

Hopefully this might be of use to someone sometime.

We want to know: given a neagtive BinaxNOW rapid antigen test, what is the probability that someone has a coronavirus infection?

For example per current guidelines if you are exposed, vaccinated and have a negative test you can act differently than if you are exposed, vaccinated and have positive test.

These tests are broadly designed such that a positive result implies positive (there are few false positives, or high specificity), but a negative result might be a false negative. Those last sentences are essentially what is given in the test kit

It is however sort of difficult to interpret this.

We want to know the probability that someone has the disease given a test, 1-NPV This is more intuitive. It is possible to get this, but you have to calculate. So I will do the calculations here

The posterior is

$P(dz+|test-) = \frac{P(test-|dz+)}{P(test-)}P(dz+) = \frac{1-P(test+|dz+)}{P(test-|dz-)P(dz-)+P(test-|dz+)P(dz+)}P(dz+).$

Note that

$Sensitivity = P(test+|dz+)$ $Specificity = P(test-|dz-)$

Hence, $\frac{1-P(test+|dz+)}{P(test-|dz-)P(dz-)+P(test-|dz+)P(dz+)} = \frac{1-sens}{spec*(1-P(dz+))+(1-sens)*P(dz+)}$

the issue is that any posterior probability depends on a prior.
Sometimes this is "prevalence".
However, eg, your prior might be different than the prevalence; you may stay in more, for example, or have had contact recently with an infected individual. For a large prior, we see that a negative test result is not very conclusive. Doing serial testing and getting 2 negative results is more conclusive, but of course it depends on the original prior.

We could of course say that the prior is too difficult to determine and throw our hands up but in doing so we are implicitly acting according to some prior. Hence, here, I will show post test probabilities for a variety of priors. this at least helps us think about what that prior is explicitly

Note that the numbers below are applicable to symptomatic adults or children - both have different sensitivities and specificities. The code could be changed though for that

I checked the number again the PPV/NPV for one of the studies listed below, and it was close but not identical

I also checked my calculation against

Diagnostic test calculator (version 2010042101). Copyright (c) 2002-2006 by Alan Schwartz alansz@uic.edu.

and our values matched. Use this at your own risk however. These are fairly standard calculations, but if you find a mistake defintiely let me know!

To calculate the probability of disease given a negative BinaxNOW test, you must calculate the likelihood ratio, which depends on sensitivity and specificity. Some believe this is not the ideal way to do this. See, eg

Moons, Karel GM, and Frank E. Harrell. "Sensitivity and specificity should be de-emphasized in diagnostic accuracy studies." Academic radiology 10.6 (2003): 670-672. http://hbiostat.org/papers/feh/moons.radiology.pdf

However we must work with these quantities here. Hence

Likelihood ratio

```
like.rat=function(sens,spec,pretest){(1-sens)/((1-sens)*pretest+(spec)*(1-pretest))}
pretest=0.2
```

posterior probability of disease given negative test is likelihood ratio * prior

```
post.test.prob = function(sens,spec,pretest){
  like.rat(sens=sens,spec=spec,pretest=pretest)*pretest
}
```

compute over a grid of priors

```
pre.tests = seq(0,1,0.01)
get.post.tests = function(sens,spec,pretests){
post.tests = c()
for(i in 1:length(pre.tests)){
  post.tests[i]=post.test.prob(sens=sens,spec=spec,pretest=pre.tests[i])
}
post.tests
}
```

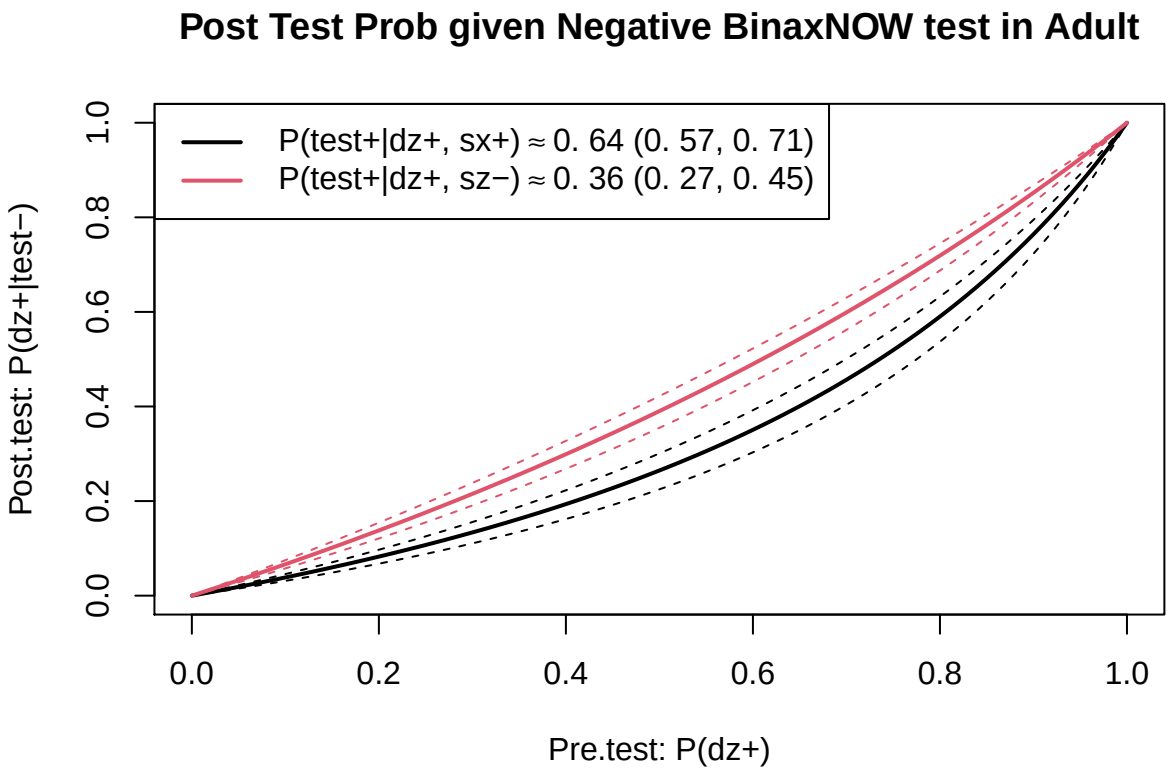
compute separately for two studies [1,2] using sens/spec for asymptomatic each study has diff sens, but similar spec

```
post.tests.6=get.post.tests(sens=0.64,spec=1,pretests)
post.tests.6l=get.post.tests(sens=0.57,spec=1,pretests)
post.tests.6u=get.post.tests(sens=0.71,spec=1,pretests)

plot.p = function(){
lwd.point = 2
plot(pre.tests,post.tests.6,type='l',xlab="Pre.test: P(dz+)",ylab="Post.test: P(dz+|test-)",lty=1,lwd=lw
lines(pre.tests,post.tests.6u,lty=2,col=1)
lines(pre.tests,post.tests.6l,lty=2,col=1)
post.tests.36=get.post.tests(sens=0.36,spec=1,pretests)
lines(pre.tests,post.tests.36,lty=1,lwd=lwd.point,col=2)
post.tests.36u = get.post.tests(sens=.45,spec=1)
post.tests.36l = get.post.tests(sens=.27, spec=1)
lines(pre.tests,post.tests.36u,lty=2,col=2)
lines(pre.tests,post.tests.36l,lty=2,col=2)
legend("topleft",
       c(TeX(" P(test+|dz+,sx+)$\\approx$0.64 (0.57,0.71)"),TeX(" P(test+|dz+,sz-)$\\approx$0.36 (0.27,
       lty=c(1,1),col=c(1,2),lwd=c(lwd.point,lwd.point))
}

png("post.test.png")
plot.p()
dev.off()
```

```
## pdf
```

```
##   2
```

```
plot.p()
```



With serial testing, you update your value on the x axis to reflect your previous post test probability eg if your posterior after one test is 0.2, that becomes your prior for the second test hence serial testing is much better than one test

References

[1] Prince-Guerra JL, Almendares O, Nolen LD, Gunn JKL, Dale AP, Buono SA, Deutsch-Feldman M, Suppiah S, Hao L, Zeng Y, Stevens VA, Knipe K, Pompey J, Atherstone C, Bui DP, Powell T, Tamin A, Harcourt JL, Shewmaker PL, Medrzycki M, Wong P, Jain S, Tejada-Strop A, Rogers S, Emery B, Wang H, Petway M, Bohannon C, Folster JM, MacNeil A, Salerno R, Kuhnert-Tallman W, Tate JE, Thornburg NJ, Kirking HL, Sheiban K, Kudrna J, Cullen T, Komatsu KK, Villanueva JM, Rose DA, Neatherlin JC, Anderson M, Rota PA, Honein MA, Bower WA. Evaluation of Abbott BinaxNOW Rapid Antigen Test for SARS-CoV-2 Infection at Two Community-Based Testing Sites - Pima County, Arizona, November 3-17, 2020. MMWR Morb Mortal Wkly Rep. 2021 Jan 22;70(3):100-105. doi: 10.15585/mmwr.mm7003e3. Erratum in: MMWR Morb Mortal Wkly Rep. 2021 Jan 29;70(4):144. PMID: 33476316; PMCID: PMC7821766.