Predictive Value of P Wave–Triggered Signal Averaging of the Electrocardiogram

Using P wave–triggered signal averaging of the electrocardiogram, Fukunami et al suggested that patients with paroxysmal atrial fibrillation (PAF) can be distinguished from those without, with a sensitivity of 91%, a specificity of 76%, and a positive predictive value of 83%. Using the standard method of calculating predictive accuracy (predictive accuracy=true positives/[true positives+false positives]), there is an error in the calculation. For the population studied, the calculated predictive accuracy using the stated sensitivity and specificity would be 76% and not 83%. However, this error is minor compared with the conceptual error made by the authors when they conclude that they have defined criteria “of clinical use for detecting patients with paroxysmal atrial fibrillation.” The predictive value of a test is dependent on the sensitivity, specificity, and prevalence of the disease in the population being studied. Their population consisted of 42 patients with PAF and 50 controls (i.e., the prevalence of PAF was 46%), thus resulting in a high predictive accuracy. However, this does not represent the prevalence of PAF in the general population or the anticipated prevalence in a population in whom the test might have the greatest potential, that is, in patients with stroke of unknown etiology (cryptogenic stroke).

From previously published data, certain assumptions can be made regarding the likely prevalence of PAF as a cause of stroke. The Lausanne Stroke Registry found that atrial fibillation was present in 8.7% of 778 patients with new nonhemorrhagic strokes. The Framingham study indicated that PAF occurs with approximately the same incidence as chronic atrial fibrillation. Because the risk of thromboembolic stroke in chronic atrial fibrillation is at least twice as great as in PAF, 4–5% of patients at most, in an unselected stroke series, might be anticipated to have PAF as a cause of their stroke. It is reasonable to assume that at least half of these would present with atrial fibrillation, leaving approximately 2.5% of a total stroke population whose stroke can be attributed to paroxysmal arrhythmia but whose presenting rhythm is sinus.

Assuming that there are 500,000 new ischemic strokes per annum in the United States then, based on the Lausanne data, approximately 45,000 (9%) will present in atrial fibrillation. If P wave signal averaging was applied to all 455,000 new strokes presenting in sinus rhythm (500,000–45,000), the predictive value for detecting individuals with PAF within this group will be only 9.7% (as opposed to 83%, calculated by Fukunami et al.). This is computed as follows: 1) Out of the total annual stroke population, patients who are anticipated to have PAF as a cause of their stroke but present in sinus rhythm=2.5%×500,000=12,500. 2) Out of all stroke patients presenting in sinus rhythm (the studied population), those without PAF=455,000–12,500=442,500. 3) True positive tests (sensitivity of 91%)=0.91×12,500=11,375. 4) True negative tests (specificity of 76%)=0.76×442,500=336,300. 5) False positive tests=442,500–336,300=106,200. 6) Predictive accuracy, from formula above=11,375/11,375+106,200=9.7%.

Mohr has suggested that, despite intensive investigations, the cause of stroke eludes diagnosis in approximately one third of cases. Thus 165,000 of the total annual stroke population would be regarded as cryptogenic. Even if the same test were targeted toward this population in whom no obvious cause of stroke could be found, similar calculations would still yield a low predictive value of 23.7%. Thus, using the techniques described by Fukunami, signal averaging of the P wave is not of value for identifying patients at risk of stroke resulting from PAF, particularly because therapy based on a positive test might expose a large number of subjects to unnecessary anticoagulation.

Knowledge of the predictive value of a test is extremely important when assessing the significance of a positive result. However, as seen from our calculations, it is vital to calculate predictive value from the population to which a new test will be applied and not to derive it from an artificial population from which only sensitivity and specificity can be evaluated.

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References


Reply

We thank Drs. Pollack and Falk for their interest in our work. They raised two interesting points: 1) how to calculate the predictive accuracy or value and 2) the importance of prevalence in the general population to use our method as a diagnostic tool. First, we would like to state the difference in the definition of the predictive accuracy and positive predictive value, because they are likely to be confused. "Predictive accuracy is defined as the proportion of all test results, both positive and negative, that are correct, which means the accuracy of the house staff's diagnostic impression" (cited from Reference 2). Accordingly, the predictive accuracy of "Ad>120 msec and LPw<0.5 μV" was calculated as follows.

True positive (38 patients) + true negative (38 patients) = Total number tested (92 patients) × 100

= 83%

On the other hand, "a positive predictive value is defined as the probability of disease with a positive test result" (cited from Reference 2). Accordingly, the positive predictive value is supposed to be calculated as follows.

True positive (38 patients) + true negative (38 patients) × 100

= 76%

The above equation and value are identical to those of "predictive accuracy" that Drs. Pollack and Falk showed in their letter to the editor.

What we calculated in the article was not the positive predictive value of 76% but the predictive accuracy of 83%. We should apologize to them and to the readers for the confusing description in the article (page 166, left column): "Predictive value" of
Predictive value of P wave-triggered signal averaging of the electrocardiogram.
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