Does my patient have SARS-CoV-2 infection? A reminder of clinical probability formulas

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Introduction

Around the world, people are wondering, ‘Do I have SARS-CoV-2?’ Determining a person’s probability of illness is central to the practice and teaching of evidence-based medicine (EBM). Probabilities can be calculated through mathematical formulas, but studies find that many clinicians have difficulty with the calculations.1–4 For many conditions in medicine, clinicians can rely on experience and/or established algorithms. However, with SARS-CoV-2 infection, clinicians lack experience and, given the rapidly changing prevalence of the illness, algorithms are difficult to establish. In this manuscript, we use the example of SARS-CoV-2 as an educational reminder of how clinicians can roughly gauge the probability of illness in different contexts and to highlight some conceptual issues in the estimates needed for the formulas.

Clinical diagnostic process and the formulas

Broadly speaking, the diagnostic process involves a sequence of estimating the probability of an illness and then adjusting this estimate with each new piece of information. Clinicians are generally taught to calculate the probability of illness given new information through either the use of Bayes probability theorem or the use of a 2×2 contingency table.

Mathematically, Bayes theorem and the 2×2 table are the same calculation. The 2×2 table calculation appears less complex than Bayes theorem, because it converts conditional probabilities into numbers that are entered into the cells of the table.

Bayes probability theorem

In writing formulas, the term ‘given’ is symbolised as a straight vertical line. Letting ‘P’=probability, ‘A’SARS-CoV-2 and ‘B’=new information, Bayes probability theorem is: P(A I B)=P(A)×P(B I A)/P(B).

Imagine that B, the new information, is the symptom of a cough. Then the probability of SARS-CoV-2 for a patient given the presence of cough, P(A I B), is equal to the probability of SARS-CoV-2 in the patient’s community, P(A), multiplied by the probability of cough given that the patient has SARS-CoV-2, P(B I A), all divided by the probability of cough in the patient regardless of their SARS-CoV-2 status, P(B).

The 2×2 table calculation shown in table 1 may be more familiar to clinicians as it is often applied to laboratory tests where there is evidence of the accuracy of the test in those with and without the illness. The probability of illness given a positive test is termed the ‘positive predictive value’. The probability of illness given a negative test is the complement of the ‘negative predictive value’.

Clinical scenario

Consider a patient calling into your clinic with a report of a cough and asking, ‘do I have SARS-CoV-2?’ To calculate the probability that this patient has SARS-CoV-2, you would need to estimate: (1) the prevalence of SARS-CoV-2 in the patient’s community, (2) the probability of cough in those with SARS-CoV-2 and also either (3a) the probability of cough in the person regardless of SARS-CoV-2 infection (for Bayes theorem) or (3b) the probability of cough in the person if it were known that they did not have SARS-CoV-2 (for the 2×2 table). This calculated probability then represents the estimated prevalence for further calculations if new information about the patient is gathered, for example, a PCR test.

Assume that the patient is living in a community with a 10% prevalence of SARS-CoV-2, that the prevalence of cough in those with SARS-CoV-2 is 80% and that the probability of cough in the patient irrespective of SARS-CoV-2 is 20%. Furthermore, assume that the PCR test returns positive in 75% with SARS-CoV-2 (75% sensitivity) and returns negative in 95% without SARS-CoV-2 (95% specificity). To apply the formulas, any new information can be considered a test result, for example, the report of a cough can represent a ‘positive cough test’.

The formulas with corresponding figures

In the figures, people are represented as yellow dots, those with SARS-CoV-2 are within the black background and those with a positive test are within the plaid background. The black area that overlaps with the plaid contains those who have SARS-CoV-2 and also test positive. Figure 1 displays a 10% prevalence of SARS-CoV-2; among the 100 yellow dots, 10 (10%) are within the black background. Since 20% of the people have a cough, 20 of the 100 yellow dots are within the plaid background, and since the probability of cough in those with SARS-CoV-2 is 80%, 8 of the 20 in the black background are also within the plaid background. The formulas calculate a 40% probability of SARS-CoV-2 given a cough. This
The prevalence of SARS-CoV-2 in the population and the probability of cough in the patient irrespective of SARS-CoV-2 status were chosen for educational purposes.
EBM learning

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EBM learning has recently published an interactive online graphic that allows readers to input different estimates of pretest probability, sensitivity and specificity and then calculate the probability of illness given a test result.7

Some conceptual issues in the estimates needed for the formulas

The prevalence of the illness (here, SARS-CoV-2) in the patient’s community

The prevalence or the ‘pretest probability’, symbolised as P(A) in Bayes theorem, is the probability that a person like our patient has the illness prior to knowing the additional information (test result). For many conditions in medicine, this estimate may be highly subjective. The current situation with SARS-CoV-2 is unique as many communities are receiving daily reports of community prevalence. Of course, if the patient has been exposed to someone with SARS-CoV-2 or is living in a specific area with a surge of SARS-CoV-2 cases, then the pretest probability estimate should be higher than the prevalence in the larger community.

The probability of the new information (here, the report of cough or the negative PCR test) in those with the illness (here, SARS-CoV-2)

The probability of the new information (test result) occurring in those with the illness is symbolised as P(B|A) in Bayes theorem. The evidence for this probability comes from people with known illness. In the case of SARS-CoV-2, many with the virus are asymptomatic and may not be included in studies. Consequently, studies reporting the probability of a symptom in those with SARS-CoV-2 likely overestimates the probability of the symptom in all with SARS-CoV-2.

There is another reason why evidence may overestimate the probability of a symptom given an illness. Imagine that the patient with the cough in our example also denied having a fever. We

Figure 2  The prevalence of 40% was calculated in Figure 1. The sensitivity and specificity were selected from a range of values in different studies.7–9

CALCULATIONS

BAYES THEOREM CALCULATION

Let A = SARS-CoV-2
Let B = PCR negative
P(A | B) = P(A) x P(B|A) / P(B) = 0.40 × 0.25 / 0.60 = 0.15 = 15%

2X2 TABLE CALCULATION

<table>
<thead>
<tr>
<th>SARS-CoV-2</th>
<th>No SARS-CoV-2</th>
<th>Probability of SARS-CoV-2 given PCR-</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCR+</td>
<td>6</td>
<td>1</td>
</tr>
<tr>
<td>PCR-</td>
<td>2</td>
<td>11</td>
</tr>
<tr>
<td>Population</td>
<td>8</td>
<td>12</td>
</tr>
<tr>
<td>2/13 = 15%</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 2 The prevalence of 40% was calculated in Figure 1. The sensitivity and specificity were selected from a range of values in different studies.7–9
are now interested in the proportion with SARS-CoV-2 who have cough but are without fever, yet evidence from studies is rarely so granular. For example, the US Naval Theodore Roosevelt ship provides evidence of symptoms in non-hospitalised sailors with SARS-CoV-2. Approximately 35% of those with SARS-CoV-2 had a cough, and a similar proportion had a fever. Clearly, sailors with a cough and no fever represent a subset of the 35% sailors with SARS-CoV-2 who had a cough. So, relying solely on this information, the probability of a cough and no fever would be lower than 35%.

The probability of a positive test given illness is termed the sensitivity. For the conditional probabilities of sensitivity and specificity (the probability of a negative test given no illness), clinicians are often taught the message of a 1975 publication that stated, ‘For tests with binary outcomes, these measures are fixed.’ However, the measures are fixed only within a population similar to the particular patient and under the same testing circumstances. As an example, the sensitivity of the PCR test for SARS-CoV-2 differs depending on a variety of issues, such as time since exposure, symptoms and age.

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**The probability of the new information (here, the report of cough or the negative PCR test) in those without the illness (here, without SARS-CoV-2)**

The probability of the new information in those without the illness is termed the specificity with a negative test result or the false-positive rate with a positive test result. This probability contributes to the denominator of both formulas, that is, P(B) in Bayes theorem. If the patient with a cough also had an underlying reason for coughing such as asthma, then the probability of cough without SARS-CoV-2 would be higher than if the patient had no underlying reason for developing a cough. With consistency in prevalence and sensitivity, the higher the probability of the new information in those without the illness, the lower the calculated probability of SARS-CoV-2 infection.

**Conclusion**

The current pandemic has clinicians around the world trying to gauge the likelihood that their patients have SARS-CoV-2. The purpose of this manuscript is to remind clinicians of two forms of a calculation to determine the probability of illness when presented with new information such as a patient symptom or the result of a laboratory test. The original Bayes probability theorem uses only proportional factors. The 2×2 contingency table calculation may be more familiar to clinicians and can be solved by converting the proportional factors of the Bayes formula into numbers for the cells of the table. The calculations require estimates that may be speculative and clinicians should recall that EBM recognises uncertainty, asking clinicians to use the "best available evidence." Understanding the calculations as well as the uncertainties inherent in some of the estimates needed for the calculations may help clinicians answer patient questions about SARS-CoV-2 as well as for more routine medical conditions.

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