Quantitative Analysis for

Interpreting Diagnostic Tests for Covid-19

Rev. Thomas Bayes Can Help

Yakov Ben-Haim[1]

Contents

1 Introduction: Epidemiological Problem and Background

Clinical response to the covid-19 epidemic depends, in part, on interpreting diagnostic PCR tests of body fluids. Serological surveys assess disease prevalence.

The Positive Predictive Value of a test (PPV) answers the question: What is the probability that a positive test indicates presence of disease? In statistical terms it is a conditional probability: the probability that a person is sick given that the person's test is positive. The Negative Predictive Value of a test (NPV) is the conditional probability that the person is not sick, given a negative test result.

The PPV and NPV are crucial in clinical decision making. If the PPV is large, then clinical intervention is strongly indicated for people whose tests results are positive. Similarly, if the NPV is large, then intervention is not indicated for people with negative test results. However, both PPV and NPV depend on test results (positive or negative) and other probabilities that may be very uncertain. We use info-gap theory to explore the robustness to this uncertainty.

More background discussion is available. See working paper:
Yakov Ben-Haim and Shai Linn, Preliminary thoughts on Interpreting Diagnostic Tests for Covid-19: Rev. Thomas Bayes Can Help
File: \papers\corona-diag-prob2020\viewpoint010.docx

\papers\corona-diag-prob2020\cdp005.tex. 26.4.2020.

[1]Yitzhak Moda'i Chair in Technology and Economics, Technion—Israel Institute of Technology, Haifa, Israel. yakov@technion.ac.il

2 Definition of Probabilities

Consider a new and unfamiliar disease such as covid-19, and for now consider only a single diagnostic test. Define the following variables.

t_+ denotes a positive result of the diagnostic test, indicating presence of the disease in the tested person.

t_- denotes a negative result of the diagnostic test, indicating absence of the disease in the tested person.

s_+ denotes actual presence of the disease in the tested person.

s_- denotes actual absence of the disease in the tested person.

$p(s_+)$ is the probability that the disease is present in an individual chosen randomly from the population. This is the fraction of the population that is infected. It is called the **prevalence** of the disease. It can be estimated from epidemiological data about the disease, but at present its true value is highly uncertain due to our lack of knowledge about the current health of the population. We will subsequently denote the prevalence as π. Its estimated value is denoted $\widetilde{\pi}$.

$p(t_+|s_+)$ is the conditional probability of a positive test result for a person, given true presence of the disease in that person. It is called the **sensitivity** of the test, and a large value is desirable. It can be estimated from laboratory data on the test for this disease. We will subsequently denote the sensitivity as σ. The sensitivity is a property of the test, and its value is fairly reliably known.

$p(t_-|s_-)$ is the conditional probability of a negative test result for a person, given true absence of the disease in that person. It is called the **specificity** of the test, and a large value is desirable. It can be estimated from laboratory data on the test for this disease. We will subsequently denote the specificity as ψ. The specificity, like the sensitvity, is a property of the test, and its value is fairly reliably known.

$p(s_+|t_+)$ is the conditional probability that the disease is actually present in a tested person, given a positive test result for that person. This is called the **positive predictive value** (PPV) of the test, and is of great clinical significance.

$p(s_-|t_-)$ is the conditional probability that the disease is actually not present in a tested person, given a negative test result for that person. This is called the **negative predictive value** (NPV) of the test, and is of great clinical significance.

From Bayes' law and the definition of complete probability, we can relate the PPV, $p(s_+|t_+)$, to the prevalence and the test characteristics, as:

$$
\begin{aligned}
p(s_+|t_+) &= \frac{p(t_+|s_+)p(s_+)}{p(t_+|s_+)p(s_+) + p(t_+|s_-)p(s_-)} && (1)\\
&= \frac{p(t_+|s_+)p(s_+)}{p(t_+|s_+)p(s_+) + [1 - p(t_-|s_-)][1 - p(s_+)]} && (2)\\
&= \frac{\sigma\pi}{\sigma\pi + (1-\psi)(1-\pi)} && (3)\\
&= \frac{\sigma}{\sigma + (1-\psi)\left(\frac{1}{\pi} - 1\right)} && (4)
\end{aligned}
$$

We note that σ, π and ψ are all probabilities, so their values all fall in the interval $[0,\ 1]$.

Likewise, the NPV, $p(s_-|t_-)$, is related to the prevalence and the test characteristics, as:

$$
p(s_-|t_-) = \frac{p(t_-|s_-)p(s_-)}{p(t_-|s_-)p(s_-) + p(t_-|s_+)p(s_+)} \qquad (5)
$$

$$= \frac{(1-\pi)\psi}{(1-\pi)\psi + (1-\sigma)\pi} \tag{6}$$

$$= \frac{\psi}{\psi + (1-\sigma)\frac{\pi}{1-\pi}} \tag{7}$$

3 PPV Robustness to Uncertainty in the Prevalence

3.1 Formulation

The most uncertain probability is the prevalence of the new and unfamiliar disease, π, whose estimated value is $\widetilde{\pi}$ for which an error estimate is w_s. The value of w_s may be a statistical estimate of error. However, we are considering situations where the error is much greater than just the statistical sampling error, and derives from non-random sampling, heterogeneous population, non-stationarity, and general lack of knowledge about the extent of infection. In these situations we face deep, non-probabilistic uncertainty, and w_s is a contextual judgment of error. For instance, expert judgment may be: "$p(s_+)$ equals about 0.15, but may err by thirty percent or more." Thus $p(s_+) = 0.15$ and $w_2 = 0.05$. In general, we use the following fractional-error info-gap model for uncertainty in the prevalence (Ben-Haim, 2006, 2018):

$$\mathcal{U}(h) = \left\{ \pi : \ \pi \in [0, \ 1], \ \left| \frac{\pi - \widetilde{\pi}}{w_s} \right| \leq h \right\}, \quad h \geq 0 \tag{8}$$

We assume that the sensitivity, σ, and specificity, ψ, of the diagnostic test are each known.

The estimated conditional probability of true disease, that is, the estimate of the PPV, based on eq.(3) and the estimated prevalence, $\widetilde{\pi}$, is:

$$\widetilde{\mathsf{PPV}} = \frac{\sigma\widetilde{\pi}}{\sigma\widetilde{\pi} + (1-\psi)(1-\widetilde{\pi})} \tag{9}$$

Let PPV_e denote a clinician's judgment of the probability that the tested individual truly has the disease. This could be $\widetilde{\mathsf{PPV}}$, or it could be any other value based on the physician's clinical judgment. We will evaluate the robustness to uncertainty of various choices of PPV_e.

Our requirement is that the clinician's judgment, PPV_e, differ from the true conditional probability, PPV, no more than ε:

$$|\mathsf{PPV}_\mathrm{e} - \mathsf{PPV}| \leq \varepsilon \tag{10}$$

That is, ε is the greatest acceptable error in the clinical judgment of the conditional probability of disease in the individual. Recall that the true value of the PPV depends on the uncertain prevalence, as stated in eq.(4).

The robustness is the greatest horizon of uncertainty, h, up to which all realizations of the true prevalence, π, cause the judgment, PPV_e, to err no more than ε:

$$\widehat{h}_{\mathrm{ppv}}(\varepsilon; \mathsf{PPV}_\mathrm{e}) = \max \left\{ h : \ \left(\max_{\pi \in \mathcal{U}(h)} |\mathsf{PPV}_\mathrm{e} - \mathsf{PPV}| \right) \leq \varepsilon \right\} \tag{11}$$

Let $m(h)$ denote the inner maximum in eq.(11). $m(h)$ is the inverse of the robustness function. From eq.(4) we see that the PPV is monotonic in π. Hence this inner maximum occurs for an extremal value of the prevalence, π, either minimal or maximal. Denote the two resulting values of $m(h)$ by $m_+(h)$ and $m_-(h)$. The value of $m(h)$ is the greater of these two alternatives:

$$m(h) = \max \{ m_-(h), \ m_+(h) \} \tag{12}$$

Note that this maximum may switch between $m_+(h)$ and $m_-(h)$ as h changes.

Based on eq.(4) and the info-gap model in eq.(8), we have the following explicit expressions:

$$m_+(h) = \left| \text{PPV}_\text{e} - \frac{\sigma}{\sigma + (1-\psi)\left(\frac{1}{(\widetilde{\pi}+w_s h)^+} - 1\right)} \right| \tag{13}$$

$$m_-(h) = \left| \text{PPV}_\text{e} - \frac{\sigma}{\sigma + (1-\psi)\left(\frac{1}{(\widetilde{\pi}-w_s h)^+} - 1\right)} \right| \tag{14}$$

where we have defined the function:

$$x^+ = \begin{cases} 0 & x < 0 \\ x & 0 \le x \le 1 \\ 1 & x > 1 \end{cases} \tag{15}$$

3.2 Numerical Example

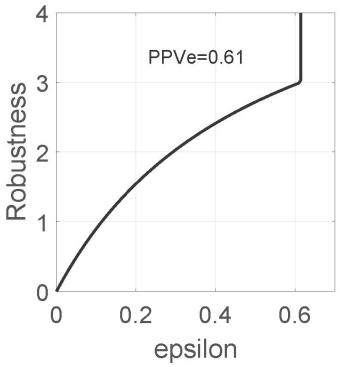

Figure 1: PPV Robustness function. $\sigma = \psi = 0.9$, $\widetilde{\pi} = 0.15$, $w_s = 0.05$. Computed with dpr001ppv.m

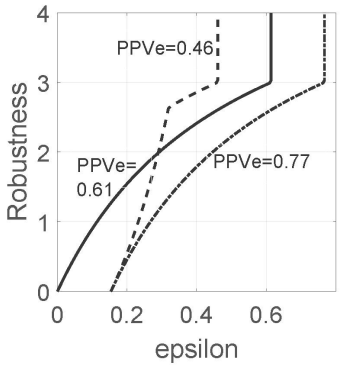

Figure 2: PPV Robustness functions. $\sigma = \psi = 0.9$, $\widetilde{\pi} = 0.15$, $w_s = 0.05$. Computed with dpr001ppv.m

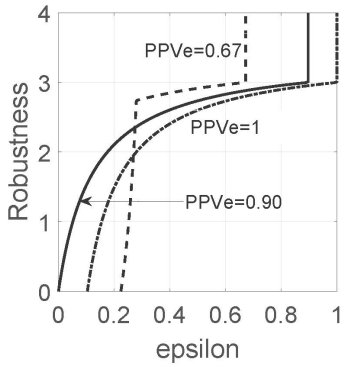

Figure 3: PPV Robustness functions. $\sigma = \psi = 0.98$, $\widetilde{\pi} = 0.15$, $w_s = 0.05$. Computed with dpr001ppv.m

We now discuss PPV robustness curves, defined in eq.(11), with the symmetric fractional-error info-gap model of eq.(8). The sensitivity, σ, and specificity, ψ, each equal 0.9. The estimated prevalence is $\widetilde{\pi} = 0.15$ with uncertainty weight $w_s = 0.05$. The estimated PPV, eq.(9), is $\widetilde{\text{PPV}} = 0.61$, and we consider 3 alternative expert judgments, PPV_e, of the PPV, equal to 0.46, 0.61 and 0.77, where the lower and upper values are 25% less, and 25% more, than the putative best estimate which is 0.61.

The robustness curve in fig. 1 is based on the estimated value of the PPV, and it displays two properties of all info-gap robustness curves: zeroing and trade off.

The zeroing property asserts that predicted outcomes have zero robustness to uncertainty. In fig. 1 the predicted error is zero, because PPV_e is based on the best estimate of the prevalence. The robustness — to uncertainty in the prevalence — is zero.

The trade off property asserts that the robustness, $\widehat{h}_{\text{ppv}}(\varepsilon)$, increases (gets better) as the performance requirement is relaxed (ε increases). This is displayed by the positive slope of the robustness

curve in fig. 1. The robustness of zero prediction error is zero (the zeroing property), while positive robustness is obtained by allowing positive error, ε.

For example, in fig. 1 we see that $\widehat{h}_{\rm ppv} = 1.5$ if $\varepsilon = 0.20$. This means that the estimated PPV will err no more than $\pm$0.20 for all values of the prevalence, π, in the interval $\widetilde{\pi} \pm 1.5 w_s$. This is modest robustness in light of the fact that the initial judgment of uncertainty in $\widetilde{\pi}$ could error by $\pm w_s$ or more. Greater robustness is obtained by allowing greater error in the prediction. For instance, $\widehat{h}_{\rm ppv}(\varepsilon = 0.6) = 3$.

Fig. 2 shows robustness curves for three different values of PPV_e: the nominal estimate reproduced from fig. 1, and a lower and greater value. These curves all display zeroing and trade off. The most significant element of the curves in fig. 2 is the intersection between two of them. We see that the robustness of the sub-optimal estimate, $\text{PPV}_\text{e} = 0.46$, exceeds the robustness of the putative optimum, $\text{PPV}_\text{e} = 0.61$, for ε exceeding 0.29. For instance, at $\varepsilon = 0.32$, the robustness with $\text{PPV}_\text{e} = 0.46$ equals 2.6, while the robustness with $\text{PPV}_\text{e} = 0.61$ equals 2.1. These are both reasonable robustnesses, but the sub-optimal estimate is more robust than the putative optimum.

Fig. 3 shows robustness curves as in fig. 2 with a single change: the sensitivity and specificity, σ and ψ, are now much greater. The resulting estimated PPV is also greater, equalling 0.90. Robustness curves are shown PPV_e values of 0.90, 0.67 (25% lower) and for 1.00 which is the maximum possible value. The robustness curves rise more rapidly, reaching reasonably large robustness at smaller ε values than in fig. 2. We note that the curves corresponding to non-optimal PPV_e values (dash and dot-dash) do not sprout off the ε-axis at the same value, unlike fig. 2. This is because they differ from the estimated PPV_e by different fractions.

4 NPV Robustness to Uncertainty in the Prevalence

We now develop an expression for the NPV robustness, and study its implications, in analogy to the analysis of the PPV robustness in section 3. We employ the symmetric fractional-error info-gap model of eq.(8).

4.1 Formulation

The estimated conditional probability of no disease given a negative test result, that is, the estimate of the NPV based on the estimated prevalence, $\widetilde{\pi}$, is, from eq.(7):

$$\widetilde{\text{NPV}} = \frac{\psi}{\psi + (1-\sigma)\frac{\widetilde{\pi}}{1-\widetilde{\pi}}} \tag{16}$$

Let NPV_e denote the clinician's expert judgment of the value of the NPV. This could be $\widetilde{\text{NPV}}$ or any other value. In analogy to eqs.(10) and (11), the performance requirement is:

$$|\text{NPV}_\text{e} - \text{NPV}| \le \varepsilon \tag{17}$$

That is, ε is the greatest acceptable error in the clinical judgment of the conditional probability that the individual is free of disease. Recall that the true value of the NPV depends on the uncertain prevalence, as stated in eq.(7).

The robustness is the greatest horizon of uncertainty, h, up to which all realizations of the true prevalence, π, cause the judgment, NPV_e, to err no more than ε:

$$\widehat{h}_{\rm npv}(\varepsilon; \text{NPV}_\text{e}) = \max\left\{h: \left(\max_{\pi \in \mathcal{U}(h)} |\text{NPV}_\text{e} - \text{NPV}|\right) \le \varepsilon\right\} \tag{18}$$

This is the NPV analog of the PPV robustness in eq.(11), and we derive an expression for the inverse of the NPV robustness function in analogy to eqs.(12)–(14).

Let $m(h)$ denote the inner maximum in eq.(18). $m(h)$ is the inverse of the NPV robustness function. From eq.(7) we see that the NPV is monotonic in π. Hence this inner maximum occurs for an extremal value of the prevalence, π, either minimal or maximal. Denote the two resulting values of $m(h)$ by $m_+(h)$ and $m_-(h)$. The value of $m(h)$ is the greater of these two alternatives:

$$m(h) = \max\left\{m_-(h),\ m_+(h)\right\} \tag{19}$$

Note that this maximum may switch between $m_+(h)$ and $m_-(h)$ as h changes.

Based on eq.(7) and the info-gap model in eq.(8), we have the following explicit expressions:

$$m_+(h) \quad = \quad \left| \text{PPV}_\text{e} - \frac{\psi}{\psi + (1-\sigma)\left(\frac{\left(\widetilde{\pi}+w_s h\right)^+}{1-\left(\widetilde{\pi}+w_s h\right)^+}\right)} \right| \tag{20}$$

$$m_-(h) \quad = \quad \left| \text{PPV}_\text{e} - \frac{\psi}{\psi + (1-\sigma)\left(\frac{\left(\widetilde{\pi}-w_s h\right)^+}{1-\left(\widetilde{\pi}-w_s h\right)^+}\right)} \right| \tag{21}$$

We are again using the function defined in eq.(15).

4.2 Numerical Example

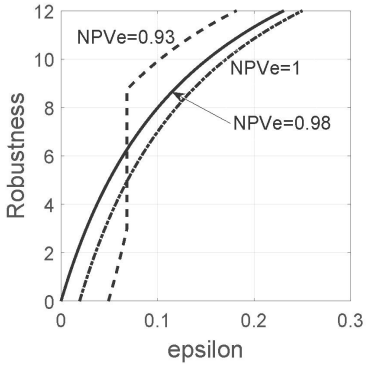

Figure 4: NPV Robustness functions. $\sigma = \psi = 0.9$, $\widetilde{\pi} = 0.15$, $w_s = 0.05$. Computed with dpr002npv.m

We now discuss a numerical example of the NPV robustness function defined in eq.(18), with the fractional-error info-gap model in eq.(8). We assume sensitivity and specificity values of $\sigma = \psi = 0.9$. The estimated value of the prevalence is $\widetilde{\pi} = 0.15$ with an uncertainty weight of $w_s = 0.05$.

The estimated NPV value, with these coefficients, is $\widetilde{\text{NPV}} = 0.98$. This is the estimated probability that a person, whose diagnostic test was negative, is in fact free of disease. This is an encouragingly large value, though we must now consider the robustness to uncertainty in the prevalence.

Fig. 4 shows NPV robustness curves for three values of the expert's judgment of the NPV: NPV_e = 0.93, 0.98, and 1.00. One sees some similarity to the PPV robustness curves in fig. 2, though the scales of the axes are quite different. In both figures the robustness curve of the lower value of NPV_e crosses the robustness curve for $\widetilde{\text{NPV}}$, while this is not the case for the larger value of NPV_e for the range of robustness values shown.

A distinctive feature of the robustness curves in fig. 4 is their steep slope at low values of ε. The steep slope implies a low cost of robustness: the robustness increases greatly by increasing the allowed error, ε, only slightly. For instance, the robustness for the estimated NPV increases from $\widehat{h}_{\text{npv}}(\varepsilon) = 0$ to $\widehat{h}_{\text{npv}}(\varepsilon) = 5.0$ as ε increases from 0 to 0.05. A robustness of 5.0 means that the true prevalence can deviate from its estimated value by $\pm 5.0 w_s$ (subject to non-negativity) and the true NPV will deviate from its estimate by no more than 0.05.

We see in fig. 4 that $\text{NPV}_\text{e} = 0.98$ is robust-dominant over $\text{NPV}_\text{e} = 1$ throughout the range of the figure. In contrast, the comparison of $\text{NPV}_\text{e} = 0.93$ and $\text{NPV}_\text{e} = 0.98$ shows a reversal of preference, depending on the allowed error, ε: $\text{NPV}_\text{e} = 0.98$ is more robust than $\text{NPV}_\text{e} = 0.93$ at low ε, and the robustness-based preference is reversed at larger ε.

In summary, the putative estimate, $\text{NPV}_\text{e} = 0.98$, has large robustness at quite small ε, and should therefore provide the basis for clinical decision. This large probability of the absence of disease, given a negative test result, would seem to strongly support refraining from medical intervention.

We can understand why the NPV is much more robust to uncertainty in the prevalence than the PPV, in this numerical example, by comparing eqs.(4) and (7). Their dependence on the prevalence, π, is different. Note that:

$$\text{PPV:} \quad \frac{\partial}{\partial \pi}\left(\frac{1}{\pi} - 1\right) = -\frac{1}{\pi^2} \tag{22}$$

$$\text{NPV:} \quad \frac{\partial}{\partial \pi}\left(\frac{\pi}{1-\pi}\right) = \frac{1}{(1-\pi)^2} \tag{23}$$

Using the estimated prevalence, $\widetilde{\pi} = 0.15$, the absolute values of the expressions in eqs.(22) and (23) are approximately 44 and 1.4, respectively. In other words, the PPV is far more sensitive to the value of prevalence. Hence the robustness, to uncertainty in the prevalence, is far lower for the PPV than for the NPV. This is seen clearly in comparing figs. 2 and 4.

We can also immediately see that the situation is reversed if the estimated prevalence is $\widetilde{\pi} = 0.85$, in which case absolute values of the expressions in eqs.(22) and (23) are reversed and approximately equal 1.4 and 44, respectively.

Summarizing the relative robustnesses of PPV and NPV, we can say that PPV is less robust to uncertainty in the prevalence than NPV, when the prevalence is low; the situation is reversed when the prevalence is high. However, when prevalence is low, most test results are negative and therefore interpretation of positive test results is more significant than interpretation of negative test results.[2] That is, at low prevalence, when PPV has lower robustness than NPV, it is the PPV determination that is more important but less robust. The situation is reversed at high prevalence. Nonetheless, that PPV is less robust than NPV does not mean that PPV has negligible robustness, as we saw in our discussion of figs. 1–3.

[2]For instance, with $\sigma = \psi = 0.9$, eqs.(4) and (7) yield $\text{NPV}(\pi = 0.15) = 0.98$ and $\text{PPV}(\pi = 0.15) = 0.61$. With $\pi = 0.15$, the naive pre-test judgment is that an individual has probability 0.85 to be free of disease and probability of 0.15 of illness. Thus, at low prevalence, a negative test result has only a modest impact on the judgment, while a positive test result entails a major revision of the assessment. The situation is precisely reversed at high prevalence: $\text{NPV}(\pi = 0.85) = 0.61$ (naive probability of health: 0.15) and $\text{PPV}(\pi = 0.85) = 0.98$ (naive probability of disease: 0.85).

5 PPV Robustness to Uncertainty in Prevalence and Sensitivity

We now formulate the info-gap robustness of the PPV to uncertainty in both prevalence and sensitivity.

Extending eq.(8), the fractional-error info-gap model for uncertainty in both prevalence, π, and sensitivity, σ, is:

$$\mathcal{U}(h) = \left\{ \pi, \sigma : \ \pi \in [0,\ 1],\ \left| \frac{\pi - \widetilde{\pi}}{w_\pi} \right| \leq h,\ \sigma \in [0,\ 1],\ \left| \frac{\sigma - \widetilde{\sigma}}{w_\sigma} \right| \leq h \right\}, \quad h \geq 0 \tag{24}$$

The extension of the robustness in eq.(11) is:

$$\widehat{h}_{\mathrm{ppv}}(\varepsilon; \mathsf{PPV}_\mathrm{e}) = \max \left\{ h : \ \left(\max_{\pi, \sigma \in \mathcal{U}(h)} |\mathsf{PPV}_\mathrm{e} - \mathsf{PPV}| \right) \leq \varepsilon \right\} \tag{25}$$

Let $m(h)$ denote the inner maximum, which is the inverse of the PPV robustness function.

From eq.(4) we can write the PPV as:

$$\mathsf{PPV} = \frac{1}{1 + \frac{1-\psi}{\sigma} \left(\frac{1}{\pi} - 1 \right)} \tag{26}$$

Thus the PPV is maximal when σ and π are both maximal, and PPV is minimal when σ and π are both minimal. In analogy to eqs.(13) and (14), define:

$$m_+(h) \ = \ \left| \mathsf{PPV}_\mathrm{e} - \frac{\sigma}{\sigma + \frac{1-\psi}{\left(\widetilde{\sigma} + w_\sigma h\right)^+} \left(\frac{1}{\left(\widetilde{\pi} + w_\pi h\right)^+} - 1 \right)} \right| \tag{27}$$

$$m_-(h) \ = \ \left| \mathsf{PPV}_\mathrm{e} - \frac{1}{1 + \frac{1-\psi}{\left(\widetilde{\sigma} - w_\sigma h\right)^+} \left(\frac{1}{\left(\widetilde{\pi} - w_\pi h\right)^+} - 1 \right)} \right| \tag{28}$$

The inverse of the PPV robustness function, $\widehat{h}_{\mathrm{ppv}}(\varepsilon; \mathsf{PPV}_\mathrm{e})$, is the greater of these two functions:

$$m(h) = \max \left\{ m_-(h),\ m_+(h) \right\} \tag{29}$$

6 NPV Robustness to Uncertainty in Prevalence and Sensitivity

We now formulate the info-gap robustness of the NPV to uncertainty in both prevalence and sensitivity, based on the info-gap model of eq.(24).

The application of the robustness in eq.(25) is:

$$\widehat{h}_{\mathrm{npv}}(\varepsilon; \mathsf{NPV}_\mathrm{e}) = \max \left\{ h : \ \left(\max_{\pi, \sigma \in \mathcal{U}(h)} |\mathsf{NPV}_\mathrm{e} - \mathsf{NPV}| \right) \leq \varepsilon \right\} \tag{30}$$

Let $m(h)$ denote the inner maximum, which is the inverse of the NPV robustness function.

For convenience we reproduce here the NPV from eq.(7):

$$\mathsf{NPV} = \frac{\psi}{\psi + (1 - \sigma) \frac{\pi}{1-\pi}} \tag{31}$$

Thus the NPV is maximal when σ is maximal and π in minimal, and NPV is minimal when σ in minimal and π is maximal. In analogy to eqs.(27) and (28), define:

$$m_+(h) = \left| \mathrm{NPV_e} - \frac{\psi}{\psi + \left[1 - (\widetilde{\sigma} + w_\sigma h)^+\right] \left(\frac{(\widetilde{\pi} - w_\pi h)^+}{1 - (\widetilde{\pi} - w_\pi h)^+} \right)} \right| \tag{32}$$

$$m_-(h) = \left| \mathrm{NPV_e} - \frac{\psi}{\psi + \left[1 - (\widetilde{\sigma} - w_\sigma h)^+\right] \left(\frac{(\widetilde{\pi} + w_\pi h)^+}{1 - (\widetilde{\pi} - w_\pi h)^+} \right)} \right| \tag{33}$$

The inverse of the NPV robustness function, $\widehat{h}_{\mathrm{npv}}(\varepsilon; \mathrm{PPV_e})$, is the greater of these two functions:

$$m(h) = \max\left\{m_-(h),\ m_+(h)\right\} \tag{34}$$

Acknowledgement The author is indebted to invaluable conversations with Prof. Shai Linn, School of Public Health, University of Haifa.

7 References

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