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PLOS Computational Biology
PLOS
Nine Hills Road
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12 December 2023

Dear Editor,

Re: Methods paper: Combined multiplex panel test results are a poor estimate of disease prevalence without adjustment for test error.

Please consider our submission of this paper for publication in PLOS Computational Biology.

During recent research on the epidemiology of community acquired pneumococcal disease, we identified an issue with the correct interpretation of multiplex panel tests, when they are being used to infer population level disease burden. Interpreted naively, combination of multiplex panel test results have the potential to significantly over-estimate disease incidence and prevalence. Accurate estimates of burden are essential for decision making on resource allocation and vaccine policy, and over-estimates have clear implications for both cost and population health.

In this manuscript we show that combining multiplex panel test results to estimate the burden of disease is highly sensitive to even small degrees of test error. Proper interpretation and uncertainty quantification requires substantial extension of previous mathematical and computational methods. We present this analysis in the paper, validate the results through simulation, and present new methods that correct for test error, expressed in terms of sensitivity and specificity. Our paper is accompanied by an open source R package[1] which can be used to transparently correct for test error when using multiplex testing to estimate disease burden.

Multiplex testing is becoming more commonly adopted as a screening test for multiple pathogens. Methods to correctly interpret multiplex test results when estimating incidence of disease are key to making evidence based decisions in public health, which can have wide reaching consequences. We believe this manuscript is of interest to your readership and will be grateful if you could consider this submission for publication in PLOS Computational Biology.

Yours sincerely,

Dr. Robert Challen Ph.D. MBBS

[1] https://github.com/bristol-vaccine-centre/testerror