Pathogens tested for by QIAstat-Dx Respiratory SARS-CoV-2 Panel

Viruses

SARS-CoV-2 (Covid-19)

Influenza A

Influenza A subtype H1N1/2009

Influenza A subtype H1

Influenza A subtype H3

Influenza B

Coronavirus 229E

Coronavirus HKU1

Coronavirus NL63

Coronavirus OC43

Parainfluenza 1

Parainfluenza 2

Parainfluenza 3

Parainfluenza 4

Respiratory Syncytial Virus A/B

Human Metapneumovirus A/B

Adenovirus

Bocavirus

Rhino/Enterovirus

Bacteria

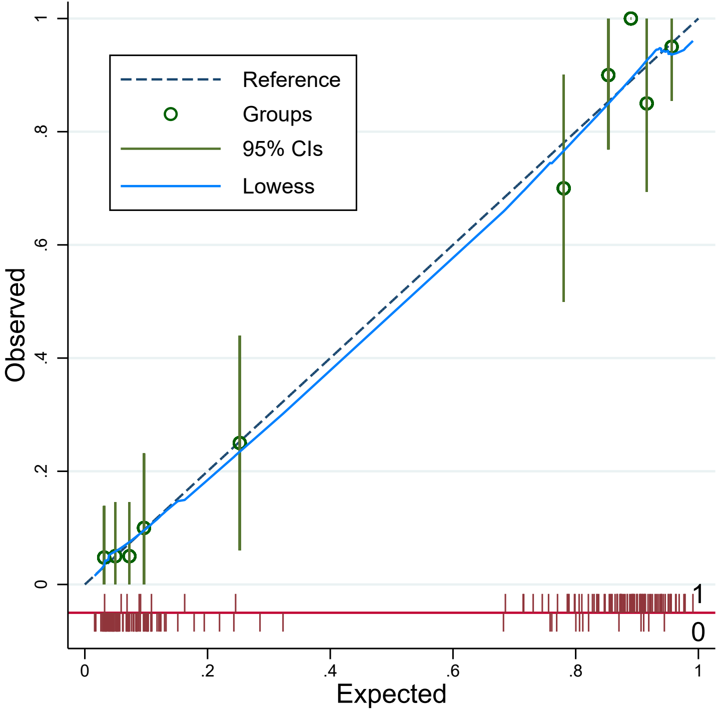
Mycoplasma pneumonia

Legionella pneumophilia

Bordatella pertussis

Sample size justification for multivariable analysis

Nine variables were expected to be included in the multivariable model. Riley et al. suggest three criteria for sample size considerations in multivariable predictive models, where n is chosen to: 1) limit optimism in predictor effects (represented by a shrinkage factor >0.9; this is to avoid overfitting, which can result in a model that performs well in the sample it is derived from, but does not perform well under other samples/external validation), 2) ensure a small difference (≤0.05) between apparent and adjusted Nagelkerke's R2 (a measure of proportion of variance explained in the outcome; again to avoid overfitting) and 3) provide a precise estimate of overall risk. With n=236 and prevalence of 40%, overall risk could be estimated within 6.5%; fixing shrinkage to 0.9 (as recommended) and with R2 of 0.3, the sample size of 236 would meet all three criteria (based on pmsampsize command in Stata). R2 was anticipated to be much higher, given the nature of the diagnostic test; for R2 of 0.65, this would allow all criteria to be met under the assumption that we might estimate 15 parameters based on modelling continuous variables, using restricted cubic splines.


Reference
Groups
95% CIs
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Observed
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