**Evaluation of TB diagnostic test accuracy using Bayesian latent class analysis in the presence of conditional dependence between the diagnostic tests used in a community-based TB screening study**

**Supplementary material**

## 1. Model

Let the random variable $Y_j, j = 1,2,\ldots,J$ denote the $j^{th}$ diagnostic test and the random variable $D$ denote the latent disease status such that $Y_j = 0(1)$ if the $j^{th}$ diagnostic test result is negative (positive) and $D = 0(1)$ if the true disease status is negative (positive). Under the assumption of conditional independence, the joint probability of a combination of test results from a set of $J$ diagnostic tests $\boldsymbol{Y} = (Y_1, Y_2, \cdots, Y_J)$ is given by [1]

$$Pr(\boldsymbol{Y}) = \sum_{d=0}^{1} Pr(D = d) \prod_{j=1}^{J} Pr(Y_j = y_j | D = d) \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

However, for $J$ dependent diagnostic tests, $Pr(\boldsymbol{Y})$ can be expressed using the chain rule of conditional probability as follows

$$Pr(\boldsymbol{Y}) = \sum_{d=0}^{1} Pr(D = d) \prod_{j=1}^{J} Pr\left( Y_j = y_j |\, D = d \bigcap_{j'=1|j>1}^{j-1} Y_{j'=y_{j'}} \right)$$

$$= \sum_{d=0}^{1} \theta_d \prod_{j=1}^{J} {p_{dj}}^{y_j} (1 - p_{dj})^{1-y_j} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots.\ldots\ldots\ldots (2)$$

where

$$p_{dj} = Pr\left( Y_j = 1 |\, D = d \bigcap_{j'=1|j>1}^{j-1} Y_{j'=y_{j'}} \right) \text{and } \theta_d = Pr(D = d), d \in \{0,1\}$$

The probabilities $p_{dj}$ and $\theta_d = Pr(D = d), d \in \{0,1\}$ can be calculated using regression methods.

Consequently,

$$Pr(Y_j = 1 | D = d) = \sum_{Y_{j-1} \in (0,1)} \cdots \sum_{Y_2 \in (0,1)} \sum_{Y_1 \in (0,1)} \prod_{k=1}^{j} p_{dk} \ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

and $Pr(Y_j = 0|D = d) = 1 - Pr(Y_j = 1|D = d)$.

The model can be extended to include covariates known to affect the diagnostic accuracy and/or prevalence such that for a binary variable $X$, $Pr(\boldsymbol{Y})$ can be re-expressed as

$$Pr(\boldsymbol{Y}) = \sum_{d=0}^{1}\sum_{x=0}^{1} Pr(X = x)Pr(D = d|X = x)\prod_{j=1}^{J} Pr\left(Y_j = y_j|\ X = x \bigcap D = d \bigcap_{j'=1|j>1}^{j-1} Y_{j'=y_{j'}}\right)$$

For a vector $\boldsymbol{X}$ of p covariates, $Pr(\boldsymbol{X}) = Pr(X_1, X_2, \ldots, X_p) = Pr(X_1)Pr(X_2|X_1) \ldots Pr(X_p|X_1, X_2, \ldots X_{p-1})$.

**1.1. Bayesian Inference**

Since the likelihood function of $\boldsymbol{y_i} = (y_{i1}, y_{i2}, \cdots, y_{iJ})$ depends on the (latent) disease status $d_i, i = 1,2,3, \cdots, N$, we have

$$Pr(\boldsymbol{y_i}, d_i|\theta, p_{d_ij}) = \left(\theta \prod_{j=1}^{J} p_{d_ij}^{y_{ij}}(1 - p_{d_ij})^{1-y_{ij}}\right)^{d_i}\left((1-\theta)\prod_{j=1}^{J} p_{d_ij}^{y_{ij}}(1 - p_{d_ij})^{1-y_{ij}}\right)^{1-d_i} \ldots\ldots\ldots (4)$$

We will only focus on the case where we have data on J diagnostic tests. Extension to incorporate covariates is straight forward. From (4) we have J conditional probability models to fit to determine $p_{d_ij}, j = 1,2, \ldots J$. Since the outcome is Bernoulli distributed and $p_{d_ij}$ is related to a set of (binary) independent variables we can define a binary regression model as $p_{id_ij} = H(\boldsymbol{y_i^T\beta_{dj}})$, where $\boldsymbol{y_i^T} = (y_{i0}, y_{i1}, \cdots, y_{ij})$ is a $(j+1) \times 1$ vector of observed variables (or diagnostic tests) with $y_{i0} = 1$, $\boldsymbol{\beta_{dj}}$ is a $(j+1) \times 1$ vector of unknown parameters to be estimated, and $H(.)$ is a known cumulative distribution function (CDF) linking the probabilities $p_{id_ij}$ with the linear component $\boldsymbol{y_i^T\beta_{dj}}$ [2]. The unknown parameters $\boldsymbol{\beta_{dj}}$ were assigned $g(\boldsymbol{\beta_{dj}}) = N(\boldsymbol{\mu_{dj}}, \boldsymbol{\sigma_{dj}^2} I_{j+1})$ priors, where $I_{j+1}$ is an identity matrix of dimension $(j+1)$ and $\boldsymbol{\sigma_{dj}^2}$ is a $(j+1) \times 1$ vector of variances among subjects whose true PTB status is $d$. The variances may not necessarily be the same (Tables S1 – S5). Similarly, the unobserved PTB status is a Bernoulli distributed latent variable. Therefore, the probability $\theta_i$ that the $i^{th}$ subject has PTB is related to a constant or a (set of) covariate(s) as follows: $\theta_i = H(\boldsymbol{x_i^T\omega})$, where $\boldsymbol{x_i^T} = (x_{i0}, x_{i2}, \cdots, x_{ip})$ is a $(p+1) \times 1$ vector of observed covariates $(x_{i0} = 1)$, $\boldsymbol{\omega}$ is a $(p+1) \times 1$ vector of unknown parameters to be estimated, and $H(.)$ is a known CDF linking the probabilities $\theta_i$ with the linear component $\boldsymbol{x}_i^T\boldsymbol{\omega}$ . The unknown parameter(s) $\boldsymbol{\omega}$ were assigned $g(\boldsymbol{\omega}) = N(\boldsymbol{\mu}_{\boldsymbol{\theta}}, \boldsymbol{\sigma}_{\boldsymbol{\theta}}^2 \boldsymbol{I}_{p+1})$ priors, where $I_{p+1}$ is an identity matrix of dimension $p+1$ and $\boldsymbol{\sigma}_{\boldsymbol{\theta}}^2$ is a $(p+1)\times 1$ vector of variances (for now we are working with $p+1=1$). Thus, the posterior distribution $g(\boldsymbol{\omega}, \boldsymbol{\beta}_{\boldsymbol{dj}} \mid \boldsymbol{y}_{\boldsymbol{i}}, d)$ is proportional to

$$g(\boldsymbol{\omega})\prod_{i=1}^{N}\left(H(\boldsymbol{x}_i^T\boldsymbol{\omega})^{d_i}\left(1-H(\boldsymbol{x}_i^T\boldsymbol{\omega})\right)^{1-d_i}\right)\times\left(\prod_{j=1}^{J}g(\boldsymbol{\beta}_{\boldsymbol{1j}})\prod_{i=1}^{N}\left(H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{1j}})\right)^{y_{ij}d_i}\left(1-H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{1j}})\right)^{(1-y_{ij})d_i}\right)$$

$$\times\left(\prod_{j=1}^{J}g(\boldsymbol{\beta}_{\boldsymbol{0j}})\prod_{i=1}^{N}\left(H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{0j}})\right)^{y_{ij(1-d_i)}}\left(1-H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{0j}})\right)^{(1-y_{ij})(1-d_i)}\right)\dots\dots\dots\dots(5)$$

where $\int g(\boldsymbol{\beta}_{\boldsymbol{dj}})\prod_{i=1}^{N}\left(H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{dj}})\right)^{y_{ij}}\left(1-H(\boldsymbol{y}_i^T\boldsymbol{\beta}_{\boldsymbol{dj}})\right)^{1-y_{ij}}d\boldsymbol{\beta}_{\boldsymbol{dj}}$ , $d\epsilon\{0,1\}$ and $\int g(\boldsymbol{\omega})\prod_{i=1}^{N}\left(H(\boldsymbol{x}_i^T\boldsymbol{\omega})\right)^{y_{ij}}\left(1-H(\boldsymbol{x}_i^T\boldsymbol{\omega})\right)^{1-y_{ij}}d\boldsymbol{\omega}$ are not easy to determine analytically. Thus, the unknown parameters $\boldsymbol{\omega}$, and $\boldsymbol{\beta}_{\boldsymbol{dj}}$, $j=1,2,3,\dots,J$ will be estimated using Markov Chain Monte Carlo (MCMC) approach.

## 2. Prior distributions

Table S1 presents the models and the prior distributions for the parameters in the probit regression models for the analysis of CPTB study. Similarly, Tables S4 – S5 present the models and the prior distributions for the parameters in the probit regression models for the analysis of Vukuzazi study. The assumptions made on the potential dependencies for all the models were presented in the analysis section of the main document.

### 2.1. CPTB Data

In the analysis of CPTB data, we allowed TST $(Y_1)$, radiography $(Y_2)$, microscopy $(Y_3)$, Xpert $(Y_4)$ and culture $(Y_5)$ as the possible ordering of the diagnostic tests.

Table S1: Prior distributions for the parameters in the probit regression models for childhood pulmonary TB data

| Response | Model structure | Model 0 | Model 1 | Model 2 | Model 3 | Model 4 |
|---|---|---|---|---|---|---|
| D | $Pr(D = 1) = \emptyset(\omega)$ | $g(\omega)$~N(0,1) | $g(\omega)$~N(0,1) | $g(\omega)$~N(0,1) | $g(\omega)$~N(0,1) | $g(\omega)$~N(0,1) |
| $Y_1$ | $Pr(Y_{i1} = 1 \vert D_i = 1) = \emptyset(\beta_{11})$ | $g(\beta_{11})$~N(0,10) | $g(\beta_{11})$~N(0,10) | $g(\beta_{11})$~N(0,10) | $g(\beta_{11})$~N(0,10) | $g(\beta_{11})$~N(0,10) |
| | $Pr(Y_{i1} = 1 \vert D_i = 0) = \emptyset(\alpha_{11})$ | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) |
| $Y_2$ | $Pr\ (Y_{i2} = 1 \vert Y_{i1}, D_i{=}1) = \emptyset(\beta_{12} + \beta_{22} y_{i1})$ | $g(\beta_{12})$~N(0,10)<br>- | $g(\beta_{12})$~N(0,10)<br>- | $g(\beta_{12})$~N(0,10)<br>- | $g(\beta_{12})$~N(0,10)<br>$g(\beta_{22})$~N(0,10) | $g(\beta_{12})$~N(0,10)<br>$g(\beta_{22})$~N(0,10) |
| | $Pr\ (Y_{i2} = 1 \vert Y_{i1}, D_i{=}0) = \emptyset(\alpha_{12} + \alpha_{22} y_{i1})$ | $g(\alpha_{12})$~N(0,10)<br>- | $g(\alpha_{12})$~N(0,10)<br>- | $g(\alpha_{12})$~N(0,10)<br>$g(\alpha_{22})$~N(0,10) | $g(\alpha_{12})$~N(0,10)<br>$g(\alpha_{22})$~N(0,10) | $g(\alpha_{12})$~N(0,10)<br>- |
| $Y_3$ | $Pr(Y_{i3} = 1 \vert Y_{i1}, Y_{i2}, D_i{=}1)$<br>$= \emptyset(\beta_{13} + \beta_{23} y_{i1} + \beta_{33} y_{i2})$ | $g(\beta_{13})$~N(0,10)<br>-<br>- | $g(\beta_{13})$~N(0,10)<br>$g(\beta_{23})$~N(0,10)<br>- | $g(\beta_{13})$~N(0,10)<br>$g(\beta_{23})$~N(0,10)<br>- | $g(\beta_{13})$~N(0,10)<br>$g(\beta_{23})$~N(0,10)<br>$g(\beta_{33})$~N(0,10) | $g(\beta_{13})$~N(0,10)<br>$g(\beta_{23})$~N(0,10)<br>$g(\beta_{33})$~N(0,10) |
| | $Pr\ (Y_{i3} = 1 \vert D_i{=}0) = \emptyset(\alpha_{13})$ | $g(\alpha_{13})$~N(-3, 0.1) | $g(\alpha_{13})$~N(-3,0.1) | $g(\alpha_{13})$~N(-3,0.1) | $g(\alpha_{13})$~N(-3,0.1) | $g(\alpha_{13})$~N(-3,0.1) |
| $Y_4$ | $Pr(Y_{i4} = 1 \vert Y_{i1}, Y_{i2}, Y_{i3}, D_i{=}1)$<br>$= \emptyset(\beta_{14} + \beta_{24} y_{i1} + \beta_{34} y_{i2} + \beta_{44} y_{i3})$ | $g(\beta_{14})$~N(0,10)<br>-<br>-<br>- | $g(\beta_{14})$~N(0,10)<br>$g(\beta_{24})$~N(0,10)<br>-<br>$g(\beta_{44})$~N(0,10) | $g(\beta_{14})$~N(0,10)<br>$g(\beta_{24})$~N(0,10)<br>-<br>$g(\beta_{44})$~N(0,10) | $g(\beta_{14})$~N(0,10)<br>$g(\beta_{24})$~N(0,10)<br>$g(\beta_{34})$~N(0,10)<br>$g(\beta_{44})$~N(0,10) | $g(\beta_{14})$~N(0,10)<br>$g(\beta_{24})$~N(0,10)<br>$g(\beta_{34})$~N(0,10)<br>$g(\beta_{44})$~N(0,10) |
| | $Pr\ (Y_{i4} = 1 \vert D_i{=}0) = \emptyset(\alpha_{14})$ | $g(\alpha_{14})$~N(-3,0.1) | $g(\alpha_{14})$~N(-3,0.1) | $g(\alpha_{14})$~N(-3,0.1) | $g(\alpha_{14})$~N(-3,0.1) | $g(\alpha_{14})$~N(-3,0.1) |
| $Y_5$ | $Pr(Y_{i5} = 1 \vert Y_{i1}, Y_{i2}, Y_{i3}, Y_{i4}, D_i{=}1)$<br>$= \emptyset(\beta_{15} + \beta_{25} y_{i1} + \beta_{35} y_{i2} + \beta_{45} y_{i3} + \beta_{55} y_{i4})$ | $g(\beta_{15})$~N(0,10)<br>-<br>-<br>-<br>- | $g(\beta_{15})$~N(0,10)<br>$g(\beta_{25})$~N(0,10)<br>-<br>$g(\beta_{45})$~N(0,10)<br>$g(\beta_{55})$~N(0,10) | $g(\beta_{15})$~N(0,10)<br>$g(\beta_{25})$~N(0,10)<br>-<br>$g(\beta_{45})$~N(0,10)<br>$g(\beta_{55})$~N(0,10) | $g(\beta_{15})$~N(0,10)<br>$g(\beta_{25})$~N(0,10)<br>$g(\beta_{35})$~N(0,10)<br>$g(\beta_{45})$~N(0,10)<br>$g(\beta_{55})$~N(0,10) | $g(\beta_{15})$~N(0,10)<br>$g(\beta_{25})$~N(0,10)<br>$g(\beta_{35})$~N(0,10)<br>$g(\beta_{45})$~N(0,10)<br>$g(\beta_{55})$~N(0,10) |
| | $Pr(Y_{i5} = 1 \vert D_i{=}0) = \emptyset(\alpha_{15})$ | $g(\alpha_{15})$~N(-3,0.1) | $g(\alpha_{15})$~N(-3,0.1) | $g(\alpha_{15})$~N(-3,0.1) | $g(\alpha_{15})$~N(-3,0.1) | $g(\alpha_{15})$~N(-3,0.1) |

D – Disease (CPTB), $Y_1$ – TST, $Y_2$ – Radiography, $Y_3$ – Smear microscopy, $Y_4$ – Xpert MTB/RIF, $Y_5$ – Culture, "-" implies the parameter is not included (i.e set to zero) in the model, Model 0 was based on the assumption of conditional independence, Model 1 was based on expert opinion [3], Model 2 adds dependency between TST and radiography in non-CPTB cases to Model 1, Model 3 additionally allows dependency of all diagnostic tests with radiography among the true CPTB cases. Model 4 is the reduced version of Model 3 that omits the dependence between TST and radiography in non-CPTB cases

Table S2: Prior distributions for the parameters in the probit regression models for Vukuzazi data

| | Model structure | Model 0 | Model 1 | Model 2 |
|---|---|---|---|---|
| D | $Pr(D = 1) = \emptyset(\omega)$ | $g(\omega)$~N(-3,0.1) | $g(\omega)$~N(-3,0.1) | $g(\omega)$~N(-3,0.1) |
| $Y_1$ | $Pr(Y_{i1} = 1 \vert D_i = 1)$<br>$= \emptyset(\beta_{11})$ | $g(\beta_{11})$~N(0,0.1) | $g(\beta_{11})$~N(0,0.1) | $g(\beta_{11})$~N(0,0.1) |
| | $Pr(Y_{i1} = 1 \vert D_i = 0)$<br>$= \emptyset(\alpha_{11})$ | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) | $g(\alpha_{11})$~N(0,10) |
| $Y_2$ | $Pr(Y_{i2} = 1 \vert D_i=1) = \emptyset(\beta_{12})$ | $g(\beta_{12})$~N(0,0.1) | $g(\beta_{12})$~N(0,0.1) | $g(\beta_{12})$~N(0,0.1) |
| | $Pr(Y_{i2} = 1 \vert Y_{i1}, D_i=0) =$<br>$\emptyset(\alpha_{12} + \alpha_{22} y_{i1})$ | $g(\alpha_{12})$~N(0,10)<br>- | $g(\alpha_{12})$~N(0,10)<br>- | $g(\alpha_{12})$~N(0,10)<br>$g(\alpha_{22})$~N(0,10) |
| $Y_3$ | $Pr(Y_{i3} = 1 \vert Y_{i2}, D_i=1)$<br>$= \emptyset(\beta_{13}+ \beta_{23} y_{i2})$ | $g(\beta_{13})$~N(0,0.1)<br>- | $g(\beta_{13})$~N(0,0.1)<br>$g(\beta_{23})$~N(0,0.1) | $g(\beta_{13})$~N(0,0.1)<br>$g(\beta_{23})$~N(0,0.1) |
| | $Pr(Y_{i3} = 1 \vert Y_{i1}, Y_{i2}, D_i=0)$<br>$= \emptyset(\alpha_{13} + \alpha_{23} y_{i1}+ \alpha_{33} y_{i2})$ | $g(\alpha_{13})$~N(0,10) | $g(\alpha_{13})$~N(0,10)<br>- | $g(\alpha_{13})$~N(0,10)<br>$g(\alpha_{23})$~N(0,10)<br>$g(\alpha_{33})$~N(0,10) |
| $Y_4$ | $Pr(Y_{i4} = 1 \vert Y_{i2}, Y_{i3}, D_i=1)$<br>$= \emptyset(\beta_{14}+ \beta_{24} y_{i2}+ \beta_{34} y_{i3})$ | $g(\beta_{14})$~N(0,0.1)<br>- | $g(\beta_{14})$~N(0,0.1)<br>$g(\beta_{24})$~N(0,0.1)<br>$g(\beta_{34})$~N(0,0.1) | $g(\beta_{14})$~N(0,0.1)<br>$g(\beta_{24})$~N(0,0.1)<br>$g(\beta_{34})$~N(0,0.1) |
| | $Pr(Y_{i4} = 1 \vert Y_{i1}, Y_{i2}, Y_{i3}, D_i=0)$<br>$= \emptyset\begin{pmatrix} \alpha_{14} + \alpha_{24} y_{i1} + \\ \alpha_{34} y_{i2}+ \alpha_{44} y_{i3} \end{pmatrix}$ | $g(\alpha_{14})$~N(0,10)<br>- | $g(\alpha_{14})$~N(0,10)<br>- | $g(\alpha_{14})$~N(0,10)<br>$g(\alpha_{24})$~N(0,10)<br>$g(\alpha_{34})$~N(0,10)<br>$g(\alpha_{44})$~N(0,10) |
| $Y_5$ | $Pr(Y_{i5} = 1 \vert D_i=1) = \emptyset(\beta_{15})$ | $g(\beta_{15})$~N(0,0.1) | $g(\beta_{15})$~N(0,0.1) | $g(\beta_{15})$~N(0,0.1) |
| | $Pr(Y_{i5} = 1 \vert D_i=0)$<br>$= \emptyset(\alpha_{15})$ | $g(\alpha_{15})$~N(-1.88,0.01)<br>- | $g(\alpha_{15})$~N(-1.88,0.01)<br>- | $g(\alpha_{15})$~N(-1.88,0.01)<br>- |
| $Y_6$ | $Pr(Y_{i6} = 1 \vert D_i=1)$<br>$= \emptyset(\beta_{16}+\beta_{26} y_{i5})$ | $g(\beta_{16})$~N(0,0.1)<br>- | $g(\beta_{16})$~N(0.84,0.1)<br>$g(\beta_{26})$~N(0,0.1) | $g(\beta_{16})$~N(0.84,0.1)<br>$g(\beta_{26})$~N(0,0.1) |
| | $\Pr(Y_{i6} = 1 \vert D_i=0)$<br>$= \emptyset(\alpha_{16})$ | $g(\alpha_{16})$~N(-3.09,0.01) | $g(\alpha_{16})$~N(-3.09,0.01) | $g(\alpha_{16})$~N(-3.09,0.01) |

D – Disease (PTB), $Y_1$ – any TB symptom, $Y_2$ – Radiologist conclusion, $Y_3$ – CAD4TBv5≥53 $Y_4$ – CAD4TBv6≥53, $Y_5$ – Xpert Ultra, $Y_6$ – Culture, "-" implies the parameter is not included (i.e set to zero) in the model, Model 0 – Based on the assumption of conditional independence, Model 1 – Accounts for conditional dependence between radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 and between Xpert Ultra and culture among the PTB cases and allows conditional independence between all the diagnostic tests among non-PTB cases, Model 2 – Accounts for conditional dependence between radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 and between Xpert Ultra and culture among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases

Table S3: Prior distributions for the parameters in the probit regression models for Vukuzazi data

| | Model structure | Model 3 |
|---|---|---|
| D | $Pr(D = 1) = \emptyset(\omega)$ | $g(\omega)$~N(-3,0.1) |
| $Y_1$ | $Pr(Y_{i1} = 1 \mid D_i = 1) = \emptyset(\beta_{11})$ | $g(\beta_{11})$~N(0,0.1) |
| | $Pr(Y_{i1} = 1 \mid D_i = 0) = \emptyset(\alpha_{11})$ | $g(\alpha_{11})$~N(0,10) |
| $Y_2$ | $Pr(Y_{i2} = 1 \mid Y_{i1}, D_i{=}1) = \emptyset(\beta_{12})$ | $g(\beta_{12})$~N(0,0.1) |
| | $Pr(Y_{i2} = 1 \mid Y_{i1}, D_i{=}0) = \emptyset(\alpha_{12} + \alpha_{22} y_{i1})$ | $g(\alpha_{12})$~N(0,10)<br>$g(\alpha_{22})$~N(0,10) |
| $Y_3$ | $Pr(Y_{i3} = 1 \mid Y_{i2}, D_i{=}1) = \emptyset(\beta_{13} + \beta_{23} y_{i2})$ | $g(\beta_{13})$~N(0,0.1)<br>$g(\beta_{23})$~N(0,0.1) |
| | $\Pr(Y_{i3} = 1 \mid Y_{i1}, Y_{i2}, D_i{=}0) = \emptyset(\alpha_{13} + \alpha_{23} y_{i1} + \alpha_{33} y_{i2})$ | $g(\alpha_{13})$~N(0,10)<br>$g(\alpha_{23})$~N(0,10)<br>$g(\alpha_{33})$~N(0,10) |
| $Y_4$ | $Pr(Y_{i4} = 1 \mid Y_{i2}, Y_{i3}, D_i{=}1) = \emptyset(\beta_{14} + \beta_{24} y_{i2} + \beta_{34} y_{i3})$ | $g(\beta_{14})$~N(0,0.1)<br>$g(\beta_{24})$~N(0,0.1)<br>$g(\beta_{34})$~N(0,0.1) |
| | $\Pr(Y_{i4} = 1 \mid Y_{i1}, Y_{i2}, Y_{i3}, D_i{=}0) = \emptyset(\alpha_{14} + \alpha_{24} y_{i1} + \alpha_{34} y_{i2} + \alpha_{44} y_{i3})$ | $g(\alpha_{14})$~N(0,10)<br>$g(\alpha_{24})$~N(0,10)<br>$g(\alpha_{34})$~N(0,10)<br>$g(\alpha_{44})$~N(0,10) |
| $Y_5$ | $Pr(Y_{i5} = 1 \mid Y_{i2}, Y_{i3}, Y_{i4}, D_i{=}1) = \emptyset(\beta_{15} + \beta_{25} y_{i2} + \beta_{35} y_{i3} + \beta_{45} y_{i4})$ | $g(\beta_{15})$~N(0,0.1)<br>$g(\beta_{25})$~N(0,0.1)<br>$g(\beta_{35})$~N(0,0.1)<br>$g(\beta_{45})$~N(0,0.1) |
| | $Pr(Y_{i5} = 1 \mid D_i{=}0) = \emptyset(\alpha_{15})$ | $g(\alpha_{15})$~N(-1.88,0.01) |
| $Y_6$ | $Pr(Y_{i6} = 1 \mid Y_{i2}, Y_{i3}, Y_{i4}, Y_{i5}, D_i{=}1) = \emptyset(\beta_{16} + \beta_{26} y_{i2} + \beta_{36} y_{i3} + \beta_{46} y_{i4} + \beta_{56} y_{i5})$ | $(\beta_{16}) \sim \mathrm{N}(0.84, 0.1)$<br>$g(\beta_{26}) \sim \mathrm{N}(0, 0.1)$<br>$g(\beta_{36}) \sim \mathrm{N}(0, 0.1)$<br>$g(\beta_{46}) \sim \mathrm{N}(0, 0.1)$<br>$\mathrm{g}(\beta_{56}) \sim \mathrm{N}(0, 0.1)$ |
| | $Pr(Y_{i6} = 1 \mid D_i{=}0) = \emptyset(\alpha_{16})$ | $g(\alpha_{16})$~N(-3.09,0.01) |

D – Disease (PTB), $Y_1$ – any TB symptom, $Y_2$ – Radiologist conclusion, $Y_3$ – CAD4TBv5≥53 $Y_4$ – CAD4TBv6≥53, $Y_5$ – Xpert Ultra, $Y_6$ – Culture, Model 3 – Accounts for conditional dependence between all the diagnostic tests except any TB symptom among the PTB cases and dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases.

Table S4: Prior distributions for the parameters in the probit regression models for Vukuzazi data

| | Model structure | Model 4 |
|---|---|---|
| D | $Pr(D = 1) = \emptyset(\omega)$ | $g(\omega)$~N(-3,0.1) |
| $Y_1$ | $Pr(Y_{i1} = 1 \mid D_i = 1) = \emptyset(\beta_{11})$ | $g(\beta_{11})$~N(0,0.1) |
| | $Pr(Y_{i1} = 1 \mid D_i = 0) = \emptyset(\alpha_{11})$ | $g(\alpha_{11})$~N(0,10) |
| $Y_2$ | $Pr(Y_{i2} = 1 \mid Y_{i1}, D_i\text{=1}) = \emptyset(\beta_{12}+ \beta_{22}y_{i1})$ | $g(\beta_{12})$~N(0,0.1)<br>$g(\beta_{22})$~N(0,0.1) |
| | $Pr(Y_{i2} = 1 \mid Y_{i1}, D_i\text{=0}) = \emptyset(\alpha_{12} + \alpha_{22}y_{i1})$ | $g(\alpha_{12})$~N(0,10)<br>$g(\alpha_{22})$~N(0,10) |
| $Y_3$ | $Pr(Y_{i3} = 1 \mid Y_{i1}, Y_{i2}, D_i\text{=1}) = \emptyset(\beta_{13}+ \beta_{23}y_{i1}+ \beta_{33}y_{i2})$ | $g(\beta_{13})$~N(0,0.1)<br>$g(\beta_{23})$~N(0,0.1)<br>$g(\beta_{33})$~N(0,0.1) |
| | $\Pr(Y_{i3} = 1 \mid Y_{i1}, Y_{i2}, D_i\text{=0}) = \emptyset(\alpha_{13} + \alpha_{23}y_{i1}+ \alpha_{33}y_{i2})$ | $g(\alpha_{13})$~N(0,10)<br>$g(\alpha_{23})$~N(0,10)<br>$g(\alpha_{33})$~N(0,10) |
| $Y_4$ | $Pr(Y_{i4} = 1 \mid Y_{i1}, Y_{i2}, Y_{i3}, D_i\text{=1}) = \emptyset(\beta_{14}+ \beta_{24}y_{i1}+ \beta_{34}y_{i2}+ \beta_{44}y_{i3})$ | $g(\beta_{14})$~N(0,0.1)<br>$g(\beta_{24})$~N(0,0.1)<br>$g(\beta_{34})$~N(0,0.1)<br>$g(\beta_{44})$~N(0,0.1) |
| | $\Pr(Y_{i4} = 1 \mid Y_{i1}, Y_{i2}, Y_{i3}, D_i\text{=0}) = \emptyset(\alpha_{14}+\alpha_{24}y_{i1}+ \alpha_{34}y_{i2}+ \alpha_{44}y_{i3})$ | $g(\alpha_{14})$~N(0,10)<br>$g(\alpha_{24})$~N(0,10)<br>$g(\alpha_{34})$~N(0,10)<br>$g(\alpha_{44})$~N(0,10) |
| $Y_5$ | $Pr(Y_{i5} = 1 \mid Y_{i1}, Y_{i2}, Y_{i3}, Y_{i4}, D_i\text{=1}) = \emptyset(\beta_{15}+ \beta_{25}y_{i1}+ \beta_{35}y_{i2}+ \beta_{45}y_{i3}+ \beta_{55}y_{i4})$ | $g(\beta_{15})$~N(0,0.1)<br>$g(\beta_{25})$~N(0,0.1)<br>$g(\beta_{35})$~N(0,0.1)<br>$g(\beta_{45})$~N(0,0.1)<br>$g(\beta_{55})$~N(0,0.1) |
| | $Pr(Y_{i5} = 1 \mid D_i\text{=0}) = \emptyset(\alpha_{15})$ | $g(\alpha_{15})$~N(-1.88,0.01) |
| $Y_6$ | $Pr(Y_{i6} = 1 \mid Y_{i1}, Y_{i2}, Y_{i3}, Y_{i4}, Y_{i5}, D_i\text{=1})$<br>$= \emptyset(\beta_{16}+ \beta_{26}y_{i1}+ \beta_{36}y_{i2}+ \beta_{46}y_{i3}+ \beta_{56}y_{i4}+ \beta_{66}y_{i5})$ | $g(\beta_{16})$~N(0.84,0.1)<br>$g(\beta_{26})$~N(0, 0.1)<br>$g(\beta_{36})$~N(0, 0.1)<br>$g(\beta_{46})$~N(0, 0.1)<br>g($\beta_{56}$)~N(0, 0.1)<br>$g(\beta_{66})$~N(0,0.1) |
| | $Pr(Y_{i6} = 1 \mid D_i\text{=0}) = \emptyset(\alpha_{16})$ | $g(\alpha_{16})$~N(-3.09,0.01) |

D – Disease (PTB), $Y_1$ – any TB symptom, $Y_2$ – Radiologist conclusion, $Y_3$ – CAD4TBv5≥53 $Y_4$ – CAD4TBv6≥53, $Y_5$ – Xpert Ultra, $Y_6$ – Culture, Model 4 – Accounts for conditional dependence between all the diagnostic tests among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases

Table S5: Prior distributions for the parameters in the probit regression models for Vukuzazi data

| | Model structure | Model 2 with covariates |
|---|---|---|
| D | $Pr(D=1 \mid X_{i1}, X_{i2}, X_{i3}) = \emptyset\begin{pmatrix}\omega_0+\omega_1 x_{i3}+\omega_2 x_{i2}+\omega_3 I(x_{i1}=2)+\\ \omega_4 I(x_{i1}=3)+\omega_5 I(x_{i1}=4)\end{pmatrix}$ | $g(\omega_0)$~N(-5,0.1)<br>$g(\omega_1)$~N(0,0.01), …,<br>$g(\omega_5)$~N(0,0.01) |
| $Y_1$ | $Pr(Y_{i1}=1 \mid X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{11}+\beta_{21}x_{i3}+\beta_{31}x_{i2}+\beta_{41}I(x_{i1}=2)+\\ \beta_{51}I(x_{i1}=3)+\beta_{61}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{11})$~N(0,10)<br>$g(\beta_{21})$ … $g(\beta_{61})$~N(0,1) |
| | $Pr(Y_{i1}=1 \mid X_{i1}, X_{i2}, X_{i3}, D_i=0) = \emptyset\begin{pmatrix}\alpha_{11}+\alpha_{21}x_{i3}+\alpha_{31}x_{i2}+\alpha_{41}I(x_{i1}=2)\\ +\alpha_{51}I(x_{i1}=3)+\alpha_{61}I(x_{i1}=4)\end{pmatrix}$ | $g(\alpha_{11})$~N(0,10)<br>$g(\alpha_{21})$ … $g(\alpha_{61})$~N(0,1) |
| $Y_2$ | $Pr(Y_{i2}=1 \mid X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{12}+\beta_{22}x_{i3}+\beta_{32}x_{i2}+\beta_{42}I(x_{i1}=2)+\\ \beta_{52}I(x_{i1}=3)+\beta_{62}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{12})$ … $g(\beta_{62})$~N(0,1) |
| | $Pr(Y_{i2}=1 \mid Y_{i1}, X_{i1}, X_{i2}, X_{i3}, D_i=0) = \emptyset\begin{pmatrix}\alpha_{12}+\alpha_{22}y_{i1}+\alpha_{32}x_{i3}+\alpha_{42}x_{i2}+\alpha_{52}I(x_{i1}=2)\\ +\alpha_{62}I(x_{i1}=3)+\alpha_{72}I(x_{i1}=4)\end{pmatrix}$ | $g(\alpha_{12}), g(\alpha_{22})$~N(0,10)<br>$g(\alpha_{32})$ … $g(\alpha_{72})$~N(0,1) |
| $Y_3$ | $Pr(Y_{i3}=1 \mid Y_{i2}, X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{13}+\beta_{23}y_{i2}+\beta_{33}x_{i3}+\beta_{43}x_{i2}+\beta_{53}I(x_{i1}=2)\\ +\beta_{63}I(x_{i1}=3)+\beta_{73}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{13})$ … $g(\beta_{73})$~N(0,1) |
| | $\mathrm{Pr}(Y_{i3}=1 \mid Y_{i1}, Y_{i2}, X_{i1}, X_{i2}, X_{i3}, D_i=0) = \emptyset\begin{pmatrix}\alpha_{13}+\alpha_{23}y_{i1}+\alpha_{33}y_{i2}+\alpha_{43}x_{i3}+\alpha_{53}x_{i2}\\ +\alpha_{63}I(x_{i1}=2)+\alpha_{73}I(x_{i1}=3)+\alpha_{83}I(x_{i1}=4)\end{pmatrix}$ | $g(\alpha_{13})$ … $g(\alpha_{33})$~N(0,10)<br>$g(\alpha_{43})$ … $g(\alpha_{83})$~N(0,1) |
| $Y_4$ | $Pr(Y_{i4}=1 \mid Y_{i2}, Y_{i3}, X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{14}+\beta_{24}y_{i2}+\beta_{34}y_{i3}+\beta_{44}x_{i3}+\beta_{54}x_{i2}\\ +\beta_{64}I(x_{i1}=2)+\beta_{74}I(x_{i1}=3)+\beta_{84}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{14})$ … $g(\beta_{84})$~N(0,1) |
| | $\mathrm{Pr}(Y_{i4}=1 \mid Y_{i1}, Y_{i2}, Y_{i3}, X_{i1}, X_{i2}, X_{i3}, D_i=0) = \emptyset\begin{pmatrix}\alpha_{14}+\alpha_{24}y_{i1}+\alpha_{34}y_{i2}+\alpha_{44}y_{i3}+\alpha_{54}x_{i3}+\alpha_{64}x_{i2}\\ +\alpha_{74}I(x_{i1}=2)+\alpha_{84}I(x_{i1}=3)+\alpha_{94}I(x_{i1}=4)\end{pmatrix}$ | $g(\alpha_{14})$ … $g(\alpha_{44})$~N(0,10)<br>$g(\alpha_{54})$ … $g(\alpha_{94})$~N(0,1) |
| $Y_5$ | $Pr(Y_{i5}=1 \mid X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{15}+\beta_{25}x_{i3}+\beta_{35}x_{i2}+\beta_{45}I(x_{i1}=2)+\beta_{55}\\ I(x_{i1}=3)+\beta_{65}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{15})$ … $g(\beta_{65})$~N(0,1) |
| | $Pr(Y_{i5}=1 \mid D_i=0) = \emptyset(\alpha_{15})$ | $g(\alpha_{15})$~N(-1.88,0.01) |
| $Y_6$ | $Pr(Y_{i6}=1 \mid Y_{i5}, X_{i1}, X_{i2}, X_{i3}, D_i=1) = \emptyset\begin{pmatrix}\beta_{16}+\beta_{26}y_{i5}+\beta_{36}x_{i3}+\beta_{46}x_{i2}+\beta_{56}I(x_{i1}=2)+\\ \beta_{66}I(x_{i1}=3)+\beta_{76}I(x_{i1}=4)\end{pmatrix}$ | $g(\beta_{16})$~N(0.84,0.1)<br>$g(\beta_{26})$ … $g(\beta_{76})$~N(0,1) |
| | $Pr(Y_{i6}=1 \mid D_i=0) = \emptyset(\alpha_{16})$ | $g(\alpha_{16})$~N(-3.09,0.01) |

D – Disease (PTB), $Y_1$ – any TB symptom, $Y_2$ – Radiologist conclusion, $Y_3$ – CAD4TBv5 ≥53 $Y_4$ – CAD4TBv6 ≥53, $Y_5$ – Xpert Ultra, $Y_6$ – Culture; Model 2 – Accounts for conditional dependence between radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 and between Xpert Ultra and culture among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases, adjusted for covariates (age, sex and HIV status).

In Table S5, D denotes disease (PTB), $Y_1$, $Y_2$, $Y_3$, $Y_4$, $Y_5$ and $Y_6$ denotes any TB symptom , Radiologist conclusion, CAD4TBv5 ≥53, CAD4TBv6 ≥53, Xpert Ultra and Culture respectively. $X_1$ denotes age (categorical variable), $X_2$ denotes sex (Male/Female) and $X_3$ denotes HIV status (+/-)

The choice of the informative prior for the parameters of the probit regression models was adapted based on the expert opinion and previously published material. This was chosen in order to yield a posterior distribution that spans the range of plausible values for the parameter.

The joint probability of random variables $Y$ and $X_1, X_2, X_3$ given by $Pr(Y, X_1, X_2, X_3)$ can be expressed using chain rule of conditional probabilities as $Pr(X_1)Pr(X_2|X_1)Pr(X_3|X_1, X_2)Pr(Y|X_1, X_2, X_3)$. Where $Y$ is either the disease status or diagnostic test and $X_1$ – Age ( four level categorical variable: 15-19 years, 30-49 years, 50-69 years, ≥70 years) with reference category as 15-19 years, $X_2$ - Sex (Male/Female), $X_3$ – HIV status (+/-). The conditional probabilities were computed using probit regression models with priors from Gaussian distribution. The unknown parameters of$X_1, X_2$ and $X_3$ in the model $Pr(Y|X_1, X_2, X_3)$ are assigned priors from N(0,10) (Table S5). The unknown parameters of $X_1$ and $X_2$ in the models $Pr(X_2|X_1)$ and $Pr(X_3|X_1, X_2)$ are assigned priors from N(0,10). To model $Pr(X_1)$ we assigned non-informative dirichlet prior, $Dir(\vartheta_1 = 1, \vartheta_2 = 1, \vartheta_3 = 1, \vartheta_4 = 1)$, to the parameters of the multinomial distribution.

## 3. Computer-Aided Detection for TB (CAD4TB) Threshold

Given all the diagnostic tests in use are imperfect, the true TB status is unknown. This is the complexity in diagnostic studies without a perfect reference standard. However, as alluded to in the background of the abstract and in the introduction, this problem can be handled using latent class analysis, a statistical methodology that has been in use over the past four decades in many disciplines but scarcely used in the field of infectious diseases, including the field of TB. This method identifies unobserved mutually exclusive subgroups in the population using information from the measured subject characteristics. In our case, using the information (test results) from all the imperfect diagnostic tests the model can stochastically tease out the TB and non-TB cases. Consequently, using the derived subgroups, the sensitivity and specificity of the tests can be calculated.

CAD4TB thresholds were determined based on secondary analysis of data from the community-based multi-morbidity survey in KwaZulu-Natal, South Africa (“Vukuzazi” study) using Bayesian latent class analysis. In this survey, the digital chest X-ray images were interpreted using CAD4TB version 5 (CAD4TBv5) and CAD4TBv6. The thresholds for both CAD4TBv5 and CAD4TBv6 were determined by performing LCA to estimate the sensitivity and specificity of CAD4TB at integer thresholds $S_k$, k = 2, 3, …, K-1, for K distinct CAD4TB scores. Thus, there were K-2 models fit and for each model, the estimates of pulmonary TB prevalence and diagnostic test sensitivity and specificity were obtained. The estimates of sensitivity and specificity for CAD4TB were used to construct a receiver operating characteristic (ROC) curve to help identify a plausible CAD4TB cut-off score.

Determination of CAD4TB cut-off scores proceeded by first fitting a two-class latent class model with any TB symptom, radiologist interpretation (chest X-ray abnormality suggestive of active TB), CAD4TBv5≥$S_k$, Xpert Ultra (excluding trace) and culture. Using the estimates of sensitivity and specificity for CAD4TBv5 obtained from the fitted models we constructed a ROC curve and determined CAD4TBv5 threshold, say $S_{t1}$. Next, we fitted a two-class latent class model with any TB symptom, radiologist interpretation (chest X-ray abnormality suggestive of active TB), CAD4TBv5≥$S_{t1}$, CAD4TBv6≥$S_k$, Xpert Ultra (excluding trace) and culture, where we now set threshold for CAD4TBv5 at $S_{t1}$. Again, using the same approach, we determined the threshold for CAD4TBv6, say $S_{t2}$. For both CAD4TBv5 and CAD4TBv6, we aimed at a threshold score that produced sensitivity and specificity estimates close to 80%. The cut-off values were 53 for CAD4TBv5 and 52 for CAD4TBv6 (Fig S1). Nonetheless, we opted for the same cut-off of 53 for both CAD4TBv5 and CAD4TBv6 based on the lowess smoother that revealed overlap of the two curves at around 80% for both the sensitivity and specificity for CAD4TBv5 and CAD4TBv6. The cut-off score of 53 yielded a sensitivity of 83% and a specificity of 80% for CAD4TBv5. In the model that included CAD4TBv5≥53 and CAD4TBv6 the threshold score of 52 for CAD4TBv6 yielded a sensitivity of 84% and a specificity of 81% While a threshold score of 53 for CAD4TBv6 yielded a sensitivity and specificity of 80% and 83% respectively (Fig S1). This is no surprise given the distribution of the difference in scores between the two versions of CAD4TB that is centered around zero (Fig S2). Fig S1 shows the receiver operating characteristic (ROC) curves of the estimates of sensitivity and specificity for CAD4TBv5 and CAD4TBv6.

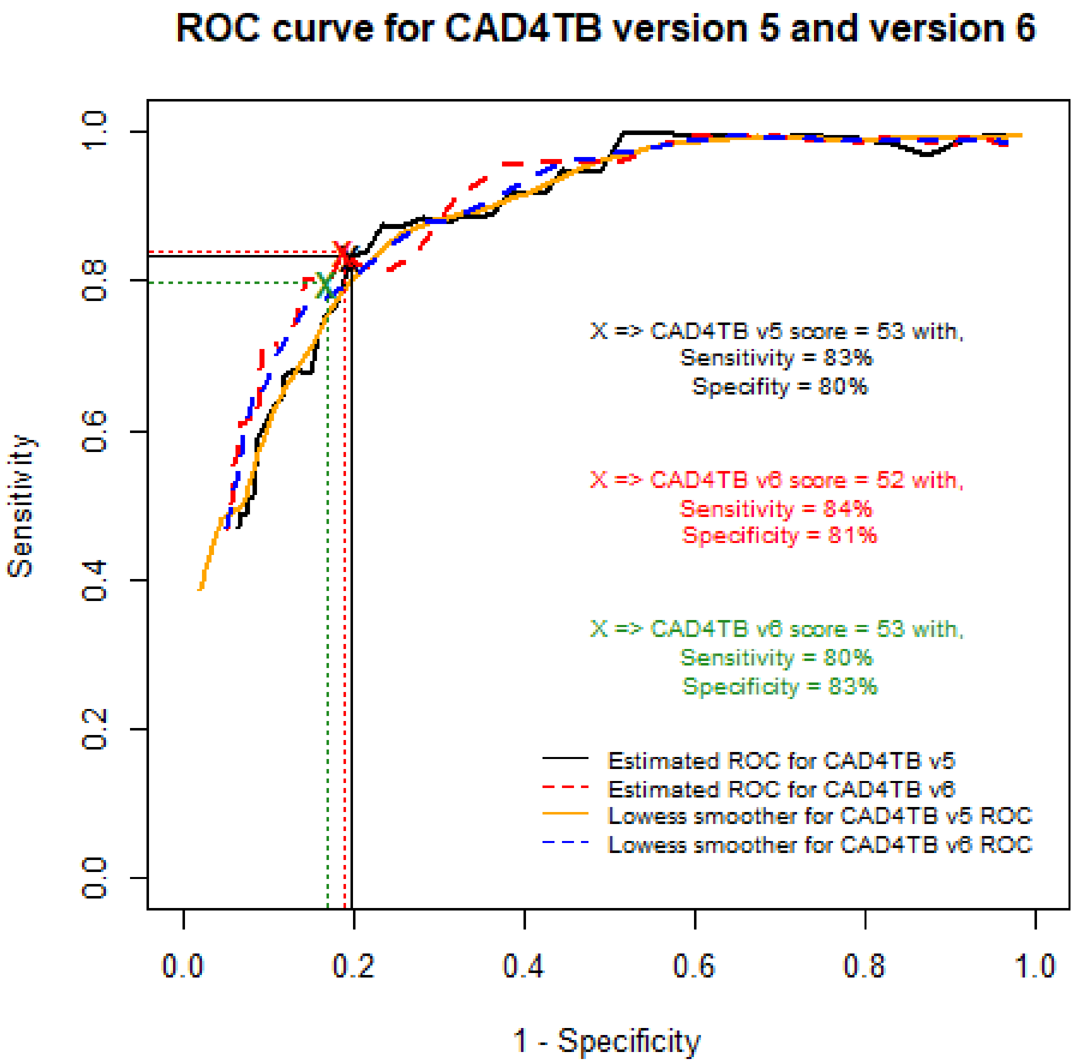


Fig S1: Receiver operating characteristic curves depicting the cut-off values used in the final latent class models

With these CAD4TB thresholds defined, we fitted a final model with any TB symptom, radiologist interpretation (chest X-ray abnormality suggestive of active TB), CAD4TBv5≥$S_{t1}$, CAD4TBv6≥$S_{t2}$, Xpert Ultra (excluding trace) and culture to estimate PTB prevalence, and diagnostic test sensitivity and specificity of the six diagnostic tests. We repeated the same analysis with chest X-ray abnormality suggestive of active TB replaced by any chest X-ray abnormality.

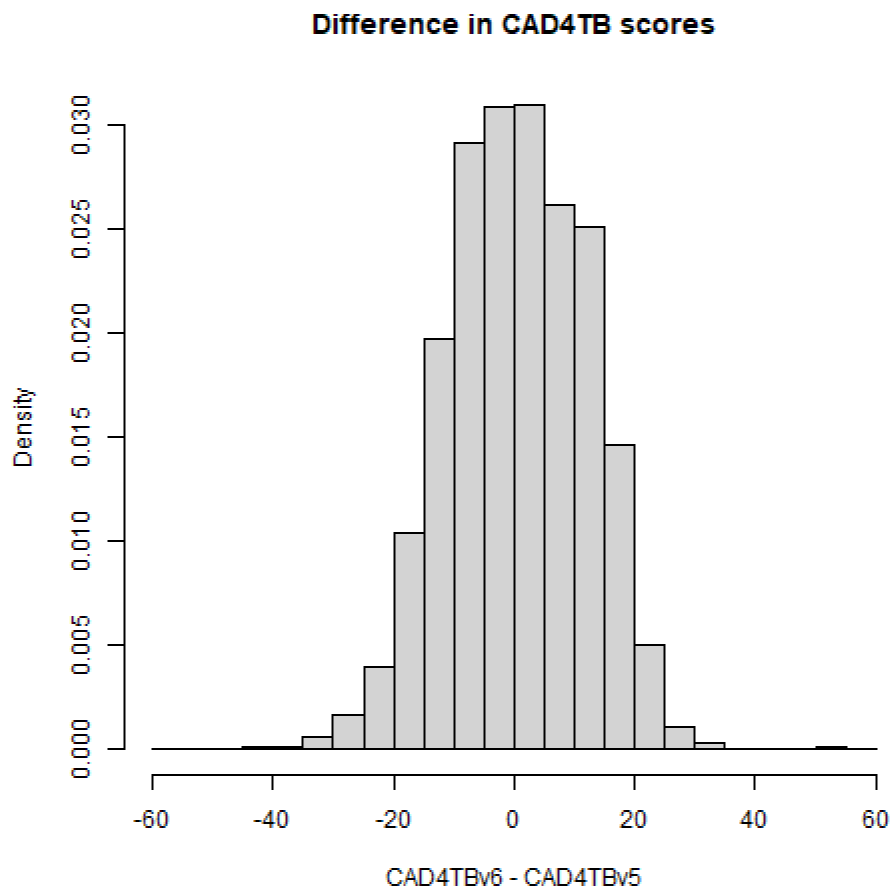


Fig S2: Distribution of difference in CAD4TB scores between version 6 and version 5

Fig S3 shows a scatter plot of CAD4TBv5 and CAD4TBv6 scores. The scatter plot reveals some trend in the scores. However, it is imperative to understand that the two devices are used to evaluate chest X-ray images of the same person. Therefore, they are paired. From the scatter plot, the positive correlation between version 6 and version 5 is not sufficiently strong to result in strong dependencies between the two versions in the model.

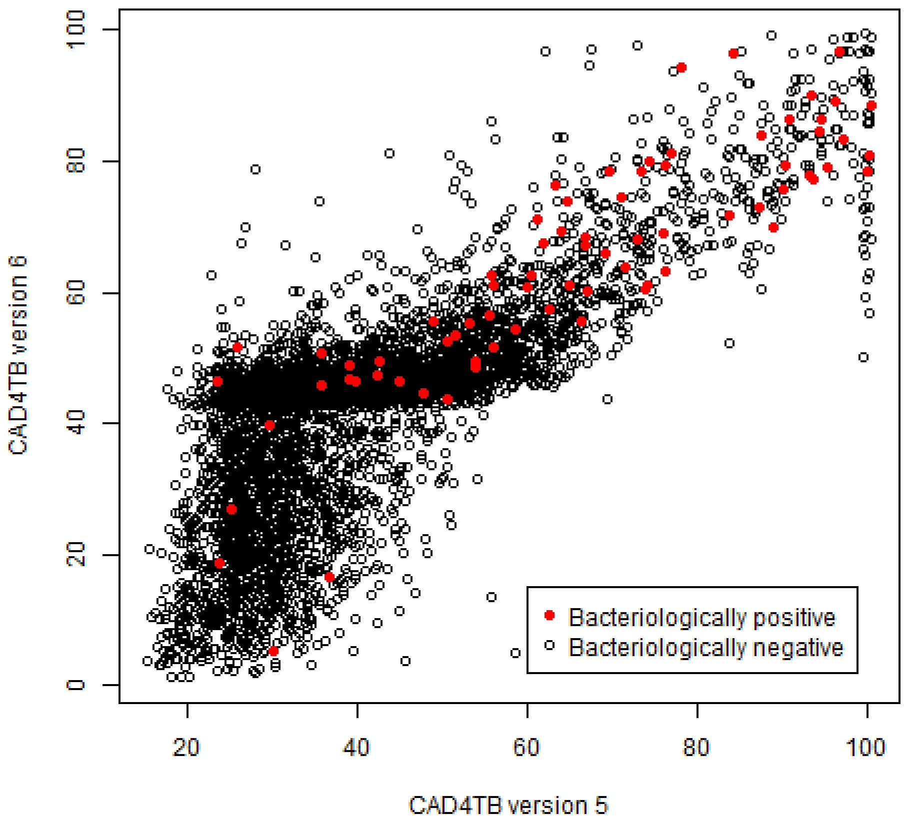


Fig S3: Scatter plot of CAD4TB version 5 and CAD4TB version 6 scores

**4. Supplementary Tables**

Table S7 presents results of four models. The results of Model 1, Model 2 and Model 3 were already presented in the main document but shown here to aid comparison with Model 4. These findings suggest that conditional dependence between TST and radiography among the children without CPTB cannot be ignored.

Table S6: Posterior median and 95% credible intervals (95% CrI) of the prevalence and diagnostic test accuracy of the parameters of childhood pulmonary tuberculosis dataset

| | | **Model 0** | **Model 1** | **Model 2** | **Model 3** | **Model 4** |
|---|---|---|---|---|---|---|
| **Test** | **Parameter** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** |
| | Prevalence | 16.3 (13.6, 19.3) | 21.6 (15.6, 28.6) | 18.4 (14.7, 26.4) | 18.9 (15.1, 27.0) | 19.9 (15.4, 29.7) |
| TST | Sensitivity | 69.2 (60.5, 76.9) | 73.2 (61.8, 82.4) | 68.3 (58.5, 79.9) | 69.5 (59.4, 81.5) | 70.5 (60.2, 83.0) |
| | Specificity | 62.3 (58.4, 66.1) | 65.2 (59.6, 71.8) | 62.7 (58.5, 69.6) | 63.1 (58.8, 70.4) | 63.7 (59.2, 72.8) |
| Rad. | Sensitivity | 66.0 (57.1, 74.1) | 65.1 (56.1, 73.8) | 64.5 (55.5, 73.3) | 60.1 (42.5, 72.2) | 62.7 (51.8, 76.8) |
| | Specificity | 73.1 (69.5, 76.5) | 74.8 (70.5, 79.2) | 73.2 (69.4, 77.9) | 72.2 (67.8, 76.5) | 73.7 (69.4, 79.9) |
| SMM | Sensitivity | 33.8 (25.5, 42.5) | 24.3 (16.7, 34.8) | 28.4 (18.7, 37.6) | 28.4 (19.0, 37.2) | 26.7 (16.7, 36.4) |
| | Specificity | 99.9 (99.5, 100) | 99.9 (99.5, 100) | 99.9 (99.5, 100) | 99.9 (99.5, 100) | 99.9 (99.5, 100) |
| Xpert | Sensitivity | 74.8 (66.3, 82.5) | 59.1 (44.2, 75.7) | 69.4 (47.8, 78.4) | 70.3 (47.9, 79.5) | 66.3 (43.2, 79.1) |
| | Specificity | 98.2 (97.0, 99.3) | 98.7 (97.1, 99.9) | 98.7 (97.2, 99.9) | 99.2 (97.5, 100) | 99.0 (97.2, 100) |
| Culture | Sensitivity | 99.9 (91.0, 100) | 75.3 (56.9, 97.2) | 88.0 (61.8, 98.4) | 86.4 (60.3, 98.5) | 82.7 (55.1, 98.2) |
| | Specificity | 99.8 (99.0, 100) | 99.8 (99.2, 100) | 99.8 (99.2, 100) | 99.8 (99.2, 100) | 99.8 (99.2, 100) |
| | Deviance | 183.7 | 104.7 | 102.1 | 101.7 | 107.8 |
| | RMSE | 42.4 | 38.0 | 12.0 | 9.1 | 32.9 |

Model 0 – Based on the assumption of conditional independence
Model 1 – Based on the expert opinion as detailed in [3]. The model accounts for conditional dependence between all the diagnostic tests except radiography among children with CPTB and conditional independence between all the diagnostic tests among children without CPTB
Model 2 – The model accounts for conditional dependence between all the diagnostic tests except radiography among children with CPTB and conditional dependence between TST and radiography among children without CPTB
Model 3 – Accounts for conditional dependence between all the diagnostic tests among children with CPTB and conditional dependence between TST and radiography among children without CPTB
Model 4 – Accounts for conditional dependence between all the diagnostic tests among children with CPTB and allows conditional independence between all the diagnostic tests among children without CPTB
TST – Tuberculin skin test, Rad. – Radiography, SMM – Sputum smear microscopy, Xpert – Xpert MTB/RIF
RMSE – Root mean squared error deviations. This is calculated as the square root of the sum of squared differences between the observed frequencies and the predicted frequencies. It shows how good the model is in explaining the variability in the data
Note model 3 seems to do better prediction compared to model 1 although model 1 seems to best fit the data. This may be explained by the fact that model 3 accounts for dependence between radiography and other diagnostic tests among the true CPTB cases. Hence extra penalty
CrI – Credible Intervals

Table S7: Distribution of the number of participants included in LCA by age, sex and HIV status

| | | Age (Years) | | | | |
|---|---|---|---|---|---|---|
| | | 15 – 29 years | 30 – 49 years | 50 – 69 years | ≥ 70 years | Total |
| Male | HIV + | 56 (8.9%) | 235 (48.4%) | 148 (29.0%) | 18 (9.6%) | 457 (25.2%) |
| | HIV - | 573 (91.1%) | 251 (51.6%) | 363 (71.0%) | 169 (90.4%) | 1356 (74.8%) |
| | Total | 629 (34.7%) | 486 (26.8%) | 511 (28.2%) | 187 (10.3%) | 1813 (100%) |
| | | | | | | |
| Female | HIV + | 140 (26.6%) | 507 (63.0%) | 355 (29.3%) | 37 (6.1%) | 1039 (33.0%) |
| | HIV - | 387 (73.4%) | 298 (37.0%) | 857 (70.7%) | 566 (93.9%) | 2108 (67.0%) |
| | Total | 527 (16.7%) | 805 (25.6%) | 1212 (38.5%) | 603 (19.2%) | 3147 (100%) |
| | | | | | | |
| Total | HIV + | 196 (17.0%) | 742 (57.5%) | 503 (29.2%) | 55 (7.0%) | 1496 (30.2%) |
| | HIV - | 960 (83.0%) | 549 (42.5%) | 1220 (70.8%) | 735 (93.0%) | 3464 (69.8%) |
| | Total | 1156 (23.3%) | 1291 (26.0%) | 1723 (34.7%) | 790 (15.9%) | 4960 (100%) |

Table S8: Posterior median and 95% credible intervals (95% CrI) of the age, sex and HIV adjusted PTB prevalence and diagnostic test sensitivity and specificity among male individuals in Vukuzazi dataset

| | | | 15 – 29 years | 30 – 49 years | 50 – 69 years | ≥70 years |
|---|---|---|---|---|---|---|
| **Group** | **Test** | **Parameter** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** |
| **HIV+ Male** | | Prevalence | 1.5 (0.8, 2.4) | 1.6 (0.9, 2.7) | 1.9 (1.1, 3.2) | 1.6 (0.8, 3.0) |
| | Any TB symptom | Sensitivity | 28.1 (12.0, 51.2) | 22.2 (7.2, 46.0) | 27.8 (11.0, 50.1) | 26.7 (7.6, 55.3) |
| | | Specificity | 82.3 (78.8, 85.4) | 84.4 (81.6, 87.0) | 84.4 (81.3, 87.2) | 83.9 (79.7, 87.6) |
| | Radiologist conclusion‡ | Sensitivity | 90.2 (72.9, 97.7) | 90.8 (72.8, 98.3) | 94.9 (82.0, 99.2) | 93.2 (74.0, 99.1) |
| | | Specificity | 77.8 (74.1, 81.4) | 54.8 (51.1, 58.6) | 44.3 (40.2, 48.5) | 37.2 (32.0, 42.6) |
| | CAD4TBv5≥53 | Sensitivity | 86.4 (67.3, 96.2) | 88.2 (67.5, 97.6) | 88.6 (70.1, 97.3) | 88.6 (65.8, 97.9) |
| | | Specificity | 87.3 (84.0, 90.2) | 68.7 (65.1, 72.4) | 56.3 (51.7, 60.7) | 37.5 (32.0, 43.3) |
| | CAD4TBv6≥53 | Sensitivity | 83.3 (63.7, 94.7) | 83.7 (60.8, 96.0) | 86.6 (66.8, 96.6) | 85.3 (59.9, 96.9) |
| | | Specificity | 89.8 (86.7, 92.3) | 69.9 (66.2, 73.5) | 57.0 (52.5, 61.6) | 41.2 (35.7, 47.0) |
| | Xpert Ultra† | Sensitivity | 65.1 (40.6, 85.3) | 70.1 (42.7, 89.5) | 69.9 (45.5, 88.0) | 62.5 (31.9, 87.1) |
| | | Specificity | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) |
| | Culture | Sensitivity | 76.7 (52.0, 94.1) | 76.7 (47.7, 95.8) | 71.1 (44.8, 92.9) | 81.4 (52.8, 96.8) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| **HIV- Male** | | Prevalence | 0.9 (0.5, 1.4) | 1.0 (0.6, 1.7) | 1.2 (0.7, 2.0) | 1.0 (0.5, 1.8) |
| | Any TB symptom | Sensitivity | 26.1 (12.0, 44.6) | 20.2 (6.4, 42.3) | 25.5 (10.5, 47.1) | 24.8 (7.9, 49.7) |
| | | Specificity | 81.9 (79.2, 84.3) | 84.0 (81.1, 86.6) | 84.0 (81.6, 86.3) | 83.5 (80.1, 86.3) |
| | Radiologist conclusion‡ | Sensitivity | 83.4 (66.8, 93.8) | 84.2 (63.2, 95.8) | 90.5 (74.7, 97.7) | 88.1 (67.3, 97.3) |
| | | Specificity | 85.9 (83.6, 88.1) | 66.6 (63.0, 70.1) | 56.6 (53.3, 60.0) | 49.3 (45.0, 53.6) |
| | CAD4TBv5≥53 | Sensitivity | 82.5 (64.9, 93.7) | 84.8 (63.0, 96.2) | 85.5 (65.4, 96.1) | 85.2 (63.2, 96.6) |
| | | Specificity | 91.2 (89.2, 93.1) | 76.2 (72.7, 79.5) | 64.8 (61.4, 68.2) | 46.2 (41.7, 50.7) |
| | CAD4TBv6≥53 | Sensitivity | 80.8 (62.5, 92.7) | 81.5 (58.3, 94.7) | 84.8 (65.2, 95.6) | 83.2 (60.0, 95.7) |
| | | Specificity | 94.4 (92.8, 95.8) | 80.0 (76.7, 83.0) | 69.0 (65.6, 72.2) | 53.9 (49.4, 58.3) |
| | Xpert Ultra† | Sensitivity | 69.3 (48.8, 85.3) | 73.7 (49.0, 90.7) | 73.5 (51.5, 89.6) | 66.8 (39.2, 87.8) |
| | | Specificity | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) |
| | Culture | Sensitivity | 78.2 (58.4, 92.9) | 78.1 (51.6, 95.2) | 72.6 (48.6, 92.5) | 82.6 (58.1, 96.2) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

‡ - Any chest X-ray abnormality, † - Excluding trace

Table S9: Posterior median and 95% credible intervals (95% CrI) of the age, sex and HIV adjusted PTB prevalence and diagnostic test sensitivity and specificity among female individuals in Vukuzazi dataset

| | | | **15 – 29 years** | **30 – 49 years** | **50 – 69 years** | **≥70 years** |
|---|---|---|---|---|---|---|
| **Group** | **Test** | **Parameter** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** |
| **HIV+ Female** | | Prevalence | 0.9 (0.5, 1.5) | 1.0 (0.5, 1.7) | 1.2 (0.6, 2.0) | 1.0 (0.5, 1.8) |
| | Any TB symptom | Sensitivity | 30.2 (14.8, 51.4) | 24.1 (9.1, 46.8) | 29.8 (12.5, 52.3) | 28.9 (9.5, 55.7) |
| | | Specificity | 81.4 (77.8, 84.5) | 83.6 (81.1, 85.9) | 83.6 (80.9, 85.9) | 83.0 (79.3, 86.4) |
| | Radiologist conclusion‡ | Sensitivity | 84.9 (67.3, 94.8) | 85.7 (65.7, 96.3) | 91.6 (74.8, 98.2) | 89.2 (67.6, 97.9) |
| | | Specificity | 84.2 (81.1, 86.9) | 63.8 (60.7, 66.9) | 53.6 (50.2, 57.1) | 46.3 (41.5, 51.0) |
| | CAD4TBv5≥53 | Sensitivity | 79.5 (60.4, 92.4) | 81.8 (59.8, 95.3) | 82.6 (61.5, 94.8) | 82.4 (57.6, 95.8) |
| | | Specificity | 96.1 (94.7, 97.3) | 86.8 (84.5, 88.9) | 78.4 (75.4, 81.2) | 62.1 (57.1, 66.9) |
| | CAD4TBv6≥53 | Sensitivity | 80.8 (61.9, 92.7) | 81.5 (59.2, 94.7) | 84.7 (65.1, 95.4) | 83.2 (58.1, 95.8) |
| | | Specificity | 96.8 (95.5, 97.9) | 86.9 (84.7, 89.0) | 78.3 (75.3, 81.2) | 64.8 (59.9, 69.5) |
| | Xpert Ultra† | Sensitivity | 52.2 (31.4, 72.4) | 57.4 (33.2, 79.8) | 57.3 (32.8, 78.7) | 49.3 (23.5, 76.3) |
| | | Specificity | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) |
| | Culture | Sensitivity | 76.9 (55.5, 92.6) | 77.1 (50.6, 94.5) | 71.4 (45.6, 92.0) | 81.5 (55.5, 96.1) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| **HIV- Female** | | Prevalence | 0.5 (0.3, 0.9) | 0.6 (0.3, 1.0) | 0.7 (0.4, 1.2) | 0.6 (0.3, 1.1) |
| | Any TB symptom | Sensitivity | 28.1 (15.4, 44.0) | 22.2 (8.2, 43.4) | 27.4 (11.9, 49.1) | 26.6 (9.9, 50.5) |
| | | Specificity | 80.9 (78.1, 83.6) | 83.2 (80.3, 85.8) | 83.1 (81.0, 85.1) | 82.6 (79.8, 85.2) |
| | Radiologist conclusion‡ | Sensitivity | 76.4 (60.8, 87.8) | 77.5 (54.9, 91.6) | 85.5 (66.8, 95.5) | 82.1 (59.7, 94.7) |
| | | Specificity | 90.5 (88.6, 92.2) | 74.6 (71.4, 77.7) | 65.6 (62.9, 68.1) | 58.5 (54.8, 62.0) |
| | CAD4TBv5≥53 | Sensitivity | 74.6 (57.5, 87.3) | 77.4 (54.7, 92.5) | 78.5 (56.6, 92.5) | 78.1 (55.0, 93.0) |
| | | Specificity | 97.6 (96.8, 98.3) | 91.0 (89.0, 92.7) | 84.3 (82.3, 86.2) | 70.2 (66.9, 73.3) |
| | CAD4TBv6≥53 | Sensitivity | 77.9 (61.8, 89.8) | 78.8 (56.4, 93.0) | 82.4 (62.4, 94.1) | 80.7 (58.3, 94.0) |
| | | Specificity | 98.5 (97.9, 99.0) | 92.5 (90.8, 94.1) | 86.4 (84.5, 88.2) | 75.7 (72.7, 78.5) |
| | Xpert Ultra† | Sensitivity | 56.5 (40.0, 72.6) | 61.9 (37.6, 82.3) | 61.4 (38.5, 81.6) | 53.7 (30.1, 77.2) |
| | | Specificity | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) |
| | Culture | Sensitivity | 78.5 (61.9, 90.6) | 78.5 (54.7, 93.8) | 73.0 (48.8, 91.7) | 82.8 (60.8, 95.2) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

‡ - Any chest X-ray abnormality, † - Excluding trace

## 5. Supplementary Figures

### Model Diagnostics

Trace plots for assessing mixing in the chains

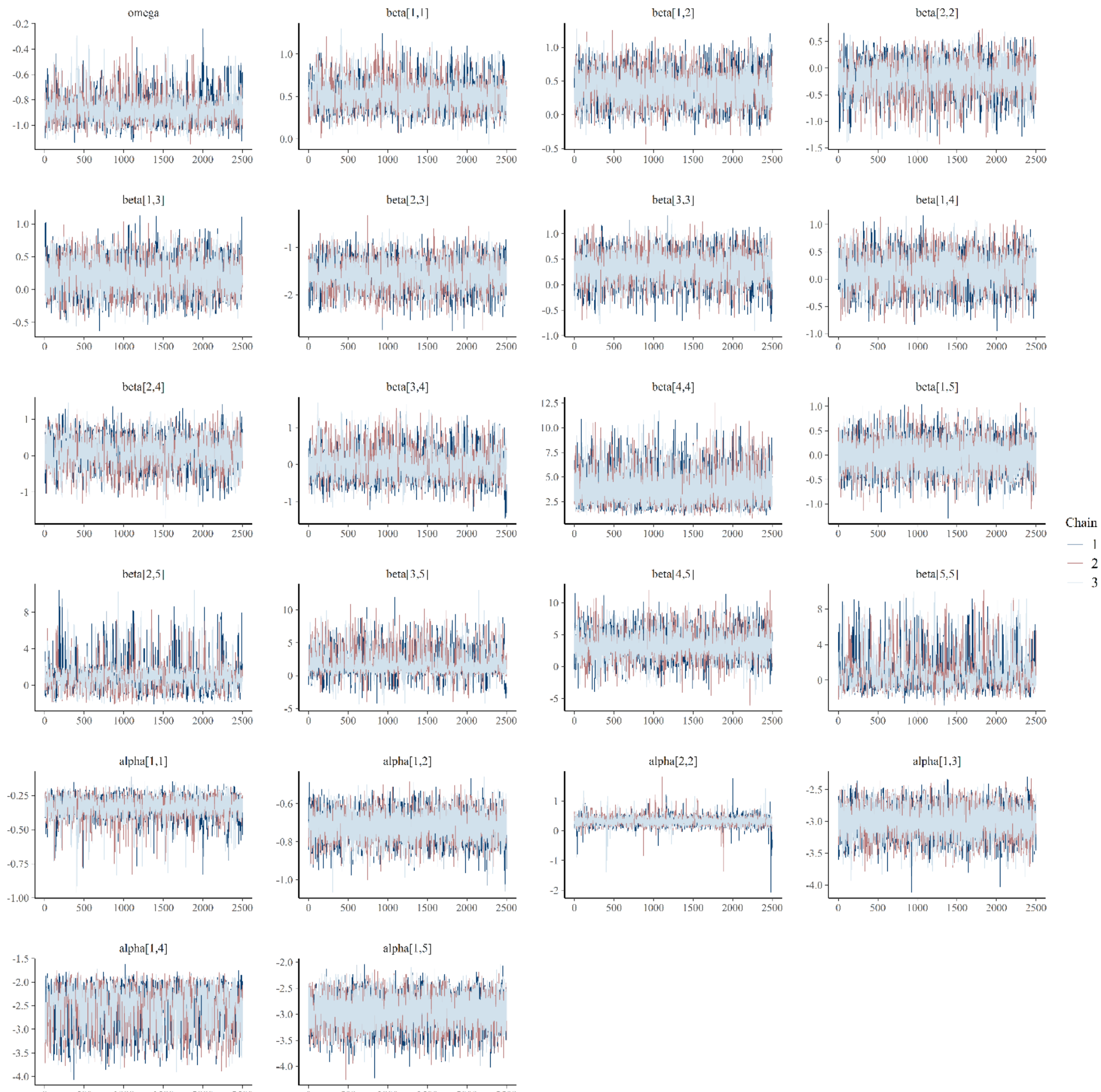


Fig S4: Trace plots of parameters on the probit scale corresponding to prevalence ($\omega$) and parameters of the probit regression models for conditional probabilities of diagnostic tests in the childhood pulmonary TB data analyzed using Model 2 presented in Table S1

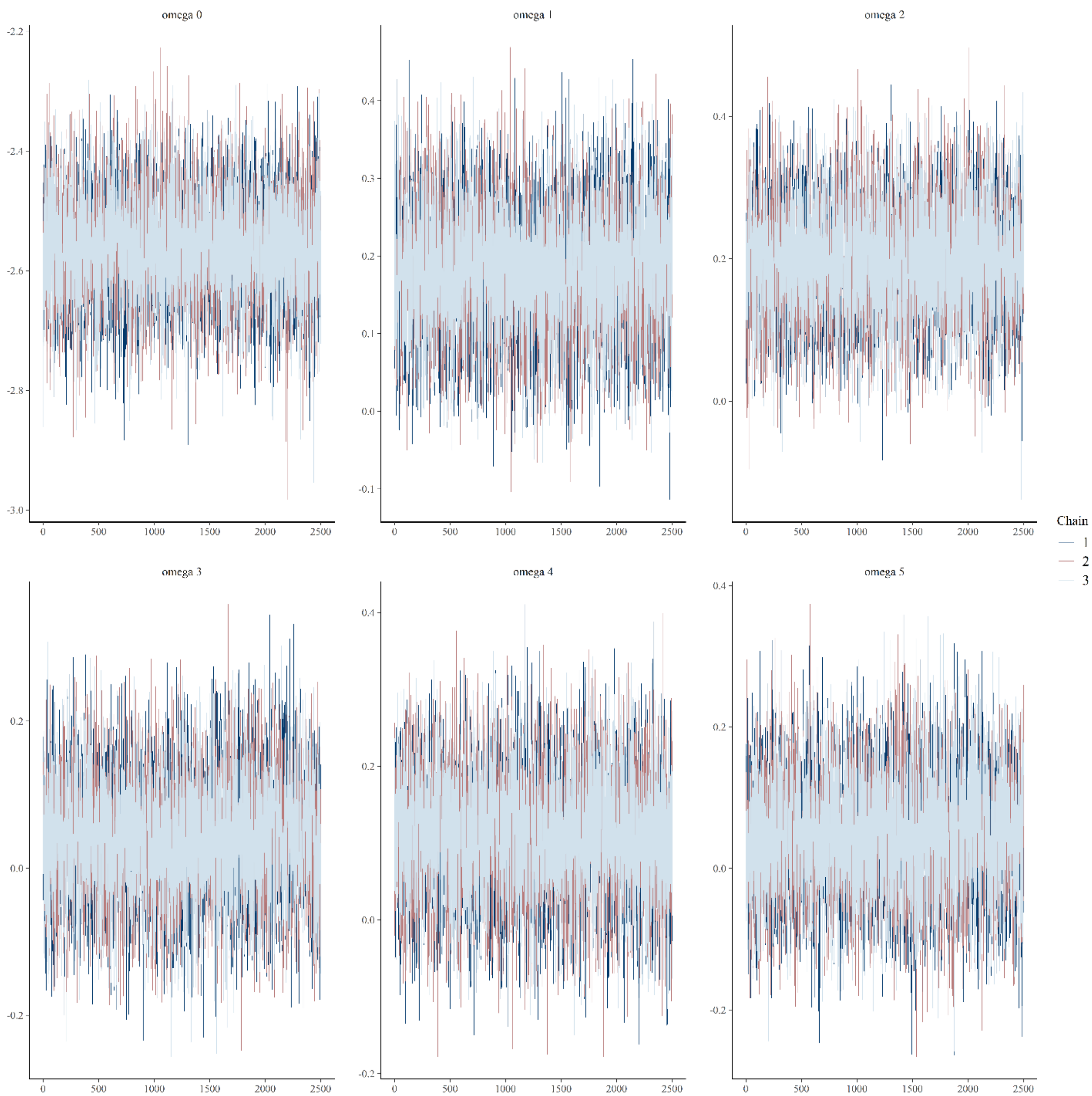


Fig S5: Trace plots of parameters of probit regression model for pulmonary TB prevalence in Vukuzazi dataset analyzed using Model 2 presented in Table S4

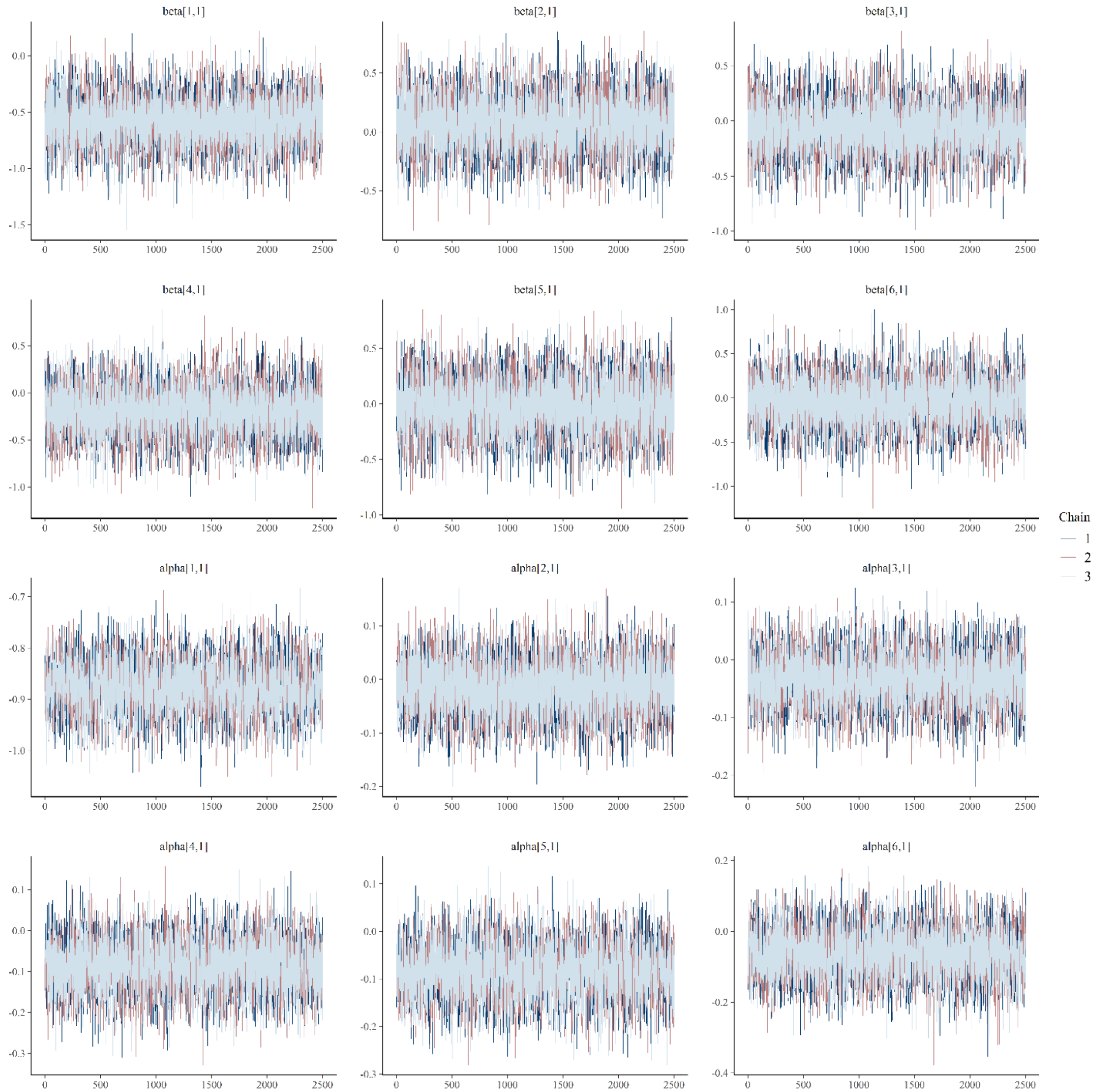


Fig S6: Trace plots of parameters of the probit regression model for conditional probability of any TB symptom among the true PTB cases ($\beta$) and among the true non-PTB cases ($\alpha$) in the Vukuzazi dataset analyzed using Model 2 presented in Table S4

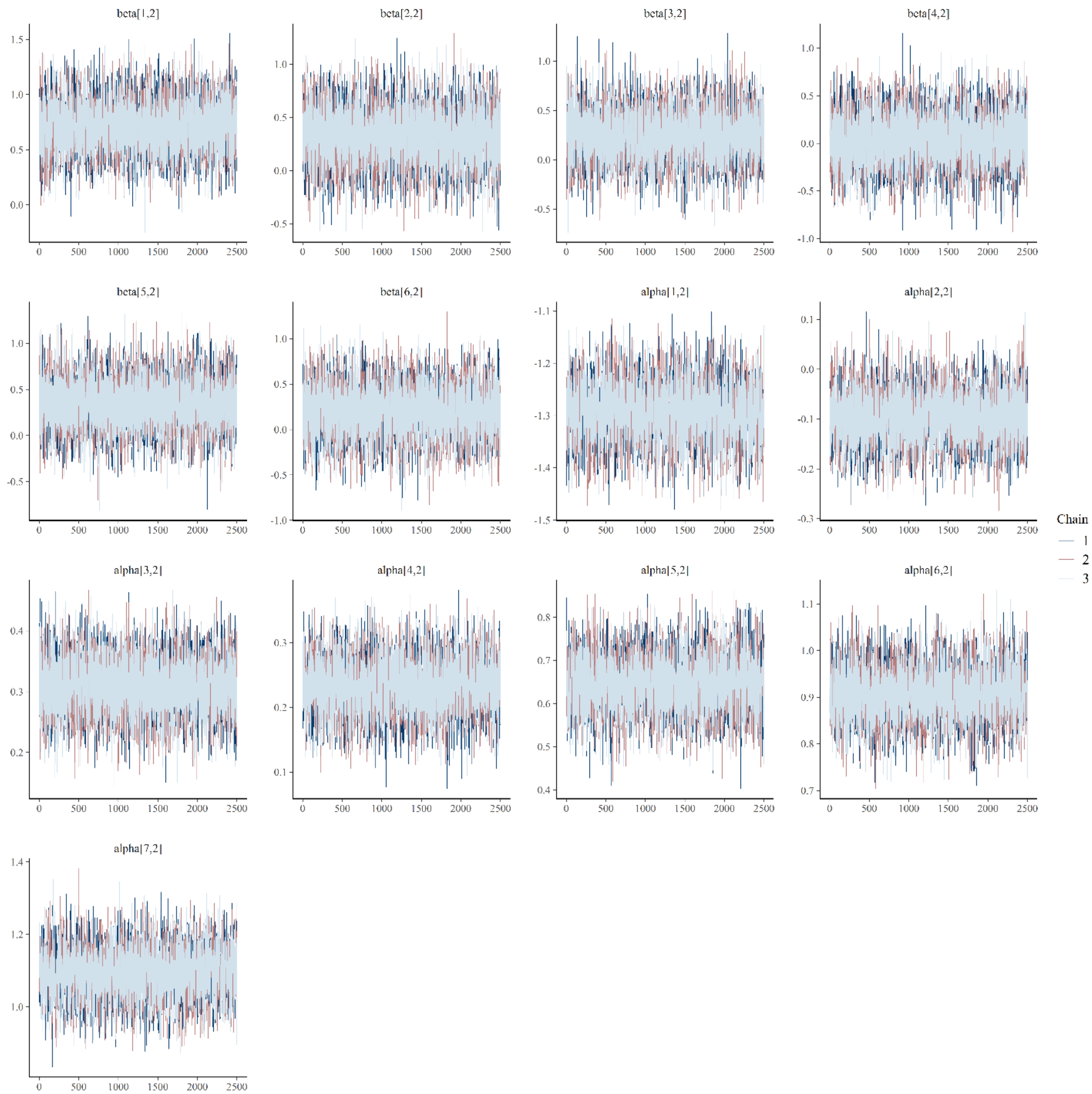


Fig S7: Trace plots of parameters of the probit regression model for conditional probability of radiologist conclusion (any chest X-ray abnormality) among the true PTB cases ($\beta$) and among the true non-PTB cases ($\alpha$) in the Vukuzazi dataset analyzed using Model 2 presented in Table S4

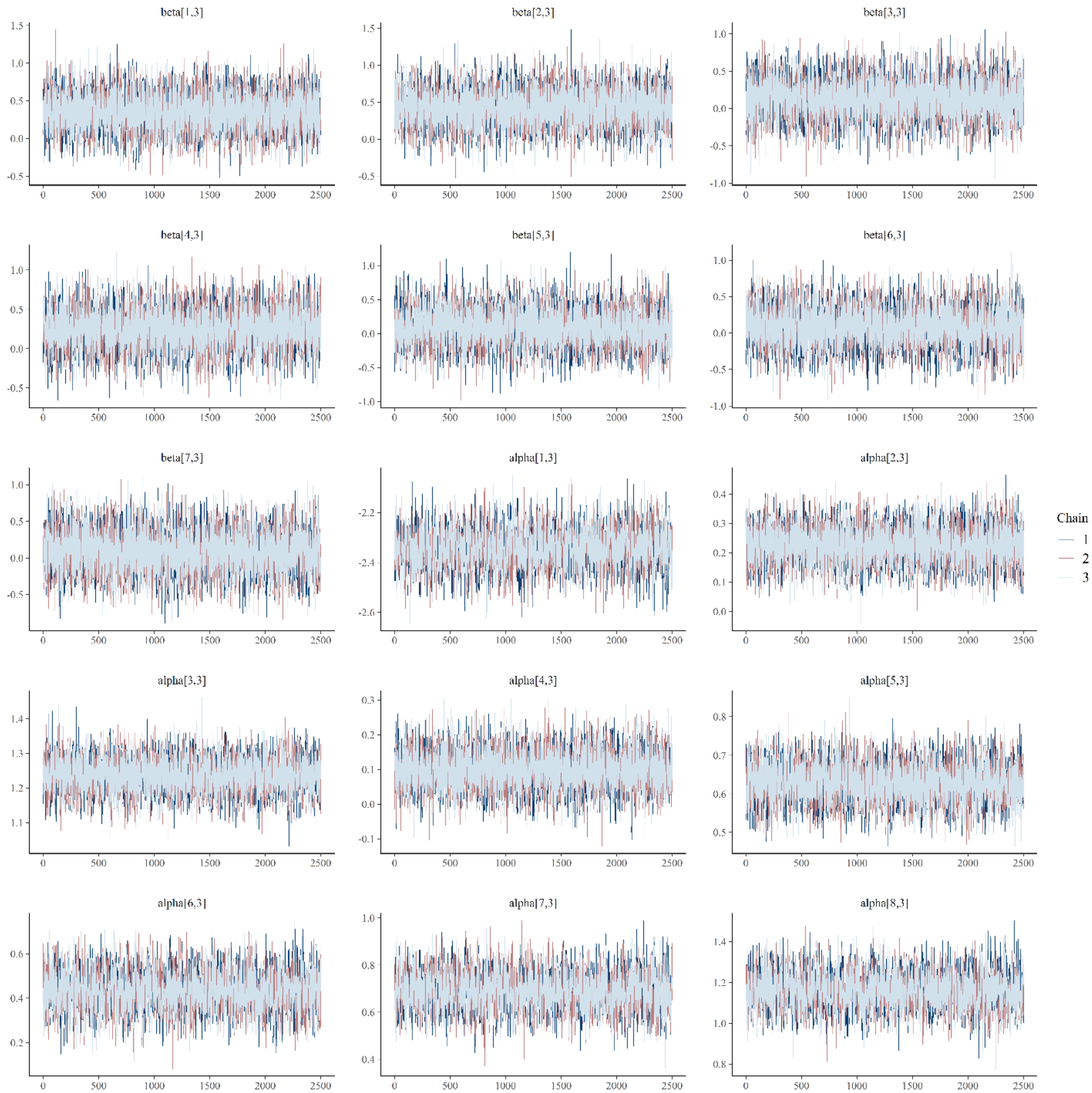


Fig S8: Trace plots of parameters of the probit regression model for conditional probability of CAD4TBv5≥53 among the true PTB cases ($\beta$) and among the true non-PTB cases ($\alpha$) in the Vukuzazi dataset analyzed using Model 2 presented in Table S4

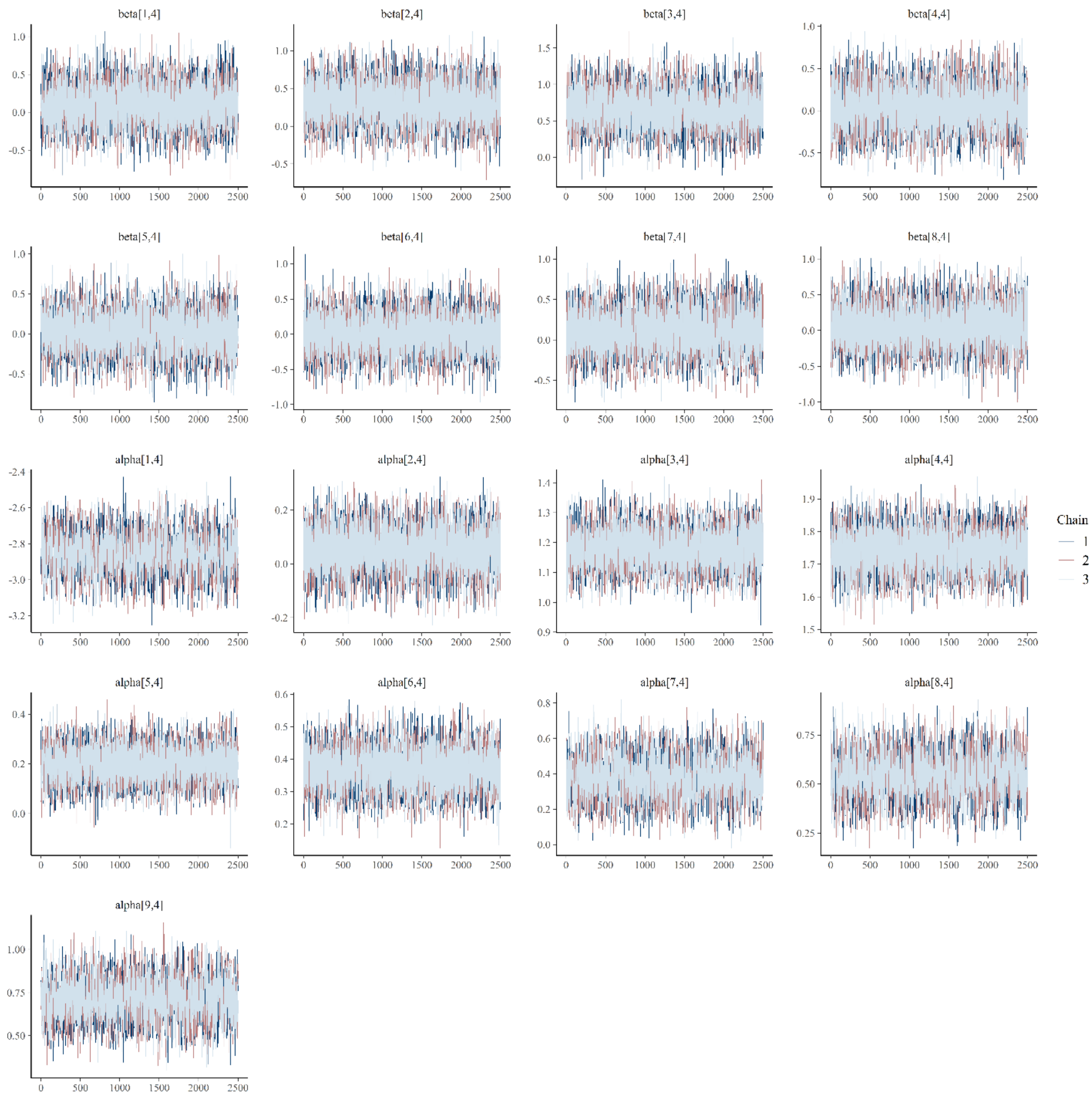


Fig S9: Trace plots of parameters of the probit regression model for conditional probability of CAD4TBv6≥53 among the true PTB cases ($\beta$) and among the true non-PTB cases ($\alpha$) in the Vukuzazi dataset analyzed using Model 2 presented in Table S4

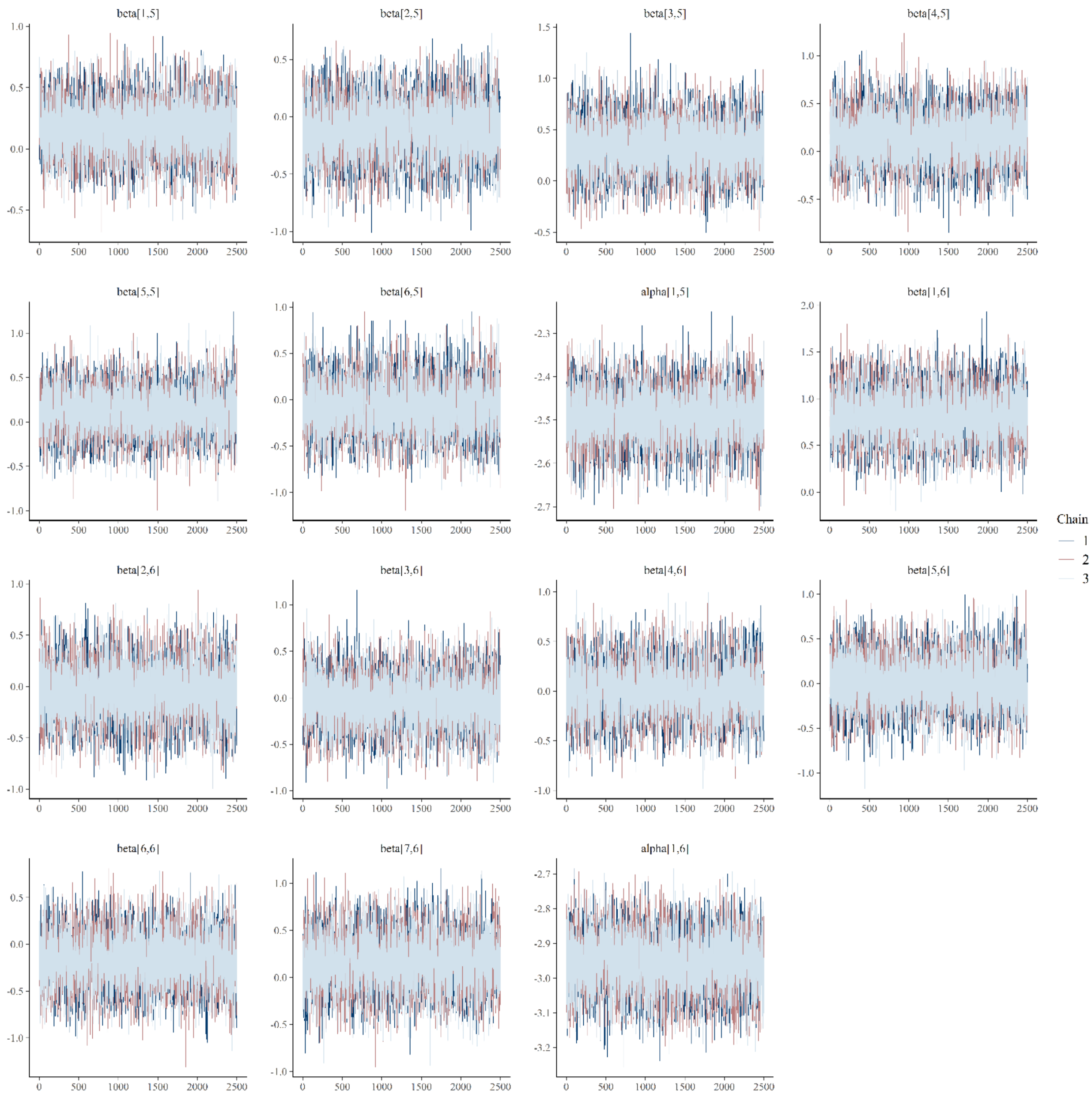


Fig S10: Trace plots of parameters of the probit regression model for conditional probability of Xpert Ultra and culture among the true PTB cases ($\beta$) and among the true non-PTB cases ($\alpha$) in the Vukuzazi dataset analyzed using Model 2 presented in Table S4

## 6. Analysis scripts

Below is the Rjags script for model 2 used for analyzing childhood pulmonary TB data. The other models can be adapted from this model.

```
model2 <- function(){
#K is the number of columns in y
#The first column of y is 1s
#We have K-1 tests
  ## likelihood --------------------------------------------------------------------------------------
  Freqobs[1:J] ~ dmulti(p[1:J],N)
  for (j in 1:J) {      # Prob. of a combination of J test results
    p[j] <- pi*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
      (1-pi)*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))

      cp1[j,1]  =  phi( inprod( y[j,c(1:1)], beta[1:1,1] ) )  #Modeling pr(y_1 = + | D=+)
      cp1[j,2]  =  phi( inprod( y[j,c(1:2)], beta[1:2,2] ) )  #Modeling pr(y_2 = + | y_1, D=+)
      cp1[j,3]  =  phi( inprod( y[j,c(1:3)], beta[1:3,3] ) )  #Modeling pr(y_3 = + | y_1, y_2, D=+)
      cp1[j,4]  =  phi( inprod( y[j,c(1:4)], beta[1:4,4] ) )  #Modeling pr(y_4 = + | y_1, y_2, y_3, D=+)
      cp1[j,5]  =  phi( inprod( y[j,c(1:5)], beta[1:5,5] ) )  #Modeling pr(y_5 = + | y_1, y_2, y_3, y_4, D=+)

       #Predict conditional probabilities
      jp1x[j,1] = y[j,2]*cp1[j,1] + (1-y[j,2])*(1-cp1[j,1])
      jp1x[j,2] = y[j,3]*cp1[j,2] + (1-y[j,3])*(1-cp1[j,2])
      jp1x[j,3] = y[j,4]*cp1[j,3] + (1-y[j,4])*(1-cp1[j,3])
      jp1x[j,4] = y[j,5]*cp1[j,4] + (1-y[j,5])*(1-cp1[j,4])
      jp1x[j,5] = y[j,6]*cp1[j,5] + (1-y[j,6])*(1-cp1[j,5])

      cp0[j,1]  =  phi( inprod( y[j,c(1:1)], alpha[1:1,1] ) )  # Modeling pr(y_1 = + | D=-)
      cp0[j,2]  =  phi( inprod( y[j,c(1:2)], alpha[1:2,2] ) )  # Modeling pr(y_2 = + | y_1, D=-)
      cp0[j,3]  =  phi( inprod( y[j,c(1:1)], alpha[1:1,3] ) )  # Modeling pr(y_3 = + | y_1, y_2, D=-)
      cp0[j,4]  =  phi( inprod( y[j,c(1:1)], alpha[1:1,4] ) )  # Modeling pr(y_4 = + | y_1, y_2, y_3, D=-)
      cp0[j,5]  =  phi( inprod( y[j,c(1:1)], alpha[1:1,5] ) )  #Modeling pr(y_5 = + | y_1, y_2, y_3, y_4, D=-)

       #Predict conditional probabilities
      jp0x[j,1] = y[j,2]*cp0[j,1] + (1-y[j,2])*(1 - cp0[j,1])
      jp0x[j,2] = y[j,3]*cp0[j,2] + (1-y[j,3])*(1 - cp0[j,2])
      jp0x[j,3] = y[j,4]*cp0[j,3] + (1-y[j,4])*(1 - cp0[j,3])
      jp0x[j,4] = y[j,5]*cp0[j,4] + (1-y[j,5])*(1 - cp0[j,4])
      jp0x[j,5] = y[j,6]*cp0[j,5] + (1-y[j,6])*(1 - cp0[j,5])

    jp1[j,1] = prod( jp1x[j,1] )
    jp1[j,2] = prod( jp1x[j,1:2] )
    jp1[j,3] = prod( jp1x[j,1:3] )
    jp1[j,4] = prod( jp1x[j,1:4] )
    jp1[j,5] = prod( jp1x[j,1:5] )

    jp0[j,1] = prod( jp0x[j,1] )
    jp0[j,2] = prod( jp0x[j,1:2] )
    jp0[j,3] = prod( jp0x[j,3] )
    jp0[j,4] = prod( jp0x[j,4] )
    jp0[j,5] = prod( jp0x[j,5] )
```

```
   }
 #calculate the sensitivity and specificity
     se[1] =     sum( jp1[c(1:1), 1] )
     se[2] =     sum( jp1[c(1:2), 2] )
     se[3] =     sum( jp1[c(1:4), 3] )
     se[4] =     sum( jp1[c(1:8), 4] )
     se[5] =     sum( jp1[c(1:16), 5] )

     sp[1] = 1 - sum( jp0[c(1:1), 1] )
     sp[2] = 1 - sum( jp0[c(1:2), 2] )
     sp[3] = 1 - sum( jp0[c(1:1), 3] )
     sp[4] = 1 - sum( jp0[c(1:1), 4] )
     sp[5] = 1 - sum( jp0[c(1:1), 5] )

   pi <- phi(omega)

   ## priors ---------------------------------------------------------------------------------------------
 for(g in 1:(K-1)){
   for(r in 1:g1[g]){
     beta[r,g] ~ dnorm(mu1[r,g], s1[r,g])
   }
 }
   for(g in 1:(K-1)){
     for(r in 1:g0[g]){
       alpha[r,g] ~ dnorm(mu0[r,g], s0[r,g])
     }
   }
   # Prior for prevalence
   omega ~ dnorm( mu.prev, s.prev )
 }

 #Choice of priors (Determined outside jags and issued as part of the data)
 g1 = c(1,2,3,4,5)  # Number of parameters in models for CPTB cases
 g0 = c(1,2,1,1,1)  # Number of parameters in models for non-CPTB cases

 mu1 = matrix(NA, nrow = max(g1), ncol = K)  #Mean among CPTB cases
 s1 = matrix(NA, nrow = max(g1), ncol = K)  # Precision for mean among the CPTB cases

 for(c in 1:ncol(mu1)){
   for(r in 1:c){
   mu1[r,c] = 0
   }
 }

 for(c in 1:ncol(s1)){
   for(r in 1:c){
     s1[r,c] = 0.1
   }
 }
 for(c in 1:ncol(s1)){
   for(r in 1:1){
     s1[r,c] = 1
   }
```

```
}

s1[1,c(3,4,5)] <- 10

mu0 = matrix(NA, nrow = max(g0), ncol = K)  #Mean among non CPTB cases
s0 = matrix(NA, nrow = max(g0), ncol = K)  # Precision for mean among the non CPTB cases

for(c in 1:ncol(mu0)){
  for(r in 1:2){
    mu0[r,c] = 0
  }
}
mu0[1,3:5] <- -3

for(c in 1:ncol(s0)){
  for(r in 1:2){
    s0[r,c] = 1
  }
}
for(c in 1:ncol(s0)){
  for(r in 1:1){
    s0[r,c] = 10
  }
}
#mean and precision for the prior distribution of CPTB prevalence
mu.prev = 0
s.prev = 1
```

Below is the Rjags script for model 2 used for analyzing Vukuzazi data. The other models can be adapted from this model.

```
cond.prob.jags.model1_11_2 <- function(){
#K is the number of columns in y
#The first column of y is 1s
#We have K-1 tests
 ## likelihood ---------------------------------------------------------------------------------------
 Freqobs[1:J] ~ dmulti(p[1:J],N)
 for (j in 1:J) {    # Prob. of test j yielding +ve result given disease status
   p[j] <- ( pa[1]*(psij[j]*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                          ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                    (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-
y[j,8])))^y[j,9]*
          ((1-psij[j])*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                          ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                    (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^(1-
y[j,9]) )^((y[j,10]==1)*1)*
    ( pa[2]*(psij[j]*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                              (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                       ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^y[j,9]*
       ((1-psij[j])*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                              (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                       ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^(1-y[j,9])
)^((y[j,10]==2)*1)*
    ( pa[3]*(psij[j]*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                              (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                       ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^y[j,9]*
       ((1-psij[j])*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                              (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                       ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^(1-y[j,9])
)^((y[j,10]==3)*1)*
    ( (pa[4])*(psij[j]*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                               (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                        ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                  (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^y[j,9]*
       ((1-psij[j])*((gammaj[j]*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                              (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^y[j,8]*
                       ((1-gammaj[j])*(pij[j]*prod(cp1[j,1:(K-1)]^y[j,2:K]*(1-cp1[j,1:(K-1)])^(1-y[j,2:K])) +
                                 (1-pij[j])*prod(cp0[j,1:(K-1)]^(y[j,2:K])*(1-cp0[j,1:(K-1)])^(1-y[j,2:K]))))^(1-y[j,8])))^(1-y[j,9])
)^((y[j,10]==4)*1)
```

```
    #Modeling pr(y_j = + | y_j-1 ... y_1, D=+)
    cp1[j,1]  =  phi( inprod( y[j,c(1,8,9,11:13)], beta[1:6,1] ) )
    cp1[j,2]  =  phi( inprod( y[j,c(1,8,9,11:13)], beta[1:6,2] ) )
    cp1[j,3]  =  phi( inprod( y[j,c(1,3,8,9,11:13)], beta[1:7,3] ) )
    cp1[j,4]  =  phi( inprod( y[j,c(1,3:4,8,9,11:13)], beta[1:8,4] ) )
    cp1[j,5]  =  phi( inprod( y[j,c(1,8,9,11:13)], beta[1:6,5] ) )
    cp1[j,6]  =  phi( inprod( y[j,c(1,6,8,9,11:13)], beta[1:7,6] ) )
    #Conditional probabilities
    jp1x[j,1] = y[j,2]*cp1[j,1] + (1-y[j,2])*(1-cp1[j,1])
    jp1x[j,2] = y[j,3]*cp1[j,2] + (1-y[j,3])*(1-cp1[j,2])
    jp1x[j,3] = y[j,4]*cp1[j,3] + (1-y[j,4])*(1-cp1[j,3])
    jp1x[j,4] = y[j,5]*cp1[j,4] + (1-y[j,5])*(1-cp1[j,4])
    jp1x[j,5] = y[j,6]*cp1[j,5] + (1-y[j,6])*(1-cp1[j,5])
    jp1x[j,6] = y[j,7]*cp1[j,6] + (1-y[j,7])*(1-cp1[j,6])

    #Modeling pr(y_j = + | y_j-1 ... y_1, D=-)
    cp0[j,1]  =  phi( inprod( y[j,c(1,8,9,11:13)], alpha[1:6,1] ) )
    cp0[j,2]  =  phi( inprod( y[j,c(1:2,8,9,11:13)], alpha[1:7,2] ) )
    cp0[j,3]  =  phi( inprod( y[j,c(1:3,8,9,11:13)], alpha[1:8,3] ) )
    cp0[j,4]  =  phi( inprod( y[j,c(1:4,8,9,11:13)], alpha[1:9,4] ) )
    cp0[j,5]  =  phi( inprod( y[j,c(1)], alpha[1:1,5] ) )
    cp0[j,6]  =  phi( inprod( y[j,c(1)], alpha[1:1,6] ) )

    #Conditional probabilities
    jp0x[j,1] = y[j,2]*cp0[j,1] + (1-y[j,2])*(1 - cp0[j,1])
    jp0x[j,2] = y[j,3]*cp0[j,2] + (1-y[j,3])*(1 - cp0[j,2])
    jp0x[j,3] = y[j,4]*cp0[j,3] + (1-y[j,4])*(1 - cp0[j,3])
    jp0x[j,4] = y[j,5]*cp0[j,4] + (1-y[j,5])*(1 - cp0[j,4])
    jp0x[j,5] = y[j,6]*cp0[j,5] + (1-y[j,6])*(1 - cp0[j,5])
    jp0x[j,6] = y[j,7]*cp0[j,6] + (1-y[j,7])*(1 - cp0[j,6])

    jp1[j,1] = prod( jp1x[j,c(1:1)] )
    jp1[j,2] = prod( jp1x[j,c(2:2)] )
    jp1[j,3] = prod( jp1x[j,c(2:3)] )
    jp1[j,4] = prod( jp1x[j,c(2:4)] )
    jp1[j,5] = prod( jp1x[j,c(5:5)] )
    jp1[j,6] = prod( jp1x[j,c(5:6)] )

    jp0[j,1] = prod( jp0x[j,c(1:1)] )
    jp0[j,2] = prod( jp0x[j,c(1:2)] )
    jp0[j,3] = prod( jp0x[j,c(1:3)] )
    jp0[j,4] = prod( jp0x[j,c(1:4)] )
    jp0[j,5] = prod( jp0x[j,c(5:5)] )
    jp0[j,6] = prod( jp0x[j,c(6:6)] )

    #Cond. prob of TB given HIV, sex, age
    pij[j] <- phi( a_prev[1] + a_prev[2]*y[j,8]  + a_prev[3]*y[j,9] + a_prev[4]*y[j,11] +
                a_prev[5]*y[j,12] + a_prev[6]*y[j,13] )
    #Cond. prob. of HIV+ given sex, age
    gammaj[j] = phi( b.x[1] + b.x[2]*y[j,9] + b.x[3]*y[j,11] + b.x[4]*y[j,12] + b.x[5]*y[j,13] )
    #Cond. prob of male given age
    psij[j] = phi( z.x[1] + z.x[2]*y[j,11] + z.x[3]*y[j,12] + z.x[4]*y[j,13])
  }
```

```
pi[1] = phi( sum( a_prev[c(1,2,3)]) )      #TB+, HIV+ male aged 15-29
pi[2] = phi( sum( a_prev[c(1,3)]) )       #TB+, HIV- male aged 15-29
pi[3] = phi( sum( a_prev[c(1,2)]  ) )       #TB+, HIV+ female aged 15-29
pi[4] = phi( sum( a_prev[c(1)]  ) )         #TB+, HIV- female aged 15-29

pi[5] = phi( sum( a_prev[c(1,2,3,4)] ) )    #TB+, HIV+ male aged 30-49
pi[6] = phi( sum( a_prev[c(1,3,4)] ) )      #TB+, HIV- male aged 30-49
pi[7] = phi( sum( a_prev[c(1,2,4)] ) )      #TB+, HIV+ female aged 30-49
pi[8] = phi( sum( a_prev[c(1,4)] ) )       #TB+, HIV- female aged 30-49

pi[9] = phi( sum( a_prev[c(1,2,3,5)]  ) )    #TB+, HIV+ male aged 50-69
pi[10] = phi( sum( a_prev[c(1,3,5)]  ) )     #TB+, HIV- male aged 50-69
pi[11] = phi( sum( a_prev[c(1,2,5)]  ) )     #TB+, HIV+ female aged 50-69
pi[12] = phi( sum( a_prev[c(1,5)]  ) )       #TB+, HIV- female aged 50-69

pi[13] = phi( sum( a_prev[c(1,2,3,6)]  ) )   #TB+, HIV+ male aged 70+
pi[14] = phi( sum( a_prev[c(1,3,6)]  ) )     #TB+, HIV- male aged 70+
pi[15] = phi( sum( a_prev[c(1,2,6)]  ) )     #TB+, HIV+ female aged 70+
pi[16] = phi( sum( a_prev[c(1,6)]  ) )       #TB+, HIV- female aged 70+

gamma[1] = phi( sum( b.x[c(1,2)]  ) )    #HIV+ male aged 15-29
gamma[2] = phi( sum( b.x[c(1)]  ) )      #HIV+ female aged 15-29
gamma[3] = phi( sum( b.x[c(1,2,3)]  ) )  #HIV+ male aged 30-49
gamma[4] = phi( sum( b.x[c(1,3)]  ) )    #HIV+ female aged 30-49
gamma[5] = phi( sum( b.x[c(1,2,4)]  ) )  #HIV+ male aged 50-69
gamma[6] = phi( sum( b.x[c(1,4)]  ) )    #HIV+ female aged 50-69
gamma[7] = phi( sum( b.x[c(1,2,5)]  ) )  #HIV+ male aged 70+
gamma[8] = phi( sum( b.x[c(1,5)]  ) )    #HIV+ female aged 70+

psi[1] = phi( z.x[1] )               #Male aged 15-29
psi[2] = phi( sum( z.x[c(1,2)] ) )    #Male aged 30-49
psi[3] = phi( sum( z.x[c(1,3)] ) )    #Male aged 50-69
psi[4] = phi( sum( z.x[c(1,4)] ) )    #Male aged 70+

# Total/Overall TB prevalence
pit[1] =(pi[1]*gamma[1]*psi[1]*pa[1] + pi[2]*(1-gamma[1])*psi[1]*pa[1] + pi[3]*gamma[2]*(1-psi[1])*pa[1] +
pi[4]*(1-gamma[2])*(1-psi[1])*pa[1] +
        pi[5]*gamma[3]*psi[2]*pa[2] + pi[6]*(1-gamma[3])*psi[2]*pa[2] + pi[7]*gamma[4]*(1-psi[2])*pa[2] +
pi[8]*(1-gamma[4])*(1-psi[2])*pa[2] +
        pi[9]*gamma[5]*psi[3]*pa[3] + pi[10]*(1-gamma[5])*psi[3]*pa[3] + pi[11]*gamma[6]*(1-psi[3])*pa[3] +
pi[12]*(1-gamma[6])*(1-psi[3])*pa[3] +
        pi[13]*gamma[7]*psi[4]*pa[4] + pi[14]*(1-gamma[7])*psi[4]*pa[4] + pi[15]*gamma[8]*(1-psi[4])*pa[4] +
pi[16]*(1-gamma[8])*(1-psi[4])*pa[4]) /
  ( gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1] +
    gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
    gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3] +
    gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])
 #TB in HIV+
```

```
  pit[2] = (pi[1]*gamma[1]*psi[1]*pa[1] + pi[3]*gamma[2]*(1-psi[1])*pa[1] + pi[5]*gamma[3]*psi[2]*pa[2] +
pi[7]*gamma[4]*(1-psi[2])*pa[2] +
         pi[9]*gamma[5]*psi[3]*pa[3] + pi[11]*gamma[6]*(1-psi[3])*pa[3] + pi[13]*gamma[7]*psi[4]*pa[4] +
pi[15]*gamma[8]*(1-psi[4])*pa[4])/
   (gamma[1]*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + gamma[3]*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] +
     gamma[5]*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + gamma[7]*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4])
  #TB in HIV-
  pit[3] =(pi[2]*(1-gamma[1])*psi[1]*pa[1] + pi[4]*(1-gamma[2])*(1-psi[1])*pa[1] +  pi[6]*(1-
gamma[3])*psi[2]*pa[2] + pi[8]*(1-gamma[4])*(1-psi[2])*pa[2] +
        pi[10]*(1-gamma[5])*psi[3]*pa[3] + pi[12]*(1-gamma[6])*(1-psi[3])*pa[3] + pi[14]*(1-
gamma[7])*psi[4]*pa[4] + pi[16]*(1-gamma[8])*(1-psi[4])*pa[4])/
   ((1-gamma[1])*psi[1]*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  (1-gamma[3])*psi[2]*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
     (1-gamma[5])*psi[3]*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + (1-gamma[7])*psi[4]*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])

  #TB in male
  pit[4] =(pi[1]*gamma[1]*psi[1]*pa[1] + pi[2]*(1-gamma[1])*psi[1]*pa[1] + pi[5]*gamma[3]*psi[2]*pa[2] +
pi[6]*(1-gamma[3])*psi[2]*pa[2] +
        pi[9]*gamma[5]*psi[3]*pa[3] + pi[10]*(1-gamma[5])*psi[3]*pa[3] + pi[13]*gamma[7]*psi[4]*pa[4] +
pi[14]*(1-gamma[7])*psi[4]*pa[4] )/
   (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] +
     gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4])
  #TB in female
  pit[5] = (pi[3]*gamma[2]*(1-psi[1])*pa[1] + pi[4]*(1-gamma[2])*(1-psi[1])*pa[1] +  pi[7]*gamma[4]*(1-
psi[2])*pa[2] + pi[8]*(1-gamma[4])*(1-psi[2])*pa[2] +
         pi[11]*gamma[6]*(1-psi[3])*pa[3] + pi[12]*(1-gamma[6])*(1-psi[3])*pa[3] + pi[15]*gamma[8]*(1-
psi[4])*pa[4] + pi[16]*(1-gamma[8])*(1-psi[4])*pa[4])/
   (gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
     gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])
  # TB in each age group
  pit[6] = (pi[1]*gamma[1]*psi[1]*pa[1] + pi[2]*(1-gamma[1])*psi[1]*pa[1] + pi[3]*gamma[2]*(1-psi[1])*pa[1] +
pi[4]*(1-gamma[2])*(1-psi[1])*pa[1])/
   (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1])
  pit[7] = (pi[5]*gamma[3]*psi[2]*pa[2] + pi[6]*(1-gamma[3])*psi[2]*pa[2] + pi[7]*gamma[4]*(1-psi[2])*pa[2] +
pi[8]*(1-gamma[4])*(1-psi[2])*pa[2])/
   (gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2])
  pit[8] = (pi[9]*gamma[5]*psi[3]*pa[3] + pi[10]*(1-gamma[5])*psi[3]*pa[3] + pi[11]*gamma[6]*(1-psi[3])*pa[3] +
pi[12]*(1-gamma[6])*(1-psi[3])*pa[3])/
   (gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3])
  pit[9] = (pi[13]*gamma[7]*psi[4]*pa[4] + pi[14]*(1-gamma[7])*psi[4]*pa[4] + pi[15]*gamma[8]*(1-psi[4])*pa[4] +
pi[16]*(1-gamma[8])*(1-psi[4])*pa[4])/
   (gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])

  se[1,1] = sum( jp1[c(1:1), 1] )
  se[2,1] = sum( jp1[c(1:1), 2] )
  se[3,1] = sum( jp1[c(1,3), 3] )
```

```
 se[4,1] = sum( jp1[c(1,3,5,7), 4] )
 se[5,1] = sum( jp1[c(1:1), 5] )
 se[6,1] = sum( jp1[c(1,17), 6] )

 sp[1,1] = 1 - sum( jp0[c(1:1), 1] )
 sp[2,1] = 1 - sum( jp0[c(1:2), 2] )
 sp[3,1] = 1 - sum( jp0[c(1:4), 3] )
 sp[4,1] = 1 - sum( jp0[c(1:8), 4] )
 sp[5,1] = 1 - sum( jp0[c(1:1), 5] )
 sp[6,1] = 1 - sum( jp0[c(1:1), 6] )
 for(g in c(1:15)){
   se[1,g+1] = sum( jp1[c(1:1)+g*2^(K-1), 1] )
   se[2,g+1] = sum( jp1[c(1:1)+g*2^(K-1), 2] )
   se[3,g+1] = sum( jp1[c(1,3)+g*2^(K-1), 3] )
   se[4,g+1] = sum( jp1[c(1,3,5,7)+g*2^(K-1), 4] )
   se[5,g+1] = sum( jp1[c(1)+g*2^(K-1), 5] )
   se[6,g+1] = sum( jp1[c(1,17)+g*2^(K-1), 6] )

   sp[1,g+1] = 1 - sum( jp0[c(1:1)+g*2^(K-1), 1] )
   sp[2,g+1] = 1 - sum( jp0[c(1:2)+g*2^(K-1), 2] )
   sp[3,g+1] = 1 - sum( jp0[c(1:4)+g*2^(K-1), 3] )
   sp[4,g+1] = 1 - sum( jp0[c(1:8)+g*2^(K-1), 4] )
   sp[5,g+1] = 1 - sum( jp0[c(1:1)+g*2^(K-1), 5] )
   sp[6,g+1] = 1 - sum( jp0[c(1:1)+g*2^(K-1), 6] )
 }

 for(g in 1:6){
   # Total/Overall sensitivity
   set[g,1] =(se[g,1]*gamma[1]*psi[1]*pa[1] + se[g,2]*(1-gamma[1])*psi[1]*pa[1] + se[g,3]*gamma[2]*(1-
psi[1])*pa[1] + se[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +
            se[g,5]*gamma[3]*psi[2]*pa[2] + se[g,6]*(1-gamma[3])*psi[2]*pa[2] + se[g,7]*gamma[4]*(1-
psi[2])*pa[2] + se[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
            se[g,9]*gamma[5]*psi[3]*pa[3] + se[g,10]*(1-gamma[5])*psi[3]*pa[3] + se[g,11]*gamma[6]*(1-
psi[3])*pa[3] + se[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] +
            se[g,13]*gamma[7]*psi[4]*pa[4] + se[g,14]*(1-gamma[7])*psi[4]*pa[4] + se[g,15]*gamma[8]*(1-
psi[4])*pa[4] + se[g,16]*(1-gamma[8])*(1-psi[4])*pa[4]) /
     ( gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1] +
       gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
       gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3] +
       gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])

   #sensitivity in HIV+
   set[g,2] = (se[g,1]*gamma[1]*psi[1]*pa[1] + se[g,3]*gamma[2]*(1-psi[1])*pa[1] +
se[g,5]*gamma[3]*psi[2]*pa[2] + se[g,7]*gamma[4]*(1-psi[2])*pa[2] +
             se[g,9]*gamma[5]*psi[3]*pa[3] + se[g,11]*gamma[6]*(1-psi[3])*pa[3] + se[g,13]*gamma[7]*psi[4]*pa[4]
+ se[g,15]*gamma[8]*(1-psi[4])*pa[4])/
     (gamma[1]*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + gamma[3]*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] +
       gamma[5]*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + gamma[7]*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4])
   #sensitivity in HIV-
```

```
    set[g,3] =(se[g,2]*(1-gamma[1])*psi[1]*pa[1] + se[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +  se[g,6]*(1-
gamma[3])*psi[2]*pa[2] + se[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
            se[g,10]*(1-gamma[5])*psi[3]*pa[3] + se[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] + se[g,14]*(1-
gamma[7])*psi[4]*pa[4] + se[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
      ((1-gamma[1])*psi[1]*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  (1-gamma[3])*psi[2]*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
        (1-gamma[5])*psi[3]*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + (1-gamma[7])*psi[4]*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])



    #sensitivity in male
    set[g,4] =(se[g,1]*gamma[1]*psi[1]*pa[1] + se[g,2]*(1-gamma[1])*psi[1]*pa[1] + se[g,5]*gamma[3]*psi[2]*pa[2]
+ se[g,6]*(1-gamma[3])*psi[2]*pa[2] +
            se[g,9]*gamma[5]*psi[3]*pa[3] + se[g,10]*(1-gamma[5])*psi[3]*pa[3] + se[g,13]*gamma[7]*psi[4]*pa[4]
+ se[g,14]*(1-gamma[7])*psi[4]*pa[4] )/
      (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] +
        gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4])
    #TB in female
    set[g,5] = (se[g,3]*gamma[2]*(1-psi[1])*pa[1] + se[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +  se[g,7]*gamma[4]*(1-
psi[2])*pa[2] + se[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
             se[g,11]*gamma[6]*(1-psi[3])*pa[3] + se[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] + se[g,15]*gamma[8]*(1-
psi[4])*pa[4] + se[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
      (gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
        gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])
    # sensitivity in each age group
    set[g,6] = (se[g,1]*gamma[1]*psi[1]*pa[1] + se[g,2]*(1-gamma[1])*psi[1]*pa[1] + se[g,3]*gamma[2]*(1-
psi[1])*pa[1] + se[g,4]*(1-gamma[2])*(1-psi[1])*pa[1])/
      (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1])
    set[g,7] = (se[g,5]*gamma[3]*psi[2]*pa[2] + se[g,6]*(1-gamma[3])*psi[2]*pa[2] + se[g,7]*gamma[4]*(1-
psi[2])*pa[2] + se[g,8]*(1-gamma[4])*(1-psi[2])*pa[2])/
      (gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2])
    set[g,8] = (se[g,9]*gamma[5]*psi[3]*pa[3] + se[g,10]*(1-gamma[5])*psi[3]*pa[3] + se[g,11]*gamma[6]*(1-
psi[3])*pa[3] + se[g,12]*(1-gamma[6])*(1-psi[3])*pa[3])/
      (gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3])
    set[g,9] = (se[g,13]*gamma[7]*psi[4]*pa[4] + se[g,14]*(1-gamma[7])*psi[4]*pa[4] + se[g,15]*gamma[8]*(1-
psi[4])*pa[4] + se[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
      (gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])


    # Total/Overall specificity
    spt[g,1] =(sp[g,1]*gamma[1]*psi[1]*pa[1] + sp[g,2]*(1-gamma[1])*psi[1]*pa[1] + sp[g,3]*gamma[2]*(1-
psi[1])*pa[1] + sp[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +
            sp[g,5]*gamma[3]*psi[2]*pa[2] + sp[g,6]*(1-gamma[3])*psi[2]*pa[2] + sp[g,7]*gamma[4]*(1-
psi[2])*pa[2] + sp[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
            sp[g,9]*gamma[5]*psi[3]*pa[3] + sp[g,10]*(1-gamma[5])*psi[3]*pa[3] + sp[g,11]*gamma[6]*(1-
psi[3])*pa[3] + sp[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] +
```

```
              sp[g,13]*gamma[7]*psi[4]*pa[4] + sp[g,14]*(1-gamma[7])*psi[4]*pa[4] + sp[g,15]*gamma[8]*(1-
psi[4])*pa[4] + sp[g,16]*(1-gamma[8])*(1-psi[4])*pa[4]) /
     ( gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1] +
        gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
        gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3] +
        gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])


   #specificity  in HIV+
   spt[g,2] = (sp[g,1]*gamma[1]*psi[1]*pa[1] + sp[g,3]*gamma[2]*(1-psi[1])*pa[1] +
sp[g,5]*gamma[3]*psi[2]*pa[2] + sp[g,7]*gamma[4]*(1-psi[2])*pa[2] +
              sp[g,9]*gamma[5]*psi[3]*pa[3] + sp[g,11]*gamma[6]*(1-psi[3])*pa[3] + sp[g,13]*gamma[7]*psi[4]*pa[4]
+ sp[g,15]*gamma[8]*(1-psi[4])*pa[4])/
     (gamma[1]*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + gamma[3]*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] +
       gamma[5]*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + gamma[7]*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4])
   #specificity  in HIV-
   spt[g,3] =(sp[g,2]*(1-gamma[1])*psi[1]*pa[1] + sp[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +  sp[g,6]*(1-
gamma[3])*psi[2]*pa[2] + sp[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
              sp[g,10]*(1-gamma[5])*psi[3]*pa[3] + sp[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] + sp[g,14]*(1-
gamma[7])*psi[4]*pa[4] + sp[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
     ((1-gamma[1])*psi[1]*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  (1-gamma[3])*psi[2]*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
       (1-gamma[5])*psi[3]*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + (1-gamma[7])*psi[4]*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])

   #specificity  in male
   spt[g,4] =(sp[g,1]*gamma[1]*psi[1]*pa[1] + sp[g,2]*(1-gamma[1])*psi[1]*pa[1] + sp[g,5]*gamma[3]*psi[2]*pa[2]
+ sp[g,6]*(1-gamma[3])*psi[2]*pa[2] +
              sp[g,9]*gamma[5]*psi[3]*pa[3] + sp[g,10]*(1-gamma[5])*psi[3]*pa[3] + sp[g,13]*gamma[7]*psi[4]*pa[4]
+ sp[g,14]*(1-gamma[7])*psi[4]*pa[4] )/
     (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] +
       gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4])
   #specificity in female
   spt[g,5] = (sp[g,3]*gamma[2]*(1-psi[1])*pa[1] + sp[g,4]*(1-gamma[2])*(1-psi[1])*pa[1] +  sp[g,7]*gamma[4]*(1-
psi[2])*pa[2] + sp[g,8]*(1-gamma[4])*(1-psi[2])*pa[2] +
              sp[g,11]*gamma[6]*(1-psi[3])*pa[3] + sp[g,12]*(1-gamma[6])*(1-psi[3])*pa[3] + sp[g,15]*gamma[8]*(1-
psi[4])*pa[4] + sp[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
     (gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-psi[1])*pa[1] +  gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2] +
       gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-psi[3])*pa[3] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])
   # specificity  in each age group
   spt[g,6] = (sp[g,1]*gamma[1]*psi[1]*pa[1] + sp[g,2]*(1-gamma[1])*psi[1]*pa[1] + sp[g,3]*gamma[2]*(1-
psi[1])*pa[1] + sp[g,4]*(1-gamma[2])*(1-psi[1])*pa[1])/
     (gamma[1]*psi[1]*pa[1] + (1-gamma[1])*psi[1]*pa[1] + gamma[2]*(1-psi[1])*pa[1] + (1-gamma[2])*(1-
psi[1])*pa[1])
   spt[g,7] = (sp[g,5]*gamma[3]*psi[2]*pa[2] + sp[g,6]*(1-gamma[3])*psi[2]*pa[2] + sp[g,7]*gamma[4]*(1-
psi[2])*pa[2] + sp[g,8]*(1-gamma[4])*(1-psi[2])*pa[2])/
```

```
      (gamma[3]*psi[2]*pa[2] + (1-gamma[3])*psi[2]*pa[2] + gamma[4]*(1-psi[2])*pa[2] + (1-gamma[4])*(1-
psi[2])*pa[2])
    spt[g,8] = (sp[g,9]*gamma[5]*psi[3]*pa[3] + sp[g,10]*(1-gamma[5])*psi[3]*pa[3] + sp[g,11]*gamma[6]*(1-
psi[3])*pa[3] + sp[g,12]*(1-gamma[6])*(1-psi[3])*pa[3])/
      (gamma[5]*psi[3]*pa[3] + (1-gamma[5])*psi[3]*pa[3] + gamma[6]*(1-psi[3])*pa[3] + (1-gamma[6])*(1-
psi[3])*pa[3])
    spt[g,9] = (sp[g,13]*gamma[7]*psi[4]*pa[4] + sp[g,14]*(1-gamma[7])*psi[4]*pa[4] + sp[g,15]*gamma[8]*(1-
psi[4])*pa[4] + sp[g,16]*(1-gamma[8])*(1-psi[4])*pa[4])/
      (gamma[7]*psi[4]*pa[4] + (1-gamma[7])*psi[4]*pa[4] + gamma[8]*(1-psi[4])*pa[4] + (1-gamma[8])*(1-
psi[4])*pa[4])
  }

  ## priors ------------------------------------------------------------------------------------------
  for(g in 1:(K-1)){
    for(r in 1:g1[g]){
      beta[r,g] ~ dnorm(mu1[r,g], s1[r,g])
    }
  }
  for(g in 1:(K-1)){
    for(r in 1:g0[g]){
      alpha[r,g] ~ dnorm(mu0[r,g], s0[r,g])
    }
  }
  # Prior for prevalence
  a_prev[1] ~ dnorm( mu.prev[1], s.prev[1] )
  a_prev[2] ~ dnorm( mu.prev[2], s.prev[2] )
  a_prev[3] ~ dnorm( mu.prev[3], s.prev[3] )
  a_prev[4] ~ dnorm( mu.prev[4], s.prev[4] )
  a_prev[5] ~ dnorm( mu.prev[5], s.prev[5] )
  a_prev[6] ~ dnorm( mu.prev[6], s.prev[6] )

  b.x[1] ~ dnorm( mu.x[1], s.x[1] )
  b.x[2] ~ dnorm( mu.x[2], s.x[2] )
  b.x[3] ~ dnorm( mu.x[3], s.x[3] )
  b.x[4] ~ dnorm( mu.x[4], s.x[4] )
  b.x[5] ~ dnorm( mu.x[5], s.x[5] )

  z.x[1] ~ dnorm( mu.z[1], s.z[1] )
  z.x[2] ~ dnorm( mu.z[2], s.z[2] )
  z.x[3] ~ dnorm( mu.z[3], s.z[3] )
  z.x[4] ~ dnorm( mu.z[4], s.z[4] )

  pa[1:4] ~ ddirch( mu.a[1:4] )
}
#=========================================================================

#Choice of priors (Determined outside jags and issued as part of the data)
g1 = c(6,6,7,8,6,7)  # Number of parameters in models for non-PTB cases
g0 = c(6,7,8,9,1,1)  # Number of parameters in models for non-PTB cases

mu1 = matrix(NA, nrow = max(g1), ncol = 6)  #Mean among PTB cases
s1 = matrix(NA, nrow = max(g1), ncol = 6)     # Precision for mean among the PTB cases
```

```
for(c in 1:ncol(mu1)){
  for(r in 1:g1[c]){
    mu1[r,c] = 0
  }
}
mu1[1,6] = qnorm(0.8)   # Informative prior of the parameter corresponding to Pr(culture =+ | Xpert ultra = -, D+)

for(c in 1:ncol(s1)){
  for(r in 1:g1[c]){
    s1[r,c] = 1
  }
}
s1[1,1] = 10
s1[1,6] = 10  #precision for the informative prior of the parameter corresponding to Pr(cult =+ | Xpert ultra = -, D+)

mu0 = matrix(NA, nrow = max(g0), ncol = 6)  #Mean among non PTB cases
s0 = matrix(NA, nrow = max(g0), ncol = 6)  # Precision for mean among the non PTB cases

for(c in 1:ncol(mu0)){
  for(r in 1:g0[c]){
    mu0[r,c] = 0
  }
}
mu0[1,5] <- -qnorm(0.97) # prior for Pr(Xpert Ultra =+ | D = -)
mu0[1,6] <- -qnorm(0.999) # prior for Pr(culture =+ | D = -)

for(c in 1:ncol(s0)){
  for(r in 1:g0[c]){
    s0[r,c] = .1
  }
}
s0[1,5:6] <- 100 # precision for prior for Pr(Xpert Ultra =+ | D = -) and prior for Pr(culture =+ | D = -) resp.

mu.prev = numeric(6)
s.prev = numeric(6)
mu.prev = c(-5,0,0,0,0,0)
s.prev = c(10,100,100,100,100,100)

#Prior for covariates in the models
mu.x = numeric(5)
s.x = numeric(5)
mu.x = c(0,0,0,0,0)
s.x = c(1,1,1,1,1)
mu.z = c(0,0,0,0)
s.z = c(1,1,1,1)

mu.a = c(1,1,1,1)  # Dirichlet prior for age groups
```

**Analysis that replaces any chest X-ray abnormality with chest X-ray abnormality suggestive of active TB**

Tables S10 – S14 present the results obtained following the alternative analysis that replaces any chest X-ray abnormality with chest X-ray abnormality suggestive of active TB. Table S15 presents a side-by-side comparison of the overall results from the two alternative analyses.

Table S10: Posterior median and 95% credible intervals (95% CrI) of the prevalence and diagnostic test sensitivity and specificity of Vukuzazi dataset

| | | Model 0 | Model 1 | Model 2 | Model 3 | Model 4 |
|---|---|---|---|---|---|---|
| Test | Parameter | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) |
| | Prevalence | 15.0 (13.9, 16.2) | 16.6 (15.1, 18.5) | 1.1 (0.8, 1.5) | 1.1 (0.8, 1.5) | 1.1 (0.8, 1.6) |
| Any TB | Sensitivity | 22.1 (19.1, 25.1) | 21.8 (18.9, 24.8) | 27.4 (17.7, 39.5) | 27.1 (17.1, 39.3) | 27.7 (17.2, 40.1) |
| symptom | Specificity | 83.7 (82.6, 84.8) | 83.8 (82.6, 84.9) | 83.0 (81.9, 84.0) | 83.0 (81.9, 84.0) | 83.0 (81.9, 84.0) |
| Radiologist | Sensitivity | 23.1 (20.1, 26.2) | 21.2 (18.2, 24.5) | 44.1 (32.0, 57.0) | 43.6 (31.5, 56.4) | 43.7 (31.5, 56.6) |
| conclusion Ŧ | Specificity | 99.9 (99.7, 100) | 99.9 (99.7, 100) | 96.9 (96.4, 97.4) | 96.9 (96.4, 97.4) | 96.9 (96.4, 97.4) |
| CAD4TBv5≥53 | Sensitivity | 95.0 (92.3, 97.1) | 88.9 (82.7, 93.7) | 80.6 (69.1, 89.3) | 80.0 (67.9, 89.0) | 80.3 (68.5, 89.1) |
| | Specificity | 92.9 (92.1, 93.8) | 93.3 (92.3, 94.5) | 80.2 (79.0, 81.3) | 80.2 (79.0, 81.3) | 80.2 (79.0, 81.3) |
| CAD4TBv6≥53 | Sensitivity | 95.1 (92.4, 97.2) | 90.5 (84.6, 94.8) | 81.4 (70.1, 89.9) | 81.3 (69.8, 89.9) | 80.9 (69.1, 89.6) |
| | Specificity | 96.0 (95.2, 96.7) | 96.6 (95.7, 97.7) | 82.7 (81.6, 83.8) | 82.7 (81.7, 83.7) | 82.8 (81.6, 83.8) |
| Xpert Ultra† | Sensitivity | 13.7 (11.5, 16.0) | 6.2 (4.7, 8.0) | 62.4 (48.9, 75.3) | 60.0 (45.6, 73.7) | 62.3 (47.5, 76.1) |
| | Specificity | 99.9 (99.8, 100) | 99.4 (99.2, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.6) |
| Culture | Sensitivity | 13.3 (11.2, 15.6) | 6.6 (5.0, 8.6) | 74.1 (60.2, 86.6) | 71.4 (56.4, 85.4) | 71.6 (55.8, 85.6) |
| | Specificity | 99.7 (99.5, 99.8) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| | Deviance | 4823.3 | 4640.3 | 4614.7 | 4610.4 | 4609.7 |
| | RMSE | 126.2 | 50.8 | 31.0 | 30.1 | 29.8 |

Model 0 – Based on the assumption of conditional independence
Model 1 – Accounts for conditional dependence between radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 and between Xpert Ultra and culture among the PTB cases and allows conditional independence between all the diagnostic tests among non-PTB cases
Model 2 – Accounts for conditional dependence between radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 and between Xpert Ultra and culture among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases
Model 3 – Accounts for conditional dependence between all the diagnostic tests except any TB symptom among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases
Model 4 – Accounts for conditional dependence between all the diagnostic tests among the PTB cases and conditional dependence between any TB symptom, radiologist conclusion, CAD4TBv5≥53 and CAD4TBv6≥53 among non-PTB cases
RMSE – Root mean square error. This is calculated as the square root of the sum of squared differences between the observed frequencies and the predicted frequencies. It shows how good the model is in explaining the variability in the data (smaller is better)
CrI – Credible Intervals
Ŧ - Chest X-ray abnormality suggestive of active PTB, † - Excluding trace
Note: The estimates presented in the table are percentages

Table S11: Posterior median and 95% credible intervals (95% CrI) of PTB prevalence and diagnostic test sensitivity and specificity for Vukuzazi dataset adjusted for HIV status, sex and age, by HIV status adjusted for age and sex and by sex adjusted for HIV status and age

| | | Overall | HIV+ | HIV- | Male | Female |
|---|---|---|---|---|---|---|
| | N | 4960 (100%) | 1496 (30.2%) | 3464 (69.8%) | 1813 (36.6%) | 3147 (63.4%) |
| Test | Parameter | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) |
| | Prevalence | 0.9 (0.6, 1.3) | 1.2 (0.8, 1.9) | 0.8 (0.5, 1.1) | 1.1 (0.7, 1.7) | 0.8 (0.5, 1.1) |
| Any TB symptom | Sensitivity | 25.8 (15.9, 38.0) | 26.3 (13.5, 43.4) | 25.4 (14.8, 39.0) | 23.8 (11.5, 39.9) | 26.7 (15.7, 40.5) |
| | Specificity | 83.0 (81.9, 84.0) | 83.5 (81.5, 85.3) | 82.7 (81.4, 83.9) | 83.3 (81.5, 84.9) | 82.8 (81.4, 84.1) |
| Radiologist conclusion Ŧ | Sensitivity | 44.1 (32.0, 56.8) | 44.2 (27.9, 62.1) | 43.9 (30.4, 57.9) | 50.0 (33.5, 66.6) | 40.6 (27.2, 55.2) |
| | Specificity | 96.9 (96.3, 97.4) | 95.3 (94.1, 96.3) | 97.6 (97.0, 98.1) | 95.3 (94.3, 96.3) | 97.8 (97.2, 98.3) |
| CAD4TBv5≥53 | Sensitivity | 81.5 (70.2, 90.2) | 84.9 (69.9, 94.5) | 80.3 (67.5, 89.8) | 85.8 (72.0, 94.5) | 79.4 (65.9, 89.6) |
| | Specificity | 80.1 (78.9, 81.2) | 78.7 (76.6, 80.8) | 80.6 (79.3, 82.0) | 72.8 (70.7, 74.9) | 84.2 (82.9, 85.4) |
| CAD4TBv6≥53 | Sensitivity | 82.5 (71.3, 90.8) | 84.3 (69.2, 93.8) | 82.1 (69.3, 91.0) | 84.4 (69.8, 93.7) | 81.8 (69.0, 90.7) |
| | Specificity | 82.6 (81.6, 83.7) | 79.2 (77.1, 81.3) | 84.1 (82.9, 85.3) | 76.2 (74.1, 78.1) | 86.4 (85.1, 87.5) |
| Xpert Ultra† | Sensitivity | 64.0 (50.6, 76.5) | 61.9 (43.7, 78.9) | 65.0 (50.1, 78.5) | 72.2 (55.8, 86.2) | 59.4 (43.8, 74.0) |
| | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| Culture | Sensitivity | 75.2 (61.6, 88.0) | 73.4 (53.4, 89.9) | 76.3 (61.5, 89.1) | 76.7 (59.3, 91.0) | 74.7 (59.2, 88.2) |
| | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

CrI – Credible Intervals

Ŧ - Chest X-ray abnormality suggestive of active PTB

† - Excluding trace

Note: The estimates presented in the table are percentages

Table S12: Age, sex and HIV adjusted posterior median and 95% credible intervals (95% CrI) of PTB prevalence and diagnostic test sensitivity and specificity for Vukuzazi dataset presented by age groups

| | | 15 – 29 years | 30 – 49 years | 50 – 69 years | ≥70 years |
|---|---|---|---|---|---|
| | N | 1156 (23.3%) | 1291 (26.0%) | 1723 (34.7%) | 790 (15.9%) |
| Test | Parameter | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) |
| | Prevalence | 0.8 (0.5, 1.2) | 1.0 (0.6, 1.6) | 1.0 (0.6, 1.6) | 0.7 (0.4, 1.2) |
| Any TB symptom | Sensitivity | 26.5 (15.1, 41.4) | 23.1 (9.7, 42.3) | 26.9 (12.8, 45.1) | 24.9 (9.0, 47.8) |
| | Specificity | 81.5 (79.1, 83.7) | 83.7 (81.7, 85.7) | 83.5 (81.6, 85.2) | 82.8 (80.0, 85.4) |
| Radiologist conclusion[Ŧ] | Sensitivity | 44.3 (30.1, 59.1) | 39.7 (21.5, 60.0) | 51.5 (33.1, 70.5) | 33.5 (15.2, 56.7) |
| | Specificity | 98.4 (97.5, 99.0) | 96.3 (95.2, 97.2) | 96.1 (95.2, 97.0) | 97.4 (96.1, 98.4) |
| CAD4TBv5≥53 | Sensitivity | 80.0 (66.4, 90.0) | 83.3 (66.2, 94.3) | 83.3 (66.5, 93.7) | 79.6 (57.8, 93.2) |
| | Specificity | 93.8 (92.3, 95.1) | 82.2 (80.0, 84.3) | 76.6 (74.5, 78.6) | 64.1 (60.7, 67.4) |
| CAD4TBv6≥53 | Sensitivity | 81.1 (67.2, 90.7) | 82.0 (64.1, 93.2) | 85.2 (69.2, 94.6) | 82.5 (61.5, 94.5) |
| | Specificity | 95.6 (94.3, 96.7) | 83.5 (81.4, 85.5) | 78.9 (76.9, 80.8) | 70.4 (67.2, 73.4) |
| Xpert Ultra[†] | Sensitivity | 64.5 (48.4, 78.3) | 65.2 (44.2, 83.2) | 65.7 (45.9, 82.1) | 58.9 (35.2, 81.7) |
| | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| Culture | Sensitivity | 77.7 (62.5, 89.6) | 77.3 (54.0, 93.4) | 70.4 (50.3, 88.3) | 81.5 (59.9, 95.0) |
| | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

CrI – Credible Intervals

Ŧ - Chest X-ray abnormality suggestive of active PTB

† - Excluding trace

Note: The estimates presented in the table are percentages

Table S13: Posterior median and 95% credible intervals (95% CrI) of the age, sex and HIV adjusted PTB prevalence and diagnostic test sensitivity and specificity among male individuals in Vukuzazi dataset

| | | | **15 – 29 years** | **30 – 49 years** | **50 – 69 years** | **≥70 years** |
|---|---|---|---|---|---|---|
| **Group** | **Test** | **Parameter** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** |
| **HIV+ Male** | | Prevalence | 1.4 (0.8, 2.4) | 1.5 (0.8, 2.6) | 1.9 (1.0, 3.1) | 1.6 (0.8, 2.9) |
| | Any TB symptom | Sensitivity | 26.5 (10.2, 49.6) | 21.7 (6.8, 46.4) | 25.9 (9.5, 48.5) | 23.9 (6.4, 53.4) |
| | | Specificity | 82.2 (78.7, 85.5) | 84.4 (81.6, 86.9) | 84.3 (81.2, 87.1) | 83.8 (79.6, 87.4) |
| | Radiologist conclusion [Ŧ] | Sensitivity | 49.8 (27.6, 72.9) | 46.4 (22.3, 71.5) | 59.8 (36.4, 80.7) | 42.0 (16.2, 72.1) |
| | | Specificity | 95.9 (93.4, 97.6) | 92.6 (90.0, 94.6) | 90.2 (86.8, 92.9) | 91.3 (86.5, 94.8) |
| | CAD4TBv5≥53 | Sensitivity | 87.6 (69.3, 96.9) | 89.7 (70.6, 98.0) | 90.9 (73.9, 98.2) | 89.6 (64.9, 98.3) |
| | | Specificity | 86.8 (83.3, 89.7) | 67.8 (63.9, 71.5) | 55.1 (50.4, 59.7) | 37.1 (31.4, 43.1) |
| | CAD4TBv6≥53 | Sensitivity | 85.7 (65.6, 95.8) | 85.8 (63.7, 96.5) | 89.2 (71.3, 97.6) | 87.7 (62.8, 97.8) |
| | | Specificity | 88.9 (85.7, 91.8) | 68.6 (64.7, 72.3) | 55.6 (50.8, 60.2) | 39.9 (34.1, 46.0) |
| | Xpert Ultra[†] | Sensitivity | 67.9 (43.8, 86.6) | 72.2 (46.1, 90.7) | 72.5 (48.9, 90.0) | 66.3 (36.2, 89.8) |
| | | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| | Culture | Sensitivity | 76.7 (51.1, 93.5) | 77.5 (48.3, 95.5) | 70.0 (44.1, 91.2) | 81.0 (50.7, 96.5) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| **HIV- Male** | | Prevalence | 0.9 (0.5, 1.4) | 0.9 (0.5, 1.6) | 1.2 (0.7, 1.9) | 1.0 (0.5, 1.7) |
| | Any TB symptom | Sensitivity | 24.5 (10.7, 43.8) | 19.7 (6.4, 42.9) | 23.8 (9.2, 45.0) | 22.3 (6.3, 47.9) |
| | | Specificity | 81.8 (79.2, 84.3) | 84.1 (81.2, 86.6) | 83.9 (81.5, 86.2) | 83.4 (80.1, 86.4) |
| | Radiologist conclusion[Ŧ] | Sensitivity | 48.6 (30.1, 67.6) | 44.8 (22.6, 69.2) | 58.4 (36.1, 78.6) | 40.8 (17.6, 67.5) |
| | | Specificity | 98.0 (96.9, 98.8) | 96.1 (94.4, 97.4) | 94.7 (92.9, 96.1) | 95.3 (93.0, 97.1) |
| | CAD4TBv5≥53 | Sensitivity | 83.2 (66.2, 93.9) | 85.9 (65.6, 96.3) | 87.4 (69.4, 96.6) | 85.5 (62.4, 96.6) |
| | | Specificity | 91.3 (89.3, 93.2) | 75.7 (72.2, 79.2) | 64.2 (60.7, 67.7) | 45.6 (41.1, 50.0) |
| | CAD4TBv6≥53 | Sensitivity | 82.7 (65.0, 93.5) | 83.0 (61.3, 95.1) | 87.0 (68.8, 96.4) | 85.2 (62.6, 96.5) |
| | | Specificity | 94.3 (92.5, 95.8) | 79.6 (76.2, 82.7) | 68.6 (65.1, 71.9) | 53.1 (48.4, 57.6) |
| | Xpert Ultra[†] | Sensitivity | 71.4 (51.6, 86.9) | 75.4 (51.1, 92.1) | 75.9 (54.7, 90.8) | 69.6 (42.8, 90.4) |
| | | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| | Culture | Sensitivity | 79.0 (59.2, 93.0) | 79.9 (54.3, 95.6) | 72.6 (49.4, 91.4) | 82.9 (57.9, 96.3) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

Ŧ - Chest X-ray abnormality suggestive of active PTB, † - Excluding trace

Table S14: Posterior median and 95% credible intervals (95% CrI) of the age, sex and HIV adjusted PTB prevalence and diagnostic test sensitivity and specificity among female individuals in Vukuzazi dataset

| | | | **15 – 29 years** | **30 – 49 years** | **50 – 69 years** | **≥70 years** |
|---|---|---|---|---|---|---|
| **Group** | **Test** | **Parameter** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** | **Median (95% CrI)** |
| **HIV+ Female** | | Prevalence | 0.9 (0.5, 1.5) | 1.0 (0.5, 1.7) | 1.2 (0.6, 2.0) | 1.0 (0.5, 1.8) |
| | Any TB | Sensitivity | 29.8 (14.1, 49.7) | 24.7 (9.4, 47.5) | 29.2 (11.9, 51.9) | 26.9 (8.8, 54.7) |
| | symptom | Specificity | 81.4 (77.9, 84.6) | 83.6 (81.2, 86.0) | 83.5 (80.9, 85.9) | 83.0 (79.1, 86.4) |
| | Radiologist | Sensitivity | 39.7 (21.5, 60.8) | 36.3 (16.7, 60.3) | 49.6 (27.9, 72.6) | 32.2 (12.0, 60.5) |
| | conclusion[Ŧ] | Specificity | 98.5 (97.3, 99.2) | 96.9 (95.7, 97.9) | 95.7 (94.1, 97.0) | 96.3 (93.9, 97.9) |
| | CAD4TBv5≥53 | Sensitivity | 80.6 (61.0, 93.0) | 83.4 (62.1, 95.6) | 85.1 (64.6, 95.8) | 83.0 (57.0, 96.1) |
| | | Specificity | 96.1 (94.7, 97.3) | 86.9 (84.7, 88.9) | 78.6 (75.6, 81.5) | 63.0 (57.8, 67.9) |
| | CAD4TBv6≥53 | Sensitivity | 82.1 (63.8, 93.2) | 82.5 (60.9, 94.6) | 86.5 (67.5, 96.4) | 84.8 (60.6, 96.4) |
| | | Specificity | 96.6 (95.2, 97.7) | 87.0 (84.7, 88.9) | 78.8 (75.7, 81.7) | 65.9 (61.0, 70.6) |
| | Xpert Ultra[†] | Sensitivity | 53.8 (32.9, 74.1) | 59.0 (33.9, 81.3) | 59.2 (34.8, 80.7) | 52.3 (25.0, 80.1) |
| | | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| | Culture | Sensitivity | 75.2 (53.5, 91.3) | 76.2 (49.4, 93.8) | 68.1 (43.8, 89.8) | 79.6 (51.4, 95.4) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| **HIV- Female** | | Prevalence | 0.5 (0.3, 0.8) | 0.6 (0.3, 1.0) | 0.7 (0.4, 1.2) | 0.6 (0.3, 1.0) |
| | Any TB | Sensitivity | 27.8 (15.1, 43.8) | 22.8 (8.6, 44.2) | 27.0 (11.3, 48.7) | 25.3 (8.9, 49.0) |
| | symptom | Specificity | 81.0 (78.2, 83.6) | 83.2 (80.4, 85.8) | 83.1 (81.0, 85.1) | 82.6 (79.7, 85.3) |
| | Radiologist | Sensitivity | 38.5 (23.6, 55.0) | 34.9 (16.8, 58.1) | 48.4 (27.0, 70.4) | 31.1 (13.0, 55.1) |
| | conclusion[Ŧ] | Specificity | 99.3 (98.8, 99.7) | 98.6 (97.7, 99.1) | 97.9 (97.1, 98.6) | 98.2 (97.2, 99.0) |
| | CAD4TBv5≥53 | Sensitivity | 74.7 (59.0, 87.2) | 78.2 (56.3, 92.3) | 80.2 (59.5, 93.0) | 77.5 (54.3, 92.5) |
| | | Specificity | 97.8 (97.0, 98.4) | 91.2 (89.2, 92.9) | 84.6 (82.6, 86.5) | 70.6 (67.3, 73.7) |
| | CAD4TBv6≥53 | Sensitivity | 78.7 (63.2, 89.5) | 79.2 (57.8, 92.4) | 83.8 (64.4, 94.6) | 81.6 (59.6, 94.3) |
| | | Specificity | 98.5 (97.9, 99.0) | 92.9 (91.1, 94.3) | 87.2 (85.4, 88.9) | 76.9 (73.8, 79.6) |
| | Xpert Ultra[†] | Sensitivity | 57.9 (40.4, 73.9) | 62.7 (38.7, 82.9) | 63.2 (40.2, 82.2) | 56.1 (31.4, 80.1) |
| | | Specificity | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) | 99.4 (99.1, 99.5) |
| | Culture | Sensitivity | 77.6 (61.3, 89.9) | 78.6 (54.8, 93.9) | 71.1 (47.3, 89.6) | 81.7 (59.0, 95.2) |
| | | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |

Ŧ - Chest X-ray abnormality suggestive of active PTB, † - Excluding trace

Table S15: Posterior median and 95% credible intervals (95% CrI) of PTB prevalence and diagnostic test sensitivity and specificity for Vukuzazi dataset adjusted for HIV status, sex and age

| | | Overall[‡] | Overall[Ŧ] | Overall[†] | Overall[⊥] |
|---|---|---|---|---|---|
| | N | 4960 | 4960 | 4960 | 4960 |
| Test | Parameter | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) | Median (95% CrI) |
| | Prevalence | 0.9 (0.6, 1.3) | 0.9 (0.6, 1.3) | 1.1 (0.8, 1.5) | 0.9 (0.6, 1.3) |
| Any TB | Sensitivity | 26.7 (16.6, 38.6) | 25.8 (15.9, 38.0) | 24.2 (14.8, 35.8) | 21.9 (12.1, 34.0) |
| symptom | Specificity | 83.0 (81.9, 84.0) | 83.0 (81.9, 84.0) | 83.0 (81.9, 84.0) | 82.9 (81.8, 84.0) |
| Radiologist | Sensitivity | 84.4 (74.0, 91.9) | 44.1 (32.0, 56.8) | 93.2 (83.5, 98.6) | 39.9 (27.1, 54.7) |
| conclusion | Specificity | 66.7 (65.3, 68.0) | 96.9 (96.3, 97.4) | 66.8 (65.4, 68.1) | 96.9 (96.4, 97.4) |
| CAD4TBv5≥53 | Sensitivity | 80.4 (68.4, 89.7) | 81.5 (70.2, 90.2) | 85.6 (72.3, 94.4) | 86.7 (73.5, 95.4) |
| | Specificity | 80.0 (78.9, 81.2) | 80.1 (78.9, 81.2) | 80.1 (79.0, 81.2) | 80.1 (78.9, 81.2) |
| CAD4TBv6≥53 | Sensitivity | 81.1 (69.2, 90.1) | 82.5 (71.3, 90.8) | 84.0 (70.3, 93.3) | 85.0 (72.1, 93.9) |
| | Specificity | 82.5 (81.4, 83.6) | 82.6 (81.6, 83.7) | 82.6 (81.5, 83.7) | 82.6 (81.5, 83.7) |
| Xpert Ultra | Sensitivity | 62.2 (48.7, 74.4) | 64.0 (50.6, 76.5) | 77.2 (60.9, 89.5) | 79.8 (63.8, 92.1) |
| | Specificity | 99.4 (99.1, 99.6) | 99.4 (99.1, 99.5) | 99.1 (98.8, 99.4) | 99.0 (98.7, 99.3) |
| Culture | Sensitivity | 75.9 (61.9, 89.2) | 75.2 (61.6, 88.0) | 68.7 (54.5, 82.0) | 71.7 (56.9, 85.5) |
| | Specificity | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) | 99.8 (99.7, 99.9) |
| | Deviance | 1656.8 | 1358.5 | 1692.0 | 1402.9 |

CrI – Credible Intervals

‡ - Model evaluating any TB symptom, any chest X-ray abnormality, CAD4TBv5≥53, CAD4TBv6≥53, Xpert Ultra (excluding trace) and culture

Ŧ - Model evaluating any TB symptom, chest X-ray abnormality suggestive of active PTB, CAD4TBv5≥53, CAD4TBv6≥53, Xpert Ultra (excluding trace) and culture

† - Model evaluating any TB symptom, any chest X-ray abnormality, CAD4TBv5≥53, CAD4TBv6≥53, Xpert Ultra (including trace) and culture

⊥ - Model evaluating any TB symptom, chest X-ray abnormality suggestive of active PTB, CAD4TBv5≥53, CAD4TBv6≥53, Xpert Ultra (including trace) and culture

Note: The estimates presented in the table are percentages

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