

Treatment-seeking behaviour in low- and middle-income countries estimated using a Bayesian model

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1 **Abstract**

2 **Background**

3 Seeking treatment in formal healthcare for uncomplicated infections is vital to
4 combating disease in low- and middle-income countries (LMICs). Healthcare
5 treatment-seeking behaviour varies within and between communities and is
6 modified by socio-economic, demographic, and physical factors. As a result, it
7 remains a challenge to quantify healthcare treatment-seeking behaviour using a
8 metric that is comparable across communities. Here, we present an application for
9 transforming individual categorical responses (actions related to fever) to a
10 continuous probabilistic estimate of fever treatment for one country in Sub-Saharan
11 Africa (SSA).

12 **Methods**

13 Using nationally representative household survey data from the 2013 Demographic
14 and Health Survey (DHS) in Namibia, individual-level responses ($n=1,138$) were linked
15 to theoretical estimates of travel time to the nearest public or private health facility.
16 Bayesian Item Response Theory (IRT) models were fitted via Markov Chain Monte
17 Carlo (MCMC) simulation to estimate parameters related to fever treatment and
18 estimate probability of treatment for children under five years. Different models were
19 implemented to evaluate computational needs and the effect of including
20 predictor variables such as rurality. The mean treatment rates were then estimated
21 at regional level.

22 **Results**

23 Modelling results suggested probability of fever treatment was highest in regions with
24 relatively high incidence of malaria historically. The minimum predicted threshold
25 probability of seeking treatment was 0.3 (model 1: 0.340; 95% CI 0.155-0.597),
26 suggesting that even in populations at large distances from facilities, there was still a

27 30% chance of an individual seeking treatment for fever. The agreement between
28 correctly predicted probability of treatment at individual level based on a subset of
29 data ($n=247$) was high (AUC= 0.978), with a sensitivity of 96.7% and a specificity of
30 75.3%.

31 **Conclusion**

32 We have shown how individual responses in national surveys can be transformed to
33 probabilistic measures comparable at population level. Our analysis of household
34 survey data on fever suggested a 30% baseline threshold for fever treatment in
35 Namibia. However, this threshold level is likely to vary by country or endemicity.
36 Although our focus was on fever treatment, the methodology outlined can be
37 extended to multiple health seeking behaviours captured in routine national survey
38 data and to other infectious diseases.

39 **Background**

40 Delay in seeking treatment for ill health in low- and middle-income countries (LMICs)
41 affects disease progression, management and outcomes [1-3]. Most infectious
42 diseases in LMICs are preventable by using cost-effective interventions and
43 treatable at peripheral health facilities [4]. However, weak health systems affect the
44 delivery of most interventions [5] and socio-economic and physical barriers that
45 modify health-seeking behaviour compound this, leading to under-utilisation of
46 health facilities [6]. Encouraging appropriate treatment-seeking behaviour for
47 uncomplicated infections is vital to further reduce disease burden in these countries
48 or for successful elimination. For malaria, for example, the current World Health
49 Organisation (WHO) recommendation is for malaria treatment to be sought in the
50 formal healthcare sector within 24 hours of fever onset and other malaria-related
51 symptoms [7]. This is because patients who seek treatment through the formal sector
52 are likely to receive an appropriate diagnosis and effective management [8].
53 However, there are many factors influencing population treatment-seeking
54 behaviour including, but not limited to; availability of healthcare providers, proximity
55 or travel time to healthcare facilities, condition severity and perception, and the
56 socio-demographic profile of the population at risk [9].

57 Studies on treatment-seeking behaviour can be grouped into two categories of
58 approach. The first is a qualitative description of steps undertaken by the population
59 in different settings [10-12] while the second is a quantitative association between
60 determinants (factors) and choice of health service use [13-18]. Although these
61 approaches are used widely in bio-medical research, they usually do not examine
62 the latent (i.e. theoretical) characteristics such as individual-level traits to estimate
63 variation at population level. In addition, comparability is not simply guaranteed

64 with the same questionnaire because of differential item functioning problem i.e. the
65 varying behavioural response to the same question depending on the respondent
66 [19]. Such variation can then be translated to spatially explicit applications that can
67 be combined with existing spatial data on populations [20] and disease incidence
68 to inform and optimise targeting of community-based interventions.

69 Model-based geostatistical methods have already been used to predict and
70 estimate disease incidence at fine spatial resolution [21, 22]. This has been aided by
71 public health intelligence data that are increasingly becoming available across
72 space and time from geo-located nationally representative household surveys.
73 These include the Malaria Indicator Surveys (MIS) [23], Demographic and Health
74 Surveys (DHS) [24], and Multiple Indicator Cluster Surveys (MICS) [25]. These nationally
75 representative household surveys also collect information on self-reported health
76 behaviour such as fever management [14]. However, how can responses
77 concerning fever treatment from household surveys be compared across
78 populations with varying access, demographics, cultures, and disease burdens?
79 Item response theory (IRT) has been widely used to examine surveys items (questions)
80 and person characteristics in psychology and education [26-28]. In education, for
81 example, it has been used to estimate the person-level traits (such as ability) or item-
82 level difficulty in an examination [29-31]. IRT concepts can be extended to health as
83 applied previously in delirium screening [32], longitudinal data analysis [33], and
84 interpreting medical codes from patient records [34]. IRT approaches are essentially
85 probit models with additional regression effects used to aid estimation of item
86 characteristics [35]. Extending this to a Bayesian framework has the advantages of
87 incorporating uncertainty in estimating latent traits and prior distributions can be
88 imposed on the Bayesian probability model to capture many aspects of data not

89 included in descriptive or quantitative frequentist approaches [36]. Although
90 Imputation techniques can be used to handle missing data, this was beyond the
91 current scope of this manuscript.

92 Here, the aim was to demonstrate the application of IRT to fever treatment-seeking
93 modelling using data from a low malaria transmission setting, the Namibia 2013 DHS.
94 We analyse fever treatment-seeking behaviour at a national level and derive
95 response characteristic curves based on travel times to the nearest facilities. The rest
96 of this paper is organised as follows. Section 2 provides an overview of household
97 survey data in LMICs and the proposed modelling approach. We then present
98 treatment-seeking behaviour model outputs in section 3, including evaluation of
99 model performance. The paper concludes with a brief discussion in sections 4 and 5.

100

101 **Methods**

102 *Data characteristics in low- and middle income countries*

103 Distance or proximity to healthcare provider is an important parameter in the choice
104 of treatment by patients in many LMICs [37-39]. In these countries, the majority of
105 people access facilities by walking. Therefore, it is preferable to use a facility close to
106 the place of residence because it is less costly compared to travelling greater
107 distances requiring motorised transport [40]. Other factors that influence utilisation
108 patterns include: age, gender, healthcare costs, socio-economic status, residence
109 (urban or rural), familiarity with health personnel, fever severity, and quantity as well
110 as quality of services at peripheral facilities [41, 42]. In some cases, however, the
111 phenomenon of by-passing the nearest healthcare facility can be encountered,
112 even for mild fever conditions [43, 44]. Empirical data are not always available to
113 model such nuances and we therefore assume use of the nearest facility in this case
114 study.

115

116 *Estimation of travel times to the nearest formal healthcare treatment provider.*

117 Estimating travel times between population centres and formal healthcare providers
118 has already been considered in previous research [14]. In brief, this requires a
119 combination of mode of travel (walking or motorised) and an impedance surface
120 that is constructed based on multiple data layers, including the various land use and
121 land cover characteristics, elevation, and roads [45]. Travel time to nearest
122 healthcare facility is a useful measure because it is relatively easy to estimate and to
123 relate travel times in different settings compared to estimating the actual physical
124 distance. The approach in Alegana et al. [14] shows how travel times for Namibia
125 were derived.

126 **<Insert fig 1>**

127 *Quantification of formal healthcare use based on national representative household*
128 *surveys*

129 To estimate the utilisation of healthcare facilities, this study used the reported use of
130 formal healthcare for fever treatment from the DHS. These surveys are conducted in
131 90 countries worldwide, and 44 in SSA, providing information on reproductive health,
132 fertility, population demographics and general health status, nutrition, household
133 characteristics, socio-economic status and infant and child mortality rates [46]. The
134 surveys are based on a random two-stage cluster sampling design in which clusters
135 are usually first sampled within a region on a probability-proportional-to-size basis
136 and thereafter, within each cluster, households are sampled randomly [47, 48].
137 Cluster sizes usually vary, but are typically approximately 15 to 30 households. The
138 household survey provides information on health and the socio-demographic profile
139 of consenting participants including their treatment-seeking behaviour for conditions
140 such as malaria-associated fever.

141

142 A notable feature of the fever treatment variable in the DHS is the decay in
143 treatment with increasing travel time to nearest facility (Figure 1). The geographical
144 barrier to utilisation, manifested as a distance decay, is a well-known phenomenon
145 in studies of healthcare utilization [37, 38, 49] and occurs when usage of health
146 facilities declines with increasing distance [50, 51]. This feature motivates the use of
147 probit models to characterise treatment-seeking behaviour (section 2.4). Another
148 feature of utilisation is that even for patients in close proximity to healthcare facilities,
149 treatment for fever is not always 100% as some mild conditions self-resolve, are
150 treated through informal care, or may be treated at a more distant facility [9].
151 Household survey data usually contain detailed information on other factors that
152 could affect utilisation of healthcare facilities. These explanatory variables can be
153 grouped largely into socio-economic and demographic characteristics and have
154 been used selectively in quantitative studies of healthcare utilisation [3, 10, 17, 52,
155 53].

156 *Application of Bayesian probit models to healthcare utilisation research*

157 Item response modelling was proposed in the 1960s [54-56] and is commonly applied
158 to studies in education and psychology to estimate item characteristics [28]. The first
159 applications of IRT used maximum likelihood estimation [57, 58]. Bayesian extensions
160 were proposed for one- and two-parameter models [59] and extended to the three-
161 parameter logistic model [60]. Fitting via Gibbs sampling became popular using
162 data augmentation (DAG) techniques in the 1990s particularly for application to the
163 normal-ogive models [61-63]. Fu et al. [64] provided some extensions to the three-
164 parameter model following Sahu's DAG approach [63] and compared Gibbs
165 sampling to BILOG-MG software [65] using likelihood estimation. There have also
166 been other innovations in parameter estimation [62], including extension to a multi-

167 level approach [26-28] and comparison with maximum likelihood methods [66].
 168 Here, a unidimensional three-parameter model with a hierarchical structure was
 169 used, its parameters estimated, and prior sensitivity checked by comparing model
 170 goodness-of-fit statistics. The main objective was to estimate the probability of a
 171 positive response to choice of treatment for persons with fever associated with
 172 malaria at a household level.

173 In general, let Y_{ij} represent a dichotomous response variable of an individual
 174 j ($j=1,\dots,N$) on a set of questions (items) i ($i=1,\dots,n$) on use of public healthcare for
 175 treatment. $Y_{ij}=1$ represents a positive response on one item (e.g. public healthcare
 176 use), while $Y_{ij}=0$ represents a negative response (e.g., non-public healthcare use).
 177 The probability of $Y_{ij}=1$ can then be written following [64] as:

$$178 \quad P(Y_{ij}=1 | \theta_j, a_i, b_i, c_i) = c_i + (1-c_i) \frac{\exp\left\{\sum_{k=1}^m (a_{ik}\theta_{jk} - b_{ik})\right\}}{\left[1 + \exp\left\{\sum_{k=1}^m (a_{ik}\theta_{jk} - b_{ik})\right\}\right]} \quad 1$$

179 where, $\theta_j = \theta_{j1}, \dots, \theta_{jk}, \dots, \theta_{jm}$ with $-\infty < \theta_{jk} < +\infty$ for $k=1, \dots, m$ dimension represents the
 180 person traits (i.e. the ability parameter). a_{ik} represents item discrimination
 181 parameters between individuals separated by individual-level traits, and is positive
 182 ($a_{ik} > 0$). b_{ik} ($-\infty < b_{ik} < \infty$) represents item difficulty (or location) parameters which for
 183 multiple items represents relationship between items and the underlying individual-
 184 traits. Lastly, c_i ($0 < c_i < 1$) represents the threshold (i.e., minimum) probability for the
 185 item in question (fever treatment). This specification of threshold probability is
 186 important to this application because the estimated probability is never equal to
 187 one when θ_j is zero, due to several individual characteristics. Hence, probability of

188 treatment is constrained to be greater than zero and less than one. In many
 189 applications in psychology and education, the ability parameter, for example, is
 190 modelled as a latent characteristic independent of survey observations [67, 68]. In
 191 this application, a predictor variable was introduced on the individual traits
 192 parameter in terms of travel-time to the nearest health facility. This parameterisation
 193 also enables the introduction of other variables such as residence (urban or rural),
 194 socio-economic status, or educational levels. Thus, equation 1 can be simplified to:

$$195 \quad P_{ij} = c_i + (1 - c_i)\Psi_{ij} \quad 2$$

196 Where

$$197 \quad \Psi_{ij} = \exp \left\{ \sum_{k=1}^m (a_{ik} \theta_{jk} - b_{ik}) \right\} / \left[1 + \exp \left\{ \sum_{k=1}^m (a_{ik} \theta_{jk} - b_{ik}) \right\} \right]$$

$$\theta_j = \alpha_j + \beta_{1j} X_{1j} + \dots + \beta_{Qj} X_{Qj}$$

198 with β_{Qj} representing coefficients of dependent variables X_{Qj} exploring differences
 199 in ability.

200

201 *The likelihood and posterior specification*

202 In general, let $f(\theta, a, b, c)$ denote a collection of unknown parameters, the posterior
 203 can be expressed as the product of the likelihood and prior distributions for unknown
 204 parameters given as:

$$205 \quad f(\theta, a, b, c | y) \propto L(y | \theta, a, b, c) f(\theta, a, b, c) \quad 3$$

206 where $f(\theta, a, b, c) = f(\theta)f(a)f(b)f(c)$ and the posterior density we wish to evaluate
 207 is

208

$$D \times L(y | \theta, a, b, c) \times \left\{ \prod_{j=1}^N f(\theta_j | \mu_\theta, \sigma_\theta^2) \right\} \times \prod_{i=1}^n f(a_i | \mu_a, \sigma_a^2) \\ \times I(a_{ik} > 0) \times \prod_{i=1}^n f(b_i | \mu_b, \sigma_b^2) \times \prod_{i=1}^n f(c_i | \kappa_i, \tau_i)$$

209 where D is a proportionality constant and

$$L(y | \theta, a, b, c) = \prod_{i=1}^n \prod_{j=1}^N [P_{ij}^{y_{ij}} (1 - P_{ij})^{1 - y_{ij}}]$$

and

210

$$\prod_{j=1}^N f(\theta_j | \mu_\theta, \sigma_\theta^2) = \prod_{j=1}^N \exp \left\{ -\frac{1}{2} (\theta_j - \mu)^\top \Sigma_\theta^{-1} (\theta_j - \mu) \right\}$$

$$\prod_{i=1}^n f(b_i | \mu_b, \sigma_b^2) \times \prod_{i=1}^n f(a_i | \mu_a, \sigma_a^2) = \frac{1}{\sigma^2} \prod_{i=1}^n \prod_{k=1}^m \frac{1}{\sigma^2} \exp \left\{ -\frac{(a_{ik} - \delta_a)^2 + (b_{ik} - \delta_b)^2}{2\sigma^2} \right\}$$

$$\prod_{i=1}^n f(c_i | \kappa_i, \tau_i) = \prod_{i=1}^n c_i^{\kappa_i - 1} (1 - c_i)^{\tau_i - 1}$$

211

212 *Goodness-of-fit statistics, prior specification and Markov chain Monte Carlo*
213 *implementation*

214 The same notation was used for the item discrimination parameter, with $a_i > 0$,

215 where a half-normal or truncated normal prior was used such that

216 $a_i \sim N(\mu_a, \sigma_a^2) I(a_i > 0)$ and $I(\cdot)$ is an indicator function. The rationale for this

217 specification is to ensure that the parameter estimate is positive. The probability

218 threshold parameter was constrained on $c \in (0, 1]$ using a beta distribution such

219 that $\pi(c_k; \kappa, \tau) \propto c_k^{\kappa - 1} (1 - c_k)^{\tau - 1}$ for suitable parameters values κ_{c_k} and τ_{c_k} .

220 The recommended procedure for selecting suitable estimates of these parameters is

221 such that the $E(c) = \kappa / (\kappa + \tau)$ and weakly informative priors may be used for

222 parameters of beta distribution.

223 Two different specifications were used for the difficulty parameter. The first was a

224 normal prior $b_i \sim N(0, 10)$ (model 1) and the second a truncated normal (model 2)

225 restricting $b_i \sim N(\mu_b, \sigma_b^2) \mathbf{I}(b_i > 0)$ to be positive. Thus, the difference between
 226 model 1 and model 2 was only in the prior specification for the b parameter. Figure
 227 2a represents the overall parameter structure for Model 1 and Model 2. The rationale
 228 for using different priors for b was to evaluate the effect of constraining item
 229 difficulty to positivity ($b_i > 0$) compared to allowing for flexible Gaussian density.

230 Lastly, the individual-trait parameter θ_j was modelled in a hierarchical approach
 231 following Fox and Glas [30] such that the joint distribution of θ_j parameters follows a
 232 multivariate normal distribution. Thus, in general, α and β are the intercept terms
 233 and regression coefficients, respectively, modelled as independent effects in model
 234 1 and model 2 (Figure 2a). In extending the model to a multi-level representation,
 235 time to the nearest facility could then be used to explain individual traits. Normal
 236 priors (e.g. $\alpha \sim N(0,1)$) were used for α and β in Figure 2a. Secondly, this was
 237 extended to a random intercept in model 3 (Figure 2b) and lastly, as a random
 238 slope and intercept model including residence (urban or rural) as a centering
 239 variable (model 4, Figure 2c). For model 4, the random slope and intercept were
 240 modelled jointly as:

$$241 \quad \begin{pmatrix} \alpha_j \\ \beta_j \end{pmatrix} \sim MVN \left\{ \begin{pmatrix} \beta_{\alpha,j} \\ \beta_{\beta,j} \end{pmatrix}, \Sigma = \begin{pmatrix} \tau_{11} & \tau_{12} \\ \tau_{21} & \tau_{22} \end{pmatrix} \right\} \quad 4$$

242 with a Wishart (multivariate scaled χ^2) distribution (Barnard et al. 2000) with density
 243 $f(\Sigma) \propto |\Sigma|^{-(\nu+d+1)/2} e^{-\frac{1}{2}tr(\wedge\Sigma^{-1})}$; d dimension matrix; ν degrees of freedom;
 244 specified for covariance matrix Σ . Thus, the inverse is specified as
 245 $\Sigma^{-1} = Wishart(\Omega, p)$ where Ω is a scale matrix, usually identity, and p is the degrees
 246 of freedom equal to the number of random components. Alternative approaches

247 could employ a scaled inverse-Wishart distribution because of the large standard
248 errors associated with large variances in the use of the inverse-Wishart prior [69].

249 < Insert fig 2 >

250 Validation was considered via a subset of 40% of the data selected randomly ($n=247$
251 of the 1,138 children) with the remaining 60% ($n=891$) used in model estimation.
252 Model 1 was then applied to the validation set and the predicted probability of
253 treatment transformed to a binary outcome. A receiver operating characteristic
254 (ROC) curve was then used to derive the specificity and sensitivity of predictions
255 when compared to observed responses from survey data. For estimation, different
256 model specifications were also used to check the sensitivity of different prior
257 specifications (i.e. models differ only on prior structure) and complexity. Model
258 outputs were evaluated and compared via goodness-of-fit statistics, for example,
259 the Deviance Information Criterion (DIC). The DIC summarises model fit based on a
260 combination of model deviance and complexity (effective number of parameters)
261 [70, 71]. This is defined as:

$$262 \quad DIC = \bar{D} + pD \quad 5$$

263 where $\bar{D} = E_{\theta|y}[D]$ is the mean deviance for $D = -2 \times \log\{P(y|\theta)\}$ with

$$264 \quad \begin{aligned} \bar{D} &= -\int 2 \log\{P(y|\theta)\} d\theta \\ \hat{D} &= -2 \log\{P(y|\bar{\theta})\} \end{aligned}$$

265 and complexity (effective number of parameters) given by $pD = \bar{D} - \hat{D}$. The two
266 parameters were monitored in the MCMC implementation using five chains in JAGS
267 version 4.2.0 and the *rjags* package in R version 3.3.1 [72]. A combination of
268 Gelman-Rubin [73] with Raftery-Lewis diagnostic [74] approaches were used to
269 check for convergence. For the former, we checked for a reduction factor of <1.05

270 while the latter provided estimates of burn-in and thinning factors given an
271 accuracy of 0.0005 at quantile (0.025) and coverage probability of 0.975.

272

273 **Results**

274 We used the Namibia 2013 DHS data to estimate the probability of fever treatment
275 in the formal sector (reported fever treatment in public and private sectors) for
276 children under five years. There were 4,818 children under five years enumerated, of
277 which 1,138 (23.6%) reported at least one fever episode in the preceding fortnight.
278 Of those that reported a fever episode, 726 (63.8%) sought treatment in the formal
279 sector (public and private sector excluding traditional healers). Overall, the
280 proportion of children with reported fever was fairly homogeneous across all the
281 regions surveyed but varied by estimated travel times. Estimation of probability of
282 treatment focussed on children reporting fever ($n=1,138$) rather than all children
283 examined in the cross-sectional survey.

284 **<Insert Table 1>**

285 In terms of computation, the Gelman-Rubin test was less than or equal to 1.05 for all
286 the parameters monitored in the MCMC implementation. However, the Raftery-
287 Lewis method showed that a minimum of 55,318 iterations were required to achieve
288 an accuracy of 0.0005 at coverage probability of 0.999 with quantile at 0.05. More
289 than 100,000 iterations with a burn-in of 50,000 were implemented. Table 1 shows the
290 DIC estimates and the effective number of parameters from the four models
291 implemented. Comparison between model 1 (M1 DIC 3615.9) and model 2 (M2 DIC
292 3685.1) suggests that using truncated normal priors for the b parameter did not
293 improve model fit. Increasing DIC (for model 3 and 4) was also directly proportional
294 to the increase in model complexity by including random intercept and slope. This
295 also increased computational demands for M3 and M4 requiring at least 250,000

296 iterations with longer burn-in (slow convergence). The difference in DIC estimates
297 also suggested that the models were sensitive to changes in model structure. Based
298 on a binary classification of predicted probability at the individual level from model
299 1, the area under the curve (AUC) was 0.978 with a sensitivity of 96.7% and a
300 specificity of 75.3% (155 true positive, 21 false positive, 64 true negative, and 7 false
301 negative).

302 Table 2 shows posterior estimates of the parameters along with 95% equal-tailed
303 credible intervals. A plot of fever-response curves based on the fitted parameters is
304 shown in Figure 3a along with a scatterplot of α and β parameters from Model 4
305 (Figure 3b), posterior density of parameters (Figure 3c) and ROC plot (Figure 3d).
306 Different mean combinations of parameters a , b , and c resulted in response
307 characteristics based on travel time to nearest health facility (Figure 3a). Parameter
308 estimates could be compared and interpreted jointly in this manner because they
309 apply to one item (on estimating fever treatment). Comparison between model 1
310 and model 2 suggested that constraining the b parameter did not have a major
311 impact on mean estimates of the individual-level traits, a or the threshold
312 parameter c . Overall, model 4 had larger person discriminant parameter estimates
313 (mean and median) compared to all the other model specifications. The correlation
314 between mean estimates for α and β as estimated from the model was weak
315 (mean -0.011, median 0.006 scatterplot Figure 2b). The combination of correlation
316 and DIC estimates suggested a fixed prior independent specification as a better
317 choice. It also imposes less computational demand. The threshold probability was
318 >0.3 for all model estimates, suggesting this as the lower limit probability of use of
319 nearest facility for fever treatment in the four models implemented from the 2013
320 Namibia DHS.

321 **<Insert table 2 and fig 3>**

322 Table 3 shows the estimated mean probabilities for malaria related fever treatment
323 at a regional level in Namibia with associated confidence intervals and population
324 estimates. Population estimates are useful in estimating fever treatment burden
325 based on probability estimate at regional level. For malaria, the probability of fever
326 treatment among febrile cases was highest in endemic areas in Zambezi and
327 Kavango (mean probability in Zambezi 0.546 (95% Credible Interval (CI): 0.369-
328 0.671)) compared to Kunene with less than one case per 1000 population with mean
329 probability 0.433 (95% CI: 0.364-0.614). Overall mean probability of fever treatment
330 was greater than 0.5 in areas with malaria incidence >1 per 1000 population.

331 **<Insert Table 3>**

332

333 **Discussion**

334 Characterising treatment-seeking behaviour in LMICs is valuable because it varies by
335 geographic location, type of disease and severity, person characteristics including
336 age and gender, as well as health system based factors such as availability, cost
337 among other enabling factors [9, 75, 76]. Here, the focus was on the estimation of
338 latent parameters of a survey question on fever and estimating the probability of
339 seeking treatment based on a dichotomous response. We used data from a
340 nationally representative household survey from the DHS in one country to estimate
341 fever treatment latent characteristics using a Bayesian IRT approach. By using this
342 method, we estimated the parameters of fever response curves that characterise
343 geographical decay in the use of formal health care based on travel time to the
344 nearest facility. The method is particularly appealing because of the joint estimation
345 of IRT parameters related to fever treatment with uncertainties incorporated in prior
346 distributions and the ability to extract the full posterior distribution compared to point

347 estimates from maximum likelihood approaches [26, 61]. This is important because
348 estimates from such probabilistic modelling can then be applied in estimating
349 numbers of symptomatic infections (treatment burden) when such probabilistic
350 estimates are transformed into gridded metrics that vary spatially [77, 78]. The
351 modelling approach can also be extended to other items in household surveys to
352 further understand human behaviour response to health conditions.

353

354 The lower limit probability estimated here, related to the threshold parameter (e.g.
355 from table 2 model 1: 0.340; 95% CI 0.155-0.597), for Namibia suggests that even at
356 large distances from health facilities, there was still a 30% chance of individuals
357 seeking fever treatment. We suggest that this is an important property in treatment-
358 seeking behaviour for individuals living far from health facilities in Namibia, although
359 this threshold may be different by country or endemicity and was not explored
360 further in this analysis. In this study, estimates of probability of fever treatment at the
361 regional level showed that the mean probability was highest in regions with relatively
362 high incidence of malaria historically (Table 3). Another operational application of
363 the probability response characteristics curves, derived from the latent parameters
364 in Figure 3a, could be in identifying areas where community health workers could be
365 deployed [79, 80]. This, however, requires definition of a cut-off probability (y-axis on
366 Figure 3a), currently not established for malaria transmission settings, to delineate
367 areas with limited access. Constraining the b parameter (item parameter) did not
368 influence estimates of the individual-level traits and the threshold parameters. This is
369 primarily because only one item was used in this application resulting in similar
370 parameter estimate for the location parameter.

371

372 In extending the model to a multilevel framework, travel times were used as
373 predictors. Comparison between constant intercept and slope model parameters
374 with a random parameter model showed that the former resulted in shorter MCMC
375 runs and better model fit compared to the latter (i.e., the random slope and
376 intercept), which experienced slow convergence as the number of effective
377 parameters increased exponentially. We are not discouraging use of a more
378 complex modelling approach while estimating IRT parameters, but this highlights the
379 increasing computational demands and efficiency related to increased complexity.

380

381 MCMC techniques were used to estimate and jointly interpret IRT parameters. The
382 three-parameter logistic model [60] was particularly useful compared to the two-
383 parameter model [59], because, the third parameter C represents the threshold
384 probability on the fever response curve, ensuring that probability is always greater
385 than or equal to zero. Despite the known benefits of IRT in other fields [28], this
386 approach has seldom been applied to modelling human behavioural aspects for
387 treatment-seeking behaviour. The current study was confined to patients' responses
388 to a fever question in household survey data and how latent (rather than observed)
389 properties can be quantified in relation to patient behaviour and travel time.
390 Dichotomous responses are common in many health surveys in LMICs and methods
391 used here can be extended to other health conditions. Although we did not have to
392 deal with missing data (NAs), several data imputation techniques can be used for
393 non-ignorable NAs [81]. These may arise when there is lack of response, or,
394 associated with refusal to participate or simply unobserved variable for survey items.
395 When NAs are imputed into the data matrix, for example, these do not usually
396 contribute to likelihood estimation [82] of the ability parameter and the higher the

397 number of missing values the more likely that there will be an increase in uncertainty
398 for the parameter estimate.

399

400 There exist some additional limitations aside from those related to computational
401 speed and efficiency. While fever in the Namibia 2013 DHS was associated with
402 malaria treatment, the survey data did not include a laboratory confirmation of
403 malaria infection [83]. Moreover, the sampling methodology for children with fever in
404 the DHS may be inferior because the survey is not powered for fever detection [47].
405 Most current surveys however incorporate rapid diagnostic tests (RDTs) and future
406 identification of febrile cases could include laboratory results as a preprocessing
407 step in identifying malaria-related fever cases. In addition, although prior
408 specifications introduce a measure of uncertainty in a hierarchical way, assumptions
409 in generating input data such as use of the nearest facility may not be sufficient in
410 understanding treatment-seeking behaviour. It has been shown in separate
411 population surveys that patients may bypass the nearest health centre due to
412 various individual- or supply-based factors such as quality [84]. While an obvious
413 recommendation is to include such effects, increasing model complexity to capture
414 such differences may have an impact on computational efficiency as seen in model
415 3 and model 4. More importantly, identifying measures of quality of care in public or
416 private health sectors can be challenging [40].

417

418 **Conclusion**

419 In the context of fever treatment, we have demonstrated that there is potential to
420 use nationally representative household data to provide a probabilistic measure of
421 treatment using a Bayesian method. Our estimates of threshold probability apply to
422 one low malaria transmission country and may be different in other countries with

423 varying malaria endemicity. Future studies will aim to conduct such comparative
424 analysis between and within countries via spatially varying parameters. The
425 methodology can be extended to multiple human behavioural questions (items)
426 related to health and demographics in the routine national survey data.

Declarations

Consent for publication: Not Applicable

Availability of data and material: DHS data available in the public domain at <http://dhsprogram.com/data/available-datasets.cfm>

Competing interests: Authors declare no competing interests.

Ethics approval and consent to participate

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Authors' contributions

VA, PMA, and AJT were responsible for study design, analysis, interpretation, and production of final manuscript. CP and JW contributed to data assembly and management, interpretation and production of final manuscript. All authors have read and approved the final version of the manuscript.

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Abbreviations

AUC: area under curve; CHW: community health worker; DAG: data augmentation; DHS: demographic health surveys; DIC: deviance information criterion; iCCM: integrated community-case management; IRT: item response theory; LMICs: low- and middle-income countries; MCMC: Markov chain Monte Carlo; MICS: multiple indicator cluster surveys; MIS: malaria indicator surveys; ROC: receiver-operating characteristics; SSA: Sub-Saharan Africa; WHO: World Health Organization.

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Appendix

Parameter notations

j	Individual/person
i	Item/survey question
k	Dimension for items
q	Dimension for dependent variables
a	Discrimination parameter
b	Difficulty parameter on items
c	Probability threshold parameter
θ	Individual trait/ability parameter
$P(Y)$	Probability that event Y occurs
$I(\cdot)$	Indicator function for event in sample space
$E(X)$	Expectation for random parameter X
μ	Mean
DIC	Deviance Information Criterion
\bar{D}	Mean deviance
$\{(\cdot)\}$	Order of brackets

Legends to figures

Fig 1: Visualisation of malaria-associated fever treatment from DHS data by **A)** age (Children 0-5 years) and **B)** by travel time to the nearest health facility generated from GIS methods combining spatial data (Land cover, roads), population centres and the locations of health facilities.

Fig 2: Graphical representation of the form of the models used. **A)** simplified fixed parameter specification used for model 1 and model 2; **B)** allowing for a random slope (model 3) on the α parameter; **C)** random slope and intercept (model 4) for the α and β parameters, respectively, centering on residence (urban and rural) with correlation estimated via the Wishart prior specification. Model 1 and Model 2 differ only in the prior specification for item difficulty (b) parameter.

Fig 3: Panel plots showing: **A)** Fever response decay curves from the four model parameter values from the DHS survey in Namibia for 2014. The data are from 1,138 ($n=891$ training, 247 validation) children under the age of five reporting fever 2 weeks prior to survey of which 726 sought treatment in the formal sector. **B)** A scatterplot for mean estimates on α (intercept) and β (slope) parameters based on model 4

(random slope and intercept model at individual level). **C)** Posterior density for IRT parameters (a individual discriminant parameter, b item difficulty, and c probability threshold). **D)** Receiver operating characteristic (ROC) plot based on the validation dataset ($n=247$ children). The binary classification was based on the predicted probability of seeking treatment for fever (from model 1) with a cut-off at 0.65. ROC had AUC=0.978 and an accuracy measure of 0.887.

Table 1: Model comparison based on goodness-of-fit statistics. DIC is the deviance information criterion while PD is the model complexity (number of model parameters)

Model	DIC	PD	Inverse log likelihood	Number of chains
M1*	3615.9	2178.9	-0.001	3
M2*	3685.1	2256.1	-0.001	3
M3	5098.7	3693.1	-0.001	3
M4	23874.1	22754.0	-0.002	3

*Model 1 and model 2 only differ in prior specification for the b parameter

Table 2: Estimated summary statistics and the 95% Bayesian credible intervals of parameters based on all four models. M1 and M2 use a fixed parameter specification for α and β using normal priors but different priors for item parameters, M3 allows random intercepts only, and M4 is both a random slope and intercepts model. Only M4 include a measure of correlation between the multi-level regression parameters.

Mod el	Estimate	a	b	c	α	β	Corr(α, β)
M1	Mean	0.704	0.807	0.340	-0.084	-0.098	-
	Median	0.556	0.850	0.326	-0.087	-0.112	-
	95% CI	[0.016 - 2.194]	[-1.044 - 2.346]	[0.1554 - 0.597]	[-0.682 - 0.523]	[-0.439 - 0.394]	-
	Gelman-Rubin						-
	Convergence estimate	1.000	1.000	1.000	1.000	1.000	-
	Gelman-Rubin						-
	Convergence upper CI	1.000	1.010	1.000	1.000	1.030	-
M2	mean	0.784	1.060	0.352	-0.080	-0.123	-
	median	0.654	0.978	0.344	-0.081	-0.121	-
	95% CI	[0.042 - 2.243]	[0.100 - 2.452]	[0.172 - 0.572]	[-0.661 - 0.518]	[-0.417 - 0.218]	-
	Gelman-Rubin						-
	Convergence estimate	1.001	1.000	1.001	1.001	1.020	-
	Gelman-Rubin						-
	Convergence upper CI	1.010	1.000	1.000	1.000	1.040	-
M3	mean	0.789	0.977	0.376	-0.582	-0.140	-
	median	0.660	0.895	0.372	-0.581	-0.150	-
	95% CI	[0.046 - 2.225]	[0.055 - 2.423]	[0.176 - 0.597]	[-2.208 - 1.069]	[-0.434 - 0.248]	-
	Gelman-Rubin						-
	Convergence estimate	1.000	1.000	1.000	1.000	1.000	-
	Gelman-Rubin						-
	Convergence upper CI	1.000	1.000	1.000	1.000	1.000	-
M4	mean	0.870	1.003	0.313	-0.133	-0.008	-0.011
	median	0.768	0.912	0.311	-0.152	-0.012	0.006
	95% CI	[0.059 - 2.244]	[0.063 - 2.477]	[0.095 - 0.527]	[-0.665 - 0.501]	[-0.880 - 0.873]	[-0.957 - 0.952]
	Gelman-Rubin						-
	Convergence estimate	1.000	1.000	1.000	1.010	1.000	1.010
	Gelman-Rubin						-
	Convergence upper CI	1.000	1.000	1.010	1.040	1.000	1.050

Table 3: Estimated probability for fever treatment (mean and 95% Bayesian Credible Interval) at the nearest health facility. Data for health facilities represent public and private entities based on facility census 2009 [85] updated based on HMIS reports. Probability of use for fever treatment estimated from parameters of model 1

Region	Population estimate 2015 ¹	Estimated mean malaria incidence per 1000 population in 2014 ²	Estimated Average travel time to nearest health facility (minutes)	Probability of using a dispensary or clinic for fever treatment mean (95% CI)	Probability of using a health centre for fever treatment mean (95% CI)	Probability of using a Regional or district hospital for fever treatment mean (95% CI)
Zambezi	105,804	1.612	23.0	0.546 (0.369-0.671)	0.537 (0.369-0.667)	0.531 (0.369-0.661)
Kavango	259,984	1.467	29.7	0.513 (0.368-0.649)	0.498 (0.368-0.633)	0.503 (0.368-0.638)
Ohangwena	283,188	1.426	29.3	0.522 (0.368-0.650)	0.494 (0.367-0.630)	0.497 (0.368-0.632)
Oshikoto	210,881	1.256	37.3	0.504 (0.368-0.644)	0.492 (0.367-0.633)	0.496 (0.367-0.637)
Otjozondjupa	167,186	1.227	31.8	0.504 (0.368-0.643)	0.486 (0.367-0.623)	0.499 (0.368-0.637)
Omusati	281,050	1.131	35.6	0.513 (0.368-0.650)	0.497 (0.367-0.637)	0.498 (0.367-0.638)
Omaheke	82,441	1.126	38.3	0.490 (0.367-0.631)	0.496 (0.367-0.637)	0.493 (0.367-0.634)
Oshana	207,218	1.096	17.6	0.561 (0.369-0.677)	0.545 (0.369-0.661)	0.547 (0.369-0.663)
Kunene	102,986	0.967	146.4	0.433 (0.364-0.614)	0.426 (0.364-0.608)	0.429 (0.364-0.612)
Khomas ³	418,742	-	43.9	0.487 (0.367-0.636)	0.483 (0.367-0.631)	0.482 (0.367-0.631)
Karas ³	88,977	-	110.2	0.447 (0.365-0.619)	0.440 (0.365-0.613)	0.446 (0.365-0.618)
Hardap ³	93,447	-	86.7	0.471 (0.366-0.628)	0.470 (0.366-0.626)	0.461 (0.366-0.616)
Erongo ³	180,672	-	98.4	0.443 (0.365-0.620)	0.440 (0.365-0.618)	0.440 (0.365-0.617)

¹ Population estimates derived from worldpop [20]

² Mean malaria incidence derived from Alegana et al. [86]

³ Regions designated as no malaria risk with case incidence of less than 1 per 10,000 population