APPENDIX 4. MODEL CODE AND EXAMPLE EQUATION

We developed the model code using R version. The code is hosted in a publicly-available repository located at https://github.com/ihmeuw/gf/tree/develop/impact_evaluation. The table below indicates the URL for the script that contains the equations that determine the model objects.

Model Name	URL for model code
DRC Malaria (first half)	https://github.com/ihmeuw/gf/blob/develop/impact_evaluation/drc/models/drc_malaria6.r
DRC Malaria (second half)	https://github.com/ihmeuw/gf/blob/develop/impact_evaluation/drc/models/drc_malaria_impact4.r
Guatemala TB	https://github.com/ihmeuw/gf/blob/develop/impact_evaluation/gtm/models/gtm_tb_pub.R
Senegal TB	https://github.com/ihmeuw/gf/blob/develop/impact_evaluation/sen/models/sen_tb_model1.R

The general form for equations in the model is a Bayesian structural equation model made up of linear regression equations with correlated error terms. The equations are fit using either gamma priors(1,1) or normal priors (mean 0 and precision 0.01) for each term. The code referenced in the table above contains the equations that determine each model. We provide an example below to assist the reader in translating between the equations from a narrative form to the code. The regression equations are run in parallel for each health zone.

Narrative form of Equation 1 from DRC model

> ITNs Received (#) ~ intercept + β_1* Lag of ITN mass distribution (\$) by Global Fund + β_2 * Lag of ITN continuous distribution (\$) by Global Fund + β_3 * Lag of ITN (\$) from other donors + β_4 * Date + β_5 *ITN Reporting Completeness

Coded form of Equation 1 from DRC model

```
ITN_received_cumulative ~ prior("dgamma(1,1)")*lag_exp_M1_1_cumulative
+ prior("dgamma(1,1)")*lag_exp_M1_2_cumulative +
prior("dgamma(1,1)")*lag_other_dah_M1_1_cumulative + date +
completeness_ITN_received
```