Multi100 Project

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1 Introduction

This document reports on a contribution (ID: YMESM) to the **Multi100 Project** of the Center for Open Science. The re-analysis concerns the following paper:

Cohen, J., Dupas, P., & Schaner, S. (2015). Price subsidies, diagnostic tests, and targeting of malaria treatment: evidence from a randomized controlled trial. *American Economic Review*, *105*(2), 609-45.

The study was a randomized controlled trial on the effect of price subsidies on access and uptake of a particular malaria treatment, artemisinin combination therapies (ACTs), between households. The focal claim to be assessed is: *'... a very high subsidy ... increases access [to antimalarials]'* (p. 609.). In this document, I first spell out the statistical approach of my re-analysis (Section 2), report key results (Section 3), and a brief conclusion (Section 4). Finally, I report supplementary plots (Section 5) and all `R` (R Core Team 2021, version 4.1.2) packages and dependencies used (Section 6).

2 Statistical model

Since the outcome – self-reported treatment of an illness episode with an ACT – is binary (either an ACT was used or it wasn't), we model the data with an aggregated binomial likelihood. That is, each row in the data set is a household. We fit two Bayesian multilevel regression models that are identical except that one collapses the ACT subsidies into a single variable and the other treats the subsidy levels as separate. We refer to the first model as `pAfit` and the second as `pBfit`, based on Table 2, Panel A and B, of the original study. We subset the data similarly to the original study, such that we 1) only focus on the first illness episode reported by each household subsequent to voucher distribution and 2) exclude households that were also provided with a subsidy for rapid diagnostic malaria tests (p. 627). Our choice of covariates is likewise fully informed by the original study.

In formal notation, our models take the following form, including prior distributions[1]:

$$y_i \sim \text{Binomial}(n_i, p_i) \tag{1}$$
$$\text{logit}(p_i) = \alpha_{\text{STRATUM}[i]} + \beta_{\text{STRATUM}[i]} A_i + \gamma H_i \tag{2}$$
$$H_i \sim \text{Normal}(\nu, \sigma_H) \tag{3}$$
$$\nu \sim \text{Normal}(0, 1) \tag{4}$$
$$\sigma_H \sim \text{Exponential}(1) \tag{5}$$
$$\alpha \sim \text{Normal}(0, 1.5) \tag{6}$$
$$\beta \sim \text{Normal}(0, 1) \tag{7}$$
$$\gamma \sim \text{Normal}(0, 1) \tag{8}$$

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[1]Note that we use a 'centered' multilevel parameterization in notation, but `brms` by default employ a 'non-centered' variant for computational efficiency.

where y is the binary outcome, and p is the probability of taking an ACT for the ith household (line 1). Since some households reported more than one illness episodes, we allow the number of illness episode n (i.e., the number 'trials' in the binomial model) to vary by household, denoted by subscript i. In the multilevel linear model (line 2), each randomization stratum gets its own varying intercept α_{STRATUM} and varying slopes for subsidy level β_{STRATUM}. We also include age of household head as a fixed effect γ, while we (line 3) impute missing values in household head age H with draws from a Normal distribution with mean ν and standard deviation σ_H estimated from the sample, which are themselves given weakly regularizing priors (line 4-5). The prior for the average intercept α and for the average slope of subsidy level β are both given weakly regularizing priors (line 6-7), as are the fixed effect of household head age, which is standardized and hence centered on zero (line 8).

The varying effects for randomization strata ensure *partial pooling* across strata, such that each stratum is simultaneously and proportionally *informing* and *informed by* the average intercept and slope estimates (cf., McElreath 2020). This reduces the risk of over-fitting and improves computational efficiency. Partial pooling is facilitated via a variance-covariance matrix with multivariate Gaussian priors, where $\mathbf{S}$ is a diagonal matrix of intercept α and slope β, and $\mathbf{R}$ is their correlation matrix with a prior distribution of LKJcorr(4) (Lewandowski, Kurowicka, and Joe 2009). The standard deviations among intercepts σ_α and slopes σ_β are both given an Exponential(1) prior.

$$\begin{bmatrix} \alpha_{\text{STRATUM}} \\ \beta_{\text{STRATUM}} \end{bmatrix} \sim \text{Multivariate Normal}\left(\begin{bmatrix} \alpha \\ \beta \end{bmatrix}, \mathbf{S} \right)$$

$$\mathbf{S} = \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} \mathbf{R} \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix}$$

Analyses are conducted with the `brms` package (Bürkner 2017a, 2018a, 2021a), an interface to the probabilistic programming language `Stan` (Carpenter et al. 2017; Stan Development Team 2021a). MCMC diagnostics and posterior predictive checks were reasonable. Data wrangling and plotting are primarily facilitated by the `tidyverse` (H. Wickham et al. 2019), `ggplot2` (H. Wickham 2016), and `tidybayes` (Kay 2022b) packages[2]. The report is written in `R Markdown` (Allaire et al. 2021; Xie, Allaire, and Grolemund 2018a).

3 Results

Here, we report results. Our target quantity of interest is *the contrast in posterior predicted probabilities of taking an ACT between the price subsidy interventions compared to no subsidy.* This contrast is akin to an average treatment effect and we compute it (in percentage) as

$$\frac{\mathbb{E}(Y = 1|\text{Subsidy} = 1) - \mathbb{E}(Y = 1|\text{Subsidy} = 0)}{\mathbb{E}(Y = 1|\text{Subsidy} = 0)} \times 100$$

for each draw of the posterior distribution (in this case, 4000 post-warmup draws), which we then in turn summarize by its mode and 95% highest posterior density interval (HPDI; i.e., the smallest possible interval containing 95% of the parameter estimates). A positive contrast thus means that the subsidies increase the likelihood of taking an ACT. Further, the contrast marginalizes over the distribution of age as well as the randomization strata by simulating a counter-factual population, wherein all households were assigned to both the treatment and the control group while retaining covariates as observed[3]. This procedure is often referred to as *g-computation* or *standardisation.*

3.1 Any subsidy level & across subsidy levels

Figure 1 shows the computed contrast as a posterior predicted density for any amount of subsidy (`pAfit` model). Zero (the dotted line) represents equal chance of taking an ACT between the two groups.

[2]The package `renv` (Ushey 2022) ensures a reproducible package environment. See Section 6 for a list of `R` packages, their dependencies, and version number used for this project, created using `grateful` (Rodríguez-Sánchez, Jackson, and Hutchins 2022).

[3]For the households with missing values in age of household head, we get predictions for the posterior mean of the imputed values.

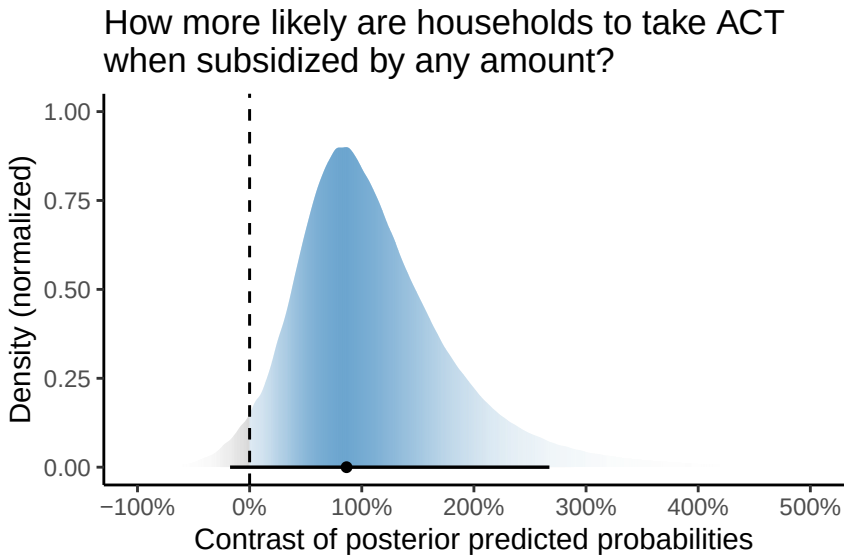

Figure 1: Results from `pAfit` model. Contrast in predicted probabilities of taking an ACT between the price subsidy intervention (any of the subsidy levels) compared to no subsidy. Zero (the dotted line) represents equal chance of taking an ACT between the two groups. The density is normalized and the gradient reflects posterior mass. The point represents the mode of the distribution with a 95% HPDI.

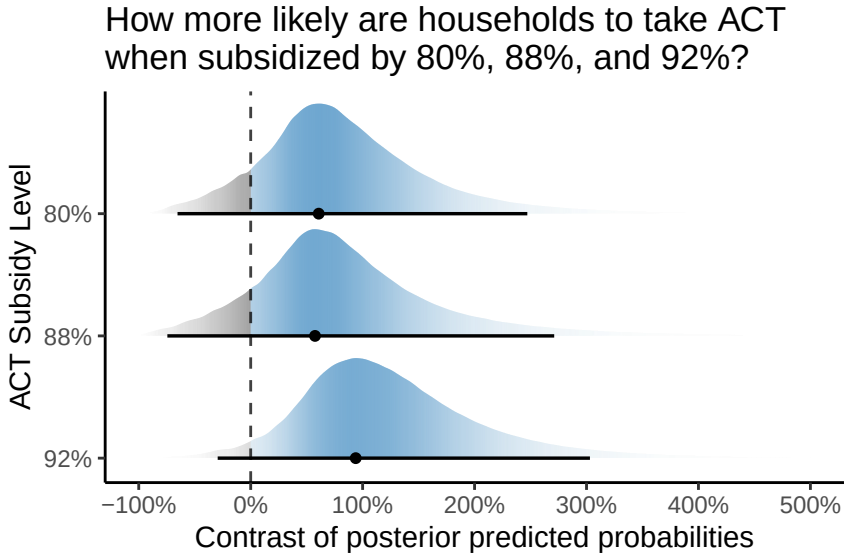

Figure 2: Results from `pBfit` model. Contrast in predicted probabilities of taking an ACT between the price subsidy intervention (for each subsidy level) compared to no subsidy. Zero (the dotted line) represents equal chance of taking an ACT between the treatment and control groups. The densities are normalized and the gradients reflect posterior mass. The point represents the mode of the distribution with a 95% HPDI.

The mode (black point) and 95% HPDI of the posterior predicted contrast between the treatment and the control group is thus 83.83% [-22.68, 266.95], or roughly a doubling with the bulk of the posterior mass being above zero. This is a substantial effect given that the posterior predicted base rate of taking ACT in the control group is 16.2% [2.6, 45.2].

Likewise, Figure 2 illustrates the computed contrast in posterior predicted probabilities across subsidy levels. The inference is very similar: there is roughly a doubling of chance of taking an ACT between the control and intervention groups, and the bulk of the posterior masses is above zero. Again, this is a substantial effect. While there is little difference between the three subsidy levels overall, perhaps unsurprisingly, the highest subsidy level (92%) has the highest posterior predicted change (94.73% [-32.59, 313.06]), with the effects of the 80% price subsidy (57.58% [-67.94, 250.66]) and the 88% price subsidy (64.8% [-79.97, 284.46]) being almost indistinguishable.

4 Conclusion

In conclusion, this re-analysis finds substantial evidence for the claim of the original study that *'... a very high subsidy ... increases access [to antimalarials]'* (p. 609.). Providing households with high price subsidies roughly doubles the chances of taking an ACT for an illness event with malaria-like symptoms, with a baseline likelihood of around 16%. This inference largely matches the original authors' findings, namely that '[s]ubsidies of 80 percent or more increase the likelihood that an illness is treated with an ACT by 16-23 percentage points (an 85-118 percent increase) [...]' (p. 628).

With that said, the present re-analysis yields a large degree of uncertainty in inference. This is at least partly due to the fact that the re-analysis marginalizes over the distribution of covariates. Excluding the random effects of strata (i.e., getting predictions for an average stratum and ignoring stratum-specific variance) reduces the uncertainty such that all 95% intervals no longer (or only barely) include zero (i.e., a 'statistically significant' difference; see Figures 3 and 4).

Note, finally, that given the overlap between the presently obtained results and those of the original study (and also due to time and timing), I did not attempt to replicate any follow-up analyses reported in the original study, such as the ones reported in their Panel A and B, Figure 4, where the self-reported data were cross-checked with observational and behavioral data. For the same reasons, I also did not attempt to replicate their baseline summary statistics (their Table 1). A reasonable balance between control and treatment groups is essential for the assumption of conditional exchangeability that underlies our average treatment effect estimates.

5 Supplementary plots

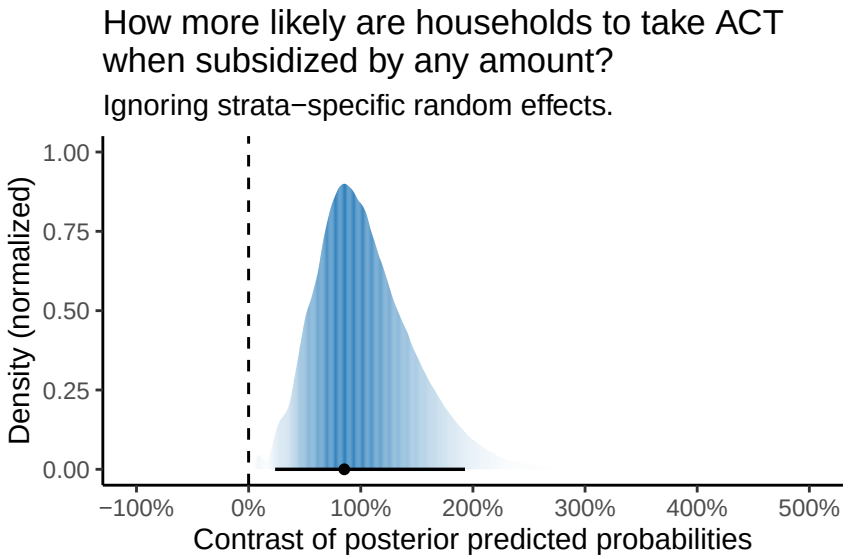

Figure 3: Same as Figure 1, but ignoring strata-specific random effects.

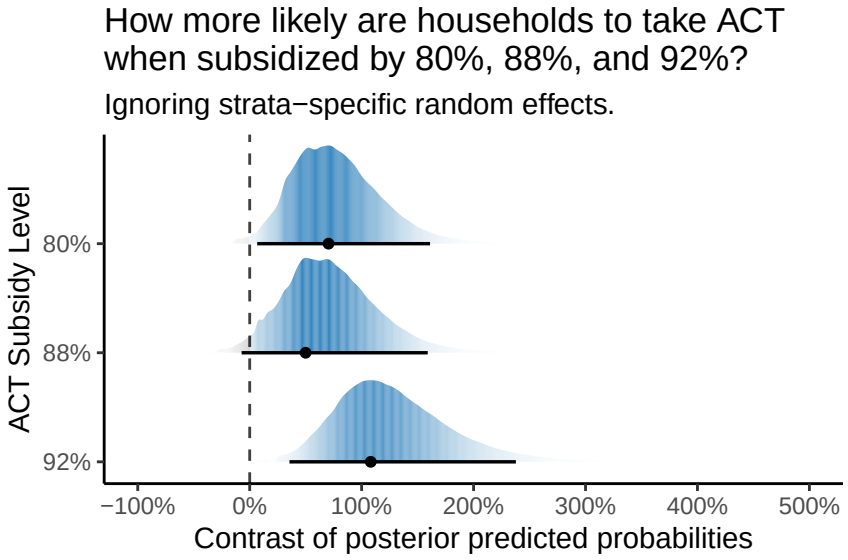

Figure 4: Same as Figure 2, but ignoring strata-specific random effects.

6 R packages and dependencies

We used R version 4.1.2 (R Core Team 2021) and the following R packages: abind v. 1.4.5 (Plate and Heiberger 2016), arrayhelpers v. 1.1.0 (Beleites 2020), backports v. 1.4.1 (Lang and R Core Team 2021), base64enc v. 0.1.3 (Urbanek 2015), bayesplot v. 1.8.1 (Gabry et al. 2019; Gabry and Mahr 2021), BH v. 1.78.0.0 (Eddelbuettel, Emerson, and Kane 2021), bit v. 4.0.4 (Oehlschlägel and Ripley 2020), bit64 v. 4.0.5 (Oehlschlägel and Silvestri 2020), bridgesampling v. 1.1.2 (Gronau, Singmann, and Wagenmakers 2020), brms v. 2.17.0 (Bürkner 2017b, 2018b, 2021b), Brobdingnag v. 1.2.7 (Hankin 2007), bslib v. 0.3.1 (Sievert and Cheng 2021a), cachem v. 1.0.6 (Chang 2021a), callr v. 3.7.0 (Csárdi and Chang 2021a), checkmate v. 2.0.0 (Lang 2017), clipr v. 0.8.0 (Lincoln 2022), coda v. 0.19.4 (Plummer et al. 2006), colorspace v. 2.0.3 (Zeileis, Hornik, and Murrell 2009; Stauffer et al. 2009; Zeileis et al. 2020), colourpicker v. 1.1.1 (Attali 2021a), commonmark v. 1.7 (Ooms 2018), cpp11 v. 0.4.2 (Hester and François 2021), crosstalk v. 1.2.0 (Cheng and Sievert 2021), desc v. 1.4.0 (Csárdi, Müller, and Hester 2021), digest v. 0.6.29 (Antoine Lucas et al. 2021), distributional v. 0.3.0 (O'Hara-Wild, Kay, and Hayes 2022), DT v. 0.20 (Xie, Cheng, and Tan 2021), dygraphs v. 1.1.1.6 (Vanderkam et al. 2018), ellipsis v. 0.3.2 (H. Wickham 2021), evaluate v. 0.15 (H. Wickham and Xie 2022), fansi v. 1.0.2 (Gaslam 2022), farver v. 2.1.0 (Pedersen, Nicolae, and François 2021), fastmap v. 1.1.0 (Chang 2021b), fontawesome v. 0.2.2 (Iannone 2021), fs v. 1.5.2 (Hester, Wickham, and Csárdi 2021), future v. 1.24.0 [@], generics v. 0.1.2 (H. Wickham, Kuhn, and Vaughan 2022), ggdist v. 3.1.1 (Kay 2022a), ggridges v. 0.5.3 (Wilke 2021), globals v. 0.14.0 (Bengtsson 2020), glue v. 1.6.1 (Hester and Bryan 2022), grateful v. 0.1.11 (Rodríguez-Sánchez, Jackson, and Hutchins 2022), gridExtra v. 2.3 (Auguie 2017), gtable v. 0.3.0 (H. Wickham and Pedersen 2019), gtools v. 3.9.2 (Warnes, Bolker, and Lumley 2021), HDInterval v. 0.2.2 (Meredith and Kruschke 2020), highr v. 0.9 (Xie and Qiu 2021), htmltools v. 0.5.2 (Cheng et al. 2021), htmlwidgets v. 1.5.4 (Vaidyanathan et al. 2021), httpuv v. 1.6.5 (Cheng and Chang 2022), igraph v. 1.2.11 (Csardi and Nepusz 2006), inline v. 0.3.19 (Sklyar et al. 2021), isoband v. 0.2.5 (Wilke and Pedersen 2021), jquerylib v. 0.1.4 (Sievert and Cheng 2021b), knitr v. 1.39 (Xie 2014, 2015, 2022a), labeling v. 0.4.2 (Justin Talbot 2020), later v. 1.3.0 (Chang and Cheng 2021), lazyeval v. 0.2.2 (H. Wickham 2019), lifecycle v. 1.0.1 (Henry and Wickham 2021), listenv v. 0.8.0 (Bengtsson 2019), loo v. 2.4.1 (Vehtari, Gelman, and Gabry 2017; Yao et al. 2017; Vehtari et al. 2020), markdown v. 1.1 (Allaire et al. 2019), matrixStats v. 0.61.0 (Bengtsson 2021a), mime v. 0.12 (Xie 2021a), miniUI v. 0.1.1.1 (Cheng 2018), munsell v. 0.5.0 (C. Wickham 2018), mvtnorm v. 1.1.3 (Genz and Bretz 2009; Genz et al. 2021), nleqslv v. 3.3.2 (Hasselman 2018), numDeriv v. 2016.8.1.1 (Gilbert and Varadhan 2019), parallelly v. 1.30.0 (Bengtsson 2021b), pkgbuild v. 1.3.1 (H. Wickham, Hester, and Csárdi 2021), pkgconfig v. 2.0.3 (Csárdi 2019), plyr v. 1.8.6 (H. Wickham 2011), posterior v. 1.2.0 (Vehtari et al. 2021; Bürkner et al. 2022), prettyunits v. 1.1.1 (Csardi 2020), processx v. 3.5.2 (Csárdi and Chang 2021b), progress v. 1.2.2 (Csárdi and FitzJohn 2019), promises v. 1.2.0.1 (Cheng 2021), ps v. 1.6.0 (Loden et al. 2021), R6 v. 2.5.1 (Chang 2021c), rappdirs v. 0.3.3 (Ratnakumar, Mick, and Davis 2021), RColorBrewer v. 1.1.2 (Neuwirth 2014), Rcpp v. 1.0.8 (Eddelbuettel and François 2011; Eddelbuettel 2013; Eddelbuettel and Balamuta 2018), RcppEigen v. 0.3.3.9.1 (Bates and Eddelbuettel 2013), RcppParallel v. 5.1.5 (Allaire, Francois, et al. 2022), renv v. 0.15.4 (Ushey 2022), reshape2 v. 1.4.4 (H. Wickham 2007), rmarkdown v. 2.14 (Xie, Allaire, and Grolemund 2018b; Xie, Dervieux, and Riederer 2020; Allaire, Xie, et al. 2022), rprojroot v. 2.0.2 (Müller 2020), rstan v. 2.21.3 (Stan Development Team 2021b), rstantools v. 2.1.1 (Gabry, Goodrich, and Lysy 2020), sass v. 0.4.1 (Cheng et al. 2022), scales v. 1.1.1 (H. Wickham and Seidel 2020), shiny v. 1.7.1 (Chang et al. 2021), shinyjs v. 2.1.0 (Attali 2021b), shinystan v. 2.5.0 (Gabry 2018), shinythemes v. 1.2.0 (Chang 2021d), sourcetools v. 0.1.7 (Ushey 2018), StanHeaders v. 2.21.0.7 (Stan Development Team 2020), stringi v. 1.7.6 (Gagolewski 2021a, 2021b), svUnit v. 1.0.6 (Grosjean 2021), tensorA v. 0.36.2 (van den Boogaart 2020), threejs v. 0.3.3 (Lewis 2020), tidybayes v. 3.0.2 (Kay 2022b), tidyselect v. 1.1.2 (Henry and Wickham 2022), tidyverse v. 1.3.1 (H. Wickham et al. 2019), tinytex v. 0.38 (Xie 2019, 2022b), tzdb v. 0.2.0 (Vaughan 2021), utf8 v. 1.2.2 (Perry 2021), vctrs v. 0.3.8 (H. Wickham, Henry, and Vaughan 2021), viridisLite v. 0.4.0 (Garnier et al. 2021), vroom v. 1.5.7 (Hester, Wickham, and Bryan 2021), withr v. 2.4.3 (Hester et al. 2021), xfun v. 0.29 (Xie 2021b), xtable v. 1.8.4 (Dahl et al. 2019), xts v. 0.12.1 (Ryan and Ulrich 2020), yaml v. 2.3.5 (Garbett et al. 2022), zoo v. 1.8.9 (Zeileis and Grothendieck 2005).

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