
Technical Appendix

Methods

We used Monte Carlo sampling with 1 million realizations to estimate case numbers and resources required. Each realization drew a value of the Guillain-Barré syndrome (GBS) baseline risk, the risk for Zika virus infection, the risk of GBS after Zika virus infection, and the relative incidence at the peak compared with an average week from the distributions specified in the previous section. Once these parameters were selected, the different components of our model were obtained as follows:

Total Number of Baseline and Zika Virus–Associated GBS Cases

The number of baseline GBS cases during the outbreak was sampled from a binomial process for the population of Puerto Rico with a probability equal to the baseline rate, assuming a time span of 1 year. The total number of Zika virus–associated GBS cases during the outbreak was sampled from a binomial process for the population of Puerto Rico with a probability equal to the product of the attack rate and the GBS risk after a Zika virus infection.

Number of Weekly Baseline GBS Cases in the Absence of Zika Virus

The mean number of weekly baseline GBS cases was sampled from a Poisson process with a mean equal to the total number of baseline GBS cases divided by 52, the number of weeks in a year.

Number of Zika Virus–Associated GBS Cases in an Average Week and Peak Week during Zika Virus Transmission

The mean number of weekly Zika virus–associated GBS cases was sampled from a Poisson process with a mean equal to the total number of Zika virus–associated cases divided by
the outbreak duration in weeks (52, the assumed length of the epidemic). The mean number of weekly Zika virus–associated GBS cases in the peak week was sampled by using a Poisson process. The mean was equal to the average number of Zika virus–associated cases per week multiplied by the relative sampled incidence at peak compared with an average week.

**Resource Needs for GBS Patients**

For each weekly estimate of cases, we estimated the proportion requiring different levels of healthcare from a binomial process with the respective probability (Technical Appendix Table) and the number of estimated cases.

**Code**

Estimates were generated using R (1). The following code was used:

```r
rm(list = ls())
require(data.table)
require(dplyr)
require(triangle)
set.seed(8675309)
n_samples <- 1e6
### fixed parameters
PR_population <- 3474182
GBS_long_term_care_fraction <- 0.45
GBS_IVIG_fraction <- 0.9
GBS_novent_ICU_fraction <- 0.2
GBS_vent_ICU_fraction <- 0.2
GBS_hosp_nonICU_fraction <- 0.6
zika_outbreak_duration_weeks <- 52
### simulation table
sim.data <- data.table(
```

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GBS_baseline_rate = rnorm(n_samples, 1.7e-5, 0.2e-5),

zika_attack_rate = rtriangle(n_samples, 0.1, 0.7, 0.25),

GBS_zika_rate = rnorm(n_samples, 1.6e-4, 0.31e-4),

peak_mean_weekly_incidence_ratio = runif(n_samples, 2, 4)

) %>%

mutate(

GBS_total_background_cases =
  rbinom(n_samples, PR_population, GBS_baseline_rate),

GBS_weekly_background_cases_mean =
  rpois(n_samples, GBS_total_background_cases / zika_outbreak_duration_weeks),

GBS_total_zika_cases =
  rbinom(n_samples, PR_population, zika_attack_rate * GBS_zika_rate),

GBS_weekly_zika_cases_mean =
  rpois(n_samples, GBS_total_zika_cases / zika_outbreak_duration_weeks),

GBS_total_cases = GBS_total_zika_cases + GBS_total_background_cases,

GBS_weekly_cases_mean = GBS_weekly_zika_cases_mean +
  GBS_weekly_background_cases_mean,

GBS_weekly_cases_peak = GBS_weekly_background_cases_mean +
  rpois(n_samples, GBS_weekly_zika_cases_mean *
  peak_mean_weekly_incidence_ratio),

GBS_total_cases_long_term = rbinom(n_samples, GBS_total_cases,
  GBS_long_term_care_fraction),

GBS_total_cases_background_long_term = rbinom(n_samples,
  GBS_total_background_cases,
  GBS_long_term_care_fraction)
get_resource_needs = function(GBS_weekly_cases) {

  output = rbind(
    data.table(Resource = “Cases per Week,”
                Value = GBS_weekly_cases),
    data.table(Resource = “Long-Term Care Patients,”
                Value = rbinom(n_samples, GBS_weekly_cases, GBS_long_term_care_fraction)),
    data.table(Resource = “Ventilators,”
                Value = rbinom(n_samples, GBS_weekly_cases, GBS_vent_ICU_fraction)),
    data.table(Resource = “IVIg per Week,”
                Value = rbinom(n_samples, GBS_weekly_cases, GBS_IVIG_fraction)),
    data.table(Resource = “Non-ICU Beds,”
                Value = rbinom(n_samples, GBS_weekly_cases, GBS_hosp_nonICU_fraction)),
    data.table(Resource = “ICU Beds,”
                Value = rbinom(n_samples, GBS_weekly_cases,
                              GBS_novent_ICU_fraction + GBS_vent_ICU_fraction)))

  return(output)
}

raw_weekly_resources <- rbind(
  cbind(get_resource_needs(sim.data$GBS_weekly_background_cases_mean),
        Estimate = “No Zika”),
  cbind(get_resource_needs(sim.data$GBS_weekly_cases_mean),
        Estimate = “Average Zika”),
  cbind(get_resource_needs(sim.data$GBS_weekly_cases_peak),
        Estimate = “Peak Zika”))
Estimate = “Peak Zika”) %>%
mutate(
Estimate = factor(Estimate, c("No Zika," "Average Zika," "Peak Zika")),
Resource = factor(Resource, c("Cases per Week," "Long-Term Care Patients,"
"IVIg per Week," "Ventilators," "Non-ICU Beds," "ICU Beds")))
### summarize
summarized_data <- raw_weekly_resources %>%
as.data.frame() %>%
group_by(Resource, Estimate) %>%
do({
quantile_frame =
data.frame(t(quantile(.Value, probs = c(0.025, 0.25, 0.5, 0.75, 0.975))))
colnames(quantile_frame) = c("Low," "IQR_Low," "Mid," "IQR_High," "High")
return(quantile_frame)
}) %>%
mutate(
Median = signif(Mid, 2),
IQR = paste0(signif(IQR_Low, 2), "–", signif(IQR_High, 2)),
`95% UI` = paste0(signif(Low, 2), "–", signif(High, 2))) %>%
select(Resource, Estimate, Median, IQR, `95% UI`) %>%
arrange(Resource, Estimate)
summarized_data[]
References
### Technical Appendix Table

Parameters used in the model for a study of Guillain-Barré syndrome and healthcare needs during Zika virus transmission, Puerto Rico, 2016

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimated value</th>
<th>Distribution</th>
<th>Source</th>
<th>Citation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Puerto Rico population, 2016</td>
<td>3,474,182</td>
<td>Fixed</td>
<td>US Census</td>
<td>US Census (2)</td>
</tr>
<tr>
<td>Baseline GBS rate</td>
<td>1.7/100,000 population/year</td>
<td>Gaussian, σ = 0.20</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Zika virus infection risk in Puerto Rico, 2016</td>
<td>25% peak probability</td>
<td>Triangle, min 10%, max 70%</td>
<td>Historic CHIKV and DENV epidemics in Puerto Rico</td>
<td>(3)</td>
</tr>
<tr>
<td>Fraction of Zika virus infections developing GBS</td>
<td>1.6/10,000 infections</td>
<td>Gaussian, σ = 0.31</td>
<td>Analysis of country-level GBS and Zika virus reports</td>
<td>(L. Mier-y-Teran, unpub. data) (3–5)</td>
</tr>
<tr>
<td>Relative Zika virus incidence during peak week compared with an average week</td>
<td>2–4 times</td>
<td>Uniform</td>
<td>Analysis of country-level GBS and Zika virus reports</td>
<td>(L. Mier-y-Teran, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing long-term care</td>
<td>45</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing IVIg</td>
<td>90</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing an ICU bed</td>
<td>40</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing an ICU bed and a ventilator</td>
<td>20</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing an ICU bed but no ventilator</td>
<td>20</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
<tr>
<td>Percentage of GBS patients needing a regular ward bed</td>
<td>60</td>
<td>Fixed</td>
<td>Chart review of Puerto Rico GBS patients</td>
<td>(J.L. Salinas, unpub. data)</td>
</tr>
</tbody>
</table>

*CHIKV, chikungunya virus; DENV, dengue virus; GBS, Guillain-Barré syndrome; ICU, intensive care unit; IVIg, intravenous immunoglobulin.