Project 2: Birth Year

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The next table summarizes, based on a survey, the number of children that had at least one dose of the Varicella vaccine. It gives the number of vaccinated children (Vaccinated) among the number of children in the survey (Sample Size). The information is provided for 3 regions of the US, and split according to birth cohort (2011-2020).

Table 1: Vaccination Data

Geography	Birth.Year	Vaccinated	Sample.Size	Coverage
Georgia	2011	196	219	0.895
Georgia	2012	248	270	0.919
Georgia	2013	261	276	0.946
Georgia	2014	252	284	0.887
Georgia	2015	276	306	0.902
Georgia	2016	311	334	0.931
Georgia	2017	265	292	0.908
Georgia	2018	246	282	0.872
Georgia	2019	251	273	0.919
Georgia	2020	165	188	0.878
Wisconsin	2011	207	225	0.920
Wisconsin	2012	205	226	0.907
Wisconsin	2013	212	235	0.902
Wisconsin	2014	195	224	0.871
Wisconsin	2015	231	262	0.882
Wisconsin	2016	246	275	0.895
Wisconsin	2017	215	238	0.903
Wisconsin	2018	214	241	0.888
Wisconsin	2019	197	224	0.879
Wisconsin	2020	156	177	0.881
Mississippi	2011	171	198	0.864
Mississippi	2012	208	230	0.904
Mississippi	2013	190	217	0.876
Mississippi	2014	215	239	0.900
Mississippi	2015	243	272	0.893
Mississippi	2016	276	307	0.899
Mississippi	2017	290	321	0.903
Mississippi	2018	242	276	0.877
Mississippi	2019	304	324	0.938
Mississippi	2020	161	181	0.890

Question 1

Derive analytically the posterior of the vaccination coverage per birth year and region. Use a conjugate prior that (1) reflects no knowledge on the vaccination coverage, and (2) reflects that vaccination coverage is typically around 90% or higher. Give posterior summary measures of the vaccination coverage per birth year and region. Is the choice of the prior impacting your results?

Answer:

The experiment can be model using a binomial likelihood:

$$P(x|\theta) = \binom{n}{x}\theta^x(1-\theta)^{n-x}$$

Where:

- x is the number of vaccinated children (observed data),
- n is the sample size (total number of children in the survey),
- θ is the vaccination rate (probability of a child being vaccinated), which is the parameter we want to estimate.

The conjugate prior of a binomial likelihood is a beta distribution. To reflect no knowledge on the vaccination coverage we can set α and β parameters of the *beta* prior distribution equal to 1. This gives us a uniform prior on θ, meaning that all values of vaccination rate are equally likely for $\theta \in [0, 1]$.

Indeed, given the beta distribution:

$$f(\theta; \alpha, \beta) = \frac{\theta^{\alpha-1}(1-\theta)^{\beta-1}}{B(\alpha, \beta)}$$

for α and β equal to 1, $f(\theta; \alpha, \beta)$ boils down to 1.

The posterior distribution can be found analytically using the formula:

$$P(\theta|x, n) \propto \theta^{x+\alpha-1}(1-\theta)^{n-x+\beta-1}$$

This is a Beta distribution with updated parameters:

$$P(\theta|x, n) \sim \text{Beta}(x + \alpha, n - x + \beta)$$

We now substitute x and n with the corresponding value per birth year and region and calculate the posterior summary measures as follows:

posterior mean

$$\text{Posterior Mean} = \frac{\alpha_{\text{posterior}}}{\alpha_{\text{posterior}} + \beta_{\text{posterior}}}$$

posterior variance

$$\text{Posterior Variance} = \frac{\alpha_{\text{posterior}} \cdot \beta_{\text{posterior}}}{(\alpha_{\text{posterior}} + \beta_{\text{posterior}})^2(\alpha_{\text{posterior}} + \beta_{\text{posterior}} + 1)}$$

posterior mode (if $\alpha_{\text{posterior}} > 1$ and $\beta_{\text{posterior}} > 1$)

$$\text{Posterior Mode} = \frac{\alpha_{\text{posterior}} - 1}{\alpha_{\text{posterior}} + \beta_{\text{posterior}} - 2}$$

We report the results for the first case (uninformative prior assumption) in table 2. We also plot the posterior densities for each year and each region in figure 1.

We now repeat the same procedure but we assume a prior density that reflects a vaccination rate of 90% or more as most likely. We set $\alpha = 18$ and $\beta = 2$ so that the mean and mode of the prior are around 0.9 or more (mean=0.9 and mode=0.944). Results are reported in table 3 and figure 2.

In this second case, since the prior and the likelihood tend to convey similar information, we observe a smaller posterior variance and also a tendency for higher values of posterior mean and median.

Final answer (short)

In conclusion the choice of the prior does impact the posterior density even if mildly in this specific case.

Table 2: Posterior summary measures with a non informative prior beta(1,1)

Geography	Birth.Year	posterior_mean	posterior_variance	posterior_mode
Georgia	2011	0.8914027	0.0004361	0.8949772
Georgia	2012	0.9154412	0.0002835	0.9185185
Georgia	2013	0.9424460	0.0001944	0.9456522
Georgia	2014	0.8846154	0.0003556	0.8873239
Georgia	2015	0.8993506	0.0002929	0.9019608
Georgia	2016	0.9285714	0.0001968	0.9311377
Georgia	2017	0.9047619	0.0002921	0.9075342
Georgia	2018	0.8697183	0.0003976	0.8723404
Georgia	2019	0.9163636	0.0002777	0.9194139
Georgia	2020	0.8736842	0.0005778	0.8776596
Wisconsin	2011	0.9162996	0.0003364	0.9200000
Wisconsin	2012	0.9035088	0.0003807	0.9070796
Wisconsin	2013	0.8987342	0.0003824	0.9021277
Wisconsin	2014	0.8672566	0.0005071	0.8705357
Wisconsin	2015	0.8787879	0.0004020	0.8816794
Wisconsin	2016	0.8916968	0.0003474	0.8945455
Wisconsin	2017	0.9000000	0.0003734	0.9033613
Wisconsin	2018	0.8847737	0.0004178	0.8879668
Wisconsin	2019	0.8761062	0.0004782	0.8794643
Wisconsin	2020	0.8770950	0.0005989	0.8813559
Mississippi	2011	0.8600000	0.0005990	0.8636364
Mississippi	2012	0.9008621	0.0003833	0.9043478
Mississippi	2013	0.8721461	0.0005069	0.8755760
Mississippi	2014	0.8962656	0.0003842	0.8995816
Mississippi	2015	0.8905109	0.0003545	0.8933824
Mississippi	2016	0.8964401	0.0002995	0.8990228
Mississippi	2017	0.9009288	0.0002755	0.9034268
Mississippi	2018	0.8741007	0.0003944	0.8768116
Mississippi	2019	0.9355828	0.0001843	0.9382716
Mississippi	2020	0.8852459	0.0005521	0.8895028

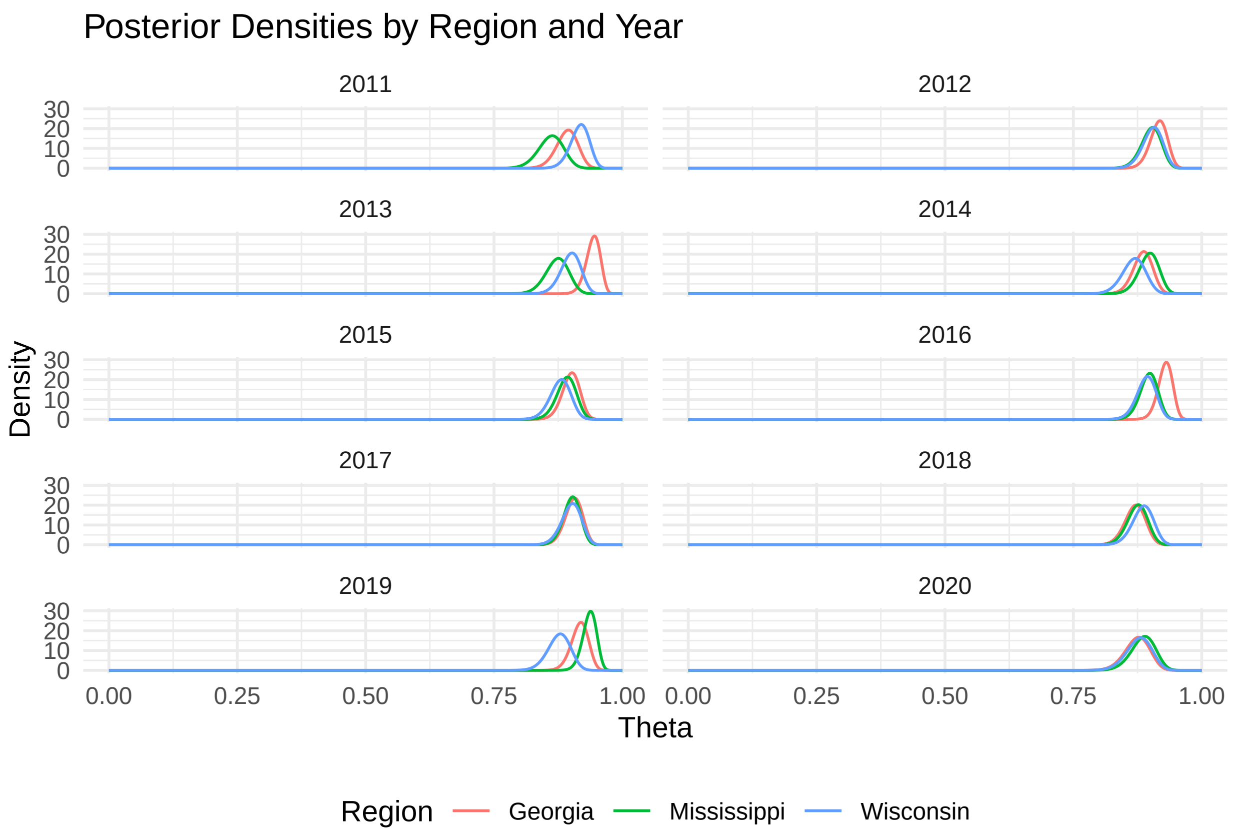


Figure 1: Posterior densities by region and year assuming a non informative prior.

Table 3: Posterior summary assuming a prior knowledge with beta(18,2)

Geography	Birth.Year	posterior_mean	posterior_variance	posterior_mode
Georgia	2011	0.8953975	0.0003903	0.8987342
Georgia	2012	0.9172414	0.0002609	0.9201389
Georgia	2013	0.9425676	0.0001823	0.9455782
Georgia	2014	0.8881579	0.0003257	0.8907285
Georgia	2015	0.9018405	0.0002707	0.9043210
Georgia	2016	0.9293785	0.0001849	0.9318182
Georgia	2017	0.9070513	0.0002694	0.9096774
Georgia	2018	0.8741722	0.0003630	0.8766667
Georgia	2019	0.9180887	0.0002558	0.9209622
Georgia	2020	0.8798077	0.0005060	0.8834951
Wisconsin	2011	0.9183673	0.0003048	0.9218107
Wisconsin	2012	0.9065041	0.0003431	0.9098361
Wisconsin	2013	0.9019608	0.0003454	0.9051383
Wisconsin	2014	0.8729508	0.0004527	0.8760331
Wisconsin	2015	0.8829787	0.0003651	0.8857143
Wisconsin	2016	0.8949153	0.0003177	0.8976109
Wisconsin	2017	0.9031008	0.0003379	0.9062500
Wisconsin	2018	0.8888889	0.0003770	0.8918919
Wisconsin	2019	0.8811475	0.0004275	0.8842975
Wisconsin	2020	0.8832487	0.0005208	0.8871795
Mississippi	2011	0.8669725	0.0005266	0.8703704
Mississippi	2012	0.9040000	0.0003458	0.9072581
Mississippi	2013	0.8776371	0.0004512	0.8808511
Mississippi	2014	0.8996139	0.0003473	0.9027237
Mississippi	2015	0.8938356	0.0003239	0.8965517
Mississippi	2016	0.8990826	0.0002766	0.9015385
Mississippi	2017	0.9032258	0.0002556	0.9056047
Mississippi	2018	0.8783784	0.0003597	0.8809524
Mississippi	2019	0.9360465	0.0001735	0.9385965
Mississippi	2020	0.8905473	0.0004825	0.8944724

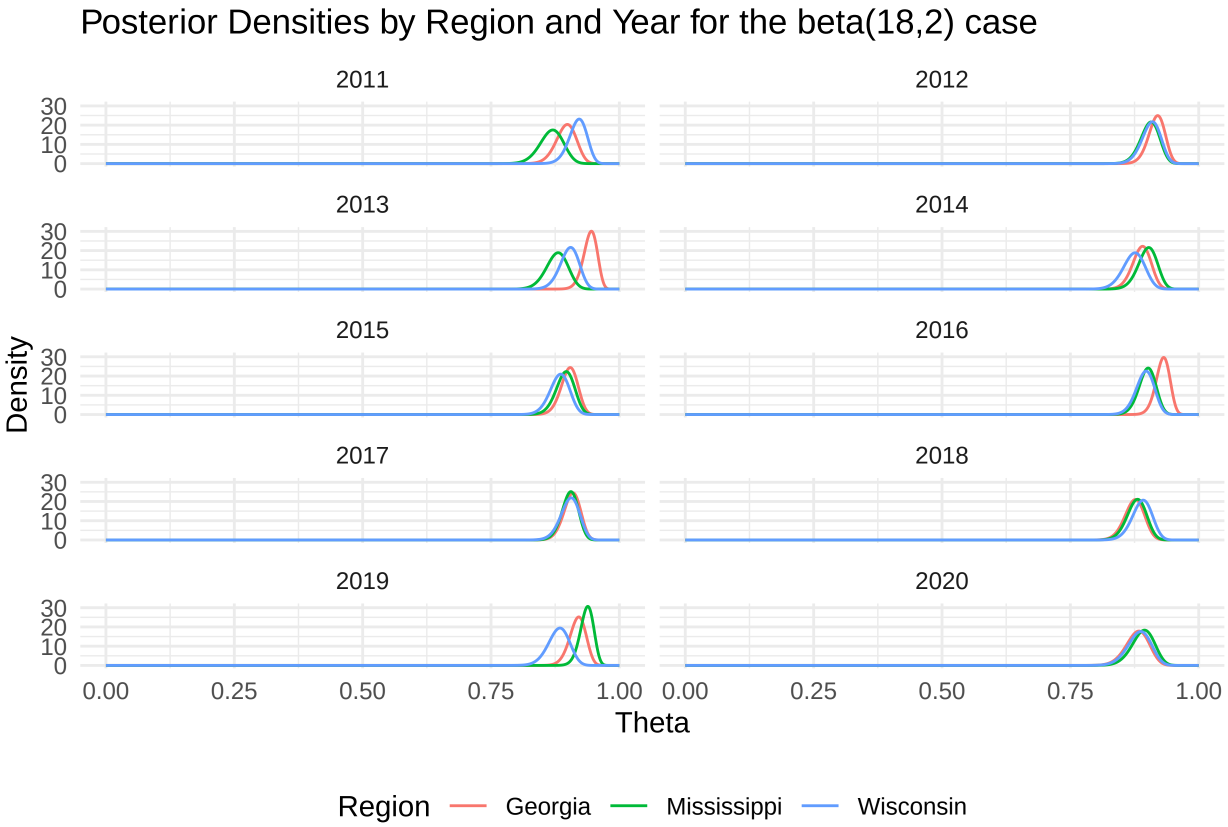


Figure 2: Posterior densities by region and year assuming an expected vaccination rate of 90% or higher.

Question 2

Investigate whether there is a change in the vaccination coverage over the birth years 2011-2019 using a logistic regression model:

$$Y_{ij} \sim Binom(\pi_{ij}, N_{ij})$$

with

$$\text{logit}(\pi_{ij}) = \beta_{0i} + \beta_{1i} \cdot \text{BirthYear}_j$$
$$\text{logit}(\pi_{ij}) = \log\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right)$$

where:

- i is the location,
- j is birth cohort,
- π_{ij} is the vaccination coverage.

Assume non-informative priors for the parameters to be estimated. Write and explain the code in BUGS language

Answer

The code written in BUGS language is provided below. First we specify the model structure. For each region and year cohort we ask to calculate the binomial likelihood by using a loop function (see chunk below).

```
for (i in 1:N_region) {  # Loop over regions
for (j in 1:N_year) {  # Loop over years (cohorts)
Y[i, j] ~ dbin(pi[i, j], N[i, j]) # Likelihood for region i and year j
```

Then we specify the logistic function. As it can be seen below we did not index the beta coefficients. This way only one intercept and one beta coefficient for the effect of year of birth will be calculated for all regions as requested in the question.

```
logit(pi[i, j]) <- beta0 + beta1 * BirthYear[j] # same beta0, beta1 for all regions
```

Then a non informative prior is specified. Since we are working with the logit of the vaccination rate, we cannot use a beta distribution as in question one, since this would be bounded between 0 and 1. The support for the logit of the vaccination rate is indeed $(-\infty, \infty)$. Therefore we use a normal distribution centered around zero but with very high variance. In BUGS language this means low precision (inverse of the variance), hence the code below.

```
# Non-informative priors for intercept and slope (shared across regions)
  beta0 ~ dnorm(0, 0.0001)
  beta1 ~ dnorm(0, 0.0001)
```

The rest of the code specifies the matrix to be used as data input and finally the model run commands. We used a burn-in of 500 (meaning that the first 500 samples are discarded), thinning equal to 2 (meaning only every other sample are retained), and then three chains are run. Since BUGS is a declarative language, we have to explicitly tell what the model structure is, then the software will automatically choose the Markov Chain Monte Carlo algorithm (by default Gibbs sampling).

```
# Run the model
fit <- jags(
  data = bugs_data,
  parameters.to.save = params,
  model.file = "logistic_model.bug",
  n.chains = 3,
  n.iter = 5000,
  n.burnin = 500,
  n.thin = 2
)
```

Overall, the full code is:

```
# Model structure assuming one intercept and one slope for all regions
model_structure <- "
model {
  for (i in 1:N_region) {  # Loop over regions
  for (j in 1:N_year) {  # Loop over years (cohorts)
  Y[i, j] ~ dbin(pi[i, j], N[i, j]) # Likelihood for region i and year j
  logit(pi[i, j]) <- beta0 + beta1 * BirthYear[j] # same beta0, beta1 for all regions
   }
  }

  # Non-informative priors for intercept and slope (shared across regions)
  beta0 ~ dnorm(0, 0.0001)
  beta1 ~ dnorm(0, 0.0001)
}
"
# Save the model structure in a text file
writeLines(model_structure, "logistic_model_Q.2.bug")

# Prepare the matrix for Y (vaccinated) and N (sample size)
# by region and year of birth
vacc_data_2019 <- vacc_data %>%
  filter( Birth.Year!= 2020)

Y <- matrix(vacc_data_2019$Vaccinated,
            nrow=length(unique(vacc_data_2019$Geography)), byrow=TRUE)

N <- matrix(vacc_data_2019$Sample.Size,
            nrow=length(unique(vacc_data_2019$Geography)), byrow=TRUE)


# Define the rows as regions and the columns as years
row.names(Y) <- unique(vacc_data_2019$Geography)
colnames(Y) <- min(vacc_data_2019$Birth.Year):max(vacc_data_2019$Birth.Year)

row.names(N) <- unique(vacc_data_2019$Geography)
```

```r
colnames(N) <- min(vacc_data_2019$Birth.Year):max(vacc_data_2019$Birth.Year)

bugs_data <- list(
  Y = Y,
  N = N,
  BirthYear = vacc_data_2019$Birth.Year,
  N_region = length(unique(vacc_data_2019$Geography)),
  N_year = length(unique(vacc_data_2019$Birth.Year))
)

# Parameters to monitor
params <- c("beta0", "beta1")

# Run the model
regression_Q2 <- jags(
  data = bugs_data,
  parameters.to.save = params,
  model.file = "logistic_model_Q.2.bug",
  n.chains = 3,
  n.iter = 5000,
  n.burnin = 500,
  n.thin = 2
)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 27
##    Unobserved stochastic nodes: 2
##    Total graph size: 114
##
## Initializing model
```

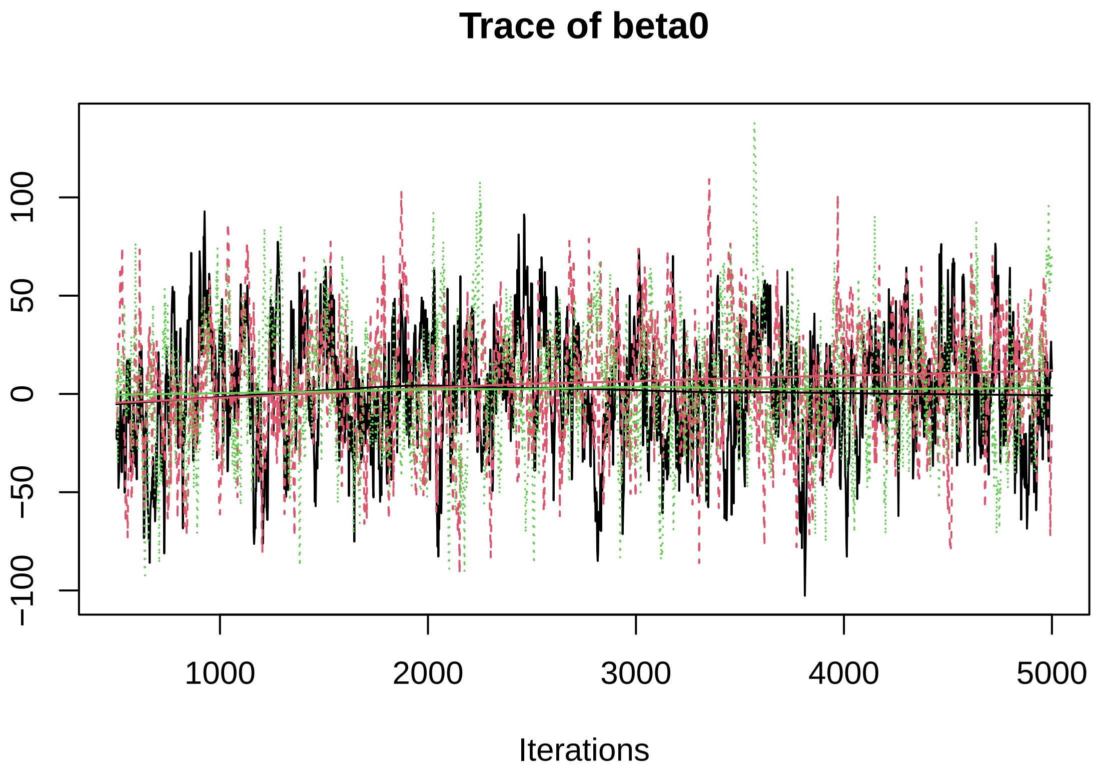
Question 3

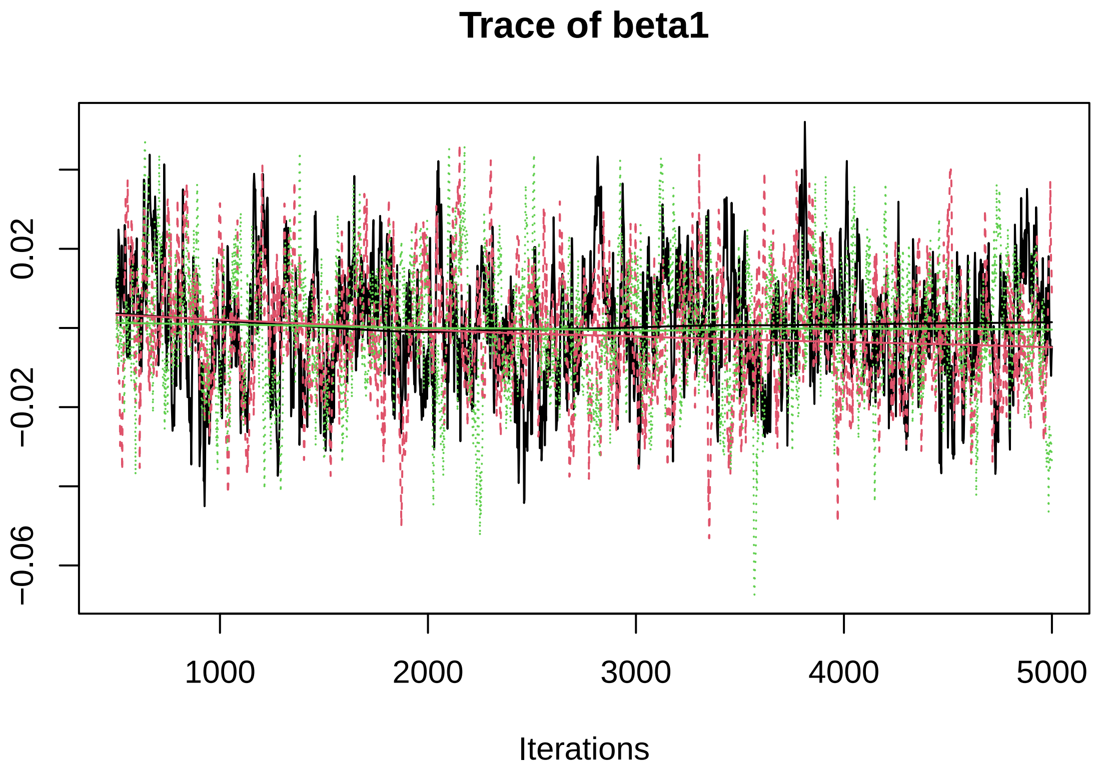
Run the MCMC method and check convergence of the MCMC chains. Give the details on how you checked convergence.

Answer

Looking at the trace plots below, for both β_0 and β_1 we can see that the chains jump around the same mean and visit different areas of the parameter space. No drift is apparent. All chains seem to oscillate within a similar range of values. A visual check favours a good convergence of the model.

We then present Gelman-Rubin diagnostic plots which compare the variance within each Markov chain to the variance between multiple chains.




Trace of beta1
0.02
−0.02
−0.06
1000
2000
3000
4000
5000
Iterations

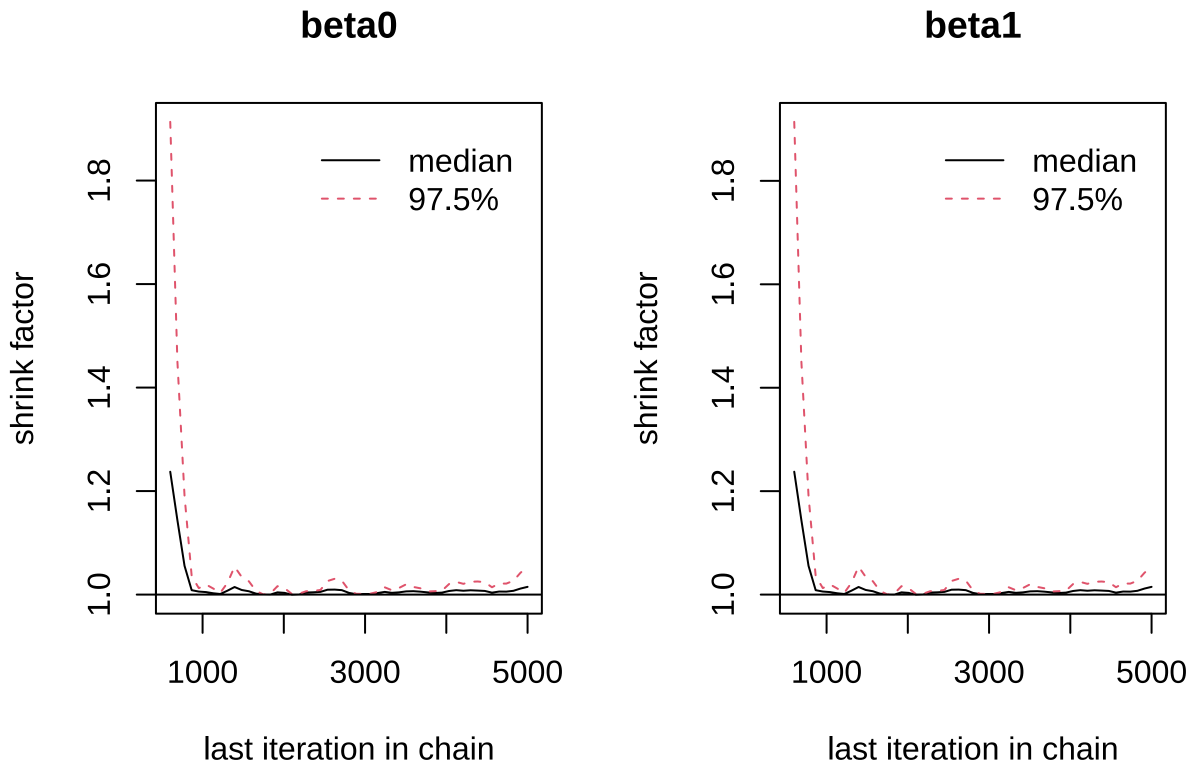


Figure 3: Gelman plots for the logistic model in question 2

The plot reports on the y axis the variance between multiple chains and traces its reduction as the iterations on the x axis increase. In essence, a decrease towards a value of 1 is a sign of convergence. In our case, for both β_0 and β_1 we see a quick drop of the shrink factor (variance within and between the chains for each parameter) before 1000 iterations and the shrink factor stabilizes around 1 thereafter particularly after 4000 iterations when also the 97.5th percentile of the shrink factor seems to be close to 1. This can be interpreted as a good convergence.

Final answer (short)

The convergence of the model has been inspected visually (traces plots) and numerically (Gelman's plot). Both tend to show a good convergence of the model.

Question 4

Make a plot of the posterior densities and give summary measures of the posterior distributions of the model parameters. Interpret the results.

Answer

The posterior density for β_0 should captures the baseline vaccination coverage when year of birth is zero. Therefore, here it does not have a direct interpretation in terms of vaccination coverage, but it is still necessary for the model. Looking at $\beta_1$posterior density we see that is centered very close to 0, and its mass spans both positive and negative values. This means that the effect of year of birth is limited and there is high uncertainty regarding its estimate. This might also be caused by the fact that we did re-scale the variable *year of birth* and consequently uncertainty gets amplified due to the large magnitude of the numerical value when taken as face value (see answer to questions 6 to 10 on this). Posterior summary measures for β_0 and β_1 are provided in table 3. If we then apply the inverse logit transformation to the linear predictor we can obtain the estimated vaccination coverage per year by using as β_0 and β_1 their mean. Data are reported in the table 4 below and indeed reflect an approximate vaccination around 90%.

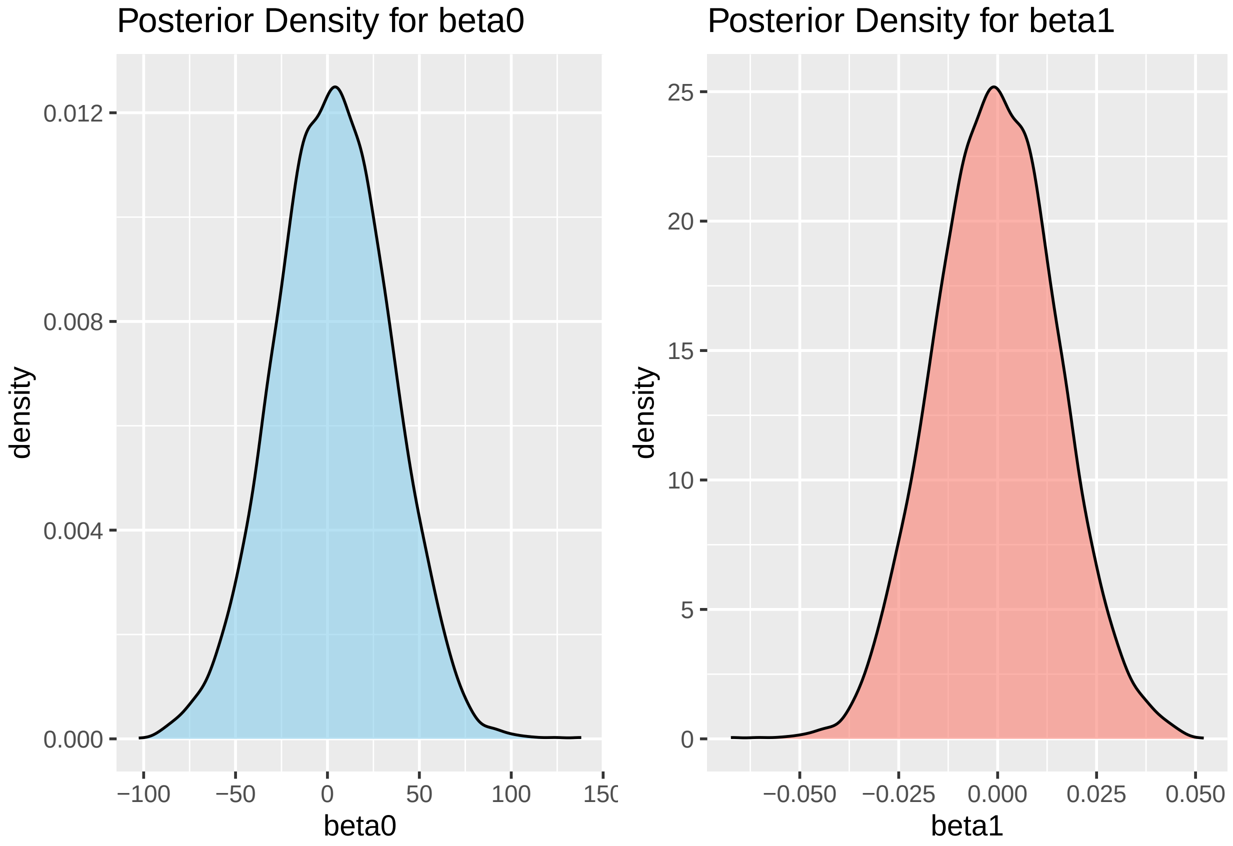


Table 4: Posterior summary measures for baysan regression model in Q.2

Parameter	Mean	Median	SD	Median Abs.Dev	5th Percentile	95th Percentile
beta0	2.8668	3.0923	31.0266	31.2018	-48.0892	53.8016
beta1	-0.0003	-0.0004	0.0154	0.0155	-0.0256	0.0249
deviance	170.5763	169.9648	1.9810	1.3859	168.7012	174.5050

Table 5: Vaccination coverage estimates per year based on model in Q2

Coverage	Year of birth
2011	90.06
2012	90.06
2013	90.06
2014	90.05
2015	90.05
2016	90.05
2017	90.05
2018	90.04
2019	90.04

Final answer (short)

The estimated effect of year on vaccination rates is close to zero with a very large credible interval that includes zero suggesting that there is no meaningful trend in vaccination rates over time.

Question 5

Give the posterior estimate of the vaccination coverage per birth year. Compare with the analytically results you obtained in Question 1.

Answer

Posterior estimate of the vaccination coverage per birth year calculated in question 1 assuming a non informative prior are reported below side by side with those estimated in question 4. Since in question 1 we actually had the break-down of the coverage per year and per region, we averaged the yearly data over the three regions for an easier comparison with question 4. The differences are small and mostly limited to approximately one percentage point.

Table 6: Vaccination coverage estimates per year based on model in Q1 and Q5

Yea of birth	estimate from Q1	estimate from Q5	difference (Q1-Q5)
2011	88.92	90.06	-1.14
2012	90.66	90.06	0.60
2013	90.44	90.06	0.38
2014	88.27	90.05	-1.78
2015	88.95	90.05	-1.10
2016	90.56	90.05	0.51
2017	90.19	90.05	0.14
2018	87.62	90.04	-2.42
2019	90.94	90.04	0.90

Question 6

Secondly, investigate whether the vaccination coverage trends are distinct at the different locations by adding a location-specific intercept and slope:

$$\text{logit}(\pi_{ij}) = \beta_{0i} + \beta_{1i} \cdot \text{BirthYear}_j$$

Use data from the years 2011-2019. Assume non-informative priors for the parameters to be estimated. Write the code in BUGS language. Give a brief summary of the convergence checks you performed. Give the posterior estimates of this model.

Answer

To evaluate whether trends in vaccination coverage differ across regions, we use a hierarchical logistic regression model. The number of vaccinated children in each region and birth year is assumed to follow a Binomial distribution with region-specific probabilities. In addition, we decided to re-scale the variable *year of birth* in the attempt of making the model numerically more stable and give to β_0 a more interpretable meaning. Years of birth were centered around their mean, without dividing by the standard deviation.

$$Y_{ij} \sim \text{Binomial}(\pi_{ij}, N_{ij})$$

$$\text{logit}(\pi_{ij}) = \beta_{0i} + \beta_{1i} \cdot \text{BirthYear}_j$$

$$\text{logit}(\pi_{ij}) = \log\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right)$$

Where:

- Y_{ij} is the number of vaccinated children in region i and year j,
- N_{ij} is the number of children surveyed in region i and year j,
- π_{ij} is the probability of being vaccinated,
- β_{0i} is the region-specific intercept, capturing baseline coverage,
- β_{1i} is the region-specific slope, capturing the change in coverage over time.

To reflect minimal prior knowledge, we use vague, non-informative priors for the intercepts and slopes:

$$\beta_{0i} \sim \text{Normal}(0, 0.001)$$

$$\beta_{1i} \sim \text{Normal}(0, 0.001)$$

This hierarchical model structure allows each region to have its own baseline coverage and trend while still sharing the same model form.

We implemented this model in **JAGS** using three MCMC chains with 5000 iterations, a burn-in of 500, and thinning of 2. Convergence was assessed using **trace plots** and **Gelman-Rubin diagnostics**, confirming good mixing and $\hat{R} \approx 1$ for all parameters.

```
model_structure <- "
model {
  for (i in 1:N_region) { # number of regions
    for (j in 1:N_year) { # number of year cohorts
      Y[i, j] ~ dbin(pi[i, j], N[i, j]) # likelihood
      logit(pi[i, j]) <- beta0[i] + beta1[i] * BirthYear[j] # regression
    }

    beta0[i] ~ dnorm(0, 0.001)
    beta1[i] ~ dnorm(0, 0.001)
  }
}
"

writeLines(model_structure, "logistic_model_q6B.bug")
```

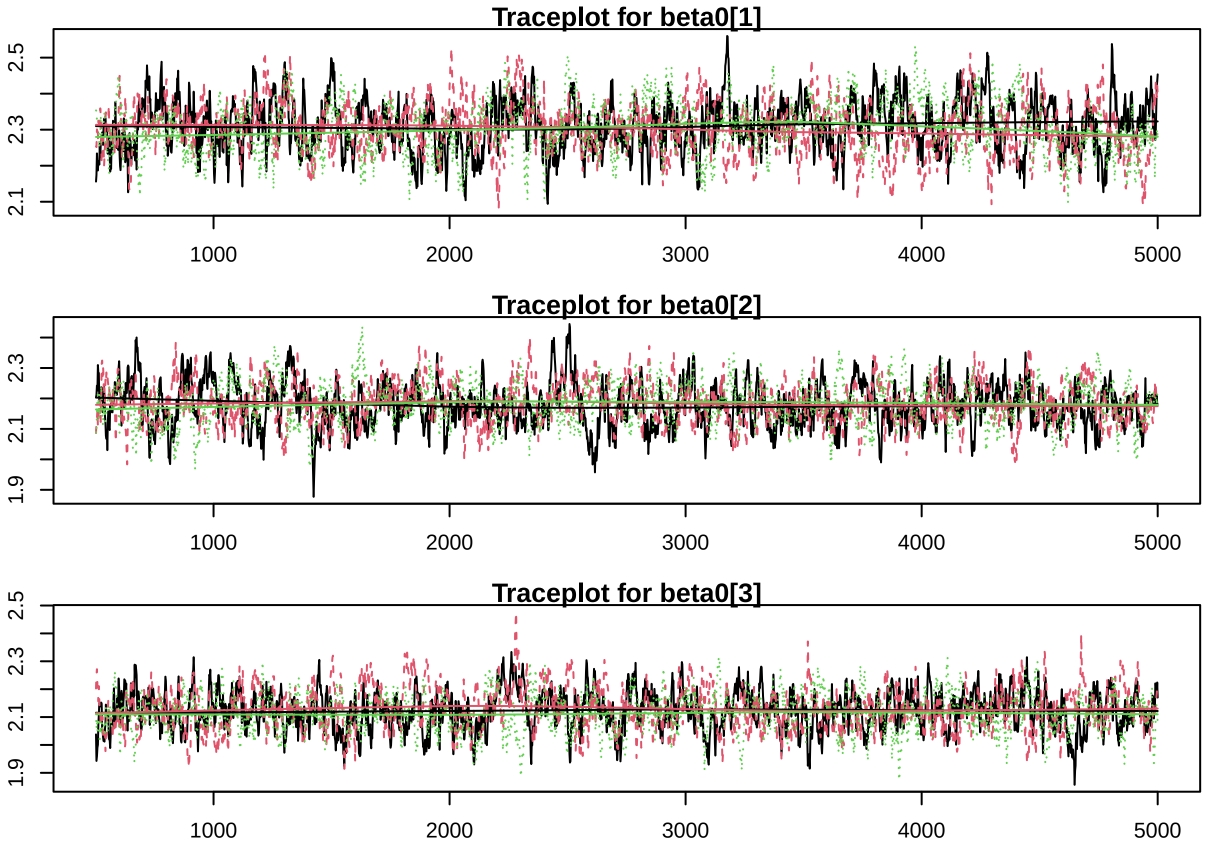
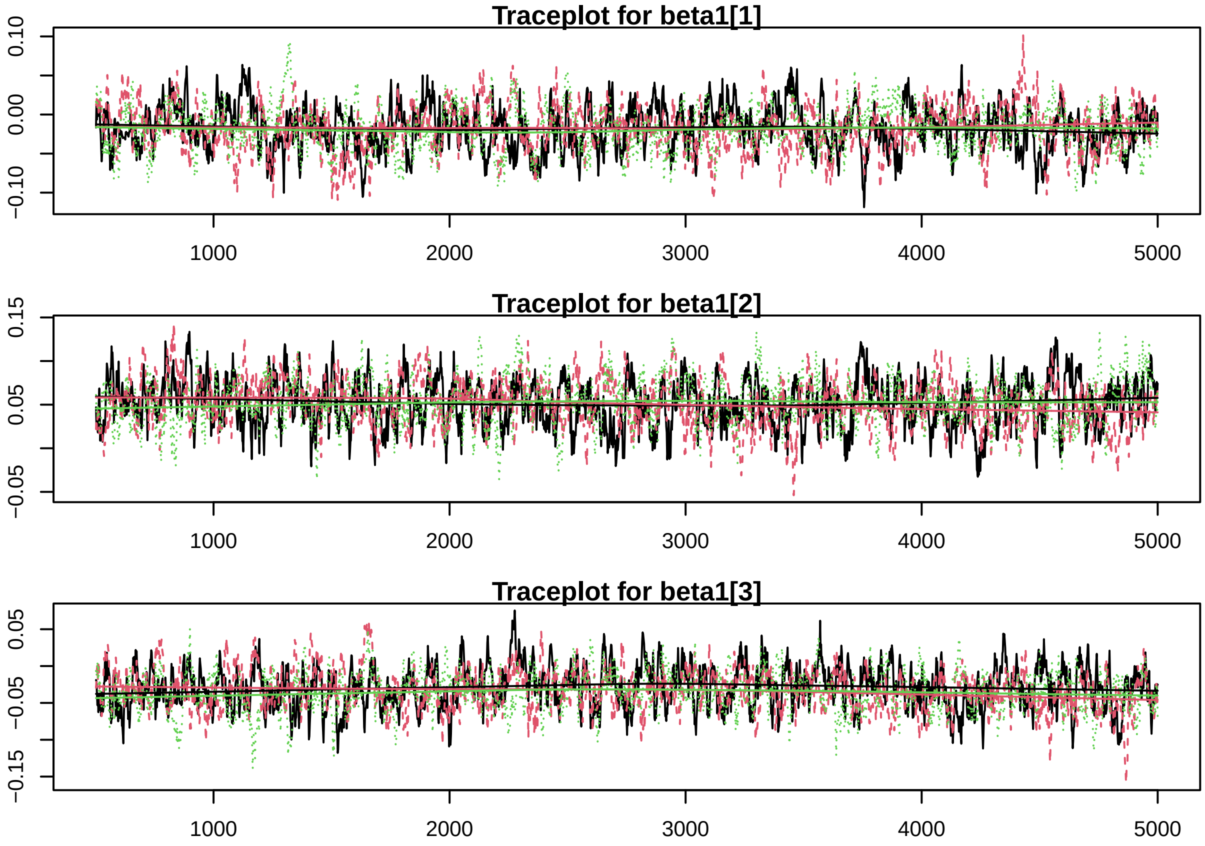


Figure 4: Trace plots for beta 0 for each region. From top to bottom: Georgia, Mississippi, Winsonsin.



Traceplot for beta1[1]

Traceplot for beta1[2]

Traceplot for beta1[3]

Figure 5: Trace plots for beta 1 for each region. From top to bottom: Georgia, Mississippi, Winsonsin.

Table 7: Posterior estimates of vaccination coverage (percent) by region and year

Region	Year_Scaled	Estimated Coverage (percent)	Year
Georgia	-4.5	91.58	2011
Mississippi	-4.5	87.53	2011
Wisconsin	-4.5	90.63	2011
Georgia	-3.5	91.44	2012
Mississippi	-3.5	88.08	2012
Wisconsin	-3.5	90.35	2012
Georgia	-2.5	91.30	2013
Mississippi	-2.5	88.61	2013
Wisconsin	-2.5	90.06	2013
Georgia	-1.5	91.15	2014
Mississippi	-1.5	89.13	2014
Wisconsin	-1.5	89.76	2014
Georgia	-0.5	91.01	2015
Mississippi	-0.5	89.62	2015
Wisconsin	-0.5	89.45	2015
Georgia	0.5	90.86	2016
Mississippi	0.5	90.09	2016
Wisconsin	0.5	89.14	2016
Georgia	1.5	90.71	2017
Mississippi	1.5	90.54	2017
Wisconsin	1.5	88.82	2017
Georgia	2.5	90.55	2018
Mississippi	2.5	90.98	2018
Wisconsin	2.5	88.48	2018
Georgia	3.5	90.40	2019
Mississippi	3.5	91.40	2019
Wisconsin	3.5	88.15	2019

Based on the visual inspection (Figure 4 and 5), the chains appear to fluctuate around the same mean value and do not show any clear drifting or trends, which is generally a good indicator of convergence.

For each of these parameters, there is a significant amount of mixing between chains (denoted by different colored lines). The chains appear to be exploring the parameter space independently while staying within the same range.

Question 7

What is the probability (a posteriori) that there is an increase in vaccination coverage (per location)?

Answer

Table 8: Posterior probability of increase in vaccination coverage per region

Region	Posterior Probability of Increase
Mississippi	0.9717
Georgia	0.2630
Wisconsin	0.1213

Interpretation

The posterior probabilities represent the likelihood that vaccination coverage is increasing in each region, based on the posterior distribution of the slope β_{1i}. A probability close to 1 suggests strong evidence of a positive trend over time, while values near 0.5 reflect uncertainty or no clear directional change. If a region exhibits a posterior probability above 0.95, it provides strong Bayesian evidence for an increase in vaccination coverage. On the other hand, probabilities near or below 0.5 may indicate stability or even a potential decline. In this case, Mississippi shows strong evidence for an increase in coverage, with a posterior probability greater than 0.95. This indicates a high degree of confidence (from a Bayesian perspective) that vaccination coverage is increasing in this region. By contrast, the probability is low in the other regions, underscoring a probable decrease or stagnation in coverage over the years, indeed in model from question two, when aggregating data from all regions (same intercept for all regions) the prediction was approximately 90% for all years.

Question 8

Make a plot of the estimated vaccination coverage (per location and birth year), including the uncertainty on the estimates. Include also the observed vaccination proportion in the plot.

Answer

The following plot shows the estimated vaccination coverage by region and birth year, along with 95% credible intervals for the model estimates.

As mentioned above, for this model we decided to re-scale the variable *year of birth*. Initially, when calculating the 95% credible interval using the row data set, we noticed that the inverse-logit transformation was unstable. Without appropriate scaling, the inverse-logit transformation of large linear predictors such as *year of birth* (2011-2020 treated a snumeric) produced very wide credible intervals approaching 0 and 1, therefore making them uninformative. Possible solutions could have been re-scaling of the variable *year of birth*; regularizing priors in order to reduce its variance and prevent implausible values; cap the range of the linear predictor before applying the inverse logit transformation. The first solution was chosen as it was computationally economic and also data driven.

Therefore, in the plot, observed rates are the white centered dots. Estimated credible intervals are represented by the shaded areas. Predicted coverage are the full triangular marks. Years are reported on centered scale where 2011 corresponds to -4.5 and 2019 to 3.5 with the other years at one unit interval.

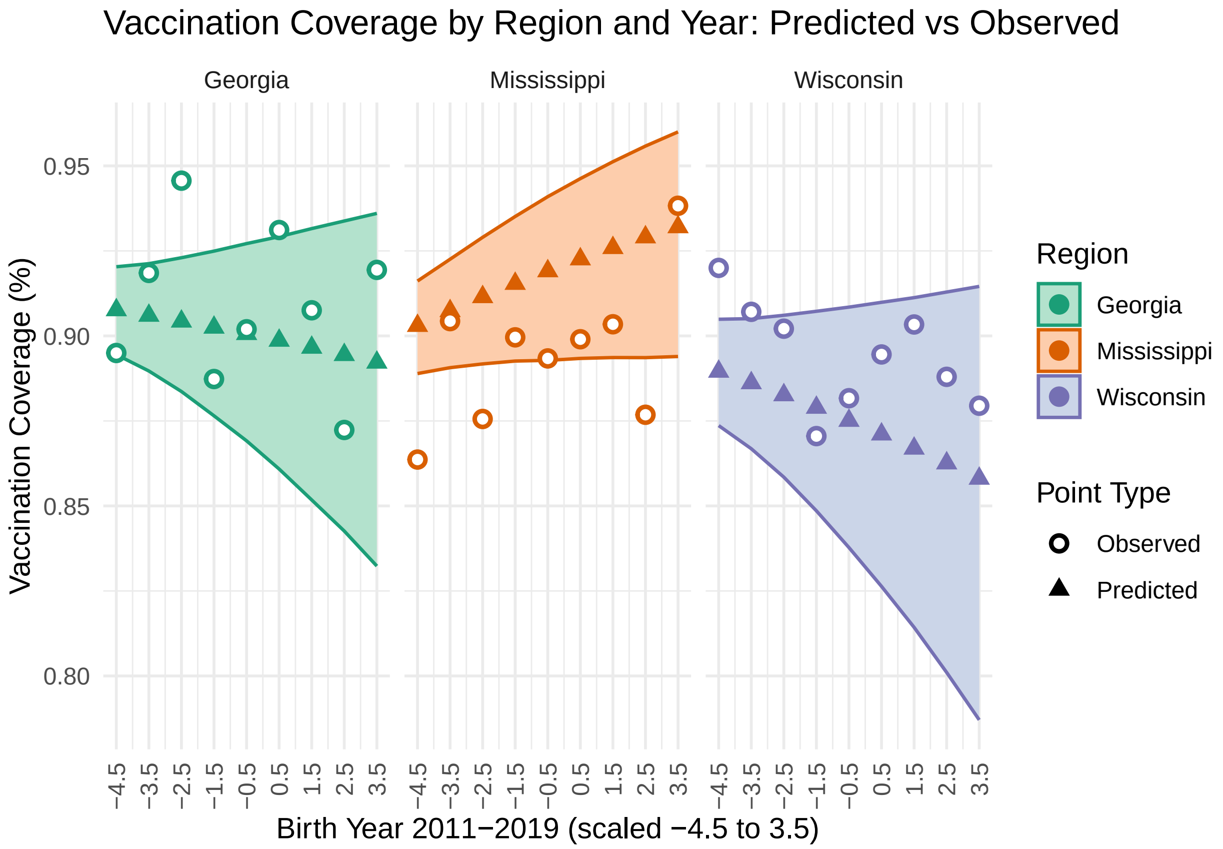


Figure 6: Estimated vaccination coverage by region and birth year. Observed rates are white centered dot, Shaded area: stimated credible interval; Full dots: predicted coverage. Years are reported on centered scale where 2011 corresponds to -4.5 and 2019 to 3.5 with the other years at one unit interval

Question 9

Investigate whether the observed number of vaccinated children in 2020 is in line with the expectations from earlier years. For this, compare the observed number of vaccinated children in 2020 with the prediction intervals for number of vaccinated children in 2020.

Answer

Table 9: Prediction intervals vs. observed number of vaccinated children in 2020

Region	Observed	Pred_Mean	Pred_Lower	Pred_Upper
Georgia	165	179.9932	172	186
Mississippi	161	176.2166	171	180
Wisconsin	156	166.7433	157	174

Interpretation

Table 9 compares the observed number of vaccinated children in 2020 with the predictive distributions derived from earlier years. For each region, the observed counts fall outside the 95% predictive intervals, indicating that actual vaccination numbers were consistently lower than what the model predicted for the year 2020.

Specifically, Georgia observed 165 vaccinations, which is below the lower bound of the 95% predictive interval [172, 186]. Mississippi observed 161, which is also below its interval [171, 180]. Wisconsin observed 156, falling below the lower bound of [158, 173].

These results suggest that vaccination counts in all three states were significantly lower than expected based on historical data and model predictions. This might indicate that year of birth is not a good predictor of vaccination coverage or that in 2020 other factors (not captured in the model) contributed to a change in the rate of vaccinated people.

Question 10

Make pairwise comparisons of the vaccination coverage in 2019 by estimating the ratio of the vaccination coverage in 2019 in two locations. Interpret the results.

Answer

Table 10 presents the pairwise mean ratios of vaccination coverage across regions in 2019. A ratio above 1 suggests that the region in the numerator has higher vaccination coverage than the one in the denominator; a ratio below 1 indicates the opposite. If the 95% credible interval includes 1, the difference is not statistically significant.

Georgia vs. Mississippi: The mean ratio is 0.958 with a 95% credible interval of [0.889, 1.019]. Since the interval includes 1, there is no strong evidence that vaccination coverage in Georgia differed from that in Mississippi.

Georgia vs. Wisconsin: The mean ratio is 1.045 with a credible interval of [0.952, 1.150]. Again, the interval includes 1, so the difference is not statistically significant, although the point estimate suggests slightly higher coverage in Georgia.

Mississippi vs. Wisconsin: The mean ratio is 1.090 with a 95% credible interval of [1.012, 1.190]. Since this interval does not include 1, we might conclude that Mississippi had significantly higher vaccination coverage than Wisconsin in 2019, despite the difference seems marginal.

These results indicate that among the three regions, only the difference between Mississippi and Wisconsin is statistically credible. Differences involving Georgia are inconclusive based on the posterior comparisons. Overall, the vaccination rates are similar across regions and years and actually fluctuate arund the mean value from one year to the other.

Table 10: Full posterior comparisons of vaccination coverage ratios in 2019

Comparison	Mean Ratio	Lower 95 CI	Upper 95 CI
Georgia / Mississippi	0.958	0.890	1.020
Georgia / Wisconsin	1.041	0.945	1.149
Mississippi / Wisconsin	1.088	1.006	1.187