# Sensitivity Analysis: Omitting Subsets of Variables

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## Contents

```
library(here)
```

```
## Warning in readLines(f, n): line 1 appears to contain an embedded nul
```

```
## Warning in readLines(f, n): incomplete final line found on '/Volumes/
## ALVINDRIVE2/flood-risk-health-effects/._flood-risk-health-effects.Rproj'
```

```
## here() starts at /Volumes/ALVINDRIVE2/flood-risk-health-effects
```

```
library(coda)
library(CARBayes)
```

```
## Loading required package: MASS
```

```
## Loading required package: Rcpp
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
library(ggplot2)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.0
## v readr   2.1.1      v forcats 0.5.1
## v purrr   0.3.4
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x dplyr::select() masks MASS::select()
```

```
fhs_model_df <- readRDS("intermediary_data/fhs_model_df_fr_and_pollute_pc.rds")

var_names <- c("Intercept", names(fhs_model_df[, 19:(ncol(fhs_model_df) - 4)]))
```

```
names_omit_svi <- var_names[!(var_names %in% c("EP_POV", "EP_UNEMP", "EP_PCI", "EP_NOHSDP",
                                             "EP_AGE65", "EP_AGE17", "EP_DISABL", "EP_SNGPNT",
                                             "EP_MINRTY", "EP_LIMENG", "EP_MUNIT", "EP_MOBILE",
                                             "EP_CROWD", "EP_NOVEH", "EP_GROUPQ"))]
```

Function for post-processing the inference

```
pc_idx <- 2:6
pc2flip <- c(-1, 1, -1, -1, -1)

post_flip <- function(beta_inf_subset, pc2flip) {
  names_temp <- colnames(beta_inf_subset)
  beta_inf_subset[pc2flip == -1, ] <- beta_inf_subset[pc2flip == -1, c(1, 3, 2)]
  colnames(beta_inf_subset) <- names_temp
  return(sweep(beta_inf_subset, 1, pc2flip, FUN = "*"))
}
```

# CAR model results, Coronary Heart Disease, Omitting SVI

Inference is based on 3 markov chains, each of which has been run for 110000 samples, the first 10000 of which has been removed for burn-in. The remaining 100000 samples are thinned by 2, resulting in 150000 samples for inference across the 3 Markov chains.

```
load(here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/CHD_omit_SVI.RData"))
```

## Beta samples

```
beta_samples <- mcmc.list(chain_list[[1]]$samples$beta, chain_list[[2]]$samples$beta,
                          chain_list[[3]]$samples$beta)
```

```
effectiveSize(beta_samples)
```

```
##        var1        var2        var3        var4        var5        var6 
## 118293.2136  19294.8213  17638.7457  26481.3651  33488.2709  36803.3486 
##        var7        var8        var9       var10       var11       var12 
##  25122.6708   1077.2927    629.9440    818.3618    310.6115    604.5310 
##       var13 
##  12494.0905
```

## Examining sigma2, nu2, rho

```
sigma2_samples <- mcmc.list(chain_list[[1]]$samples$sigma2, chain_list[[2]]$samples$sigma2,
                          chain_list[[3]]$samples$sigma2)

nu2_samples <- mcmc.list(chain_list[[1]]$samples$nu2, chain_list[[2]]$samples$nu2,
                          chain_list[[3]]$samples$nu2)
```

```
effectiveSize(sigma2_samples)
```

```
##     var1 
## 8506.588
```

```
effectiveSize(nu2_samples)
```

```
##     var1 
## 7001.059
```

## Examining a sample of the 3108 phi parameters

```
phi_samples <- mcmc.list(chain_list[[1]]$samples$phi, chain_list[[2]]$samples$phi,
                          chain_list[[3]]$samples$phi)
```

```
set.seed(1157, kind = "Mersenne-Twister", normal.kind = "Inversion", sample.kind = "Rejection")

phi_subset_idx <- sample(1:ncol(phi_samples[[1]]), size = 10)

phi_samples_subset <- phi_samples[, phi_subset_idx]
```

```
effectiveSize(phi_samples_subset)
```

```
##      var1      var2      var3      var4      var5      var6      var7      var8 
##  55330.46  28272.73  12741.53  83225.89 136580.70  90191.29  60974.97  90332.31 
##      var9     var10 
## 111332.19  57230.14
```

## Inference

```
beta_samples_matrix <- rbind(chain_list[[1]]$samples$beta, chain_list[[2]]$samples$beta,
                             chain_list[[3]]$samples$beta)

colnames(beta_samples_matrix) <- names_omit_svi
```

```
beta_inference <- round(t(apply(beta_samples_matrix, 2, quantile, c(0.5, 0.025, 0.975))),5)

# flipping the inference results according to the flipped PCs
beta_inference[pc_idx, ] <- post_flip(beta_inference[pc_idx, ], pc2flip)

beta_inference
```

```
##                          50%     2.5%    97.5%
## Intercept            6.66851  6.66278  6.67424
## flood_risk_pc1       0.06123  0.04511  0.07725
## flood_risk_pc2       0.00238 -0.01557  0.02047
## flood_risk_pc3       0.02183  0.00824  0.03552
## flood_risk_pc4      -0.00109 -0.01345  0.01117
## flood_risk_pc5       0.02138  0.00951  0.03318
## EP_UNINSUR          -0.06841 -0.08513 -0.05166
## pollute_conc_pc1    -0.24288 -0.30096 -0.18375
## pollute_conc_pc2    -0.51017 -0.59414 -0.42923
## pollute_conc_pc3    -0.36204 -0.43589 -0.28392
## tmmx                 0.02246 -0.10094  0.14309
## rmax                 0.11529  0.02433  0.20249
## Data_Value_CSMOKING  0.87054  0.84991  0.89070
```

```
saveRDS(beta_inference, file = here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/beta
```

List of significant beta coefficients:

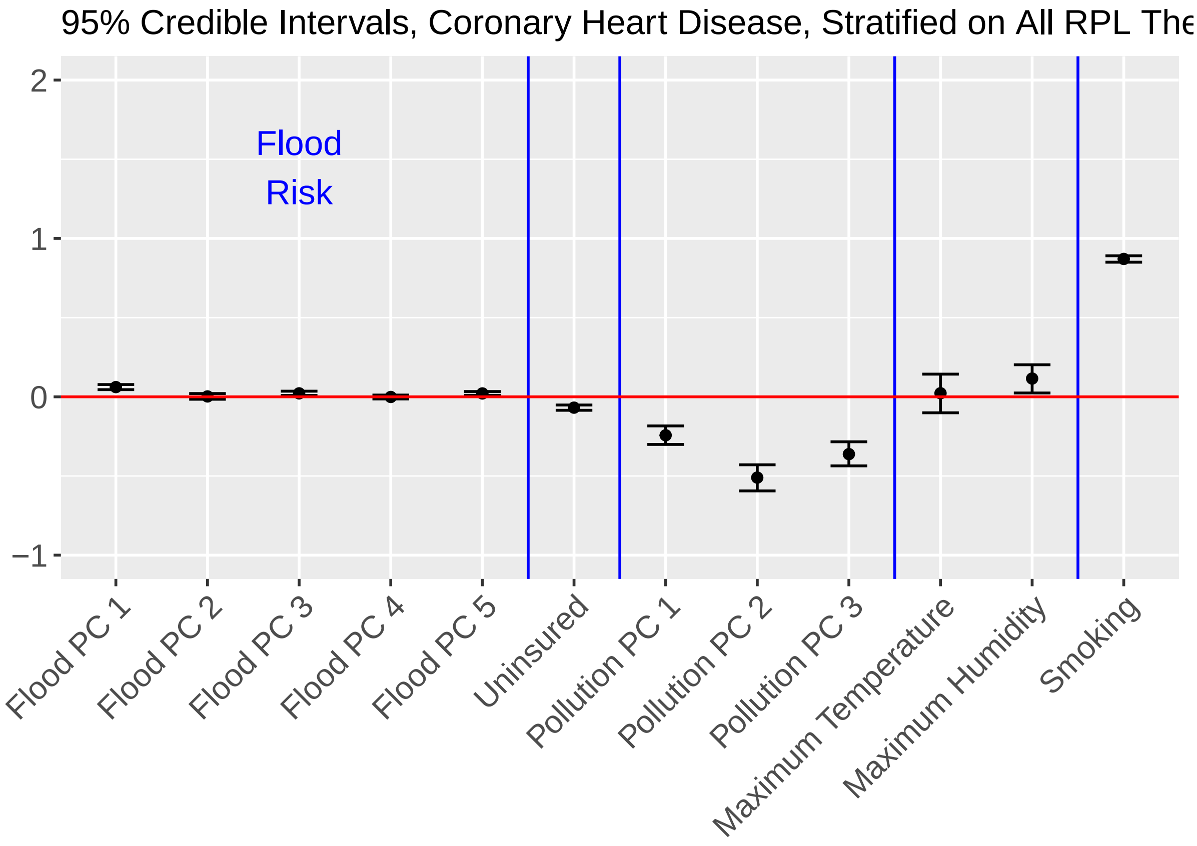
```
colnames(beta_samples_matrix)[sign(beta_inference[, 2]) == sign(beta_inference[, 3])]
```

```
##  [1] "Intercept"           "flood_risk_pc1"      "flood_risk_pc3"     
##  [4] "flood_risk_pc5"      "EP_UNINSUR"          "pollute_conc_pc1"   
##  [7] "pollute_conc_pc2"    "pollute_conc_pc3"    "rmax"               
## [10] "Data_Value_CSMOKING"
```

## Credible Interval plots for the coefficients, in ggplot

```
# first, process the beta_inference matrix in a form ggplot can understand

beta_inference_df <- as.data.frame(beta_inference)
beta_inference_df <- mutate(beta_inference_df, var_name = row.names(beta_inference_df))

beta_inference_df <- rename(beta_inference_df,
                            post_median = `50%`,
                            post_2.5 = `2.5%`,
                            post_97.5 = `97.5%`)

beta_inference_df$var_name <- factor(beta_inference_df$var_name, levels = beta_inference_df$var_name)
```

```
p <- ggplot(beta_inference_df[-1, ], aes(x = var_name, y = post_median)) +
  geom_point() +
  ylim(c(-1, 2)) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1), axis.title.x = element_blank(), axis
        axis.text=element_text(size=12),
        plot.margin = margin(5.5, 5.5, 5.5, 25)) +
  geom_errorbar(aes(ymin = post_2.5, ymax = post_97.5, width = 0.4)) +
  geom_vline(xintercept = c(5.5, 6.5, 9.5, 11.5), col = "blue") +
  geom_hline(yintercept = 0, col = "red") +
  annotate(geom = "text", x = 3, y = 1.45, label = "Flood\nRisk",
           col = "blue", size = 4.5) +
  scale_x_discrete(labels = c("Flood PC 1", "Flood PC 2", "Flood PC 3", "Flood PC 4", "Flood PC 5",
                              "Uninsured",
                              "Pollution PC 1", "Pollution PC 2", "Pollution PC 3",
                              "Maximum Temperature", "Maximum Humidity",
                              "Smoking")) + ggtitle("95% Credible Intervals, Coronary Heart Disease, St

p
```



```
ggsave(here("figures/final_figures/sensitivity_analysis/CHD_omit_SVI.pdf"),
       plot = p, device = "pdf",
       width = 8, height = 6, units = "in")
```

# CAR model results, High Blood Pressure, Omitting SVI

```
load(here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/BPHIGH_omit_SVI.RData"))
```

## Inference

```
beta_samples_matrix <- rbind(chain_list[[1]]$samples$beta, chain_list[[2]]$samples$beta,
                             chain_list[[3]]$samples$beta)

colnames(beta_samples_matrix) <- names_omit_svi
```

```
beta_inference <- round(t(apply(beta_samples_matrix, 2, quantile, c(0.5, 0.025, 0.975))),5)

# flipping the inference results according to the flipped PCs
beta_inference[pc_idx, ] <- post_flip(beta_inference[pc_idx, ], pc2flip)

beta_inference
```

```
##                           50%     2.5%    97.5%
## Intercept            32.36136 32.34803 32.37465
## flood_risk_pc1        0.05729  0.00802  0.10586
## flood_risk_pc2       -0.04157 -0.09604  0.01290
## flood_risk_pc3        0.05554  0.01386  0.09699
## flood_risk_pc4        0.01926 -0.01802  0.05619
## flood_risk_pc5        0.07317  0.03716  0.10898
## EP_UNINSUR           -0.27171 -0.32183 -0.22105
## pollute_conc_pc1     -1.00816 -1.19056 -0.82774
## pollute_conc_pc2     -2.41100 -2.67566 -2.14600
## pollute_conc_pc3     -0.30876 -0.55987 -0.06857
## tmmx                  0.01861 -0.41729  0.41541
## rmax                  0.10795 -0.19944  0.39392
## Data_Value_CSMOKING   2.15956  2.09580  2.22193
```

```
saveRDS(beta_inference, file = here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/beta
```

List of significant beta coefficients:

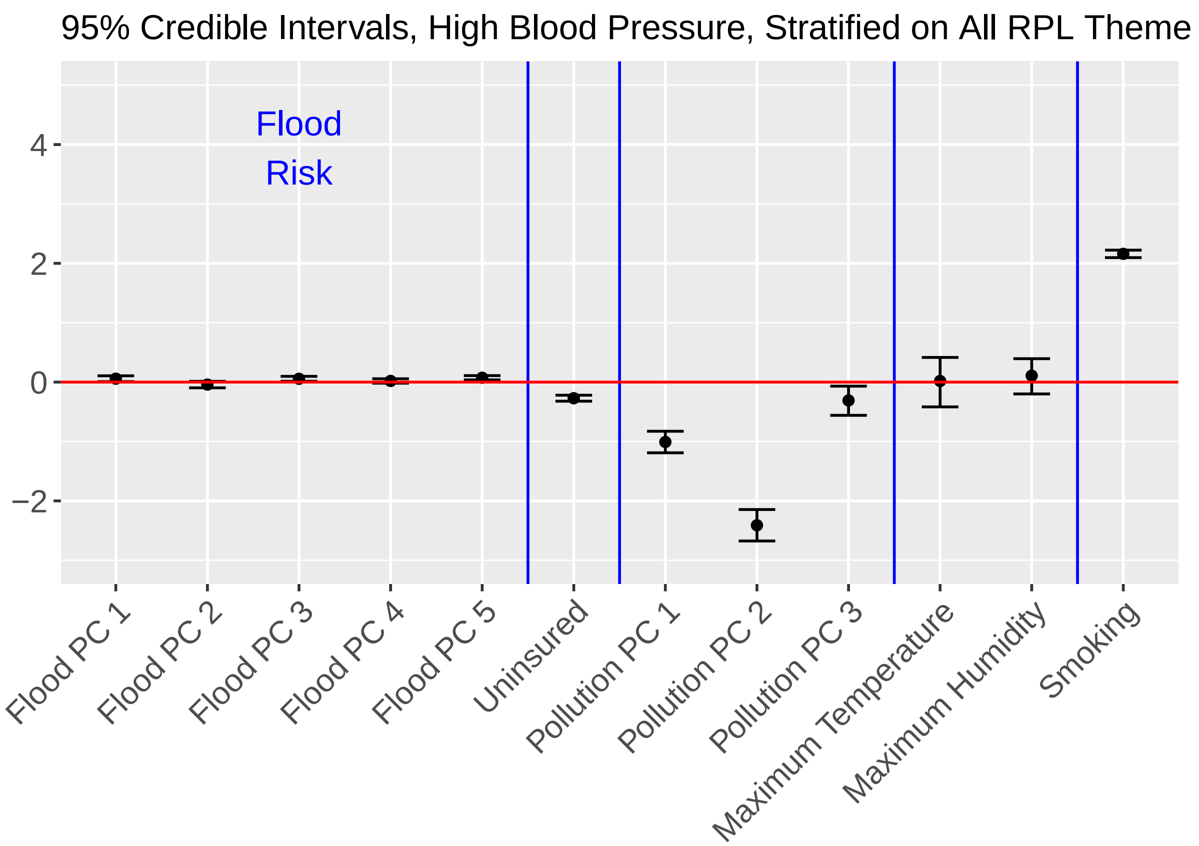
```
colnames(beta_samples_matrix)[sign(beta_inference[, 2]) == sign(beta_inference[, 3])]
```

```
## [1] "Intercept"           "flood_risk_pc1"      "flood_risk_pc3"
## [4] "flood_risk_pc5"      "EP_UNINSUR"          "pollute_conc_pc1"
## [7] "pollute_conc_pc2"    "pollute_conc_pc3"    "Data_Value_CSMOKING"
```

### Credible Interval plots for the coefficients, in ggplot

```r
# first, process the beta_inference matrix in a form ggplot can understand

beta_inference_df <- as.data.frame(beta_inference)

beta_inference_df <- mutate(beta_inference_df, var_name = row.names(beta_inference_df))

beta_inference_df <- rename(beta_inference_df,
                            post_median = `50%`,
                            post_2.5 = `2.5%`,
                            post_97.5 = `97.5%`)

beta_inference_df$var_name <- factor(beta_inference_df$var_name, levels = beta_inference_df$var_name)
```

```r
p <- ggplot(beta_inference_df[-1, ], aes(x = var_name, y = post_median)) +
  geom_point() +
  ylim(c(-3, 5)) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1), axis.title.x = element_blank(), axi
        axis.text=element_text(size=12),
        plot.margin = margin(5.5, 5.5, 5.5, 25)) +
  geom_errorbar(aes(ymin = post_2.5, ymax = post_97.5, width = 0.4)) +
  geom_vline(xintercept = c(5.5, 6.5, 9.5, 11.5), col = "blue") +
  geom_hline(yintercept = 0, col = "red") +
  annotate(geom = "text", x = 3, y = 3.95, label = "Flood\nRisk",
           col = "blue", size = 4.5) +
  scale_x_discrete(labels = c("Flood PC 1", "Flood PC 2", "Flood PC 3", "Flood PC 4", "Flood PC 5",
                              "Uninsured",
                              "Pollution PC 1", "Pollution PC 2", "Pollution PC 3",
                              "Maximum Temperature", "Maximum Humidity",
                              "Smoking")) + ggtitle("95% Credible Intervals, High Blood Pressure, Strat

p
```



```
ggsave(here("figures/final_figures/sensitivity_analysis/BPHIGH_omit_SVI.pdf"),
       plot = p, device = "pdf",
       width = 8, height = 6, units = "in")
```

## CAR model results, Asthma, Omitting SVI

```
load(here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/CASTHMA_omit_SVI.RData"))
```

### Inference

```
beta_samples_matrix <- rbind(chain_list[[1]]$samples$beta, chain_list[[2]]$samples$beta,
                             chain_list[[3]]$samples$beta)

colnames(beta_samples_matrix) <- names_omit_svi
```

```
beta_inference <- round(t(apply(beta_samples_matrix, 2, quantile, c(0.5, 0.025, 0.975))),5)

# flipping the inference results according to the flipped PCs
beta_inference[pc_idx, ] <- post_flip(beta_inference[pc_idx, ], pc2flip)

beta_inference
```

```
##                           50%     2.5%    97.5%
## Intercept             9.89994  9.89856  9.90131
## flood_risk_pc1      -0.01258 -0.01838 -0.00675
## flood_risk_pc2      -0.01449 -0.02099 -0.00807
## flood_risk_pc3       0.00440 -0.00055  0.00931
## flood_risk_pc4       0.01729  0.01292  0.02169
## flood_risk_pc5       0.00326 -0.00096  0.00750
## EP_UNINSUR          -0.06175 -0.06763 -0.05571
## pollute_conc_pc1     0.16658  0.14446  0.18857
## pollute_conc_pc2    -0.18127 -0.21124 -0.15203
## pollute_conc_pc3    -0.12326 -0.15211 -0.09590
## tmmx                 0.01235 -0.03431  0.06046
## rmax                -0.11750 -0.14901 -0.08471
## Data_Value_CSMOKING  1.30143  1.29417  1.30874
```

```r
saveRDS(beta_inference, file = here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/beta_
```

List of significant beta coefficients:

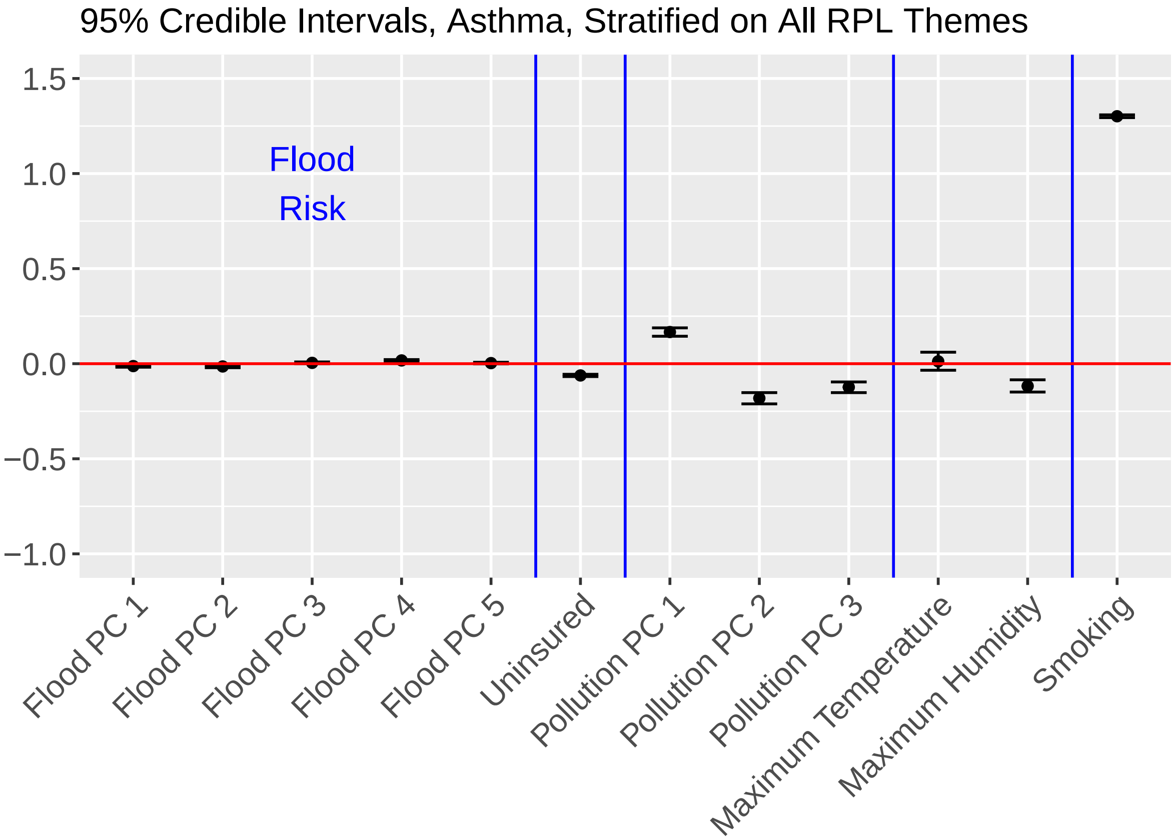
```r
colnames(beta_samples_matrix)[sign(beta_inference[, 2]) == sign(beta_inference[, 3])]
```

```
##  [1] "Intercept"           "flood_risk_pc1"      "flood_risk_pc2"
##  [4] "flood_risk_pc4"      "EP_UNINSUR"          "pollute_conc_pc1"
##  [7] "pollute_conc_pc2"    "pollute_conc_pc3"    "rmax"
## [10] "Data_Value_CSMOKING"
```

### Credible Interval plots for the coefficients, in ggplot

```r
# first, process the beta_inference matrix in a form ggplot can understand

beta_inference_df <- as.data.frame(beta_inference)

beta_inference_df <- mutate(beta_inference_df, var_name = row.names(beta_inference_df))

beta_inference_df <- rename(beta_inference_df,
                            post_median = `50%`,
                            post_2.5 = `2.5%`,
                            post_97.5 = `97.5%`)

beta_inference_df$var_name <- factor(beta_inference_df$var_name, levels = beta_inference_df$var_name)
```

```r
p <- ggplot(beta_inference_df[-1, ], aes(x = var_name, y = post_median)) +
  geom_point() +
  ylim(c(-1, 1.5)) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1), axis.title.x = element_blank(), axi
        axis.text=element_text(size=12),
        plot.margin = margin(5.5, 5.5, 5.5, 25)) +
  geom_errorbar(aes(ymin = post_2.5, ymax = post_97.5, width = 0.4)) +
  geom_vline(xintercept = c(5.5, 6.5, 9.5, 11.5), col = "blue") +
  geom_hline(yintercept = 0, col = "red") +
  annotate(geom = "text", x = 3, y = 0.95, label = "Flood\nRisk",
           col = "blue", size = 4.5) +
  scale_x_discrete(labels = c("Flood PC 1", "Flood PC 2", "Flood PC 3", "Flood PC 4", "Flood PC 5",
                              "Uninsured",
                              "Pollution PC 1", "Pollution PC 2", "Pollution PC 3",
                              "Maximum Temperature", "Maximum Humidity",
                              "Smoking")) + ggtitle("95% Credible Intervals, Asthma, Stratified on All

p
```



```
ggsave(here("figures/final_figures/sensitivity_analysis/CASTHMA_omit_SVI.pdf"),
       plot = p, device = "pdf",
       width = 8, height = 6, units = "in")
```

## CAR model results, Poor Mental Health, Omitting SVI

```
load(here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/MHLTH_omit_SVI.RData"))
```

### Inference

```
beta_samples_matrix <- rbind(chain_list[[1]]$samples$beta, chain_list[[2]]$samples$beta,
                          chain_list[[3]]$samples$beta)

colnames(beta_samples_matrix) <- names_omit_svi
```

```
beta_inference <- round(t(apply(beta_samples_matrix, 2, quantile, c(0.5, 0.025, 0.975))),5)

# flipping the inference results according to the flipped PCs
beta_inference[pc_idx, ] <- post_flip(beta_inference[pc_idx, ], pc2flip)
```

```
beta_inference
```

```
##                          50%     2.5%    97.5%
## Intercept           14.26066 14.25834 14.26298
## flood_risk_pc1      -0.00082 -0.01187  0.01005
## flood_risk_pc2       0.00330 -0.00879  0.01539
## flood_risk_pc3      -0.01693 -0.02603 -0.00790
## flood_risk_pc4       0.00957  0.00141  0.01773
## flood_risk_pc5      -0.00766 -0.01558  0.00022
## EP_UNINSUR           0.06135  0.05031  0.07251
## pollute_conc_pc1     0.69398  0.65341  0.73471
## pollute_conc_pc2     0.40920  0.35179  0.46701
## pollute_conc_pc3    -0.52482 -0.57923 -0.47073
## tmmx                 0.05782 -0.03127  0.14021
## rmax                -0.08589 -0.15206 -0.01127
## Data_Value_CSMOKING  3.34308  3.32955  3.35698
```

```
saveRDS(beta_inference, file = here("modeling_files/sensitivity_analysis/omit_subsets_of_variables/beta
```

List of significant beta coefficients:

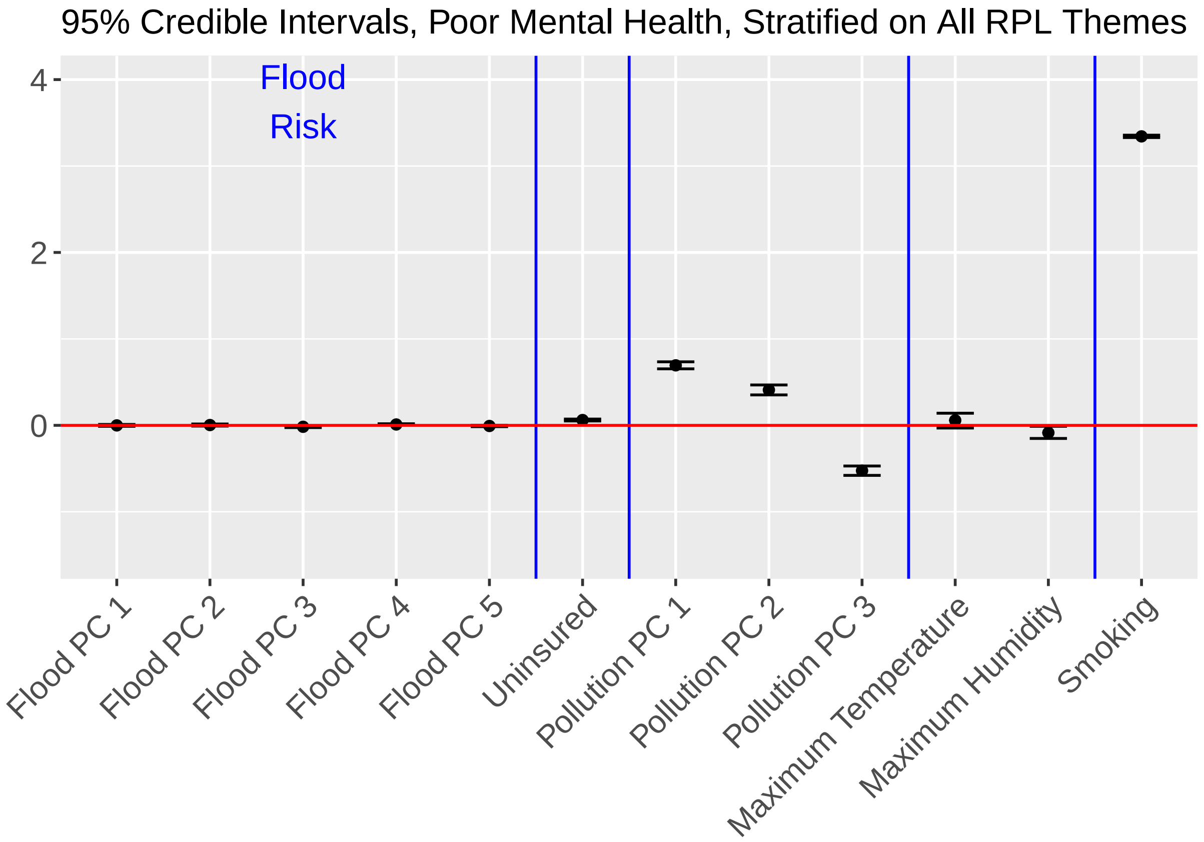
```
colnames(beta_samples_matrix)[sign(beta_inference[, 2]) == sign(beta_inference[, 3])]
```

```
## [1] "Intercept"           "flood_risk_pc3"      "flood_risk_pc4"
## [4] "EP_UNINSUR"          "pollute_conc_pc1"    "pollute_conc_pc2"
## [7] "pollute_conc_pc3"    "rmax"                "Data_Value_CSMOKING"
```

### Credible Interval plots for the coefficients, in ggplot

```
# first, process the beta_inference matrix in a form ggplot can understand

beta_inference_df <- as.data.frame(beta_inference)

beta_inference_df <- mutate(beta_inference_df, var_name = row.names(beta_inference_df))

beta_inference_df <- rename(beta_inference_df,
                            post_median = `50%`,
                            post_2.5 = `2.5%`,
                            post_97.5 = `97.5%`)

beta_inference_df$var_name <- factor(beta_inference_df$var_name, levels = beta_inference_df$var_name)
```

```
p <- ggplot(beta_inference_df[-1, ], aes(x = var_name, y = post_median)) +
  geom_point() +
  ylim(c(-1.5, 4)) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1), axis.title.x = element_blank(), axi
        axis.text=element_text(size=12),
        plot.margin = margin(5.5, 5.5, 5.5, 25)) +
  geom_errorbar(aes(ymin = post_2.5, ymax = post_97.5, width = 0.4)) +
  geom_vline(xintercept = c(5.5, 6.5, 9.5, 11.5), col = "blue") +
  geom_hline(yintercept = 0, col = "red") +
  annotate(geom = "text", x = 3, y = 3.75, label = "Flood\nRisk",
           col = "blue", size = 4.5) +
  scale_x_discrete(labels = c("Flood PC 1", "Flood PC 2", "Flood PC 3", "Flood PC 4", "Flood PC 5",
                              "Uninsured",
                              "Pollution PC 1", "Pollution PC 2", "Pollution PC 3",
                              "Maximum Temperature", "Maximum Humidity",
                              "Smoking")) + ggtitle("95% Credible Intervals, Poor Mental Health, Strati

p
```



```
ggsave(here("figures/final_figures/sensitivity_analysis/MHLTH_omit_SVI.pdf"),
       plot = p, device = "pdf",
       width = 8, height = 6, units = "in")
```