

# Basic CAR Model

Alvin Sheng

6/30/2021

```
library(here)

## here() starts at /Users/Alvin/Documents/NCSU_Fall_2021/NIH_SIP/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
```

## CAR model results

Inference is based on 3 markov chains, each of which has been run for 100000 samples, the first 10000 of which has been removed for burn-in. The remaining 90000 samples are thinned by 5, resulting in  $18000 \times 3 = 54000$  samples for inference across the 3 Markov chains.

```
load(here("modeling_files/model_3chains_var_exclude.RData"))
```

Output for the first chain is shown below.

```
chain1

##
## #####
## #### Model fitted
## #####
## Likelihood model - Gaussian (identity link function)
## Random effects model - Leroux CAR
## Regression equation - Y ~ X
## <environment: 0x7f8f8ca33700>
## Number of missing observations - 0
##
## #####
## #### Results
## #####
## Posterior quantities and DIC
##
##               Median    2.5%   97.5% n.effective Geweke.diag
## (Intercept)      77.7453 77.7253 77.7651      18000.0         1.9
```

```

## Xpct_fs_risk_2020_5      -0.1179 -0.2087 -0.0283      10734.0      1.1
## Xpct_floodfactor2        0.0171 -0.0283  0.0625      12960.6      0.8
## Xpct_floodfactor3       -0.0154 -0.0617  0.0308      12684.5     -0.5
## Xpct_floodfactor4        0.0479 -0.0024  0.0992       9935.2     -0.4
## Xpct_floodfactor5       -0.0196 -0.0827  0.0441      11001.7     -1.0
## Xpct_floodfactor6        0.0262 -0.0392  0.0918      12597.8      1.1
## Xpct_floodfactor7       -0.0120 -0.0623  0.0395      10856.9     -0.9
## Xpct_floodfactor8       -0.0144 -0.0583  0.0289      14894.6      0.1
## Xpct_floodfactor9        0.0877  0.0139  0.1609      11986.6     -1.1
## Xavg_risk_fsf_2020_100   0.1202  0.0388  0.2000       8785.6      0.2
## Xavg_risk_score_sfha     0.0083 -0.0430  0.0588      12590.9      1.9
## Xavg_risk_score_no_sfha -0.0063 -0.0954  0.0819      10668.5      0.3
## KEP_POV                  -0.1779 -0.2448 -0.1106      11811.2      0.4
## KEP_UNEMP                -0.0596 -0.1079 -0.0106      12352.9      1.1
## KEP_PCI                  0.2465  0.1733  0.3203      10025.0      0.5
## KEP_NOHSDP              -0.0541 -0.1368  0.0286       8373.5      0.0
## KEP_DISABL              -0.1211 -0.1789 -0.0630       9023.2     -1.2
## KEP_SNGPNT              -0.2182 -0.2656 -0.1727      14142.0      2.8
## KEP_MINRTY              -0.3378 -0.4233 -0.2514       5446.1     -0.7
## KEP_LIMENG               0.3492  0.2820  0.4150       8736.9     -0.3
## KEP_MUNIT               0.1100  0.0494  0.1697       8593.8     -0.1
## KEP_MOBILE              -0.0883 -0.1493 -0.0271       7809.0      0.8
## KEP_CROWD               -0.0735 -0.1215 -0.0249       9235.4     -1.1
## KEP_NOVEH               -0.1260 -0.1793 -0.0722      10100.2     -0.1
## KEP_GROUPQ              0.1105  0.0758  0.1454      14218.3      0.7
## KEP_UNINSUR             -0.0314 -0.0895  0.0286       7662.7     -0.4
## Xco                     -0.0954 -0.1659 -0.0265       4192.4      1.0
## Xno2                    -0.0193 -0.1204  0.0829       3562.1     -0.7
## Xo3                    -0.0394 -0.1733  0.0929        943.6     -0.3
## Xpm10                   0.1123  0.0308  0.1929       3248.1     -0.5
## Xpm25                   -0.2881 -0.4125 -0.1668       1405.1      0.6
## Xso2                    -0.0758 -0.1279 -0.0248       6256.1      1.3
## Xtotal_mean             -0.9107 -0.9826 -0.8377       6328.3      0.3
## nu2                     0.3197  0.2576  0.3815       1883.7     -0.3
## tau2                    1.8848  1.5878  2.2258       1910.0      0.1
## rho                     0.9924  0.9753  0.9992       7881.1      0.8
##
## DIC = 6926.558      p.d = 1660.539      LMPL = -3825.94

```

The smallest effective sample size is 935.8, for ozone (o3).

```
chain1$accept
```

```

##      beta      phi      nu2      tau2      rho
## 100.0000 100.0000 100.0000 100.0000 45.2697

```

It appears that beta, phi, nu2, and tau2 probably have Gibbs steps, whereas rho has a Metropolis-Hastings step. In any case, the acceptance probabilities are acceptable.

## Model Diagnostics

### Beta samples

```

beta_samples <- mcmc.list(chain1$samples$beta, chain2$samples$beta,
                          chain3$samples$beta)

saveRDS(beta_samples, file = here("modeling_files/model_3chains_var_exclude_beta_samples.rds"))

plot(beta_samples)

gelman.diag(beta_samples)

## Potential scale reduction factors:
##
##      Point est. Upper C.I.
## [1,]          1          1
## [2,]          1          1
## [3,]          1          1
## [4,]          1          1
## [5,]          1          1
## [6,]          1          1
## [7,]          1          1
## [8,]          1          1
## [9,]          1          1
## [10,]         1          1
## [11,]         1          1
## [12,]         1          1
## [13,]         1          1
## [14,]         1          1
## [15,]         1          1
## [16,]         1          1
## [17,]         1          1
## [18,]         1          1
## [19,]         1          1
## [20,]         1          1
## [21,]         1          1
## [22,]         1          1
## [23,]         1          1
## [24,]         1          1
## [25,]         1          1
## [26,]         1          1
## [27,]         1          1
## [28,]         1          1
## [29,]         1          1
## [30,]         1          1
## [31,]         1          1
## [32,]         1          1
## [33,]         1          1
## [34,]         1          1
##
## Multivariate psrf
##
## 1

```

## Examining tau2, nu2, rho

```
tau2_samples <- mcmc.list(chain1$samples$tau2, chain2$samples$tau2,  
                          chain3$samples$tau2)  
  
nu2_samples <- mcmc.list(chain1$samples$nu2, chain2$samples$nu2,  
                        chain3$samples$nu2)  
  
rho_samples <- mcmc.list(chain1$samples$rho, chain2$samples$rho,  
                        chain3$samples$rho)
```

```
plot(tau2_samples)
```

```
plot(nu2_samples)
```

```
plot(rho_samples)
```

```
gelman.diag(tau2_samples)
```

```
## Potential scale reduction factors:  
##  
##      Point est. Upper C.I.  
## [1,]          1          1
```

```
gelman.diag(nu2_samples)
```

```
## Potential scale reduction factors:  
##  
##      Point est. Upper C.I.  
## [1,]          1          1
```

```
gelman.diag(rho_samples)
```

```
## Potential scale reduction factors:  
##  
##      Point est. Upper C.I.  
## [1,]          1          1
```

## Examining a sample of the 3108 phi parameters

```
phi_samples <- mcmc.list(chain1$samples$phi, chain2$samples$phi, chain3$samples$phi)  
  
set.seed(1157, kind = "Mersenne-Twister", normal.kind = "Inversion", sample.kind = "Rejection")  
  
phi_subset_idx <- sample(1:3108, size = 10)  
  
phi_samples_subset <- phi_samples[, phi_subset_idx]
```

```
plot(phi_samples_subset)
```

```
gelman.diag(phi_samples_subset)
```

```
## Potential scale reduction factors:  
##  
##      Point est. Upper C.I.
```

```
## [1,]      1      1
## [2,]      1      1
## [3,]      1      1
## [4,]      1      1
## [5,]      1      1
## [6,]      1      1
## [7,]      1      1
## [8,]      1      1
## [9,]      1      1
## [10,]     1      1
##
## Multivariate psrf
##
## 1
```

## Inference

```
beta_samples_matrix <- rbind(chain1$samples$beta, chain2$samples$beta, chain3$samples$beta)
colnames(beta_samples_matrix) <- colnames(chain1$X)

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

```
##              50%      2.5%      97.5%
## (Intercept)    77.74541 77.72526 77.76547
## Xpct_fs_risk_2020_5 -0.11846 -0.20947 -0.02771
## Xpct_floodfactor2  0.01733 -0.02848  0.06292
## Xpct_floodfactor3 -0.01574 -0.06166  0.02993
## Xpct_floodfactor4  0.04814 -0.00219  0.09916
## Xpct_floodfactor5 -0.02001 -0.08280  0.04319
## Xpct_floodfactor6  0.02603 -0.03848  0.09156
## Xpct_floodfactor7 -0.01147 -0.06218  0.03928
## Xpct_floodfactor8 -0.01455 -0.05858  0.02901
## Xpct_floodfactor9  0.08748  0.01451  0.16079
## Xavg_risk_fsf_2020_100 0.12019  0.03839  0.20060
## Xavg_risk_score_sfha  0.00802 -0.04303  0.05908
## Xavg_risk_score_no_sfha -0.00614 -0.09451  0.08119
## XEP_POV          -0.17780 -0.24495 -0.11046
## XEP_UNEMP         -0.05955 -0.10768 -0.01091
## XEP_PCI           0.24681  0.17371  0.32026
## XEP_NOHSDP        -0.05413 -0.13624  0.02840
## XEP_DISABL        -0.12113 -0.17901 -0.06317
## XEP_SNGPNT        -0.21845 -0.26570 -0.17201
## XEP_MINRTY        -0.33722 -0.42218 -0.25146
## XEP_LIMENG         0.34887  0.28217  0.41493
## XEP_MUNIT         0.11002  0.04950  0.17033
## XEP_MOBILE        -0.08845 -0.14917 -0.02743
## XEP_CROWD         -0.07362 -0.12170 -0.02504
## XEP_NOVEH         -0.12598 -0.17966 -0.07259
## XEP_GROUPQ        0.11039  0.07611  0.14525
## XEP_UNINSUR       -0.03139 -0.09039  0.02834
## Xco              -0.09513 -0.16489 -0.02588
## Xno2             -0.01956 -0.12031  0.08103
```

```
## Xo3                -0.04186 -0.17364  0.09052
## Xpm10              0.11263  0.03151  0.19444
## Xpm25             -0.28796 -0.41248 -0.16528
## Xso2              -0.07616 -0.12793 -0.02453
## Xtotal_mean       -0.91055 -0.98245 -0.83768
```

List of significant beta coefficients:

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

```
## [1] "(Intercept)"      "Xpct_fs_risk_2020_5"  "Xpct_floodfactor9"
## [4] "Xavg_risk_fsf_2020_100" "XEP_POV"             "XEP_UNEMP"
## [7] "XEP_PCI"           "XEP_DISABL"          "XEP_SNGPNT"
## [10] "XEP_MINRTY"        "XEP_LIMENG"          "XEP_MUNIT"
## [13] "XEP_MOBILE"        "XEP_CROWD"           "XEP_NOVEH"
## [16] "XEP_GROUPQ"        "Xco"                 "Xpm10"
## [19] "Xpm25"             "Xso2"                "Xtotal_mean"
```

## My sparse implementation

```
load(here("modeling_files/model_1chain_var_exclude_sparse.RData"))
```

```
chain1$modelfit
```

```
##          DIC          p.d          WAIC          p.w          LMPL
##    6927.307    1660.023    6889.365    1234.289    -3816.070
## loglikelihood
##    -1803.630
```

```
mcmc_samps <- chain1$samples
```

```
effectiveSize(mcmc_samps$beta)
```

```
##      var1      var2      var3      var4      var5      var6      var7
## 18321.4446  9912.6554 12469.1992 13238.6657 10197.5822 10560.5653 12403.0199
##      var8      var9      var10     var11     var12     var13     var14
## 11985.5165 12625.7813 10659.7330  9407.1743 12192.5003 10536.4630 11308.3918
##      var15     var16     var17     var18     var19     var20     var21
## 12230.4144 10508.7540  9295.0482  9813.1030 13470.5864  5350.1551  9938.7464
##      var22     var23     var24     var25     var26     var27     var28
## 10677.3633  9163.9274 11331.1093 10783.5971 13548.4713  7717.0187  4155.9718
##      var29     var30     var31     var32     var33     var34
##  4022.9653   891.8879  2992.7464  1416.8555  6075.2460  6921.7714
```

It's easier to achieve a high sample size. I can have 10x fewer iterations.

```
effectiveSize(mcmc_samps$sigma2)
```

```
##      var1
## 1941.544
```

```
effectiveSize(mcmc_samps$nu2)
```

```
##      var1
## 1868.464
```

```
effectiveSize(mcmc_samps$rho)
```

```
##      var1  
## 7643.979
```

```
t(apply(mcmc_samps$beta, 2, quantile, c(0.5, 0.025, 0.975)))
```

```
##           50%           2.5%           97.5%  
## var1  77.745531393 77.725615386 77.76570136  
## var2  -0.118992258 -0.209991555 -0.02816716  
## var3   0.017491123 -0.028450040  0.06333074  
## var4  -0.015641929 -0.061989448  0.03023109  
## var5   0.048031777 -0.002714322  0.09909835  
## var6  -0.020180925 -0.083476256  0.04301288  
## var7   0.026119308 -0.038406765  0.09057185  
## var8  -0.011206506 -0.062177249  0.03965300  
## var9  -0.014738072 -0.058407143  0.02825494  
## var10  0.087858901  0.013848858  0.16006360  
## var11  0.121059513  0.039378964  0.20075976  
## var12  0.008084847 -0.042735653  0.05777639  
## var13 -0.005958679 -0.093608840  0.08200043  
## var14 -0.177648325 -0.244582480 -0.10966256  
## var15 -0.059781352 -0.108299958 -0.01157768  
## var16  0.246417601  0.173983917  0.31922781  
## var17 -0.054559614 -0.135833471  0.02956783  
## var18 -0.120924077 -0.178670035 -0.06354890  
## var19 -0.218863620 -0.265007603 -0.17202173  
## var20 -0.337624977 -0.422609097 -0.25114492  
## var21  0.349017968  0.281035112  0.41475156  
## var22  0.109738288  0.049267446  0.16919318  
## var23 -0.089448384 -0.149687504 -0.02896266  
## var24 -0.073529509 -0.122008807 -0.02548597  
## var25 -0.126326090 -0.180171362 -0.07244666  
## var26  0.110230356  0.076091369  0.14518724  
## var27 -0.030962559 -0.091021910  0.02952814  
## var28 -0.095475042 -0.164461999 -0.02610274  
## var29 -0.018480165 -0.116772007  0.07937906  
## var30 -0.042025281 -0.177125717  0.08732564  
## var31  0.113960175  0.032637721  0.19471096  
## var32 -0.289975263 -0.408659256 -0.17117715  
## var33 -0.075507272 -0.127299632 -0.02382415  
## var34 -0.910865188 -0.983384160 -0.83672543
```

```
quantile(mcmc_samps$nu2, c(0.5, 0.025, 0.975))
```

```
##           50%           2.5%           97.5%  
## 0.3205943 0.2579871 0.3804506
```

```
quantile(mcmc_samps$sigma2, c(0.5, 0.025, 0.975))
```

```
##           50%           2.5%           97.5%  
## 1.882348 1.583592 2.219357
```

```
quantile(mcmc_samps$rho, c(0.5, 0.025, 0.975))
```

```
##           50%           2.5%           97.5%  
## 0.9924579 0.9756118 0.9991627
```