Supplementary Information for A Bayesian Latent Variable Model for the Optimal Identification of Disease Incidence Rates Given Information Constraints

April 5th, 2024

Contents

1 CDC Serology Surveys

State	% Infected	N	Date Started	Date Ended
Connecticut	4.9%	1431	2020-04-26	2020-05-03
Connecticut	5.2%	1800	2020-05-21	2020-05-26
Connecticut	6.3%	1798	2020-06-15	2020-06-17
Connecticut	5.2%	1802	2020-07-03	2020-07-06
Louisiana	5.8%	1184	2020-04-01	2020-04-08
Louisiana	6.7%	770	2020-04-22	2020-04-27
Minnesota	2.4%	860	2020-04-30	2020-05-12
Minnesota	2.2%	1323	2020-05-25	2020-06-06
Minnesota	4.3%	1667	2020-06-15	2020-06-27
Missouri	2.6%	1882	2020-04-20	2020-04-26
Missouri	2.8%	1831	2020-05-25	2020-05-30
Missouri	0.8%	1850	2020-06-15	2020-06-20
Missouri	1.4%	1914	2020-07-05	2020-07-09
New York	3.69%	2482	2020-03-23	2020-04-01
New York	13.2%	1618	2020-04-06	2020-04-16
New York	16.49%	1116	2020-04-27	2020-05-06
New York	14.44%	1581	2020-06-15	2020-06-21
New York	13.12%	1602	2020-07-07	2020-07-11
Pennsylvania	1.98%	824	2020-04-13	2020-04-25
Pennsylvania	2.48%	1743	2020-05-26	2020-05-30
Pennsylvania	2.64%	1694	2020-06-14	2020-06-20
Pennsylvania	3.55%	1751	2020-07-06	2020-07-11
Florida	0.75%	1742	2020-04-06	2020-04-10
Florida	1.3%	1280	2020-04-20	2020-04-27
Florida	2.12%	1790	2020-05-19	2020-05-27
California	0.96%	1224	2020-04-23	2020-04-27
California	0.94%	1539	2020-05-19	2020-05-27
Utah	2.2%	1132	2020-04-20	2020-05-03
Utah	1.1%	1940	2020-05-25	2020-06-05
Utah	1.5%	1976	2020-06-15	2020-06-27
Washington	0.67%	3264	2020-03-23	2020-04-01
Washington	2.18%	1719	2020-04-27	2020-05-11
Washington	2.19%	1803	2020-06-15	2020-06-20
Washington	1.77%	1797	2020-07-06	2020-07-07

Table 1: Geographic Serological Surveys from the Centers for Disease Control

2 Model Stan Code

The Stan code used to fit the model in the paper is as follows:

```
// Coronavirus tracking model
// Robert Kubinec and Luiz Carvalho
// New York University Abu Dhabi & Getulio Vargas Foundation
// January 5, 2021
// variable type controls type of sampling:
// 1 = priors only
// 2 = priors + informative info on location of infections from seroprevalence/experts
// 3 = priors + informative info + likelihood (full model)
functions {


   // if(r_in(3,{1,2,3,4})) will evaluate as 1
  int r_in(int pos,int[] pos_var) {

    for (p in 1:(size(pos_var))) {
       if (pos_var[p]==pos) {
       // can return immediately, as soon as find a match
          return p;
       }
    }
    return 0;
    }

  real partial_sum(int[,] y_slice,
                   int start, int end,
                   int[] tests,
                   int[] cases,
                   vector phi,
                   int[] country_pop,
                   int num_country,
                   int num_rows,
                   vector mu_poly,
                   //vector sigma_poly,
                   //vector poly1,
                   //vector poly2,
                   //vector poly3,
                   real alpha_test,
                   real alpha_infect,
                   matrix count_outbreak,
                   vector month_cases,
                   vector suppress_effect_raw,
                   vector lockdown_effect_raw,
                   vector mob_effect_raw,
                   matrix Q_supp,
                   matrix Q_supp2,
                   matrix Q_lock,
                   matrix Q_mob,
                   int[] cc,
                   real pcr_spec,
                   real finding,
                   real test_baseline,
                   vector country_test_raw,
                   int S,
                   int G,
                   int L,
                   int R,
                   int RE,
                   int[] sero_row,
                   int[] sero_row_real,
                   int[,] sero,
                   matrix sero_real,
                   matrix mobility,
                   vector[] mob_array,
                   vector mob_alpha_const,
                   vector[] lockdown_med_raw,
                   vector[] suppress_med_raw,
                   vector suppress_med_raw_fear,
                   vector lockdown_med_raw_fear,
                   real sigma_test_raw,
                   vector country_test_raw2,
                   matrix lin_counter,
                   real mu_test_raw,
                   real mu_test_raw2,
                   real sigma_test_raw2,
                   matrix M_Sigma,
                   vector fear,
                   real fear_const,
                   real sigma_fear,
                   int type) {

    // big loop over states
    real log_prob = 0;
    for(r in 1:size(y_slice)) {

        int s = y_slice[r,1];
        int start2 = y_slice[r,2];
        int end2 = y_slice[r,3];

        vector[end2 - start2 + 1] prop_infected; // modeled infection rates for domestic transmission\

        int obs = end2 - start2 + 1;
        //real poly_nonc1; // non-centered poly parameters
        //real poly_nonc2; // non-centered poly parameters
        //real poly_nonc3; // non-centered poly parameters
        real country1s;
        real country2s;
        real country3s;

        vector[end2 - start2 + 1] prop_success;
        vector[end2 - start2 + 1] mu_cases;
        vector[end2 - start2 + 1] mu_tests;
        vector[G] mu_mob[end2 - start2 + 1];

        //poly_nonc1 = mu_poly[1] + sigma_poly[1]*poly1[s];
        //poly_nonc2 = mu_poly[2] + sigma_poly[2]*poly2[s];
        //poly_nonc3 = mu_poly[3] + sigma_poly[3]*poly3[s];

        country1s = mu_test_raw + sigma_test_raw*country_test_raw[s];
        country2s = mu_test_raw2 + sigma_test_raw2*country_test_raw2[s];

        // latent infection rate (unobserved), on the logit scale (untransformed)
        // constrained to *always* increase

        for(i in 1:obs) {
              if(i==1) {
```

```
        prop_infected[1] = alpha_infect +
        count_outbreak[start2+i-1,1] * mu_poly[1]  +
          count_outbreak[start2+i-1,2] *mu_poly[2] +
            count_outbreak[start2+i-1,3] * mu_poly[3] +
            Q_supp[start2,1:S]*suppress_effect_raw +
            Q_lock[start2,1:L]*lockdown_effect_raw +
            Q_mob[start2,1:G]*mob_effect_raw;
      } else {
        prop_infected[i] = exp(alpha_infect +
        count_outbreak[start2+i-1,1] * mu_poly[1]  +
          count_outbreak[start2+i-1,2] *mu_poly[2] +
            count_outbreak[start2+i-1,3] * mu_poly[3] +
            Q_supp[start2+i-1,1:S]*suppress_effect_raw +
            Q_lock[start2+i-1,1:L]*lockdown_effect_raw +
            Q_mob[start2+i-1,1:G]*mob_effect_raw) + prop_infected[i - 1];
      }
}

    //need a recursive function to transform to ordered vector

prop_success = prop_infected;


if(type==3) {

  mu_cases = inv_logit(pcr_spec + finding*prop_success);

}

log_prob += normal_lpdf(country_test_raw[s]|0,1); // more likely near the middle than the ends
log_prob += normal_lpdf(country_test_raw2[s]|0,1); // more likely near the middle than the ends

//log_prob += normal_lpdf(poly1[s]|0,1);
//log_prob += normal_lpdf(poly2[s]|0,1);
//log_prob += normal_lpdf(poly3[s]|0,1);

//mobility mediation

for(g in 1:G) {
  mu_mob[1:obs,g] = to_array_1d(mob_alpha_const[g] +
  Q_lock[start2:end2,1:L]*lockdown_med_raw[g]  +
  Q_supp[start2:end2,1:S]*suppress_med_raw[g]);
}

  log_prob += multi_normal_cholesky_lpdf(mob_array[start2:end2,1:G]|mu_mob,M_Sigma);

// fear mediation
  log_prob += normal_lpdf(fear[start2:end2]|fear_const + Q_lock[start2:end2,1:L]*lockdown_med_ra
                       Q_supp2[start2:end2,1:(S-1)]*suppress_med_raw_fear,sigma_fear);

if(type==3) {

  mu_tests = inv_logit(alpha_test +
                  country1s * lin_counter[start2:end2,1] +
                            country2s * lin_counter[start2:end2,2] +
                            test_baseline * prop_success);

        }

        // observed data model
        // loop over serology surveys to add informative prior information

        for(n in start2:end2) {

          int q = r_in(n,sero_row);
          int p = r_in(n, sero_row_real);

          if(q <= 0 && p <= 0 && type==3) {

            log_prob += beta_binomial_lpmf(cases[n]|country_pop[n],mu_cases[n-start2+1]*phi[2],(1-mu_cas
            log_prob += beta_binomial_lpmf(tests[n]|country_pop[n],mu_tests[n-start2+1]*phi[1],(1-mu_tes

          } else if(p>0 && (type==2 || type==3)) {

            // expert survey data
            // beta prior

            log_prob += beta_proportion_lpdf(sero_real[p,1]|inv_logit(prop_infected[n-start2+1]),sero_re

            } else if(q > 0 && (type==2 || type==3)) {

            // scaling function. we use seroprevalance data to
            // set a ground truth for the relationship between covariates and
            // infections measured non-parametrically

            log_prob += binomial_lpmf(sero[q,1]|sero[q,2],
                                    inv_logit(prop_infected[n-start2+1]));

          }
        }

      }

      return log_prob;
    }


}
data {
  int time_all;
  int num_country;
  int num_rows;
  int cc[num_rows]; // country counter
  int cases[num_rows];
  int tests[num_rows];
  int S; // number of suppression measures
  int G; // google mobility data (by type of mobility)
  int L; // just lockdown data (for hierarchical predictor)
  int R; // number of seroprevalence essays
  int RE; // number of expert surveys
  int type; // whether to sample from priors or from the full likelihood
  matrix[num_rows,S] suppress; // time-varying suppression measures
  matrix[num_rows,S-1] suppress2; // without COVID poll
  matrix[num_rows,G] mobility; // time-varying mobility measures
  matrix[num_rows,L] lockdown; // hierachical lockdown predictors
  vector[num_rows] fear; // COVID poll
  matrix[num_rows,3] count_outbreak;
  vector[num_rows] month_cases;
  vector[num_rows] test_max;
  int sero[R,2]; // sero-prevalence datas
  int sero_row[R];
  matrix[RE,2] sero_real; // expert survey datas
  int sero_row_real[RE];
  int country_pop[num_rows];
  matrix[num_rows,3] lin_counter;
  vector[2] phi_scale; // prior on how much change there could be in infection rate over time
  int states[num_country,3];
}
transformed data {

  matrix[num_rows,S] Q_supp;
  matrix[S, S] R_supp;
  matrix[S, S] R_supp_inverse;

  matrix[num_rows,S-1] Q_supp2;
  matrix[S-1, S-1] R_supp2;
  matrix[S-1, S-1] R_supp_inverse2;

  matrix[num_rows, G] Q_mob;
  matrix[G, G] R_mob;
  matrix[G, G] R_mob_inverse;

  matrix[num_rows, L] Q_lock;
  matrix[L, L] R_lock;
  matrix[L, L] R_lock_inverse;
  vector[G] mob_array[num_rows];


  // thin and scale the QR decomposition
  Q_supp = qr_Q(suppress)[, 1:S] * sqrt(num_rows - 1);
  Q_supp2 = qr_Q(suppress2)[, 1:(S-1)] * sqrt(num_rows - 1);
  R_supp = qr_R(suppress)[1:S, ] / sqrt(num_rows - 1);
  R_supp2 = qr_R(suppress2)[1:(S-1), ] / sqrt(num_rows - 1);
  R_supp_inverse = inverse(R_supp);
  R_supp_inverse2 = inverse(R_supp2);

  Q_mob = qr_Q(mobility)[, 1:G] * sqrt(num_rows - 1);
  R_mob = qr_R(mobility)[1:G, ] / sqrt(num_rows - 1);
  R_mob_inverse = inverse(R_mob);

  Q_lock = qr_Q(lockdown)[, 1:L] * sqrt(num_rows - 1);
  R_lock = qr_R(lockdown)[1:L, ] / sqrt(num_rows - 1);
  R_lock_inverse = inverse(R_lock);

  for(g in 1:G) {
    for(n in 1:num_rows) {
      mob_array[n,g] = mobility[n,g];
    }
  }


}
parameters {
  // real poly1; // polinomial function of time
  // real poly2; // polinomial function of time
  // real poly3; // polinomial function of time
  real mu_test_raw;
  real mu_test_raw2;
  real finding; // difficulty of identifying infected cases
  vector[S] suppress_effect_raw; // suppression effect of govt. measures, cannot increase virus transmis
  vector[L] lockdown_effect_raw;
  vector[L] lockdown_med_raw[G];
  vector[S] suppress_med_raw[G];
  vector[L] lockdown_med_raw_fear;
  vector[S-1] suppress_med_raw_fear;
  real test_baseline;
  real pcr_spec;
  vector[3] mu_poly; // hierarchical mean for poly coefficients
  vector[G] mob_effect_raw;
  //vector<lower=0>[3] sigma_poly; // varying sigma polys
  vector[G] mob_alpha_const; // mobility hierarchical intercepts
  vector[num_country] country_test_raw; // unobserved rate at which countries are willing to test vs. nu
  vector[num_country] country_test_raw2;
  real alpha_infect; // other intercepts
  real alpha_test;
  vector<lower=0>[2] phi_raw; // shape parameter for infected
  real<lower=0> sigma_test_raw; // estimate of between-state testing heterogeneity
  real<lower=0> sigma_test_raw2;
  cholesky_factor_corr[G] M_Omega; // these are for the MVN for mobility data
  vector<lower=0>[G] M_sigma;
  real fear_const;
  real<lower=0> sigma_fear;
}
transformed parameters {
  vector[2] phi;

  phi = (1 ./ phi_scale) .* phi_raw;
}
model {
  matrix[G, G] M_Sigma;
  int grainsize = 1;

  //sigma_poly ~ exponential(100);
  mu_poly ~ normal(0,50);
  mu_test_raw ~ normal(0,50);
  mu_test_raw2 ~ normal(0,50);
  lockdown_effect_raw ~ normal(0,5);
  alpha_infect ~ normal(0,10); // this can reach extremely low values
  alpha_test ~ normal(0,5);

  phi_raw ~ exponential(.1);
  mob_effect_raw ~ normal(0,5);
  suppress_effect_raw ~ normal(0,5);
  test_baseline ~ normal(0,5);

  mob_alpha_const ~ normal(0,5);
  pcr_spec ~ normal(0,5);

  finding ~ normal(0,5);
  sigma_test_raw ~ exponential(100);
  sigma_test_raw2 ~ exponential(100);
  sigma_fear ~ exponential(.1);
  fear_const ~ normal(0,5);

  for(g in 1:G) {
    suppress_med_raw[g] ~ normal(0,5);
    lockdown_med_raw[g] ~ normal(0,5);
  }

  suppress_med_raw_fear ~ normal(0,5);
  lockdown_med_raw_fear ~ normal(0,5);

  M_Omega ~ lkj_corr_cholesky(4);
  M_sigma ~ exponential(.1);

  M_Sigma = diag_pre_multiply(M_sigma, M_Omega); // Cholesky decomp for MVN for mobility

target += reduce_sum_static(partial_sum, states,
                     grainsize,
                    tests,
                     cases,
                     phi,
                     country_pop,
                     num_country,
                     num_rows,
                     mu_poly,
                     //sigma_poly,
                     //poly1,
                     //poly2,
                     //poly3,
                     alpha_test,
                     alpha_infect,
                     count_outbreak,
                     month_cases,
                     suppress_effect_raw,
                     lockdown_effect_raw,
                     mob_effect_raw,
                     Q_supp,
                     Q_supp2,
                     Q_lock,
                     Q_mob,
                     cc,
                     pcr_spec,
                     finding,
                     test_baseline,
                     country_test_raw,
                     S,
                     G,
                     L,
                     R,
                     RE,
                     sero_row,
                     sero_row_real,
                     sero,
                     sero_real,
                     mobility,
                     mob_array,
                     mob_alpha_const,
                     lockdown_med_raw,
                     suppress_med_raw,
                     suppress_med_raw_fear,
                     lockdown_med_raw_fear,
                     sigma_test_raw,
                     country_test_raw2,
                     lin_counter,
                     mu_test_raw,
                     mu_test_raw2,
                     sigma_test_raw2,
                     M_Sigma,
                     fear,
                     fear_const,
                     sigma_fear,
                     type);

}
generated quantities {

  // convert QR estimates back to actual numbers

  vector[S] suppress_effect; // suppression effect of govt. measures, cannot increase virus transmissio
  vector[L] lockdown_effect;
  vector[G] mob_effect;
  vector[L] lockdown_med[G];
  vector[S] suppress_med[G];
  vector[L] lockdown_med_fear;
  vector[S-1] suppress_med_fear;
  vector[num_rows] prop_infect_out;
  vector[num_rows] cov_out;

  suppress_effect = R_supp_inverse * suppress_effect_raw;
  lockdown_effect = R_lock_inverse * lockdown_effect_raw;
  mob_effect = R_mob_inverse * mob_effect_raw;
  for(g in 1:G) {
    lockdown_med[g] = R_lock_inverse * lockdown_med_raw[g];
    suppress_med[g] = R_supp_inverse * suppress_med_raw[g];
  }

  suppress_med_fear = R_supp_inverse2 * suppress_med_raw_fear;
  lockdown_med_fear = R_lock_inverse * lockdown_med_raw_fear;


  for(s in 1:num_country) {
        //
        // real poly_nonc1; // non-centered poly parameters
        // real poly_nonc2; // non-centered poly parameters
        // real poly_nonc3; // non-centered poly parameters

        int start2 = states[s,2];
        int end2 = states[s,3];
        int obs = end2 - start2 + 1;

        // poly_nonc1 = mu_poly[1] + sigma_poly[1]*poly1[s];
        // poly_nonc2 = mu_poly[2] + sigma_poly[2]*poly2[s];
        // poly_nonc3 = mu_poly[3] + sigma_poly[3]*poly3[s];

    for(i in 1:obs) {
              if(i==1) {
                prop_infect_out[start2] = alpha_infect + count_outbreak[start2,1] * mu_poly[1] +
                    count_outbreak[start2,2] * mu_poly[2]  +
                    count_outbreak[start2,3] * mu_poly[3]  +
                    Q_supp[start2,1:S]*suppress_effect_raw +
                    Q_lock[start2,1:L]*lockdown_effect_raw +
                    Q_mob[start2,1:G]*mob_effect_raw;

                 cov_out[start2] = alpha_infect + Q_mob[start2,1:G]*mob_effect_raw;

              } else {
                prop_infect_out[start2 + i - 1] = exp(alpha_infect + count_outbreak[start2+i-1,1] * mu_
                    count_outbreak[start2+i-1,2] * mu_poly[2] +
                    count_outbreak[start2+i-1,3] * mu_poly[3] +
                    Q_supp[start2+i-1,1:S]*suppress_effect_raw +
                    Q_lock[start2+i-1,1:L]*lockdown_effect_raw +
                    Q_mob[start2+i-1,1:G]*mob_effect_raw) + prop_infect_out[start2 + i - 2];

                cov_out[start2 + i - 1] = exp(alpha_infect + Q_mob[start2+i-1,1:G]*mob_effect_raw) + co
              }
        }
  }

}
```

3 Simulation

Because our model is fully generative, we can simulate it using Monte Carlo methods. The simulation presented here is a simplification of the model presented in the main paper for clarity of exposition. We do not have varying polynomial time trends but rather a single global time trend, and we do not implement the cumulative sum transformation on the latent vector. Despite these simplifications, the simulation is very important as it is the only way to demonstrate that the model is globally identified and can in fact capture unobserved parameters like suppression effects and relative infection rates. We also are able to show how the bias in only using observed cases and tests can affect the estimates of parameters.

The following R code generates data from the model and plots the resulted unobserved infection rate and observed values for tests and cases along with an exogenous suppression covariate:

```r
# simulation parameters
num_state <- 50

time_points <- 100
# allows for linear growth that later becomes explosive
polynomials <- c(.03,0.0003,-0.00001)

# factor that determines how many people a state is willing/able to test
# states that suppress or don't suppress
# induce correlation between the two

 cor_vars <- MASS::mvrnorm(n = num_state, mu = c(0, 5),
                              Sigma = matrix(c(1, -.5, -.5, 1), 2, 2))


state_test <- cor_vars[, 2]
suppress_measures <- cor_vars[, 1]

# size of states

state_pop <- rpois(num_state, 10000)

# assumt t=1 is unmodeled = exogenous start of the infection

t1 <- c(1, rep(0, num_state-1))

# create a suppression coefficient
# first is for preventing domestic transmission from occuring
# second is for preventing further domestic transmission once it starts

suppress1 <- -0.5
suppress2 <- -0.05

# high value of phi = high over-time stability
phi <- c(300, 300)
```

```
# parameter governing how hard it is to find infected people and test them
# strictly positive

finding <- 1.5

# recursive function to generate time-series data by state

out_poly <- function(time_pt, end_pt, time_counts, tested, case_count, rate_infected, pr_domestic) {

  if(time_pt==1) {
    time_counts <- as.matrix(c(1, rep(0, num_state-1)))
    rate_infected <- as.matrix(c(.0001, rep(0, num_state-1)))
    tested <- as.matrix(rep(0, num_state))
    case_count <- as.matrix(c(1, rep(0,num_state-1)))
  }

  # if at time = t infected, start time tracker at t
  # need to know how many states have reported at least one case = infection start

  world_count <- sum(case_count[, time_pt]>0)


  if(time_pt==1) {

    rate_infected_new <-  plogis(-5 + time_counts[, time_pt]*polynomials[1] +
                                   suppress1*suppress_measures +
                    suppress2*suppress_measures*time_counts[, time_pt] +
                    .05*sum(world_count) +
      (time_counts[, time_pt]^2)*polynomials[2] +
        (time_counts[, time_pt]^3)*polynomials[3])

    # conservative time counter that only starts when first case is recorded

    time_counts_new <- ifelse(time_counts[, time_pt]>0 | case_count[, time_pt]>0, time_counts[, time_pt

  } else {

    rate_infected_new <- plogis(-5 + time_counts[, time_pt]*polynomials[1] +
                    suppress1*suppress_measures +
                    suppress2*suppress_measures*time_counts[, time_pt] +
                    .05*sum(world_count) +
      (time_counts[, time_pt]^2)*polynomials[2] +
        (time_counts[, time_pt]^3)*polynomials[3])

    # conservative time counter that only starts when first case is recorded

    time_counts_new <- ifelse(time_counts[, time_pt]>0 | case_count[, time_pt]>0, time_counts[, time_pt
  }

  # of these, need to calculated a set number tested
  mu_test <- plogis(-7 + state_test*rate_infected_new)
  tested_new <- rbbinom(num_state, state_pop, mu_test*phi[1], (1-mu_test)*phi[1])
```

```r
  # determine case count as percentage number tested
  # this is what we always observe
  mu_case <- plogis(-2.19 + finding*rate_infected_new)
  case_count_new <- rbbinom(num_state, tested_new, mu_case*phi[2], (1-mu_case)*phi[2])


  if(time_pt<end_pt) {
    out_poly(time_pt = time_pt+1,
             end_pt = end_pt,
             time_counts = cbind(time_counts,
                                 time_counts_new),
             rate_infected = cbind(rate_infected, rate_infected_new),
             tested = cbind(tested, tested_new),
             case_count = cbind(case_count, case_count_new))
  } else {
    return(list(time_counts = time_counts,
                tested = tested,
                rate_infected = rate_infected,
                case_count = case_count))
  }

}

check1 <- out_poly(1, time_points)

check1 <- lapply(check1, function(c) {
  colnames(c) <- as.numeric(1:time_points)
  c
})

all_out <- bind_rows(list(time_counts=as_tibble(check1$time_counts),
                          `Proportion Population\nInfected`=as_tibble(check1$rate_infected),
                          `Number of Cases`=as_tibble(check1$case_count),
                          `Proportion of Cases from Domestic Transmission`=as_tibble(check1$pr_domestic)
                          `Number of Tests`=as_tibble(check1$tested)),.id="Series")

all_out$state <- rep(paste0("state_",1:num_state),times=length(check1))
all_out$suppress_measures <- rep(suppress_measures,times=length(check1))

all_out %>%
  gather(key = "time_id",value="indicator",-Series,-state,-suppress_measures) %>%
  mutate(time_id=as.numeric(time_id)) %>%
  filter(!(Series %in% c("time_counts"))) %>%
  ggplot(aes(y=indicator,x=time_id)) +
  geom_line(aes(colour=suppress_measures,group=state),alpha=0.3) +
  xlab("Days Since Outbreak") +
  ylab("") +
  facet_wrap(~Series,scales="free_y") +
  theme(panel.background = element_blank(),
        panel.grid=element_blank(),
        strip.background = element_blank(),
        strip.text = element_text(face="bold"),
        legend.position = "top")
```

Figure 1: Simulation of Observed Tests and Cases Given Unobserved Infectious Process

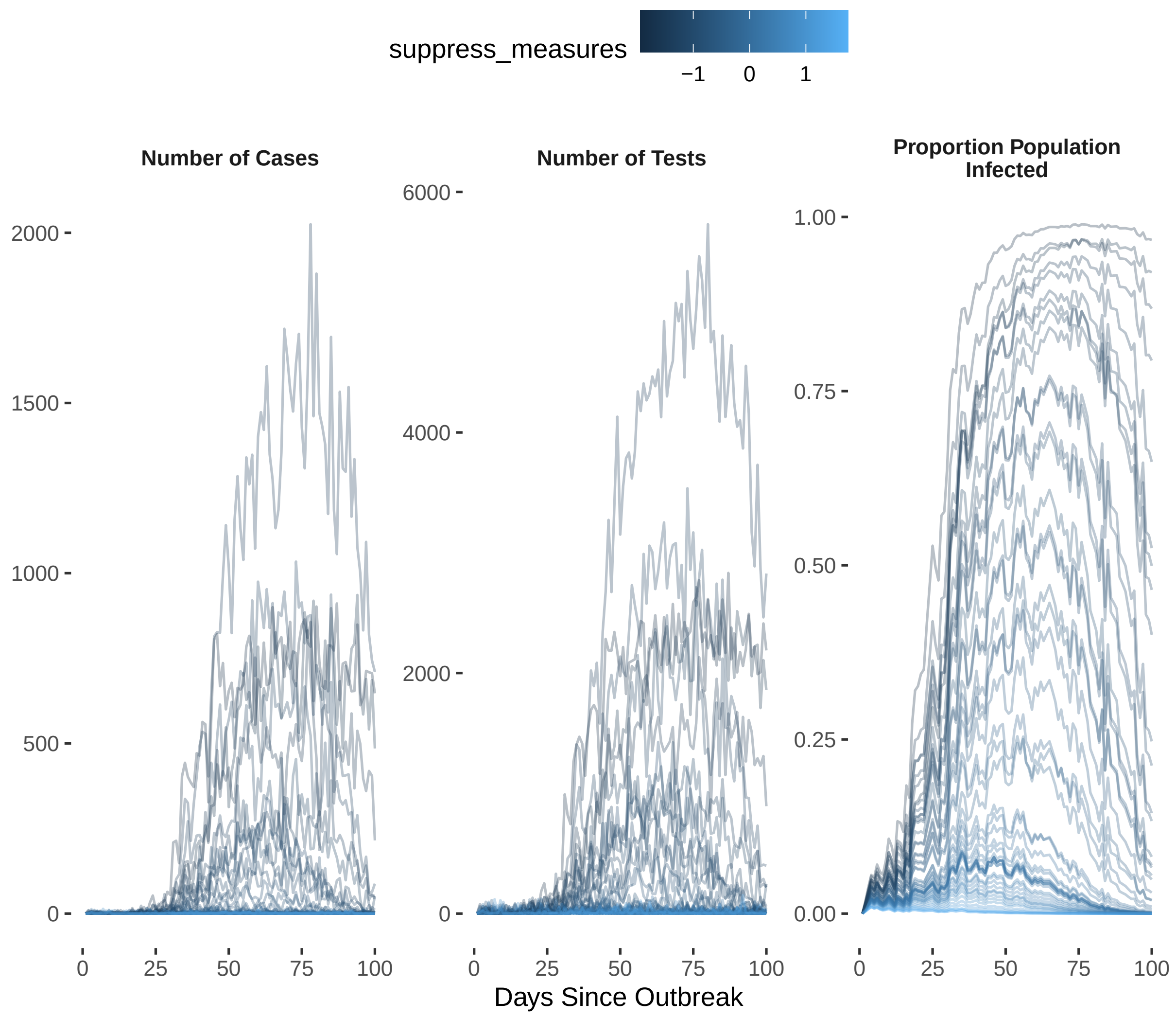


Figure 1 shows one line for each state's trajectory from a total of 100 states and 100 time points. As can be seen, the shading indicating strength of suppression policies diverges substantially over time. However, the numbers of observed tests and cases show far more random noise due to the difficulty in inferring the true rate from the observed data. It is possible that some states simply want to test more, and end up with more cases, or that the infection rate is in fact higher. As such, this model is able to incorporate that measurement uncertainty between the true (unobserved) rate and the observed indicators, tests and cases.

The data were also generated so that the suppression covariate, which shades the infection rates in Figure 1, is positively correlated with a state's willingness to test. As such, this covariation will lead a naive model to dramatically *over-estimate* the effect of suppression policies as the case/test ratio mechanically falls due to increased tests independent of the infection rate.

The primary advantage of this model is that it allows for the testing of covariates that affect the true infection rate without requiring more heavy-duty approaches like SEIR/SIR, such as modeling reproduction numbers and other disease-specific mechanisms. The intention is to have a more parsimonious model that can see how the effect of variables like suppression measures have on different states/states infection numbers over time. In particular, this model increases our understanding of the connection between contextual factors and human behavior to the virus' progression.

The model could be further extended with more complicated processes, such as spatial modeling, but for the purposes of this exposition we do not look further at such extensions. We would note that the world infection parameter is implicitly, if not explicitly, a spatial measure.

3.1 Estimation

We can then fit an empirical model using the Hamiltonian Monte Carlo (HMC) Markov Chain Monte Carlo (MCMC) sampler in Stan[1] to model the unobserved infection rate given the simulated observed data. We also fit a Bayesian binomial model of the proportion of counts to state population using the same covariates but with the observed counts as the outcome. This naive model is fitted to indicate the amount of bias that can occur in estimates as a result of ignoring the underlying infection process.

```r
# all data from simulation
# primarily case and test counts

# need to make centered, ortho-normal polynomials

ortho_time <- poly(scale(1:time_points, scale = F),degree=3)
```

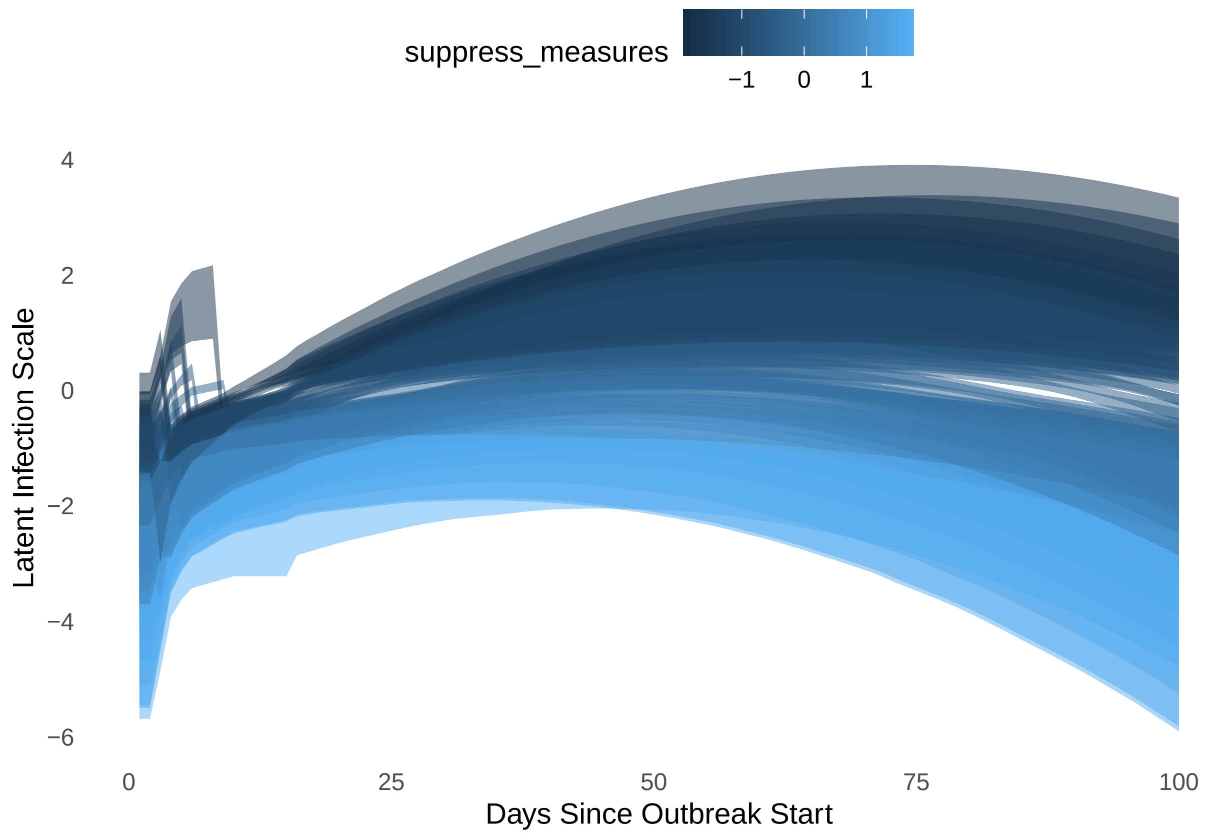
```r
init_vals <- function() {
  list(phi1 = 300,
       phi2 = 300,
       world_infect = .1,
       finding = 1,
       poly = c(0, 0, 0),
       state_test = rnorm(num_state, 5, .25),
       alpha = c(-7, 0,-2),
       sigma_test_raw = 1)
}

sim_data <- list(time_all = time_points,
                 num_country = num_state,
                 country_pop = state_pop,
                 cases = check1$case_count,
                 S = 1,
                 phi_scale = 1/100,
                 ortho_time = ortho_time,
                 tests = check1$tested,
                 count_outbreak = as.numeric(scale(apply(check1$time_counts, 2, function(c) sum(c>0)),
                                                scale = FALSE)),
                 time_outbreak = check1$time_counts,
                 time_outbreak_center = matrix(scale(c(check1$time_counts), scale = FALSE), nrow = nrow
                                                  ncol = ncol(check1$time_counts)),
                 suppress = as.matrix(suppress_measures))

# need to make a regular type data frame to do observed modeling with rstanarm

obs_data <- as_tibble(check1$case_count) %>%
  mutate(num_state = 1:n()) %>%
  gather(key = "time_points", value="cases", -num_state)


# join in outbreak timing + covariates

time_data <- as_tibble(sim_data$time_outbreak) %>%
  mutate(num_state = 1:n()) %>%
  gather(key = "time_points", value = "time_outbreak", -num_state) %>%
  mutate(time_points = stringr::str_extract(time_points, "[0-9]+"))

obs_data <- left_join(obs_data, time_data, by = c("time_points", "num_state")) %>%
  left_join(tibble(state_pop=state_pop,
                   suppress=suppress_measures,
                   num_state=1:length(state_pop)),by="num_state") %>%
  mutate(time_points=as.numeric(time_points),
         time_points_scale=as.numeric(scale(time_points,scale=T))) %>%
  left_join(tibble(count_outbreak=sim_data$count_outbreak,
                   time_points=as.numeric(1:time_points)),by="time_points")

if(run_model) {

  pan_model <- stan_model("corona_tscs_betab.stan")
# run model

pan_model_est <- sampling(pan_model,data=sim_data,chains=2,cores=2,iter=1200,warmup=800,init=init_vals,
                          control=list(adapt_delta=0.95))

naive_model <- stan_glm(cbind(cases,state_pop-cases)~poly(time_points_scale,3) +
                          count_outbreak +
                          suppress +
                          suppress:poly(time_points_scale,3)[,1],
                        data=obs_data,
                        family="binomial",
                        cores=1,
                        chains=1)

saveRDS(pan_model_est,"data/pan_model_est.rds")
saveRDS(naive_model,"data/naive_model_sim.rds")
} else {
  pan_model_est <- readRDS("data/pan_model_est.rds")
  naive_model <- readRDS("data/naive_model_sim.rds")
}
```

After fitting the latent model, we can access the estimated infection rates and plot them:

```r
all_est <- as.data.frame(pan_model_est,"num_infected_high") %>%
  mutate(iter=1:n()) %>%
  gather(key="variable",value="estimate",-iter) %>%
  group_by(variable) %>%
  mutate(estimate=estimate) %>%
  summarize(med_est=quantile(estimate,.5),
            high_est=quantile(estimate,.95),
            low_est=quantile(estimate,.05)) %>%
  mutate(state_num=as.numeric(str_extract(variable,"(?<=\\[)[1-9][0-9]?0?")),
         time_point=as.numeric(str_extract(variable,"[1-9][0-9]?0?(?=\\])")))

all_est <- left_join(all_est,tibble(state_num=1:num_state,
                                    suppress_measures=suppress_measures),by="state_num")

all_est %>%
  ggplot(aes(y=med_est,x=time_point)) +
  geom_ribbon(aes(ymin=low_est,
  ymax=high_est,
  group=state_num,
  fill=suppress_measures),alpha=0.5) +
  theme_minimal() +
  scale_color_brewer(type="div") +
  ylab("Latent Infection Scale") +
  xlab("Days Since Outbreak Start") +
  theme(panel.grid = element_blank(),
        legend.position = "top")
```

We see how the model is able to partially recover the infection rate as shown in Figure 2. The estimates reveal the same general arc as the generated data, with higher suppression policies associated with lower

Figure 2: Estimated Simulated Infection Rates



infection counts, but the scale of the infection rate is no longer identified. As such, the model is only able to recover the relative rather than absolute trajectory of the infection rate.

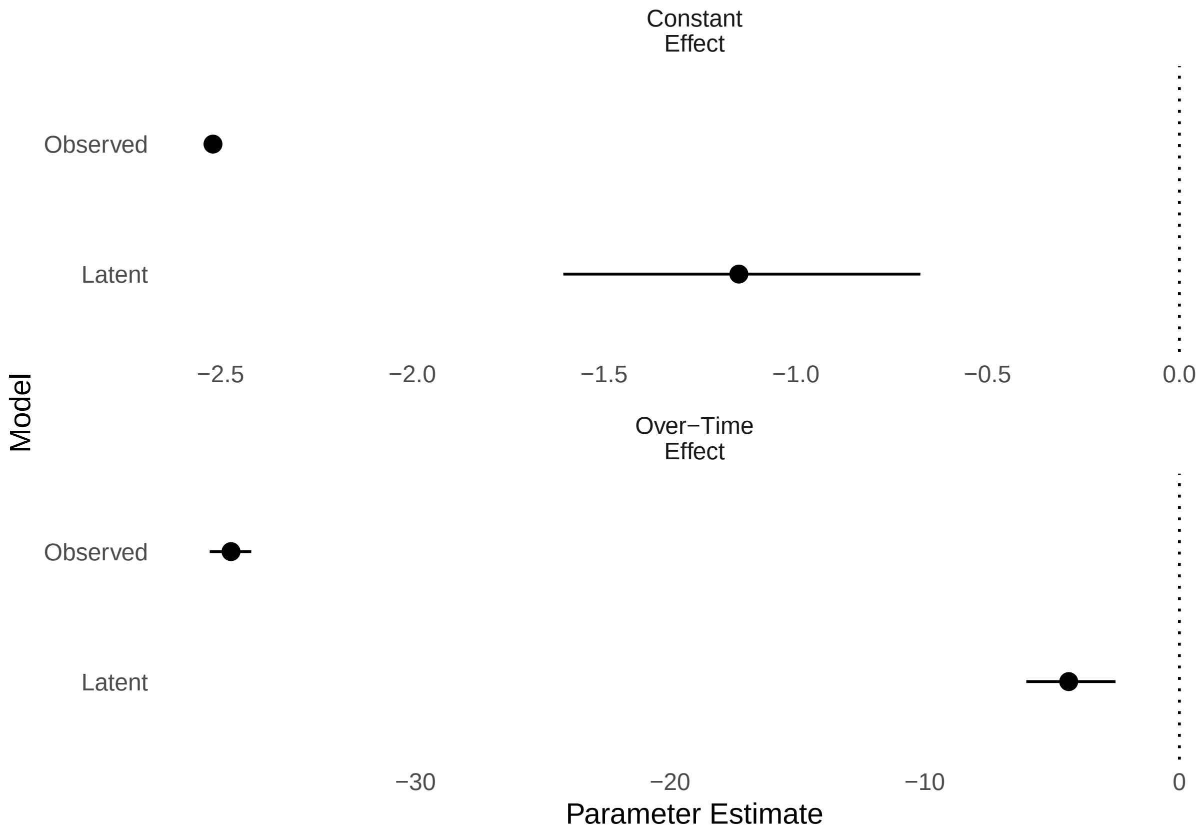
However, because we have inferred the correct arc, we can also see what the estimated suppression parameters are. We also compare those to the same suppression parameters from the naive model in Figure 3.

```r
require(bayesplot)
require(patchwork)

p1 <- mcmc_intervals_data(as.array(pan_model_est,pars=c("suppress_effect[1,1]",
                                                "suppress_effect[2,1]")))

p2 <- mcmc_intervals_data(naive_model,pars=c("suppress",
                                                "suppress:poly(time_points_scale, 3)[, 1]"))

bind_rows(list(Latent=p1,
               Observed=p2),.id="Model") %>%
  mutate(parameter=recode(parameter,
                          `suppress_effect[1,1]`="Constant\nEffect",
                          `suppress_effect[2,1]`="Over-Time\nEffect",
                          `suppress`="Constant\nEffect",
                          `suppress:poly(time_points_scale, 3)[, 1]`="Over-Time\nEffect")) %>%
  ggplot(aes(y=m,x=Model)) +
  geom_pointrange(aes(ymin=ll,ymax=hh),position=position_dodge(0.5)) +
  theme_minimal() +
  geom_hline(yintercept=0,linetype=3) +
  scale_color_brewer(type="qual") +
  guides(color="none") +
  ylab("Parameter Estimate") +
  theme(panel.grid = element_blank(),
        legend.position = "top") +
  coord_flip() +
  facet_wrap(~parameter,scales="free_x",ncol=1)
```

We can see in Figure 3 that despite the uncertainty in not perfectly observing the infection rate, we can still get a precise credible interval on the suppression effect. However, while the observed model's parameters have the same sign, they are wildly inflated, and far too precise. The constant effect in particular is ten times the size of the latent model with virtually no uncertainty interval. Because the infection process is ignored, the model obfuscates the infection/testing relationship with the effect of suppression policies, wildly over-estimating their effect at lowering infection counts.

The advantage of this model, as can be seen, is that with testing numbers and case counts, we can model the effect of state-level (or region-level) variables on the unseen infection rate up to an unknown constant. It is far simpler than existing approaches while still permitting inference on these hard-to-quantify measures. It is no substitute for infectious disease modeling–for example, it produces no estimates of the susceptible versus

Figure 3: Recovered Simulated Virus Suppression Parameters Versus Naive Model



recovered individuals in the population, nor death rates–but rather a way to measure the effect of different background factors of interest to social and natural sciences on disease outcomes as well as approximate disease trajectory. Furthermore, the model's main quantity is a better measure to share with the public than misleading numbers of positive case counts.

References

1. Carpenter, B. *et al.* Stan: A probabilistic programming language. *Journal of Statistical Software* **76**, (2017).