

Report: COVID19 Bayesian Epidemiological Model

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Model descriptions

- Model 1: The Imperial College model v3, with partial pooling of lockdown variable
- Model 2: Google Mobility and Oxford Binary Intervention indicators. Regression coefficients are assumed common for all countries (pooled alpha).
- Model 3: Google Mobility and Oxford Binary Intervention indicators. Regression coefficients are hierarchical and inform each other between countries. (hierarchical alpha)
- Model 4: Google Mobility and Oxford Binary Intervention indicators. Regression coefficients are estimated for each country. (local alpha)
- Model 5: Google Mobility, Oxford Binary Intervention indicators and b-spline. Regression coefficients are hierarchical and the b-spline is a local spline over t per country.

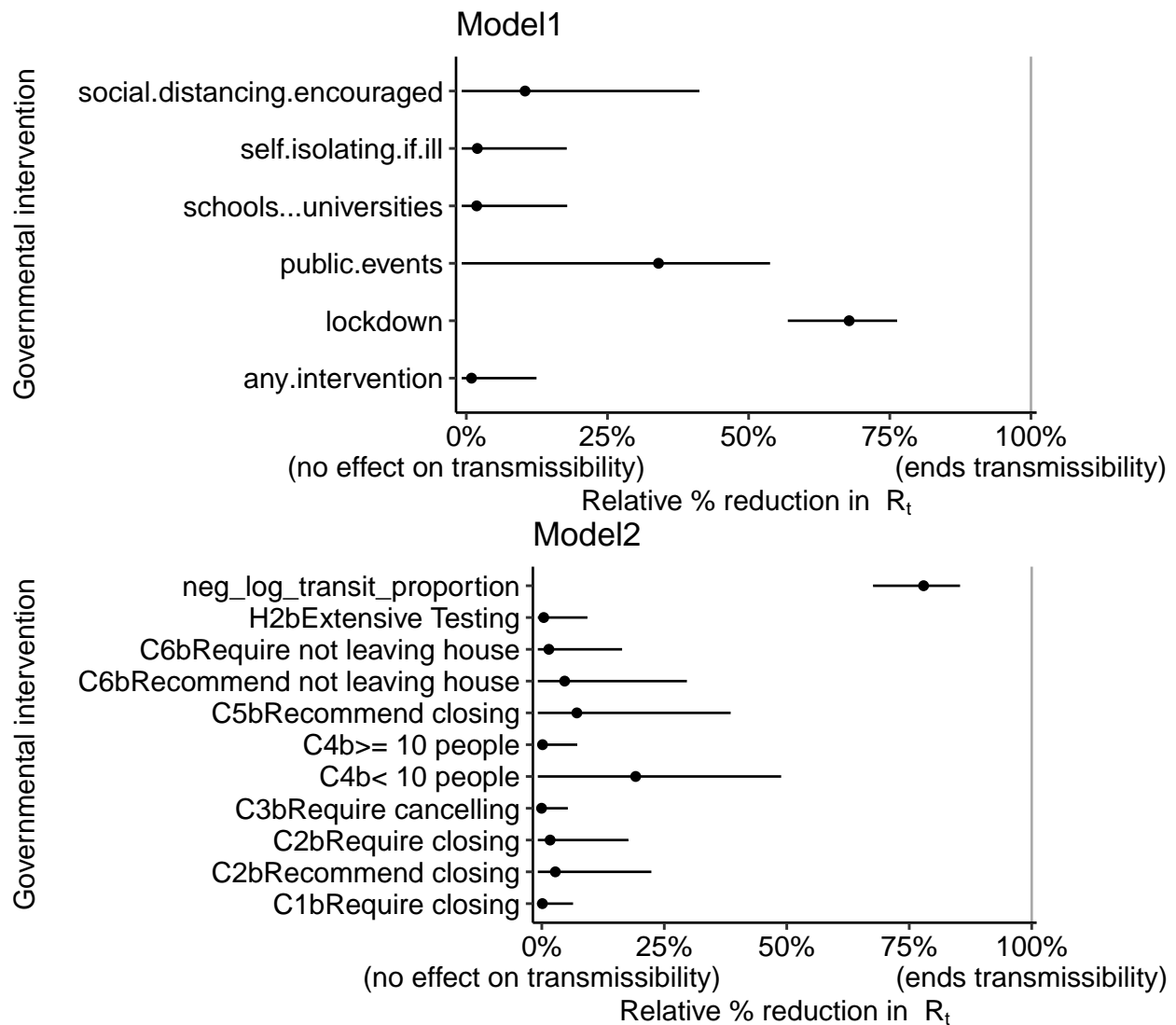
Oxford covariate descriptions

- C1: School closing
- C2: Workplace closing
- C3: Cancel public events
- C4: Restrictions on Gatherings
- C5: Close public transport
- C6: Stay at home requirements
- H2: Testing policy

Case study: The Sweden, Finland and Italy

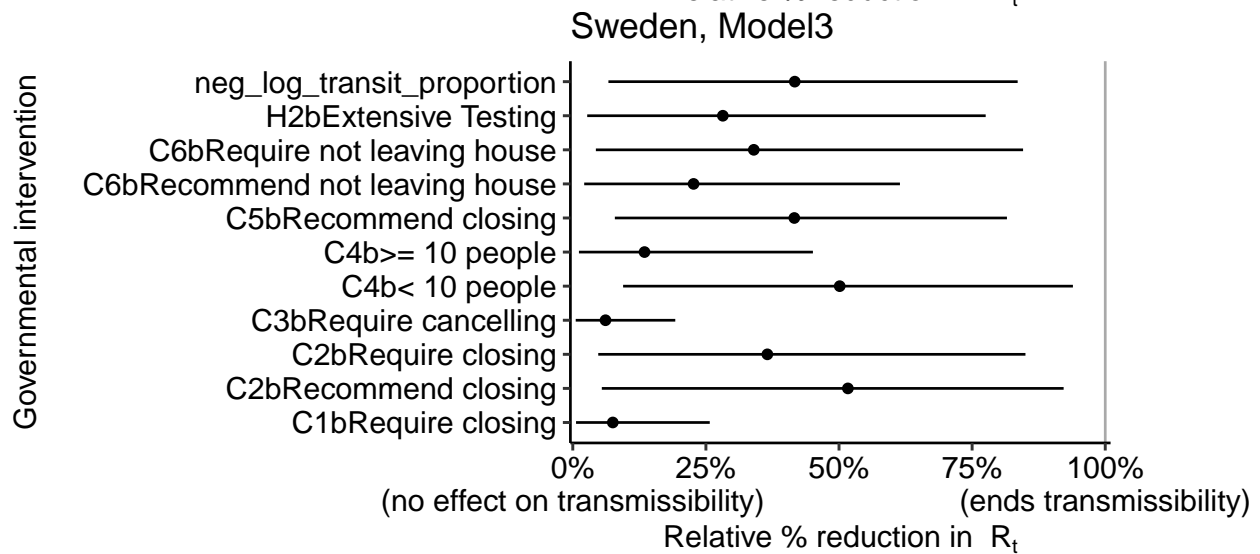
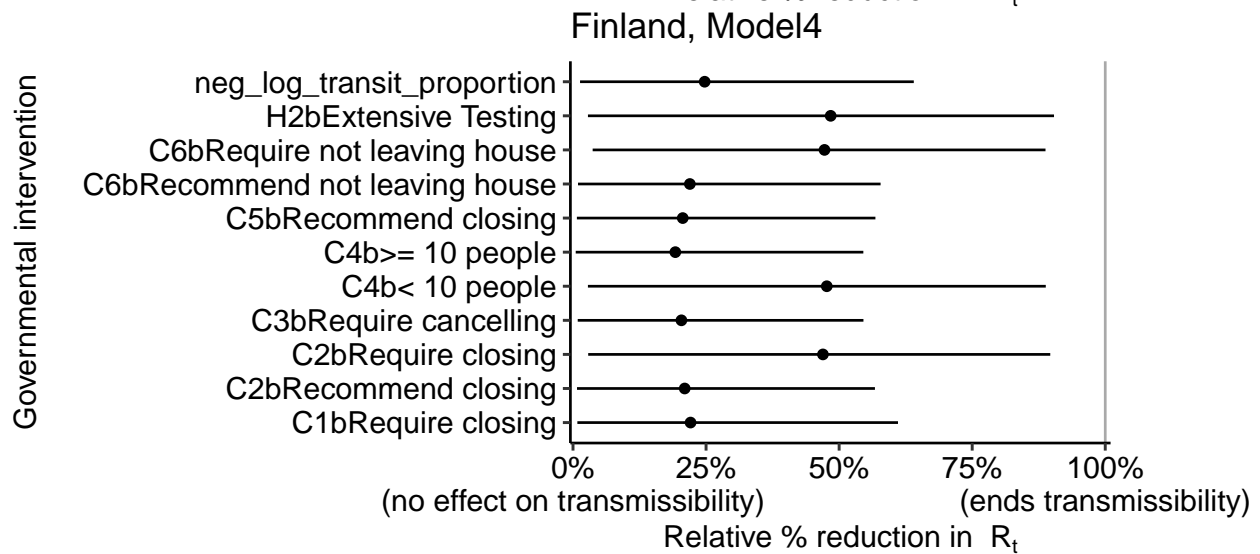
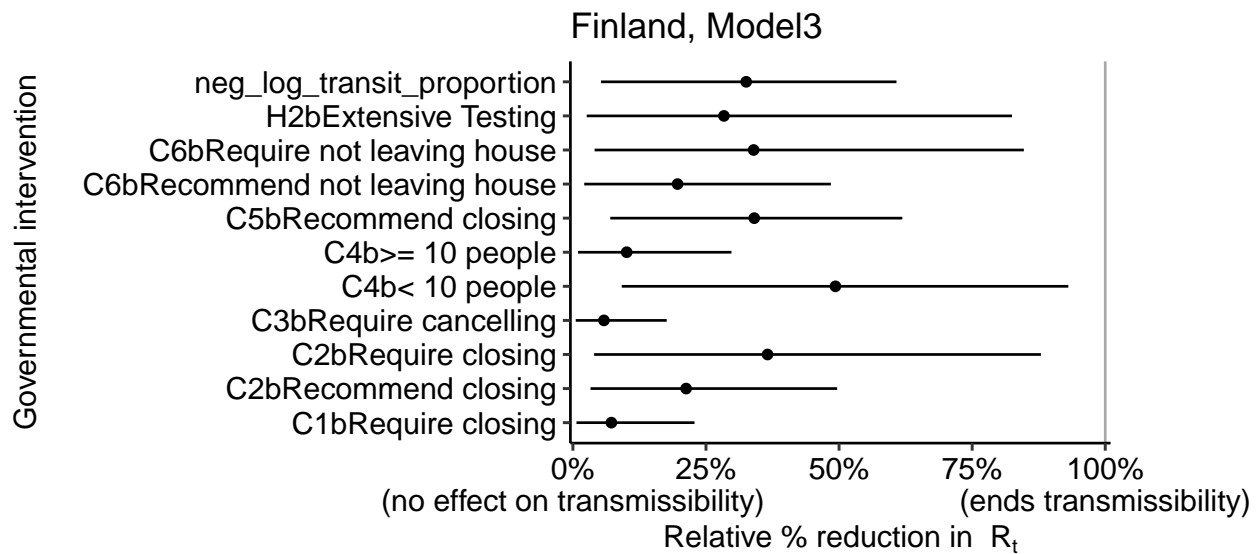
All other countries are included in the Appendix.

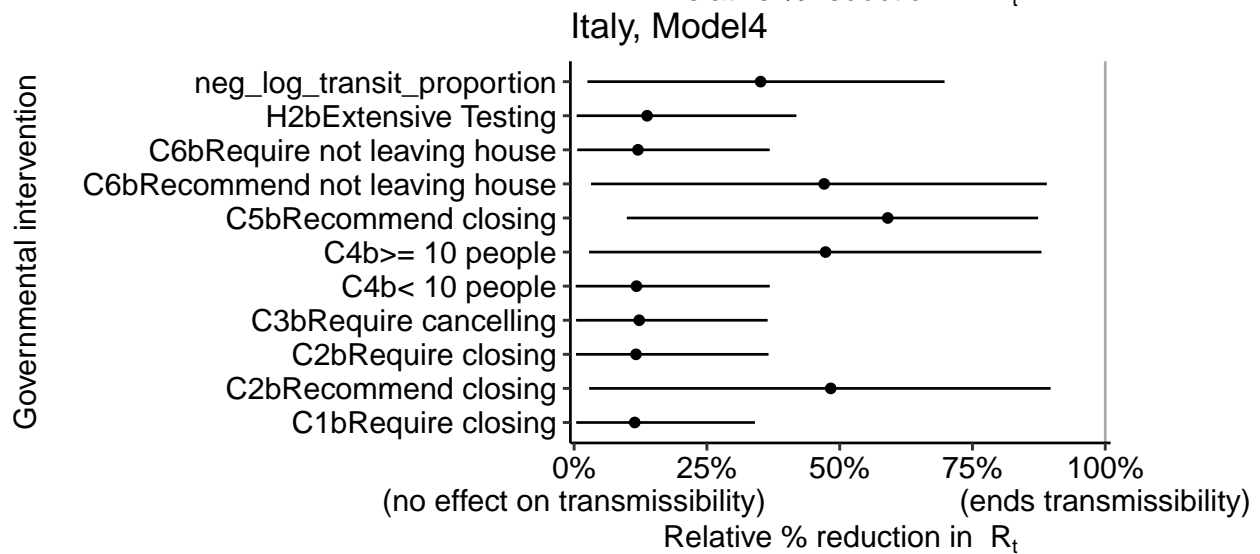
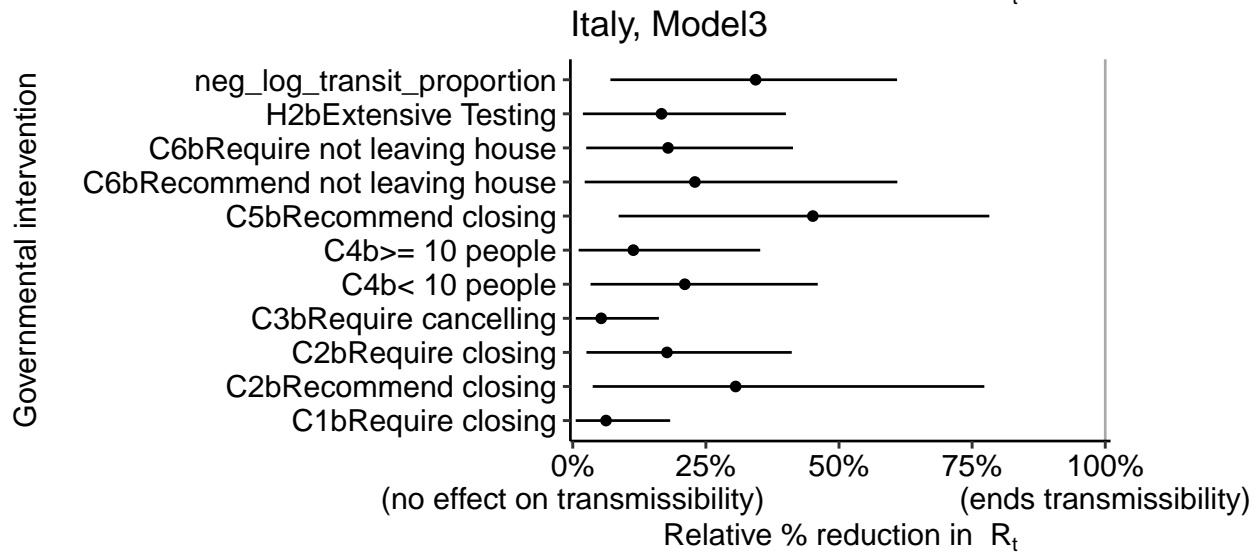
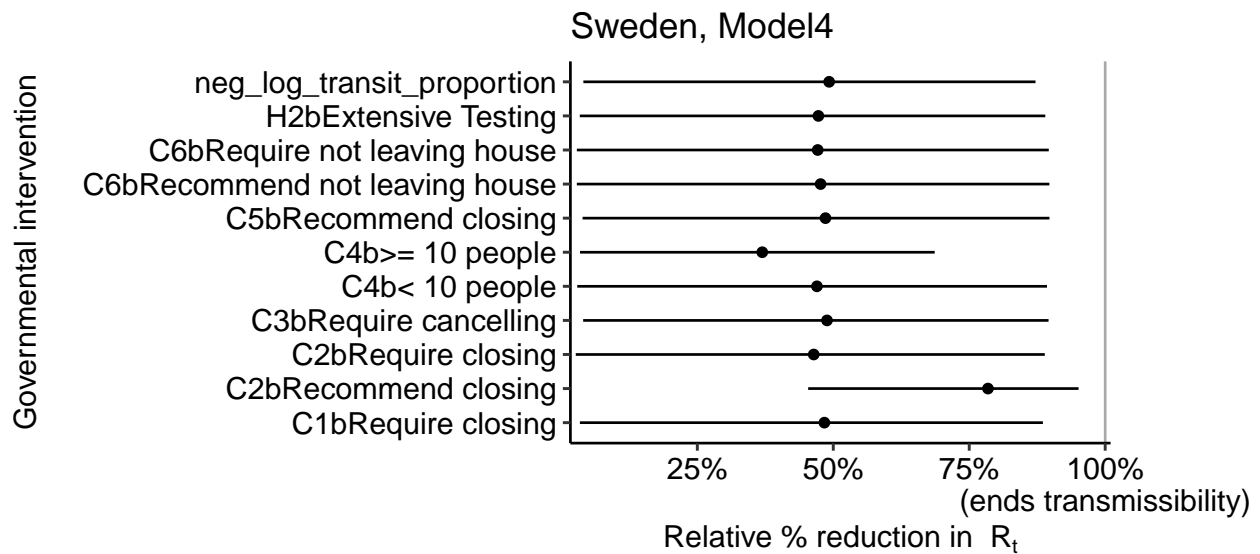
Global covariate effects (model 1 and 2)



Country specific effects (model 3 and 4)

We see that the hierarchical model has an easier time to capture the general effect that mobility has a larger effect than the stringency index. Hence the actual mobility affects R_t more than the interventions.

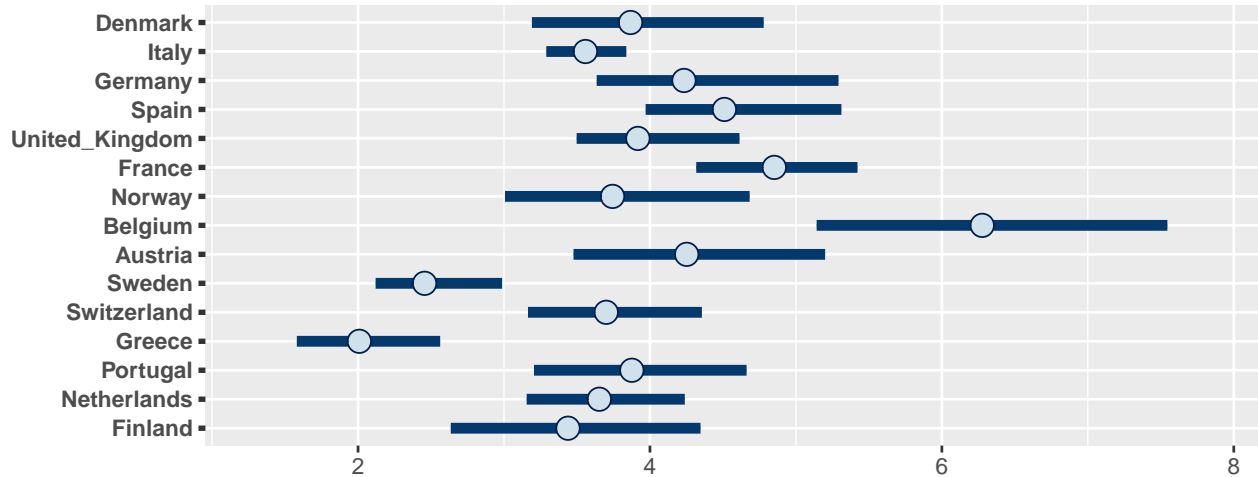




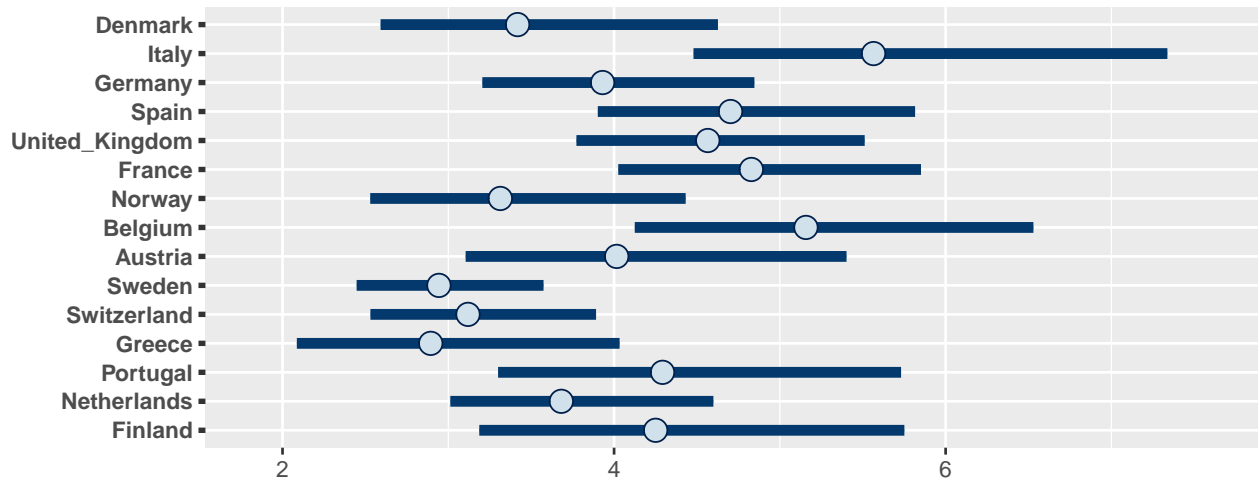
R0 for different countries

We can see that the different values for R0 vary much more between the countries when we use models with common regression coefficients.

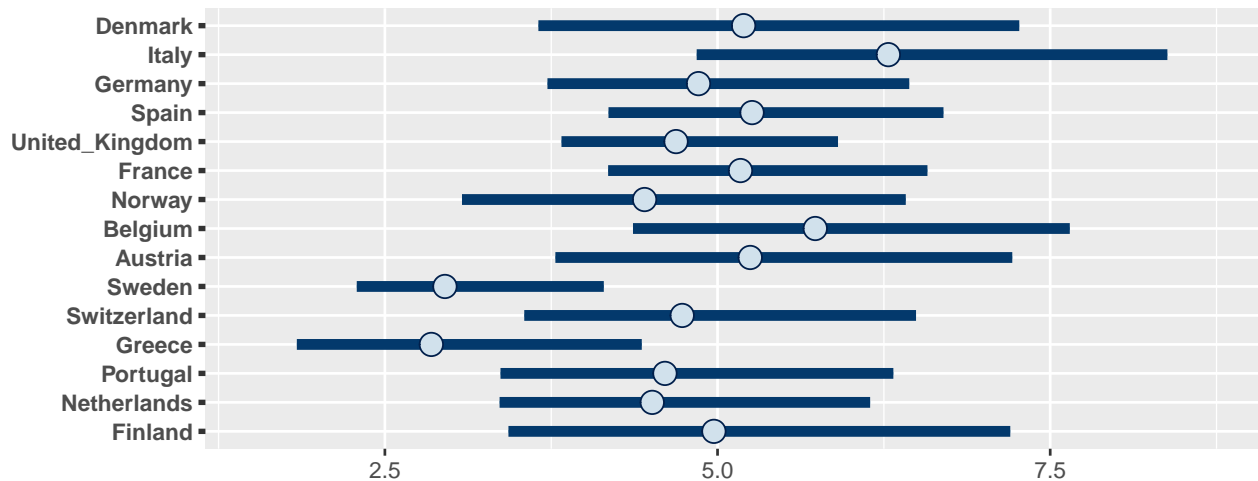
Model1



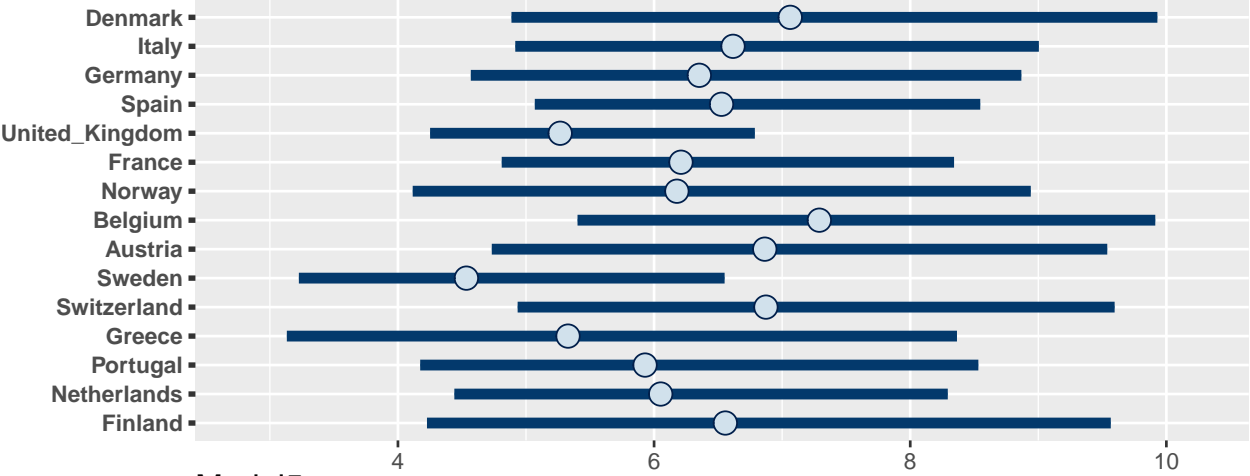
Model2



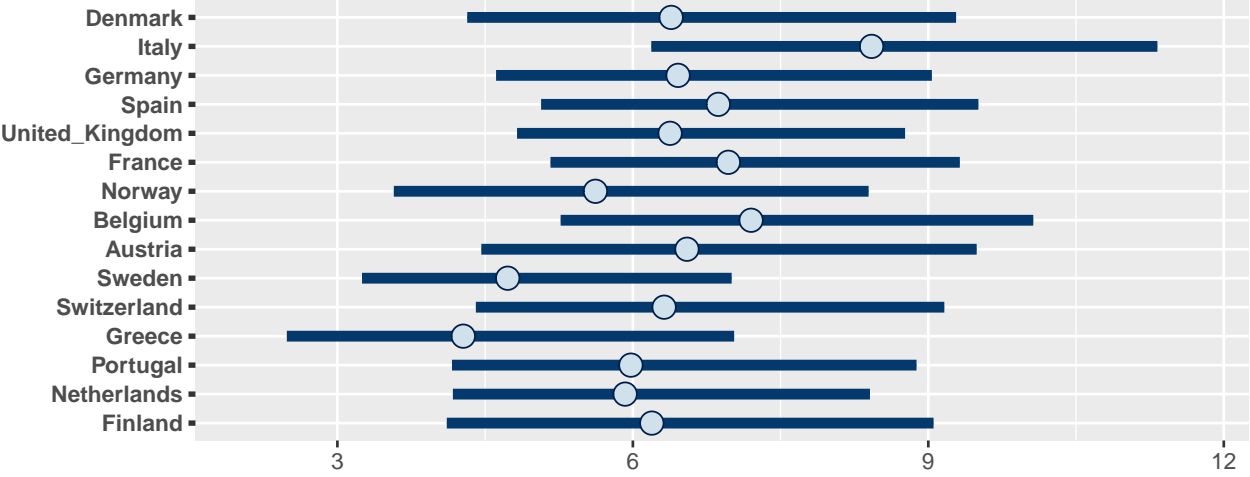
Model3



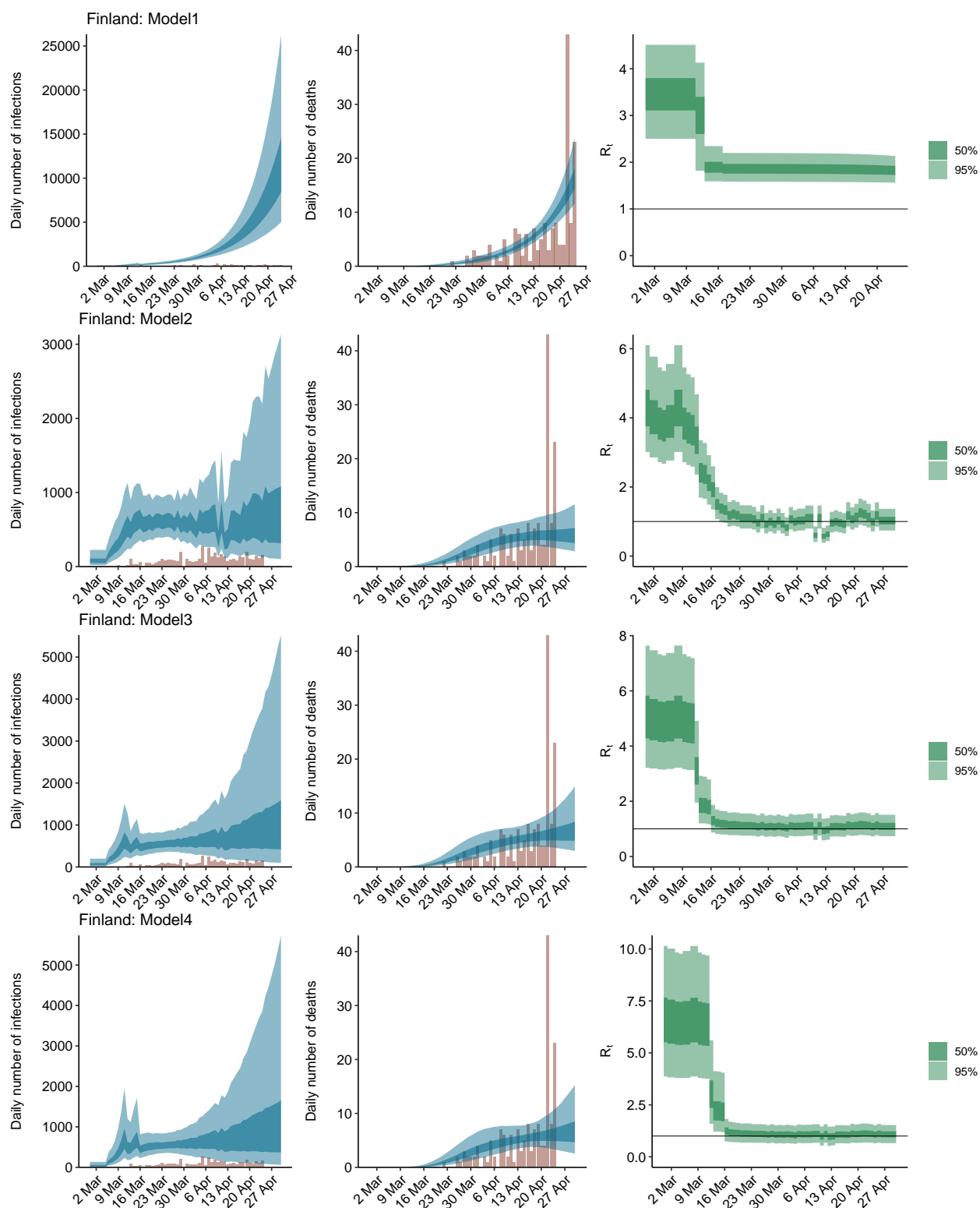
Model4

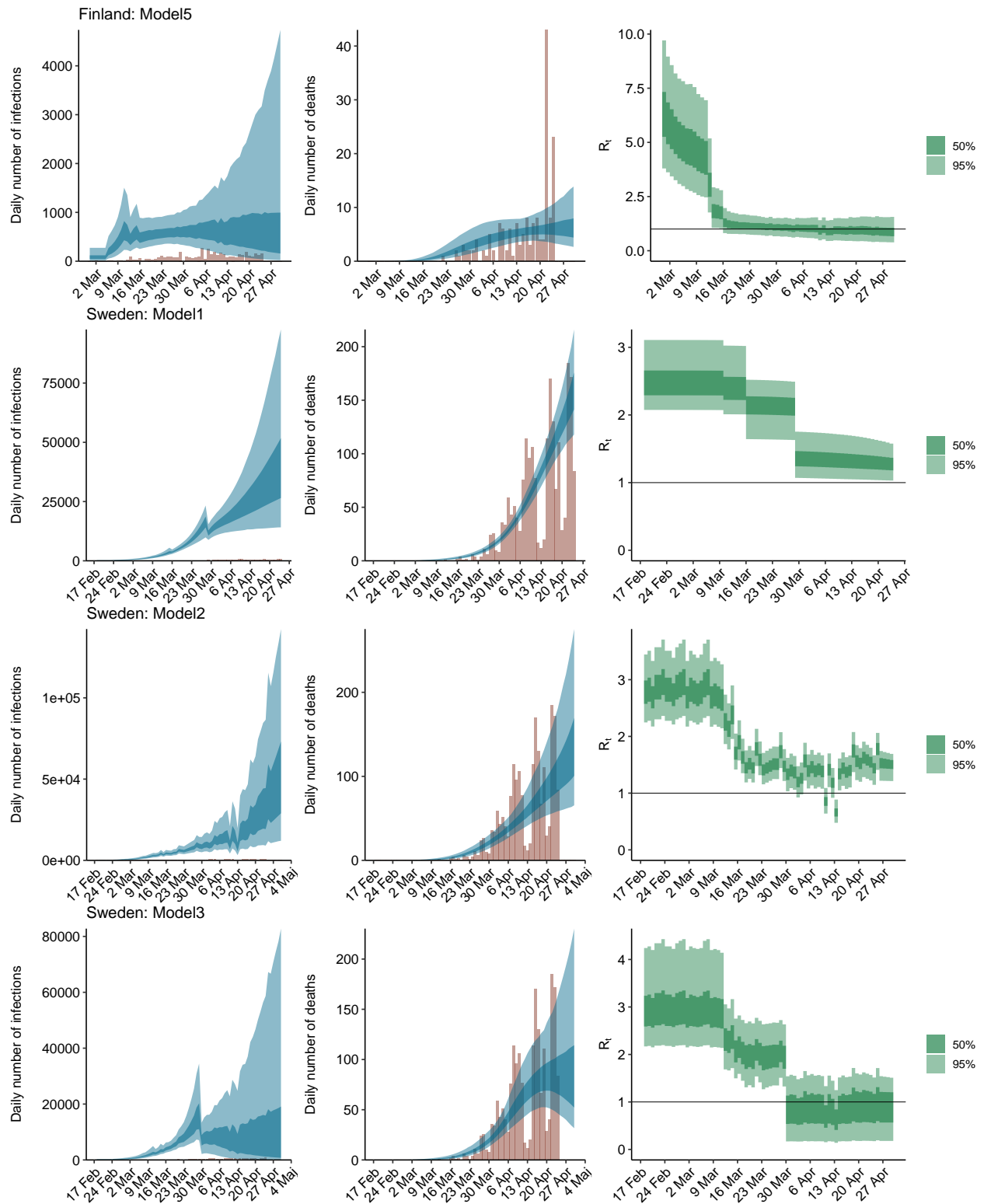


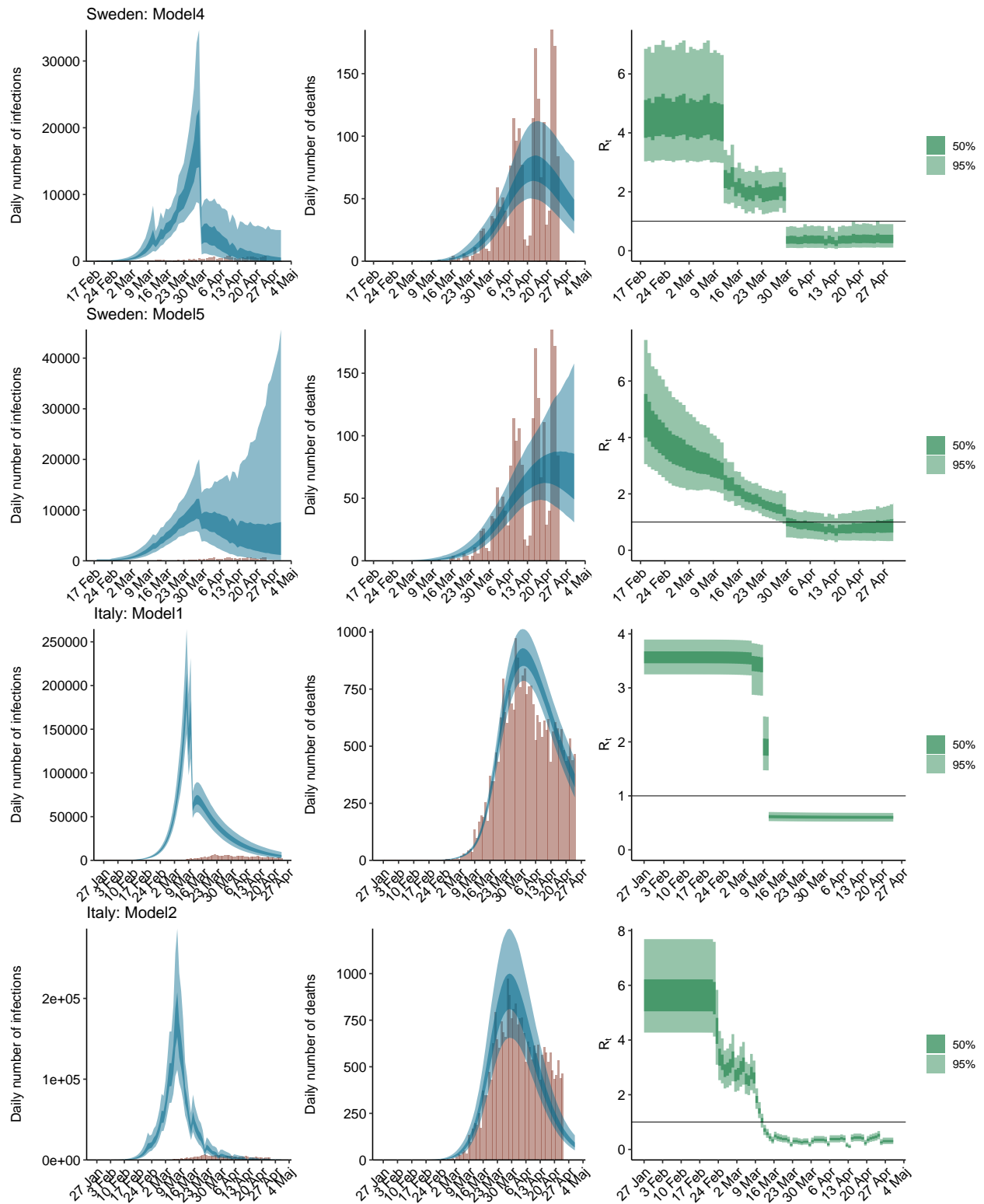
Model5

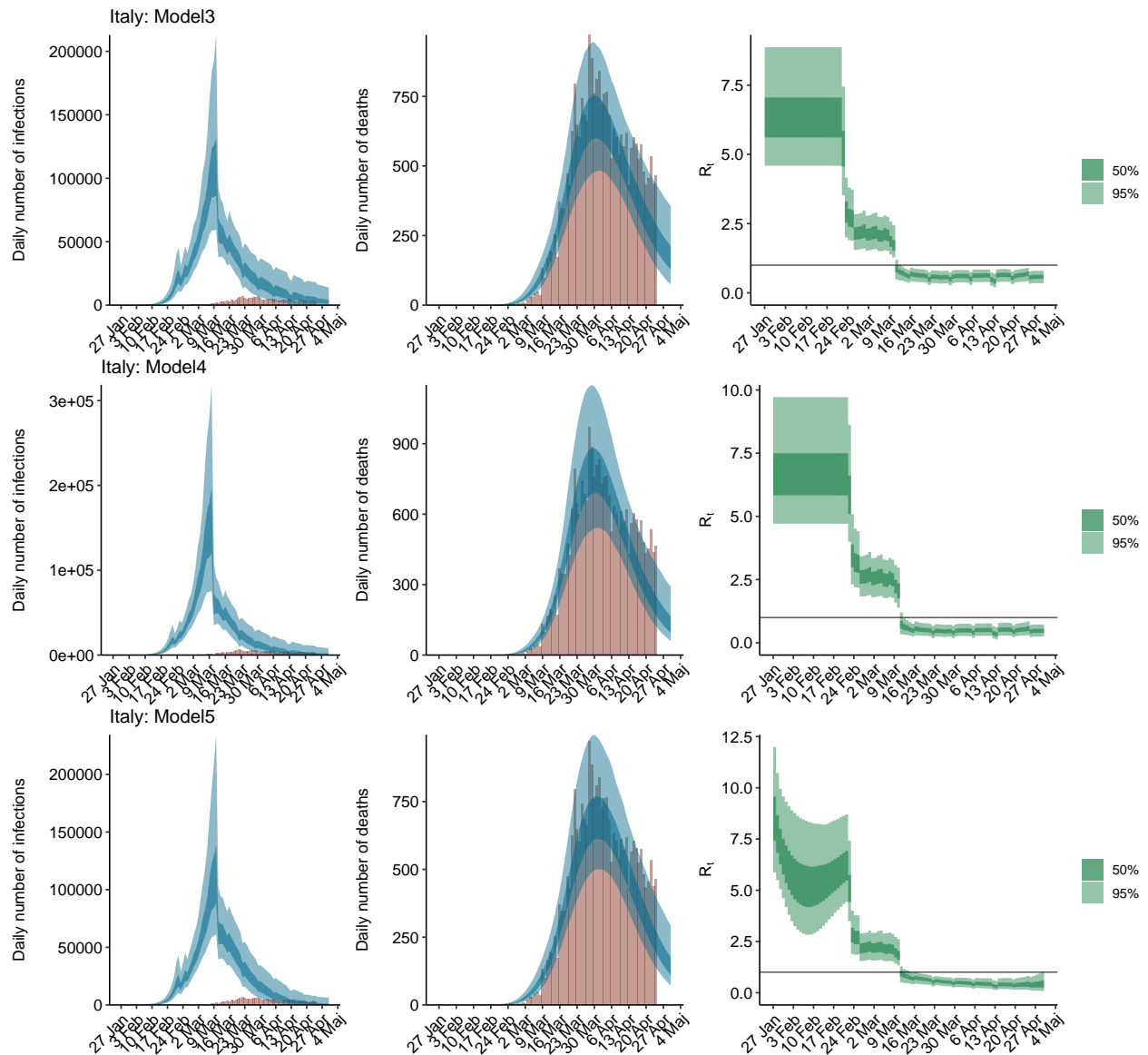


Infections, cases, deaths and R_t by country and model









Stan code

```
## S4 class stanmodel 'base' coded as follows:
## data {
##   int <lower=1> M; // number of countries
##   int <lower=1> P; // number of covariates
##   int <lower=1> N0; // number of days for which to impute infections
##   int<lower=1> N[M]; // days of observed data for country m. each entry must be <= N2
##   int<lower=1> N2; // days of observed data + # of days to forecast
##   int cases[N2,M]; // reported cases
##   int deaths[N2, M]; // reported deaths -- the rows with i > N contain -1 and should be ignored
##   matrix[N2, M] f; // h * s
##   matrix[N2, P] X[M]; // features matrix
##   int EpidemicStart[M];
##   real pop[M];
##   real SI[N2]; // fixed pre-calculated SI using emprical data from Neil
```

```

## }
##
## transformed data {
##   vector[N2] SI_rev; // SI in reverse order
##   vector[N2] f_rev[M]; // f in reversed order
##
##   for(i in 1:N2)
##     SI_rev[i] = SI[N2-i+1];
##
##   for(m in 1:M){
##     for(i in 1:N2) {
##       f_rev[m, i] = f[N2-i+1,m];
##     }
##   }
## }
##
##
## parameters {
##   real<lower=0> mu[M]; // intercept for Rt
##   real<lower=0> alpha_hier[P]; // sudo parameter for the hier term for alpha
##   real<lower=0> gamma;
##   vector[M] lockdown;
##   real<lower=0> kappa;
##   real<lower=0> y[M];
##   real<lower=0> phi;
##   real<lower=0> tau;
##   real <lower=0> ifr_noise[M];
## }
##
## transformed parameters {
##   vector[P] alpha;
##   matrix[N2, M] prediction = rep_matrix(0,N2,M);
##   matrix[N2, M] E_deaths = rep_matrix(0,N2,M);
##   matrix[N2, M] Rt = rep_matrix(0,N2,M);
##   matrix[N2, M] Rt_adj = Rt;
##
##   {
##     matrix[N2,M] cumm_sum = rep_matrix(0,N2,M);
##     for(i in 1:P){
##       alpha[i] = alpha_hier[i] - ( log(1.05) / 6.0 );
##     }
##     for (m in 1:M){
##       prediction[1:NO,m] = rep_vector(y[m],NO); // learn the number of cases in the first NO days
##       cumm_sum[2:NO,m] = cumulative_sum(prediction[2:NO,m]);
##
##       Rt[,m] = mu[m] * exp(-X[m] * alpha - X[m][,5] * lockdown[m]);
##       Rt_adj[1:NO,m] = Rt[1:NO,m];
##       for (i in (NO+1):N2) {
##         real convolution = dot_product(sub_col(prediction, 1, m, i-1), tail(SI_rev, i-1));
##         cumm_sum[i,m] = cumm_sum[i-1,m] + prediction[i-1,m];
##         Rt_adj[i,m] = ((pop[m]-cumm_sum[i,m]) / pop[m]) * Rt[i,m];
##         prediction[i, m] = Rt_adj[i,m] * convolution;
##       }
##       E_deaths[1, m]= 1e-15 * prediction[1,m];

```

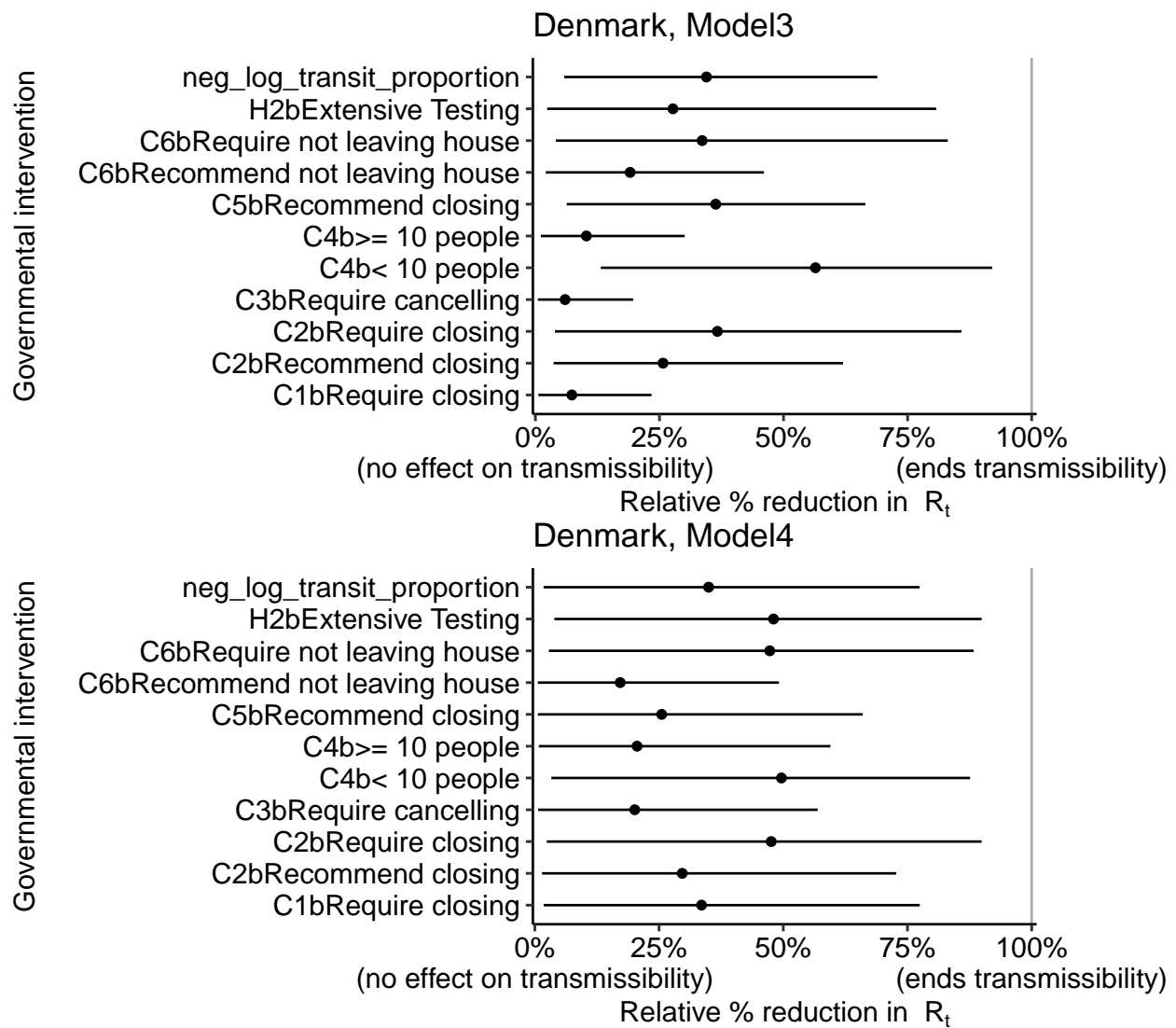
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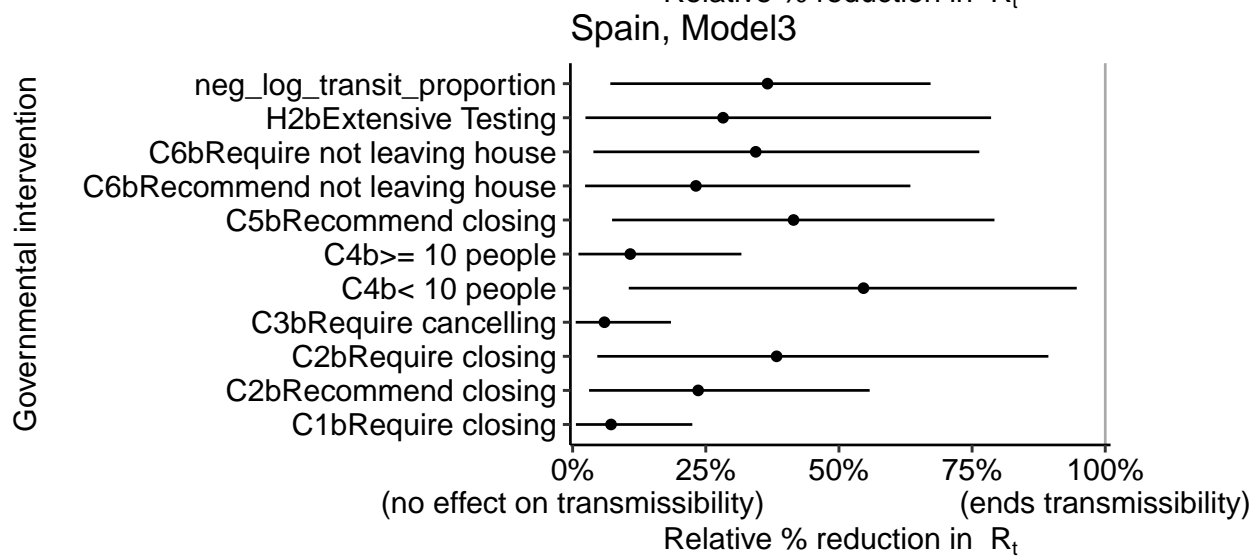
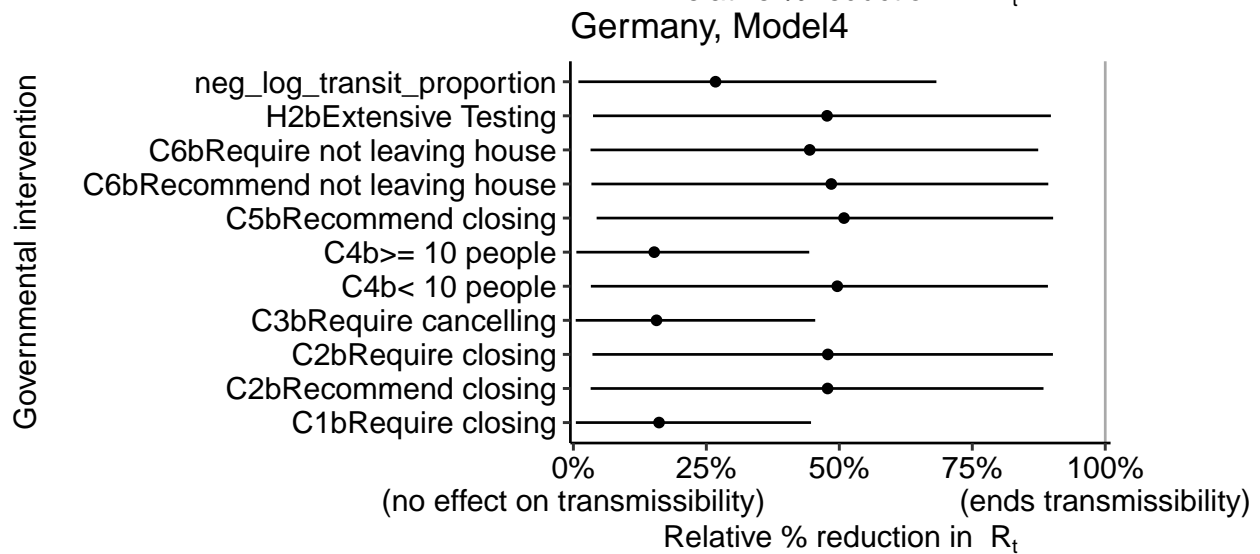
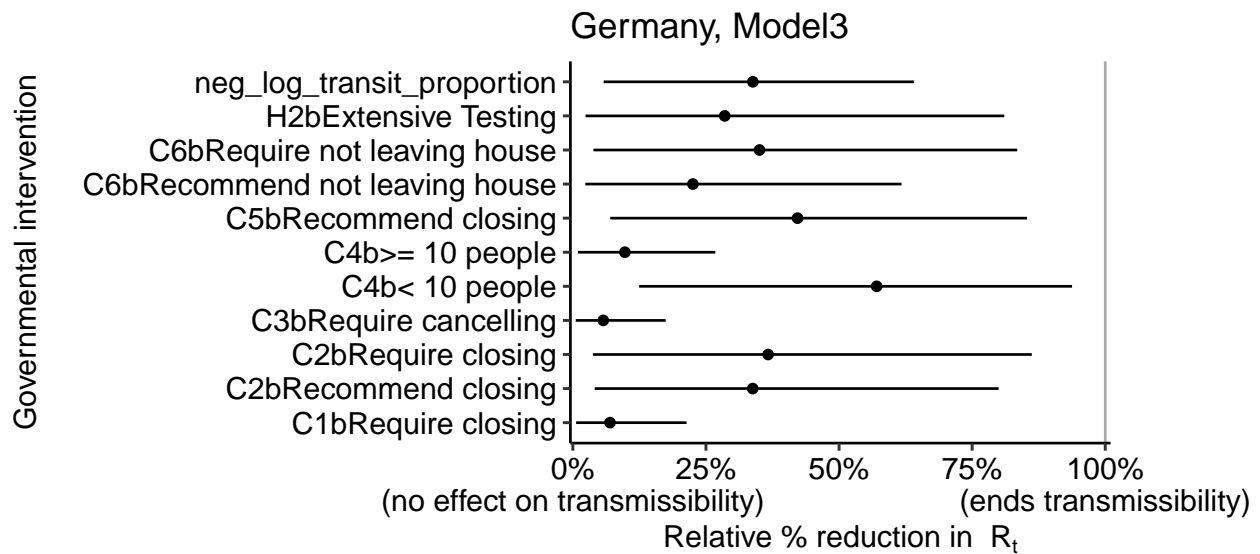
##         for (i in 2:N2){
##             E_deaths[i,m] = ifr_noise[m] * dot_product(sub_col(prediction, 1, m, i-1), tail(f_rev[m],
##         })
##     }
## }
## }
## model {
##     tau ~ exponential(0.03);
##     for (m in 1:M){
##         y[m] ~ exponential(1/tau);
##     }
##     gamma ~ normal(0,.2);
##     lockdown ~ normal(0,gamma);
##     phi ~ normal(0,5);
##     kappa ~ normal(0,0.5);
##     mu ~ normal(3.28, kappa); // citation: https://academic.oup.com/jtm/article/27/2/taaa021/5735319
##     alpha_hier ~ gamma(.1667,1);
##     ifr_noise ~ normal(1,0.1);
##     for(m in 1:M){
##         deaths[EpidemicStart[m]:N[m], m] ~ neg_binomial_2(E_deaths[EpidemicStart[m]:N[m], m], phi);
##     }
## }
##
## generated quantities {
##     matrix[N2, M] prediction0 = rep_matrix(0,N2,M);
##     matrix[N2, M] E_deaths0 = rep_matrix(0,N2,M);
##
##     {
##         matrix[N2,M] cumm_sum0 = rep_matrix(0,N2,M);
##         for (m in 1:M){
##             for (i in 2:NO){
##                 cumm_sum0[i,m] = cumm_sum0[i-1,m] + y[m];
##             }
##             prediction0[1:NO,m] = rep_vector(y[m],NO);
##             for (i in (NO+1):N2) {
##                 real convolution0 = dot_product(sub_col(prediction0, 1, m, i-1), tail(SI_rev, i-1));
##                 cumm_sum0[i,m] = cumm_sum0[i-1,m] + prediction0[i-1,m];
##                 prediction0[i, m] = ((pop[m]-cumm_sum0[i,m]) / pop[m]) * mu[m] * convolution0;
##             }
##             E_deaths0[1, m]= 1e-15 * prediction0[1,m];
##             for (i in 2:N2){
##                 E_deaths0[i,m] = ifr_noise[m] * dot_product(sub_col(prediction0, 1, m, i-1), tail(f_rev[m],
##             })
##         }
##     }
## }
##

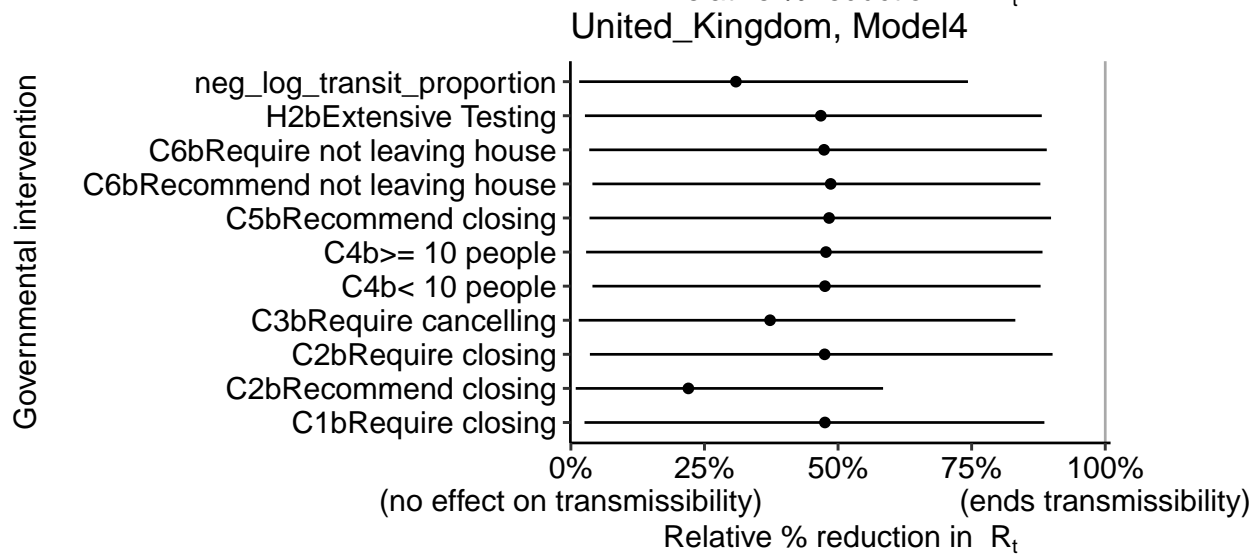
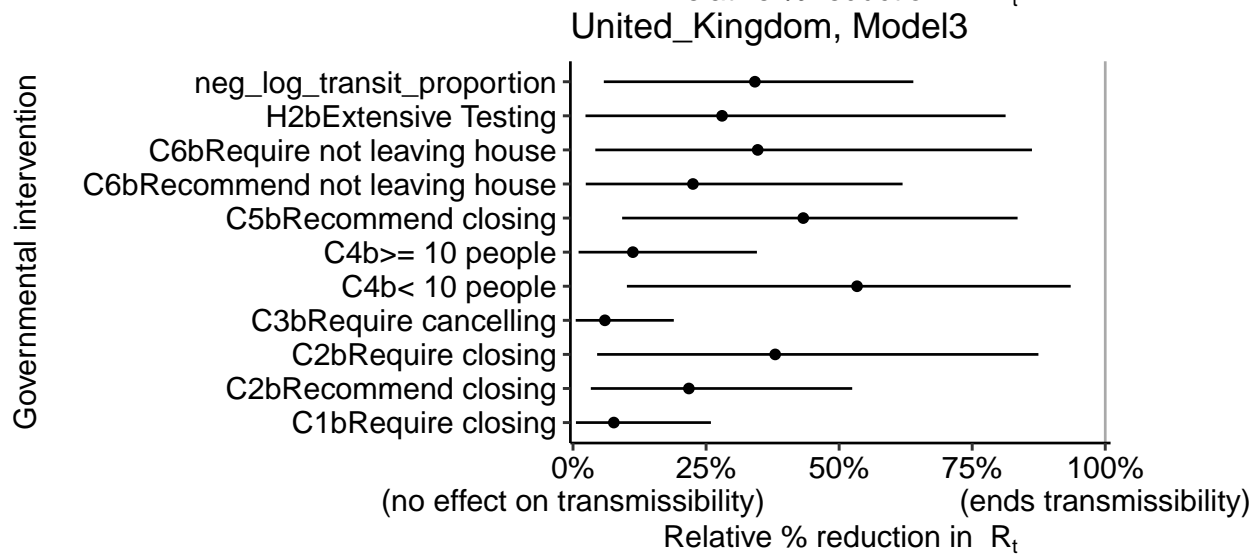
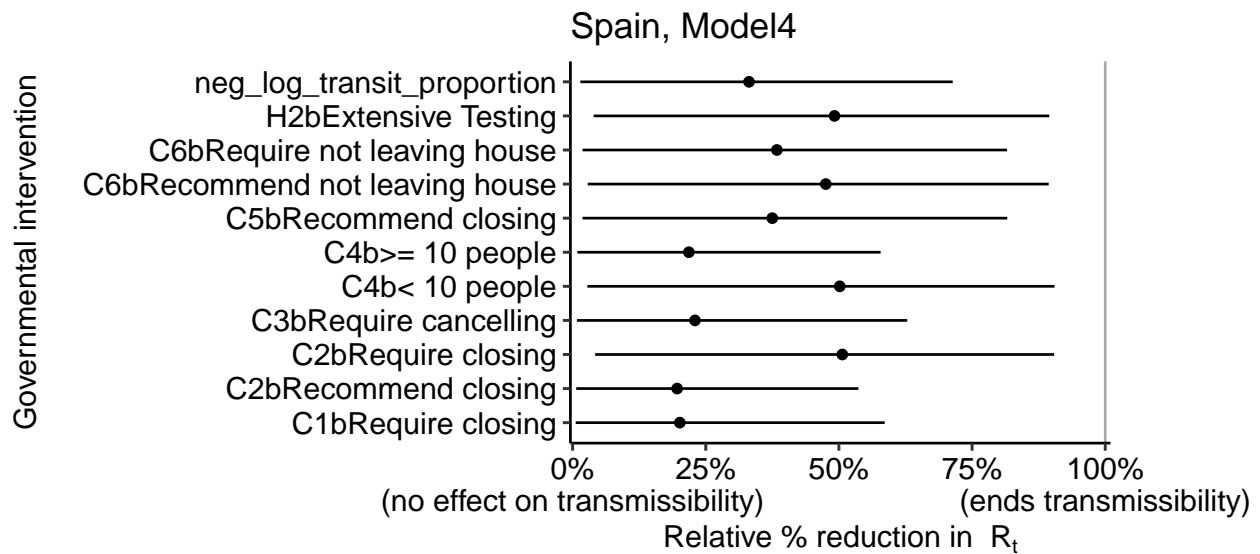
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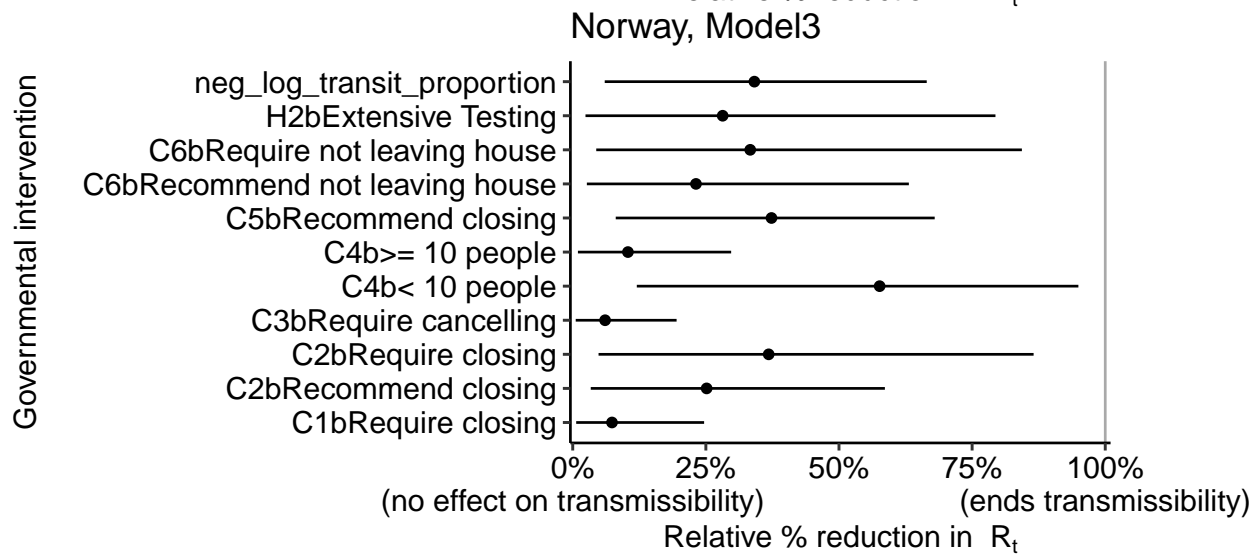
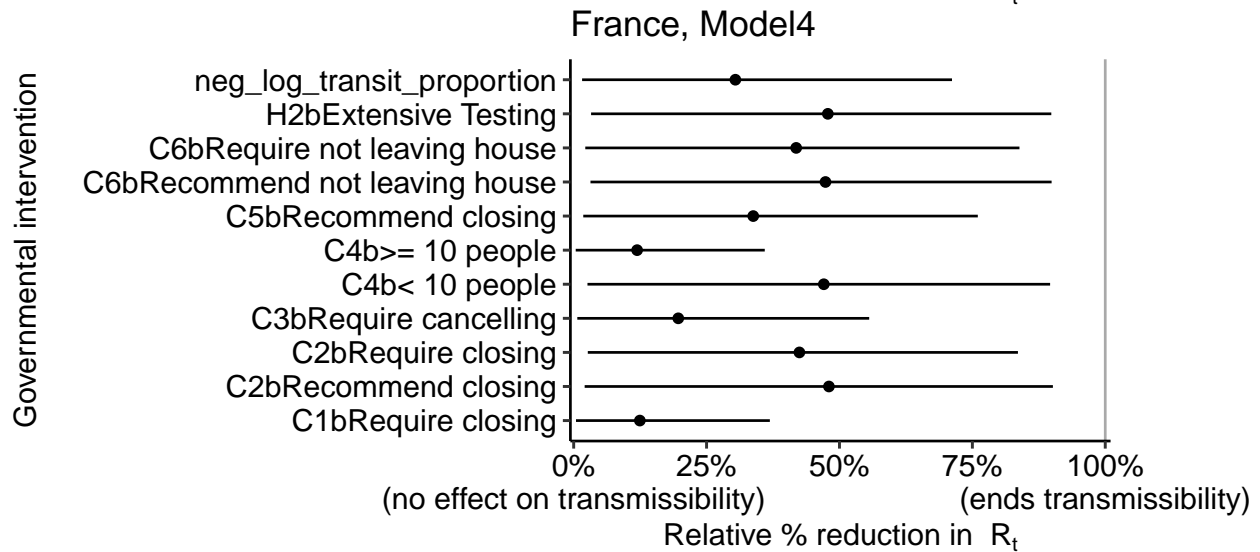
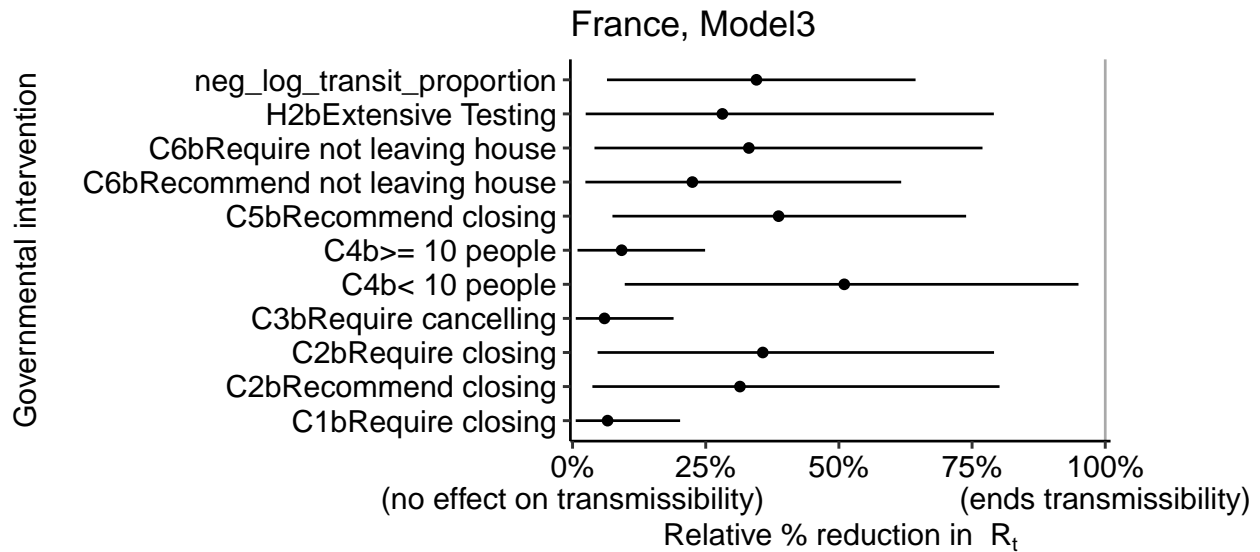
Appendix

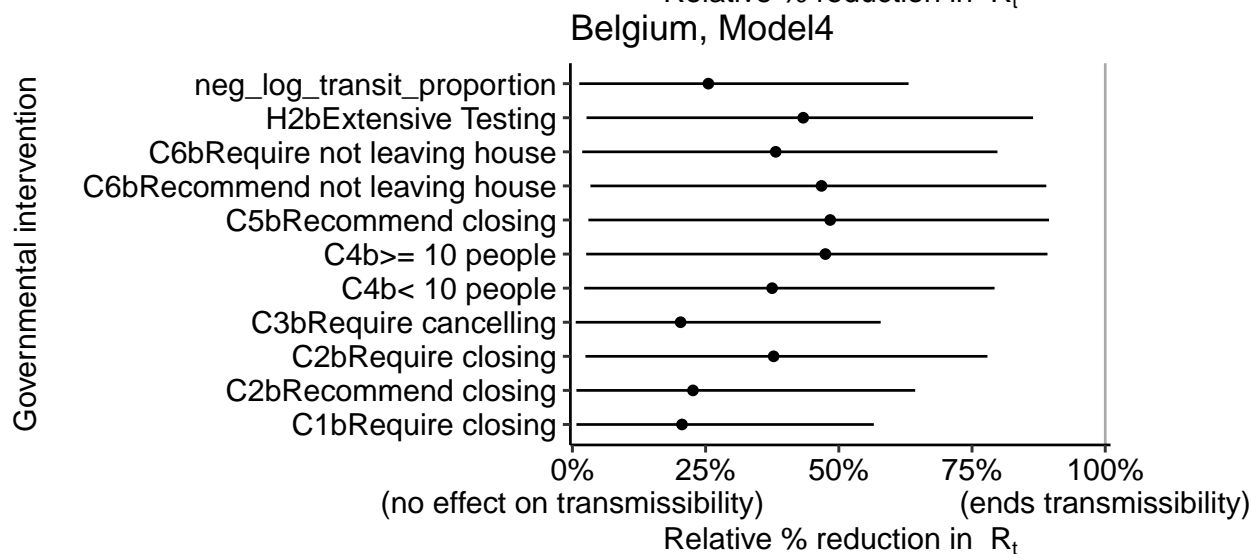
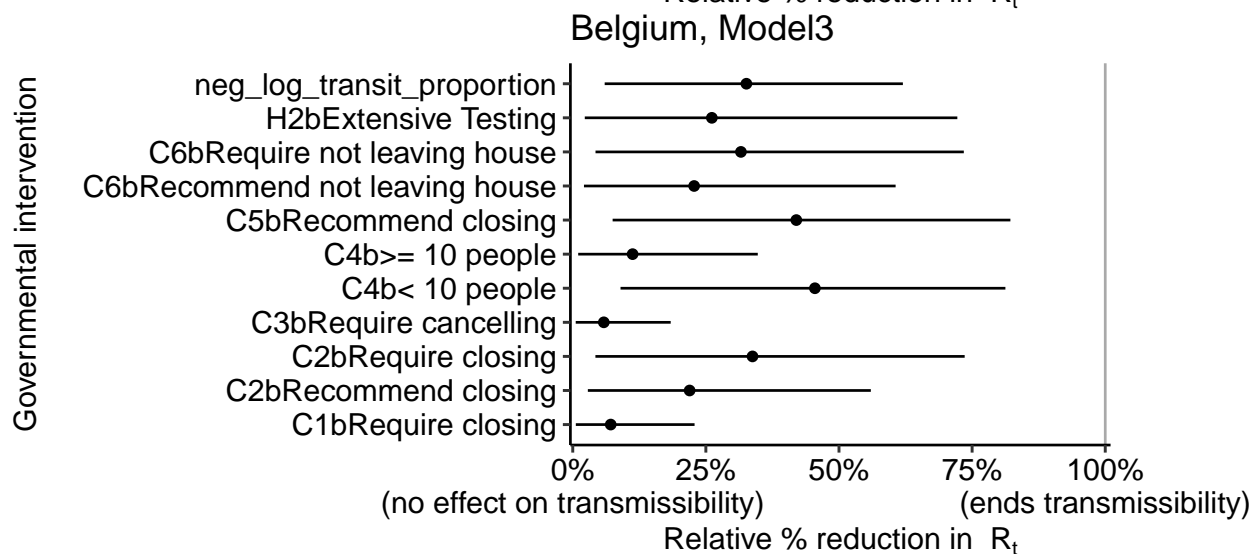
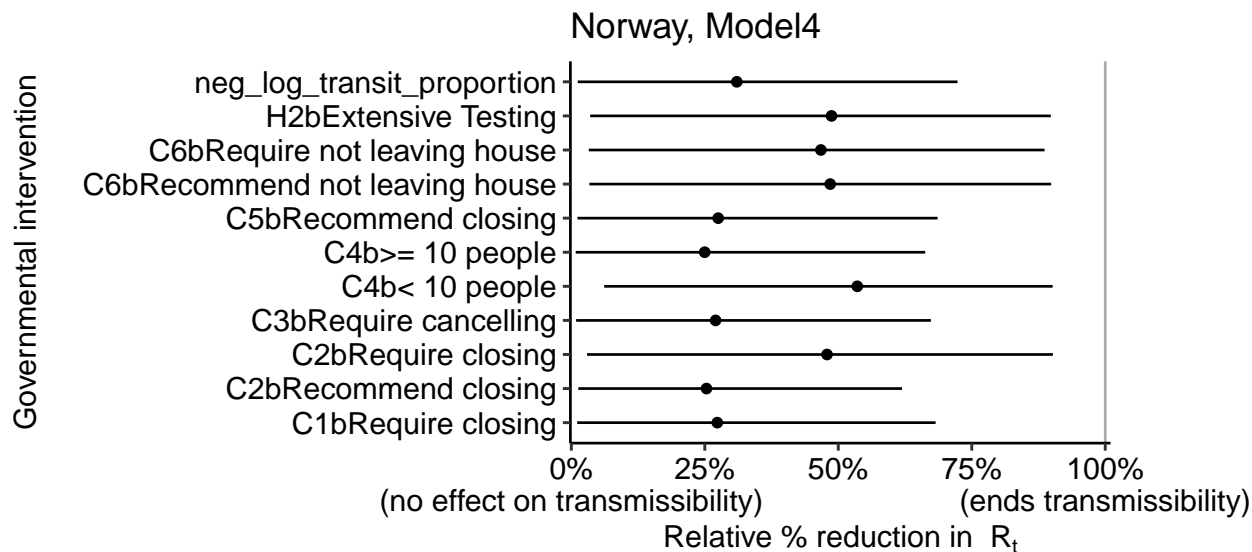
Country specific effects (model 3 to 4)

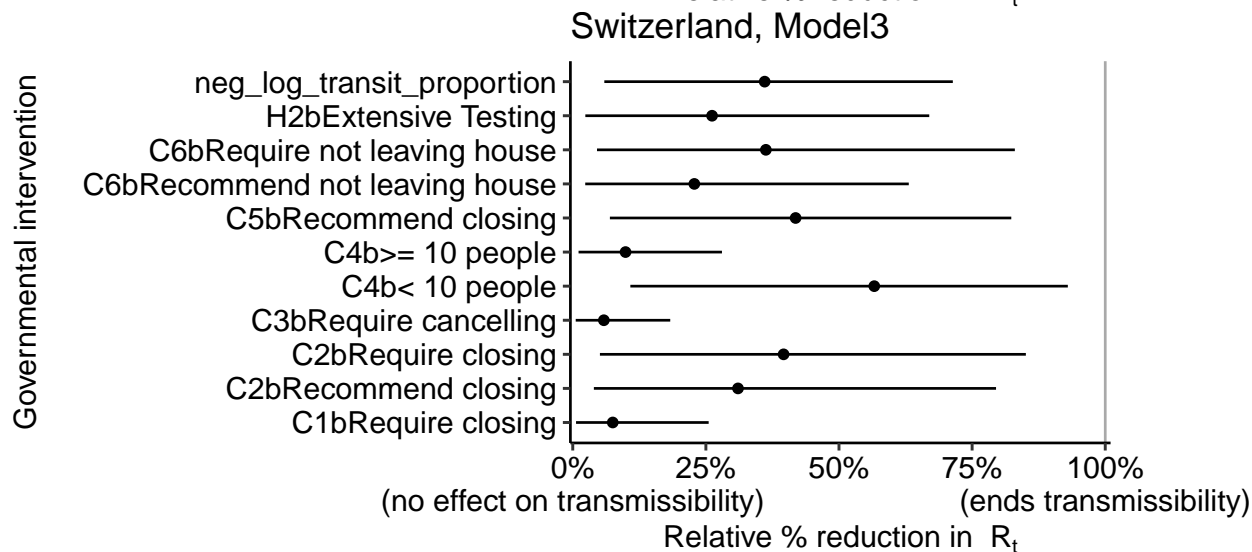
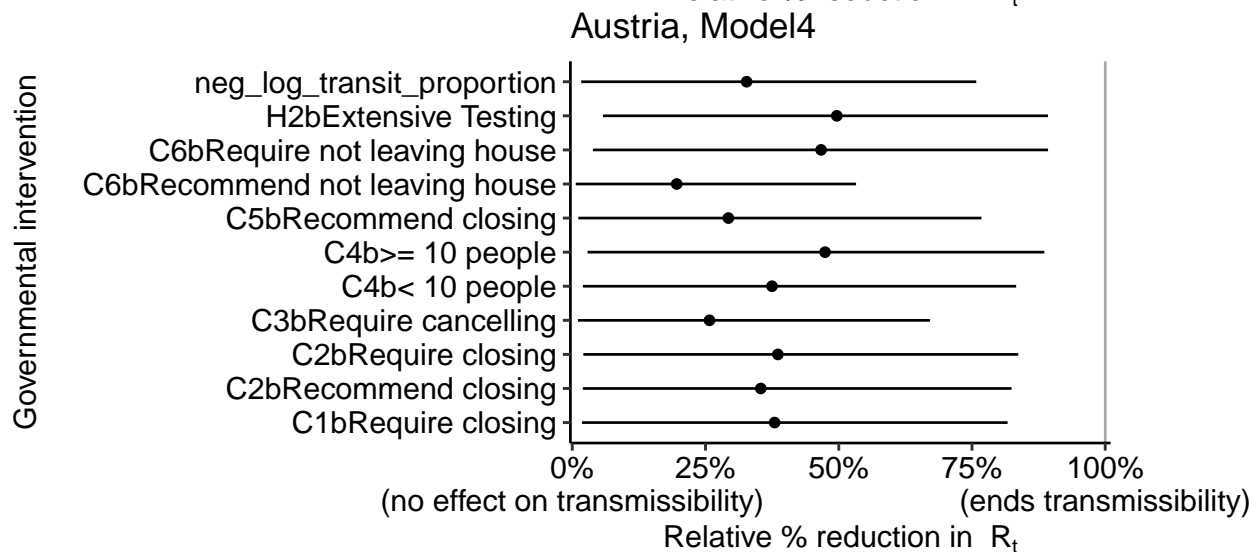
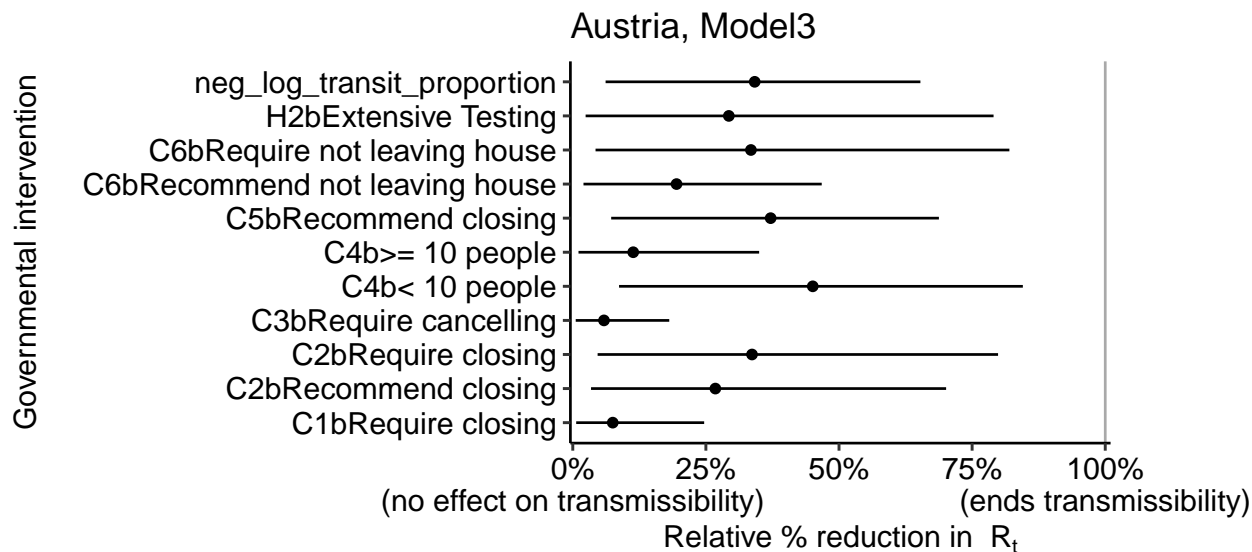


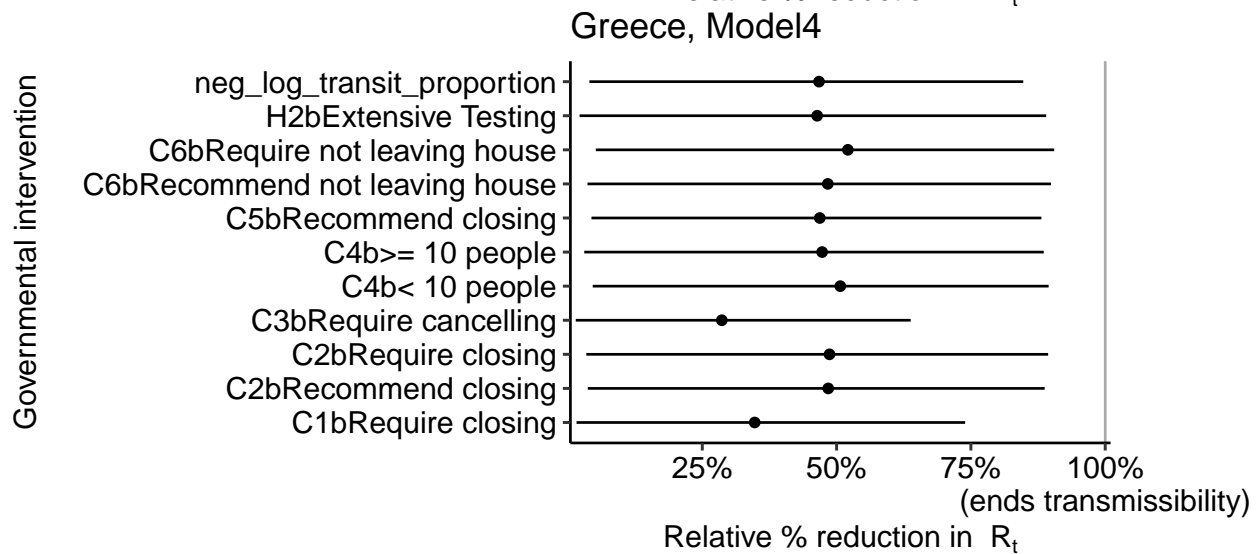
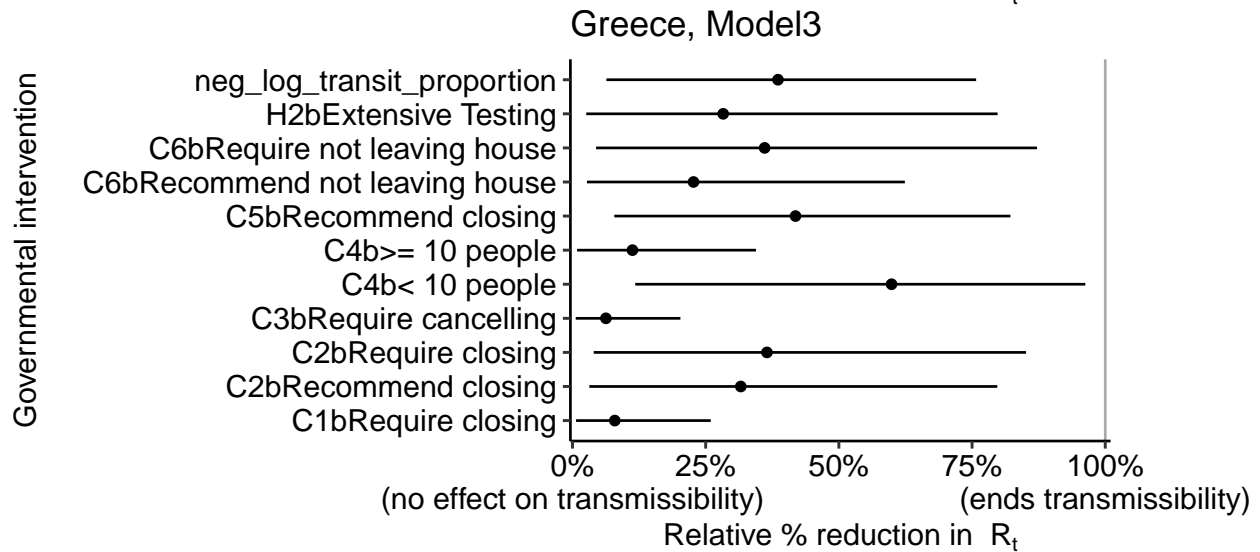
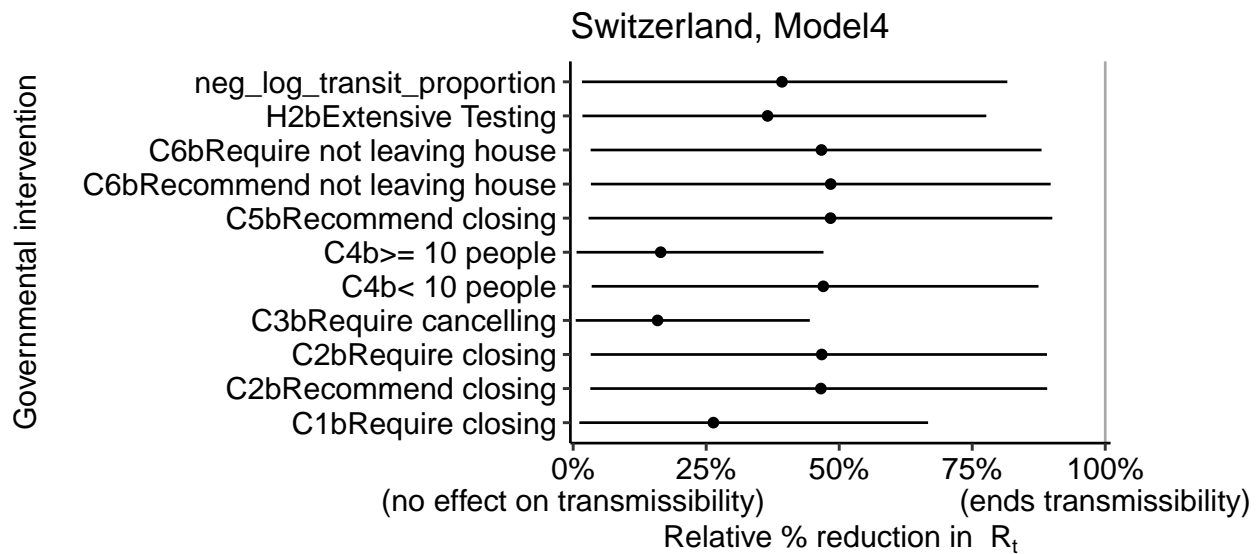


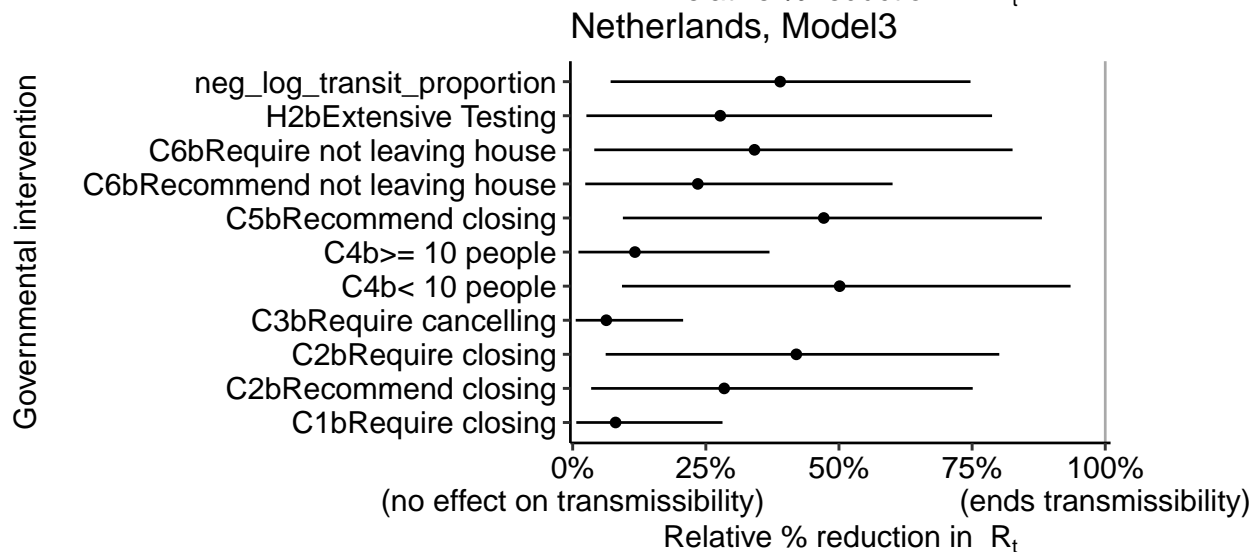
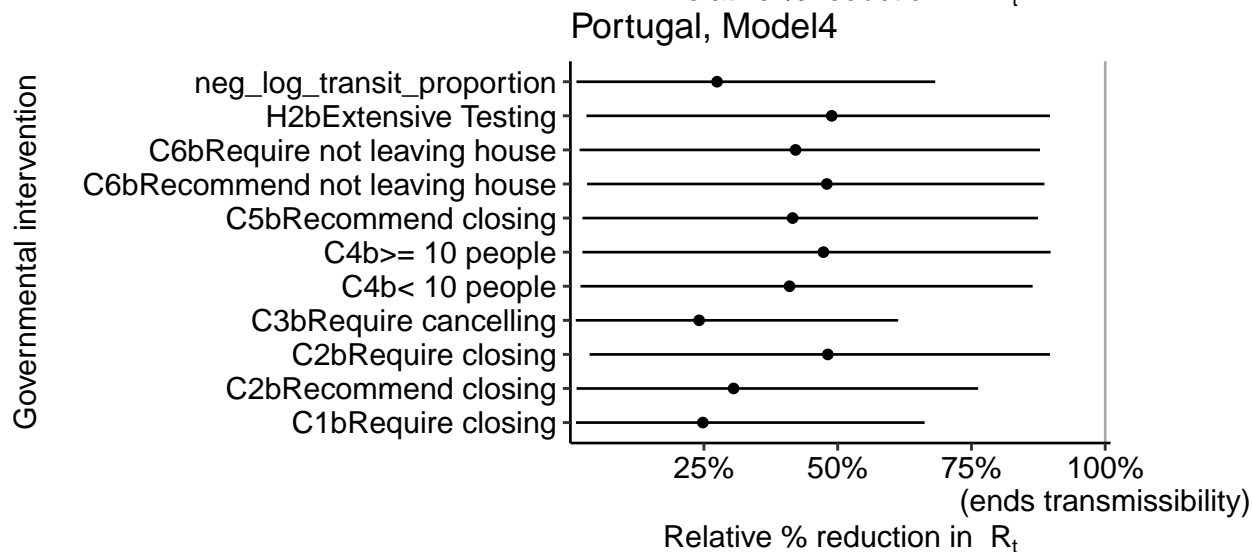
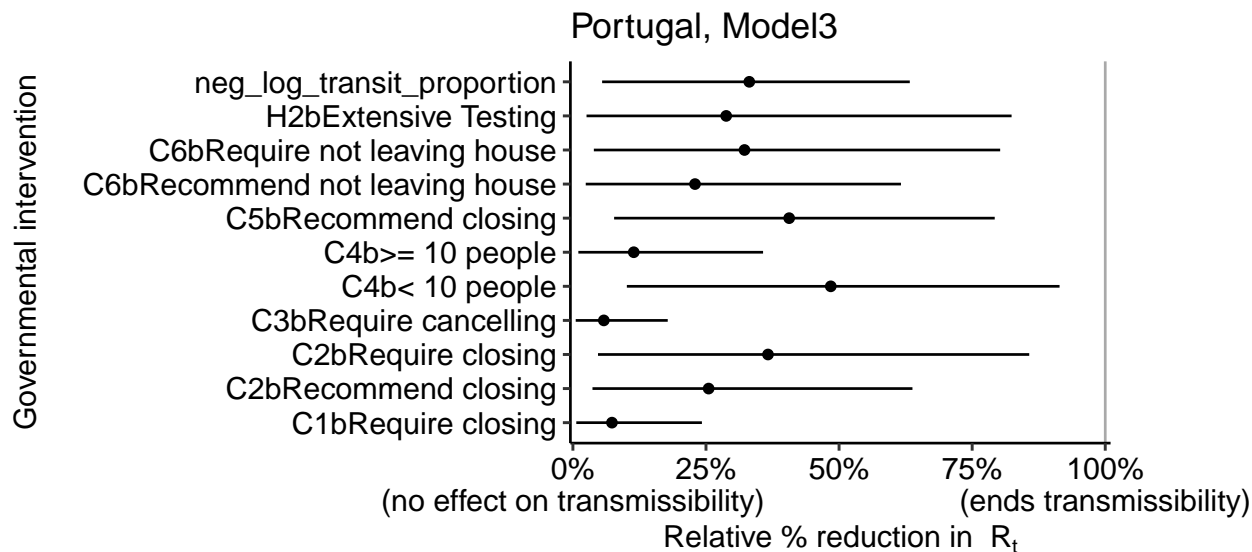


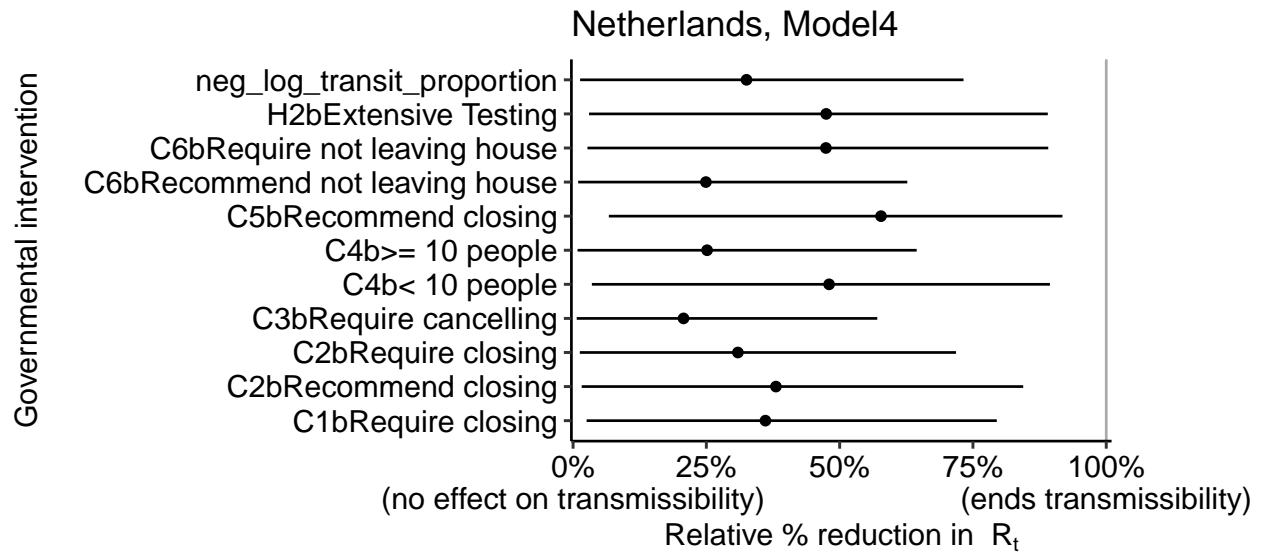




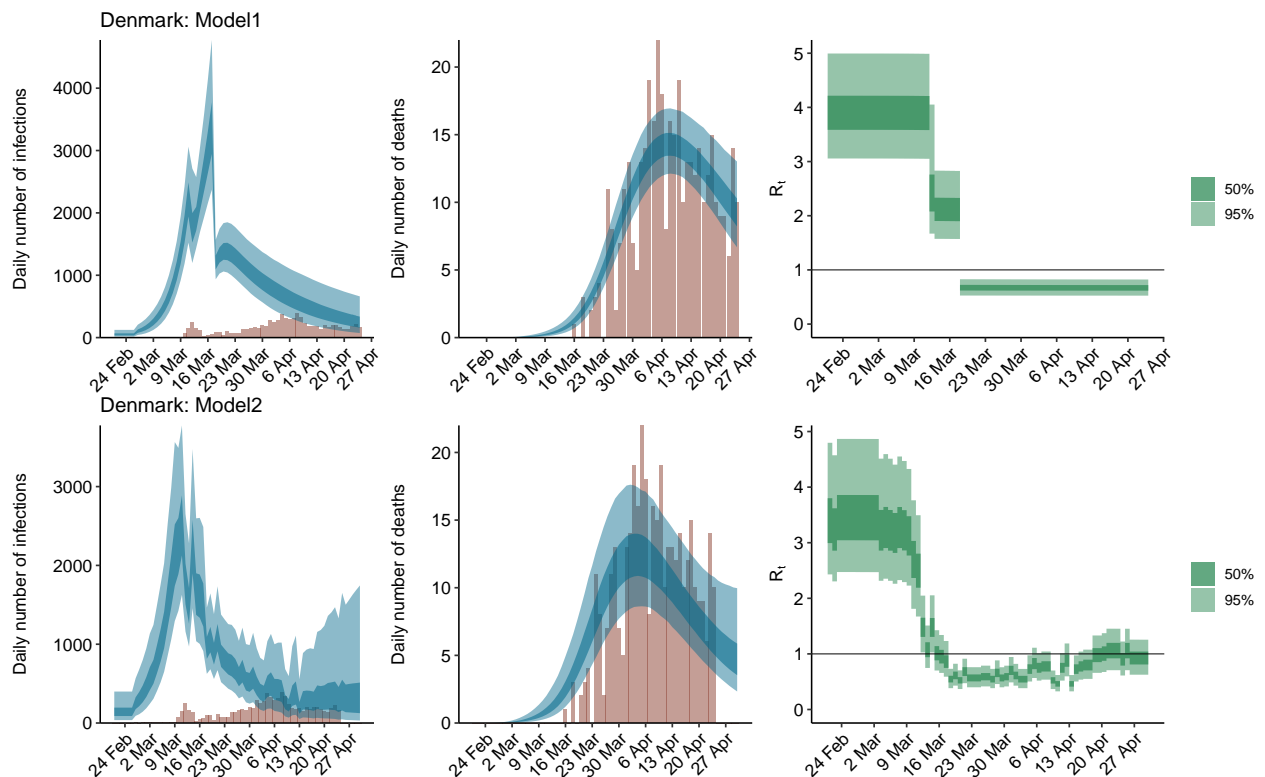


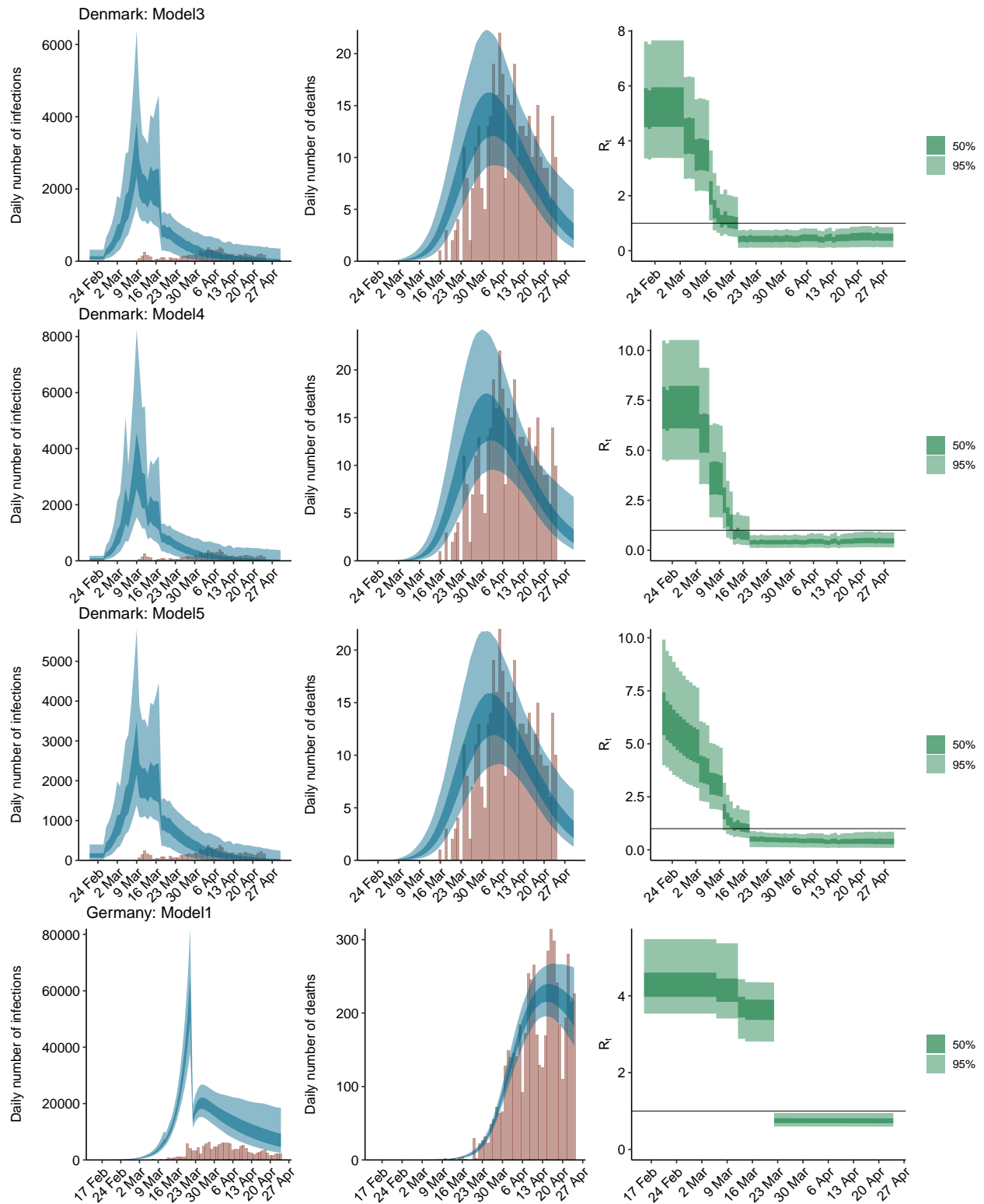


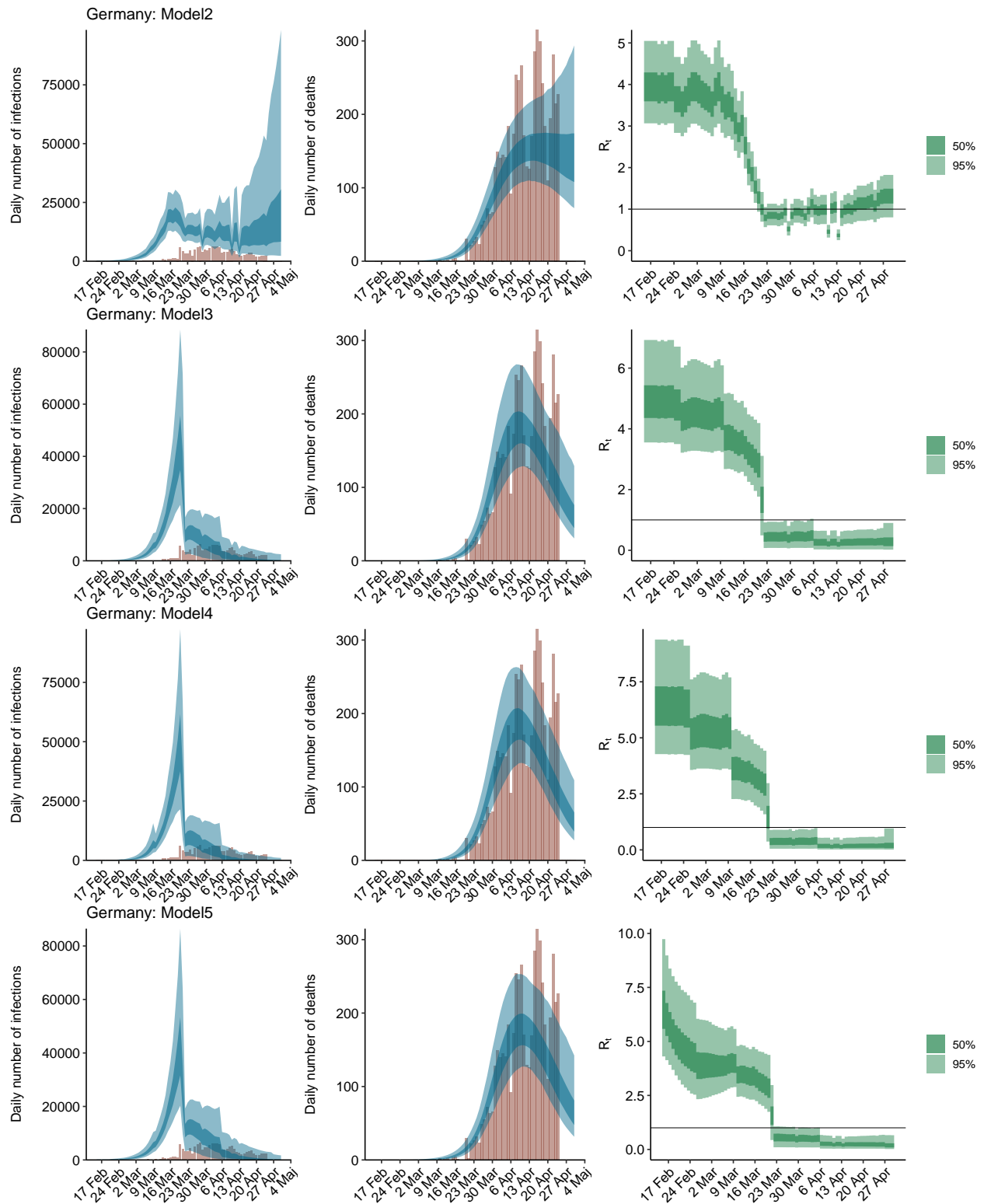


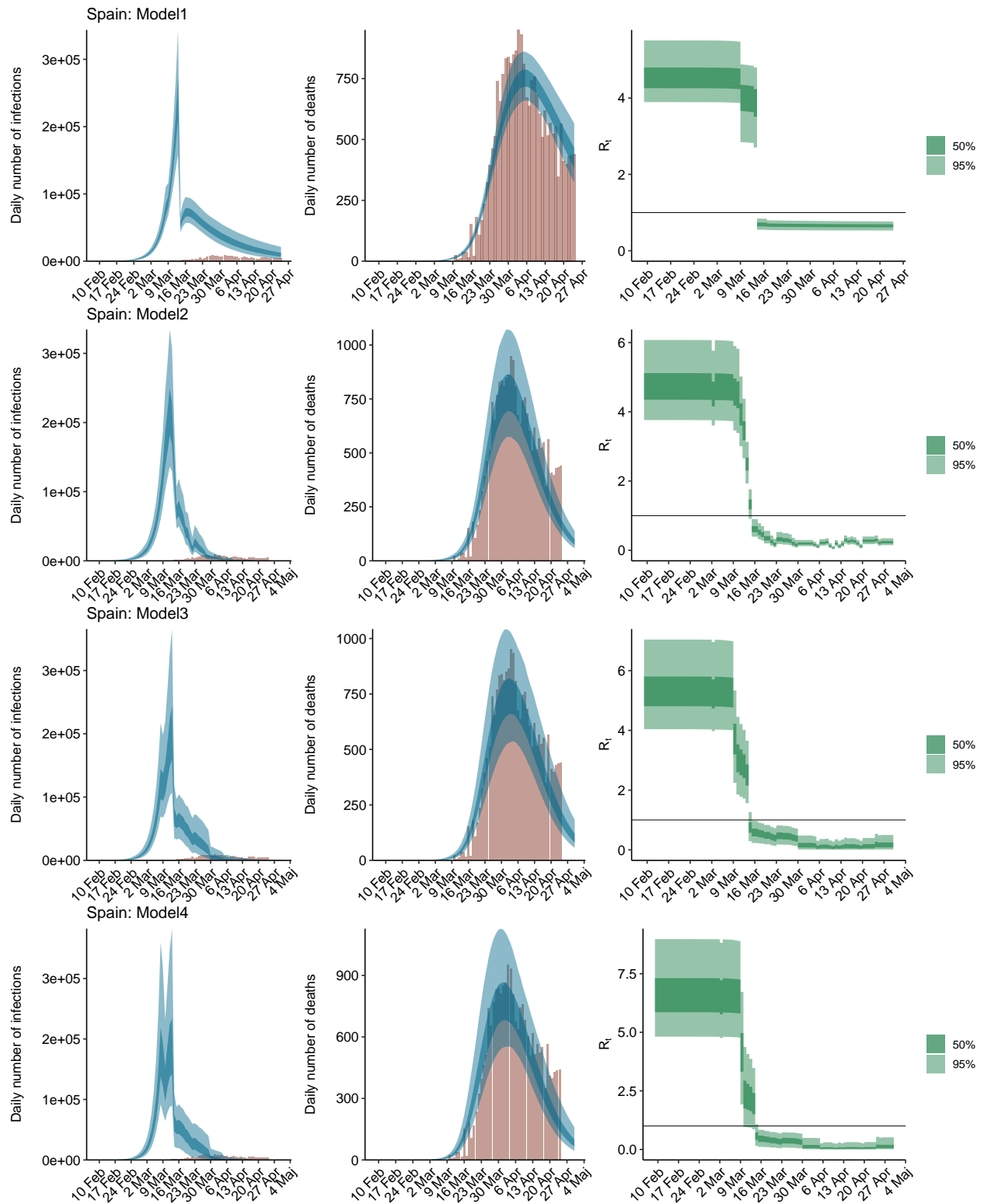


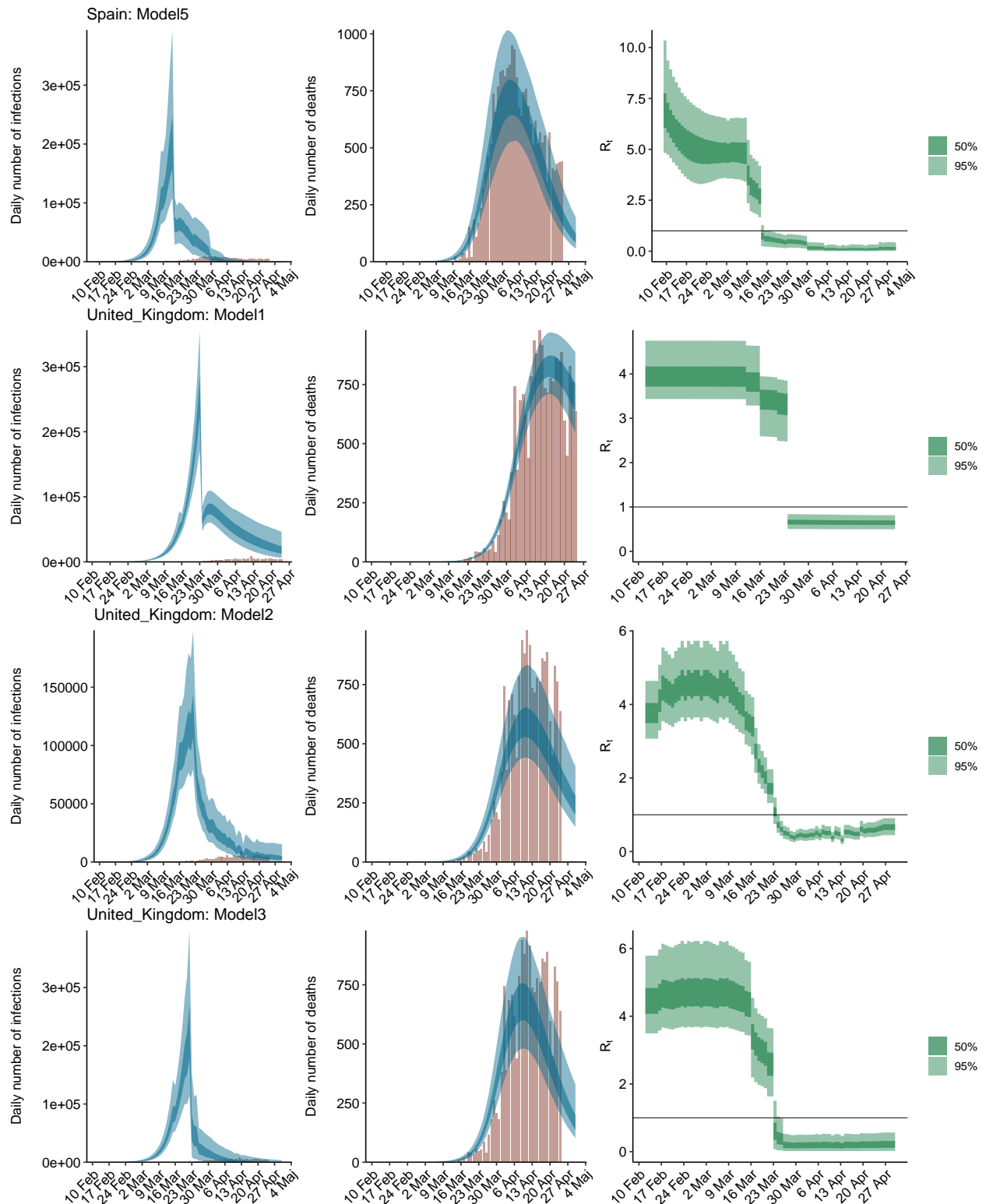
Infections, cases, deaths and R_t by country and model

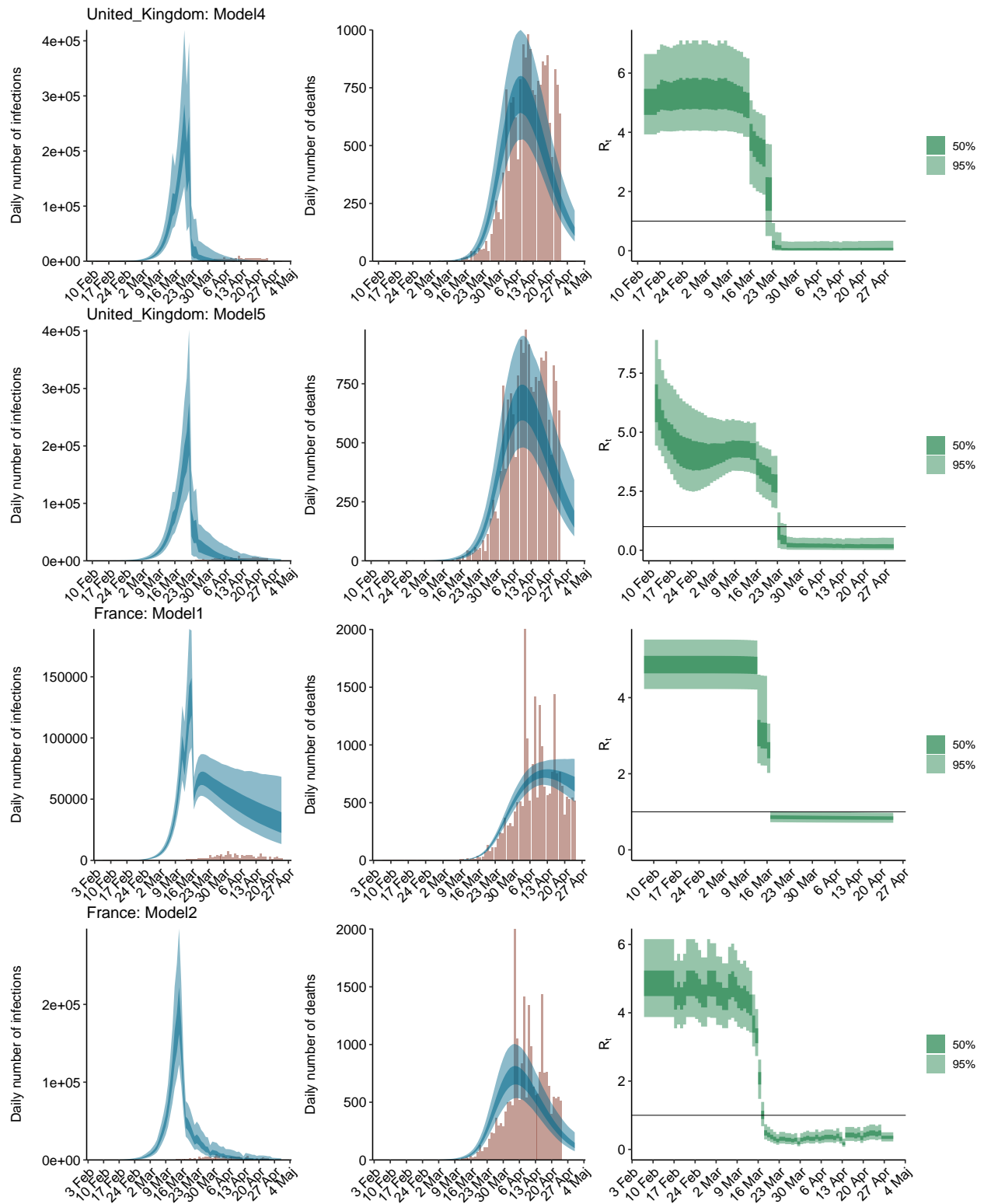


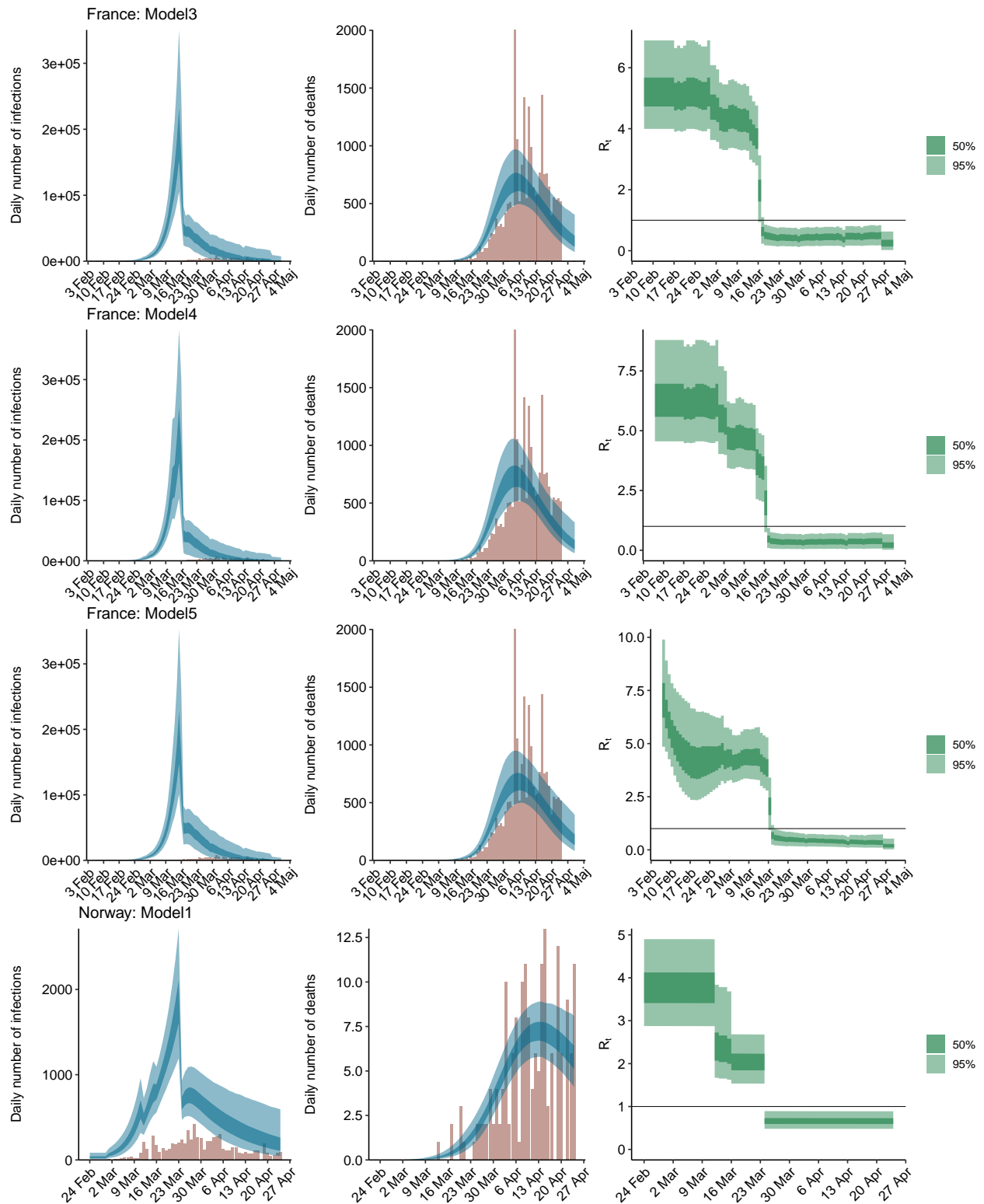


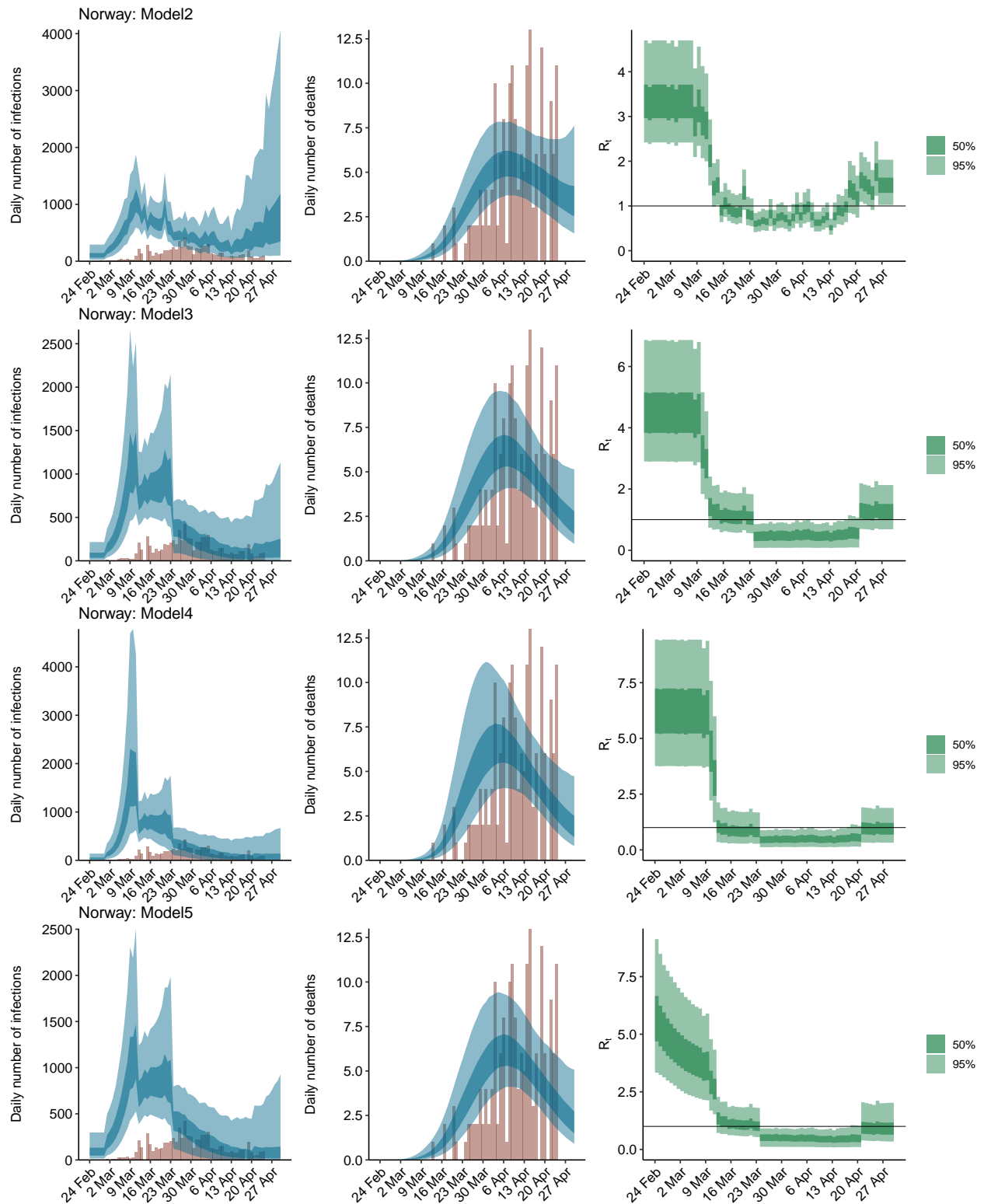


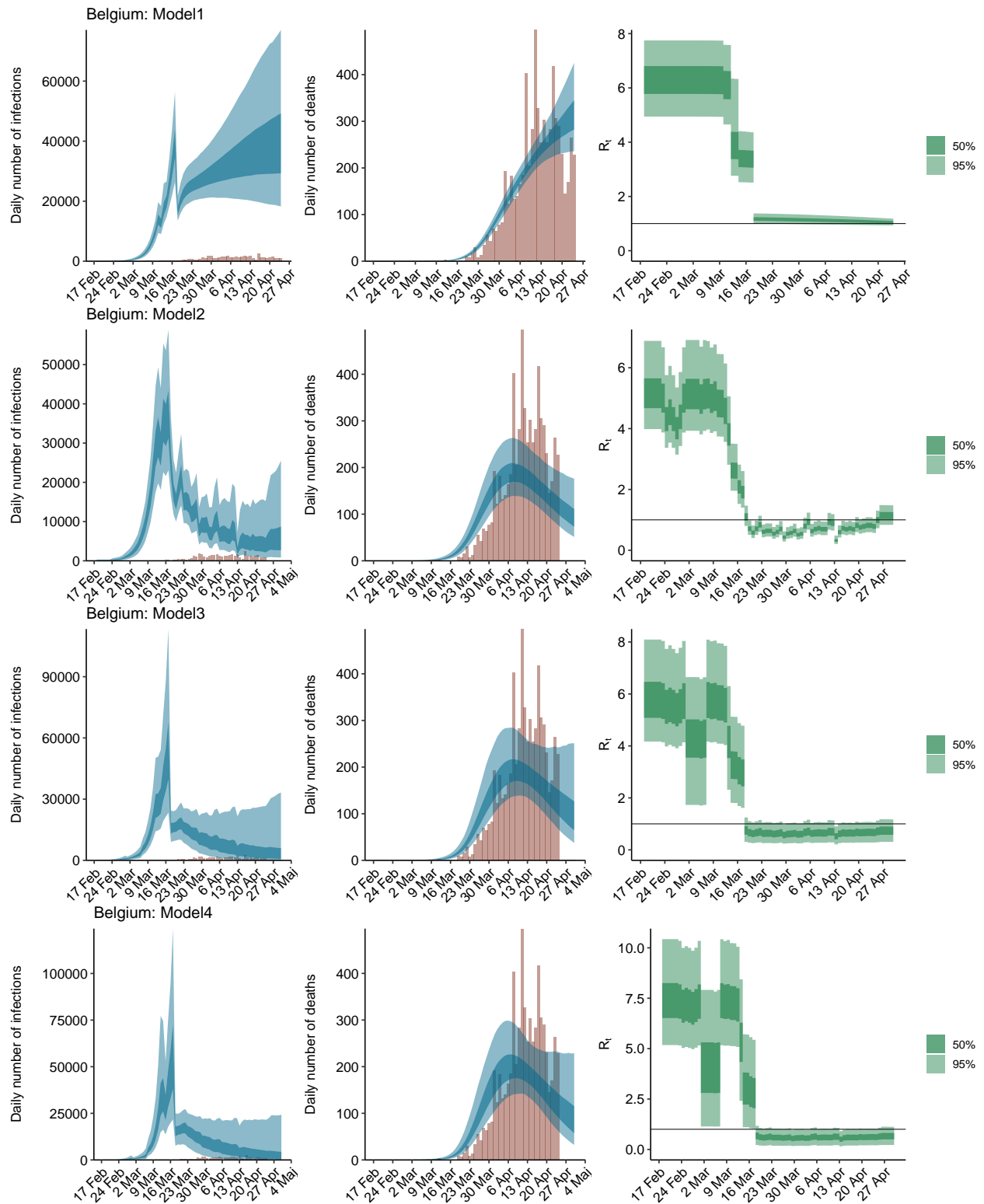


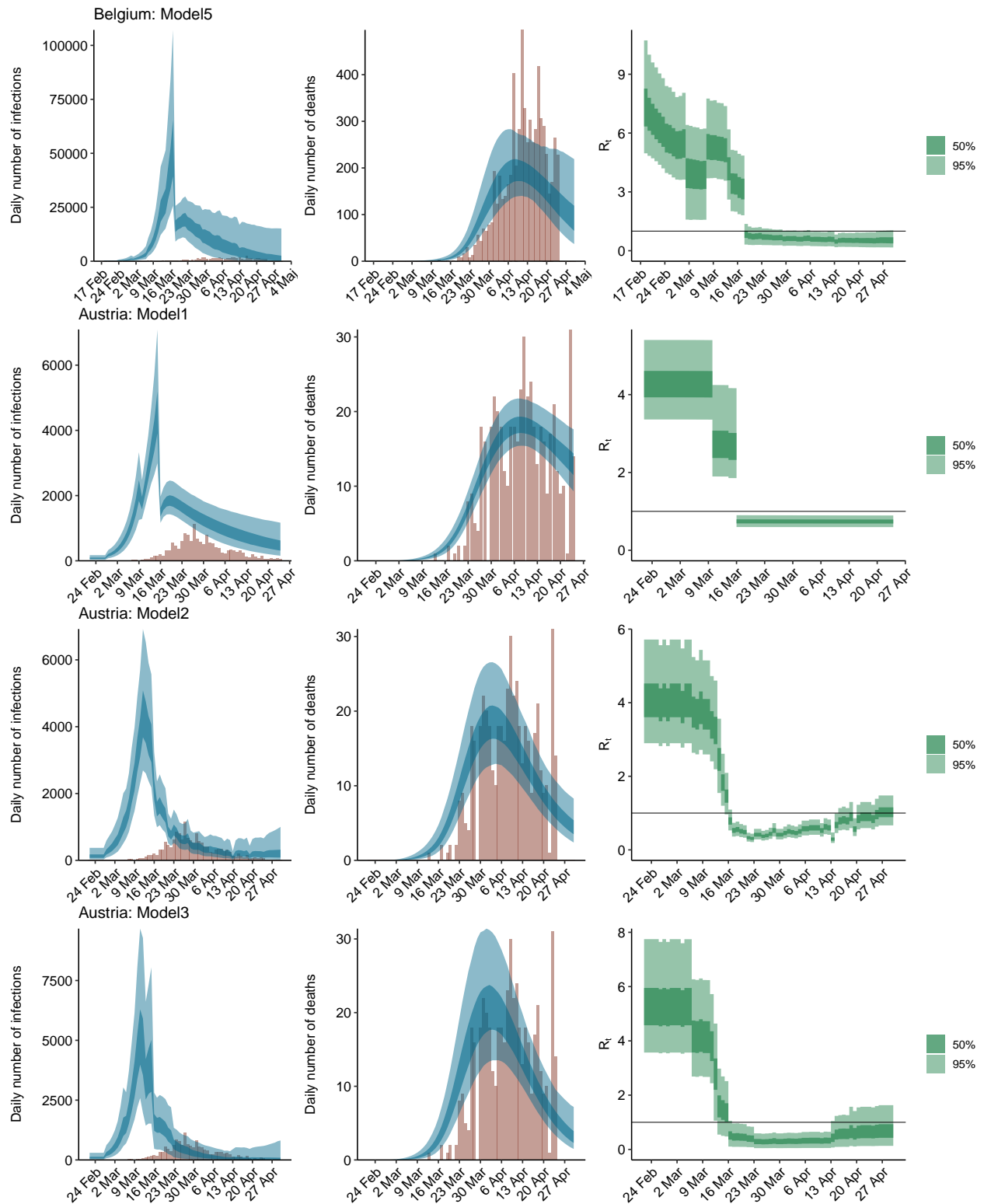


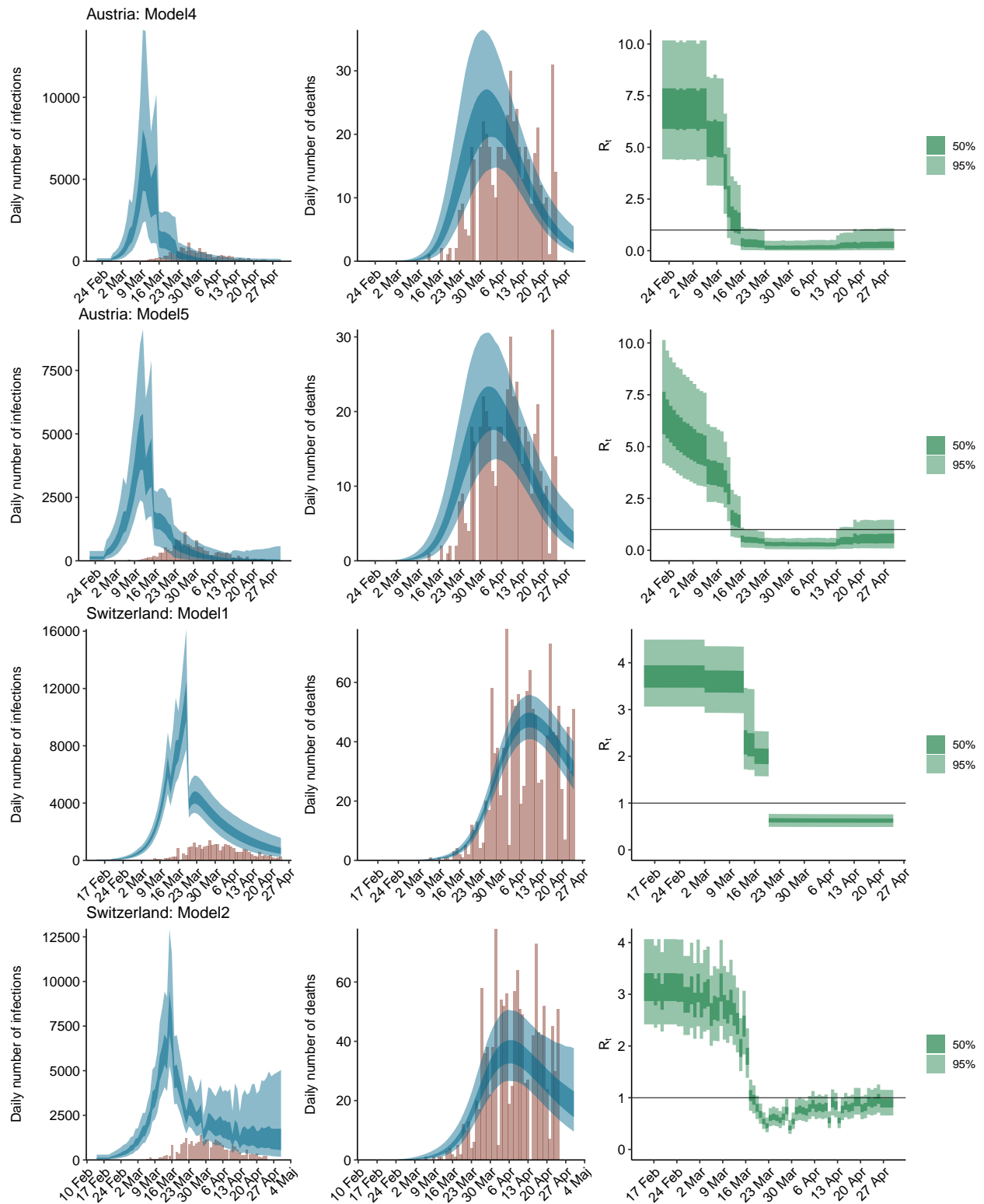


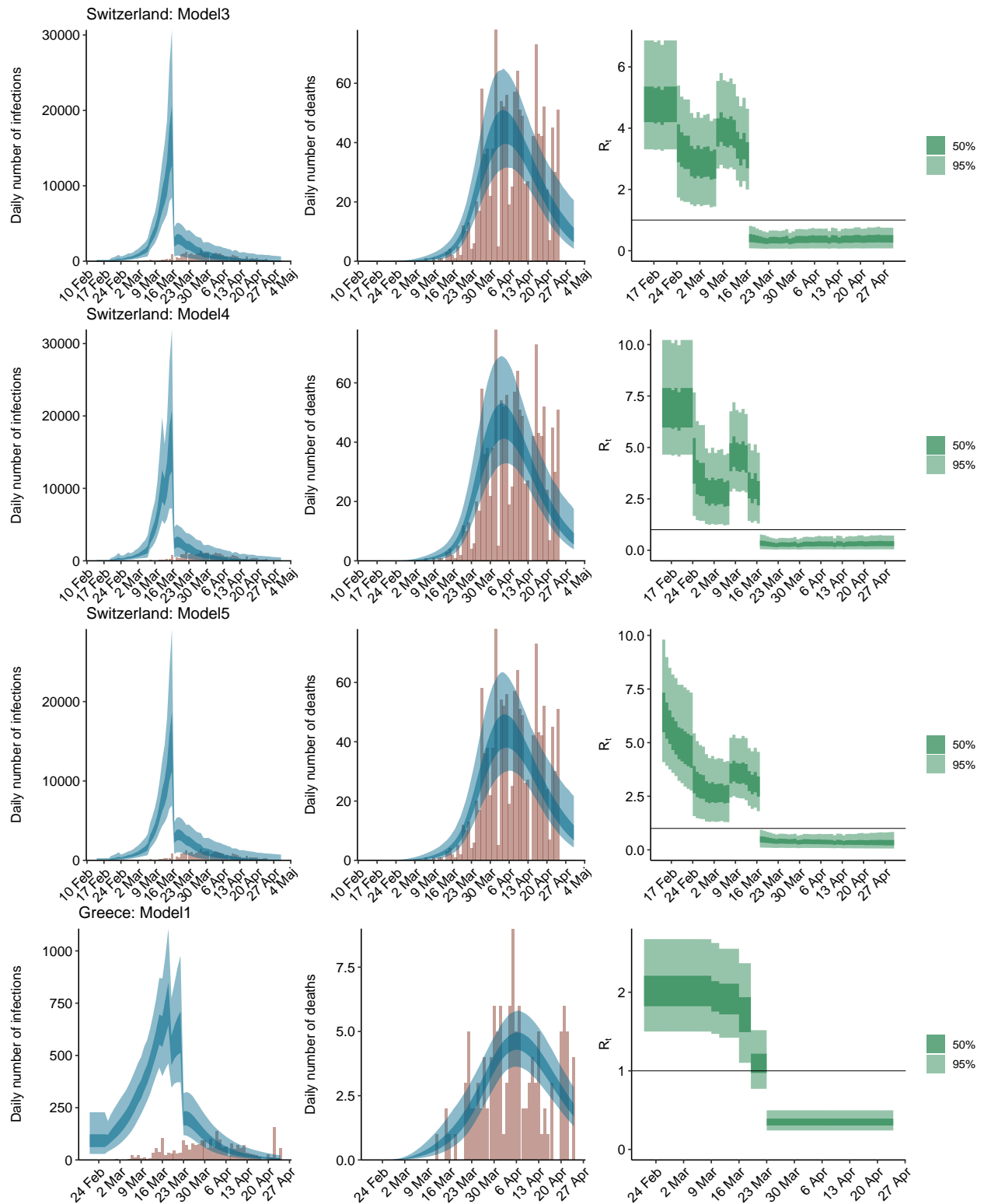


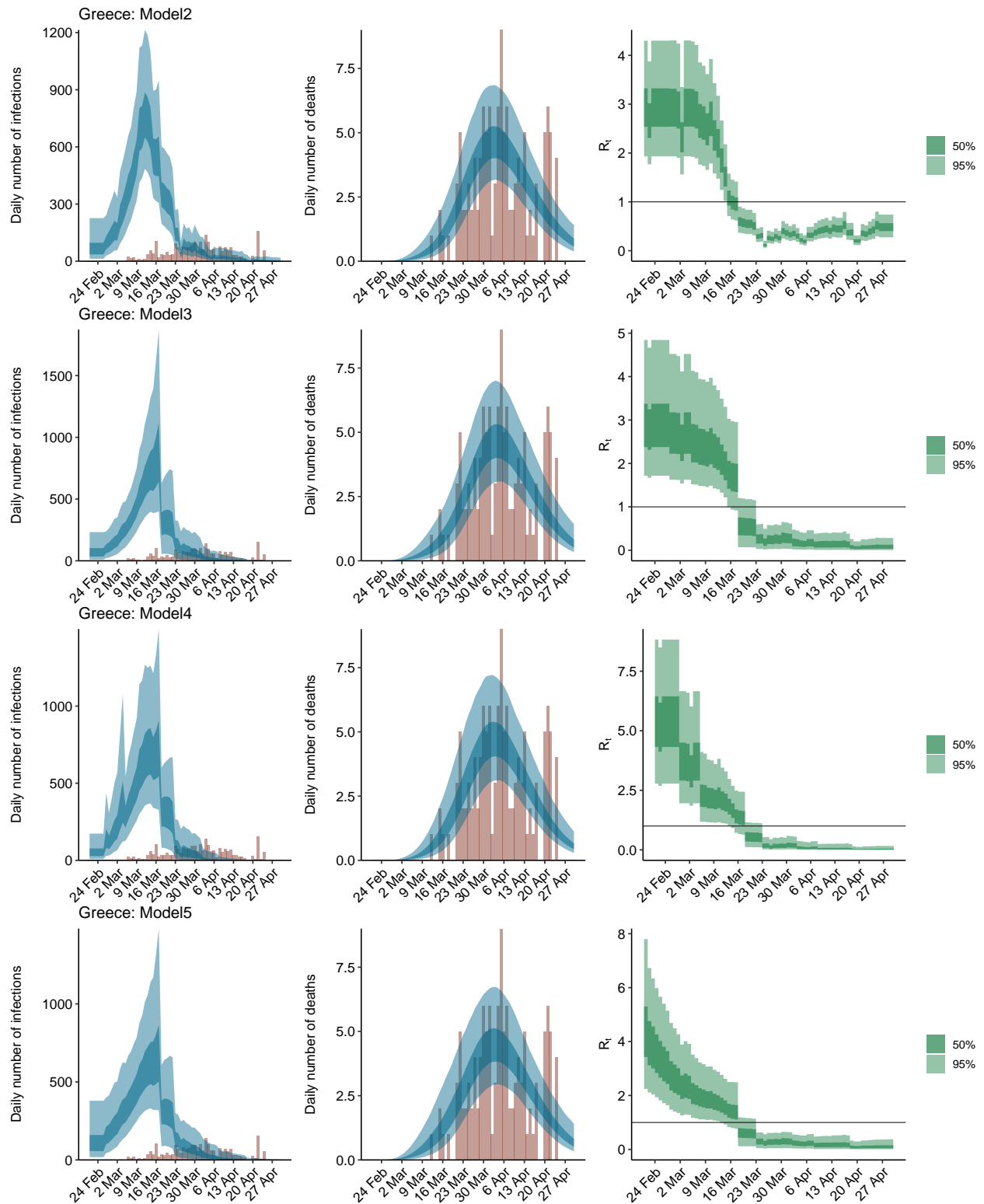


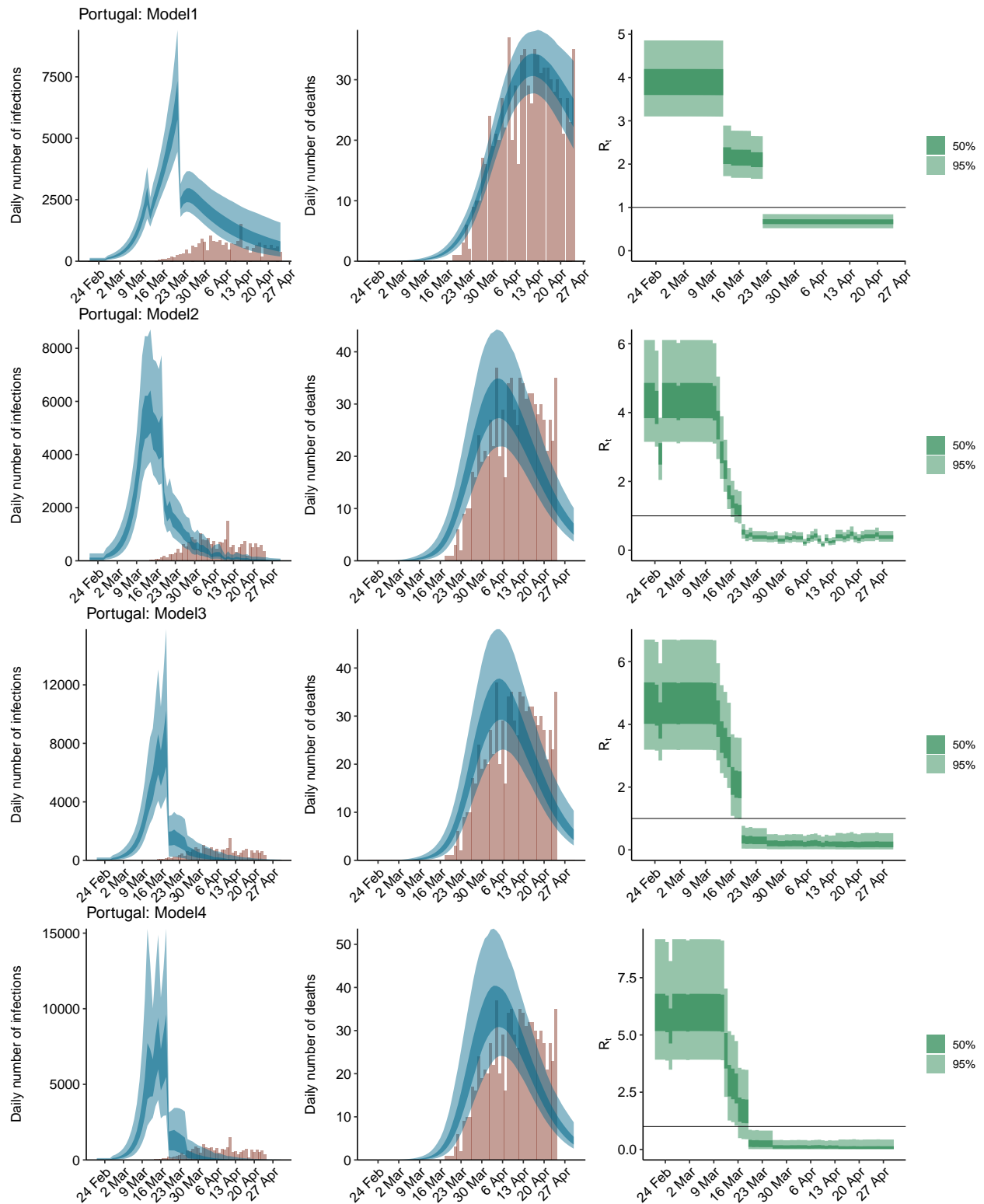


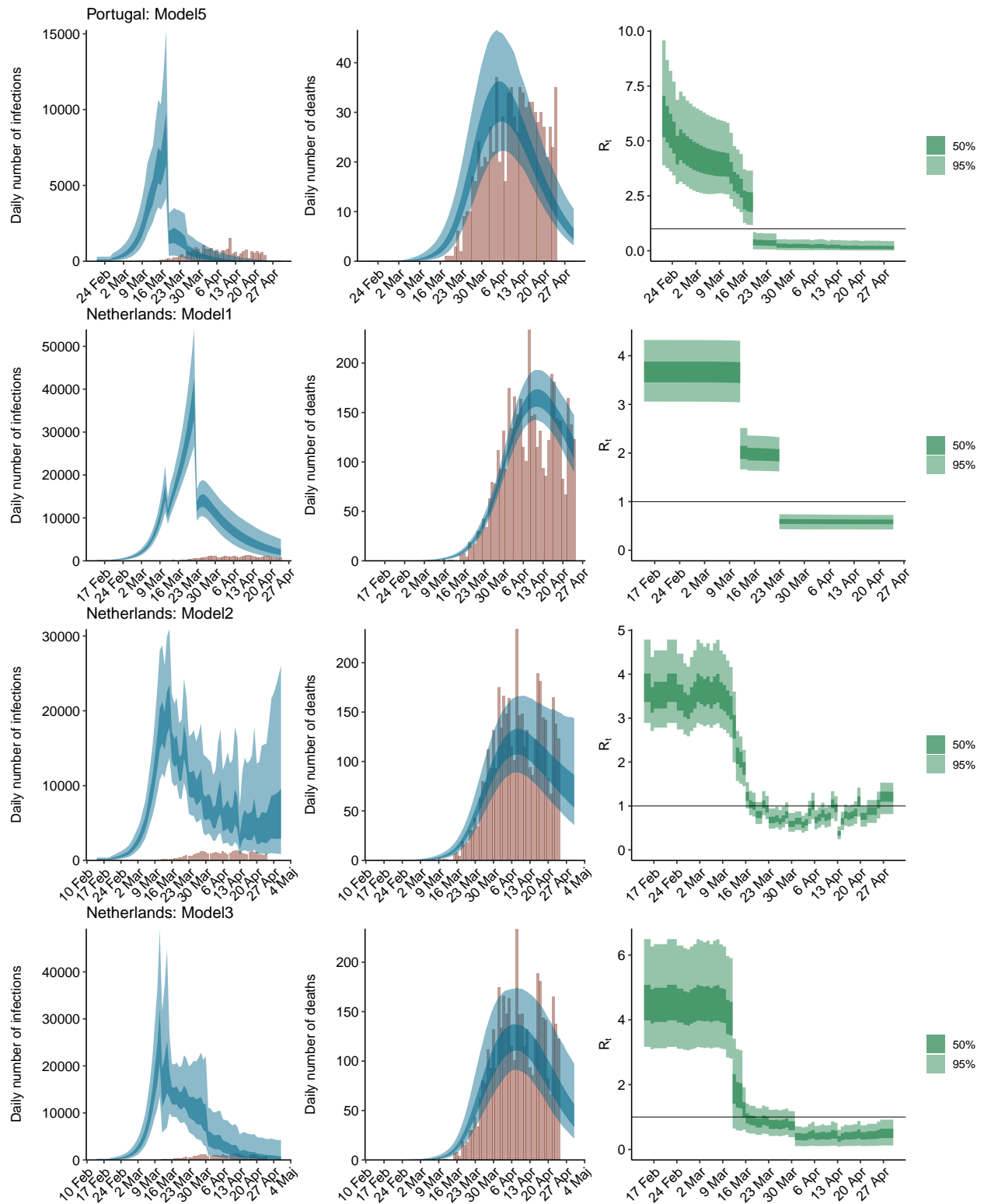


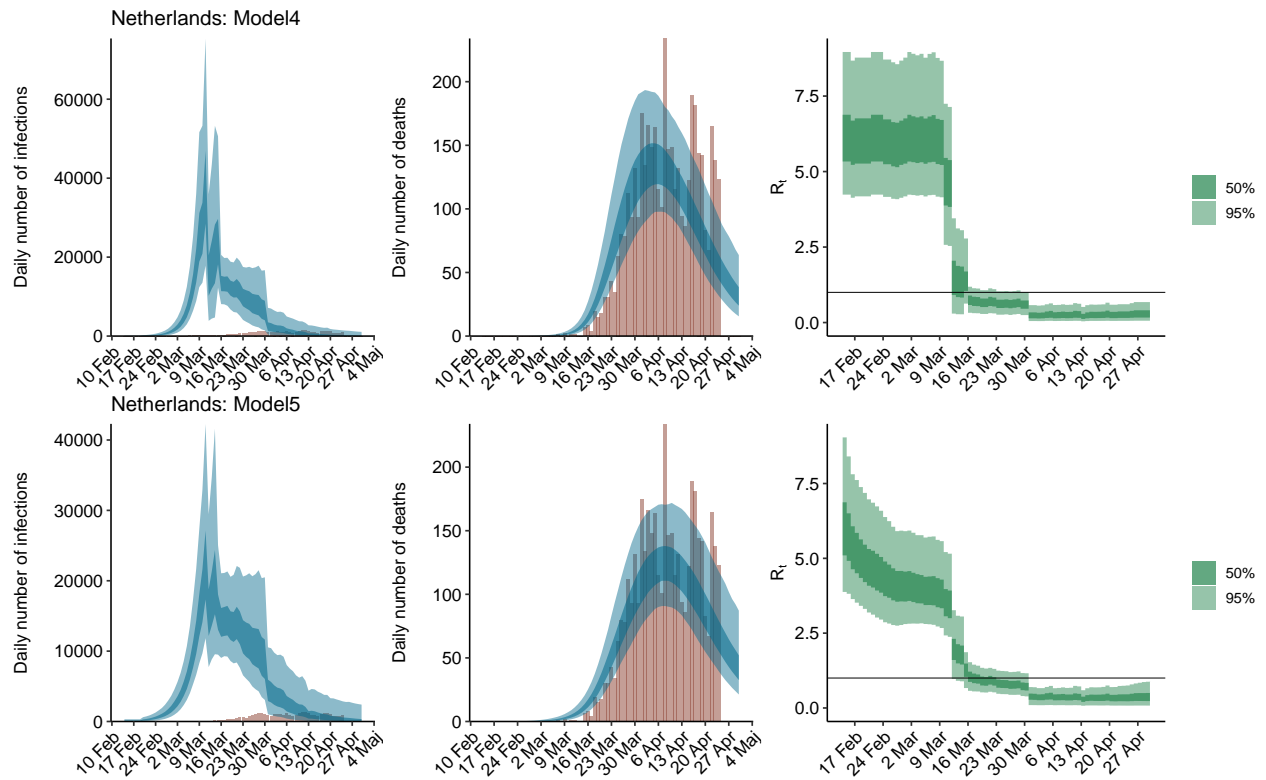












Reproducibility

Report git hash:

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