The Bucky Model

October 1, 2022

(The following documentation was manually converted to LaTeXfrom the Bucky Model online web documentation: `https://docs.buckymodel.com/en/latest/`, converted on 2022-10-01.)

The Bucky model is a spatial SEIR model for simulating COVID-19 at the county level. The Bucky model contains code for running simulations, processing data, and visualizing results.

1 Installation Guide

1. To begin, first checkout the code from GitLab:

   ```
   git clone https://gitlab.com/kinsemc/bucky.git
   ```

2. TODO

NOTE: EXTRACTION INCOMPLETE

2 Model Information

2.1 Model Description

The JHUAPL-Bucky model is a COVID-19 metapopulation compartment model initially designed to estimate medium-term (on the order of weeks) case incidence and healthcare usage at the second administrative (admin-2, ADM2) level (counties in the United States; cities or districts in various countries). These ADM2 regions are all coupled using mobility information to approximate the both inter- and intra-regional contacts between the members of the populations. Using the historical case and death data, local demographic data (see Graph Information), and a set of parameters derived from empirical studies, the model infers a number of localized features (see table below) that are related to spread of COVID-19. Projecting forward in time, Bucky then utilizes an age stratified compartment model to not only estimate the case load but additionally provide outputs relating to the healthcare burden of each locality.

These time forecasts are performed a large number of times (Monte Carlo experiments), with each individual simulation using minor modifications to the input parameters at random, scaled to the uncertainty of the estimates. The resulting collection of simulations is then used to obtain probabilistic estimates for all output variables.

2.1.1 Model Overview

At its base, the Bucky model is a spatially distributed SEIR model. SEIR models are a class of deterministic models used to model infectious diseases that are spread by person-to-person transmission in a population. The simplest versions of such models are systems of ordinary differential equations and are analysed mathematically [Het89].

Within the context of an SEIR model, disease dynamics are modeled over time by moving the population through a series of compartments (otherwise known as "bins" or "states"). Those states are as follows:

- susceptible (S): the fraction of the population that could be potentially subjected to the infection;
- exposed (E): the fraction of the population that has been infected but does not show symptoms yet;
- infectious (I): the fraction of the population that is infective after the latent period;
- recovered (R): The fraction of the population that have been infected and recovered from the infection.

The total population is represented by the sum of the compartments. Basic assumptions of this type of model include:

- Once the model is initialized, no individuals are added to the susceptible group. It follows that births and natural deaths are unaccounted for, migration in/out of the region is frozen for the duration of a simulation, and none of the population has been vaccinated or is immune to the pathogen;
- The population within each strata is uniform and each pair of individuals within the strata are equally likely to interact;
- The probability of interaction between individuals in the population is not rare;
- Once infected, an individual cannot be reinfected with the virus.

Note: The compartments E, I^{asym}, I^{mild}, I^{hosp}, R^{hosp} are gamma-distributed with shape parameters specified in the configuration file.

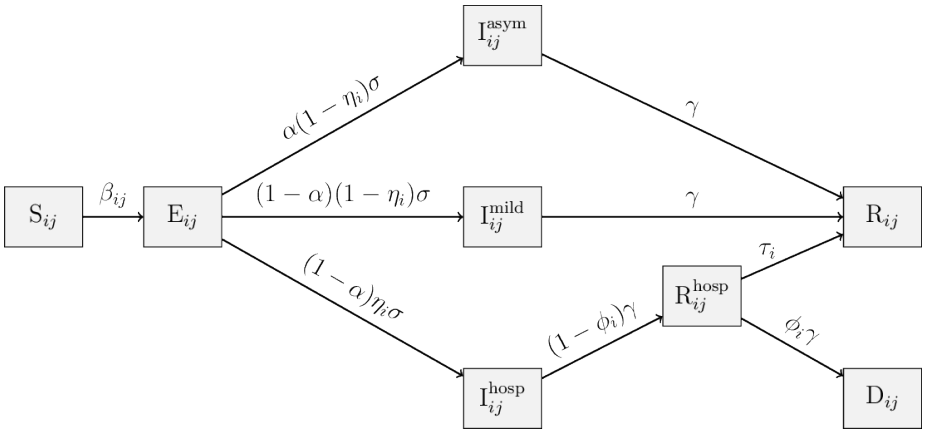


Figure 1: Model

Variable	Description
S_{ij}	Proportion of individuals who are susceptible to the virus
E_{ij}	Proportion of individuals who have been exposed to the virus
$I_{i,j}^{hosp}$	Proportion of individuals that are exhibiting severe disease symptoms and are in need of hospitalization
$I_{i,j}^{mild}$	Proportion of individuals that are exhibiting mild disease symptoms
$I_{i,j}^{asym}$	Proportion of individuals who are infected but asymptomatic
$R_{i,j}$	Proportion of individuals who have recovered from the virus and are no longer capable of infecting other individuals
$R_{i,j}^{hosp}$	Proportion of individuals who have recovered from the virus after a period of time in a hospital
$D_{i,j}$	Proportion of individuals who have succumbed as a direct result of the virus

Parameter	Description
$\beta_{i,j}$	Force of infection on a member of age group i in location j
$\frac{1}{\sigma}$	Viral latent period
α	Rate of infections that are asymptomatic
ν_i	Fraction of cases necessitating hospitalization
ϕ_i	Case fatality rate for age group i
$\frac{1}{\gamma}$	Infectious period
τ_i	Recovery period from severe infection for age group i

The Bucky model consists of a collection of coupled and stratified SEIR models. Since COVID-19 exhibits heavily age dependent properties, wherein a majority of severe cases are in older individuals, SEIR models are stratified via the age demographic structure of a geographic region in order to get accurate estimates of case severity and deaths. Additionally, to model the spatial dynamics of COVID spread, we consider a set of SEIR sub-models at the smallest geographic level for which we have appropriate data.

The basic structure of the model is displayed in the diagram above. Age is denoted by index i, and geographic regions are denoted by index j. Within each strata, Bucky models the susceptible and exposed populations, followed by one of three possible infected states: asymptomatic (I^{asym}), mild (I^{mild}), and severe (I^{hosp}). Members of the population who are either asymptomatic or exhibit mild symptoms recover from the virus at a rate γ. Those who exhibit severe symptoms and are in need of healthcare support will either recover after a period of illness at rate $1/\tau_i$ or expire as a result of the virus at rate $\phi_i\gamma$.

A critical component of the Bucky model is the parameterization of the model. A number of parameters must be derived and/or estimated from their original data sources. These include, but are not limited to those listed in tables above as well as local estimates of local case doubling time, case reporting rate, case fatality rate, and the case hospitalization rate. Further details of these quantities as well as how they are estimated are given in the Model Input and Output section. All parameter estimation for the model includes the basic assumption that, once estimated and initialized, these parameters remain constant during the simulation period.

Coupling individual age and geographically stratified sub-models occurs across a number of dimensions including disease state. Sub-models are coupled together using both the spatial mobility matrix and age-based contact matrices. Modeling of the overall interaction rates between geographic locations and age groups is an important component in accurately modeling non-pharmaceutical Interventions (NPIs). Bucky accounts for the implementation of NPIs (e.g. school closures, border closures, face mask wearing) via modifying either the social contact matrices or the basic reproductive number, R_0. For further details, see Non-pharmaceutical Interventions.

All together, these components contribute to a model that is adaptable to

a number of contexts. Bucky is calibrated to the uncertainties in both the case data and the disease parameters, leading to a model that is robust to both the quality and resolution of available input data.

2.2 Model Input and Output

2.2.1 Input

The Bucky model uses two main sources of input: the input graph and CDC-recommended parameters.

Input Graph The input graph contains data regarding demographics, geographic information, and historical case information. For details, see Graph Information.

CDC-Recommended Parameters The Centers for Disease Control and Prevention (CDC) has published pandemic planning scenarios [fDCP+20] which contain recommended parameters describing biological and epidemiological parameters. Of these five planning scenarios, Bucky utilizes scenario 5, which contains the CDC's current best estimates for disease severity and transmission. These parameters are described in detail, based on information available from the CDC, and summarized in the table below. CDC-recommended parameters are controlled by parameter files located in the `par` directory.

Parameter Description	Bucky Variable Name	Value (Interquartile Range)
Mean generation interval	T_g	7.5 (5.5, 8.5)
Mean serial interval	T_s	6 (5, 7)
Fraction of infections that are asymptomatic	asym_frac	0.4
Relative infectiousness of asymptomatic individuals	rel_inf_asym	0.75
Percentage of transmission prior to symptom onset	frac_trans_before_sym	0.5
Case fatality ratio	F	• $0-49$ years: 0.0005 • $50-64$ years: 0.002 • 65+ years: 0.013
Case hospitalization ratio	H	• $0-49$ years: 0.017 • $50-64$ years: 0.045 • 65+ years: 0.074
Time from symptom onset to hospitalization	I_TO_H_TIME	• $0-49$ years: 6 days • $50-64$ years: 6 days • 65+ years: 4 days
Duration of hospitalization	H_TIME	• $0-49$ years: 4.9 days • $50-64$ years: 7.6 days • 65+ years: 8.1 days
Time between death and reporting	D_REPORT_TIME	• $0-49$ years: 7.1 days • $50-64$ years: 7.2 days • 65+ years: 6.6 days

Disease Transmission The following parameters describe the transmissibility of the virus. The **percentage of infections that are asymptomatic**, asym_frac, refers to the percentage of infections that will never develop symptoms. This is a difficult parameter to estimate due to logistical complications (individuals would need to be tested to ensure they remain asymptomatic while infectious) and because the level of asymptomatic infections varies by age. The best estimate for this parameter is the midpoint between the lower bound of [BCB+20], the upper bound of [PTC+20], which corresponds to the estimates from [OT20].

The **relative infectiousness of asymptomatic individuals** compared to symptomatic individuals rel_inf_asym is calculated using upper and lower bounds on the difference in viral dynamics between asymptomatic and symptomatic cases. The lower bound is derived from data indicating that more severe cases have higher viral loads [LYW+20] and a study that indicates symptomatic cases shed for longer and have higher viral loads than asymptomatic

cases [NYS+20]. Other studies indicate that both symptomatic and asymptomatic cases have similar duration and viral shedding [LKL+20], which is used as the upper bound.

The final parameter relating to disease transmission is the **fraction of transmission prior to symptom onset** `frac_trans_before_sym` which corresponds to the percentage of new cases that were caused by transmission from an individual before they become symptomatic. The lower bound is derived from [HLW+20], with the upper bound derived from [CGM+20].

Disease Characteristics and Severity The mean serial interval, `Ts`, is the time in days from exposure to onset of symptoms and is taken from [MCH+20]. The mean generation interval, `Tg`, is the period of time (in days) between symptom onset for one individual and symptom onset for a person they have infected. This value is from [HLW+20].

The case fatality ratio (**CFR**) is the number of individuals who will die of the disease; the case hospitalization-severity ratio (**CHR**) corresponds to the number of cases that are severe and necessitate hospitalization. Within the context of the United States, this ratio corresponds to the individuals admitted to a hospital. In a context where access to medical care is limited, this ratio corresponds to the ratio of individuals who exhibit severe disease symptoms.

Hospital-related parameters are derived using data from COVID-Net [CDC] and the CDC's Data Collation and Integration for Public Health Event Response (DCIPHER). All data is taken from the period between March 1, 2020 to July 15, 2020 unless otherwise noted. The time it takes from symptom onset to hospitalization in days is denoted by `I_to_H_time`. The number of days an individual will be hospitalized is `H_TIME`. Finally, the number of days between death and reporting is `D_REPORT_TIME`.

2.2.2 Output

The Bucky model generates one file per Monte Carlo run. This data is post-processed to combine data across all dates and simulations. It can then be aggregated at desired geographic levels. A separate file is created for each requested administrative level, with each row indexed by data, admin ID, and quantile. The columns of this output file are described in the tables below.

Aggregated files are placed in subfolder named using the Monte Carlo ID within the specified output directory. Filenames are constructed by appending the aggregation level with the aggregation type (quantiles vs mean). For example, the following file contains quantiles at the national level:
`/output/2020-06-10__14_13_04/adm0_quantiles.csv`

An example output directory structure is shown below:

```
2020-07-28__15_21_52/
├── adm0_quantiles.csv
├── adm1_quantiles.csv
├── adm2_quantiles.csv
├── maps
│   └── ADM1
│       ├── adm1_AlabamaDailyReportedCases2020-07-26.png
│       ├── adm1_AlabamaDailyReportedCases2020-08-02.png
│       ├── ...
└── plots
    ├── ADM1
    │   ├── DailyReportedCases_Alabama.png
    │   ├── ...
    ├── US.csv
    └── US.png
```

Column and Index Names .

Index name	**Description**
adm*	The adm ID corresponding to the geographic level (i.e., adm2 ID)
date	The date
quantile	Quantile value

Column name	**Description**
case_reporting_rate	Case reporting rate
active_asymptomatic_cases	Current number of actively infectious but asymptomatic cases
cumulative_cases	Cumulative number of cumulative cases (including unreported)
cumulative_deaths	Cumulative number of deaths
cumulative_deaths_per_100k	Cumulative number of deaths per $100,000$ people
cumulative_reported_cases	Cumulative number of reported cases
cumulative_reported_cases_per_100k	Number of reported cumulative cases per $100,000$ people
current_hospitalizations	Current number of hospitalizations
current_hospitalizations_per_100k	Number of current hospitalizations per $100,000$ people
current_icu_usage	ICU bed usage
current_vent_usage	Current ventilator usage
total_population	Population
daily_cases	Number of daily new cases (including unreported)
daily_deaths	Number of daily new deaths
daily_hospitalizations	Number of daily new hospitalizations
daily_reported_cases	Number of reported daily new cases
doubling_t	Local doubling time as estimated from the historical data
R_eff	Local effective reproductive number

2.3 Graph Information

The Bucky model does not do any data manipulation, smoothing, or correcting to the data it receives from the graph (by design). If data needs to be manipulated or corrected, it should be done before it is placed on the graph.

The graph is created using admin2-level data. If data can not be found at the admin2-level, admin2-level information can be extrapolated using admin2 population and national or state level data (this is expanded upon in the *Population Data* section).

The following data sources are used to create the graph:

- admin2-level shapefile
- admin2-level population data stratified by age
- Historical admin2-level case and death data
- Contact matrix information for the country
- Mobility data (or a proxy)

All data is placed into a single dataframe, joined by the admin2-level key (e.g., FIPS for United States), with the exception of mobility data (which is used to create edges, not nodes).

2.3.1 Graph-Level Attributes

Administrative information is placed on the top graph-level. For example:

```
'adm1_key' : 'adm1',
'adm2_key' : 'adm2',
'adm1_to_str' : {1 : 'Alabama'}, ...,
'adm0_name': 'US',
'start_date' : '2020-09-25'
```

NOTE: `adm1_to_str` is a dict with key-value pairs indicating the adm1 names for each adm1 value appearing in the graph.
Contact matrices are also on this level under the key `contact_mats`.

2.3.2 Sample Node

The following is an example node on the graph for the United States. The rest of the documentation will describe what data is necessary to construct this node.

```
(0,
 {'adm1': 1,
  'Confirmed': 1757.0,
  'Deaths': 25.0,
  'adm2_name': 'Autauga County',
  'N_age_init': array([3364., 3423., 3882., 3755., 3173., 3705., 3461., 3628., 3616.,
         3966., 3811., 3927., 3237., 2589., 2311., 3753.]),
```

```
'Population': 55601.0,
'IFR': array([6.75414158e-06, 1.24643105e-05, 2.26550214e-05, 4.05345945e-05,
       7.68277004e-05, 1.38382882e-04, 2.54273120e-04, 4.63844627e-04,
       8.51898589e-04, 1.55448599e-03, 2.87077658e-03, 5.20528393e-03,
       9.47735996e-03, 1.73603179e-02, 3.14646839e-02, 9.38331984e-02]),
'case_hist': array([1207.64227528, 1234.9656055 , 1243.85366911, 1244.13444753,
       1255.27521116, 1268.95333353, 1270.38458817, 1288.05778954,
       1295.55174933, 1297.29129258, 1312.35308192, 1321.2898892 ,
       1323.10534634, 1354.97350342, 1358.88036484, 1362.43488575,
       1377.67551466, 1392.4338964 , 1406.70605635, 1446.3924143 ,
       1450.47616771, 1462.67851762, 1458.98710032, 1470.52271903,
       1481.12998684, 1501.75698721, 1508.06090303, 1513.9178672 ,
       1518.26245703, 1532.99858052, 1553.97101414, 1564.24619451,
       1579.10859377, 1590.56170754, 1597.77332362, 1616.97996262,
       1619.        , 1624.        , 1664.        , 1673.        ,
       1690.        , 1691.        , 1714.        , 1715.        ,
       1738.        , 1757.        ]),
'death_hist': array([22.76748794, 22.80142062, 22.81307638, 22.79580414, 22.79344408,
       22.79578013, 22.81581338, 22.80532061, 22.7902682 , 22.79603286,
       22.79689139, 22.79601336, 22.79344923, 22.85912123, 22.90405033,
       22.91397178, 22.97898824, 23.02565004, 23.05597481, 23.09719551,
       23.13913548, 24.12323294, 24.17184064, 24.2852927 , 24.38579416,
       24.41284998, 24.41330133, 24.41175889, 24.40910247, 24.41419481,
       24.43286524, 24.47610337, 24.52580854, 24.5245916 , 24.53522989,
       24.54591406, 24.        , 24.        , 24.        , 24.        ,
       24.        , 24.        , 25.        , 25.        , 25.        ,
       25.        ]),
'adm2': 1001.0})
```

2.3.3 Population Data

Population data should be at a admin2 level and stratified in 16 5-year age bins (if using Prem et al contact matrices):

```
0-4 years
5-9 years
10-14 years
15-19 years
20-24 years
25-29 years
30-34 years
35-39 years
40-44 years
45-49 years
50-54 years
55-59 years
60-64 years
65-69 years
70-74 years
75+ years
```

If population data for an admin2 area is known (i.e. number of total people per admin2), but it is not age-stratified, this data can be extrapolated assuming age-stratified population data exists at some level. For example, assume a country has age-stratified data provided at the national-level. To get the admin2-level age data, the data is separated into the 16 bins (as a 1-dimensional array

of length 16). These bins are then normalized by dividing by the sum. Then, the fraction of people living in the admin2 is calculated by dividing admin2 population by the total national population. For each district, this fraction is multiplied by the age vector to produce a admin2-level age vector. This vector is placed on the node under the key `N_age_init`.

The total population for an admin2 is placed on the node under the key `Population`.

2.3.4 Case Data

Case data should be at the admin2-level and include cumulative data as of the start date of the simulation and historical data for the 45-day period preceding the start date:

- `case_hist`: Cumulative historical case data
- `death_hist` : Cumulative historical death data

Historical data is structured as numerical vectors on the node with the keys `case_hist`, `death_hist`. Historical data for every node must have data points for the 45 days preceding the simulation. If there are known errors in the historical data, they must be corrected before being placed on the graph.

2.3.5 Contact Matrices

Currently, contact matrix data is downloaded from here (`https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005697`), which has contact matrices for 152 countries. If a country does not appear in this dataset, a country culturally close can be substituted (for example, Pakistan's contact rates were used for Afghanistan), or another dataset can be used. If another dataset is used, the contact matrix must be formatted such that it has the same shape as the number of age demographic bins (i.e. if there are 16 bins, the matrix must be of size 16 x 16).

2.3.6 Mobility Data

Mobility data is used to construct the edges of the graph. Mobility data, or a proxy for it, is used to describe the contact rates between counties.

The baseline mobility data shows up as an edge attribute called `weight`. `R0_frac` is a factor that is multiplied with the baseline mobility value to model the effect of NPIs, etc., on mobility. For example, given baseline mobility data from February 2020, `R0_frac` would be computed by dividing recent mobility data values with the February 2020 baseline. `R0_frac` exists to provide a knob to tune during the simulation to model NPIs.

2.4 Non-pharmeceutical Interventions

Non-pharmaceutical interventions (NPIs) are mitigations, apart from getting vaccinated and taking medicine, that people and communities can take to help slow the spread of communicable diseases. As a vaccine for COVID-19 has yet to be deployed, NPIs are among the best strategies for controlling the spread of the current COVID-19 virus. The structure of the Bucky model allows for the incorporation of NPIs via the modification of a combination of the following : the basic reproduction number, local contact matrices, and inter-regional mobility matrices.

For each country an initial list of NPIs was obtained from the ACAPS COVID-19 Government Measures Dataset (`https://data.humdata.org/dataset/acaps-covid19-government-measures-dataset`). This dataset is complemented with additional qualitative information from in-country stakeholders. The estimated compliance level are tailored to specific countries.

2.4.1 Implementation

NPIs are categorized and implemented in Bucky based on their classification into three categories:

Contact-Matrix Based NPIs These NPIs are those that effect only certain age groups within the total population. These NPI effect the ratios relating the components of the contact matrices. The NPI that fall under this category are:

- School Closure
- Shielding Elderly

Mobility Based NPI This classification is for those NPI that lead to changes in mobility/movement between administrative districts (as opposed to movement within an administrative district). The NPI that fall under this category are :

- Closing of borders, ports, and/or international flights
- Restricting inter-regional movement

Reproduction Number Based NPI This classification is for those NPI that have an effect on the overall scaling of transmissibility. It encompasses both intra-regional measures to reduce transmission as well as national level initiatives designed to reduce transmission throughout the country. The NPI that fall under this category are :

- Social distancing
- Face mask wearing
- Installation of hand washing stations

- Reduction of size of public gatherings
- Closing businesses
- Partial Lockdown
- Awareness campaigns (e.g., vaccination programs)

A summary of the NPIs that are currently implemented in Bucky are given in the table below. This table includes the classification, effects, and sources that are currently being used to approximate the effects of various NPI.

With the current implementation, we have the ability to distinguish between the effects of NPI within the categories mentioned above. For the case in which multiple NPI within category III are implemented, we have implemented a value-added approach to calculating their effectiveness in reducing the basic reproduction number. In this case, we calculate the reduction in R_0 based on the number of NPIs in place. If one NPI is in place, R_0 is reduced by 40%. If two NPI are in place, R_0 is reduced by 60%. If three or more NPI are in place, then R_0 is reduced by 70%.

NPI Classification	**Effect in Model**	**Mean Reduction (SD)**	**Source**
Contact-based: School closure	Reduce contact between school aged groups and increase the contacts in the home environment	44% reduction in overall community transmission	[WSM+20]
Mobility-based	Reduction in mobility between regions	60% (10)	[CAN+20] [WSM+20]
Reproduction number-based	60 − 8% reduction in overall community transmission	72.5% (6.25)	[JVZG+20] [JJA+20]

2.5 Model Flow

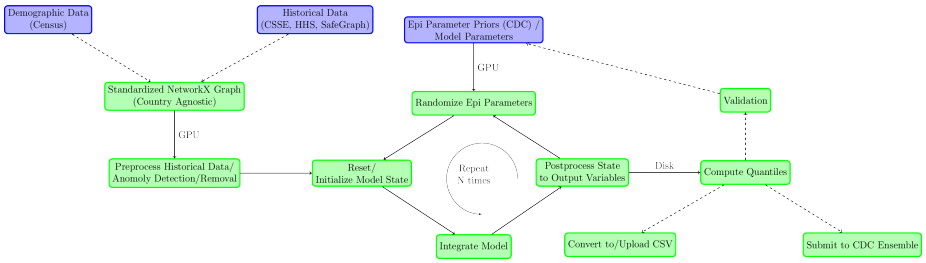


Figure 2: Model

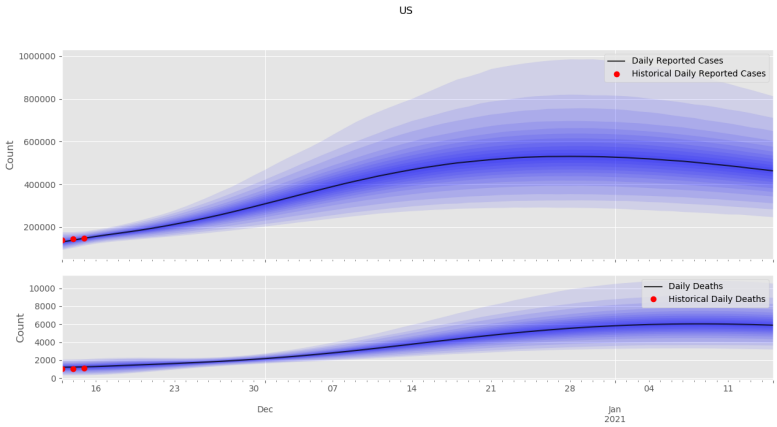
3 Visualization Tools

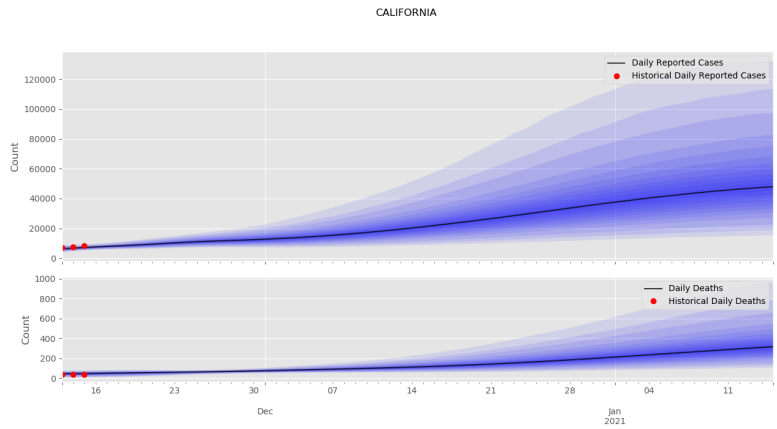
The Bucky model includes visualization tools for creating line plots with confidence intervals and maps. Maps and plots can be created at the national, state, or county (plots only) level.

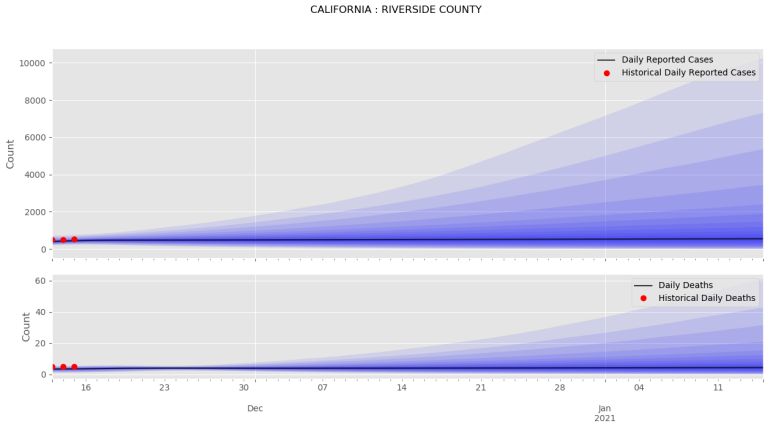
3.1 Plots

By default (i.e. without additional arguments), `bucky.viz.plot` creates line plots at the national and state level for the columns `daily_reported_cases` and `daily_deaths` for the most recently postprocessed simulation data. Historical data can be added using the `--hist` flag. For a full list of parameters and options, see TODO linkhere to documentation.

To illustrate the different available geographic levels, example plots are shown below for the United States, California, and California's Riverside county. These plots include historical data and all available confidence intervals.







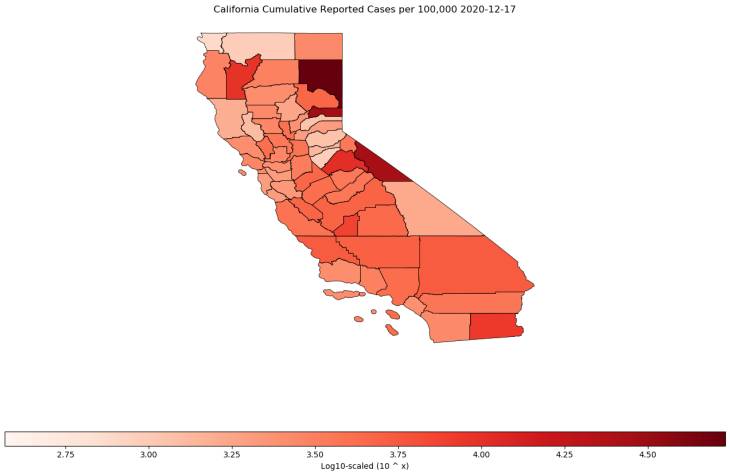
3.2 Maps

In addition to line plots, the Bucky model includes a module for creating map visualizations from simulated data. In order to create maps, the desired admin level must be supplied. Maps can be created daily, weekly, or monthly points throughout the simulation.

For example, to create state-level plots:

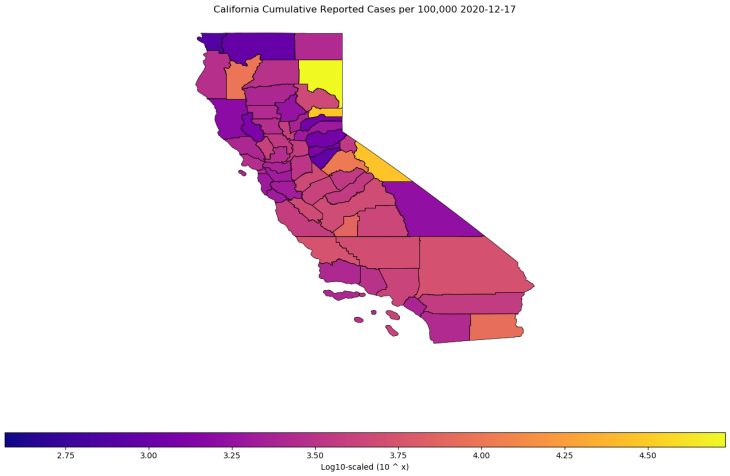
```
./bmodel viz.map --all_adm1 --columns cumulative_reported_cases_per_100k
```

This will create a map like the one shown below:



The mapping tool uses Matplotlib colormaps, defaulting to Reds. To use a different colormap:

```
./bmodel viz.map --all_adm1 --columns cumulative_reported_cases_per_100k --cmap plasma
```



4 References

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- "Measuring movement and social contact with smartphone data: a real-time application to COVID-19" by Couture, Dingel, Green, Handbury, and Williams https://github.com/COVIDExposureIndices/COVIDExposureIndices/blob/master/CDGHW.pdf
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