Simple CFR approach

Here is the basic model. We are interested in estimating the CFR among confirmed cases, ρ. Presume that the time from confirmation to report of death (censoring at recovery) follows an exponential distribution:

$$\Pr(Y_i < t) = F(t; \lambda_1)$$

Where Y_i is the time from confirmation to death for person i.

Moreover, the time from confirmation to death or recovery (composite outcome) follows an exponential distribution:

$$\Pr(T_i < t) = G(t; \lambda)$$

Where T_i is the time from confirmation to death or recovery for person i.

To ease application of the above models to our dataset, which is organized by calendar date, we will assume both time to death and time to the composite outcome follow an exponential distirbution with a constant hazard function, λ_1 and λ, respectively, for now.

Let d_{jv} be the number of reported deaths in location j and calendar date v. Based on the above:

$$E(d_{jv}) = \sum_{k=0}^{v} n_{jk}\lambda_1$$

where n_{jv} is the number in the risk set on that day (i.e., cumulative number of confirmed cases reported on day v minus the cumulative number of deaths on that day and the cumulative number of people recovered).

In addition,

$$E(n_{jv}) = c_{jv} - \sum_{k=0}^{v-1} n_{jk}\lambda$$

where n_{jv} is the number in the risk set on that day (i.e., cumulative number of confirmed cases reported on day v minus the cumulative number of deaths on that day and the cumulative number of people recovered).

Finally

$$\rho = \int_0^\infty \hat{\lambda_1}[1 - \hat{G}(t)]dt = \int_0^\infty \hat{\lambda_1} e^{-\hat{\lambda} t} dt$$

.

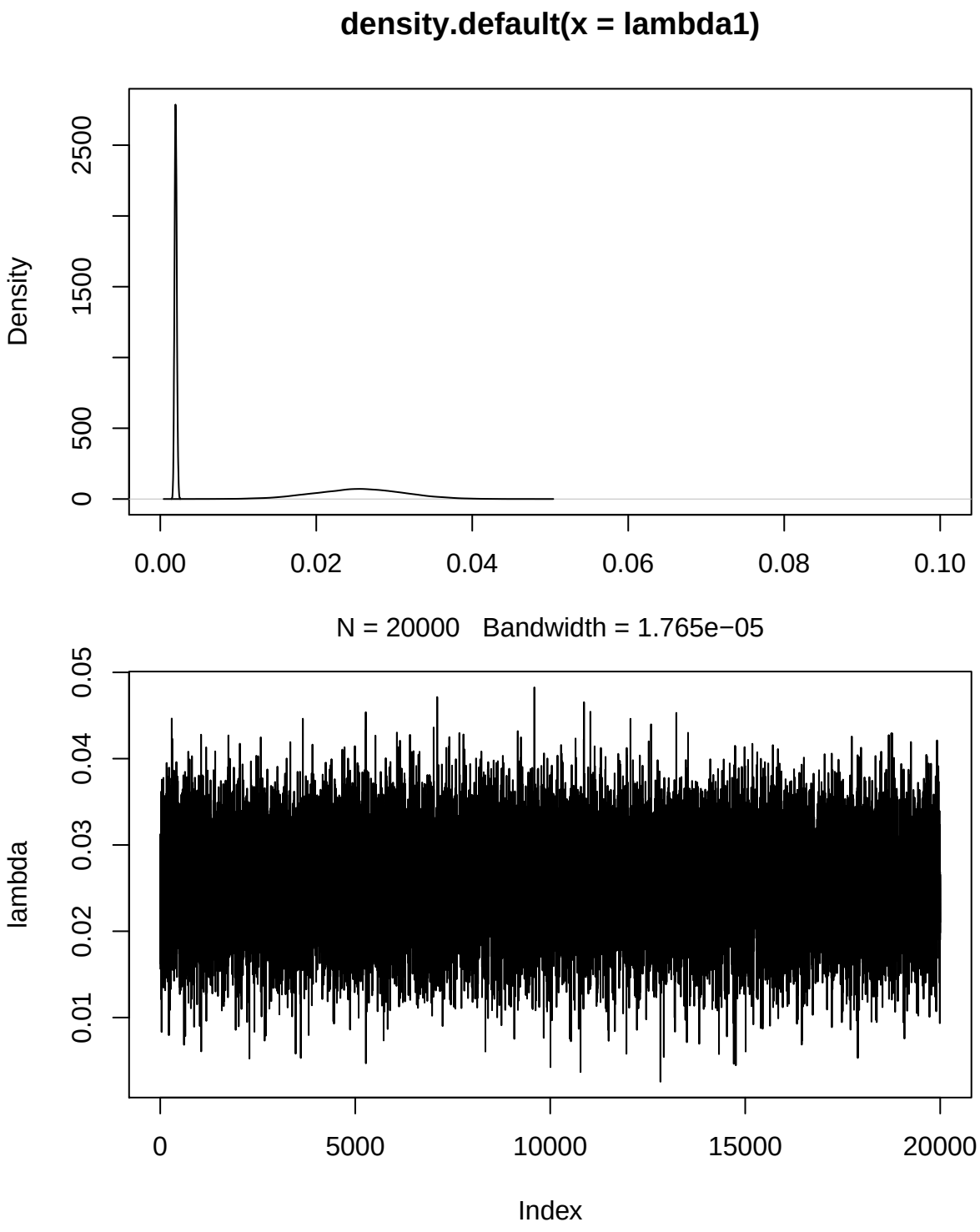
First, define the stan model.

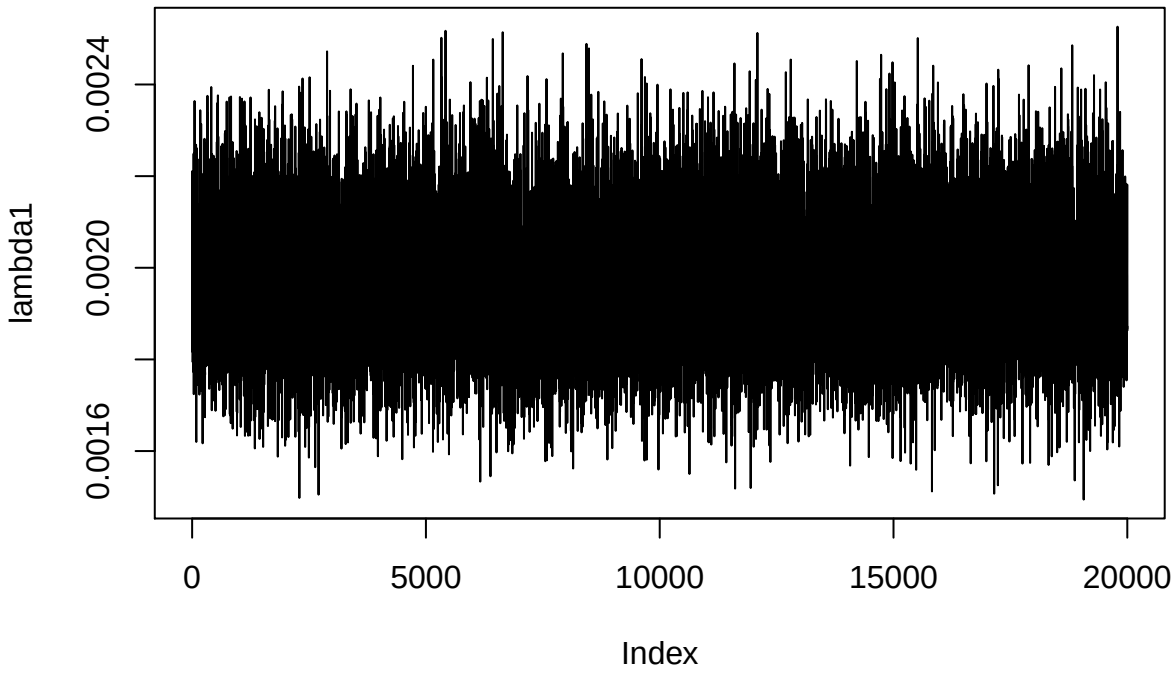
```
data {
  int <lower=0> T; //the number of time steps included
  int <lower=0> L; //the number of locations we have data from

  real <lower=0> c[T,L]; // cumulative number of confirmed cases reported on each day.
  real <lower=0> r[T,L]; // cumulative number of recovered cases reported on each day.
  int <lower=0> d[T,L]; // cumulative number of deaths reported on each day.
  int <lower=0> n[T,L]; //number of currently infected people on each day.
  int <lower = 0> V; // max infection duration (we should b e able to get rid of this)
}

parameters {
  real <lower=0> lambda1; //parameter for time to death distribution
  real <lower=0> lambda; // parameter for time to death or recovery distribution
```

```
}

transformed parameters {
  real <lower=0> expected_deaths[T,L]; // cumulative # deaths BY time T
  real <lower=0> expected_riskset[T,L]; // # infected at time T
  real <lower=0> expected_exit[T,L]; // cumulative # those who have exited due to death or recovery BY T


  //this can be made more efficient...but for now./
  for (j in 1:L) {
    for (t in 1:T) {
      expected_deaths[t,j] = 0.0001;
      expected_exit[t,j] = 0.0001;
        for (k in 1:t) {
        expected_exit[k,j] += n[k,j] * lambda;
        expected_deaths[k,j] += n[k,j] * lambda1;
        }
        expected_riskset[t,j] = c[t,j] - expected_exit[t,j];
        //expected_recovered[t,j] = (expected_exit[t,j] - expected_deaths[t,j]);

    }
  }
}

model {


  //definitely can be made more effcient.
  for (j in 1:L) {
    for (t in 1:T) {
      //target+=poisson_lpmf(d[t,j]|expected_deaths[t,j]) + poisson_lpmf(n[t,j]|expected_riskset[t,j]);
      target+=poisson_lpmf(d[t,j]|expected_deaths[t,j]) + poisson_lpmf(n[t,j]|expected_riskset[t,j]);
    }
  }
  // print(target());
}

//generated quantities {
//real  <lower = 0, upper = 1> rho;
// for (v in 1:V){
 //   rho += exp(loglambda1) * exp(-exp(loglambda) * v);
//    rho += lambda1 * exp(-lambda * v);

// }
//print(rho);
  //rho = integrate_1d(getft, 0, positive_infinity(), {lambda1, lambda}, t);

//} // The posterior predictive distribution"
```

Prep data and run model.

Summarize


density.default(x = lambda1)
Density
0
500
1500
2500
0.00
0.02
0.04
0.06
0.08
0.10
N = 20000 Bandwidth = 1.765e−05
lambda
0.01
0.02
0.03
0.04
0.05
0
5000
10000
15000
20000
Index



Results

```
#move this into stan model later
rho <- matrix(nrow = length(lambda1))
for(i in 1:length(lambda1)){
  rho[i] <- integrate(function(x) {lambda1[i]*exp(-lambda[i]*x)}, lower = 0, upper = Inf)$value
}

median(rho)
```

```
## [1] 0.07715701
```

```
quantile(rho, probs = c(.025, .975))
```

```
##       2.5%      97.5%
## 0.05242317 0.14023800
```