

Evaluate {EpiEstim} on five epidemic outbreaks

LiJin Joo lijin.joo at gmail.com

2020-08-23

(Cori et al. 2013) used the following five examples to demonstrate {EpiEstim} in thier paper. As the first step of {EpiEstim} evaluation, we reproduced Figure1 and generated a table summarize the comparison of the current version and the result resported in Cori et al.

```
library(EpiEstim)
library(ggplot2)

data(Measles1861)
data(Flu1918)
data(Smallpox1972)
data(SARS2003)
data(Flu2009)
```

Each data containis at least two varriables, a serise of number of cases (i.e. incidence) and a distirbution of serial intervals (i.e. si_distr) as in Flu 2009.

```
head(Flu2009$incidence)
```

```
##      dates I
## 1 2009-04-27 1
## 2 2009-04-28 1
## 3 2009-04-29 0
## 4 2009-04-30 2
## 5 2009-05-01 5
## 6 2009-05-02 3
```

```
Flu2009$si_distr
```

```
## [1] 0.000 0.233 0.359 0.198 0.103 0.053 0.027 0.014 0.007 0.003 0.002 0.001
```

Several options are available for different estimators for a distribution of serial intervals in {EpiEstim}: 1) nonparametric_si' with the supplied density weights (si_distr), 2)parametric_si' with options in contig', such as mean_si, std_si, or 3) learning a distribution of serial intervals from data or samples using mcmc throughmake_contig' function. Details of each option can be learned from ("EpiEstim: The R-Epi Project" 2020), ("EpiEstim: Github Repository" 2020), (Anne Cori 2020).

Reproducing Figure 1

With the provided si_distr, we can obtain Rt estimates non-parametrically with a default of 7 day sliding window as follows:

```
Rt_measles1861 <- estimate_R(incid = Measles1861$incidence,
                             method = "non_parametric_si",
                             config = make_config(list(si_distr = Measles1861$si_distr)))

round(head(Rt_measles1861$R[,c(1:4, 5, 8, 11)], 15), 1)
```

##	t_start	t_end	Mean(R)	Std(R)	Quantile.0.025(R)	Median(R)	Quantile.0.975(R)
## 1	2	8	NA	NA	NA	NA	NA
## 2	3	9	NA	NA	NA	NA	NA
## 3	4	10	NA	NA	NA	NA	NA
## 4	5	11	NA	NA	NA	NA	NA
## 5	6	12	NA	NA	NA	NA	NA
## 6	7	13	NA	NA	NA	NA	NA
## 7	8	14	NA	NA	NA	NA	NA
## 8	9	15	8.2	2.9	3.5	7.8	14.7
## 9	10	16	5.1	2.1	1.9	4.8	9.9
## 10	11	17	5.1	1.9	2.0	4.8	9.5
## 11	12	18	4.5	1.7	1.8	4.2	8.3
## 12	13	19	4.5	1.6	2.0	4.3	8.2
## 13	14	20	3.6	1.3	1.4	3.4	6.6
## 14	15	21	3.2	1.2	1.3	3.0	5.9
## 15	16	22	3.6	1.2	1.7	3.5	6.4

```
Rt_flu1918 <- estimate_R(incid = Flu1918$incidence,
  method = "non_parametric_si",
  config = make_config(list(si_distr = Flu1918$si_distr)))
```

```
round(head(Rt_flu1918$R[,c(1:4, 5, 8, 11)]),1)
```

##	t_start	t_end	Mean(R)	Std(R)	Quantile.0.025(R)	Median(R)	Quantile.0.975(R)
## 1	2	8	1.4	0.2	1.0	1.4	1.9
## 2	3	9	1.2	0.2	0.9	1.2	1.6
## 3	4	10	1.4	0.2	1.0	1.4	1.7
## 4	5	11	1.0	0.2	0.7	1.0	1.3
## 5	6	12	1.3	0.2	1.0	1.3	1.6
## 6	7	13	1.2	0.2	0.9	1.2	1.6

```
Rt_Smallpox1972 <- estimate_R(incid = Smallpox1972$incidence,
  method = "non_parametric_si",
  config = make_config(list(si_distr = Smallpox1972$si_distr)))
```

```
round(head(Rt_Smallpox1972$R[,c(1:4, 5, 8, 11)], 10),1)
```

##	t_start	t_end	Mean(R)	Std(R)	Quantile.0.025(R)	Median(R)	Quantile.0.975(R)
## 1	2	8	NA	NA	NA	NA	NA
## 2	3	9	NA	NA	NA	NA	NA
## 3	4	10	NA	NA	NA	NA	NA
## 4	5	11	NA	NA	NA	NA	NA
## 5	6	12	NA	NA	NA	NA	NA
## 6	7	13	NA	NA	NA	NA	NA
## 7	8	14	NA	NA	NA	NA	NA
## 8	9	15	NA	NA	NA	NA	NA
## 9	10	16	NA	NA	NA	NA	NA
## 10	11	17	NA	NA	NA	NA	NA

```
Rt_sars2003 <- estimate_R(incid = SARS2003$incidence,
  method = "non_parametric_si",
  config = make_config(list(si_distr = SARS2003$si_distr)))
```

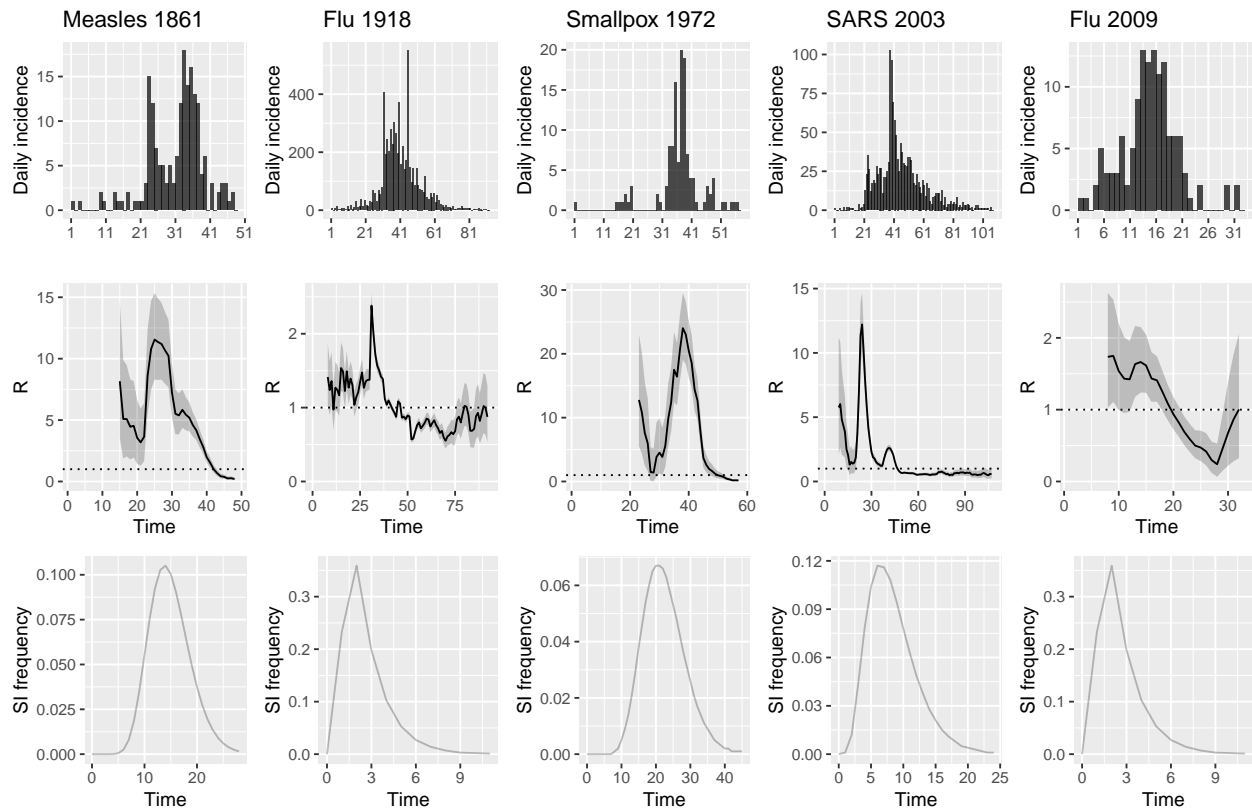
```
round(head(Rt_sars2003$R[,c(1:4, 5, 8, 11)]), 1)
```

##	t_start	t_end	Mean(R)	Std(R)	Quantile.0.025(R)	Median(R)	Quantile.0.975(R)
----	---------	-------	---------	--------	-------------------	-----------	-------------------

```
## 1      2      8      NA      NA      NA      NA      NA
## 2      3      9      5.8      2.4      2.1      5.4      11.2
## 3      4     10      6.0      2.1      2.6      5.8      10.9
## 4      5     11      4.8      1.7      2.1      4.6      8.7
## 5      6     12      4.3      1.4      2.0      4.2      7.6
## 6      7     13      3.9      1.2      1.9      3.7      6.6
```

```
Rt_flu2009 <- estimate_R(incid = Flu2009$incidence$I,
  method = "non_parametric_si",
  config = make_config(list(si_distr = Flu2009$si_distr)))
round(head(Rt_flu2009$R[,c(1:4, 5, 8, 11)]), 1)
```

```
##      t_start t_end Mean(R) Std(R) Quantile.0.025(R) Median(R) Quantile.0.975(R)
## 1          2      8      1.7   0.4              1.0       1.7         2.6
## 2          3      9      1.7   0.4              1.1       1.7         2.5
## 3          4     10      1.5   0.3              1.0       1.5         2.2
## 4          5     11      1.4   0.3              1.0       1.4         2.0
## 5          6     12      1.4   0.3              1.0       1.4         2.0
## 6          7     13      1.6   0.3              1.2       1.6         2.2
```



Comparison

Over the years, some features of {EpiEstim} have been updated thus minor differences are observed. Characteristics of each case curve and differences in the reproduced numbers are summarized as follows.

Outbreak	Cori et al (2013)	Reproduced
Measles 1861	initial : 4.3 (95 % CI: 2-8.2)	4.2 (95 Q: 1.8-8.3) at d=18
increased Rt in w3-4	mid w3: 3.0 (95 % CI: 1.3-5.9)	2.8 (95 Q: 2.2-3.4) at d=39

Outbreak	Cori et al (2013)	Reproduced
due to the high transmissibility	mid w4: 11.5 (95 % CI: 8.3–15.3)	no second peak after d=29 last d $R_t > 10$
Flu 1918	w7: below 1 end w2 : 1.4 (95 % CI: 1.0–1.9)	0.99 (95 Q: 0.7-1.3) at d=42 1.4 (95 Q: 1.0-1.9) at d =8, 10
2 days of extremely high incidence at d=31, 45	mid w5: 2.4 (95 % CI: 2.2–2.6)	2.2 (95 Q: 2.4-2.6) at d = 31
Smallpox 1972	early w7: below 1	1.0 (95 Q: 0.9 - 1.0) at d = 42 0.9 (95 Q: 0.8-0.9) at d = 47
a long induction period (4 wk)	early w4: 3.4 (95% CI: 0.8–9.3)	3.4 (95 Q: 0.8-9.3) at d = 29
SARS 2003	mid w6: 23.9 (95% CI: 19.0–29.5)	23.9 (95 Q: 19.1-29.5 at d = 38
2 peaks	early w8: below 1	0.9 (95 Q: 0.5-1.6) at d = 50
Flu 2009	mid w3: 12.2 (95% CI: 10.0–14.7)	12.2 (95 Q: 10.0-14.7) at d = 24
a constant rate	end w6: 2.6 (95% CI: 2.4–2.9)	2.4 (95 Q: 2.6-2.9) at d = 41, 42
	w7: below 1	0.9 (95 Q: 0.8-1.0) at d = 47
	early w2: 1.7 (95% CI: 1.0–2.6)	1.7 (95 Q: 1.0–2.6) at d = 8
	end w2: 1.7 (95% CI: 1.2–2.2)	1.7 (95 Q: 1.2–2.2) at d = 14
	w4: 0.2 (95% CI: 0.1–0.5)	0.2 (95 Q: 0.1–0.5) at d = 28
	w5: 0.9 (95% CI: 0.3–2.0)	0.9 (95 Q: 0.3–2.1) at d = 32

- Reproduced estimates are sample quantiles, median (quanteil at 0.025 - quantile at 0.975).
- 95Q indicates 95 sample quantile intervals. Cori et al. used a term of 95% CI but it seems they referring to the quantile intervals.
- d indicates t_end in R_t result.

Conclusion

With fixed serial interval weights, the estimates are consistent in the reproducible studies.

A true challenge in a COVID 19 study is to obtain an sensible estimate for this distribution.

Reference

Anne Cori, Neil M. Ferguson, Simon Cauchemez. 2020. *EpiEstim: Estimate Time Varying Reproduction Numbers from Epidemic Curves*. <https://cran.r-project.org/web/packages/EpiEstim/index.html>.

Cori, Anne, Neil M Ferguson, Christophe Fraser, and Simon Cauchemez. 2013. “A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics.” *American Journal of Epidemiology* 178 (9). Oxford University Press: 1505–12.

“EpiEstim: Github Repository.” 2020. <https://github.com/mrc-ide/EpiEstim>.

“EpiEstim: The R-Epi Project.” 2020. <https://sites.google.com/site/therepiproject/r-pac/epiestim>.