

PCR_positivity

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27/10/2020

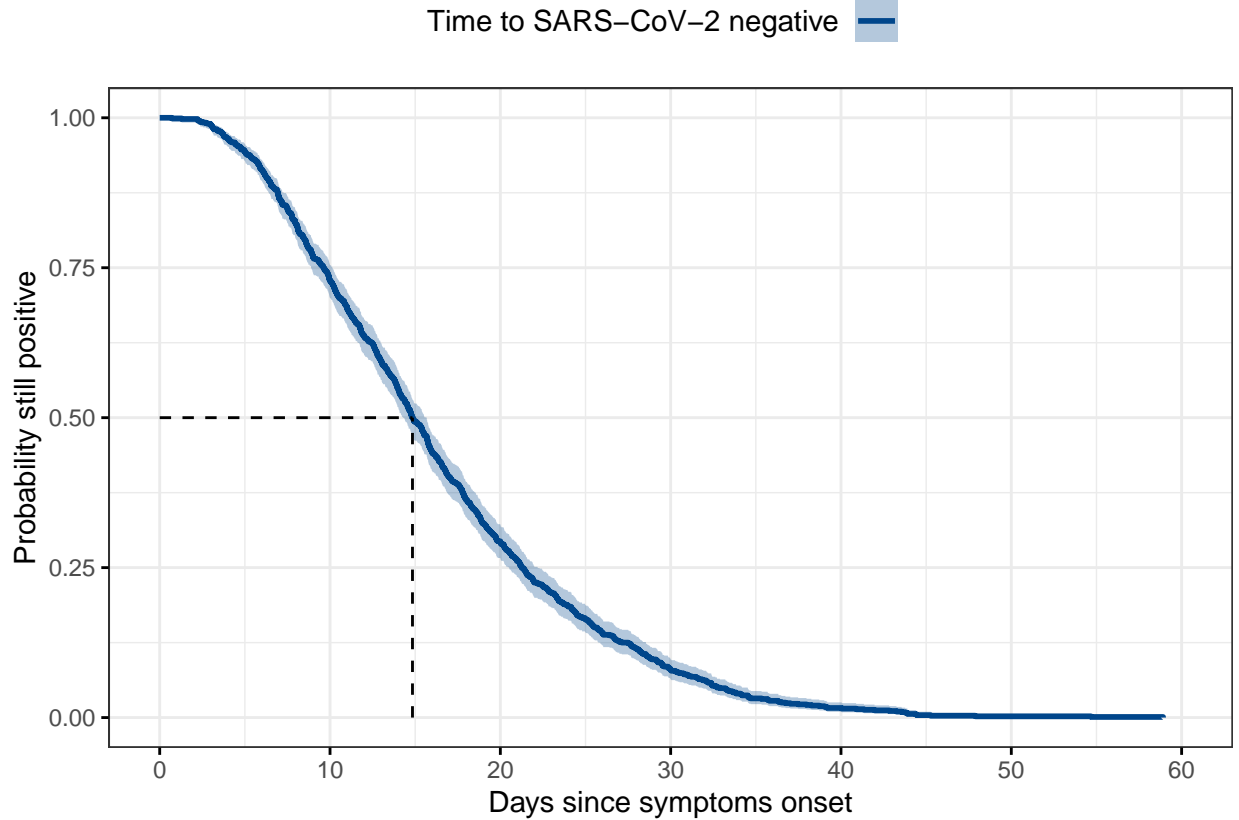
In *Eurosurveillance* 2020 Jul 30; 25(30): 2001292, Omar et al. analysed data of consecutive RT-qPCR results in 537 symptomatic patients with mild COVID-19 in home quarantine, between 28 February to 6 June 2020 in Rhineland-Palatinate, Germany. Table 1 presents their reported data on the population with an RT-qPCR positive for SARS-CoV-2 RNA at mean (95%CI) days after symptom onset. They reported a **median time to testing negative of 20 days (IQR 16-28)**.

Table 1. Cumulative population proportions, from *Omar et al.*

| ## | Days | Proportion | Number | Mean..95.CI. |
|-------|-------|------------|--------|---------------------|
| ## 1 | 2.24 | 0.990 | 532 | 2.24 (1.88-2.61) |
| ## 2 | 3.31 | 0.975 | 524 | 3.31 (2.85-3.77) |
| ## 3 | 4.48 | 0.950 | 510 | 4.48 (3.89-5.07) |
| ## 4 | 6.15 | 0.900 | 483 | 6.15 (5.33-6.97) |
| ## 5 | 9.74 | 0.750 | 403 | 9.74 (8.42-11.07) |
| ## 6 | 14.96 | 0.500 | 269 | 14.96 (13.01-16.9) |
| ## 7 | 21.43 | 0.250 | 134 | 21.43 (18.96-23.91) |
| ## 8 | 28.28 | 0.100 | 54 | 28.28 (25.5-31.06) |
| ## 9 | 32.82 | 0.050 | 27 | 32.82 (29.93-35.72) |
| ## 10 | 37.01 | 0.025 | 13 | 37.01 (34.03-40) |
| ## 11 | 42.16 | 0.010 | 5 | 42.16 (39.04-45.29) |

Using Omar et al.'s reported cumulative proportion and mean time, we fitted a gamma accelerated failure time regression line.

```
## Call: survfit(formula = edata.surv ~ 1, type = "kaplan-meier", conf.type = "log-log")
##
##           n      events      *rmean *se(rmean)      median      0.95LCL      0.95UCL
## 1000.00    1000.00    16.34      0.28      14.84      14.30      15.66
## * restricted mean with upper limit = 58.9
```

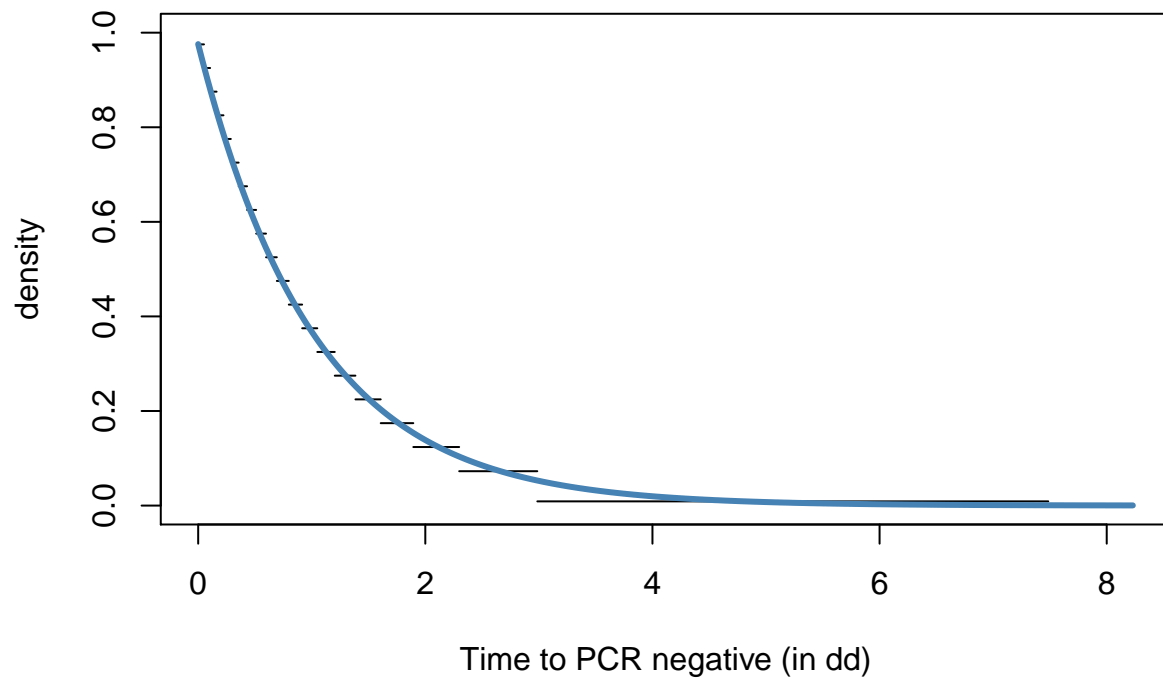


```
## Call:
## flexsurvreg(formula = edata.surv ~ 1, dist = "gamma")
##
## Estimates:
##      est      L95%      U95%      se
## shape 3.28507  3.02165  3.57145  0.14009
## rate  0.20109  0.18373  0.22010  0.00927
##
## N = 1000, Events: 1000, Censored: 0
## Total time at risk: 16336.27
## Log-likelihood = -3508.207, df = 2
## AIC = 7020.414
```

Fit Erlang distribution

From the gamma accelerated failure function, we extract the cumulative distribution function over a sequence of survival probability of length 21 (*e.g.* 0, 0.05, 0.10, ... 0.95, 0.99). That is, the likelihood of remaining **PCR positive over scaled observation time** (*dd*) and the mean, median and IQR of progression duration time (unscaled).

We used these data to fit an *Erlang* (*k*,*y*) distribution of time from symptom onset to PCR negativity, by minimizing the Kullback-Leibler divergence.



```
op_res # scaled Erlang parameters (time in dd)
```

```
## $s_min
## [1] 1
##
## $r_min
## [1] 0.9757998
```

```
scaled_gamma # re-scaled gamma over mean duration (true time)
```

```
## [1] 0.0597321
```

```
progression_durations$mean # mean duration
```

```
## [1] 16.33627
```