To: (10)(2e)[(10)(2e)@rivm.nl]
From: (10)(2e)
Sent: Tue 12/1/2020 7:51:42 AM
Subject: FW: update model-based inference
Received: Tue 12/1/2020 7:51:44 AM

From: (10)(2e) <(10)(2e)@rivm.nl>
Sent: woensdag 22 juli 2020 15:54
To: (10)(2e) <(10)(2e)@rivm.nl>; (10)(2e) <(10)(2e)@rivm.nl>
Subject: FW: update model-based inference

Hallo (10)(2e)/(10)(2e).

Ter info, onderstaande heb ik net naar (10)(2e) gestuurd zodat zij realistische parameterwaardes kan gebruiken in haar scenariostudies. (10)(2e) weten dat ik daar niet aan kan bijdragen.

Ik hoop wel dat ik tzt met oa (10)(2e) iets kan schrijven over het schatten van parameters met een nieuwe methode (zie ook hieronder). Daar had ik het gisteren kort met jullie over gehad. Graag hoor ik wat jullie daarvan vinden.

(10)(2e)

From: (10)(2e)
Sent: woensdag 22 juli 2020 15:35
To: (10)(2e). <(10)(2e)@umcutrecht.nl>; (10)(2e) <(10)(2e)@gmail.com>
Cc: (10)(2e) <(10)(2e)@umcutrecht.nl>; (10)(2e). <(10)(2e)@umcutrecht.nl>
Subject: update model-based inference

Dear all,

Attached and below you find a recent update of the code for model-based inference using actual hospitalization data and synthetic serological data (n=3,000 in the first week of April, 10 groups of 300 with 8 infections in each group). The synthetic serological data are important to ensure that the age-specific attack rates are reasonable (2-3% late March). This can at any moment be updated with actual serological data.

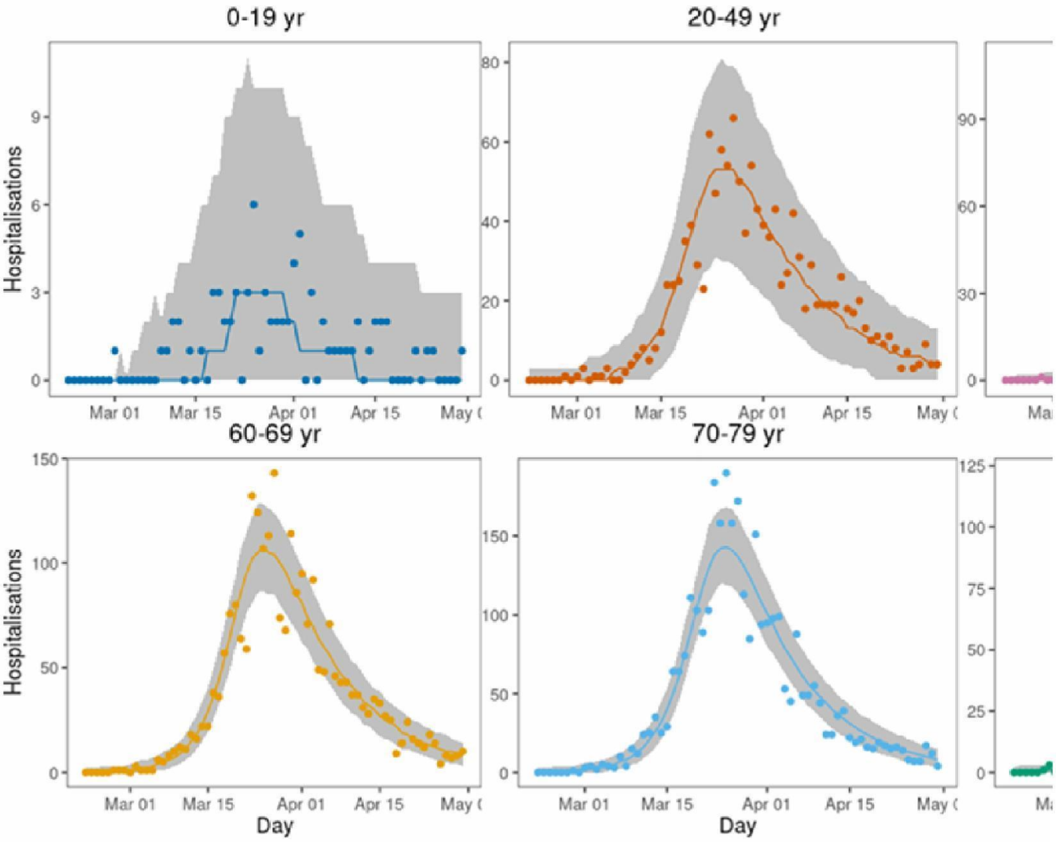
By request of ao (10)(2e) I have today
1) lumped the age groups 0-4, 5-9, and 10-19 years as well as the age groups 20-29, 30-39, 40-49 years wrt hospitalization rates,
2) included a smooth logistic transition from the pre-lockdown contact matrix to the lockdown contact matrix,
3) estimated the parameters x0 and k of the transition function as well as a reduction factor (zeta) for the additional reduction in transmission during the lockdown, and
4) included (by example) the possibility of estimation of the age-dependent fractions that were already immune (or less infectious, is also straightforward).

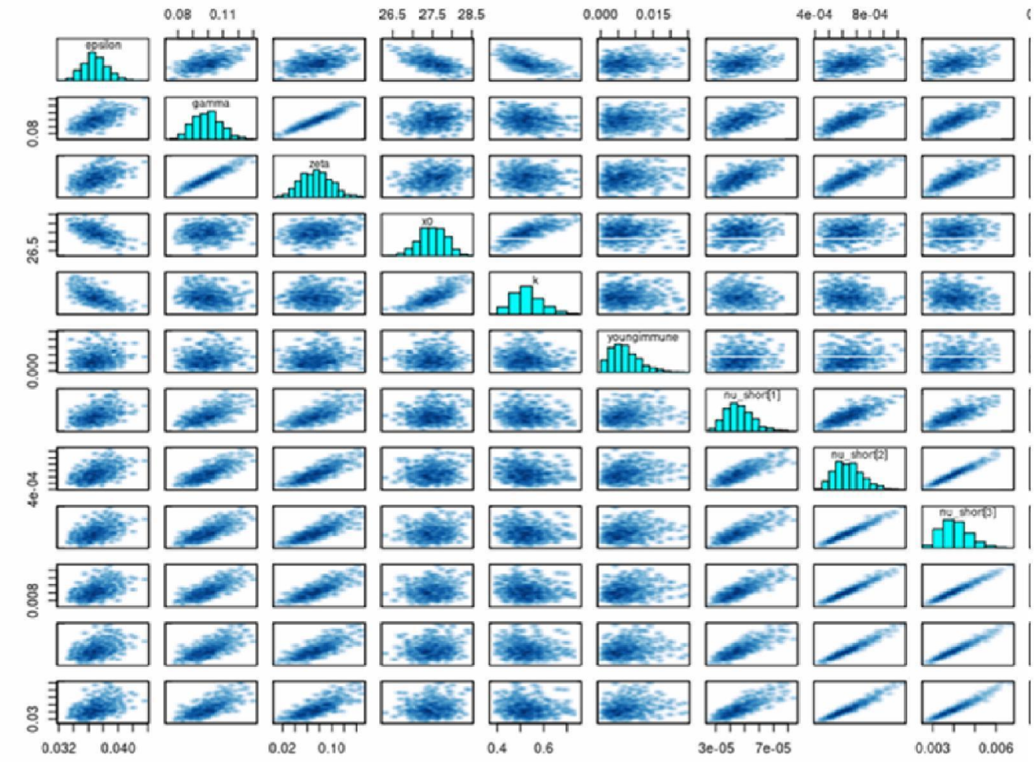
Below you also find some plots and statistics. Let me know if you have questions or remarks.

As you know I may not be able to publish with you on exit/de-escalation scenario studies, so I will now leave any further refinements as well as subsequent model scenario analyses to (10)(2e). Good luck with it!

I do hope to be able to write something on estimation of transmission parameters, attack rates, and age-dependent hospitalisation probabilities with generalized profiling (along the lines of earlier influenza/rsv work; see e.g. (10)(2e). For this I think we will ultimately need actual serological data. I was hoping that (10)(2e) ((10)(2e)) could reformulate the current model to GP and produce some figures (still with the synthetic serodata). Is that ok with you, (10)(2e)? After that, I will write a draft (shouldn't take more than a couple of days) and share this first with (10)(2e) (10)(2e) and (10)(2e) and thereafter with others (including ao (10)(2e) (10)(2e)) to see who could/would be willing and deserving to contribute.

Best,
(10)(2e)


0-19 yr
20-49 yr
60-69 yr
70-79 yr
Hospitalisations
Hospitalisations
Day
Day
0
3
6
9
0
20
40
60
80
0
30
60
90
0
50
100
150
0
50
100
150
0
25
50
75
100
125
Mar 01
Mar 15
Apr 01
Apr 15
May 0



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Inference for Stan model: corona_21072020.
10 chains, each with iter=2000; warmup=1000; thin=10;
post-warmup draws per chain=100, total post-warmup draws=1000.

                 mean  se_mean        sd      2.5%       25%       50%       75%     97.5% n_eff
Rhat
epsilon      0.036932 0.000054 0.001651  0.033973  0.035834  0.036832  0.037955  0.040519   919
0.998110
gamma        0.099491 0.000308 0.009248  0.082982  0.092866  0.099397  0.105437  0.119651   904
0.998408
zeta         0.074417 0.000810 0.024907  0.029401  0.056184  0.073972  0.091235  0.125613   945
1.000717
x0          27.500285 0.010659 0.346750 26.801352 27.272322 27.496246 27.748264 28.159879  1058
0.998025
k            0.529263 0.002107 0.063514  0.420141  0.484733  0.522537  0.568994  0.674388   908
0.994094
youngimmune  0.007151 0.000138 0.004370  0.001099  0.003931  0.006457  0.009478  0.017732  1006
1.000339
nu_short[1]  0.000046 0.000000 0.000010  0.000031  0.000039  0.000045  0.000052  0.000069  1060
0.998242
nu_short[2]  0.000644 0.000003 0.000105  0.000472  0.000566  0.000637  0.000707  0.000869  1005
1.000751
nu_short[3]  0.004071 0.000022 0.000679  0.002989  0.003564  0.004009  0.004486  0.005641   991
1.000789
```

```
nu_short[4]  0.010430 0.000056 0.001758  0.007662  0.009121  0.010278  0.011442  0.014384   992
1.001132
nu_short[5]  0.027358 0.000161 0.005103  0.019341  0.023644  0.026808  0.030218  0.039103  1003
1.000078
nu_short[6]  0.044036 0.000283 0.009041  0.030369  0.037444  0.042654  0.049252  0.065640  1019
0.999616
inoculum     0.000031 0.000000 0.000007  0.000019  0.000026  0.000030  0.000035  0.000045   919
1.000869
p_short[1]   0.000464 0.000002 0.000074  0.000333  0.000414  0.000456  0.000513  0.000629  1070
0.998066
p_short[2]   0.006411 0.000021 0.000662  0.005246  0.005924  0.006384  0.006844  0.007816  1009
1.000936
p_short[3]   0.039162 0.000130 0.004045  0.031956  0.036275  0.038776  0.041653  0.047602   965
1.001540
p_short[4]   0.094506 0.000307 0.009582  0.077494  0.088031  0.093623  0.100849  0.115218   976
1.000875
p_short[5]   0.214390 0.000699 0.021959  0.175166  0.199403  0.212917  0.227400  0.261822   987
1.000535
p_short[6]   0.304343 0.000962 0.030799  0.249242  0.282099  0.302270  0.324068  0.371028  1026
0.999536

Samples were drawn using NUTS(diag_e) at Wed Jul 22 13:30:32 2020.
For each parameter, n_eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor on split chains (at
convergence, Rhat=1).
```

[redacted] (10)(2e)
Centre for Infectious Disease Control
National Institute for Public Health and the Environment (RIVM)
web: [redacted] (10)(2e)
phone: (31) [redacted] (10)(2e)