Latest discussion:

* 1.) If we assume that both vaccination and previous infection gives the same protection you can just keep one parameter. If not, we need two
* 2.) Since they have a shorter duration of the disease, they are less likely to infect other individuals later in their infectious period. The next step is to include two other parameters: one that accounts for the vaccine effectiveness agains susceptibility to infection and one for the vaccine effectiveness against infectiousness. After doing that, we can run some simulations and see how the spreading dynamics change (varying also the contact reduction for the vaccinated and unvaccinated groups).
* There are contradictory study about whether vaccinated and unvaccinated have the same viral peak. What I suggest to do is just to represent the infectiousness measures with VL data, and add a parameter to represent possible different infectiousnesses

Tasks to do:

* 1.) Add a variable “Vaccinated” to status.matrix - if equal 1 the individual is vaccinated/immune 0 not
* 2.) when computing acc.rate, distinguish if the infector is vaccinated or not, and select the respective infectious measure
* 3.) Update the incubation period such that it returns the day at which the infectious measure peaks (distinguish also here between vaccinated and unvaccinated)

Some notes

* We are now assuming that the length of the infectious period depends only on the vaccination status (i.e., all the vaccinated have the same IP, and all the unvaccinated the same. But the IP of vaccinated is different from the one of unvaccinated). Therefore, we do not need to use that function anymore
* Yes, what you can do is to always use infectious.period.length but to make this function depend on the vaccination status. So, for example you add status.matrix as an input argument, and within the function to write an if cycle in which you check whether and individual is vaccinated (if (status.matrix$Vaccinated==1) {….})