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# A New "Non-Epidemiological" Model of the Covid19 Pandemic - Based on Potential Infection Ceilings [Maximum Number of Infected Persons] and Blocks - Taking Into Account the Results of Simple Calculations of Virus Multiplication as Well as Infection and Infectiveness of Persons Part II- The Essence of Block of Viruses. My Calculations Versus the Statistical Records

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## Abstract

The main objective was an explanation what exactly happens „during the block", -in all the affected Mankind. So I introduced once again the simple arithmetic [„2x2x2..."] model of virus multiplication but not a group of people [and so in the entire cloud] but one person [say "person zero"] from his/her infection to death; it is to show what is going on both in target cells and in an extracellular space including an exocytosis and blocking of viruses.

However the clear explanation of course of pandemic with actually all the time the block taking place had become possible only with Hill equation. Obtained numbers of infected people [in different selected time periods] enabled me to propose some methods of estimation of abundance of people sick,producing antibodies and dead.

Then my data [i.e. number of infected people]for all the population in Poland were compared with the statistical records. Mine figures were much, much bigger comparing those from statistics. However, the opposite was true with the data for the apparent beginning of pandemic [March-May]: there was something like an excess of cases of infection in that time.

***Keywords:*** *Covid19 Pandemic; Potential Infection Ceilings; Virus Multiplication*

### What really happens during the block, "its end" and just after the block?

### Exocytosis and blocking of extracellular viruses

How long will it take [because of viruses multiplying somewhere anyway] to "exceed the level of this block"? And how many people could be eventually "saved" with such a block. My first assumptions [which - as I show hereafter, were not true] were made in such a way: From the calculations with Hill equation we have the number of infected [y-axis] versus the number of viruses V [x-axis because there is n, so the logarithm from $2^n$ and V = 200 x $2^n$]. Therefore, if we assume [Table 1, part I] how many binding sites [ie block in the blood] are there, so how many viruses [indirectly axis X] can be bound, we can see what is the value of y [for a given x]. In such a way I estimated that in all the Poland there are about 1,5 million of infected people in the block [compare part I of this paper; especially just table 1]. The same way might be adopted for the number of sick, etc [data not shown]. Of course, the time ie the number n [on x axis] for above situation gives us an expected time of "end of the block" [compare text later].

Thus, this block should last until virus multiplication attains/exceeds the threshold of blood binding capacity, as I have written earlier, up to 32 to 35 doubling periods that is almost a year from the infection of "an person zero" to the time the pandemic becomes already overt.

Anyway even if there was no block the first month, or even two, after infection of „individual zero" would be asymptomatic anyway due to too few viruses and affected cells [table 3-part I and table 5]. Of course, all the time multiplication of viruses takes place but the majority of viruses first of all those exocytosed from attacked target cells are bound in the block.

My final opinion, which I will justify later, is that the block will continue until the end of pandemic and until all susceptible persons become infected.

| | **Number of viruses** | | | | | | | | **Number of infected persons [I] and…** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | **Finally present** | | | | | | |
| | **Total 2/** | **Entering the target [made in the infected cells ] 3/** | **Exocytosed 4/ [Version b]** | **Blocked 5/ [Version b]** | **Intracellular** | **In extracellular fluids** | | **9/ Block =Q+Y version a [version b] Total body** | **10/ X/ No Block total (new cases)** | **11/ Y/ Block Total (new cases)** | **12/ Y/X in %** |
| | | | | | **6/NO Block and block version a [version b] Q** | **7/ NO Block** | **8/ Block version a [version b] Y** | | | | |
| 1 | 400 → 360 | 10- [200] | 157 [189] | 278 [337] | 53 [21] | 347→ 307 | 69 [47] | 122 [68] | 1(0) | 1(0) [1(0)] | 100 [100] |
| 2 | 800 → 720 | 20- [400] | 355 [397] | 323-601 [371]-708 | 118 [[44] | 682 → 602 | 81 [53] | 199 [97] | 1(0) | 1(0) 1(0)] | 100 [100] |
| 3 | 1600 → 1440 | 40- [800] | 719 [778] | 608-1209 [692]-1400 | 239 [86] | 1361 → 1201 | 152 [99] | 391 [185] | 1(0) | 1(0) 1(0)] | 100 [100] |
| 4 | 3200 → 2880 | 80- [1600] | 1439 [1589] | 1201-2410 [1407]-2807 | 480 [177] | 2720→ 2400 | 310 [201] | 790 [378] | 1(0) | 1(0) 1(0)] | 100 [100] |
| 5 | 6400 →Inf 5760 | 160- [3200] | 2878 [3183] | 2424-4834 [2821]-5628 | 960 [354] | 5440→ 4800 | 606 [403] | 1566 [757] | 2(1) | 1(0) 1(0)] | 50 [50] |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | 12800 → 11520 Inf,A | 320- [6400] | 5760 [6367] | 4839-9673 [5643]-11271 | 1920 [707] | 10880 → 9600 | 1207 [806] | 3127 [1513] | 5(3)3 | 1(0) 1(0)] | 20 [20] |
| 7 | 25600 → 23040 Inf, A | 640- [12800] | 11520 [12732] | 9670-19343 [11120]-22391 | 3840 [1425] | 21760→ 19100 | 2417 [1612] | 6257 [3027] | 11 (6) | 2(1) 1(0)] | 18,2 [9,1] |
| 8 | 51200 → 46080 Inf, A,S | 1280- [25600] | 23040 [25464] | 19342-38685 [22240]-44631 | 7680 [2830] | 43520→ 38400 | 4835 Inf [3224] | 12515 [6054] | 23 (12) | 5(3) [2(1)] | 21,7 [8,7] |
| 9 | 102400 → 92160 Inf,A,S | 2560- [51200] | 46080 [50928] | 38684-77369 [44480]-89111 | 15360 [5660] | 87040→ 76800 | 9671 Inf [6448] inf | 25031 [12108] | 48 (25) | 11(6) [4(2)] | 22,9 [8,3] |
| 10 | 204800→ 184320 Inf,A,S | 5120- [102400] | 92160 [101856] | 77371-154740 [88960]-178071 | 30720 [11320] | 174080→ 15360 | 19343 Inf,A [12896] Inf,A | 50063 [24216] | 99 (51) | 23(12) [10(6) | 23,2 [10,1] |
| 11 | 409600 → 368640 Inf,A,S | 10240- [204800] | 184320 [203712] | 154738-309478 [177920]-355991 | 61440 [22640] | 348160 → 307200 | 38685 Inf,A [25792] Inf,A | 100125 [48432] | 201 (102) | 48(25) [22(12)] | 23,9 [10,9] |
| 12 | 819200→ 737280 Inf,A.S | 20480- [409600] | 368640 [407424] | 309476-618954 [355840]-711831 | 122880 [45280] | 696320 → 614400 | 77370 Inf,A,S [51584] Inf,A,S | 200250 [96864] | 405 (204) | 98(50) [46(24)] | 24,2 [11,4] |
| 13 | 1638400 → 1474560 Inf,A,$S_{ser}$ | 40960- [819200] | 737280 [814848] | 618952-1237906 [711680]-1423511 ! end of the block | 245760 [90560] | 1392640 → 1228800 | 154740 Inf,A,S [103168] Inf,A,S | 400500 [193728] | 814 (409) | 198 (100) [94(48)] | 24,3 [11,5] |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 14 | 3276800 → 2949120 Inf,A,$S_{ser}$ | 81920- [1638400] | 1474560 [1629696] | 0 | 491520 [181089] | 2785280→ 2457600 | already after block [a] and [b] 1547380 Inf,A,S | already after block [a] and [b] 2038900 [1832128] | 1633 (819) | 707 (509) [552(458)] | 43,3 [33,8] |
| 15 | 6553600 → 5898240 Inf,A,$S_{ser}$, | 163840- [3276800] | 2959120 [3259392] | 0 | 983040 [362173] | 5570560→ 4915290 | 4332660 Inf,A,$S_{ser}$ | 5315700 [1832128] possibly death* | 3271 (1638) | 2035 (1328) [1829 (1277)] | 62,2 [55,9] |
| 16 | 13107200 → 11796480 Inf,A,$S_{ser}$, | 327680- [6553600] | 5898240 [6518784] | 0 | 1966080 [724 | 11141120→ 9830400 | 9903220 Inf,A,$S_{ser}$ | 11869400 * | 6547 (3276) | 5002 (2967) | 76,4 |
| 17 | 26214400- 23592960 Inf,A,$S_{ser}$,D ? | 655360- [13107200] | 11796480 [13037568] | 0 | 3932160 | 22282240- 19660800 | 210 44340 Inf,A,$S_{ser}$ | 24976500 * | 13200 (6653) | 11246 (6244) | 85,2 |

***Table 5:*** *What is going on in the body of one infected person [Let it be person"0" *] ? – Taking into consideration the blocking of viruses.*

Now let us characterize [Table 5] what is really going on in a body of one person [say "person zero"] assuming some substantial % of viruses [including those exocytosed from the target cells] undergoes blocking. Initially, I assumed 75% of exocytosed and 80% blocked viruses [bound to serum ACE2 and some erythrocytes]-version a. In the "corrected" version. b. I assumed 90% exocytosed and 87,5% blocked viruses. In yet another version [Table 6] there is 92 - 98% of blocked viruses.

Well, one could ask why I did not assume 100% of block. It would simplify the reasoning but it is simply incredible, because viruses travel [in a passive diffusive way] and is hardly possible that all would bind to the blocking sites. Besides, in such a case there would not be pandemic at all. Although still some viruses were multiplied in the cytoplasm of infected cells, but if only they came out the cells they would bind with the blocking sites and in a short time there would be no multiplication thus no pandemic whatsoever [until new infection of the same person occured somehow but even then…].

Well one can say that viruses might quite easily pass directly from one cell to another [67-69]. Yes but: 1/such a way gives more local damage but at the same time strongly supress infectivity [69] 2/even with such a way -with "virus synapses" [69] sooner or later some viruses come out the cell/s and "have an opportunity" to bind to the blocking sites.

Selection of too big % of blocked viruses would result in a relatively quick complete lack of viruses in extracellular space and so the end of pandemic either.

One should take in mind that the number of intracellular viruses doesn't depend on whether or not there is a block. So two versions shown in the column 6-table5- [one of them in brackets] only show 75% of exocytosis and that in brackets 90%.The percentage of exocytosed viruses is very important factor of pandemic [regardless the block would happen or not].

In fact even if there was formation of syncytia [due to the damage of cell membranes of neighbouring cells –near tight junctions] [66] after much longer time respectively bigger amount of viruses would be finally exocytosed into extracellular space, so lumen of capillaries and be blocked. The only difference is that in such a case bigger fraction of cells would be affected in the same time [eg serious acute interstitial pneumonia [70]].

## Symptoms of pandemic and block

Most interesting are the number of infected persons [columns 10 - 12, table 5]]. They were calculated without block according the simple formula I presented earlier [so simply $I_p = V/4000$-of course just integers eg 27 not 27,245 or even not 27,879]. But with a block, where there is much less viruses especially in extracellular space, I applied formula $I_p = V_{extracellular}/4000$,which seems to be more justified as it does not overstate intracellular viruses, which do not infect.

The column 12 [still table 5] shows us summarized effect of block on number of infected persons [by one person"zero"] ie the ratio of those infected during the block to that if there was no block whatsoever. We can see that from n = 8 to n = 13 this ratio is about 8-9% for version a and 4,3-5,9% for version b.

Besides table 5 shows us clearly [in spite indirectly] what is the health of this one person ["zero"-but of course this might happen and happens with every one infected person multiplying viruses] in case there is block or is not [the block is over:full saturation of blocking sites]. How? That's simple, I assumed [and partially already discussed] that one needs to have in a whole body 40000 viruses to be sick S [at least very mildly-I later changed this limit to 300000: S], 2 millions to be seriously ill $S_{ser}$, 10000 to produce specific antibodies A [I changed this later to 80000: A], and 2 or even 5-6 $x10^7$ to die [D→D]. So in column 2 [but in the column 8 – and eventually 6-if the block takes place] there are - in proper cells of table -after respective time- signs S [V> 40000], S [> 300000], $S_{ser}$ [> 2 $x10^6$], A [>10000], A [> 80000], D [> 2 or even $5x10^7$. To be infectious [Inf] infected person should contain in the whole body not less than 4000 viruses [with 200 as an infectious dose $d_i$], but in fact [compare earlier text] not less than 32000 [Inf] [>1600 as $d_i$].

If only number of "attacked"cells mattered lower limits for sickness would be exactly the same regardles there was the block or not. However,the sickness like Covid19 needs not just a lot of damaged or disturbed cells but also certain processes related to the immune system- like "cytokin storm" [44] and thus is dependent on extracellular viruses. So I think two conditions should be met [for disease to appear]: bigger than above mentioned: a/ number of attacked cells and b/ number of viruses not just in a whole body but that in extracellular space.

So, one can see that the primary symptoms of a pandemic are weakened [quantitatively],but in a sense they are delayed, when there is a block, especially when the % of viruses blocked is greater [version b]. Fraction of viruses undergoing exocytosis plays a major role either - regardless the block. If there was both maximum possible % of exocytosis and % of block the parameters of the pandemic [the number of people infected, infectious, sick, but also producing antibodies and death cases] would delay, thus diminish, enormously.

And thus the onset of a mild disease [S]comes 40 days later [n = 10 not n = 6 without the block], pronounced disease [S] does one month later [n = 14≠ 11; note it is already after the block-if the duration of the block was extended -as it has to happen within younger people- the delay would be bigger], serious sickness ten days later [n = 15≠ 14, so after the block]. Producing of specific antibodies delays for 40 days [A: n = 10≠ 6; A: n = 13≠ 9]. People are infectious [Inf] with the block taking place 1,5 month later [n = 9/or even 10/≠ 5] or certainly contagious [Inf] [n = 12≠ 8]. The strongest effect of block concerns the infectiveness. The ratio of infected to infectious persons without a block would be more than 30 [table 3, I part] and taking the block into account is more than 100 [look in table 5- at n = 12

-without block-there is 405 infected and 11 infectious,while with block [version b] taking place at n = 16 there is 16 infectious and 1829 infected].

The above data are not shown in table 5. However, they can be obtained simply by combining the reasoning used in the arithmetic model „2 x 2 x2.." [Table 3] with the data in table 5. Since the person „0" - assuming the existence of a block - will infect the first person at time n = 8, then this person [„8"] has 200 viruses in his body, so 400 for n = 9...., so 6400 n = 13 and only then he/she is infectious [and there are already two such people - taking into account „person zero"] Thus we can see from table 6 that at n = 14 four people will become infectious, and at n = 15 ten such people. Ergo will then be 16 infectious people.

Take in mind that real danger happens not earlier than already the block is over.Then suddenly amount of non-blocked extracellular viruses increases dramatically, so infectiousness,morbidity and in consequence -later-mortality.

The numbers of infected persons deduced in such a way are striking [in spite a block,first of all when the block is already over]. If „Individual zero" infects 9223 people, and 98 of these people ["9"to "14"] are likely to die before "the end of the block" [n from 32 for the oldest group to 34.7 for the youngest group-compare part I. Why will they die [although, due to individual differences, it does not have to be]? Simply by analogy to "person zero [„described" in table 6]. Since „0" is [assuming a block in version b] infectious not earlier than for n = 9 and dies at n = 18, then specimen „9" will start to infect at n = 21, and will die at n = 27 etc.

First of all I have to emphasize strongly that the block concerns every single infected person. But in such a case if we know what is going on with one person we do know the same about any other else. So, if person "0" [infected at n = 0, say just before the beginning of doubling period No1] - with block-becomes infectious: Inf at n = 10 [really infectious Inf at n = 12/13], is sick S at n = 13 and dies at about n = 19 - 20 then person "8" respectively will become infectious not earlier than at n = 18, sick at about n = 21 and die at n = 37 - 38 etc.

What is going on with the viruses being blocked? One can only speculate they will be gradually and slowly recognized and destroyed by our immune system rather innate one and/or...reactive oxygen species [free radicals]. However the participation of an adaptive immune system with IgM, but maybe some first IgG [may be different from those against free viruses or complexes viruses with their receptors] either, can't be excluded. Well,the macrophages mentioned to be "the Troian horse of pandemic" [71] [as they travel quite freely and contain ACE2 [it is questioned [66N, 66N że nie] might simply kill internalized viruses ie destroy viruses'complexes.

It should be emphasized here that the block, i.e. the potential ability to bind viruses [in the blood], is available to everyone, even those who do not multiply them [because they do not have functional receptors]. If such person [not susceptible one] took up even 100,000 viruses from the outside, because they were not be able to multiply, they would simply be „blocked" and then destroyed. There may be about 33 million of such people in Poland [i.e. 32,9 million as 38.4 million all minus 5,5 million susceptible, i.e. those having functional SARS CoV-2 receptors].

## An evolution of my ideas concerning the block for/against viruses. Block and its effects [from one person to all population]-calculated with Hill equation

Here I have to very briefly, as much as possible, describe my subsequent views on the block, thus when it is there, in how many people, when it is no longer there and whether it should be considered that there are two subsequent phases of the pandemic [„hidden" with the block and apparently overt- after the block] or whether these phases „partially overlap".

My first idea [depicted in figure 1] has been explained on the page 1 of this [second] part. According to this idea there are two great, long lasting phases of pandemic-hidden when block takes place [it would be 31 - 34 doubling periods –for viruses "in all the cloud"]and second one apparently overt lasting next about 35 - 38 doubling periods.

But when I continued reasoning and calculations what was going on in the body of one person [say "0"]-from infection to death- [see table 5] it had become apparent that: 1/even the person "0" had -in his/her body- phase of the block,which became over and it looked like every infected person was in phase of block and thereafter in phase without block when all the blocking sites were then already saturated.

So it had become obvious that the block started with an infection of given person so some people were still in the block phase and other already not.

But if I tried to estimate number of infected persons it was then that I came to the misconception that before the end of time n = 32 [group 65+] to 34.5 [group under 25], all people - obviously susceptible i.e. having functional SARSCoV-2 receptors - would already become infected, and over 90% of them [„newly infected", i.e. infected at n = 25-29] would have so few viruses that they would be asymptomatic, would not be infectious, and even possibly very sensitive tests would not be able to detect that they were in fact already infected. Then they could be infected a second time from those less numerous, but nevertheless numerous, formerly infected people - who have large amounts of viruses per body. Especially when one considers that neither the infectious [both still in blocking and post-blocking phase] and the newly infected do not yet have any sufficient immunity.

I have to add that I have concluded that they are all already infected using a continuation of the arithmetic model „ 2 x2 x2..x2 „and, for example, since the specimen" 0 „infected more than 1000 people [Table 5], then following their further fate - in analogy to the fate of "person zero „- it is possible to reach enormous amounts of infected people [after all 1000 x 1000 = milion;compare earlier].

Then I started to think that the phases of the block and „after the block" - in the scale of the entire population, of course, taking into account the susceptible persons - overlap and that the block definitely ends only when the „blocking places" are saturated, i.e. according to "my estimations at that time" about n = 46]. At the same time, I tried to find out more precisely what the effects of the block were, as well as what happened to the unblocked viruses and how to reconcile it with a „new beginning", i.e. „outright of "evidently overt pandemic- after the block".

I thought it started at around 1 x $10^7$ viruses per million people [30 - 300 viruses per person]. This, however, would require the assumption that a large part of viruses - I'm talking now about unblocked viruses here - were also destroyed by some defense mechanisms. I had realized that I had been at a turning point and until I found some model/algorithm to calculate the number of infected - taking into account the block - I would not go on.

And then I thought that we should come back to the Hill equation, i.e. to calculate the dynamics of virus binding with the block [i.e. plasma ACE2 and some erythrocytes] with this method. But after rather short time of calculations it turned out that it was necessary to assume that the blocking rate would be slowed down with each subsequent period of viruses' doubling. Otherwise the blocking sites would be exhausted too early [and viruses were still multiplying and new people were getting infected [because I confronted the calculations of the number of blocked and „free" viruses and the number of infected people - calculated from the Hill equation]. Thus finally I have understood that block is going on in the body of every infected person, so the block would happen until the end of pandemic. It can't be that all the places of binding- "binding sites" are saturated in spite there are stilll noninfected people, can it?

All the data come from above reasoning and calculations are presented in table 6.

| **Time [n]** | **Number of viruses** | | | **Number of infected people I @$** | **Increase Of number of infected people: $I_{n+1} - I_n$ #!** | **Inf ..... A** | **S,A,Inf** | **Clearly sick S** | **Seriously sick $S_{ser}$ ..... Dead D** | **Inf = S** | **A ..... S** | **$S_{ser}$ ..... D** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Total** | **Blocked** | **& Free** | | | | | | | | | |
| 5 | 6,4 x$10^3$ | 5,917 x {128} x$10^3$ | 483 {6272} | 0 {0,37=0} * | 0 | 0 | 0 | 0 | 0 | | | |
| 10 | 2,048 x $10^5$ | 1,893 x {4,096 x$10^3$} $10^5$ | 1,55 x $10^4$ {2,007 x $10^5$ } Inf (n=8) A (n=9) | 0 {11,9=12} | 0 | 0 | 0 | 0 | 0 | | | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11 | 4,096 x $10^5$ | 3,809 x$10^5$ {8,192 x $10^3$} | 2,87 x $10^4$ {3,914 x $10^5$ } | 0 {23} | 0 | | | | | | | |
| 12 | 8,19 x $10^5$ | 7,756 x $10^5$ | 4.34 x$10^4$ {8,19 x $10^5$} Inf,S, A | 0 {49} ……. 0,93=1 | 0 | 0 | 0 | 0 | 0 | | | |
| 13 | 1,638 x $10^6$ | 9,9 x $10^5$ /// 1,515 x $10^6$ | 6,48 x $10^5$ /// 1,23 x $10^5$ S = 12,5 | 0 {98} ……. 1,85=2 | 0 | 0 | 0 | 0 | 0 | | | |
| 14 | 3,277 x $10^6$ | 9,902 x$10^5$ /// 3,03 x $10^6$ | 2,287 x $10^6$ /// 2,47 x$10^5$ $S_{ser}$ | 0,65=1 ……. 6.5=7 | 1 | 0 | 0 | 0 | 0 | | | |
| 15 | 6,554 x $10^6$ | 9,904 x$10^5$ /// 6,06 x $10^6$ | 5,564 x $10^6$ /// 4,94 x $10^5$ | 1,59=2 …….. 16 | 1 | 0 | 0 | 0 | 0 | | | |
| 16 | 1,311 x $10^7$ | 9,906 x$10^5$ | 1,212 x $10^7$ | 3,46=3 ……. 35 | 1 | 0 | 0 | 0 | 0 | | | |
| 17 | 2,622 x $10^7$ | 9,914 x$10^5$ | 2,523 x $10^7$ | 7,2=7 ……. 72 | 4 | 0 | 0 | 0 | 0 | | | |
| 18 | 5,244 x $10^7$ | 9,93 x $10^5$ //4,953 x $10^5$ | 5,145 x $10^7$ | 15 * ……. 147** | 8 | 0 | 0 | 0 | 0 | | | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 19 | 1,049 x $10^8$ ……!! 4,49 x $10^7$ because D „0" | > 9.93 x$10^5$ //4,957 x $10^5$ ----------!! 3 x$10^3$ because D „0" | *4,49 x $10^7$* because D „0" ---------- ---- 1,039 x$10^8$ | 12,8 so 15 * …….. 128 so 147** 29,6=30 | 0 | 0 | 0 | 0 | 0 | | | |
| 20 | 2,097 x $10^8$ ……. 8,98 x $10^7$ | 9,952 x $10^5$ ……. 5,2 x$10^3$ | 8,98 x $10^7$ | 25,6=26 ……. 256 | 11 | 0 | 0 | 0 | 0 | | | |
| 21 | 4,196 x $10^8$ ……. 1,796 x $10^8$ | 1,0004 x $10^6$ ……. 1,04 x $10^4$ | 1,796 x$10^8$ | 51 ……. 512 | 25 | 0 | 0 | 0 | 0 | | | |
| 22 | 3,592 x $10^8$ | 1,0108 x $10^6$ ……. 2,08 x $10^4$ | 3,592 x $10^8$ | 102 ……. 1024 | 51 | 1 ……. 0 | 0 | 0 | 0 | | | |
| 23 | 7,184 x $10^8$ | 1,032 x $10^6$ ……. 4,16 x $10^4$ | 7,184 x $10^8$ | 205 …….. 2048 | 103 | 1 ……. 1 | 0 | 0 | 0 | | | |
| 24 | 1,437 x $10^9$ | 1,073 x $10^6$ ……. 8,32 x $10^4$ | 1,437 x $10^9$ | 410 ……. 4097 | 205 | 1 ……. 1 | 0 | 0 | 0 | | | |
| 25 | 2,874 x $10^9$ | 1,156 x$10^6$ ……. 1,664 x $10^5$ | 2,874 x$10^9$ | 819 ……. 8194 | 409 | 4 ….. 1 | 0 | 0 | 0 | | | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 28 | 2,299 x $10^{10}$ | 2,321 x $10^6$ ……. 1,331 x $10^6$ | 2,299 x $10^{10}$ …… 5,37 x $10^{10}$ | 6555 …… 64900 | 5736/3 = 1912 | 11 …….. 0 | 1 | 1 | 1 …… 0 | | | 1 ……. 0 |
| | | 6,314 x $10^6$ | 9,196 x $10^{10}$ | | | | 8 | 6 | | | | |
| 30 | 9,196 x $10^{10}$ | …… 5,324 x$10^6$ 26220 ……. 240115 | 19665/2 = 9832 | 51 ……. 25 | | | 1 …….. 0 | | | | | |
| 31 | 1,839 x $10^{11}$ | 1,143 x $10^7$ & 222 ……. 1,044 x $10^7$ | 1,839 x $10^{11}$ | 51487 ……. 442888 | 25267 | 103 ……. 51 | 0 | 0 | 4 ……. 0 | | | 7 ……. 0 |
| 32 | 3,678 x $10^{11}$ | 2,187 x$10^7$ ……., 2,088 x $10^7$ | 3,678 x $10^{11}$ | 101147 …….. 766685 | 49660 | 205 …….. 103 | 11 | 9 | 8 ….. 0 | | | 15 …….. 0 |
| 33 | 7,356 x $10^{11}$ | 4,275 x $10^7$ ……. 4,176 x $10^7$ | 7,356 x $10^{11}$ | 195363 ……. 1237995 | 94216 | 409 ……. 205 | 25 | 18 | 0 ……. 1 | | | 15 ……. 1 |
| 34 | 1,471 x $10^{12}$ | 8,451 x $10^7$ ……. 8,352 x $10^7$ | 1,471 x $10^{12}$ | 365628 …… 1697335 | 170265 | 1912 ……. 409 | 51 | 38 | 11 ……. 1 | | | 26 ……. 2 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 35 | 2,943 x $10^{12}$ | 1,68 x $10^{8}$ ...& 259..... 1,67 x $10^{8}$ | 2,943 x $10^{12}$ | 648310 ..... 2128096 | 282682 | 1912 ..... 1912 | 103 | 77 | 25 ..... 1 | | | 51 ..... 3 |
| 36 | 5,885 x $10^{12}$ | 3,35 x $10^{8}$ ..... 3,34 x $10^{8}$ | 5,885 x $10^{12}$ | 1056299 ..... 2437082 | 407989 | 1912 ..... 1912 | 205 | 154 | 51 ..... 4 | | | 102 ..... 7 |
| 37 | 1,177 x $10^{13}$ | 6,69 x $10^{8}$ ..... 6,68 x $10^{8}$ | 1,177 x $10^{13}$ | 1541508 ..... 2627927 | 485209 max | 9832 ..... 1912 | 409 | 308 | 103 ..... 8 | | | 205 ..... 15 |
| 38 | 2,354 x $10^{13}$ | 1,337 x $10^{9}$ ..... 1,336 x$10^{9}$ | 2,354 x $10^{13}$ | 2001111 ..... 2735014 | 459603 | 9832 ..... 9832 | 819 | 616 | 205 ..... 0 | | | 410 ..... 15 |
| 39 | 4,708 x $10^{13}$ | 2,673 x $10^{9}$ ..... 2,672 x $10^{9}$ | 4,708 x $10^{13}$ | 2351691 ..... 2791899 | 350580 | 25627 ..... 9832 | 1638 | 1230 | 409 ..... 11 | | | 819 ..... 26 |
| 40 | 9,416 x $10^{13}$ | 5,345 x $10^{9}$ .....& 2074..... 5,344 x$10^{9}$ | 9,416 x $10^{13}$ | 2577467 ..... 2821238 | 225776 | 49660 ..... 25627 | 3276 | 2458 | 819 ..... 25 | | | ..... 51 |
| 42 | 3,766 x $10^{14}$ | 2,1381 x$10^{10}$ //& 7700..... 2,138 x$10^{10}$ | 3,766 x $10^{14}$ | 2777449 ..... 2843649 | 199982/2 = 99991 | 170265 ..... 94216 | 13110 | 9833 | 1641 ..... 103 | | | 6555 ..... 205 |
| 44 | 1,507 x $10^{15}$ | 8,5521 x$10^{10}$ ..... 8,552 x $10^{10}$ | 1,507 x $10^{15}$ | 2832405 ..... 2849309 | 54956/2 = 27478 | 407989 ..... 282682 | 49660 | 37464 | 3276 ..... 409 | | | 26220 ..... 819 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 45 | 3,013 x $10^{15}$ | 1,71 x $10^{11}$ // & 6,017 x $10^{4}$ ……. 1,71 x $10^{11}$ | 3,013 x $10^{15}$ | 2841768 ……. 2850254 | 9363 | 485209 ……. 407989 | 94216 | 71938 | 6555 ……. 819 | | | 51487 |
| 46 | 6,026 x $10^{15}$ | 3,42 x$10^{11}$ / 11,6 % satur. of block ……. *2,868 x$10^{11}$* // 3,42 x $10^{11}$ | 6,026 x $10^{15}$ | 2846476 ……. 2850727 | 4708 | 459603 ……. 485209 | 169905 | 132060 | 13110 1641 | | | 101147 |
| 47 | 1,205 x $10^{16}$ | 6,82 x $10^{11}$ | 1,205 x $10^{16}$ | 2848835 | 2359 | 350580 ……. 459603 | 283042 | 226473 | 25267 ……. 3276 | | | 195363 …….. 6555 |
| 48 | 2,411 x $10^{16}$ | 1,368 x $10^{12}$ // & 4,8 x $10^{5}$ ……. 1,368 x $10^{12}$ / 46,5 % satur. of block | 2,411 x $10^{16}$ | 2850018 ……. 2851082 | 1183 | 225776 ……. 350580 | 407989 | 345516 | 49660 ……. 6555 | | | 365628 |
| 49 | 4,822 x $10^{16}$ | 2,736 x$10^{12}$ // & 9,6 x $10^{5}$ 93 % satur. of block ……. 2,736 x$10^{12}$ | 4,822 x $10^{16}$ | 2850609 ……. 2851141 | 591 | 99991 ……. 225776 | 485209 | 446599 | 94216 …….. 13110 | 26220 | | ……. |
| 50 | 9,642 x $10^{16}$ 2,252 x $10^{17}$ | 2,943 x $10^{12}$ /100% saturation of block ……. *2,943 x $10^{12}$* // 2,736 x $10^{12}$ | 9,642 x $10^{16}$ | 2,850904 [99,99 % of susceptible] ……. practically 2851200 | 295 | 99991 …….. 99991 | ? >485209 | 472406 | 169905 …….. 25627 ? | | | ……. 51487 ?? |

***Table 6:*** *Block and just after – So all the pandemic-- Group I [ > 65 YEARS OLD] in Poland-calculated {17.10.2020}. Ka for I = 1x 1013 . Explanations see text.*

***Citation:*** Turski Wojciech Antoni. "A New "Non-Epidemiological" Model of the Covid19 Pandemic - Based on Potential Infection Ceilings [Maximum Number of Infected Persons] and Blocks - Taking Into Account the Results of Simple Calculations of Virus Multiplication as Well as Infection and Infectiveness of Persons Part II- The Essence of Block of Viruses. My Calculations Versus the Statistical Records". *EC Nutrition* 16.7 (2021): 61-90.

Then I assumed that initially 98% of viruses was blocked. Previously I couldn't make such an assumption because arithmetic mode of calculation gave me an early "sudden end of pandemic" if I tried the calculations with too high % of block of viruses. With the Hill equation it was possible.

But anyway at n = 12 more than 80% of blocking sites in the body of one person ["0"] is saturated, so at n-13 all sites are saturated. So there are not blocking sites whatsoever until n = 17, where first new infected person appears [besides person "0" with all the blocking sites already saturated]. Then appear new blocking sites [I calculated the minimum i.e. 200 viruses as an infectious dose per one newly infected].

But at n-19 new story begins –person "0" dies, so there is the very substantial decrease of both total number of viruses as those actually blocked, so finally free viruses [as a difference of both preceding ones] and thus the calculated number of infected persons decreases, but obviously it means there is no increase of number of infected people. Still the number of freshly blocked viruses is the 200 x number of newly infected persons [it is shown in lower part of table cells-under----- from n = 21 up to the end of the table –to the n = 53 -and thus practically to the end of pandemic]. Why? Because two conditions are then [n = 53] met: 1] practically 100% of susceptible people [in group I: 65+] is infected and 2] 100% of blocking sites are saturated.

But already at n = 44 there is/was almost 2,7 million of 65+ susceptible infected, so 94%; at n = 49 there is/was 99,9%, whereas there is/was only 77,9% of saturation of blocking sites.

The additional important [for calculations] question arises: how many persons zero"are/were in the whole of Poland [38.4 million people]? It seems to me that there is one such person per million inhabitants [with today's tourism and business connections - there are not many 38 people returning from China/to the whole of Poland]. Well, but what about persons previously infected who came back or visited Poland between say May and November this year? Aren't they new persons "0"? Not at all. Even one such person with even 10 million viruses in the body [perhaps seriously ill] means nothing comparing one bilion viruses in whole the cloud let alone $10^{11}$ - $10^{14}$ viruses [compare eg table 7].

So we should calculate -from the Hill equation- for a million people of a given age group-assuming that $K_a = 1 \times 10^{13}$ and $I_{max} = 297000$ [and analogously for each of the four age groups I distinguish] and then multiplying by 9.6 [the number of each I-IV group is nearly 9.6 million] and then adding the results for the same date/n.

Let us remain within table 6, essentially concerning just age group [65+] and taking in account all the pandemic with block and post block going on all the time until the end of pandemic. I have compared number of infected persons with that calculated previously assuming then that there was "after the block [for all the population]". But there are quite another numbers of doubling periods: from 1 to 53 in table 7 and from 32 to 70 in case of older calculations [then I thought the block goes on in group I until n = 32, compare an earlier text]. So the only one way of matching dates [number n] was to look for about the same total amount of viruses. And that's it. It appeared that number of infected persons are about the same for about the same total amount of viruses [in case of table 6 of course it does concern free ie unblocked viruses]. Thus n = 32 in older calculations [figure 1; figure 3-6] corresponds about n = 17-19 from table 6. Then there remained [to the practical end of pandemic]about 35 doubling periods [up to n = 53], exactly as in older assumptions and calculations [33 +35 = 68; figure 3-6].

## Summarizing the block

Well, now summarizing up what the block gives:

1. Delaying infections, infectivity, morbidity, and thus deaths, but also the formation of specific antibodies - I mean first of all those against „free viruses", not those blocked ones.

2. Delay means a significant reduction in the abundance of the above-mentioned pandemic symptoms; here I will quote the results of the analysis using the "combined" method [Table 3 plus table 5]. Table 5 shows when infectivity begins, whether it is mild, pronounced or severe. But table 3 shows how many persons has how many viruses [on average].

3. The most important are the effects of block for every infected person - and here the block clearly delays the development of the pandemic, i.e. the appearance of subsequent symptoms/stages from infection to death, especially infectivity.

4. There is no clear division - in the scale of the entire population - into the so-called the hidden phase [with the block] and the open phase [without the block], because people get infected all the time, they enter the block and this block ends within them one day [with saturation of blocking sites]. Unless, however, [remember that I start with one single person, and not, for example, 10 out of 100,000 people], we divide the pandemic into the following phases A-D [table 6, but of course it does correspond the collective table 7 for entire Poland's population either]:

    A. With only one infected person [from n = 1 to n = 18-19, but notice the block takes place in his/her body only to n = 15 and most serious changes take place when the block is over [!!But this will take place with every infected susceptible person]; the number of free viruses is still distinctly lower than that of total ones.

    B. „Oligosymptomatic", i.e. up to 50-100 infected per 100000 inhabitants [from n = 19-20 to n = 29 -30 for group of seniors [65+]-table 6 and n = 27-29 [older numeration 43-45] in the collective table 7; in spite of block there is not evident difference of amount of total and free [unblocked] viruses.

    C. Full-blown exponential phase to infection of 80% of susceptible persons [from n = 32-33 up to n = 42, with $K_a$ attained at n = 37- group 65+ (Table 7); about n = 38 –whole population-table 8].

    D. As above, but „flattened"phase - lasting from n = 43 until the end of the pandemic [i.e. until almost all susceptible infected [unless they die] develop such an amount of anti-SARSCoV-2 IgG antibodies that virtually all viruses in their bodies would be destroyed.

Phase D can be divided into D1/when the amount of infected is still below 95% of all susceptible [about three weeks–n = 43 and 44/41 all population] and D2/when infected is over 95%, i.e. all susceptible within the limit of error. Re-infection can often occur in phase D, especially D2 „sub-phase" [from n = 45 to n = 53 but even longer].

Where would the new infections come from?

Maybe from people who came from a country where still the functional receptors for SARSCoV-2 are not saturated?

Such a scenario is only one of the possibilities. Maybe just this phase, it's like the realization of three possibilities [A, and B, C] at the same time.

Viruses continue to multiply in the bodies of previously infected people - still in the block phase, but also –even stronger-after the block, so gradually more people are mildly ill, producing antibodies, more seriously ill, etc. and at the same time.

People already infected once but having a negligible total amount of viruses in the body - become infected a second time, ie rather receive a repeated infecting dose of viruses from some people already infectious. Let's assume these three combined phenomena A-C as one scenario [with an additional infection from some contaminated surfaces]. This second infection is something like "increasing the dose of poison" or "an one more glass for the alcoholic".

## Some essential questions

The question is what might be maximal number of viruses in the body of one person -and more difficult in all the cloud ie whole population - [which might be numbers that can be substituted for the Hill equation]. Well I assumed some "ceilings" ie the numbers of cells expressing ACE-2 gene [or rather some fraction of them meeting the criteria for being the functional receptors for SARSCoV-2]. But:

1. The number of cells containing ACE-2 in the cell membrane - reported in the literature - there are very divergent data - may be underestimated.

2. We do not know how many viruses enter the target cell on average, and we do not even know how many ACE2 molecules there are located on average in the one cell membrane.

3. What % of viruses disappears with the bodies of the dead, although with the exception of the zero individual, it does not seem to be a significant percentage and

4. Is it possible for viruses to enter „from cell to cell" - „through viral synapses" - into cells that do not have receptors for the virus [notice that nobody claimed about such a possibility] - the formation of multicellular syncytia in which viruses continue to multiply using the ribosomes of cells in the syncytia and their enzymes able to „unconsciously" functionally modify the multiplied viruses [lipid and glycan attachment, transport and exocytosis]. Very recently Leroy., *et al*. [66] published the review about formation of syncytia [multinucleated giant cells] of infected target cells with non infected cells. However it looks like the formation of those syncytia [with SARSCoV-2] always needs the cells taking virus in [from infected cel] have to express genes for both ACE2 and TMPRSS-2.

According to my assumptions there is about 5 x $10^{15}$ cells containing ACE2 but if there –on average 20 viruses come into one such cell it makes totally $10^{17}$ viruses, and with formation of syncytia it might magnify this number even to $10^{18}$.

On the other hand if on average death happens when there is 60 million of viruses in the body it should be that in the bodies of all dead [susceptible] people would be no more than 4 x $10^{14}$. But this calculation is based on the assumption, there is one virus sucked into one cell. So this magnifies the maximal number in the bodies of all [!!] dead people enormously even to $10^{16}$ - $10^{17}$.

And what about if even about 90% of viruses die-one should rather call "lose"- but anyhow suitably chosen [and true] $K_a$ value/s gives us not very big difference comparing with the data I calculated and presented previously? Also there is possible that somehow in very final part of pandemic viruses already do not multiply but still directly and undirectly affect the cells and tissues thus all the body. Well, some doctors claim such a story might be actual in even quite early phase of sickness of every one patient.

## The effect of block on $K_a$ value for infection.The complexes virus-serum ACE2 as potential inhibitors of infection

I have to emphasize one more point here: It seems impossible that, even though in the body of every infected person more than 90% of emerging viruses- is blocked [even 98% at the beginning], the final calculated number of infected was almost the same as if there was no block at all. And that would be the case, because by definition the number of infected depends on the number of unblocked viruses; we can see from table 6 that practically up to n = 20 even the death of "an individual zero" seems to have a greater impact than the block - I'm talking not about one person - about the entire population.

And yet the block takes place until the end of the pandemic. So I assumed that blocking in every infected person had to increase the $K_a$ value from 1x$10^{12}$ [or even lower value] to $10^{13}$. Why?

I assume that virus-serum ACE2 [V-SA] complexes, and maybe the complexes of viruses with some erythrocytes [V-E] [so generally virus-block complexes: V-B] are the potent competitive inhibitor/s of infection, and more particularly of the viral [V] association [„recognition"] process, with functional SARSCoV-2 receptors FR [forming V-FR complex/es]. In analogy to the findings of enzyme kinetics [] [but not only], such binding reduces the affinity [and thus increases the $K_a$ value] without affecting the maximum effect [$I_{max}$]. However, it

would require binding the V-B complex [or maybe only V-SA] with the functional receptor (s), thus formation of SA-V-FR ie "three component containing" complexes.

There is a theoretical possibility, although the SARSCoV-2 literature does not mention it, that the V-SA complex, and not only the free virus (s) itself, binds to the viral membrane receptor. It would need just binding by other spikes, i.e. spike proteins especially those located at an angle of almost 180 degrees from this spike protein that would bind to the membrane receptor.

And so it would be capable with the formula [59]:

$I = I_{max} \times V_{free}/K_a \times (1/1 + [Inh]\ /K_i) + V_{free}$ .....{7 }

Where [Inh] is the amount/concentration of the competitive inhibitor ie complexes V-SA and $K_i$ is their inhibition constant also expressed as amount of V-SA exerting 50% inhibition.

$K_i$ value is perhaps extremely low eg $10^4$ - $10^5$ viruses per body; this value and an above equation concern just the body of every one infected person [such amount of viruses if expressed in terms of molar concentration of viral RNA would be enormously low!]. But $K_a$ would not increase all the time as parallelly amount of complexes V-SA [V-B] decreases due to their destroying with body defense mechanisms [innate or/and adapted immune system but not only] acting on them.

One could imagine either that complex V-SA binds [with its spike receptor binding domain RBD] not with the same receptor which actually binds free virus but the other receptor present in the same target cell membrane. It would be even less hazardous for this cell, so for the person involved. But binding of V-SA -with fusion peptide of RBD-with the receptor just beginning to bind free virus can't be excluded.

Then –in analogy with molecular mechanisms of action of non-steroid hormones [and other bioregulators] [74]– the quasi-allosteric change of structure of cell membrane [or at least neighbouring domains; maybe so called rafts] might take place finally resulting in decreasing of affinity of FR to free viruses thus preventing the cells from becoming infected. All these above mentioned possibilities are visualized schematically on the figure 8.

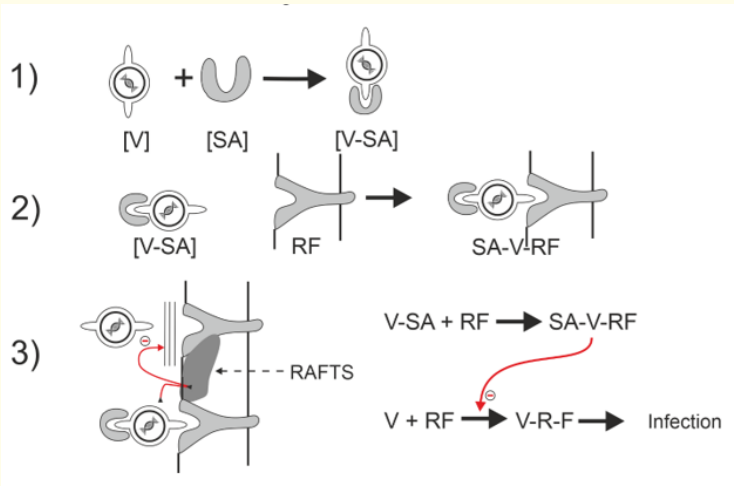


***Figure 8:*** *1/ Binding of virus with serum ACE-2. 2/Binding such a complex with the functional receptor of SARSCoV-2 [thus inhibitory against binding free virus andd its functional membrane receptor]. 3/The participation of the rafts within above assumed inhibition of infection.*

Such an increase of $K_a$ value caused that 50% effect ie 50% of infected people comes almost 40 days later [assuming doubling period as 10,5 days].

But I proved that blocking of viruses might increase $K_a$ for infection more directly looking on [and recalculating] the statistical data for pandemic in Poland and Belgium [and other countries]. But I will show it later.

### What to do further? Exact dating and duplication period for viruses

I currently have two options:

1. More labor-intensive [especially with my hardware and software], i.e. completing the calculations from table 6, i.e. the number of patients [sick], producing antibodies and possibly the dead - using the Hill equation basing on the number of free viruses - as in table 6 - for the senior group [65+], and then by analogy for the younger groups [II-IV] and summarize them to achieve the image for the entire Polish population [as in the collecting table 7] or

2. Simpler: that is, adopting the image for age groups as in figure 3-6 and-first of all- in the collecting table 7.

I adopted the latter solution because:

1. The epidemic situation becomes tragic, and so far only my considerations and calculations predict and explain this situation [not only in Poland, but practically all over the world, especially in countries affected by the pandemic] - *ergo* I do not have time for two-three months of further calculations; and

2. As I mentioned earlier, I showed data compatibility [„after the block" - older calculations and „all the time block" - newer calculations]. If this is true for the 65+ group [Table 6], the most vulnerable and most numerous [I mean the number of susceptible people], then there is no reason to believe that the calculations [*a la* Table 7] for younger age groups will give significant differences.

And here we have come to the moment where it is necessary to change time presented as the number of doubling periods [for viruses] n into real dates eg 01.05.2020. I am now convinced that doubling period [t(2)] lasts 10-11 days [previously I thought about 7 days or even –less possible-5,75 days = 138 hours.

I did this and it might be shown in collecting table 7 and further tables. Table 8 is limited just to number of infected people [during all the pandemic]-without the number of sick and so on-but it compares my calculated estimations with the statistical data.Further comparisons are in figure 9 and 10.

So it looks like there are/were two phases of pandemic at the same time [partially overlapping]: 1/hidden [or maybe better it should be called a weakened or much alleviated pandemic] for those being in phase of block until all virus binding sites are saturated and 2/ overt/visible for those "after the block" in their bodies.

But of course it does not change the main fact that in all age groups in phase D [compare earlier] everybody susceptible is infected and there might be frequent cases of second [in fact] infection. It might be this does not concern newborn babies and children before 10 years old, which might possess just negligible -near zero, amount of functional receptors of SARSCoV-2. But if they still do contain functional receptors although in a distinctly lower concentration [or even in such a case predominantly not in lung]?!

Some later [and former] fragments - excerpts - of the work could be transferred to an Addendum - or even two of them:

1. Additional theoretical comments

2. Additional practical and epidemiological comments, including suggestions for the further development of the pandemic and sources and suggestions for further research.

Yet another amazing phenomenon was revealed that I had never even foreseen before [and neither did anyone else]. As we can see from table 7 [the column with designation@$ -under ……..] even in case there was no block whatsoever [as practically everyone believes - except me] quite early [in terms of months of pandemic] more than 95% [practically all within error]of all susceptible people had become infected!

## Two clever approaches to estimate indirectly the number of persons affected during pandemic

But I have to explain yet another problems deeply related with the table 6. One could ask why the table is so long and if we can't shorten it. Well we can. But this actual version of table 6 is so long because otherwise I could not explain very clever approach how to estimate the probable number of affected persons ie not only infected but also sick, producing specific antibodies [potentially recovered], clearly and seriously ill,infectious and dead.It is quite simple and relies on an analogy ie the assumption that [in spite of some distinct differences] the fates of majority of infected people after infection are essentially similar and the disease progression goes similarly depending on multiplication of viruses in their bodies, actually as in the body of " person zero" [compare table 3 and especially 5-because the block]. Specifically from table 6 [it is shown in the column with a sign &] we can see what is going on with "person zero from his/her infection up to his/her death. So I show on the left the time [number of n-specifically the end of n-th duplication period] of appearing successive steps of Covid progress for "person zero"-and on the right side those for two from the next [after "person zero"] infected persons:

Infection n = 0 n = 8 n = 14

Infectioussness [lowest limit]-Inf n = 8 n = 16 n = 22

Production of antibodies [lowest limit] –A n = 9 n = 17 n = 23

n = 23

Infectioussness [clear]-Inf n = 12 n = 20 n = 26

Sickness [lowest limit]-S n = 12 n = 26

Production of antibodies [clear]-A n = 12 n = 26

Sickness [clear]- S n = 13 n = 21 n = 27

Serious sickness- $S_{ser}$ n = 14 n = 22 n = 28

Death D n = 19 n = 27 n = 33.

The amounts of viruses in one body for above mentioned steps [stages of Covid] were shown earlier. So at n = 13 the block is over and the amount of extracellular free [unblocked] viruses increases sharply about an order of magnitude from about $4 \times 10^4$ at the end of n = 12 to about $6 \times 10^5$ at the end of n = 13. So,"suddenly"the amount of viruses resulting in almost asymptomatic sickness [> 40000 viruses]increases to that for the clear sickness with about the full range of symptoms [> 300000 viruses]. It would be better to present the time these stages appear in days rather than the number of virus doubling periods- [n from 12 to 13]- then it would be a difference of 3 - 12 days.

But what with estimating of number affected people later ie after two-nine months? It is easy. We just have to have a look on column with the sign #!. There are shown the increases of number of infected people in susscessive doubling periods. So there is 1 newly infected person at n = 15 [rather it is an increment during the 15$^{th}$ doubling period], exactly 1 after 16$^{th}$, 4 after 17$^{th}$, 8 after 18$^{th}$ but 103 after 23$^{rd}$. So if succesively 1 person would die at n = 33, also 1 at n = 34 and 35 [that who became infected at n = 16] 4 would die at n = 36, but 8 at n = 37 and 103 at n = 42. And etc. Thus obtained data are shown in the right part of table 6.

Now it is clear why I did not shorten the table-because if I did there would be not visible amounts of people getting sick or producing quite big amount of antibodies-estimated in such simple method of analogy. I called this method the „top starting method".

I have been applying also a method „starting from the bottom", where I use the following reasoning: If 200 viruses are downloaded during an infection, this means that the newly infected e.g. in n = 53 contain in their body - on average - then 200 viruses [at least not yet 400]. Then those infected with n = 52 [one period of doubling „back"] have mean [pay attention always at n = 53!] 400 viruses, and those infected with n = 51 already 800 viruses, etc. With this method after some time n we will have about 300,000 [but > 300,000] viruses [which means expressive „full-blown" disease]. Let it be for n = 42. Then we look under #! how many such people appeared in n = 42 and for subsequent, but earlier periods of doubling [n = 41, 40, 39, 38 and so on up to n for which no one was infected yet]. The sum of the number so determined means the estimated number of people who at n = 53 are clearly ill, because at that time [e.g. from 17 to 28 December 2019] they have an average of 300,000 viruses and more in their bodies. In order to assess how many seriously ill one period of doubling [of viruses] backward have been, one should go back to n = 41 [i.e. do not include the increment in 42$^{th}$ doubling period in the summation] etc.

The last approach has the disadvantage - apart from the general disadvantage of both approaches described, that they are not algorithmized [yet] - that you have to assume that after n = 53 there are no new infections [in fact there are very few] -because those infected with n = 53 -having a minimal amount of viruses ever -this would be the end of a pandemic. If one wrongly chose date for this „as if the end of the pandemic" the estimated number of dead „in those days" could be much higher.Mind you,the amount of death cases estimated with „top starting method" [Table 6] at about the end of pandemic [n = 50] is 25627 only for seniors 65+. The same estimated for all the population [Table7] is 38563. Not bad result of comparison. But generally the results for death cases in earlier phase of pandemic as well as other parameters would be not so consistent with two applied methods [Hill equation versus an approach "top starting" and "starting from the bottom".

## View of more detailed changes during the pandemic in the entire population in Poland

Remember that I only use the results of calculations, not statistical data, so I cannot say which of those producing specific antibodies [which is rather indisputable] suffered [in the light of softer and stricter criteria determining who is sick], and who - in light of these criteria - did not get sick at all, but produced antibodies [i.e. he/she is not formally a „healer"/recovered person].

I do not know whether at a given time these people have already produced enough antibodies to bind - and thus - destroy virtually 100% of viruses present in the body. Well, there may be at any given time of a pandemic, either more people producing antibodies, but not enough yet to destroy 100% of viruses [thus not fully recovered] –possibility@-or fewer people but completely virus free [really recovered]- possibility $. „The truth is in the middle", so it is best when interpreting my calculations - in table 7 [And figure 3-7] to recognize that when for example at n = 20 [52 from the very first beginning in 2019-taking into account the block] we have 600 people producing antibodies, it is probably only after 10-34 days [i.e. at n = 21-23 (53-55)] that these 600 people are completely recovered. I do not know [who does?] if those producing antibodies were really previously ill or never got sick.

Table 7 starts with n = 17, ie from about the time when 1 person per 100,000 people is infected [throughout Poland]. Generally, all data in this table that refer to 100,000 people in the entire population are marked in red.

| Time | | | 1/ I [> 200V] | 2/ S [>4x10⁴V] | 3/ A [> 10⁴ V] | 4/ U =S-A | 5 / D {> 5x10⁷ V | 6/ AS=I-S | 7/ AC= I –A - D | 8/ S [>3x 10⁵ V] Z | 9/ S serious [>2x 10⁶ V] | 10/ REC.(?) [> 8x10⁴ V] R |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| n 1/ | Days 2/ | Date 3/ | | | | | | | | | | |
| 17 33 | 1 [180] | 15.02 2020 | 13 [0,034] | 0 | 0 | 0 | 0 | 13 | 0 | 0 | 0 | 0 |
| 22 38 | 54 [233] | 08.04 .2020 | 422 [1,1] | 0 | 0 [0] | 0 [0] | 0 | 422 [1,1] | ...422 [1,1] | 0 | 0 | 0 |
| 24 40 | 75[254] | 29.04. 2020 | 1690 [4,4] | 19 [0,05] | 0 [0] | 19 [0,05] | 0 | 1671 [4,4] | 1690 [4,4] | 2 [0,...] | 0 | 2 [0,...] |
| 29 45 | 127 [306] | 20.06 2020 | 53251 [138,7] | 365 [0,95] | 250 [0,65] | 115 [0,3] | 1 [0,...] | 52886 [138] | ...53000 [138]113813813838 | 46 [0,12] | 12 [0,03] | 32 [0,08] |
| 32 48 | 159 [338] | 22.07 2020 | 393802 [1026] | 2861 [7,5] | 2045 [5,3] | 816 [2,1] | 3[0,....] | 390941 [1018] | 391754 [1020] | 360 [0,94] | 90 [0,23] | 258 [0,67] |
| 34 50 | 179 [358] | 11.08. 2020 | 1265520 [3296] | 11270 [29,3] | 8208 [21,4] | 3062 [8] | 12[0,03] | 1254250 [3266] | 1263472 [3290] | 1420 [3,7] | 355 [0,92] | 1034 [2,7] |
| 37 53 | 211 [390] | 12.09. 2020 | 3759389 [9790] | 87418 [228] | 63062 [164] | 24356 [64] | 101[0,26] | 3671971 [9562] | ...3696226 [9626] | 11015 [28,7] | 2574 [6,7] | 7946 [20,7] |
| 39 55 | 232 [411] | 03.10 2020 | 4829827 [12578] | 299270 [779] | 241133 [628] | 51137 - [133] max | 370 [0,96] | 4530557 [11798] max | 4588324 [11949] max | 37708 [98,2] | 9247 [24,1] | 30383 [79,1] |
| 41 57 | 253 [432] | 24.10 2020 | 5126736 [13351] | 874742 - [2277] | 923462- [2405] | <0 | 1792 [4,67] | 4251994- [11073] | ...4201482 [10941] | 110217 [287] | 27554 [71,8] | 116356 [303] |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 42<br>58 | 264 [443] | 04.11.<br>2020 | 5275190<br>[13737] | 1162474<br>[3027] | 1264627<br>[3293] | < 0 | 2875<br>[7,49] | 4112716<br>[10710] | 4007688<br>[10437] | 146472<br>[381] | 36618<br>[95,4] | 159343<br>[415] |
| 44<br>60 | 285 [464] | 25.11.<br>2020 | 5328096<br>[13875] | 1624118<br>[4229] | 2162093<br>[5630] | < 0 | 8506<br>[22,2] | 3703978<br>[9646] | 3157497<br>[8223] | 204639<br>[533] | 51160<br>[133] | 272424<br>[709] |
| 46<br>62 | 306 [485] | 16.12.<br>2020 | 5339520<br>[13905] | 1864704<br>[4856] | 2712192<br>[7063] | < 0 | 15112<br>[39,3] | 3474816<br>[9049] | 2612216<br>[6803] | 231383<br>[603] | 57600<br>[150] | 339024<br>[883] |
| 47<br>63 | 317 [516] | 27.12.<br>2020 | 5345088<br>[13920] | 1946400<br>[5069] | 2987021<br>[7779] | < 0 | 20175<br>[52,5] | 3398688<br>[8851] | 2337892<br>[6088] | 245246<br>[639] | 61312<br>[160] | 376365<br>[980] |
| 49<br>65 | 338 [537] | 17.01.<br>2021 | 5345942<br>[13922] | 2008656<br>[5231] | 3282893<br>[8549] | < 0 | 27077<br>[70,5] | 3337286<br>[8691] | 2035972<br>[5307] | 253091<br>[659] | 62273<br>[162] | 426245<br>[1110] |
| 50<br>66 | 349[548] | 28.01.<br>2021 | 5346000<br>[13922]<br>max | 2041920<br>[5318]<br>max | 3421440<br>[8910]<br>max | < 0 | 33461<br>[ 87,1] | 3304080<br>[8604] | 1891099<br>[4925] | 257282<br>[670] | 64321<br>[168] | 427776<br>[1114] |
| 52<br>67<br>? | 360 [569] | 07.02.<br>2021 | 5346000<br>[13922]<br>max | 2041920<br>[5318]<br>max | 3421440<br>[8910]<br>max | < 0 | 38563<br>[100]<br>max | 3304080<br>[8604]. | 1885997<br>[4911] | 257282<br>[670] | 64321<br>[168] | 427776<br>[1114] |

***Table 7:*** *Summary of the (overt) pandemic - presumably in Poland (2020)-according to my assumptions and calculations This date means the last day of doubling period n[for viruses] shown in the column 1/.*

Thus infected I for > 200 virus downloaded [column 1]; sick S for > 40,000 v in body [column 2]; producing antibodies [assume specific IgG] for V > 10000 [A; column 3]; U = S-A as „still sick" [column 4]; dead D for V > 50 x $10^6$ [column 5]; asymptomatic AS = I-S [column 6]; so called active cases AC = I-A –D [column 7]; clearly sick S [for> 300,000 V [column 8]; seriously ill patients - in severe state –$S_{ser}$ -when V > 2 million in the body [column 9]; those producing much more IgG antibodies A for V> 80,000 [column 10].

Let's start with those infected [total number of cases]. We can see that with the admission of only 200 viruses as an infecting dose [column 1], the total number of infected [including the sick, also severely, and asymptomatic and producing antibodies - and thus convalescents, and dead-because it is impossible to take in mind them –except died] may reach almost 14% of the total population. On the other hand, when adopting „stricter" „criteria of infection [when at least 1600 viruses would have to be downloaded for it] it will be only about 1.74%. But these are percentages for the entire population. When we calculate them assuming as 100% only those susceptible, the results will be 6.8 times higher, which means that 11.8% of susceptible people will be infected - with more stringent criteria- and 100% susceptible with less severe criteria.

The comparison of the number of patients [sick people] gives similar results. The maximum percentage of mildly ill S in the whole population could reach 5.3% [column 2], but clearly ill S [column 8] only 0.67%, and seriously ill $S_{ser}$ [in poor condition] - column 9 - „only" 0.17%.

Number of deaths from Covid 19 - as it is calculated taking into account the number of viruses and target cells attacked - „should" [with some substantial delay - compare the curves in figure 3-6 and table 12] to reach 1‰ of the total population [criterion for death more demanding: 50 - 60 million viruses in the body - column 8B], but even 2‰ for just $V > 20 \times 10^6$ contribute to death - [not shown].

It is obvious that the later in the pandemic, the greater the ratio of death cases to new infections, but also to the number of mildly ill people. And so [See table 7], between October 24 and November 4 the ratio of the increase in the number of deaths to the increase in the number of infections is 0.73% [death D to mildly sick: D/ S = 0,38%], and between November 4 and 25 it is 10.66% [D/S. = 1,22%], and between November 25 and December 16.... 57% [D/S = 2,73%]. And in official statistics it is noted that this ratio is growing/has already increased from 1.5 to over 5% [although official statistics in my opinion underestimate the cumulative amount of infected people, and misinterpret that infections are „fresh".

Mind you, if the viral load was examined and reported it would be quite easy to know if the infections are really "fresh"or those from ago seweral weeks or months [I do mean the date of infection and not date of performing the test]. Simply the number of viruses in swabs [let alone in blood] of really freshly infected persons would be on average very small one [just above the practical limit of detection],but in case of old infections would be on average much bigger.

And now let's compare the calculated number of potential REC [recoveries], and thus the number of people „still sick" U [as the difference in the number of sick S and those who produce antibodies A-potential survivors]. With low criteria [10,000 viruses in the body are enough to produce IgG antibodies] the maximum may be 8,9% of „pseudo-convalescents" [column 3]; with the more stringent criteria [at least 80,000 viruses in the body; but this also implies production of higher IgG concentrations] only 1.1% of such convalescents [column 10].

The number of „still sick" people U- column 4 - reaches its maximum at October the 3rd ie on 232th day of clearly overt –symptomatic--current pandemic [411th day of that pandemic from the very beginning ie day of infection of "person zero"-probably yet in China] for U = S-A [mild criteria; column 4], and 4 - 5 days later for U = S-A [acute criteria; not shown]. After reaching the maximum this number of „still sick" decreases sharply, after a few days it equals zero. Of course, in the longer run, the number of people producing IgG continues to increase markedly [„fast"] and the number of patients /sick [calculated] to increase „weakly" [„flat curve"].

The percentage of people producing enough anti-SARSCoV-2 IgG to destroy all viruses in the body would be an obvious "measure of collective resistance to Covid 19"- „herd immunity". Taking into consideration low criteria [compare the previous text] one could talk about developing resistance in as much as 8.9% of the population [that is, about 60% of all susceptible people]. But with more plausible [higher] criteria, these expectations for „herd immunity" drop to just 1.1% of the total population, or around 7.5% of people susceptible to the current „versions" of the virus. The latter seems to be too pessimistic.

The calculated data for asymptomatic people are interesting. With „low requirements" for a person to be classified as infected and sick, the maximum of such asymptomatic people is 11.8% of the total population and this maximum takes place exactly in the about the same time as the number of still sick U = S-A ie October the 3rd. Mind you, also calculated [by me] number of active cases AC = I-A –D attains the maximum about the same day].

What does it mean? Just before attaining this maximum, the number of sick people increases slower than those who are infected, and over a period longer than that of this maximum, the number of cases of the disease increases slightly more clearly, but later distinctly, than the number of infected people.

Now I think that I could [but I did not] calculate A, S and $S_{ser}$ in another way [ie not just estimate from amount of viruses -and amount of persons with different amount of viruses- by analogy]: simply with Hill equation assuming for clear and serious sickness the same ceilingas for mild sickness [as the mildly ill might after a long time become clearly then-unfortunately-seriously ill] eg $S_{max} = S_{max}$ but parallelly "the affinity to get sick clearly –let alone seriously"-should be apparently lower, so $K_a$ should be several times higher. Well, bit later I decided to adopt yet another one mode of estimation of number of affected persons including S, S, $S_{ser}$ and…REC, [being equivalent to an assumption of bigger $K_a$ values for more serious level of sickness but the higher production of antibodies either].

Also maybe amount of still infected people but producing specific antibodies should be alternatively calculated assuming the same ceiling regardless the level of antibodies made-but with an increase of $K_a$ [for infection] by an antibody [acting like an enzyme competitive inhibitor]. In such a case the maximum of number of infected persons should be attained at number of viruses:

$$V_{max} = [K_a^I \times K_a^A]^{1/2} \text{ ……..\{8\}}$$

And very low number of infection [near zero], thus the real end of pandemic, should come with number of viruses equal more than $10 \times K_a^A$ [where $K_a^I$ is the amount of viruses needed for attaining 50% of maximal number of infected people and $K_a^A$ is the amount of viruses needed for attaining 50% of maximal number of people producing specific IgG antibodies. But it is not sure.

## An attempt to compare with statistical data for Poland. The comments concerning the statistical data and the strategy of testing. What about near future?

### The bursts

It seems the concept of „burst/s" needs to be introduced here. Researchers who have studied related phenomena, such as tumor development, tumor metastasis, or gene expression, ie transcription and translation, have introduced the concept of „burst/s", ie ejection or "spikes" [75,76]. So „new viruses" appear in the form of certain jumps [„ bursts"]. If we charted this in great detail ["day after day"], it would be a „sawtooth curve": growth lag period, and sudden ejection. If we have such jumps, we can predict that during all the pandemic [even if there is a block] we have some kind of „bursts" there. The second obvious reason of a „sawtooth curve/s"is the mitigation and tightening of laws [and human attitudes] regarding the pandemic.

An overt pandemic is going to be the typical exponential increase [the number of infected or sick people, not just the total amount of viruses in the cloud], then this curve will „flatten out" [or is flattenning out"].

### First look. Two directions [X and Y] of further analysis

Some interesting phenomena seem to be revealed by comparing my calculated numbers of infected people with the statistics since the beginning of the current pandemic. This is shown in table 8.

| Total [cumulative] number of infected People I | | 3] I- ST/ I-M % =2]/1] In [ ]: 2/1 in [ ] | 4]Total tests [stat.] % of population | 5] % of positive tests [stat.] | 6] % of infected people in population [ from stat. rec] =4] x 5] x $10^{-2}$ ……. %-as above but from my calculations | 7] Statistical records [$ST_{corr}$] &!! | 8] &!! $ST_{corr}/M$ % =7]/1] | 9] My calculations: sick people | 10]= $I_{stat-corr}$ / $M_{sick}$ % =7]/9] # | | | % of positive tests [my calcul.]] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1]My calculations[M] | 2]Statistical records [ST] | | | | | | | | | | | |
| 13 [2] | --- | ? | --- | ---------- | ---------- | -------- | --------- | 0 | | | | 3,39 x $10^{-5}$ |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 422 [53] | 4848 | 1149 | 0,262 | 4,88 | 0,0128 ..... $1,1 \times 10^{-3}$ | <0 [2421] | [573,7] | 0 | | 2606// 3028 | 160,1 | $1,1 \times 10^{-3}$ |
| 1690 [211] | 12216 | 722,8 | 0,778 | 4,15 | 0,032 ..... $4,4 \times 10^{-3}$ | <0 [4362] | [258,1] | 19 | | 8531// 10221 | 119,5 | $4,4 \times 10^{-3}$ |
| 13335 [1667] | 23151 | 173,6 | 2,17 | 2,82 | 0,061 ..... $3,47 \times 10^{-2}$ | <0 [602] | [4,51] | 92 | 654,3 | 27900// 41235 | 56,14 | $3,46 \times 10^{-2}$ |
| 53251 [6656] | 31311 | 58,8 | 3,15 | 2,63 | 0,083 ..... 0,139 | <0 [1605] | [3,01] | 365 | 439,7 | 37008// 90259 | 34,69 | 0,14 |
| 202302 [25288] | 37210 | 18,39 [147,1] | 4,18 | 2,35 | 0,1 ..... 0,527 | <0 [4493] | [2,22] | 1432 | 313,8 | 40785// 243087 | 15,31 | 0,53 |
| 393802 [49225] | 41162 | 10,45 [83,6] | 4,72 | 2,39 | 0,11 ..... 1,026 | <0 [7984] | [2,03] | 2861 | 275,9 | 41495// 435297 | 9,45 | 1,03 |
| 1265520 [158190] | 52401 | 4,14 [33,1] | 5,7 | 2,43 | 0,14 ..... 3,296 | 9980 | 0,8 | 11270 | 88,6 | 42073// 1307593 | 4 | 3,3 |
| 3759389 [469924] | 73034 | 1,94 [15,54] | 7,53 | 2,56 | 0,19 ..... 9,79 | 30794 | 0,82 | 87418 | 35,2 | 42267// 3801656 | 1,92 | 9,79 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 4829827 [603728] | 95756 | 1,98 [15,86] | 8,67 | 2,92 | 0,25 …….. 12,58 | 53516 | 1,11 | 299270 | 17,9 | 42267// 4872094 | 1,97 | 12,58 |
| 5126736 [640842] | 228276 | 4,45 [35,62] | 10,86 | 5,56 | 0,6 …….. 13,35 | 186036 | 3,63 | 874742 | 21,3 | 42267// 5169003 | 4,42 | 13,35 |
| 5275190 [659399] | 414771 | 7,86 [62,4] | 12,63 | 8,68 | 1,1 …….. 13,74 | 372531 | 7,06 | 1162474 | 32,1 | 42267// 5317457 | 7,8 | 13,74 |
| 5287790 [660974] | 544794 | 10,3 [82,4] | 13,46 | 10,7 | 1,44 …….. 13,77 | 532554 | 10,07 | 1258809 | 42,3 | 42267// 5330057 | 10,22 | |
| 5302910 [662864] | 665431 | 12,55 [100,4] | 14,17 | 12,42 | 1,76 …….. 13,81 | 623191 | 11,75 | 1385020 | 45,0 | 42267// 5345177 | 12,45 | |
| 5318016 [664752] | 819262 | 15,41 [123,2] | 14,81 | 14,62 | 2,17 …….. 13,85 | 777022 | 14,61 | 1499809 | 51,8 | 42267// 5360283 | 15,28 | |
| 5328096 [671340] | 922358 | 17,31 [137.4] | 15,42 | 15,57 | 2,4 …….. 13.88 | 880118 | 16,52 | 1624127 | 54,2 | 42267// 5370363 | 17,17 | 13,88 |
| 5339520 [667440] | Exp.[E] 1401600 ,,,,,,,,, 1032960 | [E] 26,25 ,,,,,,,,, | [E] 18,0 ,,,,,,,,, 16,28 | [E] 20,27 ,,,,,,,, 16,51 | [E] 3,65 …….. 13,91 ,,,,,,,,,,,, 2,69 | | | 1864704 | | 42267// 5381787 | 26,04 …….. 19,19 | 13,91 |
| 5345088 [668136] | [E] 1693440 ,,,,,,,,,, 1090560 | [E] 31,68 ,,,,,,,, | 19,5 ,,,,,,,,, 16,71 | 22,62 ,,,,,,,,, 16,98 | 4,41 ……. 13,91 ,,,,,,,,,,,, 2,84 | | | 1946400 | | 42267// 5387355 | 31,43 …….. 20,24 | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5345942<br>[668243] | [E]<br>2219360<br>„„„„„„„„„<br>1209600 | [E]<br>43,39<br>„„„„„„„„<br>17,57 | 22,1<br>„„„„„„„„„<br>17,92 | 27,32<br>„„„„„„„<br>17,92 | 6,04<br>……..<br>13,92<br>„„„„„„„„„„„<br>3,15 | | | 2008656 | | 42267//<br>5388209 | 41,19<br>……..<br>22,45 | 13,92 |
| 5346000<br>[668250] | [E]<br>2688000<br>„„„„„„„„„<br>1271040 | [E]<br>50,28<br>„„„„„„„„<br>18,0 | 23,6<br>„„„„„„„„<br>18,39 | 29,67<br>„„„„„„„„<br>18,39 | 7,0<br>……..<br>13,92<br>„„„„„„„„„<br>3,31 | | | 2041920 | | 42267//<br>5388267 | 49,89<br>……..<br>23,59 | 13,92 |
| 5346000<br>[668250] | [E]<br>3072000<br>„„„„„„„„„„„<br>1336320 | [E]<br>57,46<br>„„„„„„„„„<br>18,43 | 25,0<br>„„„„„„„„<br>18,86 | 32,02<br>„„„„„„„„<br>18,86 | 8,0<br>……..<br>13,92<br>„„„„„„„„„„„<br>3,48 | | | 2041920 | | 42267//<br>5388267 | 57,01<br>……..<br>24,8 | 13,92 |

***Table 8:*** *My calculated data and those from statistic records -Infected persons **except column 9] there is numer of sick people. &!! [columns 7 and 8]- Certain amount of infected people was substracted from statistical data –namely it was 42240 people ie.38.4 million [all the Poland] x 1100 per million, where 1100 is the estimated[ with Eadie –Hofstee plot kinetic analysis] maximal amount of infected people $I_{max}$ apparently lacking of the block[ for further explanations see text]. In brackets [ ] there are results as above .but only 0,8 x number of infected „from the first wave of pandemic was substracted. Without this „reduction by multiplication" corrected values [differences of „total and first wave pandemic"] would be < 0 [both as numbers and %]. [E]=Exp. means expected numbers [in future] calculated with an assumption [basing on approximation of values from the curves from statistical records from October 03 to November 25-not shown]that % of positive tests increases by 2,35 per 10,5 days [ie one duplication period- t(2)-for viruses] and % of tests [100%=all the population]increases respectively by 1,3. Under „„„„„„„ in columns 2-6 there are expected values [in future] but with values based on an assumption that daily increases of both number of tests and % of positive tests would be much smaller[1/3 ie 0,43 for total tests and 1/5 ie 0,47 per one t(2)]. Obviously multiplying the values shown in columns 4 and 5 [x $10^{-2}$ ] gives us ] % of infected people in population [column 6]. For further explanations see text.*

My data were calculated from the Hill equation for people of four age groups [compare previous text] - per million people, then multiplied by 9.6 and summed. This gave the total number of infected people in Poland [38.4 million people] - the same data are in the summary table 7.

It would be naïve to say that my calculations do not give results even close to the statistical data. I use the concept of „cloud of human breaths and viruses" [in which 90% of us live - compare before] and thus I assume that my calculations concern the whole of Poland, so as if the correct tests for the presence of the virus would be carried out for 100% of the population of Poland - from the beginning of the pandemic up to now [and approximating - also in the future]. Therefore, in my opinion, the% of infected is practically equal to the % of positive tests [of course, assuming: one test for one person - which is an assumption for understandable reasons - even for the sake of repetitions and verifications whether X „has healed" - does not apply to the number of infected people recorded in statistics]. However, to simplify it, I assumed that the %

of positive tests [column 5] x% of the tests performed -assuming the total population as 100%- [column 4] x $10^{-2}$ [because:$10^{-2}$ x $10^{-2}$/100 = $10^{-2}$] –both from the statistics-gives us % of infected people in the entire population [column 6].

Table 8 shows that the number of infected in the statistics is significantly lower than that calculated by me - both when we compare the direct numbers [column 2 versus 1] and when we compare the percentages of infected in the entire population [column 6-upper statistical and lower mine], and when we look at the ratio of statistical data to those calculated by me [expressed in % - shown in column 3].

But when we look more closely, we will see that for the beginning of the pandemic - until the end of May this year [2020] - is the opposite; that is, for April and May [as well as March] 2020 statistics report a much larger number of infected than the numbers calculated by me. In June and July the statistics give already lower figures than mine, albe it still higher than 10% of mine, while from August 11 to October 3 the statistics are "almost constant' - from 1.5 to 4.5% compared to the figures I calculated.

So in further text I will go in two directions - we will call them X and Y. The X direction will not deal with the interpretation of this „excess number of infections" according to statistical data in relation to my calculations - but I will critically analyze the statistical data and try to predict what will happen in the near future, i.e. until early February 2021. However, I do not mean what will happen, because according to my calculations, it is known that almost all susceptible [with functional virus receptors] are already infected [I was writing this text in the end of September], and now some people are getting worse [they get sick, the severity of the disease increases until to a serious and dangerous state and... to death], and in other, more and more of them, production of specific anti-SARSCoV-2 antibodies increases markedly until the viruses are completely destroyed. When talking about predicting what will happen, I have here at thoughts on what data will be reported in the official - and available worldwide – statistics [here I mention Poland] from December 5 to mid-February 2021.

Direction Y will analyze the reason of mentioned "excess number of infections" according to statistical data in relation to my calculations –from March to August. Of course both directions of reasoning will met resulting within new ideas concerning whole the pandemic all over the world.

### X direction. The comments concerning the statistical data and the strategy of testing. What about near future?

Let's go with X. Mind you, the % of infected people must increase [total cumulative data] all the time. My calculation methodology does not allow for a direct refering to the dynamics of increases and decreases in the so-called positive and negative tests for Corona virus. Well, I assume that my results refer to the entire population, i.e. if there are 1000 infected, it means that the % of negative tests in Poland should be: 38.4 million minus 1000/38.4 million x 100, which is practically almost 100% [99.96], and with one million infected, 97.4% [respectively,% of positive tests 2.6%]. Of course with my approach % of negative tests during a pandemic must decrease from 100% to..... [for me it is 86.1%], and the % of positive tests must go up from zero to... [13.9% for me].

But somebody will say that people are getting better [become healthy], so it cannot an increase of the percentage of positive tests last all the time. But it cannot be so, even if we make an adjustment to the number of people [A] producing antibodies- [even if we assume they produced enough IgG to completely get rid of viruses in their bodies]- that is taking in account something like the number of "active cases". But even then % of positive tests should also increase for a very long time -from the very first day of the pandemic until the beginning of October [See table 8]; if we assume - but it does not seem possible to me – everyone once infected produced a sufficient amount of IgG anti-SARSCoV-2 to get rid it then after attaining the maximum such data would come to zero.

If the tests were done absolutely randomly, the results in ‰ or % would be reliable and comparable with my calculations; but they certainly were not made that way. Certainly, they were made mainly for people who either had some symptoms, e.g. increased fever [e.g. 37.6 degrees C] or came from China and then from Italy, stayed with an infected, undoubtedly sick person, or were to finish quarantine or take responsible work with other people.

Therefore, my results for... the number of sick people [even mildly]-instead all so called infected- would be more similar to the number of infected people given in the statistical reports. And indeed if we compare my calculated numbers of sick [even very mildly ie with only assuming about 40000 viruses in a body] [column 9] with reported number of infected- as that with positive result of test [column 8-data little bit corrected –compare earlier]-we obtain in the column10 % of ratio I -ST/M sick [in %]"much nearer" 100% [20-90%]than the ratio of infected I- ST/I-M [column3: 2 - 18%]. Still there is an evident surplus in statistical records [April-July]- I will not deal with this now. In fact the same conclusions would be if we did not use corrected data but simply raw statistical numbers of infected [and sick] persons.

Well, we could think that statistical records are lower than my calculated figures because they show those infected but only those likely "really infected" ie only those who took more than 1600 viruses as an infectious dose not just 200 viruses [the minimal infecting dose I applied]. And indeed our calculated numbers of infected persons calculated assuming such a possibility [column 1 in brackets] are much more similar to those statistically reported-even about 100% [see also the column 3 in brackets-I mean only the time after half of July- in aim to neglect –at the moment-the surplus I mentioned-likely "the early wave of pandemic"].

So it looks like the tests are made mostly for affected people,sick even very, very mildly-practically almost asymptomatic. So they are not made randomly and thus we do not know who is in fact infected and who is not. So it is quite sure that real number of infected people is by far greater. I will show the additional supports of this view bit later.

My reservations are also raised by the % of positive tests given in the statistics [or easy to calculate from them]. It cannot decrease, especially in the first three months of the pandemic, but even if it remains constant it seems unreliable. Meanwhile [column 6] it decreases/d between April 8 and July 11 of 2020 and then hardly changes/d until mid-September.

Of course, if the subjects tested were only sick, even if mildly, the% of positive tests would be near 100%. Let's assume the following Q testing strategy: [„anyone who complains and/or feels bad", but in addition half of the tests for clearly asymptomatic people, e.g. before or after quarantine - after returning from abroad or after diagnosing infection in the family/neighborhood/gaming in the same sports team"]. Then, evidently, the % of positive tests would be about 50%. But if it were from the beginning - or from a „fairly early date"- less sensitive antigen not genetic tests, it would already give % positive tests close to 20% - supposedly recommended.

Nothing can replace random testing - including for newborn babies - on a sociologically representative sample of the entire population. Otherwise we haven't got the real picture of the pandemic. Well, we just believe that really only affected people come to the points of testing and that such a situation takes place as it had been taken place always during all the pandemics/epidemics. But look there is the terrible difference between the number of infected and even slightly affected people.

We can expect that the statistical reports in near future might give us distinctly different figures depending on the dynamics of % of tested people and even more on the dynamics of increment of positive tests. In my opinion almost all susceptible persons are already infected [in many cases already even one month or two ago], so in fact the actual figures do not show us new infections but are just result/s of increases of number of tests performed and "nonrandomness of selection to test any one".

Look at table 8 [E] = Exp. means expected numbers [in future] calculated with an assumption [basing on approximation of values from the curves from statistical records from October 03 to November 25-not shown] that % of positive tests increases by 2,35 per 10,5 days [ie one duplication period- t(2)-for viruses] and % of tests [100% = all the population]increases respectively by 1,3.

Under mark, „„„„„„„„ in columns 2-6 there are expected values [in future] but with values based on an assumption that daily increases of both number of tests and % of positive tests would be much smaller [1/3 ie 0,43 instead 1,3 for total tests and 1/5 ie 0,47 instead 2,35 for positive tests per one t(2)]. As we can see the total cumulated number of infected persons at the half of February 2021 might be even more than three milion people if we assume the same dynamics of both testing and its nonrandomness as that observed from the beginning of

October to the end of November. If we assume much slower dynamics of those we would observe only about million and three hundred thousands infected persons. Mind you,in both cases the mentioned figures are just an indirect reflection of the fact that for a long time [compare table 7] more than 5 and a half million are infected.

In fact when tests are made only for "very very slightly sick" but even if say only 10-60 % of tests is for them [and only remaining 90 - 40% of tested are asymptomatic [for some reasons not infected?]] the obtained number of positive tests say us nothing about the real number of both daily increments of infected people and cumulative numbers of infected people. Such near reality numbers might be only obtained with absolutely random performing of tests [not shown].

## Conclusion

- The block takes place for every susceptible [with functional receptors for SARSCoV-2] infected person and lasts bit longer or less in different people, age groups, and depending on the time of infection - some people are still in the block and other are not.
- During the block phase the increment of symptoms is incomparably delayed: this concerns infectiousnesses, sickness of any level and death. However tragic symptoms appear or enormously strengthen already when the block is over, so the blocking sites in the body of infected person are already saturated.
- The relatively low [even very low] number of infected people shown in statistical records apparently results/; resulted from testing too small amount of people and hardly random choice people for their testing.
- About beginning of October 2020 more than 95% of all susceptible people [ie those having the functional receptors of SARSCoV-2] are already infected. However, the most probably, quite large part of susceptible people becomes infected for the second time, and this re-infection is usually a re-collection - as if enhancing the effect - of an infecting dose [in fact there is something like „infecting the infected"].

## Bibliography

1. Rich KL. "Introduction to Ethics". Book 1, Jones and Bartlett (2018).
2. Frankena WK. "Ethics, 2nd edition". Prentice-Hall, Inc. New Jersey (1970).
3. Shannon TA. "Ethics of Nursing Practice" (1980).
4. Emanuel EJ and Persad G. "The Ethics of Covid-19 Immunity-Based Licenses (Immunity Passports")". *Journal of American Medical* 323.22 (2020): 2241-2242.
5. American Public Health Association (APHA). Ethics at center of Covid-19 vaccine distribution debate: Prioritizing vulnerable populations". *The Nation's Health* (2021).
6. Persad G., *et al*. "Public Perspectives on Covid-19 Vaccination Prioritization". *Journal of American Medical Association* (2021).
7. Hughes Gogineni Lewis and Deshpande. "Considerations for fair prioritization of COVID-19 vaccine and its mandate among healthcare personnel (2021): 33760673.
8. Heesoo J., *et al*. "Morbidity and Mortality Weekly Report. Decline in Covid-19 Hospitalizations, Growth Rates, Associated with Statewide Mask Mandates. U.S. Department of Health and Human Services". *Centers of Disease Control and Prevention* (2021): 1-6.

9. Emanual EJ and Bilinski A. "COVID-19 and Excess All-Cause Mortality in the US and 18 Comparison Countries". *Journal of Medicine* 324.20 (2020): 2100-2102.

10. Emanuel EJ., *et al.* "Fair allocation of scarce medical resources in the time of Covid-19". *New England Journal of Medicine* (2020).

11. Hawkins JS and Emanuel EJ. "Clarifying confusions about coercion". 35.5 (2005): 16-19.

12. Mullin E. "Immunity passports" could create a new category of privilege: being infected with the virus could come with more freedom". *One Zero* (2020).

13. Parfit D. "Equality and priority". *Ratio* 10.3 (1997): 202-221.

14. World Health Organization. "What we know about long-term effects of COVID-19: the latest on the COVID-19 global situation and long-term sequelae". Geneva, Switzerland: World Health Organization (2020).

15. Wright RA. "Human Values in Health Care: The practice of ethics" (1987).

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