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1	Models cannot predict future outbreaks: A/H1N1 virus, the paradigm
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22 Abstract

23 Evolution of the industrialized society had led to a risk management policy in many domains. 24 Assessment of health care risk in the case of infectious diseases often includes mathematical 25 models. Results of modelling were used in France to design emergency plans against flu 26 pandemic. We believe that models cannot predict the features of the future outbreaks 27 because the intrinsic properties of an emergent pathogen and the ecosystem in which it is 28 developing are very complex. Of course, prediction of future outbreaks is not possible 29 without using models, but we think that it is an illusion to presently believe that emerging 30 phenomenon can be anticipated by using only prediction from models. The recent pandemic 31 caused by the novel A/H1N1 virus has confirmed the unpredictability of infectious diseases. 32 The rapid evolution in several domains such as antimicrobial therapeutics, vaccine and 33 hygiene conditions make comparison with past pandemics hard. The adherence of 34 populations to prevention measures and immunisation campaigns are unpredictable. In 35 addition, the presentation of pessimistic models is deleterious. They impress governments 36 and provoke fears. There is a striking necessity to develop the number and the capacities of 37 sentinel centres to take and adapt decisions based on timely available scientific information.

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39 Evolution of society had led to a risk management policy in many domains. The 40 assessment of health care risk in infectious diseases, especially concerning future epidemics, 41 often includes mathematical models which tentatively predict in silico the burden of the 42 future outbreaks such as attack rate, dissemination, morbidity or mortality. Currently, models are designed to run with different scenarios, and probabilistic methods allow testing 43 44 their performance in a number of situation. But the question asked by physicians, scientists 45 and in fact everyone is "how many people will die, how many will be hospitalized?". Such 46 predictions from models were used in France to design the emergency plan against flu 47 pandemic [1]. We believe that models cannot predict with acceptable accuracy the features 48 of the future outbreaks because the intrinsic properties of an emergent pathogen and the 49 ecosystem in which it is developing are very complex and unstable. Of course, prediction of 50 future outbreaks is not possible without using models, but we think that it is an illusion to 51 presently believe that emerging phenomenon can be anticipated by using only prediction 52 from models. The recent pandemic caused by the novel A/H1N1 virus has confirmed the 53 unpredictability of infectious diseases.

54 Seasonality of respiratory infections is a well-known phenomenon in temperate 55 regions. Flu has long been associated with cold season, and the word "Influenza" comes 56 from "influenza di freddo" in Italian that means "cold influenced". A marked peak of 57 respiratory infections occurs during cold winter months. Several mechanisms have been 58 proposed to explain it, such as seasonal environmental changes (temperature humidity...), 59 seasonal host-behaviour changes and seasonal changes in host physiology (melatonin, vitamin D...) [2-4]. However there is still no clear understanding of this phenomenon. In 60 61 contrast, disease seasonality is less defined in tropical regions where a background of 62 influenza cases is observed throughout the year on top of which epidemics occur at 63 intermediate months between the influenza season in temperate countries of the Northern 64 and Southern hemispheres [4]. On the top, none of yet proposed determinants can explain 65 why the four last pandemics of influenza (1918, 1957, 1968, and 2009) did not initiate during the cold season. 66

67 Interference between several respiratory viruses affecting the spread of influenza
68 was recently described in Europe and drastically modified the dynamics of the outbreak [569 6]. In France and in Sweden, an epidemic of rhinovirus infections occurred after the start of

school year, and delayed the onset of the A/H1N1 pandemic. We also observed in Marseille that the epidemic of Respiratory Syncytial Virus bronchiolitis, which happens usually just before the seasonal flu epidemic, occurred later in the season, just after that the A/H1N1 pandemic started to decline. In addition interference between several Influenza viruses remains not properly known: at the beginning of the A/H1N1 pandemic, nobody was able to predict whether seasonal influenza strains (H3N2 and H1N1) would still provoke an epidemic wave or not.

77 In certain groups of population, the presence of cross-reactive antibodies against a 78 new pandemic strain of influenza can heavily affect viral dissemination and therefore impact 79 on the epidemiologic characteristics of the pandemic (total number of cases, age of the 80 cases, number of severe cases, number of deaths, death rate, length of the phenomenon...) 81 and seems unpredictable. The fact that the elderly were partially protected against the novel 82 A/H1N1 [7-9] explains that the novel A/H1N1 virus infected mostly young people. In 83 addition, at-risk groups may not be the same as for seasonal flu. For example, obesity was an 84 undisputable independent risk factor of severity and lethality during the A/H1N1 pandemic 85 [10-11].

The inherent variability of new variants makes predictions difficult. Each pandemic virus has its own intrinsic properties which can evolve during the pandemic period. Then, intrinsic pathogenicity of new pandemic variants appears to be unpredictable. Data experimental derived from animal models must not be directly extrapolated to humans: in the A/H1N1 case, experiences with ferrets predicted a severity of pneumonia intermediate between that due to seasonal virus and the highly pathogenic avian H5N1 virus [12]. But in fact, the fatality rate of the novel A/H1N1 virus was relatively mild.

93 The novel 2009 H1N1 virus reminded the 1918 pandemic, also caused by a H1N1 94 virus, despite totally distinct, which was associated with a large number of secondary 95 bacterial co-infection which could explain partially the huge number of deaths [13]. Because 96 of drastically different sanitary conditions nowadays, it is awkward to use the 1918 data as a 97 basis for anticipating the spread, severity, and health consequences of present and future 98 H1N1 pandemics. Currently, the use of antibiotics and anti-pneumococcal vaccines allow to 99 efficiently combat the historically lethal bacterial co-infections. The availability of adapted 100 vaccine and the rapid evolution on several domains such as antiviral therapeutics and

101 hygiene conditions are likely to play a critical role in the burden of these new pandemic 102 variants as well as the increase of air traffic in their spread. Some models take into account 103 the impact of human interventions such as vaccine/antiviral delivery, isolation of infected 104 patients, school closure, halting air traffic and non-pharmaceutical interventions. Moreover, 105 it remains often difficult to evaluate their real impact even without applying any model. For 106 example, it was only in the late nineties that hand washing indisputably demonstrated, 107 through randomized trials, its efficacy to prevent inter-human transmission in developed 108 countries [14-15]. In 2005, a randomized-trial in Pakistan confirmed it in low-income 109 countries [16]. Furthermore, the efficacy of mask use, largely recommended during A/H1N1 110 pandemic, to prevent respiratory infections is still to be clearly established by randomized 111 trials [17-19]. Thereby, their introduction into models seems very tricky.

112 The vast majority of studies showed that immunization against influenza has a true 113 impact in terms of hospitalization rate, global morbidity, influenza associated mortality as 114 well as global mortality [20-26]. Intriguingly, during the immunisation campaign against the 115 A/H1N1 pandemic virus, a large proportion of the population was reluctant to accept 116 vaccination in some countries such as France and Germany. Human behaviours often are 117 unpredictable and could vary among countries and vary with time. In France, the negative 118 image provided by the mass media could have contributed to the low uptake of the A/H1N1 119 vaccine. We observed and reported that in public hospitals of Marseille, the nurses were less 120 immunised against the new A/H1N1 pandemic virus than against seasonal flu [27]. Fears of 121 vaccination promoted by anti-immunization lobbies are largely relayed by the media and the 122 doubts induced and amplified by mediatisation persists for a long time, even when scientists 123 have demonstrated that there is no scientific evidence for suspicion. The association 124 between multiple sclerosis and hepatitis B vaccine on one hand [28], and between autism 125 and measles vaccine on the other hand [29] will be standing for many years to come, and 126 any model is able to predict these events. One model can predict the willingness to accept a 127 vaccine only for one specific situation. External factors cannot be included into models 128 because they are often unknown until they appear. In France, the fact that medical 129 information about the A/H1N1 vaccine was delivered and promoted primarily by politicians 130 could have a counterproductive effect. Medical recommendations bypassing the medical 131 system arouse suspicion in the population [27].

132 With hindsight, the recent pandemic reinforces the idea that presentation of 133 pessimistic models mostly based on extrapolated hypotheses is deleterious. They impress 134 governments and provoke fears. In another hand, it has been previously observed that 135 pessimistic hypothesis about bioterrorism based only on speculations led governments to 136 elaborate countermeasure plans with disproportionate measures. The Dark Winter 137 operation, a bio-terrorist attack simulation, resembles movie script more than reality. Fears 138 of a putative H5N1 avian flu pandemic amplified by pessimistic figures based on 139 unsupported prediction constrained governments to implement emergency flu plans. Later 140 on, these plans postulated that the fatality rate will be close to that observed in cases of 141 A/H5N1 infection. For example, In France the 2009 emergency plan against pandemic flu 142 predicted 91 000 to 212 000 deaths [1]. But A/H5N1 virus is still an almost pure zoonotic 143 agent with transmission properties drastically distinct from those of the human adapted 144 H1N1, H2N2 or H3N2 viruses. During the A/H1N1 pandemic in Marseille, no intermediate 145 measure had been planified between (i) maintaining the organisation and logistics of the 146 public hospital system as it was before the crisis, and (ii) the emergency opening of a 700 147 bed-hospital exclusively dedicated for A/H1N1 infected patients. In the real-life situation, 148 along 10 month pandemic period, more than 2,500 clinical specimens were laboratory-149 documented: of these patients, around 11% were hospitalized and used simultaneously less 150 than 50 beds at the peak of the pandemic.

151 In conclusion, infectious diseases remain unpredictable with mathematical models 152 because pathogens and their ecosystem evolve continuously in a very unstable manner. Of 153 course, some models which take into consideration the antiviral/antimicrobial therapies, the 154 vaccines, the sanitary condition and the non-pharmaceutical interventions are useful to 155 anticipate some logistic problems (quantity to purchase...) and can help to prepare the 156 response to the future pandemics but they cannot predict with acceptable accuracy the 157 major features of a future pandemic (number of cases, hospitalization, deaths...). The 158 pessimistic predictions resulting from bioterrorism and the putative avian flu outbreak were 159 published in highly-rated scientific journals. However they were neither supported by 160 indisputable scientific evidence nor confirmed in real-time up to now. They fuelled fears in 161 the population through amplification by the media, causing great concern amongst the 162 public and the politicians. In order to fight future outbreaks and as a complementary

163 approach of modelling methods, we need to reinforce the network of sentinel centres by 164 increasing their timely detection/diagnostics capacities and by implementing a large variety 165 of technological tools detecting abnormal events. The data from these sentinel centres 166 should not be necessarily exhaustive but they require to produce sufficient amount of data 167 to investigate emergence and epidemic tendencies. Coupled with the fact that data from 168 hospital-based surveillance systems and Google searching tools are easily and timely 169 available, such surveillance method system will not be very costly. Our capacity for analysis 170 and laboratory documentation needs to be increased and better integrated; during a crisis 171 all data must be rapidly shared using communication media such as internet [30]. Rapid 172 communication of research using specific free media such as Promed and 'PloS Currents: 173 Influenza' can also improve the information dissemination. In addition, very early data about 174 a new variant could be incorporate in some models and then produce more accurate 175 predictions. Furthermore, decision process should be based on timely available scientific 176 data to allow decision makers to take real time decision. Precautionary principle should be 177 advantageously replaced by alertness principle.

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