Letter to the Editor

Dear Editor,

I read with interest the Opinion article by Habibzadeh and Yadollahie published in the May 2009 issue of *Archives of Iranian Medicine*.[1]

In their paper, the authors have questioned the importance of *h*-index from several aspects. One point raised by them is that calculation of *h*-index depends seriously on the database in use. However, though this is true, it cannot question the very concept of the *h*-index, which is independent of any database used.

Another criticism raised is that the *h*-indices of Korotkoff and Röntgen, two influential scientists, are respectively below 4 and 6. To explain this, they wrote that "some facts are so well-accepted that they are rarely cited; the Korotkoff sounds heard during the measurement of blood pressure is so familiar to health care personnel that no one generally cites the original article of Nikolai Korotkoff." However, reference 7 of their paper indicates that they have used *Harzing's Publish or Perish* Web site to get this information. It should be pointed out that this website uses *Google Scholar* data to calculate its various statistics.[2] Importantly, *Google Scholar* does not perform as well for older publications as these publications and the publications that cite them have not been posted on the Web.[2] Meho and Yang[3] found that the majority of the citations from journals and conference papers in *Google Scholar* are made from documents after 1993. Therefore, *Google Scholar* seems to underestimate the impact of scholars who have mainly published before 1990.[2] This can explains why Korotkoff and Röntgen, whose influential papers were mainly published before 1905, do not get high *h*-indices using *Harzing's Publish or Perish* Web site's database.

Another criticism raised is that a researcher can increase his or her *h*-index through self-citations. However, Engqvist and Frommen[4] have shown that even "excessive" self-citation will cause the *h*-indices of two equivalent scientists to differ only slightly, seldom by more than one unit. Thus, the *h*-index seems robust enough against self-citations. It should be noted that I do not advocate that *h*-index is an ideal scientometric. *h*-index has several pitfalls—a single number can never give more than a rough approximation to an individual's multifaceted profile. These pitfalls are well discussed in the scientific literature as well as in *Harzing's Publish or Persish* Web site. However, given the points mentioned above, I can neither accept Habibzadeh and Yadollahie's criticisms nor advocate that their comment, *i.e.*, reading scientists' papers, is pragmatic for ranking scientists in research festivals or for granting awards.

Conflict of Interests

The author has no conflict of interests to disclose.

M. R. Namazi MD, Assistant Professor of Dermatology, Medicinal and Natural Products Chemistry Research Center and Dermatology Department, Shiraz University of Medical Sciences, Shiraz, Iran.
E-mail: namazi_mr@yahoo.com
Tel: +98-917-302-7858
Fax: +98-711-231-9049

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Authors' Reply

We read with interest the comments of Namazi on our article.[1] Although he is correct that limitation of retrieving the pertinent records from various databases does not question the basic concepts of the *h*-index, his argument is acceptable until the time when this index is not used as a tool to evaluate persons, since even a sound theoretical method would be practically worthless unless we can use it with the available resources.

We just named Korotkoff and Röntgen as prototypes of many scientists who have contributed to science by publishing only a few but brilliant masterpieces. Although each of their few articles received hundreds of citations and sometimes could be treated as a breakthrough, for the nature of the calculation of the *h*-index, they might have a low index. In our discussion, we used *Harzing's Publish or Perish*® which reports the highest *h*-index as it uses the most extensive database—the

Google Scholar®, albeit we are not sure even if we could have counted the citations to all the published articles of Korotkoff and Röntgen, we would come to a higher *h*-index.

Although, herein we are not going to challenge the robustness of *h*-index as presented by Engqvist and Frommen,[2] in our previous article[1] we could increase the *h*-index of FH from 3 to 4 by inadvertent referencing to some of his articles.[3-6] Here again, thanks to this letter and using the same trick we raise his *h*-index from 4 to 5, and believe us or not, we are pretty ready to increase his *h*-index once again simply by self-citations!

We agree with Namazi that *h*-index is not an ideal scientometric and that is why we propose that such indices should be used only as screening tools and not as the sole means for evaluation of scientists.[1] As an example, to determine the first three top scientists of an institution, probably it is better to find out the top 20 researchers by a metric, say *h*-index, and then read (peer review) their works to select the best three ones.

Finally, we would rather hear from one who has not been awarded recently by the Iranian Health Ministry for his high *h*-index,[7] a clear conflict of interests which has not been disclosed.

Conflict of Interests

We declare that we have no conflict of interests and that we have no known gain or benefit from a high or low *h*-index—we are not university faculties.

Farrokh Habibzadeh MD•*, Mahboobeh Yadollahie MD*, *Shiraz NIOC Medical Education and Research Center, Shiraz, Iran.
E-mail: Farrokh.Habibzadeh@gmail.com

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Dear Editor,

Dr. Haghdoost et al.[1], in their recent article (*Arch Iran Med.* 2009; **12(6):** 533 – 541) have estimated the health effects of the 2009 H1N1 pandemic on Tehran and Kerman populations for several different hypothetical scenarios by using the compartment model. Although the paper itself is state of the art in modeling infectious diseases, the results can mislead policymakers who are not attentive to the pitfalls of modeling for prediction. However, I decided to elucidate the disadvantages of the model and possible further steps to elaborate Haghdoost's work:

- The model is tremendously dependent on its input. Accurate input makes available truthful estimation and imprecise input endows with a deceivable estimate. The employed inputs in the Dr Haghdoost's paper have been borrowed mainly from Fraser et al.[2] who estimated case fatality ratio based on data in Mexico City as of late April. Fraser et al.[2] estimated the number of infected people and case fatality ratio, 23000 (range 6000 to 32000) and 0.4% (range 0.3 to 1.8%), respectively. However, the average case fatality rate based on laboratory-confirmed cases officially reported to WHO was 0.08% as of August 6, 2009 which was five times lower than the case fatality ratio imputed in the model.[3] This means using the more recent case fatality ratio confers a mortality level about five times less than the estimated mortalities in the paper. An explanation for the difference between the two case fatality ratio estimations comes from the underreporting of contracted cases in early phases of the pandemic.[4]

- Case fatality ratio from a population which is employed to estimate the effect of the disease for other populations needs to be standardized; since the Novel influenza A (H1N1) differentiates between younger and older age groups as well as high and low risk populations.[5] I was not able to locate a discussion on the age standardization in the paper. Considering the difference between the age structures of the two populations (Iranian and Mexican), the unadjusted estimates may be biased.

- The prediction models are deterministic which means all stochastic components contributing to the estimates such as confidence interval for case fatality ratio,

hospitalization rate, transmission rate, and R_0 (basic reproductive number) are all ignored. In the lack of appropriate tools and techniques to deal with stochastic components, scaling up the number of possible scenarios with a minimum and maximum reported case fatality ratio, hospitalization rate, transmission rate, and R0 can help demonstrate the degree of uncertainty in the estimates and functions as a sensitivity analysis of the model. However, I strongly recommend using simulation or another possible method to preserve stochastic components in future studies, because a wide confidence interval with the same mean estimate in the paper can change the preferred policy interventions.

Farshad Farzadfar MD, Harvard School of Public Health, U.S.A.
E-mail: ffarzadf@hsph.harvard.edu

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Author's reply,

We reviewed the valuable comments of Dr. Farzadefar on our paper entitled: "Modeling of H1N1 Influenza in Iran". Generally we agree with his main concepts; however, in order to address his comments specifically there are some issues we should clarify:

- As a general rule, the final results of all models are sensitive to their input. Therefore, finding the best input based on the most accurate available evidence is one of the main steps in modeling. The available epidemiological statistics regarding H1N1 are very limited. In the published literature there are currently wide variations. In our model, we systematically have explored all available information and chose our parameters based on extensive discussions. In addition, we sought the scientific contribution of experts at the CDC of Iran in order to adjust our parameters based on national experiences, as well. Dr. Farzadfar mentioned that the mortality rate in some of the WHO reports were much lower than the reported rates in published papers. However, even among the WHO reports, much greater mortality rates can be found. For example, those reported in the Eastern Mediterranean (0.6%), Europe (0.38%), and Western Pacific (0.36%).[1] Therefore, we cannot rely on only a few reports when a more general and comprehensive view is needed. In our model, we have assumed that the mortality rate is 0.36% which is very close to the lower range that Dr. Farzadfar mentioned in his letter (0.3% – 1.8%). In this stage, we cannot say anything more because of our limited knowledge. Nevertheless, we hearty wish that few people will pass away and our model overestimated the numbers. (Nevertheless, we are hopeful that our model will be an overestimate of the numbers in that less people will expire from this disease.)

- In the second comment, Dr. Farzadfar wrote about the importance of standardization based on age and possibly sex. We strongly believe that age standardization is not necessary. People in all age groups are susceptible to H1N1, and severe forms of the diseases have been recorded amongst all age groups. In addition, although the age structures of populations have differences, these heterogeneities are not large enough to substantially change the parameters. Values for R_0 were chosen after a thorough literature review. As you can see in our paper, the final results are very sensitive to R_0 changes (which were the most important element of the model). We are reasonably certain that the impact of such standardization on our final results is much lower that the impact of changing R_0.

- In the last page of the discussion, we wrote a few paragraphs about the limitations and mentioned that we did not run a sensitivity analysis and simulation. We hope that in future studies and with more accurate parameters, researchers can expand upon the models to create more sophisticated ones. The main reasons for ignoring sensitivity analysis were:
a) The lack of accurate and acceptable information to feed the model,[2] for certain by the time we can find enough evidence to

expand the analysis.[3,4]

b) The impact of R_0 changes on the epidemic curves and its sequences was large enough and convincing, such that even without sensitivity analysis we could rely on the final conclusion.

c) Generally speaking, in most models, we have to explore the impact of only a few parameters. It might not be possible to simultaneously control all sources of variations in a single model. Therefore, more models with different scenarios are recommended.

Ali Akbar Haghdoost MD*, Mohammad Mehdi Gooya MD**, Mohammad Reza Baneshi PhD˙***, *Physiology Research Center, Kerman University of Medical Sciences, Kerman, **Center for Infectious Disease Control, Ministry of Health and Medical Education, Tehran, ***Department of Biostatistics, Kerman University of Medical Sciences, Kerman, Iran. E-mail: rbaneshi@yahoo.com; m_baneshi@kmu.ac.ir

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Dear Editor,

A concern about "modeling of H1N1 Flu"

I read the recent publication on modeling of H1N1 Flu in Iran by Haghdoost et al.[1] Haghdoost et al. used an epidemiological mathematical model to predict a pandemic situation in Iran. This model is very interesting. However, there are some points to be considered. First, the model is based on a "closed" system which does not account for immigration and emigration. Indeed, the actual scenario for a pandemic in many countries is due to the transportation of the disease from old to new settings. Second, there are no concerns on the external parameters that can cause the situation to deviate. The seasonal based prediction might be grossly affected by the difference of temperature year to year, which is a common happening today with the global warming situation. Third, at present, the vaccine for swine flu is successfully being produced and implemented. Therefore, the effect of vaccination on the pandemic should be assessed when forecasting the situation in the year 2010.

Viroj Wiwanitkit MD, Wiwanitkit House, Bangkhae, Bangkok Thailand 10160
Tel: +66-241-32436
E-mail: wviroj@yahoo.com

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Author's reply,

In response to Dr. Wiwanitkit's comments, we have to mention that in the second part of our modeling we assessed the impact of the number of infectious subjects on the epidemic curve. We assumed that the population was closed without any emigrations or immigrations; we knew that in reality it is not the case, and this issue was highlighted in our paper. However, we believe that our final conclusion is somehow robust to slight violation of this assumption. First of all, the rate of movement among a healthy population is not high, particularly during a short term of 2 – 3 years. In addition, we do not have accurate information about the pattern of population movement, particularly in an unstable situation; but without any doubt as the result of the flu outbreak we expect much less population movement. Nevertheless, as shown in our paper, the epidemic curve is highly sensitive to the number of imported infectious cases.

The second comment regarding the year to year temperature variation and its impact on R_0. We could not find any evidence for that in the literature; however, the annual variation is too small to significantly change R_0. Intuitively, we think that the density of population in close spaces is more or less comparable in both 2009 and 2010 winters and a small difference in the temperature would not have a significant impact.

Finally, our model predicted epidemic curves without any interventions; we hope our interventions including the vaccine campaign would suppress the peaks. At least, our findings may help to assess the impacts of interventions by comparing the observed figures in the following two years with our predictions.

Ali Akbar Haghdoost MD*, Mohammad Mehdi Gooya MD**, Mohammad Reza Baneshi PhD˙***, *Physiology Research Center, Kerman University of Medical Sciences, Kerman, **Center for Infectious Disease Control, Ministry of Health and Medical Education, Tehran, ***Department of Biostatistics, Kerman University of Medical Sciences, Kerman, Iran. E-mail:rbaneshi@yahoo.com; m_baneshi@kmu.ac.ir

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