A practical method to target individuals for outbreak detection and control

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Abstract
Identification of individuals or subpopulations that contribute the most to disease transmission is key to target surveillance and control efforts. In a recent study in BMC Medicine, Smieszek and Salathé introduced a novel method based on readily available information about spatial proximity in high schools, to help identify individuals at higher risk of infection and those more likely to be infected early in the outbreak. By combining simulation models for influenza transmission with high-resolution data on school contact patterns, the authors showed that their proximity method compares favorably to more sophisticated methods using detailed contact tracing information. The proximity method is simple and promising, but further research is warranted to confront this method against real influenza outbreak data, and to assess the generalizability of the approach to other important transmission units, such as work, households, and transportation systems. See related research article here http://www.biomedcentral.com/1741-7015/11/35

Keywords: contact network, hotspot, dynamic network, contact pattern, wireless sensing devices, collocation ranking, class schedule, high school, influenza, disease transmission.

Background
The transmission potential of an infectious disease is directly related to the characteristics of the infectious agent, its host population and the local environment [1]. The contribution of these factors can be encapsulated in a single parameter that is key for disease control, namely, the ‘reproduction number’, which quantifies the average number of secondary cases generated by an infectious individual during the early epidemic phase [1]. Identification of individuals or subpopulations associated with high transmission potential is particularly useful to guide surveillance and control strategies, especially when resources are limited [2].

Understanding the complexity of dynamic human interactions and contact networks is crucial to identifying hotspots of disease transmission during an outbreak [3]. The dynamic social contact networks relevant for disease spread depends on a number of factors, including individual host characteristics (e.g., age, prior immunity, number of contacts), pathogen characteristics (transmission mode), characteristics of the space in which individuals interact (for example, confined versus open setting, room capacity), and the duration and proximity of human interactions.

Recent technological advances in miniature wireless sensing devices have allowed unobtrusive and unsupervised quantification of the dynamic network of human interactions in various settings, including schools [4-6], conferences [7], and hospitals [8]. In particular, these innovative technologies have increased our understanding of face-to-face contact patterns relevant for the spread of rapidly transmitted infectious agents [4,9]. Given the large amount of costly information captured by these devices, there is active debate on the minimum level of data that is required to capture the essence of disease transmission and to be sufficient to inform disease control [7,10].

Performances of various indicators of social connectivity
A recent study by Smieszek and Salathé, published in BMC Medicine [11], used high-resolution contact-network data collected by wireless sensing devices during a 1-day period at a high school in the USA, combined with extensive epidemic simulations, to evaluate the effectiveness of several metrics to identify individuals who play a significant role in outbreak dissemination.
The consolidated network dataset was limited to close
proximity interactions, based on records indicating face-
to-face contacts within a distance of less than 3 m at a
certain point in time. The dataset also included location
records indicating the presence of an individual in a
specific classroom.

The authors then quantified the performances of a vari-
ety of indicators of social connectivity, which required
different levels of information on the high-school contact
network to identify individuals with high transmission
potential. In particular, the authors introduced a low-cost
indicator of social connectivity, based on the ‘collocation-
ranking method’, which relies on the cumulative amount
of time that an individual spends with other individuals
in the same room, modulated by class size. Such informa-
tion does not rely on the detailed structure of the high-
school contact network, and can be retrieved from sche-
dule data alone. The Smieszek and Salathé study relied
on simulations of influenza transmission on the detailed
high-school contact network to assess the performances
of the different indicators, in terms of their ability to
identify individuals at higher risk of infection and those
with early disease onset.

Findings and potential applications
Epidemic simulations showed that the simple schedule-
based collocation ranking indicator clearly outperformed
methods selecting individuals at random, and compared
favorably with more data-hungry indicators. Because col-
lecting reliable data about individual-level interactions is
cumbersome and expensive to obtain at the community
level, the authors proposed that their low-cost collocation
method can be exploited for the design of sentinel surveil-
ance systems, with the potential to quickly detect the
onset of an infectious disease outbreak, and thereby opti-
mize mitigation and prevention strategies. In particular,
sentinel high-school students could be selected from those
with high collocation ranking, and these could then be
monitored for their infection status throughout the influ-
enza season, and/or be prioritized for vaccination in the
case of vaccine shortage, in an effort to stamp out an
emerging outbreak.

Limitations and future directions
This interesting proof-of-concept study by Smieszek and
Salathé addressed social interactions within a high
school, which is an important focus for seasonal and pan-
demic influenza transmission [12]. As acknowledged by
the authors, a key limitation of this study is the lack of
validation against epidemiological data from real school
outbreaks. The simulation model used to evaluate the
performances of the method is a conceptualized version
of disease transmission, and although it is driven by real
contact information, it remains one step removed from
the actual disease-transmission process. A previous study
combining outbreak data in an elementary school with
contact-network information highlighted the importance
of gender on influenza transmission, with children of the
same gender infecting each other more frequently
(reflecting assortative mixing) [4], an issue that was not
considered by Smieszek and Salathé. Interestingly, school
outbreak data have also shown that the exact location of
children within the classroom does not matter, which
supports the use of simple class-schedule information as
proposed by Smieszek and Salathé [11] rather than the
use of more detailed seating charts. Although there has
been good progress overall in elucidating social interac-
tions among school-age children, more studies are
needed to address whether contact patterns, and hence
transmission links, might differ between elementary and
high schools.

Another limitation of the school-based study by Smiesz-
zek and Salathé [11] relates to the contribution of other
units to disease transmission. About one-third of all
influenza secondary-transmission events are believed to
occur within households [13], whereas only 7 to 20% are
thought to occur in schools [14]. Hence, estimating the
relative infection risk of individuals in a variety of settings
relevant for disease transmission, including schools,
households, conferences, and transportation systems, will
be important in future research. It is not clear how the
method proposed by Smieszek and Salathé [11] could be
generalized to household and work environments, where
systematic ‘schedules’ are more difficult to obtain.

As noted by the authors, the transmission mode of
influenza and other respiratory pathogens is not clearly
understood, but probably involves a combination of
direct contact and transmission by fomites and aerosols,
which makes it difficult to capture the social network
relevant for disease transmission. Because the transmissi-
bility of influenza has been shown to be associated with
environmental conditions [15,16], actual transmission
rates could vary within the same school, house, or office
building, owing to local differences in the environment.
In the future, more elaborate studies should collect local
environmental variables such as room ventilation rates to
better quantify influenza transmission potential in con-
fined settings [17].

In summary, Smieszek and Salathé [11] have introduced
a promising and practical method to identify individuals
with high infection potential who can be targeted for out-
break detection and control. Future studies should employ
consistent methodological approaches to measure contact
networks in different settings, in parallel with careful dis-
ease monitoring. Technological advances in contact-net-
work sensing devices and pathogen identification methods
(for example, multiplex PCR), combined with innovative
approaches for disease surveillance (for example, web-based
and smart-phone technologies [18]), have huge potential to increase our understanding of infectious disease transmission and to suggest novel ways of detecting and controlling outbreaks.

Authors’ contributions
Both authors contributed to the writing and editing of this commentary. Both authors read and approved the final manuscript.

Authors’ information
GC is an associate professor in the School of Human Evolution and Social Change at Arizona State University and a research fellow at the Fogarty International Center, US National Institutes of Health. Research interests include mathematical and statistical modeling of infectious disease transmission and control interventions, with a focus on seasonal and pandemic influenza and the quantitative characterization of past influenza pandemics.

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Competing interests
The authors declare that they have no competing interests.

Acknowledgements
We are grateful for financial support from MISMS (Multinational Influenza Seasonal Mortality Study), an ongoing international collaborative effort to understand influenza epidemiological and evolutionary patterns, led by the Fogarty International Center, National Institutes of Health http://www.origem.info/misms/index.php. The MISMS study is funded by the International Influenza Unit, Office of Global Health Affairs, Department of Health and Human Services.

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Received: 30 January 2013 Accepted: 12 February 2013
Published: 12 February 2013

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Pre-publication history
The pre-publication history for this paper can be accessed here: http://www.biomedcentral.com/1741-7015/11/36/prepub

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