

2nd International Conference on Epidemiology & Evolutionary Genetics

August 18-19, 2014 DoubleTree by Hilton Beijing, China



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Modern tools to understand the epidemiology of infectious diseases

Mathematical models have been used to understand the factors which govern infectious diseases, to design better treatments and to make outcome predictions both in therapy efficacy and epidemiology. This talk will review the state of the art modelling and data interpretation obtained from anti-hepatitis B virus infection therapies, anti-HIV infection therapies and acute hepatitis B virus infection in chimpanzees. The outcome from these studies help us hypothesize that human infected with virus can be divided into four groups:

1. Individuals having no or any symptoms can recover automatically even if infected with a large amount of virus if their virus reproductive numbers are less than one.
2. Individuals having no or any symptoms can become persistent with infections even if infected with microscale virus if their virus reproductive numbers are larger than one.
3. Individuals having symptoms of acute infection and can recover automatically even if infected with a large amount of virus if their virus reproductive numbers are less than one.
4. Individuals having symptoms of acute infection can become persistent with infections even if infected with microscale virus if their virus reproductive numbers are larger than one.

This hypothesis may interpret virus infections with unclear reasons: the first two kinds of population have infected the third and fourth kind of population.

Acknowledgements This research is supported by the National Natural Science Foundation of China under Grant No. 61074192.

Biography

Lequan Min is currently a Professor in Mathematics and Physics School, and the PhD supervisor with the Automation School at the University of Science and Technology Beijing. His current research interests are modeling and simulations of complex systems in particular to the virus infections and epidemic spreading. He is also the author or co-author of over 200 scientific journal and conference papers.

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