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The Math of Flu

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The first major epidemic of a disease officially recorded by a "professional" – and actually no-one less than the acclaimed Father of Western Medicine Hippokrates of Kos (~460 to 370 BC), took place in 412BC was probably an influenza epidemic. The term Influenza was probably coined in Italy in 1357AD when the development of flu was blamed on the "influence" of the stars.

In 1485, a "sweating sickness" killed many people in Britain including the Lord Mayor of London and his successor. It was probably also an influenza epidemic that wiped out the West-Indian population of Hispaniola (the island comprising the Dominican Republic and the Republic of Haiti) in 1492 as an immediate consequence of this Island being "discovered" by Christopher Columbus. And one of the worst pandemics this planet ever hit, the H1N1 pandemic from 1918-1919 called "Spanish Flu", killed worldwide at least 20 and perhaps up to 100 million people. And it may well have been an influenza pandemic that killed the last Neanderthals when they came into contact with invading "modern" people.

So, it is easy to understand – and well reflected in the internet – that the responsible authorities in governments and NGOs get busy (as well as nervous) whenever a new outbreak of a flu-like disease is reported. And scientists and educators as well begin developing and teaching courses to make people understand the basics of epidemiological modelling including even the meaning of that famous dimensionless R_0-parameter and its critical threshold value 1 (see for example Dr. R. C. Larson's nice and playful recent introduction to the subject on
http://blossoms.mit.edu/video/larson2.html).

In this little booklet experts from various fields join forces to discuss such and other tools from mathematics to support the analysis of the evolution of viruses and of epidemics caused by them:

- Bulla and M. Stanke present a method that can be used to identify and analyse recombination events in the evolution of HIV and other viruses,
- in "Visualizing Viral Evolution", a short report on Manfred Eigen's theory of self-organization of matter and molecular evolution is given and used to interpret recent diagrams on the webpage of the Shanghai Partner Institute for Computational Biology showing phylogenetic networks presenting the evolution and spreading of the A H1N1 virus during the last "swine flu pandemic" from 2009 (see
http://www.picb.ac.cn/picb-dynamic/Desktop/news/shownews.jsp?ID=538),
- while a rather general approach to "canonically" relate proper phylogenetic trees to such networks is outlined in "A Topological Approach to Tree (Re-)Construction".
- J. Haß, S. Matuszewski, D. Cieslik and M. Haase discuss the role of pigs as a "mixing vessel" for recombining viruses,
- C. Spehr, A. Spillner and K.-E. Biebler report on methods that can be used to fit epidemic models and real-world data and
- finally M. Ziller, M. Gussmann and A. Karger deal with mathematical challenges posed by mass spectroscopy – one of the most important technologies in the molecular sciences: The classification of mass spectra.

We expect that this broad mix of aspects all of which are relevant in the analysis of viral evolution and epidemics will provide the reader with a good introduction into the various tools mathematics can provide to cope with a particular striking phenomenon in human history.