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Peter Slood is distinguished research professor at the University of Amsterdam, a professor of advanced computing in St. Petersburg, Russia and a visiting professor to the complexity program in NTU, Singapore. He is a laureate of the Russian Leading Scientist president's program and has been the PI of many European research programs on complex systems, such as www.virolab.org and www.dynanets.org. Peter Slood is editor in chief of two highly ranked Elsevier Science Journals in computational

science and computing systems and for over 10 years he has been the Scientific Chair of the International Conference on Computational Science www.iccs-meeting.org. For more than 20 years he has been a well-known advocate of studying complex systems through computational models. His main interest is in uncovering the rules by which Nature seems to process information. On this topic he has published over 400 papers, book chapters and books. His work is covered in international media such as newspapers, interviews and documentaries. Currently he is working on a theory and methods to reformulate complex systems into an information theoretic framework using concepts from thermodynamics. He latest papers are on stochastic resonance in hierarchical networks and intervening strategies of dark criminal networks.

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A Complex World from a Virus' Point of View

In 2006 the European Union posted a scientific challenge reading: *'If we could spend 1 Billion Euro on stopping the HIV Pandemic, should we spend it on better medicine or changing behavior?'* Thinking about mind boggling questions like that we realize more and more that the only answer to many relevant questions in life requires a true multi-, inter-, and cross-disciplinary approach. It is a quest from the molecule all the way up to mankind and back again. There is no escape, the only way out is to dig deep into all aspects of the elements that constitute the problem and try to uncover their intricate connection, and then hope for the best. In this presentation I will relate of such a journey and show how we can uncover emergent properties of HIV-1 dynamics using novel algorithmic and computational methods. These methods seem to have a predictive power with which we might be able to answer seemingly impossible questions as the one stated above.