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سیستم‌های پیچیده  
و ماده چگال



سمینار هفتگی ماده چگال نرم

## Influenza Virus and its Evolution

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New sequencing technologies are being developed at an enormous speed, allowing efficient sequencing of the genome of a single organism or a community of organisms. The genome of a diverse set of organisms are also being deposited in public databases. This provides a vast amount of information that needs to be understood in new ways and with new tools. The main focus of this talk is on influenza virus and quantitative genomic analyses of its evolution. In particular, the first genomic analysis on the origins of the 2009 human H1N1 influenza A virus of swine origin and the reasons behind the lack of close relatives to it, via a systemic analysis on the worldwide surveillance of the influenza viruses in different hosts, will be discussed. Furthermore, the evolutionary mechanisms of the virus, especially, its reassortment patterns will be described.

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