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## **Paradigm changes in virology using Adenovirus as a model for the integration of genomics and bioinformatics methods**

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Virology, both basic and clinical research, is undergoing dramatic changes due to the influx of whole genome data. With the rapid advances in next generation sequencing technology and the availability of bioinformatics tools developed for other systems, virology is at the leading edge of paradigm changes for broader and deeper understanding, including taxonomy, nomenclature and clinical methods. Human adenoviruses are model organisms in the past. They are also pathogens with multiple effects on the population. Whole genome data and analysis are providing an opportunity to understanding pathogen emergence and re-emergence at the molecular level and adenoviruses are a model system for developing standards, including genome annotation standards.

### **Biography**

Donald Seto has a PhD in biology from The Johns Hopkins University and completed postdoctoral studies with Leroy Hood at the California Institute of Technology. He is an Associate Professor of Bioinformatics and Computational Biology at George Mason University. He has published more than 60 scientific papers in journals and is serving as an editorial board member of Viruses.