

## High-throughput genomics and the Sword of Damocles

Jeremy F Taylor  
Division of Animal Sciences  
University of Missouri, Columbia MO 65211-5300  
[taylorjerr@missouri.edu](mailto:taylorjerr@missouri.edu)

Next-generation sequencing and high-throughput assaying technologies have dichotomized entire research communities into those individuals who have rapidly evolved in response to the technological selection pressure and those destined to become evolutionary dead-ends. The problem lies not with the ease with which these technologies may be applied to address a breadth of issues from organismal evolution to variant detection or from quantitation of gene expression and DNA methylation, but the ease with which they generate volumes of data which have never before been experienced by individual investigators. Unfortunately, the pandemic has only just begun and the rate at which data are being generated appears to exceed the exponential increases in computer hardware capabilities described by Moore's law. As a consequence, fewer and fewer investigators will have access to these technologies until user friendly software becomes available at modest price points. However, the problem really is institutional in nature since no institution can afford the disenfranchisement of a large proportion of its life sciences faculty whom are not bioinformaticians or computer systems analysts. Unless universities and corporate research entities rapidly invest in the computational processing and data storage infrastructures and bioinformatics support (personnel and software), their ability to compete within competitive funding and intellectual property generation domains will rapidly wither.