

## *Modeling the Spread of the Zika Virus in South Carolina*

**James Brown**

With the passing of the 2016 Olympic Games, the Zika virus is a pressing topic for researchers and world leaders alike as it spreads throughout the Americas. The possibility of a rapid spread and its negative impact on pregnant mothers amplifies the need for modeling Zika. Developed by Kermack and McKendrick, compartmental models in epidemiology provide a mathematical infrastructure to model complex systems and to show how a disease spreads through them. More specifically, SIR models allow us to compute the theoretical number of people infected with a disease in a closed population over time. We apply the use of this model in order to show how the Zika virus may spread through South Carolina.

## *A Rank-Sum Test for Significance of Difference in Copy Variation*

**Kendrick Hardison**

Copy number variation (CNV) results from duplications and deletions of genomic DNA, and is known to correlate with a number of genetic diseases. Typically, a subject being screened for a disease will have measures from  $k$  sections of DNA, and these are compared to an  $N$  amount of controls. Here we describe a rank sum statistic useful for determining whether the subject is at risk for disease. We derive the exact distribution of this statistic and compare the exact distribution to an approximate distribution proposed in the literature. We demonstrate that use of the approximate distribution of the rank sum statistic results in higher than nominal Type 1 error rate and an exaggeration of power.