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Ronald D Hagan* (rhagan@utk.edu) and **Michael A Langston**. *Computational Tools for the Analysis of DNA Methylation Data*.

The genetic code contained in a person's DNA is far from the only determining factor in actual gene expression. Epigenetic mechanisms such as DNA methylation and histone modifications also play a prominent role. In fact, aberrant methylation patterns have been linked to nearly all forms of cancer. In this talk we present an overview of an innovative set of computational tools with a foundation in statistical analysis and graph theory for analyzing methylation data. In addition, we explore a variety of use cases demonstrating the utility of our tools for methylation biomarker discovery in disease, tissue differentiation, mutation status, and outlier detection. (Received January 07, 2016)