1106-VG-1233 **H Wang*** (hwang@gerorgiasouthern.edu) and **G Peng**, gpeng@mdanderson.org. *Mathematical model of dynamic protein interactions regulating protein stability of tumor suppressors.*

In the field of cancer biology, numerous genes or proteins form extremely complex regulatory network. Many key tumor suppressors such as p53 are regulated through protein stability control, which determines cancer cell fate and cancer cell survival. It remains elusive how we could understand and target p53 stabilization process through network analysis of hundreds of molecules and signals, which are known involved in regulating p53 protein stability. In this presentation we discuss the use of random walk and stationary distribution to measure the compound effect of a network of genes or proteins. This method is applied to the network of nine proteins that influence the protein stability of p53 via regulating the interaction between p53 and its regulator MDM2. This work shows the importance of using mathematical analysis to dissect the complexity of biology networks in cancer. (Received September 11, 2014)