1176-92-279 **Seyyed Mahmood Ghasemi*** (sghasemi@uh.edu), **Pankaj K Singh**, **Hannah L Johnson**, **Fabio Stossi**, **Robert Azencott** and **Michael Mancini**. *Stochastic modeling of GREB1 gene transcription.* Preliminary report.

Gene transcription is an essential step in the central dogma of biology. It is usually considered a highly regulated and ordered phenomenon, however, live imaging experiments often demonstrated an intrinsic stochasticity in mRNA production. Many mathematical models based upon different types of experiments have focused on messenger RNA (mRNA) production in single cells. This complex process is influenced by many factors and has often been analyzed through stochastic models with parameters that are strongly gene dependent. Our study is centered on the effects elicited by the steroid hormone 17η-Estradiol (E2), which binds to the estrogen receptor (ER) to regulate the expression of a large number of target genes, including GREB1, which is used in this study as a paradigm for a long ER target gene, in populations of MCF7 breast cancer cells. Our goal was to describe early responses to E2 by modeling dynamics from static time points. We monitored GREB1 gene transcription using high-resolution imaging and single-molecule Fluorescence In Situ Hybridization (smFISH) using spectrally separated probe sets for GREB1 introns and exons to perform both nascent and steady-state RNA analysis to investigate the effect of inhibitor, the level of its concentration, and some other factors. (Received January 25, 2022)