1145-AA-2632 **Kamel Lahouel***, klahoue1@jhu.edu, and **Donald Geman**, **Laurent Younes** and **Cristian Tomasetti**. *A mathematical model of tumorigenesis.* Preliminary report.

We model and simulate the process of tumorigenesis in a tissue by modeling the evolutionary dynamics of all cells composing the tissue and their interactions. The stem cells belonging to the tissue can acquire different fitness advantages via driver mutations belonging to different pathways. We define the occurrence of cancer as the emergence of a surviving clone having a particular combination of driver mutations. Due to the complexity of the model, we use a stochastic approximation approach as an alternative to the analytical approach for the calibration of the model. The calibration is performed by fitting real colorectal cancer data constraints: The lifetime risk of colorectal cancer, the probability of having a polyp by 50 years old and the probability of having a polyp by 80 years old. In addition, we set a constraint ensuring the non explosion of the size of the tissue by the end of every simulation. Once the free parameters of the model are fixed, we test our model by simulating 4 different tissues, namely, colon, colon with a Familial adenomatous polyposis disorder, blood and pancreas. We compare the results of our simulations to real cancer data such as incidence curves for every tissue or the risk and number of polyps for colorectal cancer and FAP. (Received September 25, 2018)