1010-92-65 **Wai-Yuan Tan*** (waitan@memphis.edu), Department of Mathematical Sciences, The University of Memphis, Memphis, TN 38152, **Li-Jun Zhang** (lzhang1@memphis.edu), The Department of Mathematical Sciences, The Universsity of Memphis, Memphis, TN 38152, **Chao W. Chen** (Chen,chao@epa.gov), US EPA, Washington, D.C., Washington, D.C., and **Junmei Zhu** (jzhu@memphis.edu), Department of Mathematical Sciences, The University of Memphis, Memphis, TN 38152. *Stochastic Mixture Models of Human Colon Cancers.* Preliminary report.

In the past 15 years, molecular biologists and cancer researchers have shown that for human colon cancer there are at least 3 different pathways leading to carcinomas and cancer tumors: The LOH pathway (75-80%), the MSI-H (High level of MSI) pathway

(10-15%) and the MSI-L (Low level of MSI) pathway (10%). Thus, in a population at risk for colon cancer, different cancer patients derive their cancer through different pathways depending on environmental conditions. It follows that for fitting human colon cancer data such as those from the NCI/NIH SEER project, the true model should be a mixture of different pathways. In this paper we will thus consider a mixture model of 5 different pathways for human colon cancers. These pathways are: The LOH pathway, the familial LOH pathway, the FAP pathway, the MSI-H pathway and the HNPCC pathway. For this model, we derive an EM algorithm to estimate the proportion of different pathways and the parameters for each pathway. We derive the MLE for each pathway through the genetic algorithm. We have applied this model to fit the SEER data of human colon cancers. Our results indicate that the model fits the data well and fits nicely the biological observations. (Received August 18, 2005)