



In this thesis, I study three stochastic methods that can be applied for the analysis of data in cancer research and, in particular, to cancer genomic data and to images of angiogenic processes. Cancer is a multistep process where the accumulation of genomic lesions alters cell biology. The latter is under control of several pathways and thus, cancer can arise via different mechanisms affecting different pathways. Due to the general complexity of this disease and the different types of tumors, the efforts of cancer research cover several research areas such as, for example, immunology, genetics, cell biology, angiogenesis.