Mean residual life regression models attract considerable attentions in the recent study of survival data analysis. However, all the existing works focus on independent survival data incapable of applying to the analysis of clustered data, which are frequently encountered in biomedical studies. This thesis aims to develop novel methodologies based on mean residual life models to account for the dependency caused by clustered structure in data. The first method is proposed using the hierarchical quasi-likelihood in the construction of the quasi-likelihood function. It can avoid the estimation challenges and be simply implemented via an iterative algorithm. An explicit distributional assumption is still needed while it is hard to be verified in the practice. A more flexible model framework is further developed by the penalized quasi-likelihood method, leading to a broader range of application for the proposed frailty model and the estimator of regression parameters with asymptotic properties. Extensive simulation studies have been carried out and results show promising finite sample performance of both proposed methodologies. The utility of proposed models are illustrated by their applications to the data from a multi-center trials study of breast cancer.