To maximize their usefulness, core and mini core collections should be dynamic. The peanut core collection was developed in the early 1990's, and the mini core was developed in the late 1990's. Research has shown that these collections can be used to improve the efficiency and effectiveness of identifying valuable traits in the entire germplasm collection, and both of these collections have been widely used to mine valuable genes from the germplasm collection. However, both of these collections need to be updated and revised to better represent additions to the entire collection and changing needs of the peanut breeding community. The first objective was to add accessions to represent additions to the entire collection since the core was selected. Data were generated and analyzed, and it was concluded that 41 accessions need to be added to the core collection. A subsample of these accessions will also be added to the mini core collection. Recent discussions in the Peanut Crop Germplasm Committee has indicated the need for homogeneous accessions for some users of these germplasm collections. We examined evaluation data to identify accessions in the core and the mini core which appear to be heterogeneous. The possibility of the selection and storage of homogeneous subsamples will be discussed.