Lumi v. Minfi Worklfow:

1. Lumi
   1. Normalization Steps:
      1. Color Correction using a smooth Quantile Normalization
      2. Background correction on separated colors
         1. Can run without the use of control data
      3. Probe level normalization (typically using quantile normalization)
   2. Other features
      1. Functions to fit a gamma mixture model to determine methylation status and probability values
   3. Caveats
      1. Does not use included background probe data for estimations, just works off of base data
2. Minfi
   1. Normalization Steps:
      1. P value cutoffs
      2. Normalization functions
         1. preprocessFunnorm – datasets with global methylation differences (cancer/dif cell types, etc.)
         2. preprocessQuantile – datasets where we do not expect global differences (single tissue)
   2. Other features
      1. Drop probes that contain SNPs very easily (dropLociWithSnps)
      2. Built in methods for MDS and pairwise plots for EDA
      3. Well integrated with methods for finding differentially methylated regions (DMR) and visualizing results
   3. Caveats
      1. Requires complete set of background probes
      2. Requires proper feature data annotations?