Title: kimma for RNA-seq differential expression analyses with genetic kinship

Background literature

* Comparison of RNAseq analysis methods
  + <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4054597/>
  + <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4728800/>
* limma
  + <https://academic.oup.com/nar/article/43/7/e47/2414268>
  + <https://genomebiology.biomedcentral.com/articles/10.1186/gb-2014-15-2-r29>
* edgeR
  + <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2796818/>
* dream
  + <https://bioconductor.org/packages/release/bioc/vignettes/variancePartition/inst/doc/dream.html>
  + <https://academic.oup.com/bioinformatics/article/37/2/192/5878955>
* DMRcate (a similar paper outline for new bioinformatics method)
  + <https://epigeneticsandchromatin.biomedcentral.com/articles/10.1186/1756-8935-8-6>

Main findings

1. Expands on limma package to allow incorporation of a matrix co-variate (kinship)
2. Runs a true linear mixed effects model (i.e. paired samples by donor) as compared to duplicateCorrelation shortcut in limma or other paired method in dream package

Analyses

1. Simulated data
   1. Create “fake” RNAseq data
      1. 2+ effect sizes for treatment
      2. 2+ relatedness levels for kinship or some way to have RNAseq with differing levels of correlation to kinship.
   2. Run kimma, limma, and dream analyses of differential expression
   3. Compare model fit (sigma?) and other metrics (see DMRcate paper for ideas)
2. Real world data
   1. RSTR vs LTBI, media vs Mtb and another one TBD
   2. Run kimma, limma, and dream analyses of differential expression
   3. Compare model fit and other metrics

Roles

* Kim
  + Add quality weights option to kmFit( )
  + RSTR analysis (mostly already done for another paper)
* Kiana
  + Create simulated data?
  + Analysis of simulated data
* Sashank
  + Analysis of second real world data