RNA-Seq class activities
April 26

We talked about enriching for target RNAs.

A. What kinds of RNA are going to be maintained or lost in each of these techniques?
   1. Selection by hybridization to oligo-dTs

   2. rRNA depletion by binding to oligos complementary to rRNA

B. Given the way that cDNA is made from RNA, which end of the mRNA are you least likely to see in your final sequencing data? Why? What data does this mean you might be missing? How might you try to target these sequences?

C. In a genome, each base has the same probability of being seen. Is this true in RNA-seq? Why or why not? How will this change your library size calculations?