**Assignment #2 – Investigating the cellular response to exogenous DNA (cont…)**

***Introduction***

Double-stranded DNA (dsDNA) in the cytosol of human cells stimulates the type 1 interferon (IFN) response, a component of innate immunity that is active against invading pathogens and many cancers. Over the course of Assignment #1 and Assignment #2, we will examine the host genes that are transcriptionally regulated upon detection of invading dsDNA.

For assignment #2, you will generate count data using two different alignment strategies, and subsequently perform differential gene expression (DGE) analysis on each with the final aim of comparing the two alignment strategies. Here, we will use all three bioreps for each of our two conditions in the analysis.

***Steps required***

1. **Use featureCounts to generate gene counts from the alignment generated in Assignment #1.**
   1. Import into DeSeq2
   2. Perform basic data exploration and DGE analysis
2. **Use Kallisto or Salmon to pseudoalign raw fastq files to generate alternative count dataset.**
   1. Convert transcript counts to gene counts
   2. Import into DeSeq2
   3. Perform basic data exploration and DGE analysis
3. **Compare outputs from the two strategies – what have you learned?**

***Useful notes***

* Several R scripts are provided
  1. conversion of transcript counts to gene counts
  2. basic data exploration (i.e. similarity of biological replicates)
  3. DGE analysis