

# Recitation 8

1. Load 20170927\_example.gtf.csv with readr.
2. Determine how many records have an exon\_number of 2 using str\_detect().
3. Determine how many records have an exon\_id that ends in 1 using regular expressions.
4. Use str\_detect() to find any records with snRNAs.
5. Use str\_split() to split the data into useful chunks. See if you can save this as a new tibble. Don't be too detailed about this as gtf files are not always consistent.
6. Set up a R Markdown file in R-Studio. Use the default examples, the cheatsheets in R-Studio, and the file example-RNotebook.Rmd (written by Arjun Krishnan, CMSE faculty and R power user) to take your recitation from Session 5 and convert it to a nicely formatted R Markdown file.