**Meetings with Andrew**

**Meeting #2 5/29/20**

1. Regarding Tim’s Givinostat project
   1. If decreasing genesets maybe we can increase th permutation
   2. For the plots try including the Pvalue threshold
   3. Try using plotly … + theme\_bw() if plot is too long trying to show other values
2. For TGFb
   1. Perform sensitivity analysis
      1. Compare DE results of run1 to run2 when it happens
      2. Can use venn diagrams
      3. See if they differ by run in PCA or other outputs

**Meeting #3 6/2/20**

1. Regarding Givinostat
   1. Also agrees the GSEA results were limited by the small samples
   2. Its important to set deadline and gather timelines.
   3. It helps tremendously to alert the investigator of a problem that you run into if it may delay a report. They need to know why so that they might understand the delay. Things happen and problems can occur unexpectedly.
   4. Well meet again next week to discuss some results from projects that I have been working on
   5. Make copies of reports in case one is overwritten

**6/10/20**

1. **80/20 feel guilty for working on other projects**
2. **Andrew uses RMD to mostly makes the plots in RMD**
   1. **Knit options, word, pdf or Html**
   2. **Word might be nicer**
   3. **Html might not be able to show large tables**
   4. **PDF could be better**
   5. **You can source the code into RMD with absolute path or relative**
   6. **Prep like code**