Changes to make to FA\_Analyze.Rmd

* Move calculation of myd$bc1cts\_f\_a to prev script
* Move Omit calculation and application block to prev script
* Move Gen-0 treatment effect dataframe creation to prev script
* Consider Removing the “As an additional check, assess the relationship between change in fitness,dw, and weight (reads)”
  + This block is confusing to any reviewers and may cause people to suspect our relationship between weight and the response variable.
  + Move this block to a new file called FA\_Analyze\_LEGACY\_BLOCKS.Rmd
* Move: ASSESS: FITNESS CHANGE IN 500 GENERATIONS OF EVOLUTION ACROSS 7 TREATMENTS IN 4 ENVIRONMENTS AND 2 CHEMICAL STRESSORS - Create an appropriate data frame with 1 entry per bcpID (rather than 1 entry per rep\*bcpID)” block to previous script
* Add comments to all blocks
* Move: “# Look at within well VS between well fitness differences!” to prev script in place where mydwcw is created
* Consider moving “# Look at within well VS between well fitness differences!” to the legacy file…
* Move to Legacy: # look at extinction pre-fit assay -- patterns are a little weaker here than if the post fit assay data are used.
  + We will use longitudinal data for this instead.
* Move to prep code: “# Calculate covariates for SALT (MOVE THIS BLOCK TO THE PREP FRAME EVENTUALLY)”
* Move to legacy code: “It is important to look at these data a few different ways, lets zoom in on the rug plot from the treatment effect violin plots above...”
  + “PLOT(S): SALT dw rank by barcode in 0.0, 0.4, 0.8, 1.2”
  + “PLOT(S): COPR dw rank by barcode in 0.0, 0.4, 0.8, 1.2”
* Move to legacy code:
  + “PLOT(S): 3d plots for targetted sets of 3 (and one set with all treats together for context!)” – salt
  + “PLOT(S): 3d plots for targetted sets of 3 (and one set with all treats together for context!)” – copr
* Move to new script: Increase, Decrease results – we may not present this stuff.
* Move to new script: all end matter, well data etc….

Changes to make to Analyze.Rmd – methods analysis script

* Figure out what to do with : “Analysis: Assess whether detected fitness change for barcodes in the 250-generation experiment is affected by barcode-cross contamination rate” block.
* Remove old power block
* Consider changes to new power block (pending discussion with JF) – which error to use for what.
* Consider removing multimodel averaging / inference blocks as they are not used and can be confusing.
* Remove outdated block : “Analysis: Assess effects of evoluitonary treatment on change in fitness in 250-generations of experimental evolution.”