

## **Reviewer Comments** (for ShirNat/qbio577\_fall2022)

[Blocks 3 & 4] Change: Delete the code that was commented out

[Blocks 5 - 8] Change: Use a line plot instead of a scatter plot, should be on a same canvas

[Blocks 9 - 12] Change: Combine blocks 9-12, no need to have multiple blocks

[Blocks 10 - 12] Change: Blocks are removed, the original pca plot is not correct (data should be transposed)

[Block 20] Comment: It is not possible to read legend if there are too many categories

[Blocks 25-31] Change: Removed codes that were commented out

[Block 44] Change: Clean up unnecessary outputs

[Block 46] Comment: Colors should be transparent (ATAC-seq is hard to see). Plotting a single sample for each group is not sufficient, because one sample from each group may not represent the whole group. For instance, if you look at the [Block 40], in Histone ChiP-seq, the experiment "ENCFF037ACM (purple)" has a different pattern compared to the other.

[Blocks 49-50] Suggestion: Cross correlation matrix might be another option to validate the consistency of patterns

[Blocks 51-53] Change: Removed codes that were commented out

[Block 54] Comment: It is hard to read a legend with 50+ items. Separate plots for different experiment targets or different cell types would be helpful to see proximities.

[Block 55] Comment: The comment for tip position has a typo in it which can cause problems in the downstream analysis (should be 3.95 instead of 0.95).

[Blocks 56-64 ] Comment: Blocks can be combined into one block, no necessary outputs.

[Blocks 76+] Comment: No outputs generated for the remaining blocks. The Jupyter Notebook should be saved after generating the output cells.

[Blocks 77 & 81] Comment: The input data for MDS must have been transformed first.