Data Analysis Based on Provided Example:

* all python scripts can be executed either via a standard python environment (IDLE, Sypder etc.) or via shell commands
* for details on usage and help, please type “python Supplementary\_script\_XXX.py –h”
* assuming the following data structure:

|- sample1\_demo.sam

|- sample2\_demo.sam

|- sample3\_demo.sam

|- sample4\_demo.sam

|- Supplementary\_script\_A\_demo.py

|- Supplementary\_script\_B\_demo.py

|- Supplementary\_script\_C\_demo.py

|- Supplementary\_script\_D\_demo.py

|- Supplementary\_script\_E\_demo.py

|- Supplementary\_script\_F\_demo.py

|- Supplementary\_script\_G\_demo.py

|- references\_yeast\_demo

|- Asite\_offset\_demo.txt

|- yeast\_genes\_demo.pkl

|- yeast\_introns\_demo.pkl

|- yeast\_sequence\_demo.pkl

|- yeast\_tRNA\_demo.pkl

* the example reference files contain information on transcripts/sequence/tRNA of yeast’s chromosome 1 only
* sample1-4\_demo.sam are Ssb1 selective and total translatome samples from Döring et al. 2017 containing only reads mapping to yeast’s chromosome 1
* set current working directory to: main folder containing demo samples and scripts
* command lines:
  + python Supplementary\_script\_A\_demo.py sample1\_demo.sam sample1
  + python Supplementary\_script\_A\_demo.py sample2\_demo.sam sample2
  + python Supplementary\_script\_A\_demo.py sample3\_demo.sam sample3
  + python Supplementary\_script\_A\_demo.py sample4\_demo.sam sample4
  + python Supplementary\_script\_B\_demo.py sample1
  + python Supplementary\_script\_B\_demo.py sample2
  + python Supplementary\_script\_B\_demo.py sample3
  + python Supplementary\_script\_B\_demo.py sample4
  + python Supplementary\_script\_C\_demo.py sample1
  + python Supplementary\_script\_C\_demo.py sample2
  + python Supplementary\_script\_C\_demo.py sample3
  + python Supplementary\_script\_C\_demo.py sample4
  + python Supplementary\_script\_D\_demo.py sample1 sample3 sample2 sample4 experiment1
  + python Supplementary\_script\_E\_demo.py sample1 sample3 sample2 sample4 experiment1
  + python Supplementary\_script\_F\_demo.py sample1 sample3 sample2 sample4 experiment1  
    expected output:   
    Start of binding detection script  
    2019-01-21 20:14:41  
    Reading of all input files finished   
    2019-01-21 20:15:53  
    Start of binding detection  
    2019-01-21 20:15:55  
    Included based on raw reads: 63 transcripts  
    Background too high: 5 transcripts  
    Correlation too low: 0 transcripts  
    Identified Strong Binders: 7 transcripts  
    Identified Binders: 0 transcripts  
    End of binding detection script  
    2019-01-21 20:15:55
  + python Supplementary\_script\_G\_demo.py sample1 sample3 sample2 sample4 experiment1
* the expected output files are provided