NIST Statistical Test Suite: An Introduction

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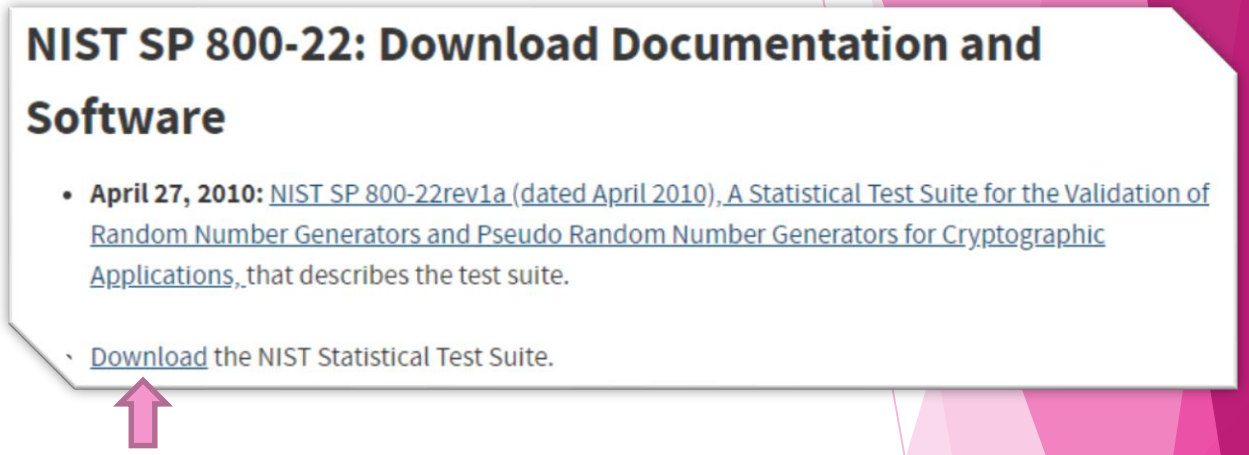
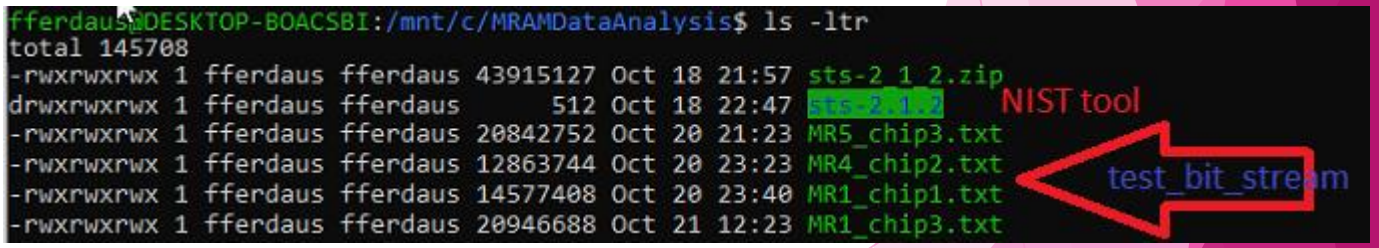
What is NIST STS?

- NIST Statistical Test Suite is an important testing suite for randomness analysis often used for formal certifications or approvals.
- For More detail visit:
  - https://csrc.nist.gov/publications/detail/sp/800-22/rev-1a/final (Manual guide by NIST)
  - https://crocs.fi.muni.cz/lib/exe/fetch.php?media=public:research:romjist_v11_for_publish.pdf (A short explanation of 15 NIST tests)

Download the NIST STS tool

- To download NIST STS tool visit:
  - https://csrc.nist.gov/Projects/Random-Bit-Generation/Documentation-and-Software
- Linux machine required
  - Tips: Use “Windows Subsystem for Linux” for windows 10 operating system (https://docs.microsoft.com/en-us/windows/wsl/install-win10)
- NOTE: Keep the unzipped version of the tool on the same folder (directory) where the test_bit_stream files are located.

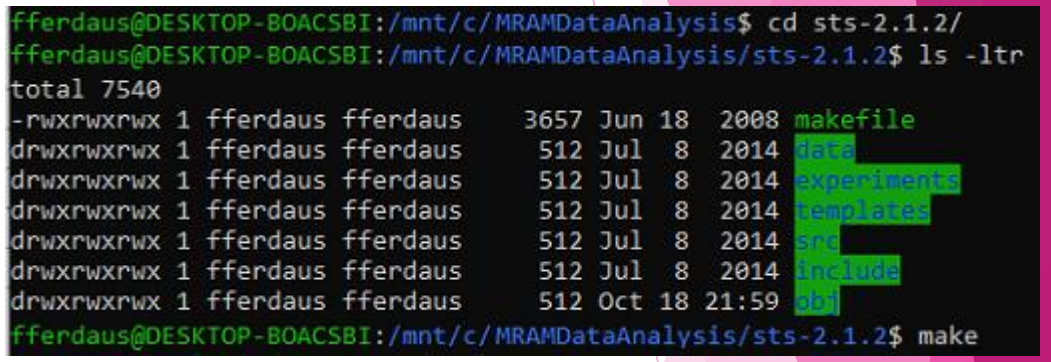




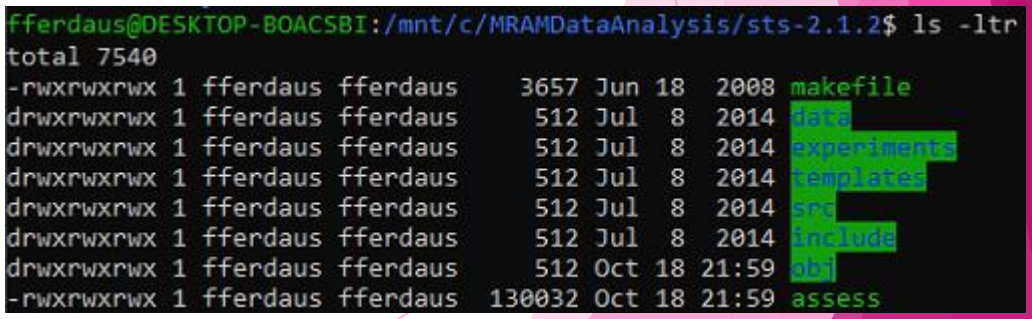
Install the NIST STS tool

- To install NIST STS tool go to the <sts-2.1.2> directory and type "***make***" to execute the ***makefile***.
  - *Might require to install make package:*

    ```
    sudo apt install make
    ```



- After successful installation, An executable file named ***assess*** should appear in the project directory.



Run the Test Code

- To invoke the NIST STS, type the following:
  - `./assess <sequenceLength>`
  - Min bit stream length (sequenceLength) should be 10^6.
- A series of menu prompts will be displayed in order to select the data to be analyzed and the statistical tests to be applied.

```
fferdaus@DESKTOP-BOACSBI:/mnt/c/MRAMDataAnalysis/sts-2.1.2$ wc ../MR1 chip1.txt
       0        1 14577408 ../MR1_chip1.txt
fferdaus@DESKTOP-BOACSBI:/mnt/c/MRAMDataAnalysis/sts-2.1.2$ ./assess 1041243
          G E N E R A T O R    S E L E C T I O N
          ---------------------------------------

   [0] Input File                 [1] Linear Congruential
   [2] Quadratic Congruential I   [3] Quadratic Congruential II
   [4] Cubic Congruential         [5] XOR
   [6] Modular Exponentiation     [7] Blum-Blum-Shub
   [8] Micali-Schnorr             [9] G Using SHA-1

  Enter Choice: 0


              User Prescribed Input File: ../MR1_chip1.txt
              S T A T I S T I C A L   T E S T S
              ---------------------------------

   [01] Frequency                       [02] Block Frequency
   [03] Cumulative Sums                 [04] Runs
   [05] Longest Run of Ones             [06] Rank
   [07] Discrete Fourier Transform      [08] Nonperiodic Template Matchings
   [09] Overlapping Template Matchings  [10] Universal Statistical
   [11] Approximate Entropy             [12] Random Excursions
   [13] Random Excursions Variant       [14] Serial
   [15] Linear Complexity

        INSTRUCTIONS
           Enter 0 if you DO NOT want to apply all of the
           statistical tests to each sequence and 1 if you DO.

  Enter Choice: 1
```

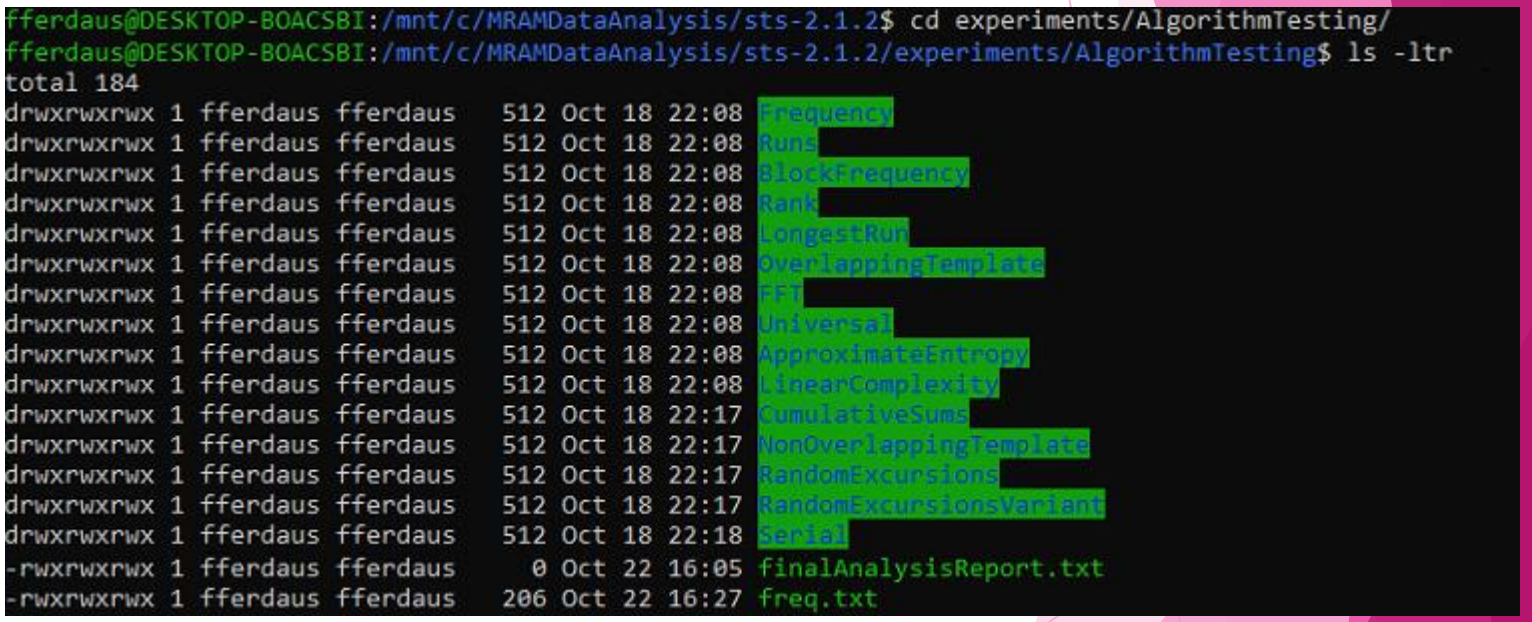
Run the Test Code

- Min number of bitstream sequence should be 10 to evaluate all tests.
  - Number of bits in the file must be ≥ (#bitstream × `sequenceLength`)
- The user must specify whether the file consists of bits stored in ASCII format (containing 0's and 1's) or binary format (packing 8-bit data in a single byte).

```
     P a r a m e t e r   A d j u s t m e n t s
     ----------------------------------------
 [1] Block Frequency Test - block length(M):         128
 [2] NonOverlapping Template Test - block length(m): 9
 [3] Overlapping Template Test - block length(m):    9
 [4] Approximate Entropy Test - block length(m):     10
 [5] Serial Test - block length(m):                  16
 [6] Linear Complexity Test - block length(M):       500

Select Test (0 to continue): 0

How many bitstreams? 14

Input File Format:
 [0] ASCII - A sequence of ASCII 0's and 1's
 [1] Binary - Each byte in data file contains 8 bits of data

Select input mode:  0

  Statistical Testing In Progress.........

  Statistical Testing Complete!!!!!!!!!!!!
```

Empirical results Location

- Once the testing process is complete, the empirical results can be found in the ***experiments/*** subdirectory.
- A file ***finalAnalysisReport.txt*** (summary report) will be generated when statistical testing is complete which is located at ***experiments/AlgorithmTesting/*** subdirectory.



Depiction of the Final Analysis Report

```
------------------------------------------------------------------------------
RESULTS FOR THE UNIFORMITY OF P-VALUES AND THE PROPORTION OF PASSING SEQUENCES
------------------------------------------------------------------------------
   generator is <../MR1_chip1.txt>
------------------------------------------------------------------------------
 C1  C2  C3  C4  C5  C6  C7  C8  C9 C10  P-VALUE  PROPORTION  STATISTICAL TEST
------------------------------------------------------------------------------
  0   0   2   0   1   1   1   3   3   3  0.066882     14/14       Frequency
  2   1   0   1   4   0   1   0   2   3  0.035174     14/14       BlockFrequency
  0   1   0   2   0   2   2   3   2   2  0.213309     14/14       CumulativeSums
  0   0   1   1   1   1   2   2   4   2  0.122325     14/14       CumulativeSums
  3   1   3   1   4   0   1   1   0   0  0.017912     14/14       Runs
  0   2   2   2   2   2   1   1   2   0  0.534146     14/14       LongestRun
  0   1   3   1   0   1   1   1   4   2  0.066882     14/14       Rank
  2   4   0   1   0   2   1   2   2   0  0.066882     14/14       FFT
  3   0   2   1   1   1   0   4   1   1  0.066882     14/14       NonOverlappingTemplate
  0   1   2   3   2   1   1   0   2   2  0.350485     14/14       NonOverlappingTemplate
  0   1   3   3   0   2   1   1   3   0  0.066882     14/14       NonOverlappingTemplate
  2   1   1   0   1   0   2   0   6   1  0.000439     14/14       NonOverlappingTemplate

  2   0   1   1   0   1   3   2   3   1  0.213309     14/14       NonOverlappingTemplate
  0   1   3   2   2   0   1   1   2   2  0.350485     14/14       NonOverlappingTemplate
  2   1   0   1   1   1   2   0   3   3  0.213309     14/14       OverlappingTemplate
  3   2   0   1   3   2   0   1   0   2  0.122325     13/14       Universal
  3   1   0   1   2   1   4   2   0   0  0.035174     13/14       ApproximateEntropy
  3   0   0   3   0   0   1   2   0   0      ----      8/9        RandomExcursions
  1   1   1   3   1   1   1   0   0   0      ----      9/9        RandomExcursions
  2   1   2   0   1   1   1   1   0   0      ----      9/9        RandomExcursions
```

Depiction of the Final Analysis Report

```
173    3   0   3   0   0   0   1   0   2   0      ----        9/9        RandomExcursions
174    1   1   1   1   0   2   0   0   2   1      ----        9/9        RandomExcursions
175    0   0   0   1   1   2   1   1   0   3      ----        9/9        RandomExcursionsVariant
176    0   0   1   0   0   2   2   0   0   4      ----        9/9        RandomExcursionsVariant

191    3   0   1   0   1   1   2   1   0   0      ----        9/9        RandomExcursionsVariant
192    3   0   0   3   0   2   0   1   0   0      ----        9/9        RandomExcursionsVariant
193    2   2   3   2   1   0   1   0   2   1  0.350485      13/14       Serial
194    2   1   0   2   4   1   0   1   2   1  0.122325      14/14       Serial
195    0   3   2   1   2   3   2   0   1   0  0.122325      14/14       LinearComplexity
196
197
198  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
199  The minimum pass rate for each statistical test with the exception of the
200  random excursion (variant) test is approximately = 12 for a
201  sample size = 14 binary sequences.
202
203  The minimum pass rate for the random excursion (variant) test
204  is approximately = 8 for a sample size = 9 binary sequences.
205
206  For further guidelines construct a probability table using the MAPLE program
207  provided in the addendum section of the documentation.
208  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
209
```