**MIPS64 Programming Project**
**Introduction:**

The DNA in our human body is composed of 4 nucleobases (i.e., the alphabet of DNA). These are adenine(A), cytosine(C), guanine(G) and thymine(T). Thus, we can view our DNA as a string composed of the "alphabets" A,C,G and T.

In computational biology, the reference DNA string is stored as suffix array in the filter-verification framework due to improvement in space requirement as compared to suffix trees.

Suffix array is defined as an array of integers containing the starting position of suffixes of an DNA string *T* in lexicographical order.

Example: T = TGCA$

| I | 0 | 1 | 2 | 3 | 4 |
|------|---|---|---|---|---|
| *T*[i] | T | G | C | A | $ |

| Suffixes | i |
|----------|---|
| TGCA$ | 0 |
| GCA$ | 1 |
| CA$ | 2 |
| A$ | 3 |
| $ | 4 |

Sorted lexicographically:

| Suffixes | i |
|----------|---|
| $ | 4 |
| A$ | 3 |
| CA$ | 2 |
| GCA$ | 1 |
| TGCA$ | 0 |

Suffix array (A):

| I | 0 | 1 | 2 | 3 | 4 |
|------|---|---|---|---|---|
| *T*[i] | 4 | 3 | 2 | 1 | 0 |

**Objective**:
Obtain the equivalent suffix array of a DNA string using both **EDUMIPS64 and MIPSers** simulation program.

**Given**: A DNA string with length of at most 40 DNA alphabets. Assume that the string is already declared in memory location DNA.
**Output**: Suffix array stored in memory location ARR

**Software**: (1) **EDUMIPS64 ver 1.2.3 (available at CANVAS)**
  **(2) MIPSers  (available at CANVAS)**

**Documentation via Google form**

**Submission: November 20, 2017 (Monday).  Upload source code for both to CANVAS**
**Filename: Grp?M.txt (for MIPSers) and Grp?E.txt (for EDUMIPS)**