**Benchmarking Results**

* **Simple Test (A…)**
  + A file containing 100000 A’s
    - **Input: 100000 bytes**
  + DNAHuffman: **5 bytes**
  + Gzip: **142 bytes**
  + Rar: **145 bytes**
  + Zip: **266 bytes**
* **Simple Test (A…C…G…T…)**
  + A file containing 1000 A’s, then 1000 C’s, then 1000 G’s, then 1000 T’s
    - **Input: 400 bytes**
  + DnaHuffman: **20 bytes**
  + Gzip: **57 bytes**
  + Rar: **109 bytes**
  + Zip: **179 bytes**
* **Random Strings (0.25 A, 0.25 C, 0.25 G, 0.25 T)**
  + Generated 10 test files (each of length 100000) where I sampled from a uniform distribution of probability 0.25 for each of the 4 nucleotides (results below are averaged)
    - **Input: 100000 bytes**
  + DnaHuffman: **25005 bytes**
  + Gzip: **29621.4 bytes**
  + Rar: **30084.8 bytes**
  + Zip: **29871.8 bytes**
* **hg19 chr1 (no N)**
  + The chr1 sequence from hg19, but with ‘N’ removed and everything made upper-case
    - **Input: 62050 bytes**
  + DnaHuffman: **15351 bytes**
  + Gzip: **17830 bytes**
  + Rar: **17743 bytes**
  + Zip: **17874 bytes**