The **Human Genome Project** was a landmark 13 year project to map the human DNA. The project made it possible for many advances in medicine. It is also useful for other fields, such as agriculture and anthropology.

The basic process used was to extract the DNA from the cells of a person. Unfortunately, the whole DNA can’t be extracted in one piece. It is usually broken up into a very large number of small pieces. The small pieces are processed in a sequencer machine capable of detecting the strand of molecules. The result of processing one strand then is a sequence of letters describing the type and order of molecules in the strand. The strands only contain four bases: adenine (A), guanine (G), cytosine (C), and thymine (T). So, strands are represented by a text string containing the letters AGCT.

In order to recreate the order of the full DNA strand, these pieces must be stitched together in the correct order. To do this, the ends of two incomplete DNA strands are compared to see if they match when overlapped. If so, it is possible that these DNA strands are two pieces of a larger whole. The strands are matched and merged repeatedly until the full DNA string is reproduced.

Here is an example of two DNA strands that match when overlapped:

| Strand 1: | AC GGACA TAGTCATT |
| Strand 2: | CATAGTCATT TCATG |
| Combined: | AC GGACA TAGTCATT | CATAGTCATT |

**Assignment**

In this step of the assignment, you will create a class that represents the DNA strand. It will be capable of storing any size of string (using the heap), checking for overlap with other strands, and merging two strands together. You will also create a program that tests your class.

**Requirements**

- The class must be declared in [Strand.h](#) and implemented in [Strand.cpp](#).
- A class **Strand** must use heap memory. May not use `std::string`, `std::vector`, or any other STL or third party storage containers.
- **Strand** must have a default constructor, a copy constructor, a destructor, and an assignment operator.
- **Strand** must have a constructor with this signature: `Strand(const char * src);`
- **Strand** accessor methods must not allow contents to be modified by external code.
- **Strand** must have a method `size_t size() const` that returns the number of bases stored in the strand.
- **Strand** must have no memory errors. This includes leaks, double deletes, writing to deleted memory, bad pointer access, etc.
- **Strand** must overload the operators: `strand + strand` and `strand += strand`. The first results in a new object whose value is the concatenation of the two inputs. The second results in the lhs operand’s value being modified by concatenating the rhs operand’s value.
- **Strand** must overload the operators: `strand == strand` and `strand < strand`. An ASCIIbetical comparison is expected.
- **Strand** must have a method `Strand substrand(size_t i, size_t j) const` that returns a copy of the strand that starts at position `i` and ends at position `j - 1`. Think “Python slice.”
- **Strand** must have a method `Strand merge(size_t i, const Strand &right) const`. This method makes a new strand that is the concatenation of a copy of the current strand object up to position `i - 1`, and all of the `right` strand.
- **Strand** must have a method `size_t overlap(const Strand &right) const`. This method finds the first position in the current strand object such that the rest of the current strand completely matches the first of the `right` strand. If there is no overlap between the two strands, then this method will return a value that is greater than or equal to the size of the current strand.
- **Strand** can have more methods as you deem useful in implementing the required methods.
- A unit test program must be created. This program will have at least one function per method of the **Strand** class. Each function will then fully exercise at least one of the **Strand** methods. In making unit tests, you should check for all interesting input conditions possible. For example, the test of overlap should test cases with complete overlap, no overlap, lots of overlap, very little overlap, and medium size overlap.
- A [Makefile](#) must be provided for this assignment. At minimum, it must have a target `unittest` that will...
be sure your unit test program is built correctly, and then run `valgrind` on your unit test program.

**Show Off Your Work**

To receive credit for this assignment, you must upload the source code (.h and .cpp files) and the Makefile to the CIT submission system linked at the top of the page.

Additionally, the programs must build and run. In addition to your unit tests, your `Strand` class will be tested by a grading unit test. Any incorrect performance or memory errors will be counted against the assignment score.