# Assignment 1

A pseudo-DNA molecule consists of two chains. Each chain, called the $\alpha$ or the $\beta$ chain, consists of a sequence of A, G, C or T-molecules. Across chains, an A-molecule can link only with a T-molecule and a C-molecule can only link with a G-molecule. A/T/C/G molecules will be called nucleotide molecules. An example pseudo-DNA molecule therefore is:

```
alpha C-C-T-C-T-T-C-T
      | | | | | | | |
beta  G-G-A-G-A-A-G-A
```

A DNA chain splits into two as follows:

```
alpha C-C-T-C-T-T-C-T
      | | | | | | | |
                <-G-A
                <-C-T
      | | | | | | | |
beta  G-G-A-G-A-A-G-A
```

Note that splits yield several pseudo-DNA molecules, all of which need to be uniquely identified. Implement in C a pseudo-DNA data structure, that has at least two types of links: within a chain, and across the chain, as shown above. Implement the following operations on the data structure:

- insert(DNA Molecule Id, Chain Id, Nucleotide, Position): insert the given nucleotide molecule at the given position in the specified chain of the specified pseudo-DNA molecule. Note that you also have to insert the corresponding nucleotide in the other chain of the same pseudo-DNA molecule.

- delete(DNA Molecule Id, Position): Delete whatever nucleotide molecule pairs exist at the given position in the specified pseudo-DNA molecule.

- Split(DNA Molecule Id): Split the DNA molecule as described above. This will result in two chains.

- PrintChain(DNA Molecule Id) and PrintAllChains() (Self explanatory).