

Data Structures and Laboratory, Fall 2014, 2nd Homework

`coupleDna` function must have five arguments that represent five RNA chains of length ten. Only two of these five RNA chains can fit together to form an adequate DNA chain. `coupleDna` function must seek for these two pairs, and after determining the fitting two RNA chains, must merge these two RNA chains to form a DNA chain. The output of the `coupleDna` function must be the DNA chain.

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- It is assumed that there are at most and at least two matching RNA chains appear among the five.
 - It is not important in which order they appear.
 - Both the DNA chain and the RNA chains in your program must use the same linked-list structure to store the genetic data.
 - Each linked-list node must store a string. The length of the string can be either one, or two.
 - If the length of the strings in each node of the linked-list is one, then the linked-list represents a RNA chain and the strings can include only one of the four letters: **A, T, G** or **C**.
 - If the length of the strings in each node of the linked-list is two, then the linked-list represents a DNA chain and the string can be any of the following four combinations: **AT, TA, GC, CG**.
 - Use capital letters to represent nucleic acids.
 - In the beginning of your program, you must call a function to print the given five RNS chains to the screen. The name of the function is `printRnas`.
 - In the end of your program, you must print the resulting DNA chain with a function named `printDna`.
 - For the sake of simplicity, all RNA chains', so the resulting DNA's length is 10.
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Code snippet to test:

```
// You may initialize linked-lists any way you like. Here, it is assumed here that
// you have written an initRna function to easily initialize RNA chains.
linkedList *rna1 = initRna("ATGATGATGC");
linkedList *rna2 = initRna("TCGCGCTAGC");
linkedList *rna3 = initRna("CGTCGTAAAC");
linkedList *rna4 = initRna("TATTTACGAA");
linkedList *rna5 = initRna("TACTACTACG");

printRnas(rna1, rna2, rna3, rna4, rna5);
linkedList *dna = coupleDna(rna1, rna2, rna3, rna4, rna5);
printDna(dna);
```

Sample run:

```
> ./a.out
>1: A T G A T G A T G C
>2: T C G C G C T A G C
>3: C G T C G T A A A C
>4: T A T T T A C G A A
>5: T A C T A C T A C G
>
>AT TA GC AT TA GC AT TA GC CG
```