**Program core: the spliceosome**

In real life, an enzyme complex that processes the pre-mRNA to mature RNA by cutting out the introns.

In this program, it is a function the takes the first sequences of the FASTA file as the pre-mRNA, and all following as the introns.

* taking the introns one by one, it then splits the sequence in the part before the intron, and the part behind it.
* those two parts are joined into one string again
* the process is then repeated for all following introns on the shortened sequence from the previous round
* for the translation of the final "mature mRNA", a dictionary that has the codons as the keys can be used, e.g. "ATG": M (methionine, the start codon).

**Pseudo code**

function spiceosome on pre-mRNA + list of introns:

**looping over all introns:**

**find start position of intron**

**find length of said intron**

**sequence before = pre-mRNA[0:start of intron]**

**sequence after = pre-mRNA[start of intron + length of intron : end of sequence]**

**join sequence before & sequence after**

return final assembled sequence

**Any advanced information**

In the setting of the problem, the sequences are give as DNA. To convert into RNA, replace the Ts with U (for uracil). Also the sugar backbone is different, but this doesn't influence the sequence analysis.