The data that you have can be roughly summarized as follows:

1. When a biologist gives a sequence of nucleotide bases (the encrypted message) from the left column of the table, out comes one of the corresponding strings of amino-acids from the right column (the decrypted message). For example, *UCUCUC..*, translates into *ser-leu-ser-leu...* etc.
2. Which of the possible amino-acid chains you get depends on where the ribosome starts reading the encrypted message
3. You know (with the benefit of hindsight that the original scientists didn't have) that
   - several different nucleotide sequences can code the same amino-acid
   - some sequences of nucleotides mean "stop the translation"
   - there are 20 amino-acids

Your tasks are:

1. To answer why the following coding schemes are incompatible with the data (including number of amino-acids and the date in the table):
   - coding with doublets
   - coding with non-overlaping quadruplets
   - coding with overlaping triplets
2. To make a table of converting from triplets of nucleotides (codons) to either amino-acids or "stop-signals"