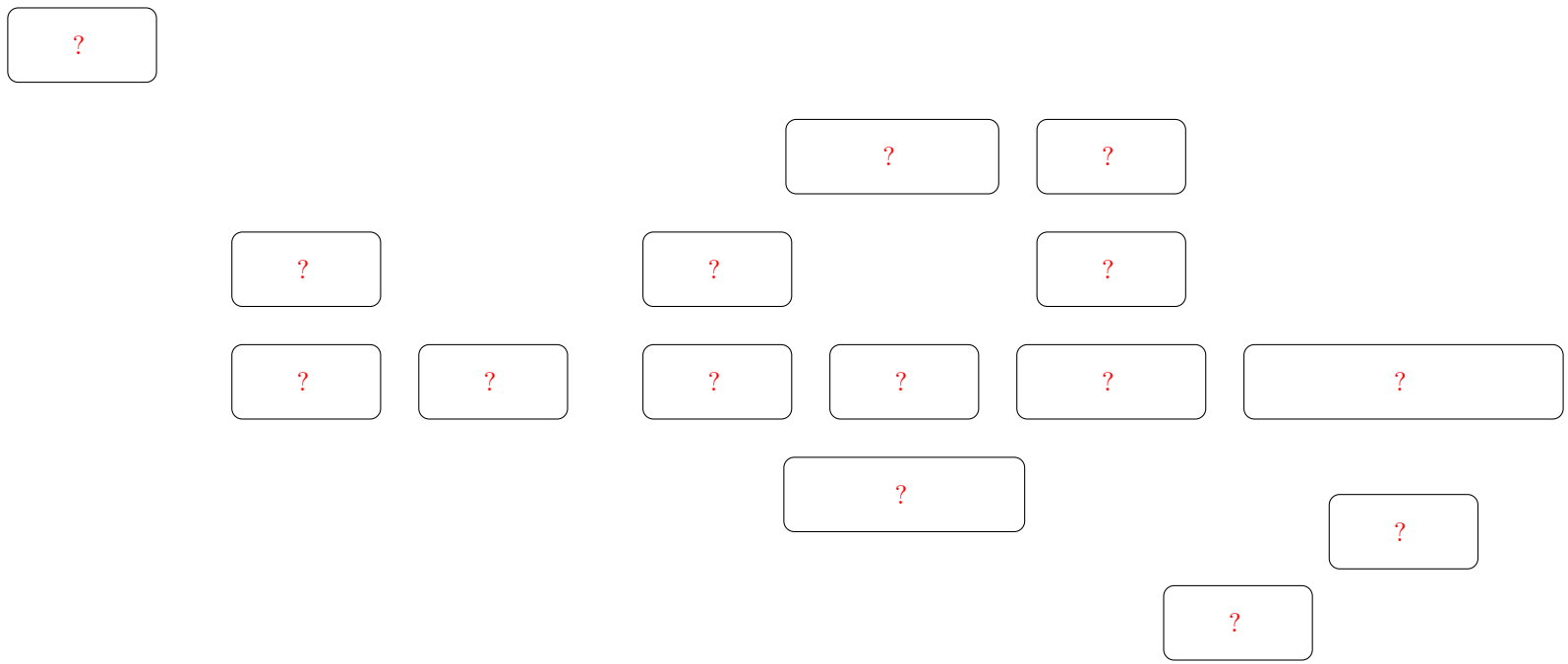
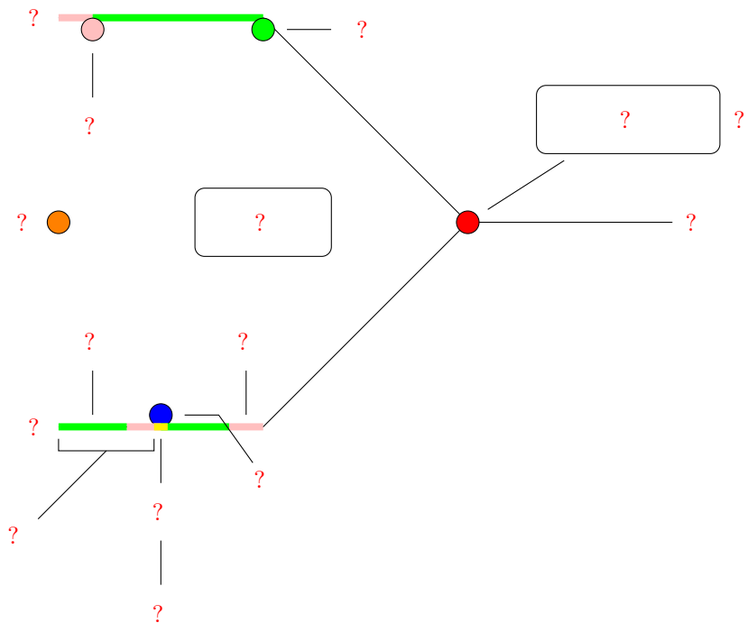
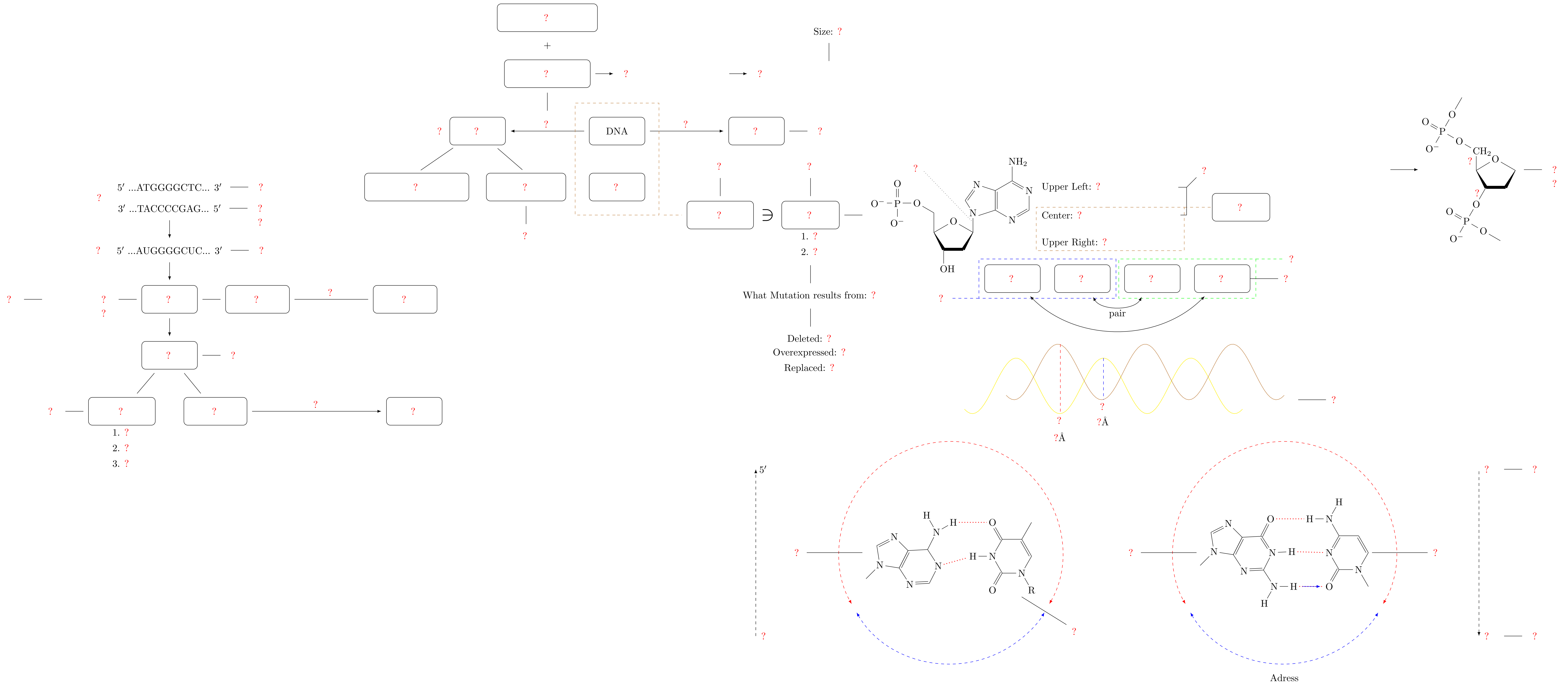
Memory



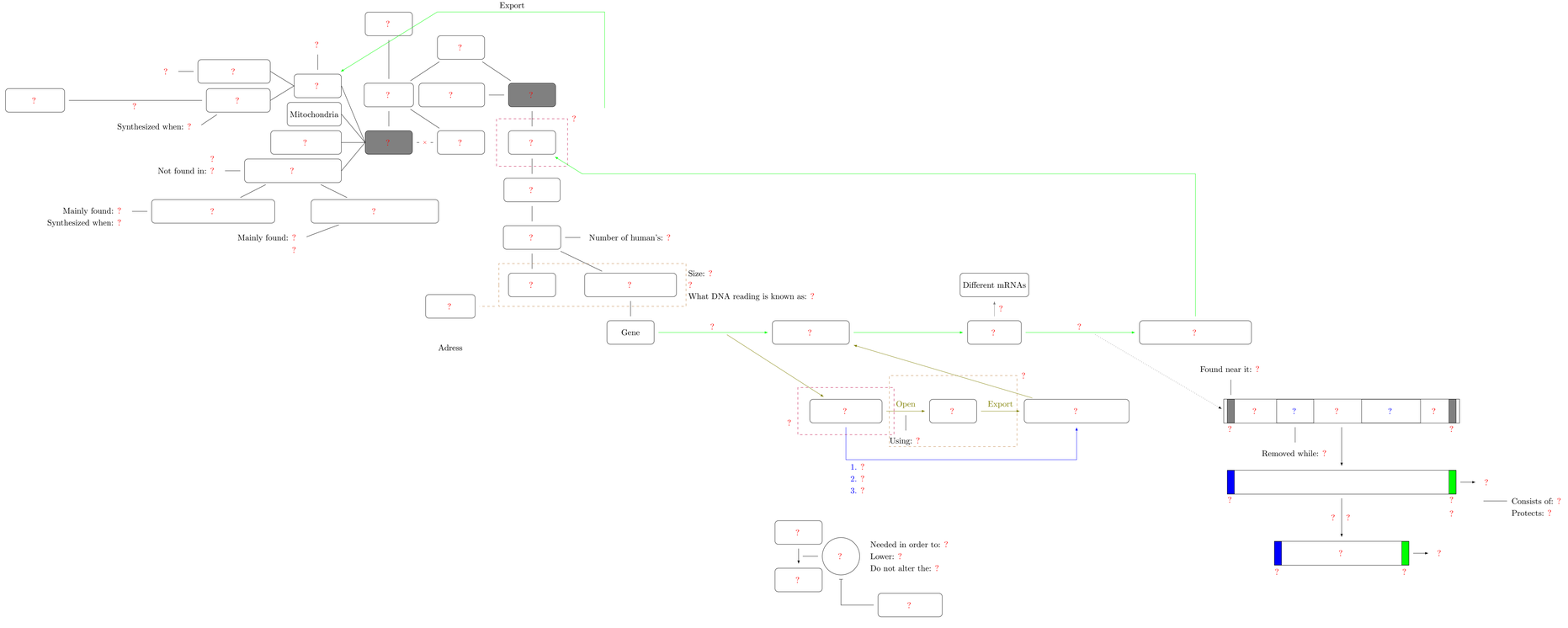
DNA Replication



Transcription



Soma


Export
?
Mitochondria
Synthesized when: ?
Not found in: ?
Mainly found: ?
Synthesized when: ?
Mainly found: ?
Number of human's: ?
Size: ?
What DNA reading is known as: ?
Adress
Gene
Different mRNAs
Open
Export
Using: ?
1. ?
2. ?
3. ?
Found near it: ?
Removed while: ?
Consists of: ?
Protects: ?
Needed in order to: ?
Lower: ?
Do not alter the: ?

Why a Triplet Code?

Prior to understanding the details of transcription and translation, geneticists predicted that DNA could encode amino acids only if a code of at least three nucleotides was used. The logic is that the nucleotide code must be able to specify the placement of 20 amino acids. Since there are only four nucleotides, a code of single nucleotides would only represent four amino acids, such that A, C, G and U could be translated to encode amino acids. A doublet code could code for 16 amino acids (4 x 4). A triplet code could make a genetic code for 64 different combinations (4 X 4 X 4) genetic code and provide plenty of information in the DNA molecule to specify the placement of all 20 amino acids. When experiments were performed to crack the genetic code it was found to be a code that was triplet. These three letter codes of nucleotides (AUG, AAA, etc.) are called codons.
The genetic code only needed to be cracked once because it is universal (with some rare exceptions). That means all organisms use the same codons to specify the placement of each of the 20 amino acids in protein formation. A codon table can therefore be constructed and any coding region of nucleotides read to determine the amino acid sequence of the protein encoded. A look at the genetic code in the codon table below reveals that the code is redundant meaning many of the amino acids can be coded by four or six possible codons. The amino acid sequence of proteins from all types of organisms is usually determined by sequencing the gene that encodes the protein and then reading the genetic code from the DNA sequence.

src: `https://passel2.unl.edu/view/lesson/3ccee8500ac8/6`

tRNA

While the specific nucleotide sequence of an mRNA specifies which amino acids are incorporated into the protein product of the gene from which the mRNA is transcribed, the role of tRNA is to specify which sequence from the genetic code corresponds to which amino acid. The mRNA encodes a protein as a series of contiguous codons, each of which is recognized by a particular tRNA. One end of the tRNA matches the genetic code in a three-nucleotide sequence called the anticodon. The anticodon forms three complementary base pairs with a codon in mRNA during protein biosynthesis.

On the other end of the tRNA is a covalent attachment to the amino acid that corresponds to the anticodon sequence. Each type of tRNA molecule can be attached to only one type of amino acid, so each organism has many types of tRNA. Because the genetic code contains multiple codons that specify the same amino acid, there are several tRNA molecules bearing different anticodons which carry the same amino acid.

The covalent attachment to the tRNA $3'$ end is catalysed by enzymes called aminoacyl tRNA synthetases. During protein synthesis, tRNAs with attached amino acids are delivered to the ribosome by proteins called elongation factors, which aid in association of the tRNA with the ribosome, synthesis of the new polypeptide, and translocation (movement) of the ribosome along the mRNA. If the tRNA's anticodon matches the mRNA, another tRNA already bound to the ribosome transfers the growing polypeptide chain from its $3'$ end to the amino acid attached to the $3'$ end of the newly delivered tRNA, a reaction catalysed by the ribosome. A large number of the individual nucleotides in a tRNA molecule may be chemically modified, often by methylation or deamidation. These unusual bases sometimes affect the tRNA's interaction with ribosomes and sometimes occur in the anticodon to alter base-pairing properties.

src: `https://en.wikipedia.org/wiki/Transfer_RNA`

rRNA

Universally conserved secondary structural elements in rRNA among different species show that these sequences are some of the oldest discovered. They serve critical roles in forming the catalytic sites of translation of mRNA. During translation of mRNA, rRNA functions to bind both mRNA and tRNA to facilitate the process of translating mRNA's codon sequence into amino acids. rRNA initiates the catalysis of protein synthesis when tRNA is sandwiched between the SSU and LSU. In the SSU, the mRNA interacts with the anticodons of the tRNA. In the LSU, the amino acid acceptor stem of the tRNA interacts with the LSU rRNA. The ribosome catalyzes ester-amide exchange, transferring the C-terminus of a nascent peptide from a tRNA to the amine of an amino acid. These processes are able to occur due to sites within the ribosome in which these molecules can bind, formed by the rRNA stem-loops. A ribosome has three of these binding sites called the A, P and E sites:

- In general, the A (aminoacyl) site contains an aminoacyl-tRNA (a tRNA esterified to an amino acid on the 3' end).
- The P (peptidyl) site contains a tRNA esterified to the nascent peptide. The free amino (NH2) group of the A site tRNA attacks the ester linkage of P site tRNA, causing transfer of the nascent peptide to the amino acid in the A site. This reaction is takes place in the peptidyl transferase center
- The E (exit) site contains a tRNA that has been discharged, with a free 3' end (with no amino acid or nascent peptide).

A single mRNA can be translated simultaneously by multiple ribosomes. This is called a polysome.

In prokaryotes, much work has been done to further identify the importance of rRNA in translation of mRNA. For example, it has been found that the A site consists primarily of 16S rRNA. Apart from various protein elements that interact with tRNA at this site, it is hypothesized that if these proteins were removed without altering ribosomal structure, the site would continue to function normally. In the P site, through the observation of crystal structures it has been shown the 3' end of 16s rRNA can fold into the site as if a molecule of mRNA. This results in intermolecular interactions that stabilize the subunits. Similarly, like the A site, the P site primarily contains rRNA with few proteins. The peptidyl transferase center, for example, is formed by nucleotides from the 23S rRNA subunit. In fact, studies have shown that the peptidyl transferase center contains no proteins, and is entirely initiated by the presence of rRNA. Unlike the A and P sites, the E site contains more proteins. Because proteins are not essential for the functioning of the A and P sites, the E site molecular composition shows that it is perhaps evolved later. In primitive ribosomes, it is likely that tRNAs exited from the P site. Additionally, it has been shown that E-site tRNA bind with both the 16S and 23S rRNA subunits.

Behavior Mechanism