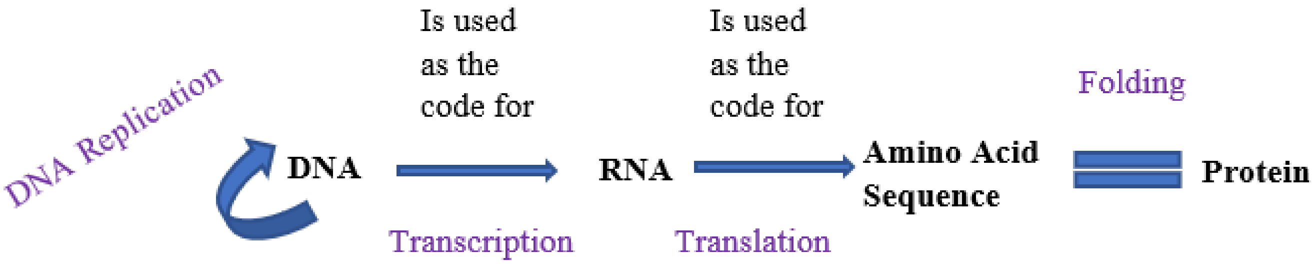
The Central Dogma of Biology

DNA acts as a blueprint for what a living organism will look like, what it will make, and how it will function. DNA is relatively stable. Genes are encoded in DNA as long sequences of nucleotides (A, T, C, and G). DNA exists in almost every living cell; very few exceptions exist such as mature red blood cells which do not have a nucleus. DNA gets replicated as cells grow and divide and transcribed and translated every time a gene is expressed. Every time a gene is expressed, a protein is made. A phenotype is an observable or measurable description of proteins. Different phenotypes are a different expression of genes. A different phenotype could be a different protein, or a different amount of the same protein being made.

The central dogma of biology explains how DNA is related to mRNA and proteins. While DNA holds the information for how life can function, DNA itself is not used directly for making of proteins. Rather, an mRNA transcript is made that is complementary to DNA. This RNA can then be used in the process of translation to make an amino acid sequence which can fold into a functional protein. Below is a simple diagram showing the relationship between DNA, RNA, and amino acid sequences.



DNA Replication:

DNA replication is the process of making a copy of DNA from an old copy. DNA replication occurs in a semi-conservative fashion meaning that for one full strand DNA, a new full strand of DNA is produced. This results in two double stranded DNA pieces where each one is composed of one new strand and one old strand.

A newly synthesized daughter strand is complementary and antiparallel to the old strand of DNA. To replicate DNA, first the double stranded DNA is opened up so its bases are revealed. Then, the old strand of DNA is read from its 3’ end to its 5’ end and new bases are recruited that are complementary to it. Adenine is paired with thymine and guanine is paired with cytosine as per Chargaff’s rule. The way the base is aligned when it is added to the new strand results in the new strand being built from its 5’ end to its 3’ end.

Both strands of the old DNA will undergo replication. The old strand is called a template strand when compared to the new strand that is created called a daughter strand. The title of template strand is a respective term. This title just means the specific strand is the one used for DNA replication for a specific daughter. Both strands can serve as a template strand, but only one is used as a template for each new daughter strand. While this can feel confusing at first, it can be helpful to think about this in terms of common everyday example. A child may call their own mother “Mom”. This title represents their relationship. This woman may not be “Mom” to someone else but instead they may be “Aunt” or “sister” or even be a stranger. A DNA template strand is only a template for the a specific daughter strand.

Transcription:

Transcription is the process of making RNA from DNA. The process of transcription is similar to but not the same as that of DNA replication. RNA is composed of the nucleotides adenine, guanine, cytosine, and uracil and exists as a single strand. RNA will be made by reading a DNA template strand from its 3’ end to its 5’ end and recruiting new bases. Adenine is paired with uracil and guanine is paired with cytosine. The RNA transcript will be antiparallel to the template strand meaning that the orientation of the bases results in the RNA being made in a 5’ to 3’ direction.

Eukaryotes store their DNA in a nucleus so the process of transcription must take place in the nucleus. After transcription occurs, the RNA can leave the nucleus. Prokaryotes do not have a nucleus and DNA floats freely in the cytoplasm, so transcription occurs in the cytoplasm. Another difference between prokaryotes and eukaryotes is what happens after the RNA is created.

RNA is transcribed directly from DNA. A prokaryote can use RNA as it is being transcribed to make a protein, but eukaryotes cannot. A eukaryote must complete post-transcriptional modifications to mRNA that is made such as adding guanine caps on the 5’ end and a poly-A tail composed of many adenines on the 3’ end. Splicing also must be completed before a mature mRNA transcript is made and then can be used in translation.

Translation:

Translation is the process of using mRNA to recruit amino acids to make a polypeptide chain. With the help of a ribosome, mRNA is read in the 5’ to 3’ direction starting at a start codon, AUG. A tRNA that is complementary to the start codon caries a methionine amino acid that will begin the polypeptide. New tRNA molecules float by and check if they are complementary to the next three bases (the next codon). If they are, they attach the amino acid they carry to the growing polypeptide chain. New tRNA molecules check the rest of the mRNA three bases at a time and the chain grows until a stop codon is reached and translation is terminated.

As the polypeptide is being made, it begins to fold. The shape is determined by the specific sequence of amino acids and their attraction to each other and aversion to the environment they are in. The types of folding that occur are categorized into four levels. Every level builds on itself. For instance, a protein with a tertiary structure has primary and secondary structures but also has tertiary level of folds as well.

Primary structure is a linear sequence of amino acids. It is rare to find a protein with just primary structure in nature. Secondary structure has alpha coils and beta pleated sheets as folds. These structures are held together by hydrogen bonds. Tertiary structure is more complex and involves many different types of folds and many bonds such as disulfide bonds, dipole-dipole interactions, and London dispersion forces, and even a multitude of ionic bonds. Primary, secondary, and tertiary structures all are composed of one strand of amino acids bound together. Quaternary structure is when multiple polypeptide chains are attracted to each other and fold with each other. Each of these polypeptide chains will be made independently from each other in translation and they may be similar or completely different sequences. The folding of the protein brings about its function in the body.

Learning Objectives:

- Understand and be able to describe the central dogma of biology as a foundational relationship for genetics.
- Understand how genes, alleles, and phenotype are all related to DNA, RNA, and proteins.
- Memorize and be able to draw and explain the process of DNA replication, transcription, and translation as well as be able to identify proteins and organelles involved in each.
- Be able to predict the sequence of a daughter strand of DNA given a template or coding strand of DNA.
- Be able to predict the sequence of mRNA given either strand of DNA, a sequence of tRNAs, or a polypeptide.
- Be able to predict the sequence of amino acids given DNA strand(s) or a RNA strand.
- Correctly deduce the result of absent or mutated machinery in DNA replication, transcription, or translation for prokaryotes and eukaryotes.
- Correctly compare and contrast DNA replication, transcription, and translation together as well as between prokaryotes and eukaryotes.

Order of Activities:

1. Review how DNA, RNA, and proteins are related by watching the following short video. https://youtu.be/gG7uCskUOrA
2. Review the steps of DNA replication using your notes, then watch this video to visualize the process. https://www.youtube.com/watch?v=TNKWgcFPHqw
3. Review the steps of transcription in both prokaryotes and eukaryotes using your notes, then watch this video to visualize the process https://youtu.be/vLz2A1cjPH8
4. Review the steps of translation in both prokaryotes and eukaryotes using your notes, then watch this video to visualize the process. https://www.youtube.com/watch?v=TfYf_rPWUdY
5. Open the corresponding worksheet for this material and complete the DNA replication, transcription, and translation note tables without using your notes to test your knowledge. Then, use your notes to change or add anything you need to make this a study review tool complete with all of the information about each process you need. Once you have completed this, move on to the application portion of the worksheet.
6. Discuss what you wrote with a partner or group if possible before checking your work using the answer key provided. This answer key provides information that will act as a foundation for other topics in genetics. While there is more information about the central dogma of biology, make sure you understand at least the information provided in the key.
7. After reviewing any topic, it is a good idea to have a metacognition check. Ask yourself the following questions:

    - What are my emotional responses to learning this material? Which material am I frustrated with and need aid in understanding?
    - What difficulties have I had with the learning tasks? What specific tasks will I do to master this content?
    - Do I understand all of the learning goals? Can I explain each of them out loud to someone clearly and concisely?
    - How is what I learned related to other things I have learned in this class? How is it related to other classes, my career, and my life?
8. Closing: Think about how splicing and alternative splicing are related to the central dogma of biology. Review these topics as needed to understand the entire process of gene expression.
9. If you would like to have more aid in learning this material, please reach out. There are numerous individuals who want to help you feel confident in your understanding. If your course has learning assistants or teaching assistant(s), you should reach out to them to review concepts you want to learn more about. Your professor is also a great resource to go to when you do not understand a topic. You can study with your peers or receive academic support through the LRC as well. If you would like help identifying how to receive the support you need, do not hesitate to contact the CU Denver Learning Resources Center at LRC@ucdenver.edu or stop by our front desk in the learning commons building.