Biology 1002B Cycle 2: Molecular Evolution Breakdown

Introduction

Dear Student,

Thank you for opening this cycle breakdown for Bio 1002B. This resource has been created by the Education Team at WebStraw. The Education Team consists of students that have previously taken and/or students that are currently taking Bio 1002B.

Purpose

This resource focuses on key concepts that are important for students to understand to succeed within this course. This resource was created by students for other students. Our goal is to help students (1) further develop their understanding of course content and (2) achieve greater academic success. (3) Our resource is also open access meaning there are no financial or legal barriers to students who wish to access and use our resource.

Instructions

To maximize the benefits of this resource, we recommend that you read carefully through the cycle breakdown with specific focus on bolded terms and the “Think about it” paragraphs. Then, try applying your knowledge with some of our custom-made questions at the end of this document. Make sure you already have a good understanding of course content before using this resource, as it will not cover ALL testable content!

Disclaimer

This resource is supplementary to your course content and is not meant to (1) replace any of the resources provided to you by your instructor nor is it meant to (2) be used as a tool to learn the course material from scratch. We assume that students who use this resource will have a basic understanding of the course content. This resource does not contain everything you need to know for your evaluations. Please refer to the course material provided by your instructors if there are any discrepancies between our resource and your course content.

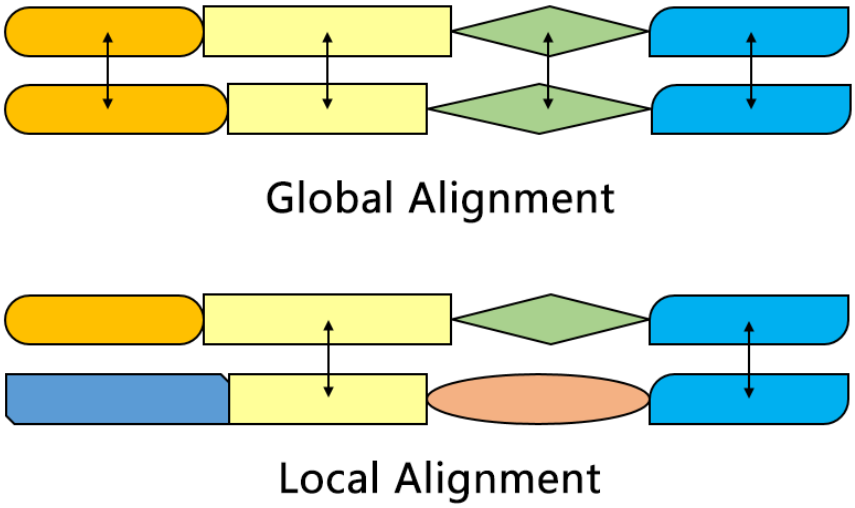
We wish you the best of luck on your exams!

- The WebStraw Team

Note to Instructors:
If this resource has been created for your course and you would like to collaborate with us, please email us at team@webstraw.ca

Sequence Alignments

A **sequence alignment** is a method of arranging sequences of genes or polypeptides to identify regions of similarity.
Global alignments attempt to align two sequences by starting at one end and moving in a linear fashion to the other. If the sizes of the two query sequences are different, many gaps in the alignment will occur.
Local alignments look for regions with identical bases and build the sequence alignments from there. Local alignments are preferable because they are less time consuming and are suitable for aligning more divergent or distantly-related sequences. Most algorithms are based on local alignments when comparing a sequence to a database.



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BLAST

BLAST (Basic Local Alignment Search Tool) is an algorithm that uses local alignments to compare a query sequence to the NCBI database.

BLAST will assign a **max score (BLAST score)** that indicates the level of similarity between the query sequence and sequences in the database. Higher BLAST scores indicate a higher similarity between the sequences.

BLAST also assigns an **E-value**, which is the likelihood that the two sequences evolved independently of each other and became similar due to chance.

Think about it; if the BLAST score between two sequences is very high, is it more plausible to assume that the sequences arose from two completely separate phylogenetic lineages or that they arose from the same common ancestor?
If there is high similarity between two gene or protein sequences, we assume that the sequences arose from the same common ancestor because that is more likely. Typically, high BLAST scores predict very low E-values and E-values decrease as the BLAST score increases. We use E-values to determine homology between two gene sequences. In general, if the E-value < 0.00001, the sequences are considered homologous.

Mutations Associated With Evolution

Mutations to DNA can be **synonymous** (silent) or **non-synonymous** (affecting the amino acid sequence of the protein). Examples of non-synonymous mutations include **missense** and **nonsense** mutations.
Synonymous mutations tend to accumulate in the genome at a higher rate due to their inability to obviously affect the phenotype of an individual. The lack of selective pressure acting on synonymous mutations allows them to become fixed in the population gene pool. By contrast, non-synonymous mutations have a lower rate of accumulation because they have the potential to be acted upon and disposed of by natural selection. The rate that synonymous mutations become fixed in the population is higher than that of non-synonymous mutations.

In homologous genes, there is a proportional relationship between the frequency of amino acid substitutions in a given gene and the time since the last common ancestor. An enzyme that can be used as an example of this is Cytochrome C, in which, the number of substitutions in its gene sequence increases as time since the last common ancestor increases.

The **neutral theory of molecular evolution** suggests that molecular evolutionary changes are due to random genetic drift of mutant alleles that are considered neutral. It contradicts **selection theory** by stating that many changes to the sequences of genes over time are neutral (or synonymous), resulting in evolution without natural selection. In other words, the sequences of genes are changing over time because of the lack of selective pressure to dispose of or propagate mutations that don't affect the phenotype of individuals in a population.

The rate of evolution for proteins is affected by the selective pressure and the degree of constraint. High selective pressure to keep an essential protein the same (i.e. cytochrome c) leads to a lower rate of evolution in a protein. Degree of constraint is how flexible a protein is to modifications in its gene sequence and still maintaining function. Some proteins are able to change a lot and their functions remain the same. Other proteins are highly conserved and little changes to their gene sequence can be detrimental to protein function.

Molecular Homology

Volvox is a type of green algae. It has a gene called GlsA that is essential for asymmetric cell division and when knocked out, Volvox dies. Chlamy has the same gene but its function is unknown and when knocked out, there is no effect. The GlsA gene in Volvox is homologous to the GlsA gene in chlamy due to high similarity between their sequences. This is a case in which two genes descended from the same common ancestor but ultimately performs different functions. Another example of molecular homology is chlamy flagella and human flagella and cilia.

Molecular Convergence

The two major theories of evolutionary change are contingency and convergence. **Contingency** is the idea that each step in evolution is dependent upon all of the steps preceding it. In theory, if we were to change the conditions under which organisms were living billions of years ago, our tree of life would look completely different than what it currently is.

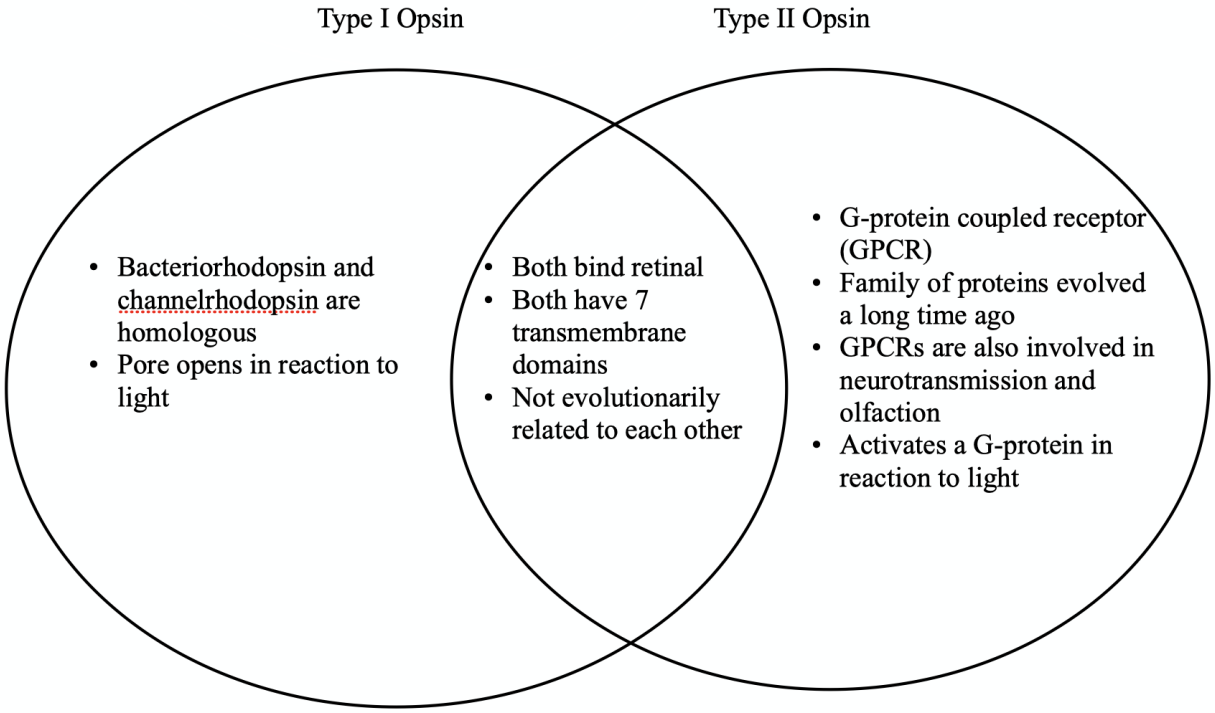
Convergence is the idea that although there are many evolutionary routes that can be taken, the destinations are limited; essentially, there are routes will all tend to converge towards the same destination. For example, life is dependent on certain basic functions (e.g. eyesight). Different organisms evolved unique mechanisms that achieve the same goal.

Think about it; are two proteins that perform the same function the result of functional convergence or homology?

Two proteins with the same function can be the result of *either* divergence from a common ancestor or convergent evolution because it is possible for two proteins to have a similar function but have different gene or polypeptide sequences.

Homology, however, can only be determined by looking at the gene or amino acid sequences of the protein. Highly similar gene sequences are presumed to have common ancestry due to the extremely low likelihood of the two gene sequences converging from separate lineages.

Channelrhodopsin in Chlammy and the rhodopsin pigment in humans is a prime example of convergent evolution. Although both have similar functions pertaining to light reception, neither are evolutionary related whatsoever. Gene sequencing reveals that the two sequences are not similar and, thus, not homologous. Not only are their gene sequences completely unrelated, but their mechanisms in carrying out the same function are different; channelrhodopsin is a type 1 opsin and rhodopsin is a type 2 opsin.



Ruminant organisms such as cows use bacteria to break down cellulose. Cows are an example of a ruminant organism in that they don't have their own enzyme to break down cell walls, but use bacteria living on the grass they eat to digest the grass' cell walls for them. Cows then use an enzyme called **digestive lysozyme** which attacks the bacterial cell membrane to kill the bacteria and gain its nutrients.
Digestive lysozyme is able to work at low pH's while **non-digestive lysozyme** is not. Digestive lysozyme is thus able to resist denaturation in harsh environments such as a cow's stomach.

The lysozyme enzyme found in cows, monkeys and birds is another example of convergent evolution. Although the lysozyme gene did not evolve from a common ancestor of the three animals, all three gene sequences have an aspartic acid residue at position 75 and an asparagine residue at position 87. These amino acids are likely critical to the function of lysozyme and evolved separately in all three lineages. Convergent evolution resulted in the lysozyme enzyme with conserved residues in certain positions, despite lack of molecular homology.

Apply Your Knowledge

Consider the following (not multiple choice, these are designed to allow you to think more freely about the testable concepts):

1. An ancient protein from 65 million years ago was isolated and its amino acid sequence determined. The sequence of the modern day equivalent protein (which has evolved since then) is also known. What would the ratio of synonymous to nonsynonymous mutations be in the molecular evolution process of this protein?

2. What would the BLAST score and E-value for the sequence alignment between the gene for lysozyme in cows and birds be like? What about the sequence alignment between the GlsA gene in Chlamy and Volvox? You don't need to give actual numbers, but describe their magnitude.

Congratulations for making it through the entire breakdown. Remember to continually reinforce your understanding over as long a period of time as possible in order to

maximize your performance. Best of luck in your studies! Here are some links that might interest you.

Want to learn more about WebStraw? Check out our website at www.webstraw.ca