

Class 04: The Central Dogma (1)

Held: Tuesday, 8 September 2009

Summary: We begin to study central issues in molecular biology and the corresponding computational problems.

Related Pages:

- EBoard.
- Reading: Chapter 2.
- Due: Writeup of Web exploration.

Notes:

- Vida has been sick. That means you get to watch the “train wreck in slow motion” of Sam trying to describe biology.
- There is no homework for Thursday. You may, however, want to look over Chapter 2 again.

Overview:

- Lab Exercises, Continued
- Basics of the Central Dogma
- Key Processes
- Some Related Issues
- Computational Problems
- Web Exploration

Lab, Continued

- We'll use the first fifteen-twenty minutes of class to wrap up the lab exercise from the previous class.
- We'll spend a few minutes reflecting on what you learned in the lab.

The Central Dogma: The Basics

- The title of the chapter is “The Central Dogma”?
 - Do the authors tell us explicitly what the central dogma is?
 - How would you phrase the central dogma?
- The term “The Central Dogma” was coined by Francis Crick
 - You should know who Francis Crick is
 - The central dogma describes information transfer between the three primary sequences we work with
 - He introduced the concept in a 1958 conference paper and revisited it in a 1970 *Nature* paper.

- Crick describes the dogma in this way: “once (sequential) information has passed into the protein, it cannot get out again”
- Crick also breaks the possible types of information transfer into three categories:
 - General transfers, which happen for most kinds of cells:
 - DNA to DNA (replication)
 - DNA to RNA (transcription)
 - RNA to Protein (translation)
 - Special transfer, which happen in a few special cases
 - DNA to protein
 - RNA to RNA
 - RNA to DNA
 - Unknown transfers, which he postulates do not happen
 - Protein to DNA
 - Protein to RNA
 - Protein to Protein
- Interestingly, Crick’s second article on the Central Dogma is immediately followed by an article whose thesis is “Several RNA tumour viruses contain an enzyme that synthesizes a DNA-RNA hybrid using the single stranded viral RNA as template. Hybridization experiments confirm that the DNA strand is complementary to the viral RNA.”
- Do you know any possible exceptions to the “proteins don’t transfer information to any kind of sequence”?

The Key Processes

- Duplication
 - Copying DNA to DNA, e.g., when cells divide
 - Lots of effort to ensure accuracy of copy
 - Not that important right now
- Transcription
 - Copying DNA to RNA
 - Process goes from the 3’ to 5’ of the template strand
 - A lot like DNA pairing, except that U pairs with A.
 - The quick hack: Start with the coding strand, replace all T’s with U’s
- Translation
 - Starts at start codon (AUG)
 - Triplets of nucleotides converted to proteins
 - Stops at stop codon
 - A promoter region gets everything started

Some Related Issues

- Chromosomes: 46 (22 pairs plus two sex chromosomes)
- Inheritance
- Mutation

Computational Problems

- So, what are the interesting computational problems we get from this initial information?
- We can encode transcription and translation
 - What input types?
 - What output types?
- As the initial examples suggest, one interesting problem is to compare two DNA sequences and see how close they are.
 - Allows us to find basic information about mutations.
- A more interesting problem is to look at comparing partial sequences to longer sequences.

Web Exploration

Make sure to turn on scripting for any site you visit!

- We're going to try the Web exploration for Chapter 2.
- You'll find that some of it is similar to what we did for Chapter 1.
- But reinforcement is good.
- No, you don't need to turn it in.
- But we will compare notes at the end.
- You may want to note what you learn from the more detailed instructions.
- Here are some notes, thoughts, and questions
 - Did this exploration help you find better ways to look for DNA?
 - Does the FASTA file for HBB use the template sequence or the coding sequence? How do you know?
 - Can you find typos in the GenBank record?
 - Stupid tidbit: Sam is likely to have an HBB mutation
 - What software can you use to compare sequences?
- What procedures would we have to write to make all of this easier to do?

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