Hi Jim,

Great solution. Interesting that you chose to create a NumberWrapper class with its own methods. I wish I thought of doing the same because I wanted to make mine a little more OO like yours, but the only thing I could think of at the time was creating another class for the array, which I decided would be a bad idea.

Emanuel

Hi John,

Great post. I never knew that stacks were used to check enclosures like curly braces and parenthesis. Do you know if IDEs like Eclipse also use them to check for this error?

Regards,

Emanuel

Hi Emanuel,

Regarding linked lists, do your nodes link backwards as well as forwards, or just forwards (one-directional)? So given the codon sequence ACT, node C either links to both A and T, or just to T?

Regards,

Jim

t

Hi Jim,

Those are good questions. Regarding direction, DNA, is doubled stranded, but only one of the strands will be translated, and this always happens in what is referred to as the 5’ to 3’ (pronounced “5 prime to 3 prime”) direction. I don’t want to bore everyone with the details of the molecular biology of this, so in a nutshell, each nucleotide of DNA contains 5 carbon atoms. The 5’ carbon marks the start, and the 3’ carbon marks the end, to which other nucleotides will be added to when replicated. When it is “read”, it also follows this direction. The “central dogma of biology” (National Center for Biotechnology Information, 2007) states that DNA is transcribed into RNA, which is then translated into protein “DNA->RNA->Protein”. Anyway, not to get too side-tracked, but, it would make sense to have the linked list follow this same 5’-3’ direction.

I had to go back to read the journal articles to see if the contents of each node contains one single nucleotide, or one codon. It looks like in the example of researchers that are completing genomes are actually assembling DNA sequences into larger fragments, which are then given IDs and quality scores. These fragment IDs and their corresponding scores are then being stored in a single node.

In the example of the ciliate organism, it appears that the model of one nucleotide per node is being used, though I can see how using a node to store a codon (3 bases) could work for other purposes.

Emanuel

Reference:

National Center for Biotechnology Information (2007) *Central Dogma of Biology: Classic View* [Online]. Available from: <http://www.ncbi.nlm.nih.gov/Class/MLACourse/Modules/MolBioReview/central_dogma.html> (Accessed: 12 August 2013)

Hi Emanuel,

The only improvements I'd suggest are to refactor the constructor, the ButtonHandler's actionPerformed method and the createArray method into smaller methods:

* In the constructor, a generic createButton(String aLabel, String anActionCommand) could replace lines 39 to 45, reducing 6 lines of code to 2 lines. You may need to keep track of those buttons with class attributes, unless the generic method also accepts an ActionListener object as a parameter; in which case lines 47-49 could be moved into the generic method.
* In actionPerformed, lines 61 and 62 could be combined into one method. Lines 70 and 71 could comprise a separate method that could be called instead.
* In createArray, the integerArray variable could be made a class attribute so that its within the scope of current and future methods. The generation of the numbers could then be separated into one method, the even number check into another method and the display of the different arrays (in the JTextArea and JOptionPane) into another method.

Jim

Hi Jim,

Thanks for taking the time to look at my code. You mentioned shortening the number of lines, and in one of your examples, you say I could shorten these 2 lines into one method:

String arrayLengthString = arrayLengthJTextField.getText();

arrayLength = Integer.parseInt(arrayLengthString);

How would you do this?

Emanuel

Hi Emmanuel,

Thanks for reading my post. I have never used an IDE before, but I looked it up and found that eclipse even asllows you to set the stack size (<http://scala-ide.org/docs/current-user-doc/faq/index.html>). And, sometimes, it comes with an Exception Stack Trace (read more:( <http://help.eclipse.org/juno/index.jsp?topic=%2Forg.eclipse.platform.doc.user%2Freference%2Fref-error_log_view.htm>).

I am hoping that we will gte to use IDEs in the following week? What do you think?

Regards,

John

Hi John,

At the start of the module, Sam said that we could use an IDE for our programming, but he prefers that we don’t use them. At my workplace, most software engineers are using Eclipse, so maybe using them is not harmful to our learning the material. However, I do have a few friends that have interviewed at Google and were made to demonstrate their programming skills by writing code on a whiteboard in front of their interviewers. I don’t know if this is the norm when interviewing for software engineering positions, but maybe not using an IDE can be a good idea.

Regards,

Emanuel

Hi Emanuel,

Superb overview of DNA theme and linked list data structure.

As I understand you work pretty close to DNA and other bioinformatic stuff, so allow me to ask, may be you know and can suggest some C++ libraries for working with DNA and/or storing human body parts representation as set of bits/bytes (sound crazy and scary I know)? May be some of your fellow at work know about it. I'm just looking at it at the moment and can't find anything pretty lightweight but efficient.

Thanks in advance! :)

With best,

Val

Hi Val,

Thanks for your question. I don’t do any C++ programming at work, so I looked at some of the bioinformatics C++ programs written by our engineers and they are mainly using libraries from the NCBI C++ Toolkit (National Center for Biotechnology Information, n.d.a.). My group mainly works with DNA, so a lot of what we do involves analyzing DNA sequence similarity by using tools that align them by implementing certain algorithms based on heuristic or probabilistic models (Wikipedia, 2013), so we make extensive use of their “Global Alignment Library” (National Center for Biotechnology Information, n.d.b.). My math skills are pretty weak now compared to when I was an undergraduate, so perhaps this is something I need to review if I want my dissertation to involve this topic.

Emanuel

References:

National Center for Biotechnology Information (n.d.a.) *NCBI C++ Toolkit* [Online]. Available from: <http://www.ncbi.nlm.nih.gov/IEB/ToolBox/CPP_DOC/> (Accessed: 13 August 2013)

Wikipedia (2013) *Sequence Alignment* [Online]. Available from: <http://en.wikipedia.org/wiki/Sequence_alignment> (Accessed: 13 August 2013)

National Center for Biotechnology Information (n.d.b.) *Biological Sequence Alignment* [Online]. Available from: <http://www.ncbi.nlm.nih.gov/books/NBK7151/> (Accessed: 13 August 2013)

Hi Emanuel/Jim,

Nice work Emanuel and nice review Jim.  Please in addition you also displayed your result and error in both DOS and GUI. Is there any reason for this?

Regards.

Fatai

Hi Fatai,

Thank you for taking the time to try my program. I often try to display results to the DOS or terminal windows before attempting to display them in the GUI. I usually remove them once I have validated the results with the GUI, but in this case, I forgot to do it. I often also do this with certain variables throughout the coding process just to make sure my program is doing what I want it to.

Regards,

Emanuel

In your two class setup, I think it is beneficial to move the user-input out of the Array class into the main method.

If I may add, I believe that it is good practice to limit variable declaration from within the blocks of code that they are actually needed. When variables are declared, resources are allocated, and when the block is done and the variable falls out of scope, the resource is released. Java’s garbage collection might take care of this, but I think it’s still a good thing to practice.

Regards,

Emanuel

H Emanuel,

Thanks for sharing your work with us.

The system did not accept 0 as a positive integer.  I would like to know why.

In mathematice, zero is regarded as positive.

Why did the system reject "+6"? "+6" and 6 are the same. The system should be smart enough

to detect this and handle it accordingly by say stripping the plus sign/. What do you think?

Best regards,

Ifeanyi

Hi Ifeanyi,

Thanks for taking the time to look at and try my program. I’ve actually read that zero in mathematics is regarded as “neither positive nor negative” (Wikipedia, 2013). I have read a few instances where it was described as positive, but ultimately decided to go with the Wikipedia answer since an array with no elements would be useless in this program.

I suppose I could have implemented the program to accept a plus sign in front of an integer to denote that it was positive, but it was unnecessary since the program was already asking for only positive integers.

Thanks for your comments.

Regards,

Emanuel

Reference

Wikipedia (2013) *Sign (Mathematics)* [Online]. Available from: <http://en.wikipedia.org/wiki/Positive_number>