

Commentary

The HTML layer and CCS layer for the summary page and the Detail page following link from summary page where done by myself Mehboob Patel. All files created or edited by me for use in my webpages end with the number 2. The commentaries for the respective files are as follows.

1. aa2.pl – this is a perl cgi script which displays the full amino acid sequence and followed by the DNA sequence coded by this amino acid. This script calls on the middle layer module cwmodule and the subroutine GetAA.
2. aa2.css – This is the css file for the aa2.pl cgi script which adds formatting like colour, border, margins, padding and the text style to the cgi script. By placing word-wrap:break-word; into the css the long string returned by the middle layer code is wrapped.
3. condon2.pl – this perl cgi script displays the coding usage frequencies within the coding region as well the overall codon usage information for all sequences in the database in a tabular format. It uses the subroutine GetGeneCodons and GetCodonFrequency using the cwmodule. Both subroutines output the results as a percentage into a hash variable. The perl script references each key in the hash (these keys are the triplet nucleotides which constitute a codon) and returns the value for them. The GetGeneCodons subroutine outputs the coding usage frequencies for that particular sequence and GetCodonFrequency outputs the codon usage for all sequences in the database. The table displays these outputs along with codon name and the amino acid or stop position these codon code for.
4. condon2.css – this is the css file for the condon2.pl script which adds border to the title as well as some padding and margin to the tables.
5. detai2.pl this perl cgi page for the detail page which links from the summary page when you click on the accession number. This page is not the same as the detail page which can be accessed from the menu bar (which is done by Yolanda). This page displays the complete DNA sequence with the coding regions highlighted, the full amino acid sequence and followed by the DNA sequence coded by this amino acid, the codon usage frequencies within the coding region with the overall codon for the accession number selected in different frames. It also allows the ability to identify sticky-end restriction enzyme sites in the genomic with the ability to search for EcoRI, BamHI and BsuMI by entering the accession number manually. By using iframe html tag this allows the individual cgi web files to be displayed on the one webpage in independent frames allowing a quick summary. The detail page uses as java script and some css from jquery website which was amended to allow the four individual frames to be maximised allow for more detail viewing. The popup buttons where placed in a div tag and labelled with a ref followed by full e.g. codonfull to indicate full screen. Each popup has its own id eg popup1 (complete DNA) which has

a link to the external cgi file (dna2.pl) which calls the java module pop-up to open the screen to the frame size set. The class attribute in the link creates a clickable plus (+) button which can call an action in this case maximise screen.

6. detail2.css – This file applies the css properties to the detail2.pl cgi script. It applies colour, padding margin and border properties to the relevant tags. The height and the width of the page had to be fixed in the body tag, this is because the frame properties have their positions set to absolute to allow overflow and viewing on different size screens caused issues (discussed further in bug testing). Each frame (called box in css file) has its size set equally, and the position properties were set so they would be displayed as four frames two next to each other and two above each other. The id boxes on top of the frames have (ref tag as name followed by full e.g. #codonfull) they each have their properties set so that they are displayed on top of their respective frames.
7. dna2.pl – this is a perl cgi script to show the complete dna sequence for the given sequence and is displayed in its respective frame using the cwmodule and the GetDNA subroutine. This script has been amended from Yolanda script, with the menu and footer bar stripped. To simplify the look.
8. dna2.css – this file applies the css properties to the dna.pl file and uses the original css properties created by Yolanda.
9. sticky2.pl – this is a perl cgi script which allows the user to identify sticky-end restriction enzyme sites in the genomic with the ability to search for EcoRI, BamHI and BsuMI by entering the accession number manually, using the cwmodule and StickyEnds subroutine. This script has been amended from Yolanda original script with the menu bar and footer bar stripped. It also displays the result of the search on the same page instead of switching pages.
10. sticky2.css – this file applies the css script to the sticky2.pl and uses the original css properties created by Yolanda.
11. summary.pl – this is a perl cgi script file which displays the summary results for all the sequences in the database using the cwmodule and the GetSummary subroutine. It displays the Gene Id, Protein Name, Accession Number and chromosome Location. As the Accession number is unique it has a hyperlink attached to it which is clickable which then takes the user to the detail page. The header & footer have been used from Yolanda script.
12. summary2.css – this file applies the css properties to the summary.pl file. It adds the font style, background colour, padding and margins to the different attributes in the webpage.
13. aatest2.pl – perl script to retrieve results using the middle layer code for the full amino acid sequence with the coding regions for using 9 random accession numbers.

14. aatest2.txt – results for aatest.pl script.
15. summarytest2.pl - perl test script to retrieve the results for getsummary subroutine.
16. summarytest2.txt – results for summarytest.pl
17. singlefrequencytest2.pl - perl test script to run the GetGeneCodons subroutine
which will return the codon frequency for the 9 random accession numbers chosen
18. singlefrequencytest2.txt – results for singlefrequencytest.pl
19. totalfrequencytest2.pl - perl test script to run the GetCodonFrequency subroutine
which will return the codon frequency for all the sequences in the database
20. totalfrequencytest2.txt results for perl script