Practice with MATLAB

CS 365: Introduction to Scientific Modeling

In Class Lab

August 27, 2014

1 Strings, output to the screen, table lookups, and simple iteration

To learn about the print command `fprintf`, type:
`doc fprintf`

Next, create Table1 as follows:

```
Table1 = [{'cat'},{'Fluffy'}; {'dog'}, {'Rover'}; {'mouse'},{'Meese'};
{'frog'},{'Kermit'}; {'rabbit'},{'Peter'}]
```

Table1 is a lookup table of pets and their names. Use a for loop to print sentences that report the name of each pet:

```
The cat is Fluffy.
The dog is Rover.
The mouse is Meece.
The frog is Kermit.
The rabbit is Peter.
```

Hints: Use the index of the for loop to refer to Table1, i.e., you should not type 'cat' or "Fluffy', and you should only type 'The' and 'is' once. Use `char` to extract a string from a cell (`help char`).

Remark: Generally, it is a poor idea to use for loops explicitly in MATLAB. They run interpreted and are excruciatingly slow compared to the built-in matrix operations. I will look for unnecessary for loops in your code and mark them down.

Extra credit: Devise an experiment to compare the efficiency of a built-in MATLAB matrix operation to that of an explicit for loop, run the experiment, and report the results.

2   Using script files and `find`

Run the bigGene.m code (by strong the .m file in your current directory and typing: `bigGene`. Learn about `find` with `help find`.

Remove the spaces from the variable `mito`. Hint: Use `find` to locate the spaces. Assign those indices in `mito` to the empty string '' (two single quotes with nothing between them).

Use `find` to count the number of a's in `mito`.

Count the number of occurrences of `ccg` in `mito`, using `strncmp` instead of `find`. Why?

3   Using external files

Load in the file `full_translation_table` by typing the command:
`load full_translation_table.mat`

Inspect the data in the `translation_table` by clicking on it in the Workspace.

Print the following for each row of the table:
`Codon x is abc.  It codes for the amino acid xyc.`

`x` stands for the row of the table, `abc` is the codon in that row (Col. 1) and `xyz` is the amino acid in the row (Col. 2).

Extra credit: Make a new table that contains one entry for each amino acid with a count of how many codons code for it. Which amino acid is most abundant in the `mito` genome string? Which codon triplet is the most abundant?

4   Creating functions and simple plotting

Create a function `myPlot` that takes as input 2 vectors, a string to label the x axis and a string to label the y axis. Use `myPlot` to display the chirp signal shown in the graphics tutorial for 2-D plots.