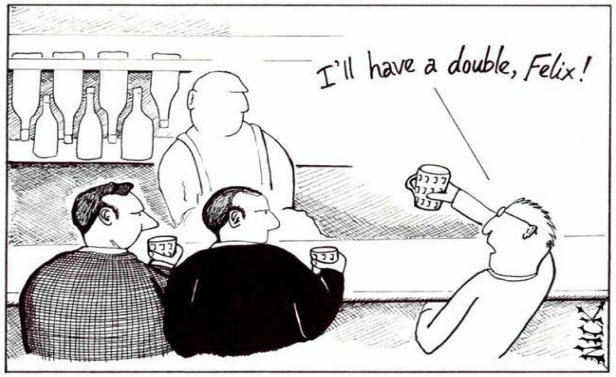

Cambridge, 1953. Shortly before discovering the structure of DNA, Watson and Crick, depressed by their lack of progress, visit the local pub.

Sequencing Protocols: Using FinchTV for analyzing and storing DNA sequences in scf file format

(Fornari Lab, DePauw University)

CEQ 8000 software should export the sequences in *scf* and *fasta* formats to your lab folders in the I:/drive. (Make arrangements with Dr. Evans to gain access to any special folders associated with faculty research or teaching labs).

In order to view the data, select the *Finch TV program* from your desktop or Program Files folder and use it to open your file by clicking on the Folder icon or the File menu, then browsing to the location of your exported scf files (see above) and selecting it. Once opened in FinchTV, note the colored peaks and the called-bases above the peaks. You can spread out or raise/lower the peaks by adjusting the sliders at the left and bottom of the electropherogram. (You may need to make these adjustments in order to manually evaluate some of the called-bases for authenticity)

Find restriction sites or any desired sequence string by going to *Edit*, scrolling down to *Find Sequence*, and entering a restriction site sequence. For example, the restriction site sequence for EcoR1 is GAATTC. Enter this sequence into the 'Find Sequence' window, and then press *Enter* repeatedly in order to find all EcoR1 sites. Highlight (by left-clicking and holding the mouse button while dragging) and copy (by right-clicking a highlighted region) the entire DNA sequence between the sites, if you want to save it for any later, downstream analyses outside of FinchTV. (See: Alternative Strategies for analyzing DNA sequences with other programs, especially for translating into amino acid sequences).

FinchTV allows you to highlight any desired stretch of sequence by left-clicking and holding the mouse key while you drag the pointer along the sequence. You can now BLAST the highlighted section by going to *Edit,* and then choose the last entry, BLAST sequence. Next, select one of the BLAST methods: BLASTn, BLASTx, TBLASTx, or MegaBlast (see the NCBI web site for a full explanation of these search options)

Look for your primer sequences or other 'landmarks' and highlight and copy the amino acids or nucleotides between them. This sequence can then be reBlasted to find similar sequences