# Sequencing Flow Charts
## (VI) Bioinformatic Analysis of Sequence Data

In addition to the basic functions provided by the CEQ 8000 software, we use other programs to analyze the DNA chromatograms, which are stored as '.scf' files in your I:/drive folder: **(1)** the very expensive Accelrys DS-Gene program located on only 2 computers, one in room 219 and the other in room 228A; **(2)** the freeware supplied by Geospiza, particularly the FinchTV program for Mac or Windows OS (works as well or better than DS-Gene for this task); **(3)** the MEGA 3.1 program and **(4)** MPI Bio-informatics Toolkit (for processed sequences only, but excellent in this regard)

To use DS-Gene, go to the Sequencing Lab in room 219 of the Olin Biology building, or to room 228A

You need to download the FinchTV program (freeware) from this site and install it onto your own computer by following some simple instructions (it's a zip file)

Follow these instructions for using the Accelrys DS-Gene program to analyze your sequences.

Folow these instructions for using the FinchTV program to analyze your sequences in the scf format

**OR**

Or use these instructions for the excellent MEGA 3.1 program

**(a)** You should store all your DNA sequences as '.scf' trace files and/or as '.fasta' files, or even as plain '.txt' files (for use with the Windows NotePad program) on your local computer or CD

**(b)** The original sequence files will be stored indefinitely in your I:/drive folder (or until your research advisor removes them).

**(c)** You can access base-call quality scores and other information in the I:/drive files

Once your raw scf files are processed out of the scf format, or if you need to re-format files, translate in 6 frames, do searches, align-ments, structure queries or make phylogenetic trees, then see the MPI Toolkit, especially the Utilities menu