

# Using GCG

## Getting Started

- Initialize the GCG Flat-file Programs  
(This is usually done automatically when logging on - You should see the GCG Welcome banner)

analyze% **gcgff**

- Initialize the GCG Relational Database Programs

analyze% **gcgrdb**  
(Provides access to the Oracle-based sequence database)

## Help

The GCG manuals are at  
<http://genome.microbio.uab.edu/GCG/GCG10/gcgmanual.html>  
(Ask Elliot for the username and password)

### While on analyze:

- **genhelp**  
On-line help arranged by program
- **genmanual**  
On-line Manual

## Copying Data or Sequence Files

- analyze% **fetch enzyme.dat**  
(Restriction enzyme list)
- analyze% **fetch GE:vsvcg**  
(The Genbank sequence for vsvcg)

## Displaying Data or Sequence Files

- analyze% **typedata Enzyme.dat**  
Display the data and documentation
- analyze% **typedata -ref GE:vsvcg**  
Display documentation only

## Running Programs

- Programs
  - Type the name of the program
  - Do not abbreviate program names
  - Program names are case sensitive
- Program Parameters
  - A dash (-) indicates a program parameter
  - Parameters can be abbreviated
  - Parameters are case insensitive

## Global Switches

- Changes your GCG environment
- Type at the analyze% prompt
- **doc**  
Displays a short paragraph describing the program being run
- **nodoc**  
Suppresses the documentation displayed for each GCG program
- **comcheck**  
Displays a list of command line options when a program is run  
Gives you a chance to enter new options after you have started a program.
- **nocomcheck**  
Turns the ComCheck option off.

## General Program Switches

- Enter on the command line following the program name
- Enter at the program prompt if -Check or ComCheck is active
  - **-DEFault**  
use default values for every parameter not on the command line
  - **-PROtein**  
sets the program to expect protein sequences.
  - **-NOPROtein**  
insists that your sequences are nucleic acids.
  - **-CHEck**  
prints a summary of the available command line parameters

## Batch Jobs

- Use for programs that may take more than a minute or two to run
- Use **-Batch** to ensure the program will run in batch mode
- Use **-NOBatch** if you do not want to use batch mode
- The program will prompt you for required information
- The program is automatically submitted to a batch queue

The following programs should be run in batch mode

- BLAST
- Compare
- FastA
- FrameAlign
- FrameSearch
- MFold
- ProfileSearch
- TFASTA

## Graphic Output

You must first specify a graphic device before running a program.

- `analyze% setplot`

PostScript Output

- Create a PostScript text file
  - Choose the Postscript option from SetPlot
  - A postscript graphic file will be created
- Create a GIF file
  - Choose the GIF option from SetPlot
  - A gif graphic file will be created

- Send the PostScript or GIF file to your computer
  - Use FTP
  - Be sure to use binary mode for gif files
- Edit/Print the GIF or Postscript file
  - Use Adobe Distiller in the Adobe Acrobat package to create a pdf file from the postscript file
  - Edit the pdf file using Adobe Illustrator

## **File Transfer**

- Use FTP

Fetch (Macintosh); WS FTP (Windows)

Available from: <http://www.dpo.uab.edu/software/ftp/ftpframe.html>

## **Printing**

- Transfer the file to your computer using FTP and print as you normally would

## **SeqLab**

The Xwindows-based user interface for GCG

- **analyze% seqlab &**
  - Launches the Xwindows interface for running GCG programs
  - Must be running an Xwindows package on your Mac or PC

## **SeqWeb**

- The Web-based GCG interface
- Use a web browser to connect to: <http://gcg.genome.uab.edu>
- Connect using your analyze username and password