# MEGA-CC (Compute Core) and MEGA-Proto

Quick Start Tutorial

# Installation

- Create a folder for MEGA (*i.e. ~\Documents\MEGA-CC*).

- Copy *M6CC.exe* and *M6Proto.exe* to the newly created directory.

- For the demo at the end of this document, also copy the *Examples* folder that came with the M6CC.zip file. This folder contains the input data file that will be used for the demo.

# MEGA-CC Input Files

- MEGA Analysis Options file
  - Specifies the calculation and desired settings.
  - Created using MEGA-Proto.
  - Has a *.mao* file extension.
- Data file (one of the following)
  - Multiple sequence alignment in MEGA or Fasta format.
  - Distance matrix in MEGA format.
  - Unaligned sequences in Fasta format (for alignment only).
- Tree file (required for some analyses)
  - Newick file format.

# MEGA-CC Output Files

- In general, two output files are produced
    1. Calculation-specific results file (Newick file, distance matrix,…).
    2. A summary file with additional info (likelihood, SBL,…).
    - Some analyses produce additional output (bootstrap consensus tree).
- Output directory/filename
    - Default is the same location as the input data file.
    - Specify an output directory and/or file name using *-o* option.
    - If no output filename is specified, MEGA-CC will assign a unique name.
- Errors/warnings
    - If MEGA-CC produces any errors or warnings, they will be logged in the the summary file.

# Running MEGA-CC

- Easiest to run using command-line or batch scripts:
  - M6CC.exe –a options.mao –d alignment.meg –o outFile
- Can also be run using custom scripts (Perl, Python, …):
  - exec('M6CC.exe –a options.mao –d alignment.meg –o outFile');
- Integrated *File Iterator* system can process multiple files without the need for using scripts (see Demo2 below)
- In addition, other applications can launch MEGA-CC:
  - status = CreateProcess("M6CC.exe…");
- To see a list of available command options, call M6CC.exe from a command-line prompt with the *–h* flag.

# MEGA-Proto (analysis prototyper)

- Has the same look and feel as the GUI edition of MEGA.
- Produces MEGA Analysis Options files.
- Has no computational capabilities.
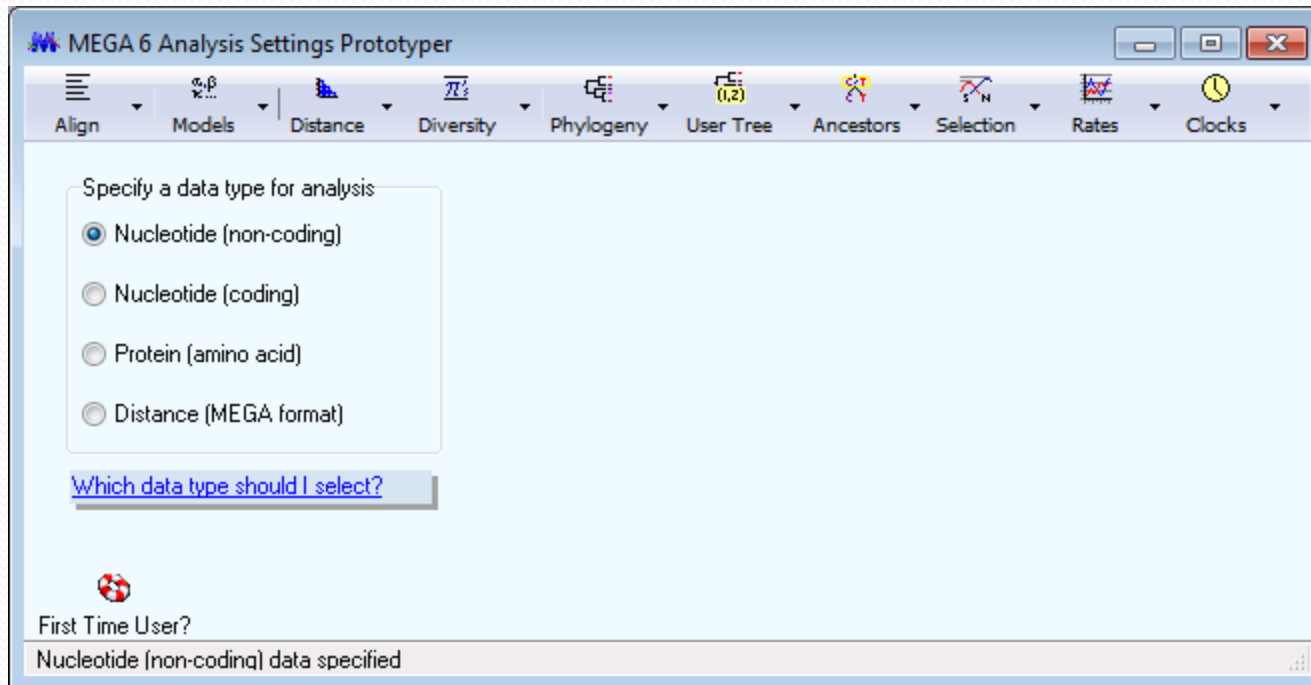
# Using MEGA-Proto

1. Select input data type.
   - Nucleotide (non-coding)
   - Nucleotide (coding)
   - Protein (amino-acid)
   - Distance matrix (MEGA format)
2. Select analysis from menu.
3. Adjust analysis settings.
4. Save the MEGA Analysis Options file.

# Demo1

- The following example demonstrates how to perform Maximum Likelihood phylogeny reconstruction using MEGA-Proto and MEGA-CC
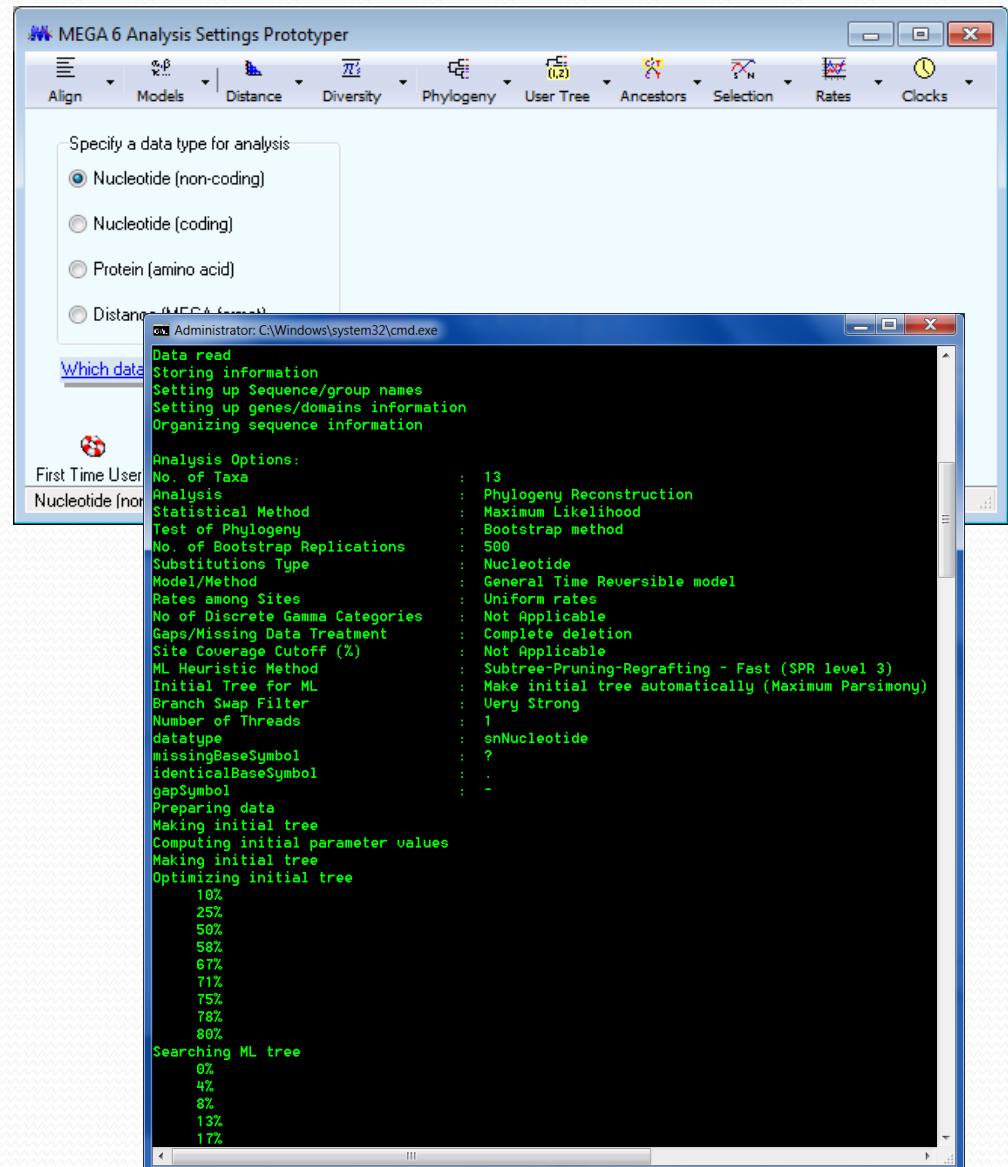
# Demo1 Setup

- For this demo, make sure that you have the M6CC.exe, M6Proto.exe, and example data files located in your working directory as shown. The example data files folder is included in the MEGA-CC.zip download.
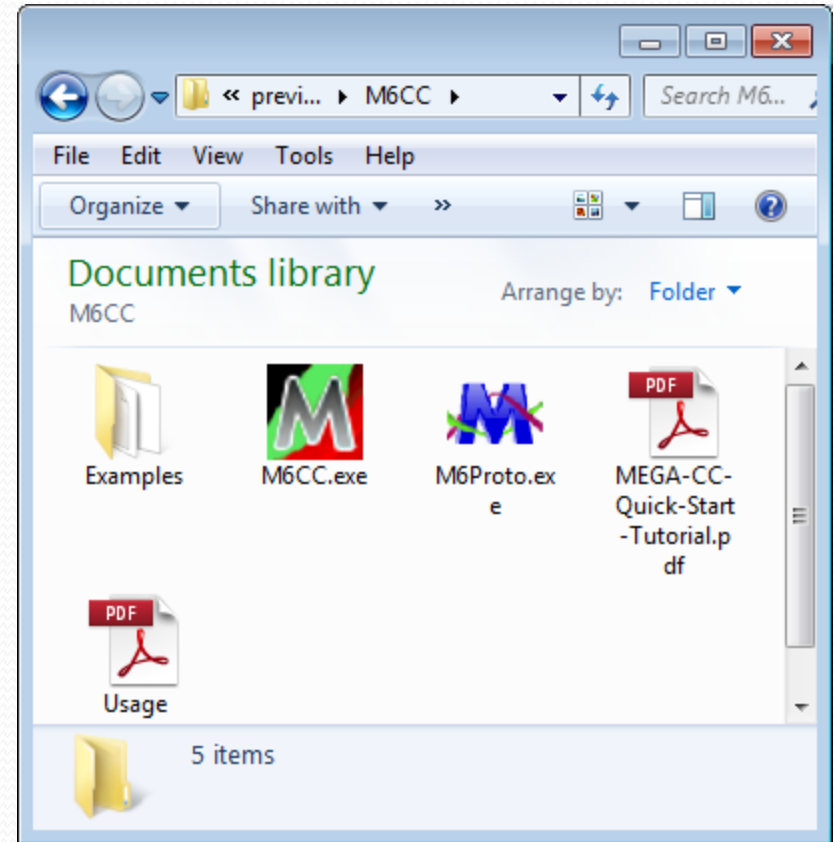
# Step 1

- Open MEGA-Proto by right-clicking the M6Proto.exe file and selecting *Open*.
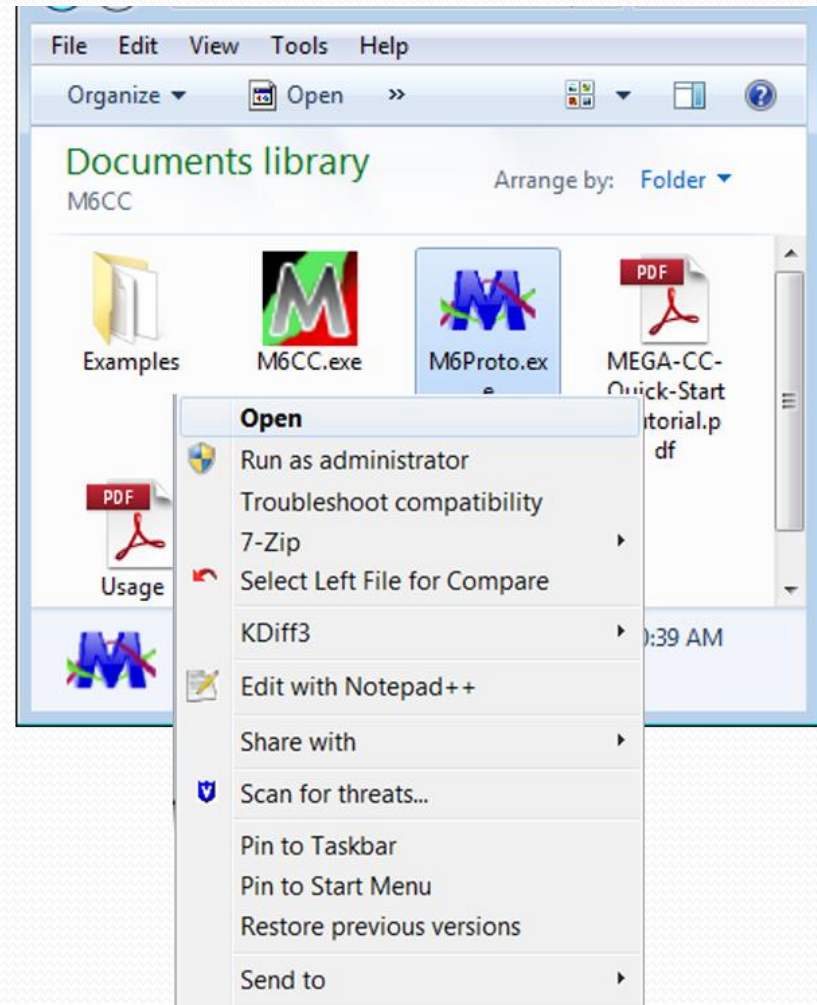
# Step 2

- Select the data type of the input data file to be analyzed. For this demo, we will accept the default setting - Nucleotide (non-coding).
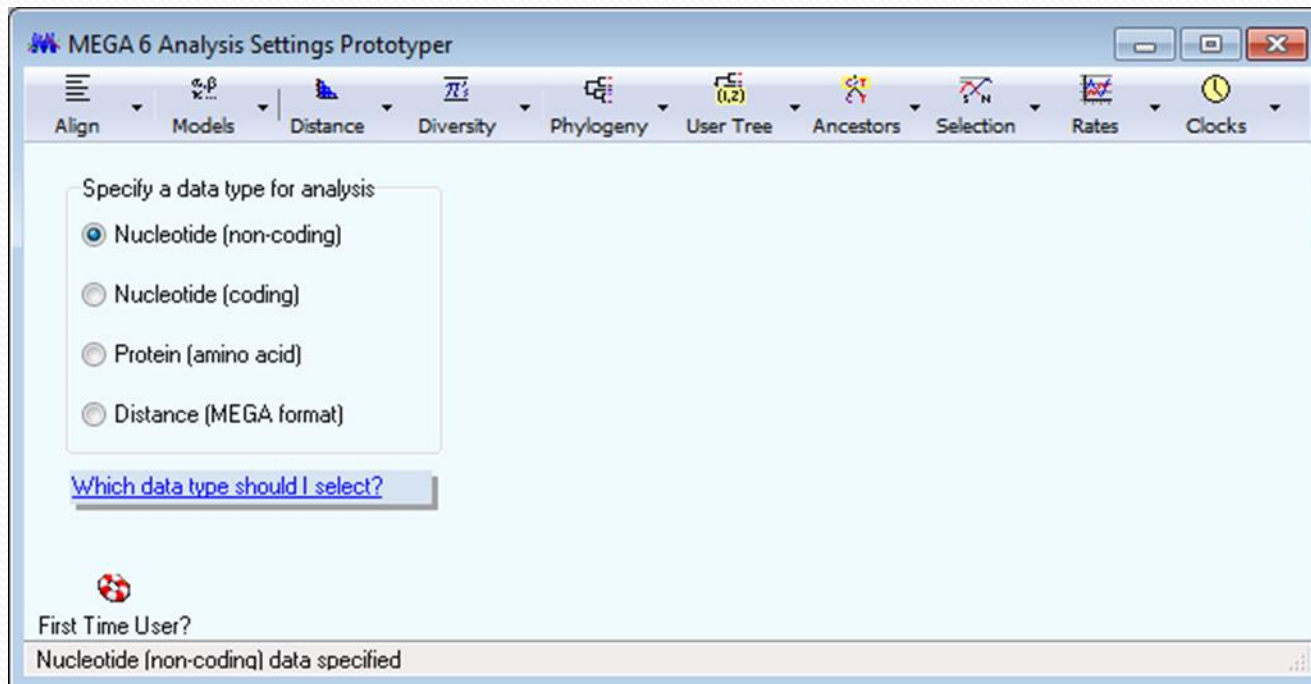
# Step 3

- Select *Construct/Test Maximum Likelihood Tree...* from the *Phylogeny* menu.
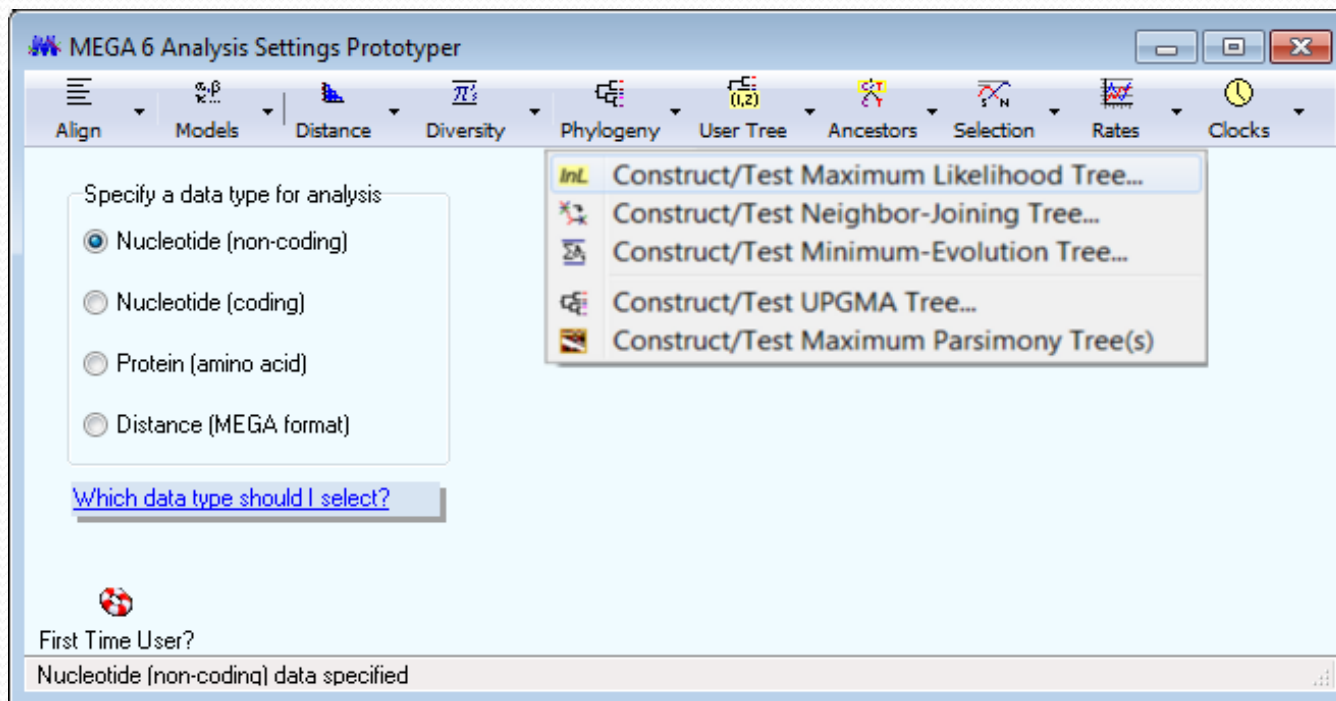
# Step 4

- Adjust the analysis preferences to match those shown.

- Click the *Save Settings...* button and save the analysis options file as *mlDemo.mao* in the current working directory.

# Step 5

- Open a command prompt.
- Navigate to the same directory as the M6CC.exe file using the *cd* command
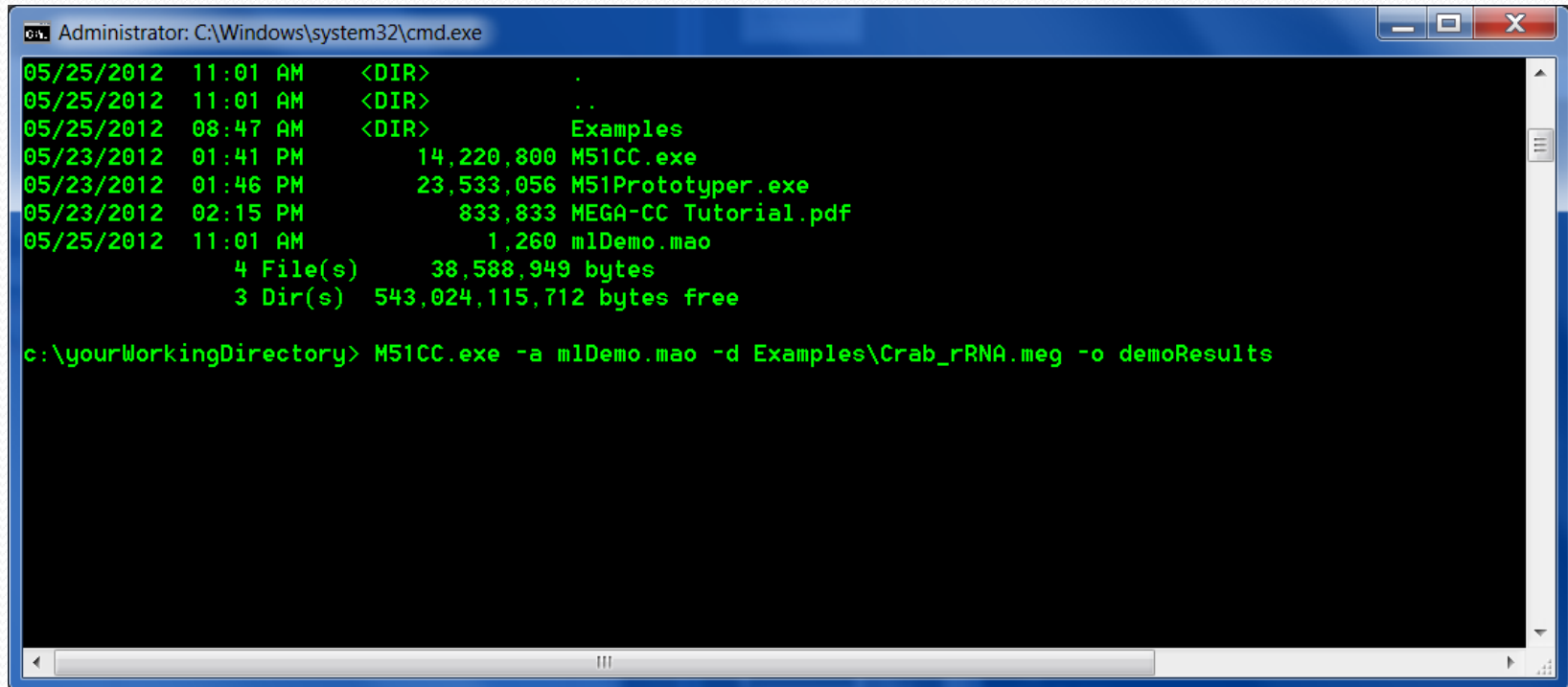
# Step 6

- Execute the analysis by calling the M6CC.exe file
  - M6CC.exe –a mlDemo.mao –d Examples\Crab_rRNA.meg –o demoResults

# Step 7

- The analysis will be launched and progress updates will be displayed in the command prompt window.

# Finally

- The analysis will produce 3 output files
  - demoResults.nwk
    - This Newick file gives the Maximum Likelihood tree found using the given settings.
  - demoResults_consensus.nwk
    - This Newick file gives the bootstrap consensus tree that MEGA produces from all bootstrap sample trees.
  - demoResults_summary.txt
    - This file gives analysis information such as the log likelihood value of the Maximum Likelihood tree, ts/tv ratio, etc...

# Demo2

- The following example demonstrates how to use the File Iterator system in MEGA-CC to process multiple input data files using a single analysis options file.
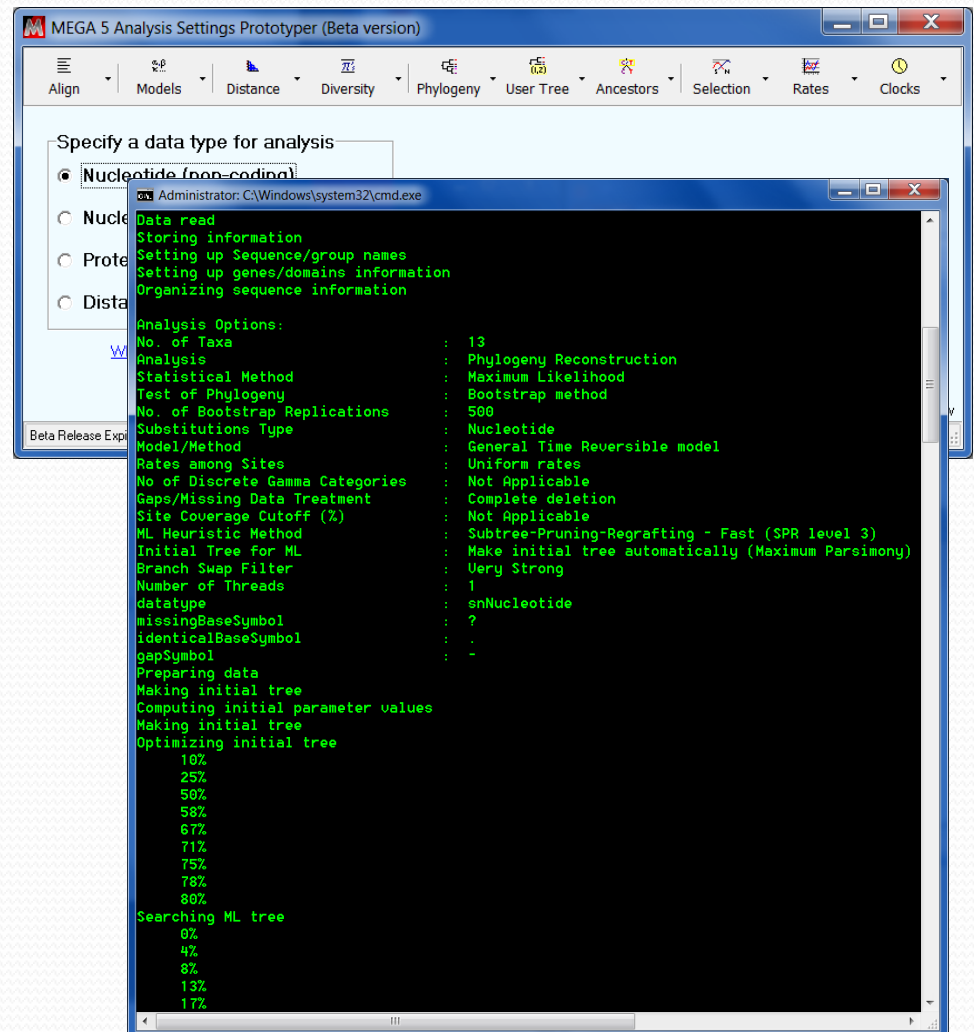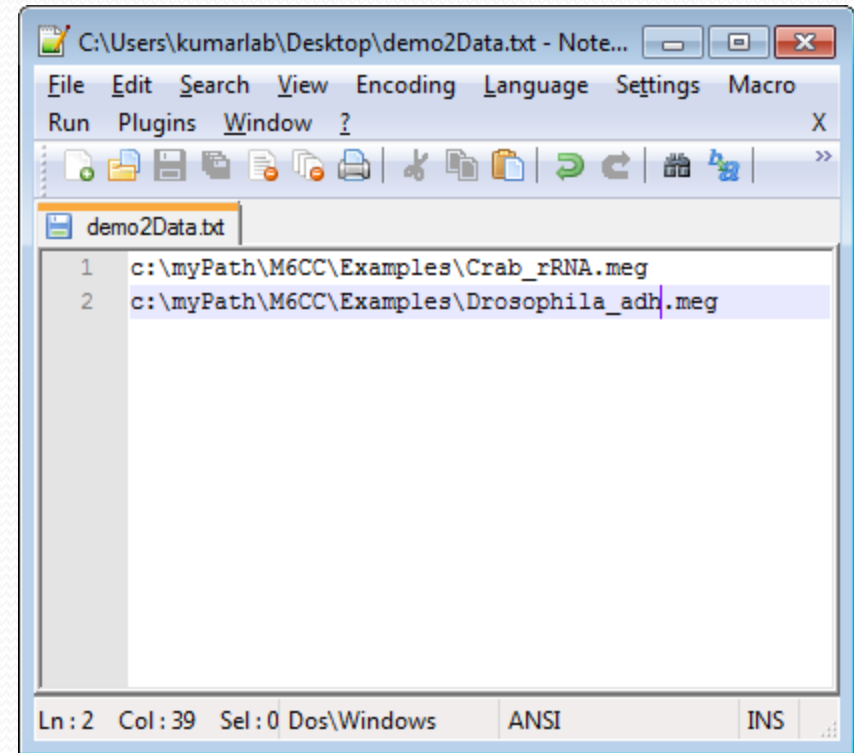
# Demo2 Setup

- If you have not already done so, perform the Demo1 Setup as well as the first 5 steps of Demo1.
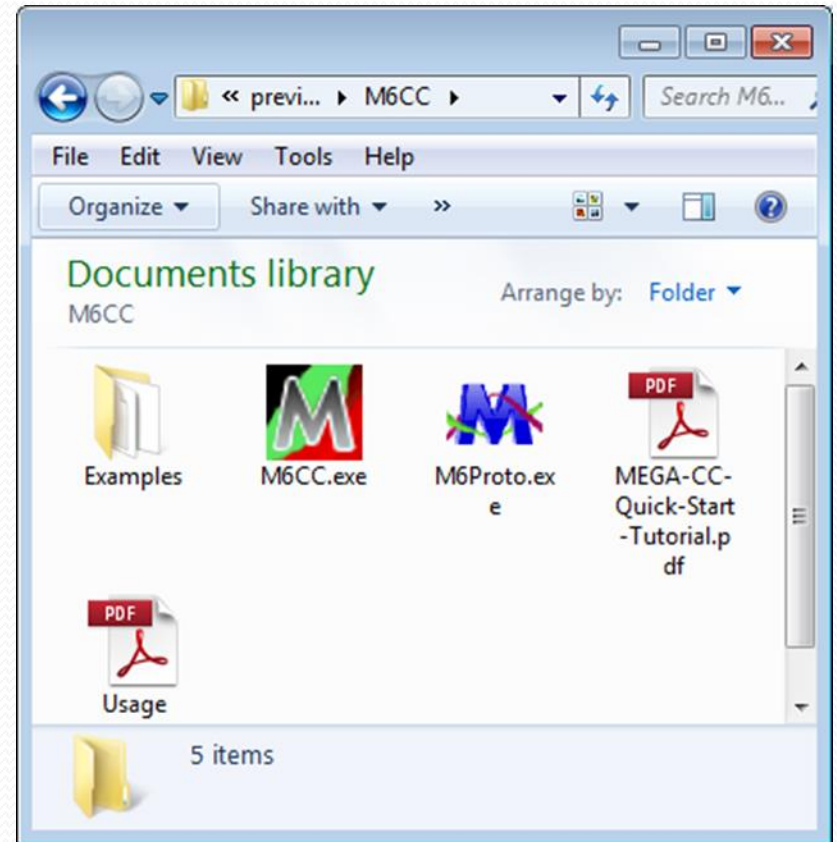
# Step 1

- Create a text file named demo2Data.txt which we will use to specify multiple alignment files for ML phylogeny inference.

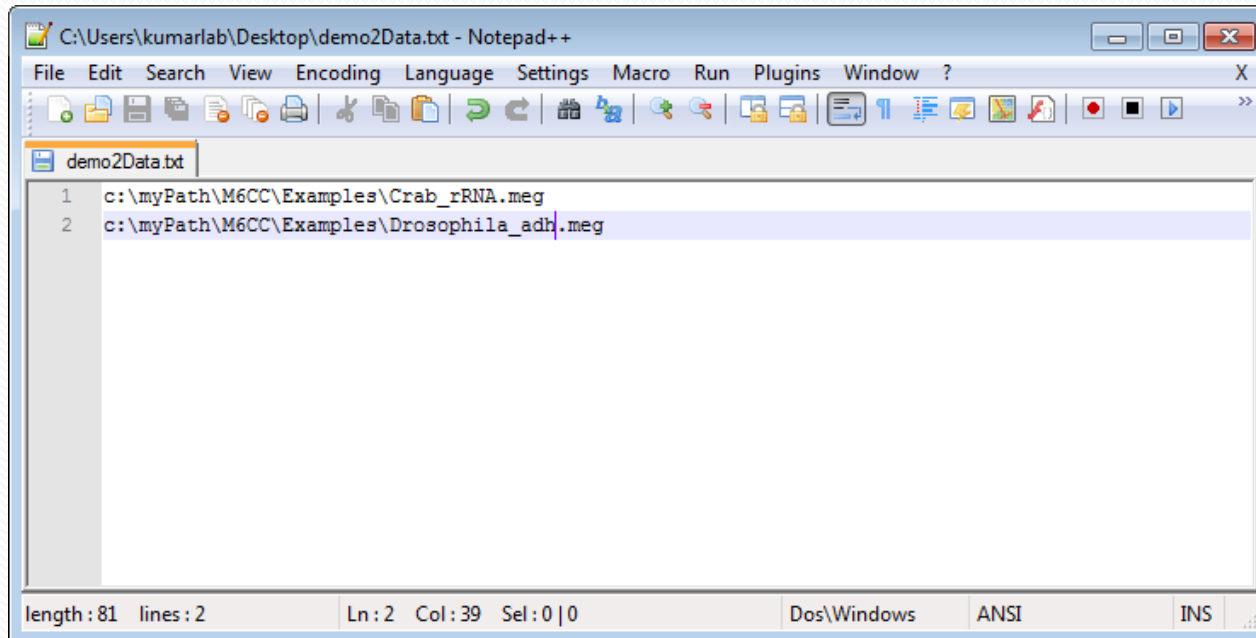- In this file, add the full paths to the Crab_rRNA.meg and Drosophila_Adh.meg example files.

# Step 2

- From a command-line prompt, call MEGA-CC as follows:
  - M6CC.exe –a mlDemo.mao –d demo2Data.txt
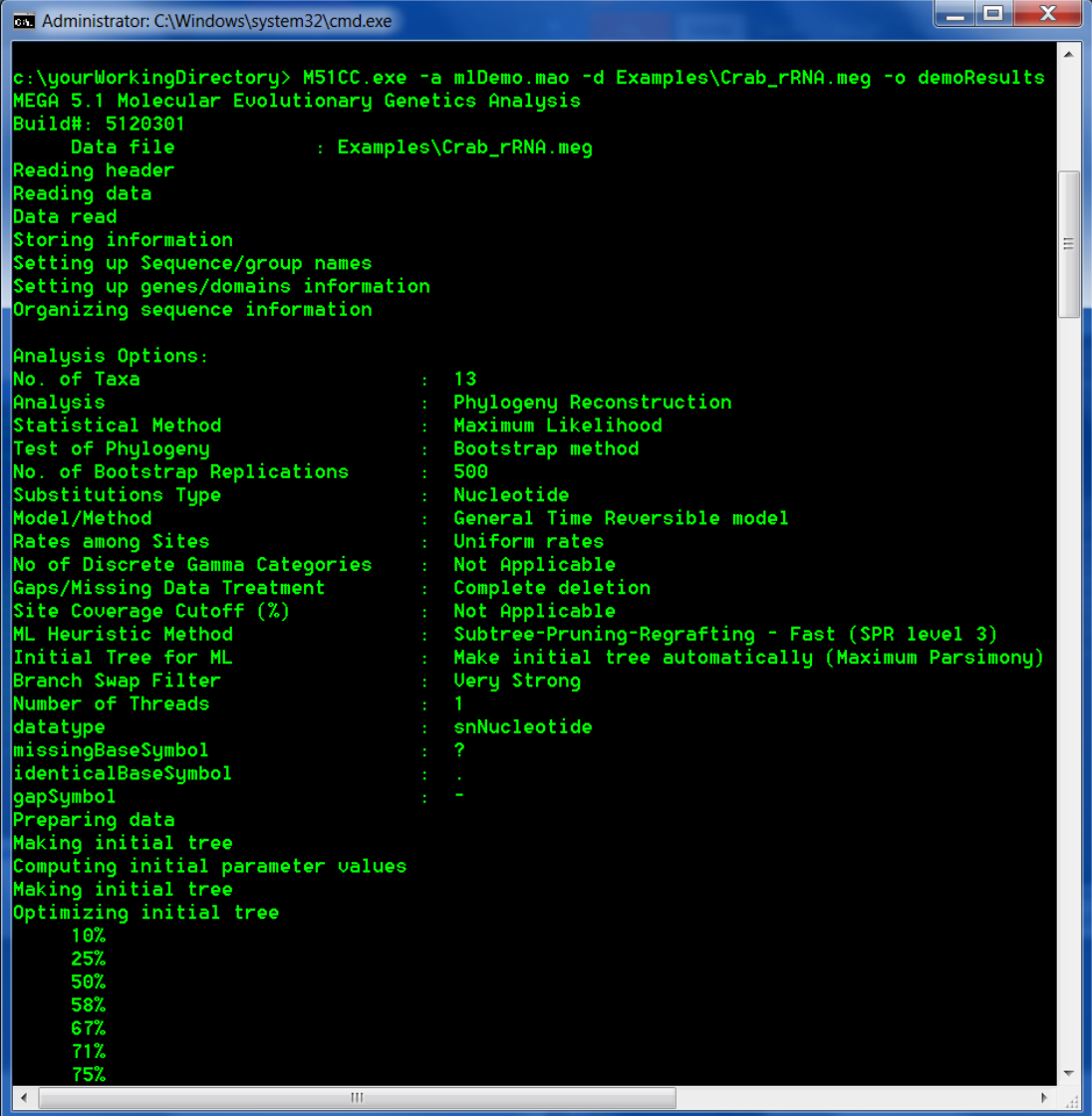
# Step 3

- The analyses will be launched sequentially and progress updates will be displayed in the command prompt window.

# Finally

- The analysis will produce output files for each input data file
- In this example, the same analysis options were used for each alignment file
- Enjoy!