DNAMAN
Sequence Analysis Software

Sequence Alignment and Phylogenetics

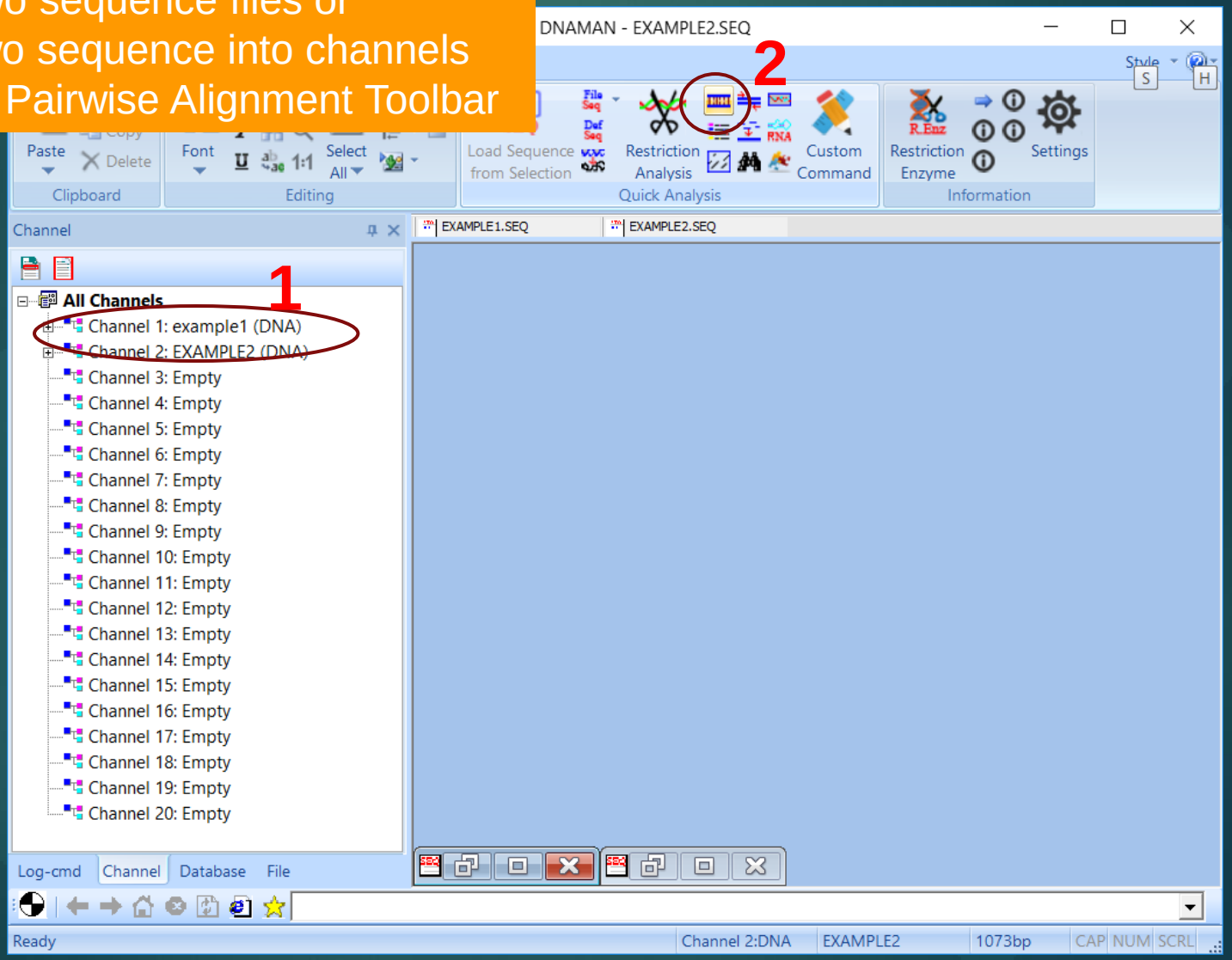
BIOINFORMATICS PLATFORM

Sequence Alignment and Phylogenetics

- Pairwise Sequence Alignment
- Multiple Sequence Alignment
- Phylogenetic Analysis

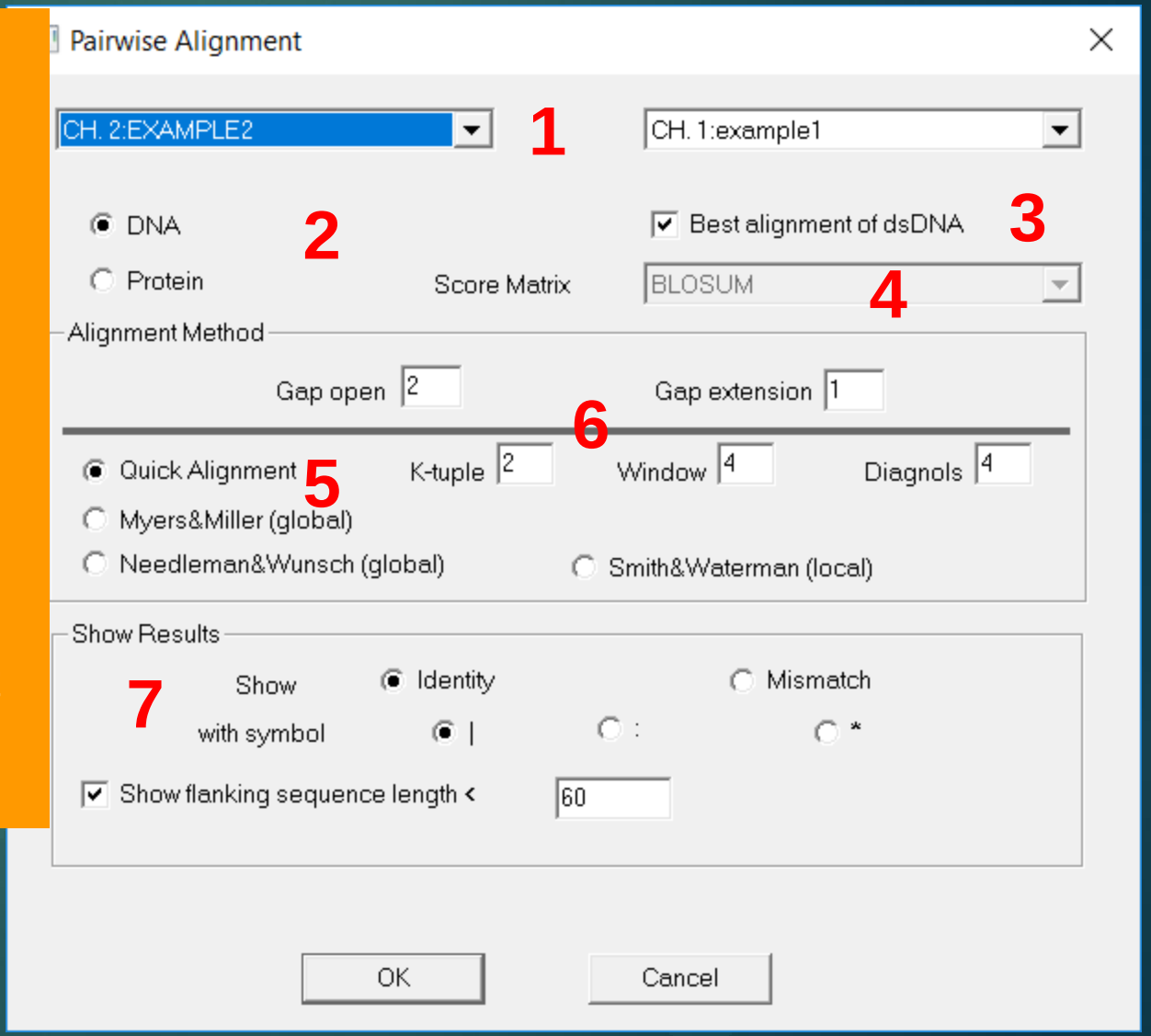
Pairwise Alignment

1. Open two sequence files or load two sequence into channels
2. Choose Pairwise Alignment Toolbar



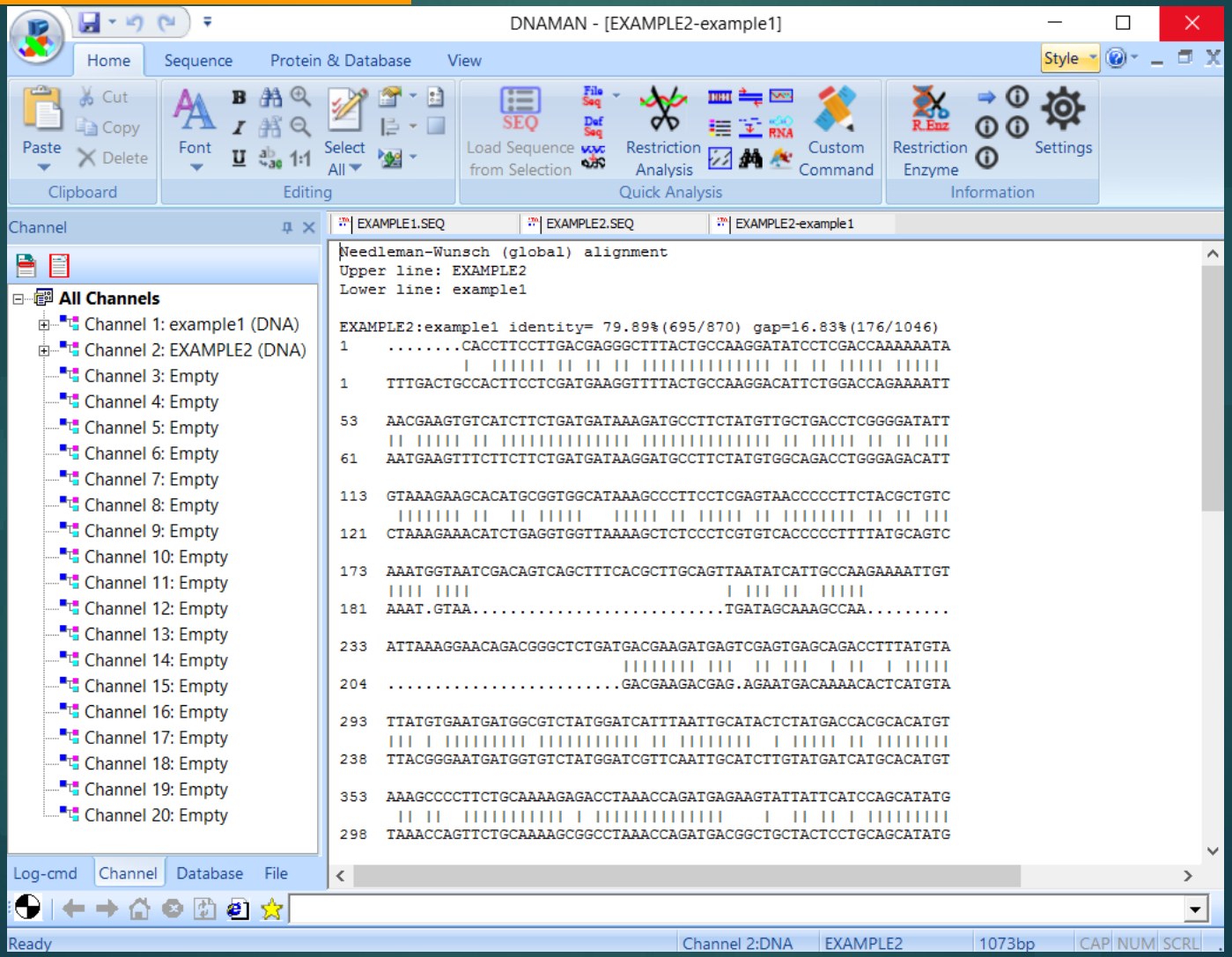
Pairwise Alignment

1. Select two sequences from channels
2. Select type of alignment
3. If DNA seq properties unknown, check “Best alignment of dsDNA
4. For Protein Seq alignment, choose a score matrix
5. Choose one of 4 alignment method
6. Choose parameters for alignment
7. Select sequence alignment display options
8. Click OK to start alignment



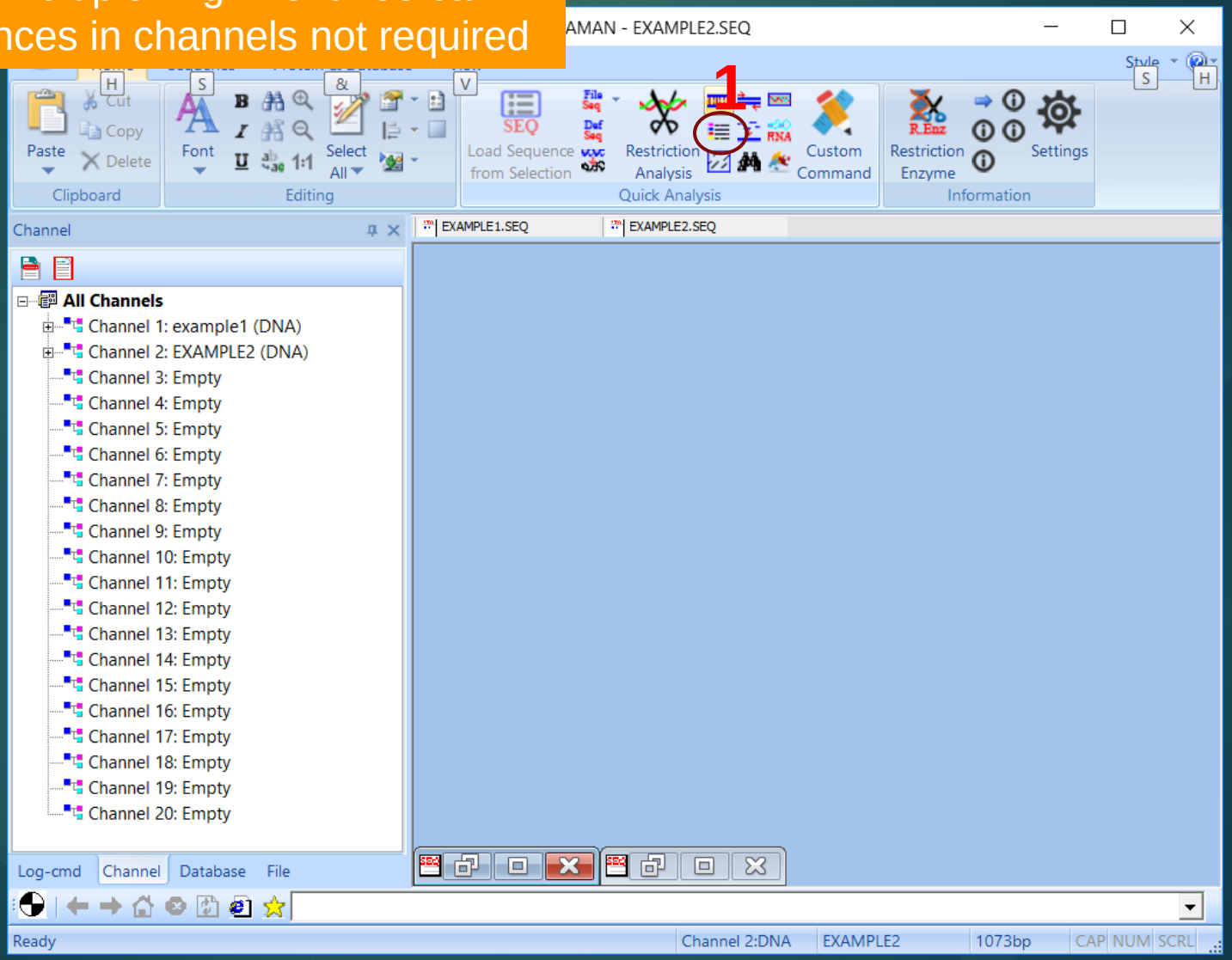
Pairwise Alignment

Result of Pairwise Alignment

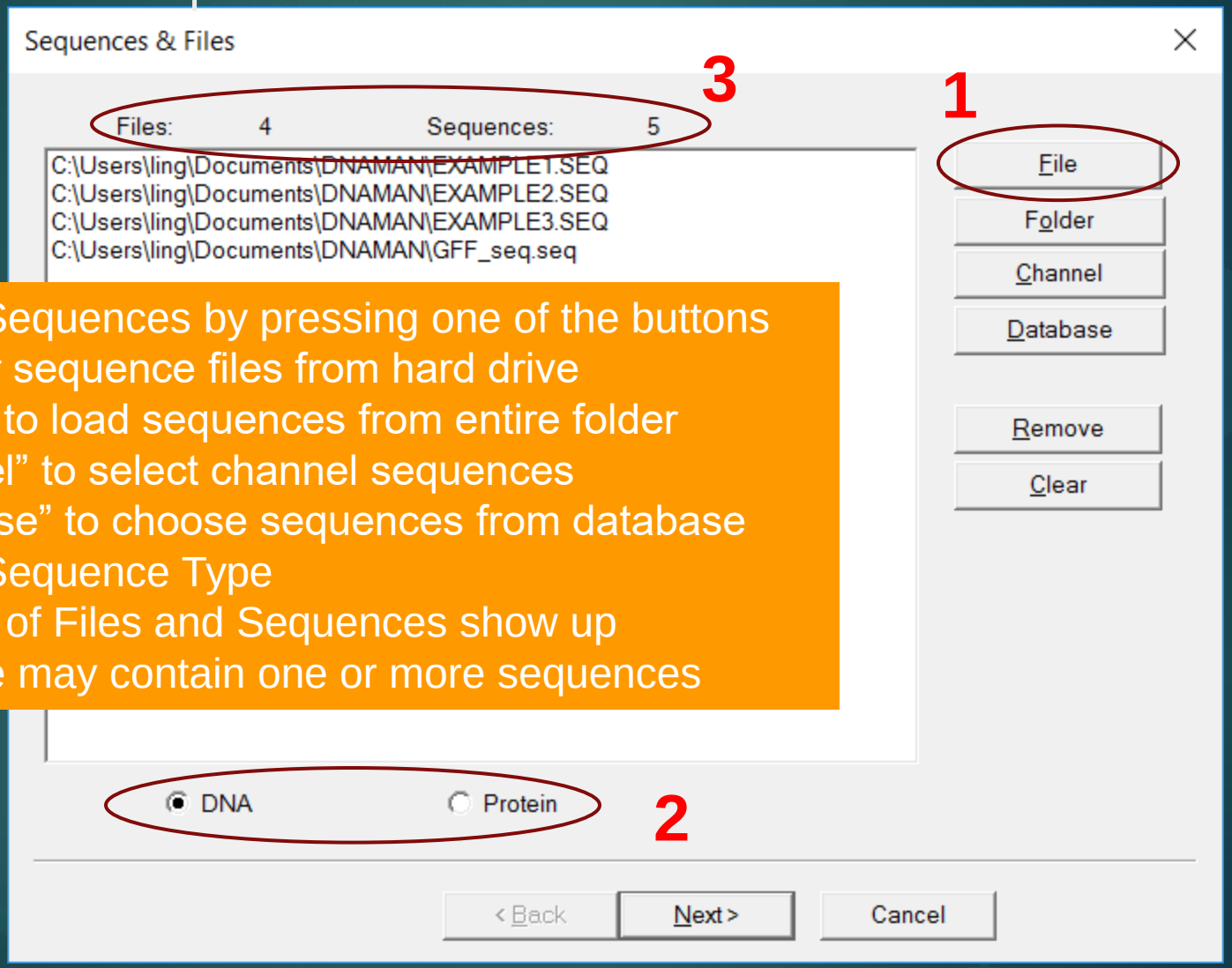


Multiple Alignment

1. Choose Multiple Alignment Toolbar
   Sequences in channels not required



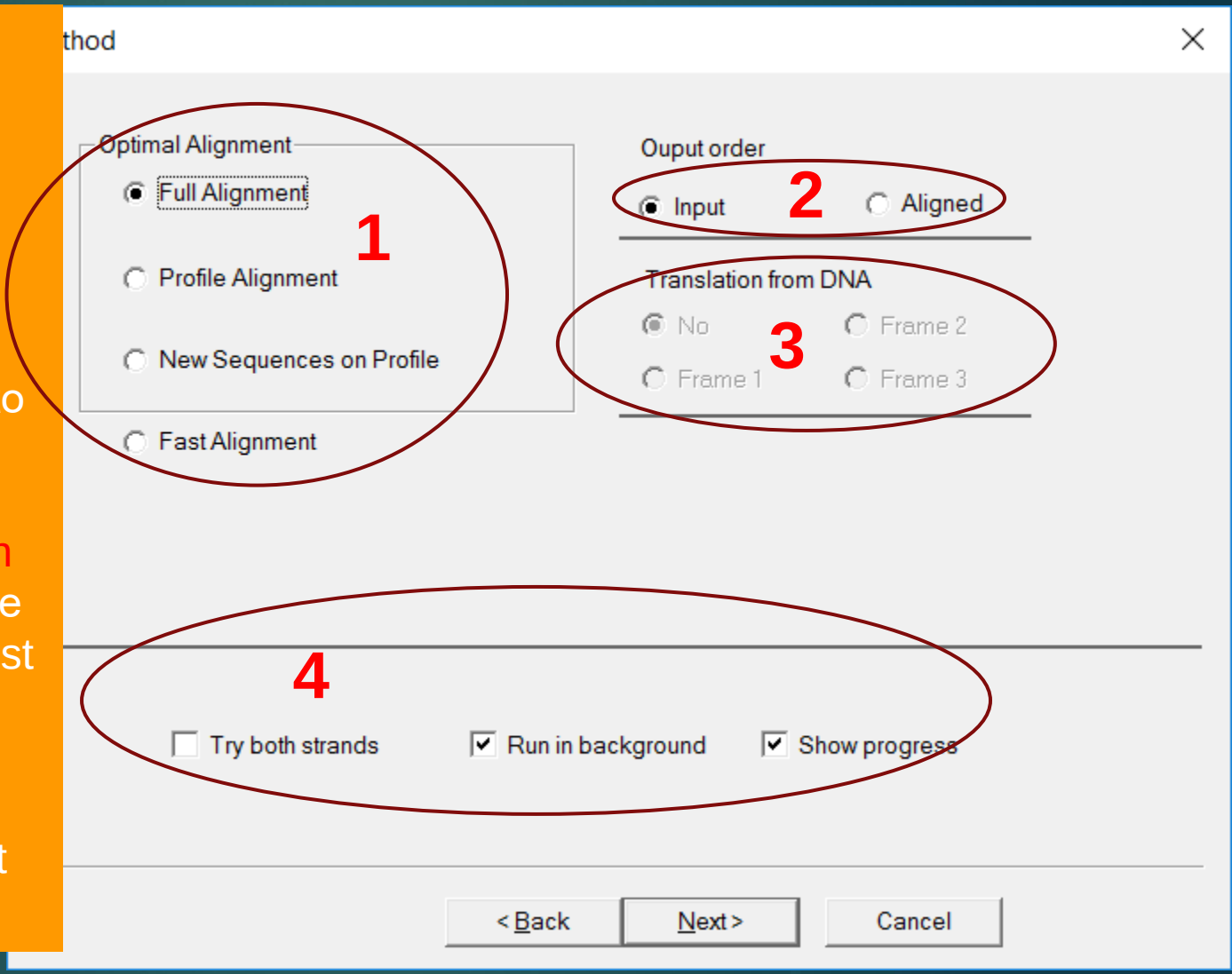
Multiple Alignment
- Select Sequences



1. Choose Sequences by pressing one of the buttons
   - "File" for sequence files from hard drive
   - "Folder" to load sequences from entire folder
   - "Channel" to select channel sequences
   - "Database" to choose sequences from database
2. Choose Sequence Type
3. Numbers of Files and Sequences show up
   - Each file may contain one or more sequences

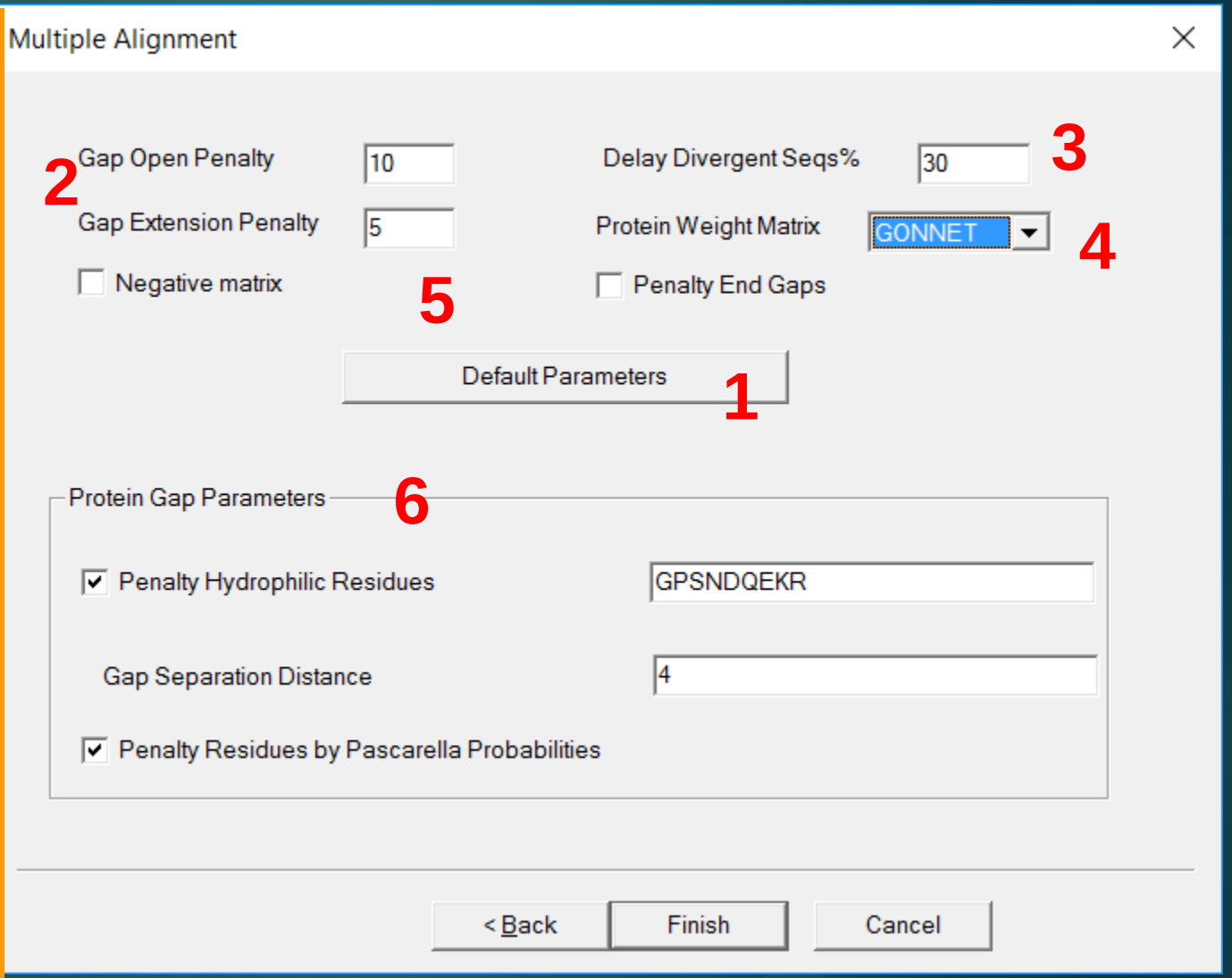
Multiple Alignment
- Alignment Methods

1. Choose Alignment Methods from 3 Optimal and 1 Fast alignment
   - "Full Alignment" to fully align all sequences
   - "Profile Alignment" to align two sets of aligned sequences
   - "New Sequences on Profile" to align more sequences to the first sequence set
   - "Fast Alignment" to align all sequences using fast alignment algorithm



Multiple Alignment
- Multiple Alignment Parameters

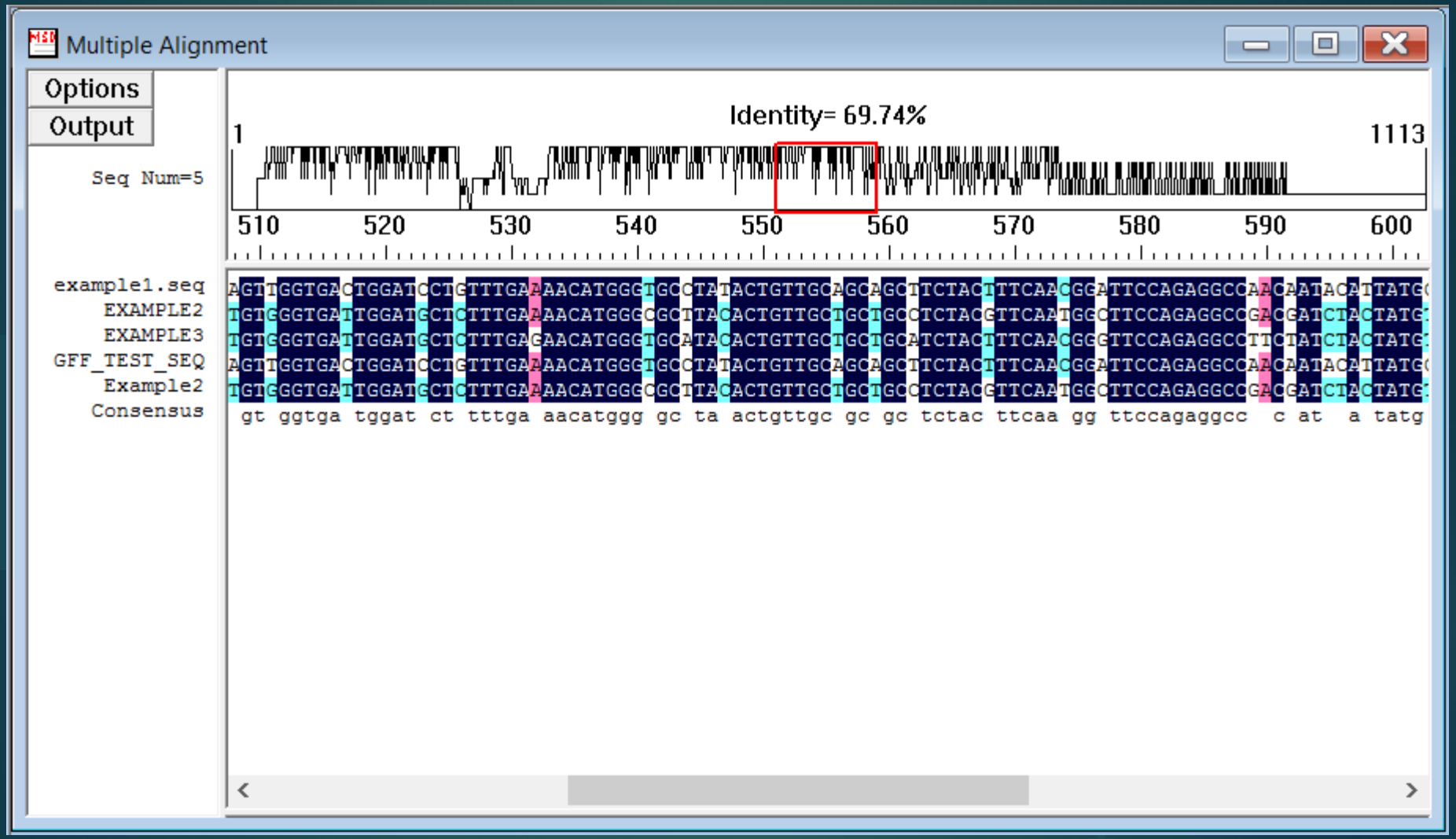
1. To use default parameters instead of user-defined ones, press Default Parameters button
2. Change Gap Open and Extension penalties if needed
3. Sequences with poor homologous score can be delayed for alignment
4. Protein specific weight matrix can be selected
5. Negative matrix and penalties for gaps at ends can be used
6. More protein gap penalties can be used



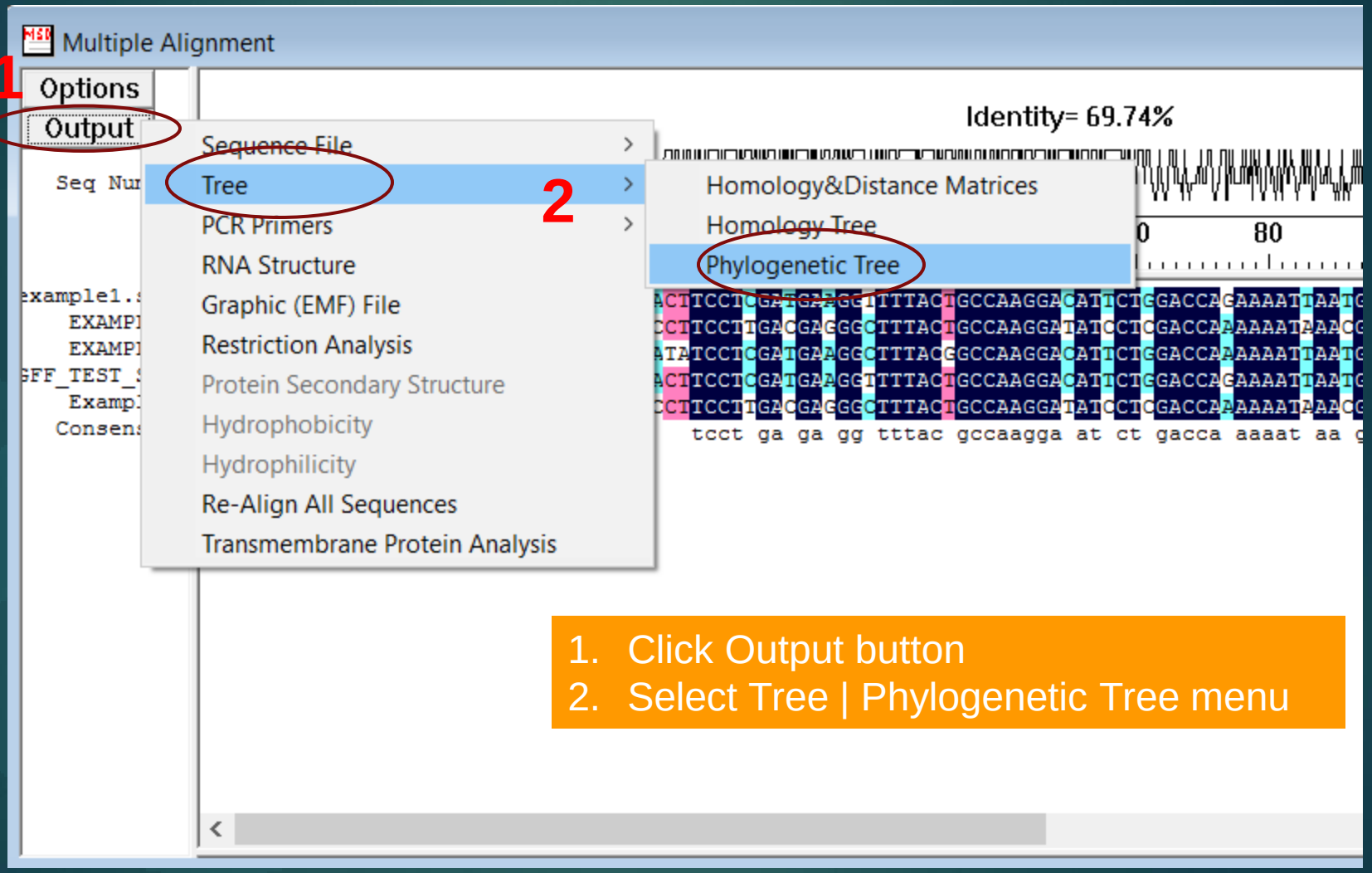
Reference:
Thompson et al (1994) ***Nucleic Acids Res.*** 22:4673

Multiple Alignment

- Multiple Alignment Result

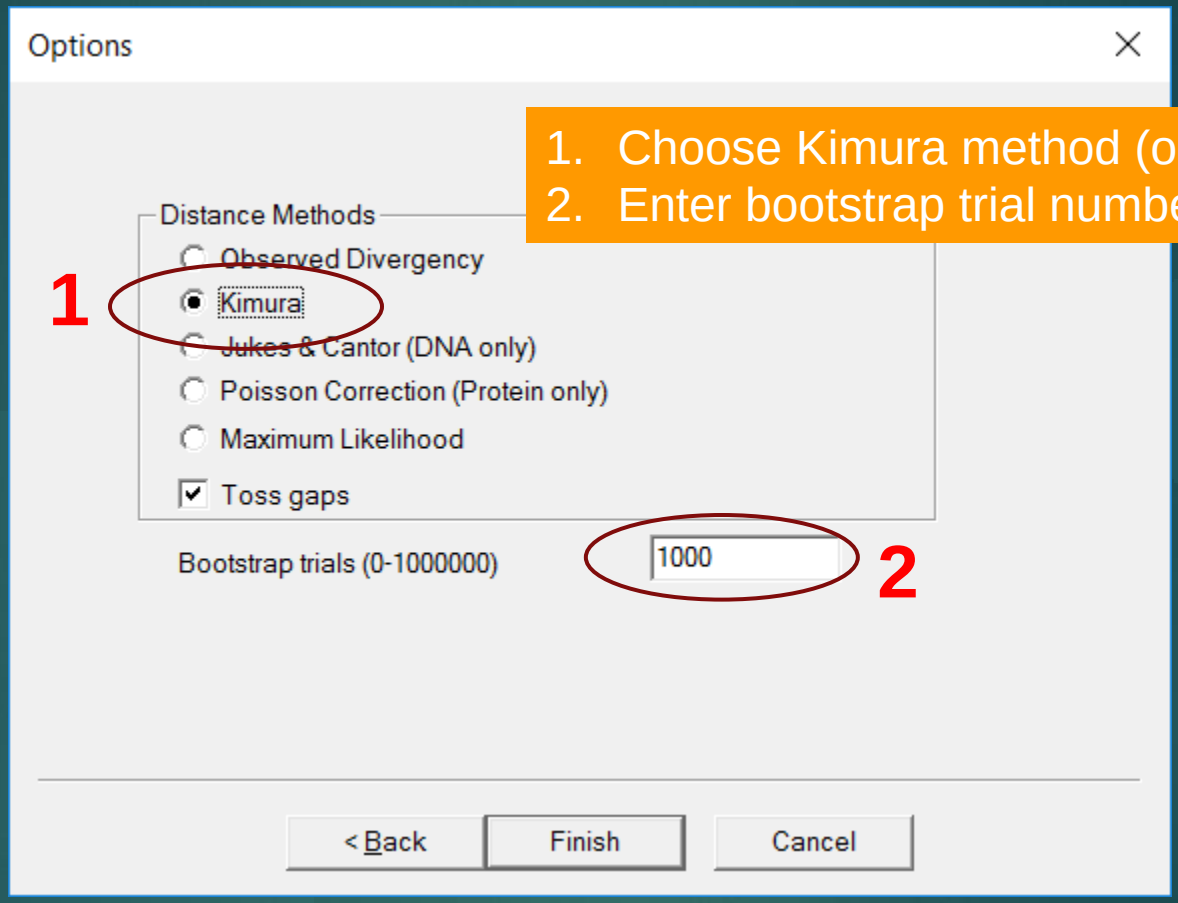


Phylogenetic Analysis

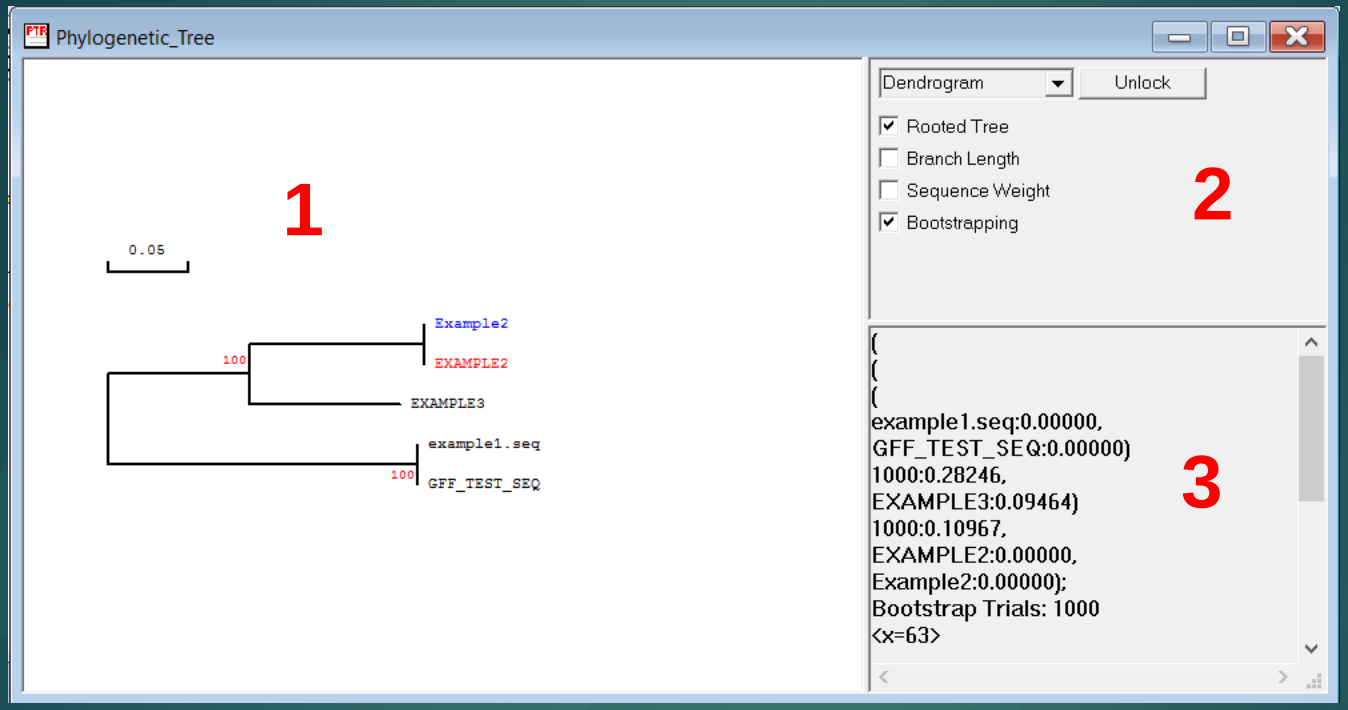


1. Click Output button
2. Select Tree | Phylogenetic Tree menu

Phylogenetic Analysis
- Tree Options

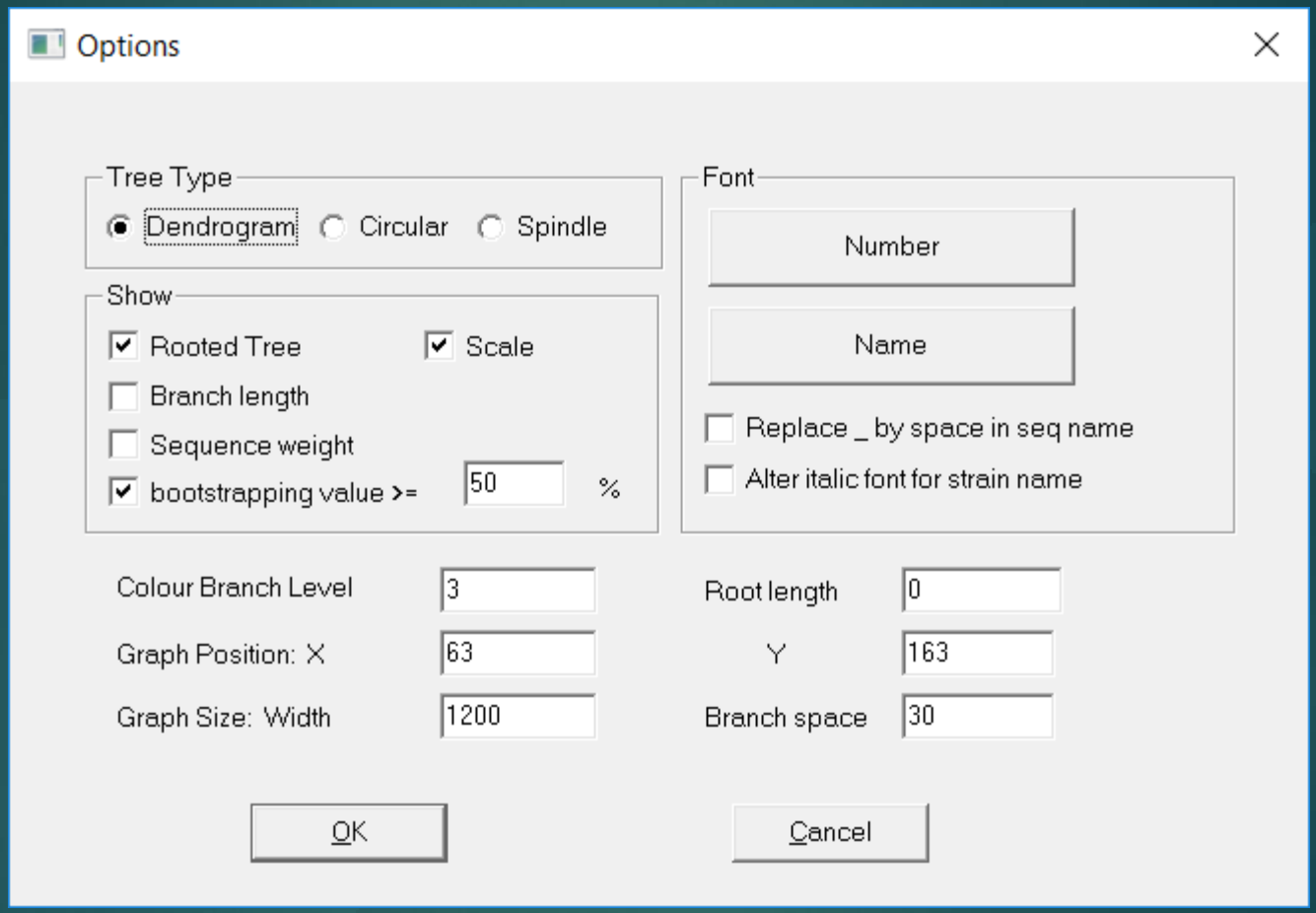


Phylogenetic Analysis
- Tree View



1. Tree graph window: Double-click to open Tree Options dialog box
2. Graph control window
3. Tree description text window

Phylogenetic Analysis
- Tree View Options



Phylogenetic Analysis
- Tree Type