DNAMAN
Sequence Analysis Software

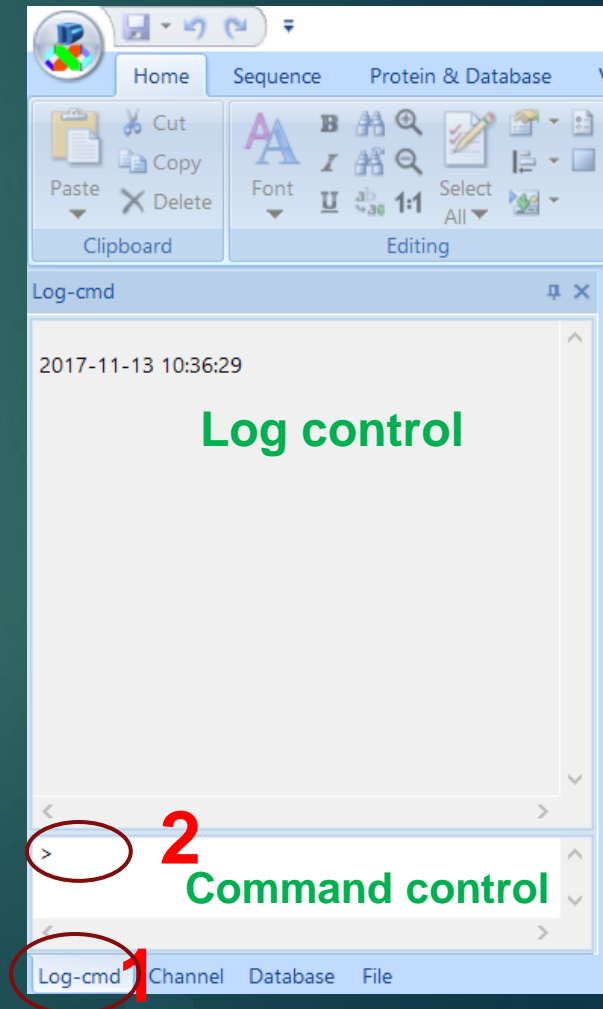# *Command Line and Batch Processing*

BIOINFORMATICS PLATFORM

DNAMAN Command Line and Batch Processing

- Command line Basics
- Command line Details
- Batch Processing
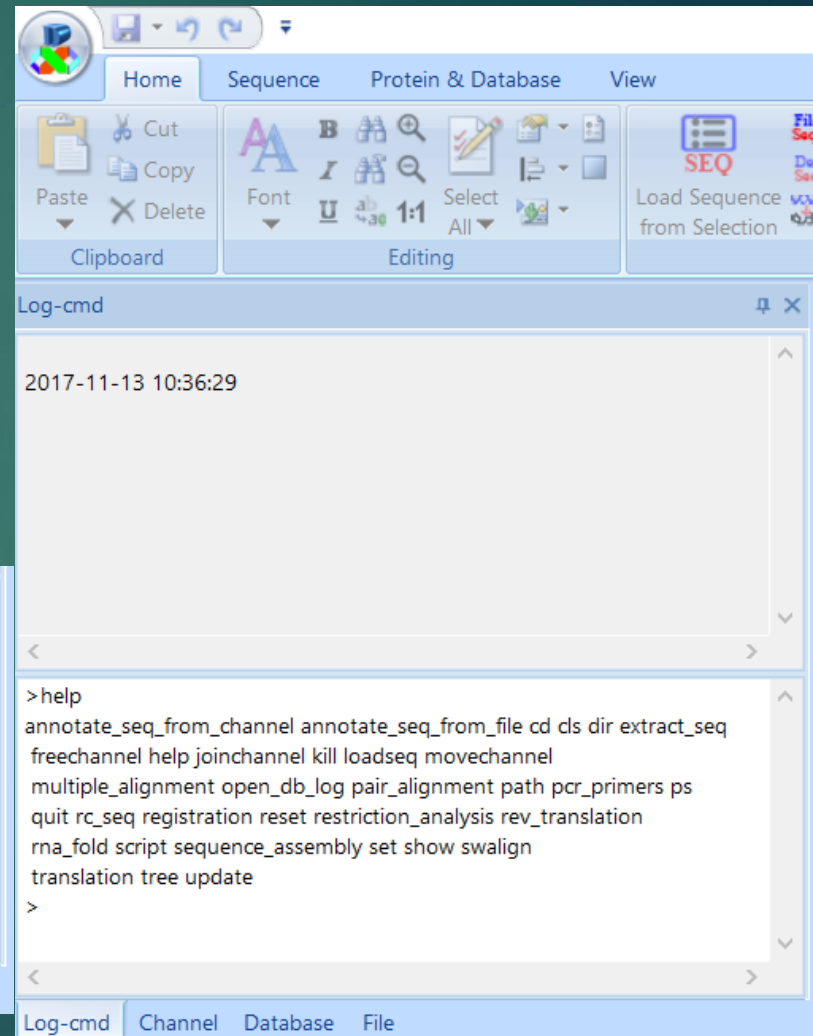- Scripting

Command Line Basics
- Getting Started

▶ Start in Log-cmd tab for command line processing

▶ Enter command at Prompt >

▶ Additional log information in Log control

▶ Type "help" to get list of available commands

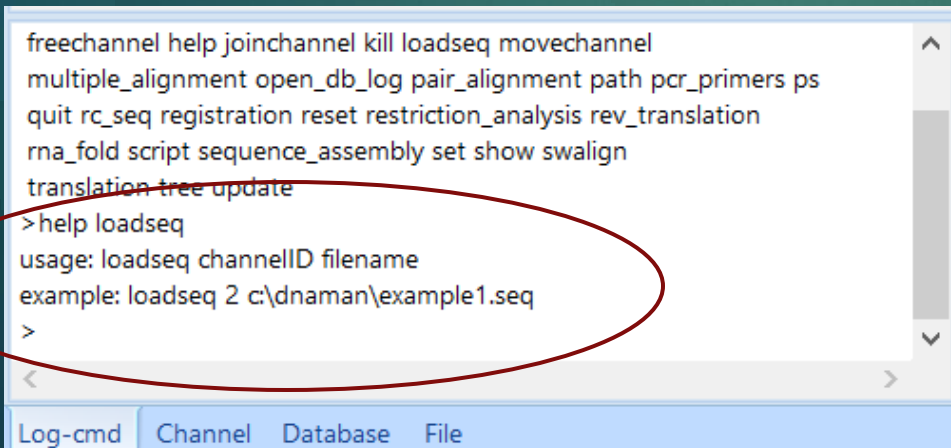▶ Type a command without parameter and DNAMAN displays its usage

Command Line Basics
- Getting Help

▶ Type "help" to get list of available commands

▶ Type "help" followed with command to get help for the specific command, eg "help loadseq"

Command Line Details
- "show"

▶ >show

usage: show function parameters

▶ example: show all

A list of parameters are shown in the Log window

▶ example: show translation

Only Translation parameters show up

....
15-Seq_Search:
Blast_Server=
http://www.ncbi.nlm.nih.gov/blast/

16-Protein_Structure:
Filter= 1
Remove_Singlet= 1
Remove_Poor= 1
Poor_Length= 40
Poor_Homology= 20

17-Translation:
AAperRow= 20
AAsymbolID= 0
Display_Parent_seq= 0
Reading_frames= 3

Command Line Details - "set"

- ▶ >set

usage: set function parameter

- ▶ example:

    set restriction_analysis enzyme_file=restric.enz

- ▶ Type "show restriction_analysis" to verify if parameters set correctly

Command Line Details

- Commands are mostly self-explanatory

- DNAMAN program may be used as command line executable

  - DNAMAN is installed on your computer and dnaman.lnk is located on your Desktop. Launch a CMD console and cd to your Desktop.

  - Type the following command:

    dnaman.lnk –e multiple_alignment folder c:\dnaman\msd *.seq

    This command will perform multiple alignment for all sequence files in the folder c:\dnaman\msd

  - Type the following command

    dnaman.lnk –s dnaman_script1.txt

    This command will execute all commands in the dnaman_script1.txt file

Batch Processing

Many commands are processed in batches
- ▶ Extracting sequences in batches
- ▶ Protein translation in batches
- ▶ Annotation processing in batches
- ▶ Scripting

Batch Processing
- "extract_seq"

► *Application: Extract specific annotations from sequences*

► >extract_seq

usage: extract_seq [channel/file/folder] ids annotation_name annotation_type

► Example:

extract_seq file c:\dnaman\puc18.seq bla gene

This command will extract a sub-sequence from puc18.seq with an annotation name "bla" and type "gene".

annotation_name can be set "none" if it is not relevant for extraction.

If folder is specified, all sequence files in the folder will be extracted.

Batch Processing
 - "translation"

- ***Application: Translate specific annotations from sequences***

- >translation

usage: translation [channel/seq/file/folder] IDs annotation_type

- Example:

      translation file c:\dnaman\puc18.seq cds

This command will translate all subsequences of puc18.seq with annotation_type "cds".

If folder is specified, all sequence files in the folder will be translated.

Batch Processing
- "translation"

- ***More samples***

- [Download translation_samples.zip from lynnon web site](#)

- Extract downloaded zip file and place the folder in DNAMAN folder in your Documents. You may see:

    c:\users\your_user_name\documents\DNAMAN\translation_samples

- Make sure "translation_samples" contain sequence files (not another folder "translation_samples")

- Type command

    translation folder translation_samaples cds

This command will translate all files in "translation_samples" folder with annotation type "cds".

Batch Processing
- "annotate_seq_from_file"

- ***Application: Add annotations to sequences***

- >annotate_seq_from_file

usage: annotate_seq_from_file [channel/file/folder]

- example: annotate_seq_from_file channel 1 annot_list.dat

This command will annotate channel 1 using annotations defined in annot_list.dat. The file annot_list.dat must be in DNAMAN consensus sequence format which example files can be found in DNAMAN\consens folder.

- example: annotate_seq_from_file folder c:\dnaman\seq promoters.dat

This command will annotate all files in c:\dnaman\seq folder using annotations defined in promoters.dat

Scripting

▶ ***Application: Execute sequentially a series of commands***

▶ >script

usage: script (filename)

▶ example:

   script c:\dnaman\dnaman_script.txt

This command will execute all commands in dnaman_script.txt file

▶ dnaman_script.txt sample content   :

   dnaman_script

   rna_fold file c:\dnaman\example1.seq

   wait 2

   translation folder c:\dnaman\seq cds