

DNAMAN

Sequence Analysis Software

*Command Line  
and Batch  
Processing*

BIOINFORMATICS PLATFORM

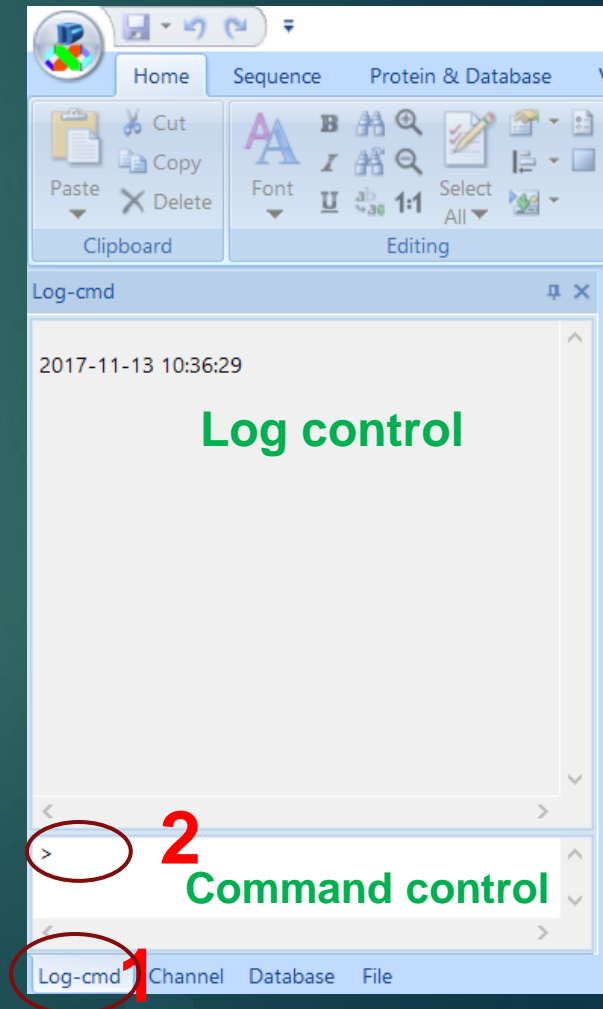
# DNAMAN Command Line and Batch Processing

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

# Command Line Basics

## - Getting Started

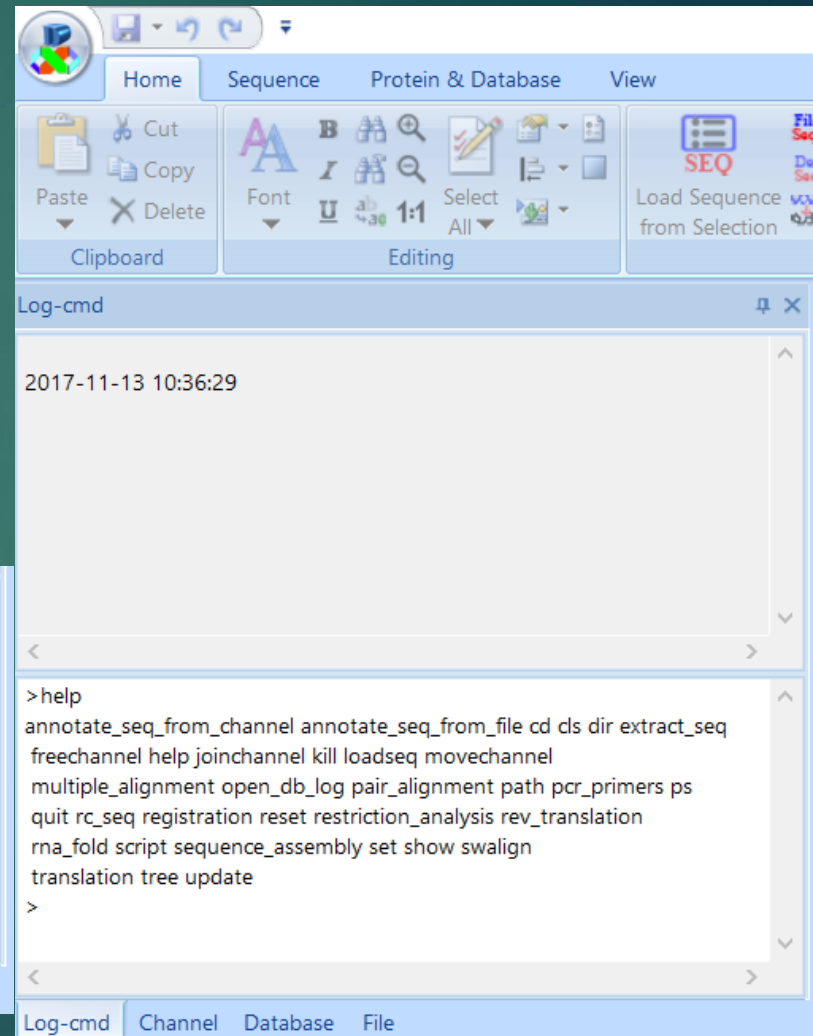
- ▶ Start in Log-cmd tab for command line processing
- ▶ Enter command at Prompt >
- ▶ Additional log information in Log control
- ▶ Type “help” to get list of available commands
- ▶ Type a command without parameter and DNAMAN displays its usage



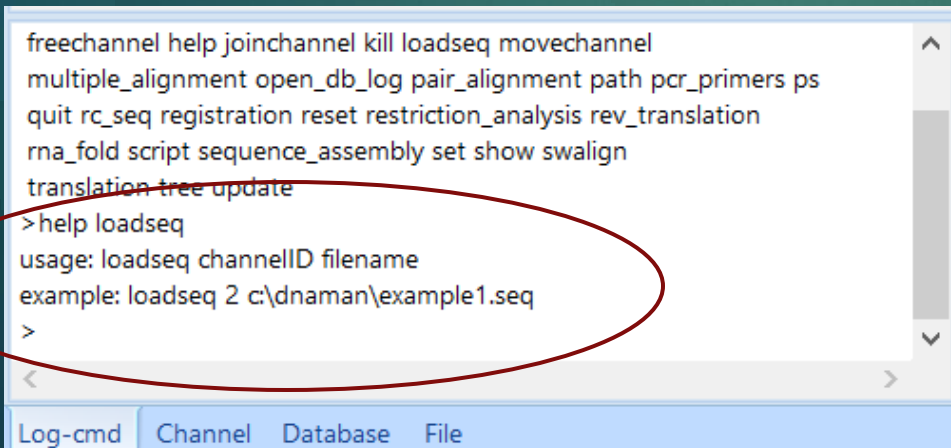
# Command Line Basics

## - 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”



The screenshot shows a software interface with a ribbon menu (Home, Sequence, Protein & Database, View) and a toolbar. Below the toolbar is a window titled "Log-cmd" containing a command prompt. The command prompt shows a list of available commands: freechannel, help, joinchannel, kill, loadseq, movechannel, multiple\_alignment, open\_db\_log, pair\_alignment, path, pcr\_primers, ps, quit, rc\_seq, registration, reset, restriction\_analysis, rev\_translation, rna\_fold, script, sequence\_assembly, set, show, swalign, translation\_tree, and update. The command ">help loadseq" is entered, and the output shows the usage: "usage: loadseq channelID filename" and an example: "example: loadseq 2 c:\dnaman\example1.seq".



This is a close-up of the command prompt window from the previous screenshot. It shows the list of commands and the help output for "loadseq". The text is as follows:

```
freechannel help joinchannel kill loadseq movechannel
multiple_alignment open_db_log pair_alignment path pcr_primers ps
quit rc_seq registration reset restriction_analysis rev_translation
rna_fold script sequence_assembly set show swalign
translation_tree update
>help loadseq
usage: loadseq channelID filename
example: loadseq 2 c:\dnaman\example1.seq
>
```

The text "usage: loadseq channelID filename" and "example: loadseq 2 c:\dnaman\example1.seq" is circled in red.

# 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
```

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