

Using tacg restriction analysis program with BioEdit.

This manual was put together by Stan Vitha. Updated 10/2016

Background:

While BioEdit has a built-in restriction analysis feature, the output is not as neat and informative as the one generated by `tacg`. `tacg` is a unix program for pattern search in DNA sequences. Its most popular application is for restriction analysis. It is a very fast command line program, thus is very suitable for execution from other programs. In order to run this software on Windows machines, it is necessary to install the basic CygWin release (www.cygwin.com) that will create a unix-like environment on your computer. It is recommended to install the optional “mc” (Midnight Commander) package, this will make file copying and editing much easier.

NOTE: Even on a 64-bit Windows system you will need a 32-bit Cygwin installation. Existing pre-compiled tacg executable will not work with 64-bit Cygwin.

Once the CygWin is installed, download the `tacg` executable that was compiled for CygWin (<http://www.mhoenicka.de/software/cygwinports/tacg.html>). Save the zipped tar file (“`cygwin1.1.4-tacg-3.04.tar.gz`”) in cygwin “tmp” directory.

Open the cygwin terminal and run the “mc” file manager.

Note: you can toggle between the graphical interface and the command line view by “Ctrl-O”

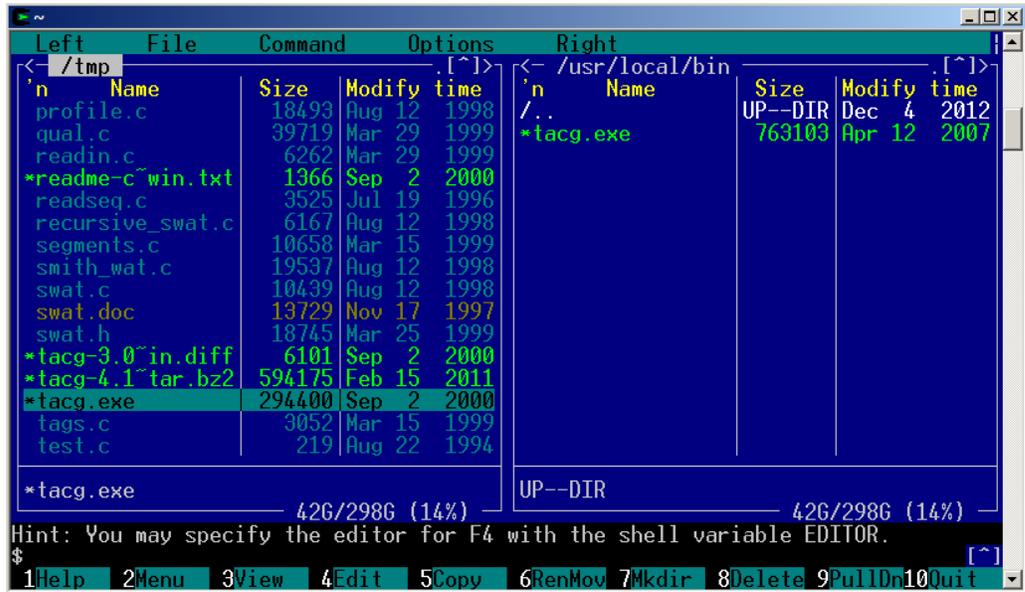
Navigate to the “tmp” directory and extract the compressed tar file:

```
$ tar -xvf cygwin*.gz
```



```
SViTha@TAMU-0108761 /tmp
$ ls cyg*
cygwin1.1.4-tacg-3.04.tar.gz
SViTha@TAMU-0108761 /tmp
$ tar -xvf cygwin*.gz
Data/codon.data
Data/matrix.dat.FULL.1998.gz
Data/matrix.data.yeast
Data/matrix.examples
Data/rebase.dam
Data/rebase.dam+dcm
Data/rebase.data
Data/rebase.dcm
Data/regex.data
Docs/tacg.1
Docs/tacg3.main.html
Docs/tacg3.main.html.old
Docs/tacg3.man.html
Docs/tacg3.man.pre
readme-cygwin.txt
tacg.exe
tacg-3.04-cygwin.diff
SViTha@TAMU-0108761 /tmp
$
```

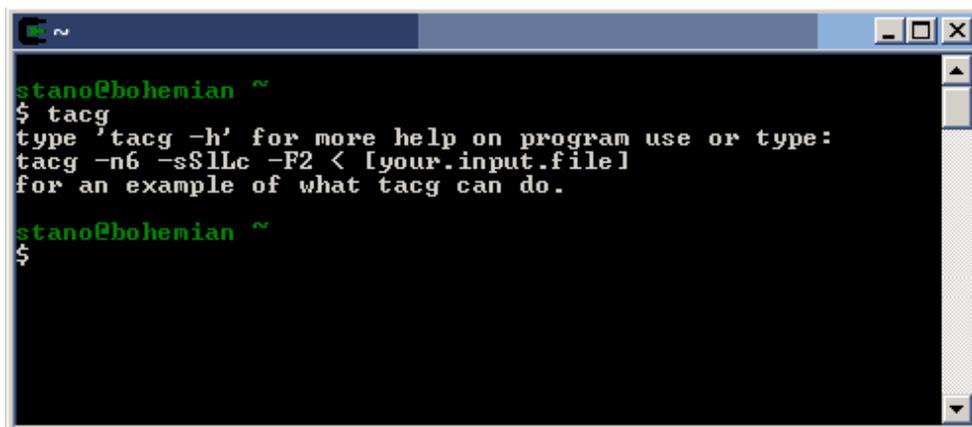
Follow the installation instructions in the “`readme-cygwin.txt`”:



- copy `tacg.exe` into `/usr/local/bin`.
- Copy the `tacg.1` man file in the `/Docs` subdirectory to your `man1` directory (`/usr/share/man/man1`)
- Copy all files in the `/Docs` and `/Data` subdirectories into one directory with read access for all users, e.g. `/usr/local/lib/tacg`,
- Create a system-wide environment variable `TACGLIB` which points to this directory- edit the file `/etc/profile` and add the following lines:

```
# set the TACG Library environmet variable
export TACGLIB=/usr/local/lib/tacg
```

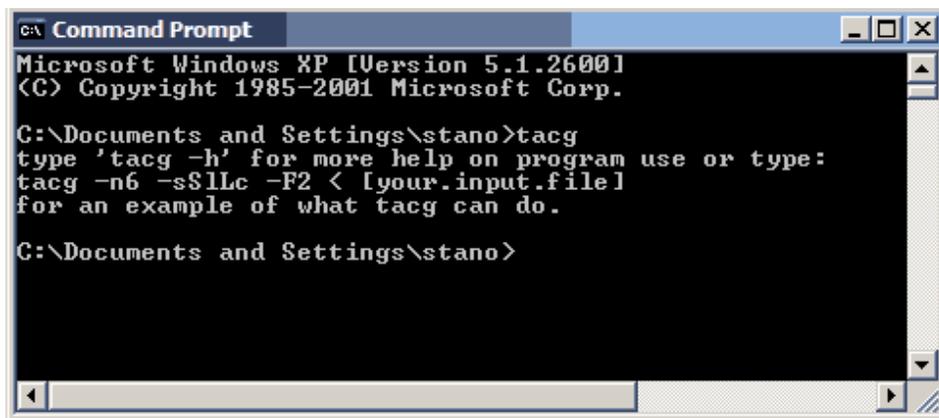
Also make sure the `PATH` environment variable includes the location where `tacg` is installed (`/usr/local/bin`). After the installation is complete, you should be able to start cygwin shell and run `tacg` without any parameters. It should return a short message (see below).



Now that tacg is installed and functional, the next step is to invoke the tacg program as if it was a DOS command, i.e. without starting the cygwin shell window. For this to work, the Windows PATH environment must include the path to the tacg executable and to its library files. In the Windows Control Panel – System, choose the “Advanced” , “Environment Variables”.

- Add a user variable PATH, value =
C:\cygwin\bin;C:\cygwin\usr\local\bin
- Alternatively, if you have administrative privileges, edit the PATH system variable and add the same string to the end of the existing path (beware that the individual paths must be separated by a semicolon):
- Create a new user or system variable TACGLIB, its value is
c:\cygwin\usr\local\lib\tacg

Now open a Command Prompt window and run tacg without any parameters. You should get the same response as when it was run from the cygwin shell:



```
C:\ Command Prompt
Microsoft Windows XP [Version 5.1.2600]
(C) Copyright 1985-2001 Microsoft Corp.

C:\Documents and Settings\stano>tacg
type 'tacg -h' for more help on program use or type:
tacg -n6 -s$llc -F2 < [your.input.file]
for an example of what tacg can do.

C:\Documents and Settings\stano>
```

Finally, In order to create the accessory application menu item for tacg in Bioedit, add the following lines to the end of “accApp.ini” file located in the “Bioedit\apps” folder:

On the first line below, edit the path to tacg as needed (on 64-bit windows, even the 32-bit version of Cygwin is located in C:\cygwin64)

```
[tacg]
Program=C:\cygwin\usr\local\bin\tacg.exe
Don't use interface=0
Don't create menu item=0
Auto-Feed=1
Degap Sequences=1
Separate Files=0
Auto-Feed File Format=1
Auto-Feed File Name Required=0
Remove redundancies=0
Truncate titles=0
Change spaces in titles=0
Specific File Name=
Prompt for Input File=0
```

Prompt for Output File=0
Open Output as Alignment=0
Open Output as Text=1
Open Output with External Program=0
External Program Name=C:\WINDOWS\system32\write.exe
Open Output with Accessory Application=0
Accessory Application to open with=
Input File Prefix=
Output File Prefix=
Specify Input File Name=0
Specify Output File Name=0
Input File Name=input.fas
Output File Name=out.txt
Input File Prefix Required=0
Space after input prefix=0
Output File Prefix Required=0
Space after output prefix=0
Input File Name Arbitrary=0
Output File Name Arbitrary=0
Redirect input from stdin=0
Redirect output from stdout=0
Default Command Line=-s < input.fas
View Documentation Option=0
Documentation File=
Description=
Include Additional Options Box=0
Redirect General stdout=1
Stdout Redirected Filename=out.txt
Redirect General stdin=0
Stdin Redirected Filename=
Add input file to command line=0
Add output file to command line=0
output command at beginning=0
input command at beginning=0
output command at end=0
input command at end=0
c0 Title=6-cutters only
c0YES="-n6"
c0NO="-n4"
c0 Default=1
c1 Title=Circular DNA
c1YES="-f0"
c1NO="-f1"
c1 Default=0
c2 Title=Table of Fragment Sizes
c2YES="-F 1"
c2NO=""
c2 Default=0
c3 Title=Ladder Map
c3YES="-l"
c3NO=""
c3 Default=0
c4 Title=Table of Cut Sites
c4YES="-S "
c4NO=""
c4 Default=1
c5 Title=dam methylated?

```

c5YES="--dam"
c5NO=""
c5 Default=0
c6 Title=dcm methylated?
c6YES="--dcm"
c6NO=""
c6 Default=0
c7 Title=Double Stranded Output?
c7YES="--strands 2"
c7NO="--strands 1"
c7 Default=1
c8 Title=Tickmarks
c8YES=""
c8NO="--notics"
c8 Default=1
i0 Title=ORF Analysis (frames,minimum size)
i0 Prefix="-O "
i0 Default=123,25
i0 CheckBox=1
i0 CheckBox Title=ORF Analysis
i0 CheckBox Default=0
i1 Title=5=5', 3=3', 0=blunt, 1=all
i1 Prefix="-o "
i1 Default=1
i1 CheckBox=1
i1 CheckBox Title=Overhang of Ends
i1 CheckBox Default=1
i2 Title=Output Width (n x 15 characters)
i2 Prefix="-w "
i2 Default=75
i2 CheckBox=0
i2 CheckBox Title=0
i2 CheckBox Default=0
i3 Title=Frames 1,3, or 6, Code 1 or 3-letter
i3 Prefix="-T "
i3 Default=3,1
i3 CheckBox=1
i3 CheckBox Title=Linear Cotranslation
i3 CheckBox Default=1
i4 Title=1 = 1st base of sequence
i4 Prefix="-b "
i4 Default=1
i4 CheckBox=1
i4 CheckBox Title=Beginning of Subsequence
i4 CheckBox Default=1
i5 Title=0 = last base of sequence
i5 Prefix="-e "
i5 Default=0
i5 CheckBox=1
i5 CheckBox Title=End of Subsequence
i5 CheckBox Default=1

```

Now start BioEdit, load some sequences, highlight one and run the “tag” accessory application. Enjoy!

