

SEQUENCHER®

Tutorial for Macintosh

Working with AppleScript

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Gene Codes Corporation

T C A G E N E
A G T C O D E S

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Sequencher and AppleScript

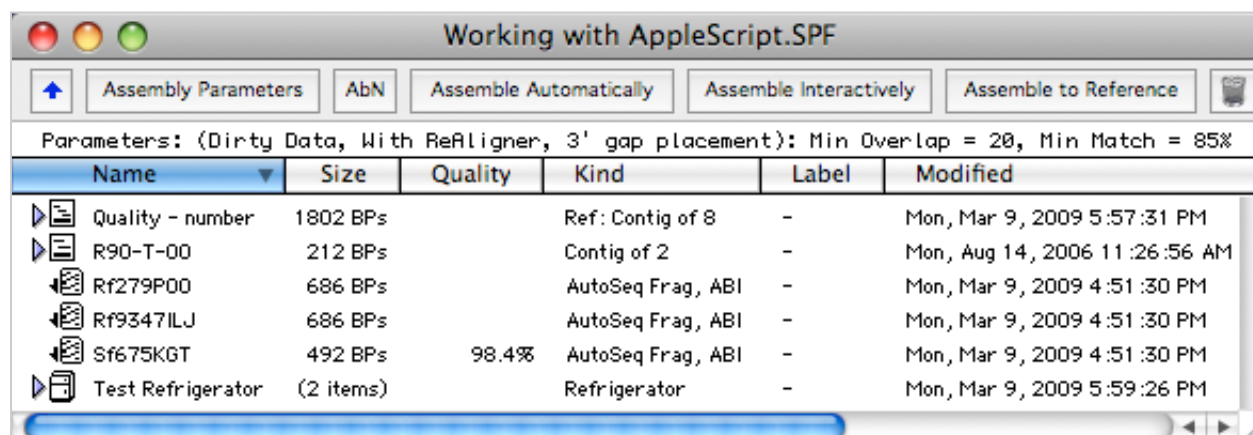
INTRODUCTION

This tutorial will show you how to use AppleScript to get more from Sequencher. This will not be a tutorial on AppleScript itself, there are many excellent web sites, books and tutorials that already do that. The tutorial will give you a glimpse into the potential of AppleScript and how it can help you get more from Sequencher. By the end of this tutorial you will be able to open an AppleScript in Sequencher, run it, and modify it.

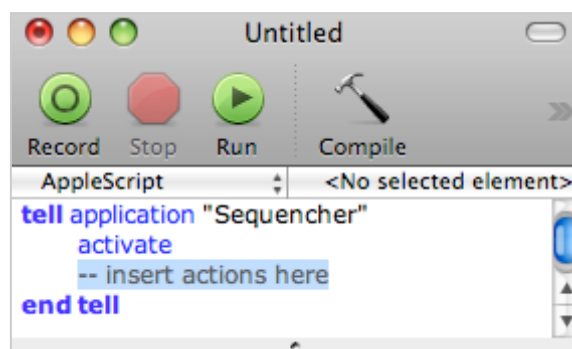
RUNNING A SCRIPT

In order to run an AppleScript with Sequencher you will need to have an open project and an open script.

- Launch Sequencher.
- From the **File** menu, choose **Open Project...** and locate the project called "Working with AppleScript" inside the AppleScript sub-folder of the Sample Data folder. This project contains contigs, fragments, and a refrigerator.
- Select the project and click the **Open** button.



- Go to the **Window** menu and choose **Script Window**. The Script Editor opens with a window ready for you to start writing a script.



- Close this window by clicking on the red **Close** button.
- A window appears asking if you wish to save your script. Click the **Don't Save** button.

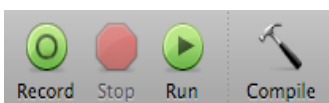
Now you need to locate the script with which you are going to work.

- From the AppleScript Editor **File** menu, choose **Open** and locate the script called "Custom Report" inside the AppleScript sub-folder of the Sample Data folder.
- Select the script and click the **Open** button.

The function of this script is to create a report of your project.

If you have not worked with AppleScript before you will see that the script is composed of colored text and gray text. The gray text is comment; in this script the comments will tell you what the different segments do or if there are any special requirements. The colored text is the actual script. Take a moment to scan through the script to see the different segments.

```
-- Get the volume name
tell Application "Finder"
  activate
  set volName to get name of startup disk
end tell
```



- Click on the green Run button to run the script.

The resultant report will be written to a text file on your Desktop called Custom report DDHHMM where DDHHMM is the time stamp representing the day of the month, hour, and minute. You can open this file in any text editor.

- Use a text editor to open the report.
- Scan through the report noting the different types of information.

You will see a comprehensive set of information including the total number of fragments assembled into contigs, the total number of edited bases, the average depth of coverage of all contigs, an example of an ABI data sheet, and more information on the contigs.

```
project name: Working with AppleScript.SPF
Monday, November 21, 2011 1:44:28 PM
```

```
----- PART 1 -----
Total Fragments: 10    with combined len: 5247 bases
Total Contigs: 2 with combined len: 2014 bases
```

```
# of fragments not incorporated into contigs: 3
Total # of edited bases in all fragments: 0
Average depth of coverage of all contigs: 2.313263041065
```

```
----- PART 2 -----
contig: Quality - number
      Quality - eight: 585 bases long, starting at 0
      2 ambiguous base calls in this sequence.
```

```
----Start an example of an ABI data sheet for fragment Quality - eight -
---
```

Data Collection

```
File Name       : glpt12.br3_k38-1512899.ab1
Sample Name     : k38-1512899
Comment        : glpt12.br3
Lane Number     : 15
Number Of Pts  : 11060
Number Of Bases : 755
```

RUNNING A MORE COMPREHENSIVE REPORT

The second script also produces a report and writes it to a file but it focuses on different items of information than the first report.

- From the AppleScript Editor **File** menu, choose **Open** and locate the script called "Report Data Attributes" inside the Sample Data's AppleScript folder.
- Select the script and click the **Open** button (you do not have to close the first script).
- Click on the green **Run** button to run the script.

The resultant report will be written to a text file on your desktop called Project_name report DDHHMM where Project_name is the name of the project you are analysing and DDHHMM is the time stamp representing the day of the month, hour, and minute. You can open this file in any text editor.

This report contains information on the contigs and sequences in the project. It writes the consensus sequence of each contig to the report file. It includes information on the overall quality, orientation, length, and number of gaps and ambiguities of each fragment in the contigs. The report also contains all the information it can find for each of the unincorporated fragments including the ABI data sheet and confidence information where it exists.

```
-----  
Sequence: Sf675KGT      length: 492      Original length: 666      ambigs: 0      edits: 0      unknowns: 0      gaps: 0  
AGACTAAAAAGAAGTATTTTCAAGAATAGGAGGCCGTGCCACCAGCTAATAATATGTAAAGCAAGTTACAAAAGGGGAAGCAAAGGCTTCTGAATTAAGTTGTGGATTACAGTCACCTC  
TGCATGACTTACAGTGACTGTCTTAAAAATGCTTGTGCTTTTGTCTTTTCTAGAAATCTCTGTGCGAGGGGAAAGGATAAGAGATTATTACAAAAGCAGCAGGGCTATGCTGCTTGC  
CAAACAACCAAGAAGGTGTCCTCGATTAGAGTGCAGAGGTGGGTGTGCAGGAGGCCAGTGCTGTGGACCCTGAGGAGCAAGCGCGGAAATACTCTTTTGAATGCACTGACGGCTCCTCC  
TTTGTGGACGAGGTTGAGAAAAGTGGTGAAGTGCAGGCTGTACGAGGTGTGTCTCTAAACACACTCCCGCAGCTCTGTCTTTGGAAAAGGTTGTATACTTCTTGACCATGTGGGACTAAT  
GAATGCTTCATA
```

Quality Values: 8 Low, 155 Medium, 329 High Confidence

```
28 35 40 35 42 40 31 26 42 35 35 42 38 38 42 42 42 42 42 44 38 27 27 42 38 42 39 46 42 39 42 42 42 46 46 42 42 42 36  
42 42 38 42 42 28 39 42 42 44 44 39 44 45 44 42 39 44 44 50 48 39 44 50 43 39 44 50 46 50 39 34 43 50 43 42 44 45 39 39  
38 39 34 31 45 44 39 39 50 45 45 48 39 42 44 50 39 39 26 17 39 45 45 39 39 39 39 50 39 25 34 39 38 39 39 25 39 43 43  
39 43 39 38 43 42 39 43 50 46 43 34 20 28 38 42 39 50 39 42 39 50 45 48 39 50 48 34 43 39 42 39 48 48 42 43 42 43 48 48  
48 48 44 39 43 44 45 48 48 48 44 45 39 27 15 34 48 43 43 45 43 48 46 48 42 43 38 21 39 43 43 43 45 43 48 43 43 42 38 39  
48 35 15 24 25 38 37 43 48 41 43 46 45 37 34 35 39 43 43 43 37 28 38 43 35 42 39 43 46 48 46 43 46 42 42 43 44 42 42 42  
38 31 39 46 46 38 42 46 42 39 35 25 42 42 38 42 38 50 50 44 46 46 42 42 42 42 28 13 27 46 42 42 42 42 21 39 39 42 42 42  
44 42 42 42 42 42 35 27 42 42 35 45 42 44 42 38 42 42 42 44 42 42 42 42 42 42 44 44 43 42 42 30 24 45 40 31 41 41 38  
42 42 44 42 42 42 40 41 42 42 50 42 42 42 50 50 50 45 20 41 42 40 40 45 41 42 45 43 43 50 42 42 50 45 45 45 44 45 42  
42 42 45 44 38 44 42 42 39 38 38 33 44 44 50 44 40 24 40 44 50 26 18 34 35 39 42 44 44 27 35 40 42 44 44 42 42 45 38 43  
34 15 38 38 50 42 44 38 42 43 42 44 44 44 42 45 24 31 38 42 42 42 42 50 50 44 50 43 50 40 42 42 50 50 50 44 45 44 50 43  
50 50 42 37 44 42 42 44 35 39 35 42 40 37 42 39 43 50 42 42 42 37 44 38 42 42 36 34 43 42 44 42 37 34 40 34 42 42 32 31  
35 42 37 29 30 35 42 43 38 31 34 29
```

Features: None

ABI Metadata:

Data Collection

```
File Name      : L16_15830_0045E1SNP88F_P1.ab1  
Sample Name   : 15830_0045E1SNP88F_P1  
Comment      :  
Lane Number  : 54  
Number Of Pts : 8112  
Number Of Bases : 666
```

- Close both scripts by clicking the red **Close** button.

EDITING A SCRIPT

You can use AppleScript to control Sequencher's commands and automate the application itself as well as running reports. The next script has a very simple function. It selects all the unincorporated fragments within your project. You are going to edit it so that it can actually open the fragment editors of each of the selected sequences.

- From the AppleScript Editor **File** menu, choose **Open** and locate the script called "Edit this Script" inside the Sample Data's AppleScript folder.
- Select the script and click the **Open** button.

The next step will show how easy it is to edit a script to do something more.

- Scroll down until you find the following line: **select all unincorporated fragments**

The next line is the one you want to edit: `--choose menu command "Open Window"`
 You will see that the line is in grey type. This is because it has been commented out with two dashes.

- Remove the `--` comment marks by simply deleting them.
- Compile the new script so that you may Run it by clicking the **Compile** button



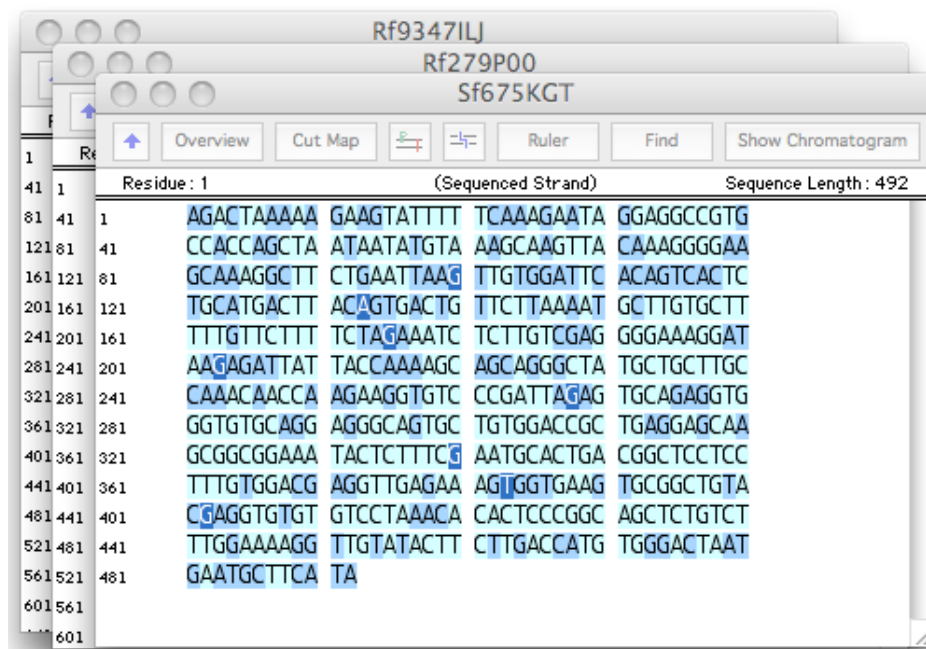
The line has changed to look like this: **choose menu command "Open Window"**

- Run the script by clicking the green **Run** button.

The unincorporated fragments are now selected:

Quality - number	1802 BPs	Ref: Contig of 8
R90-T-00	212 BPs	Contig of 2
Rf279P00	686 BPs	AutoSeq Frag, ABI
Rf9347ILJ	686 BPs	AutoSeq Frag, ABI
Sf675KGT	492 BPs 98.4%	AutoSeq Frag, ABI
Test Refrigerator	(2 items)	Refrigerator

The script then goes on to open the fragment editor windows of the selected fragments. You can see the names of each sequence in the center of its editor and these match the names of the selected fragments in the Project Window.



This last AppleScript example is a very simple sample of the type of script that can control Sequencher. All the scripts you have looked at in this tutorial illustrate how you can use AppleScript to get more out of Sequencher, whether you use it to generate reports or whether you use it to automate aspects of your assembly process.

For more information on AppleScript the Apple web site is a good place to start www.macosxautomation.com/applescript. For more information on Sequencher visit www.genecodes.com.