SEQUENCHER®

Tutorial for Macintosh

Working with AppleScript

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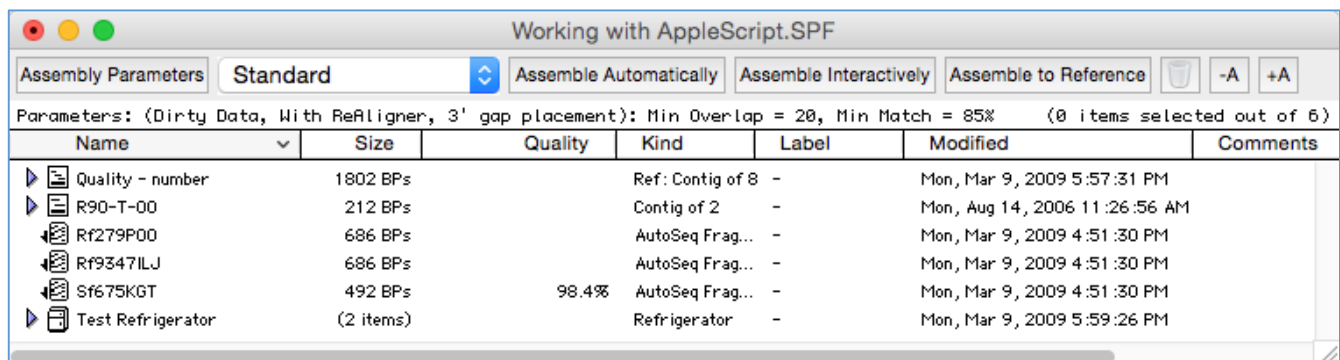A G T **C** O D E S

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. Note that if you are working with a recent version of Mac OS such as Yosemite (Mac OS 10.10), then some of the screen shots for the **Script Editor** will look different. Don't worry, all of the functionality is still there and you can still follow this tutorial.
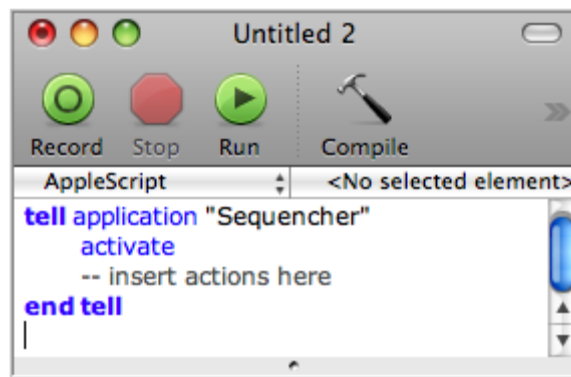
RUNNING A SCRIPT

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 on 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 **Sequencher Sample Data** folder.
- Select the script and click on 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.

- Click on the **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
Wednesday, 10 December 2014 18:53:21


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

# of fragments not incorporated into contigs: 11
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            :  g1pt12.br3_k38-1512899.ab1
Sample Name         :  k38-1512899
Comment             :  g1pt12.br3
Lane Number         :  15
Number Of Pts       :  11060
Number Of Bases     :  755
Run Started At      :  Thu, Sep 16, 2004  7:57 PM
Run Stopped At      :  Thu, Sep 16, 2004  8:53 PM
Gel Data File       :     (not available)
Dye Set/Primer      :  KB_3730_POP7_BDTv1.mob{}
Comb Name           :     (not available)
```

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 **Sequencher's AppleScript Sample Data** folder.
- Select the script and click on 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 reportDDHHMM 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
AGACTAAAAAGAAGTATTTTTCAAAGAATAGGAGGCCGTGCCACCAGCTAATAATATGTAAAGCAAGTTACAAAGGGGAAGCAAAGGCTTCTGAATTAAGTTGTGGATTCACAGTCACTC
TGCATGACTTACAGTGACTGTTCTTAAAATGCTTGTGCTTTTTGTTCTTTTCTAGAAATCTCTTGTCGAGGGGAAAGGATAAGAGATTATTACCAAAAGCAGCAGGGCTATGCTGCTTGC
CAAACAACCAAGAAGGTGTCCCGATTAGAGTGCAGAGGTGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGAGGAGCAAGCGGCGGAAATACTCTTTCGAATGCACTGACGGCTCCTCC
TTTGTGGACGAGGTTGAGAAAGTGGTGAAGTGCGGCTGTACGAGGTGTGTGTCCTAAACACACTCCCGGCAGCTCTGTCTTTGGAAAAGGTTGTATACTTCTTGACCATGTGGGACTAAT
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 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 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 30 24 45 40 31 41 41 38
42 42 44 42 43 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 on 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 but shows how a single script can be flexible. When you have followed all the instructions the script will set some of the Assembly Parameters in your project, select any fragments not in a contig and then assemble them. You are going to edit the script so that all the commands run and so you can change settings to suit your own preferences.

- Click on the **Assembly Parameters** button in **Sequencher's** button bar.
- Make a note of the **Assembly Algorithm** set as default, the **Minimum Match Percentage** and the **Minimum Overlap**. You will need these values later.
- 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 on the **Open** button.

```applescript
tell application "Sequencher"
    activate

    set projName to Name of Project 1
    get projName
    --set Assembly method of Project projName to Clean Data
    set Min match percentage of Project projName to 80
    set Min overlap of Project projName to 20
    get Min overlap of Project projName
    --select all unincorporated fragments
    --assemble all

end tell
```

Whenever you see a line in an **AppleScript** that starts with two dashes (- -), that line has been commented out. That is to say that **AppleScript** will ignore any commands or text on that line. You will see that lines of text which contain explanations about your script start in the same way. Comment lines are always in a gray font. 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: get projName

The next line is the one you want to edit: --set Assembly method of Project projName to Clean Data
- Remove the – comment marks by simply deleting them.

This line will now set the Assembly Algorithm to the Clean Data method. The next two edits you are going to make in the script will set two Assembly Parameters.

- Change the value of the Min match percentage from **80** to **70**.
- Change the value of the Min overlap from **20** to **15**.
- Finally, remove the – comment marks from the two lines of the script near the bottom of the script.
- Save your edited script. It should now look like this.

```applescript
tell application "Sequencher"
    activate

    set projName to Name of Project 1
    get projName
    set Assembly method of Project projName to Clean Data
    set Min match percentage of Project projName to 70
    set Min overlap of Project projName to 15
    get Min overlap of Project projName
    select all unincorporated fragments
    assemble all

end tell
```

- Compile your script changes by clicking on the **Compile** icon.
- Now run the script by clicking on the **Run** button.

The script now assembles most of the fragments into a single contig, two fragments do not assemble but that is expected. To confirm that the script did indeed change the Assembly Parameters as well, follow these steps.

- Click on the **Assembly Parameters** button on **Sequencher's** button bar.

- Compare the parameters with the changes you made to your script.
- If you don't intend to use these parameters in another assembly, then change them back to the settings you noted earlier in this tutorial.
- Close the **Assembly Parameters** dialog.

If you want to experiment with the script further, you can edit it again and try it on the project data once you have dissolved the contig or contigs you want to re-assemble.

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.

- Quit out of **AppleScript** and **Sequencher** if desired.

For more information on **AppleScript**, the Apple website is a good place to start: www.macosxautomation.com/applescript. For more information on **Sequencher**, visit www.genecodes.com.