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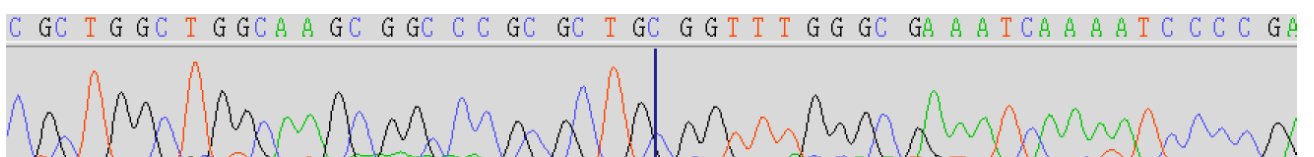
# STARS

## Sequence Typing Analysis and Retrieval System

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*[www.cbrg.ox.ac.uk/~mchan/stars/](http://www.cbrg.ox.ac.uk/~mchan/stars/)*

15 July 2005



Computational Biology Research Group

*[www.compbio.ox.ac.uk](http://www.compbio.ox.ac.uk)*

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## STARS TUTORIAL:

### *Using STARS to analyse a 96-well plate of pneumococcal MLST sequences and query the MLST database on the internet for allele assignments*

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#### Getting Started

- a. Start Exceed.
- b. Log into your CBRG account using secure shell (SSH). If you haven't done this before please refer to [http://www.compbio.ox.ac.uk/CBRG\\_accounts.shtml#using\\_molbiol](http://www.compbio.ox.ac.uk/CBRG_accounts.shtml#using_molbiol)
- c. Copy across the files for the exercise using the following command  

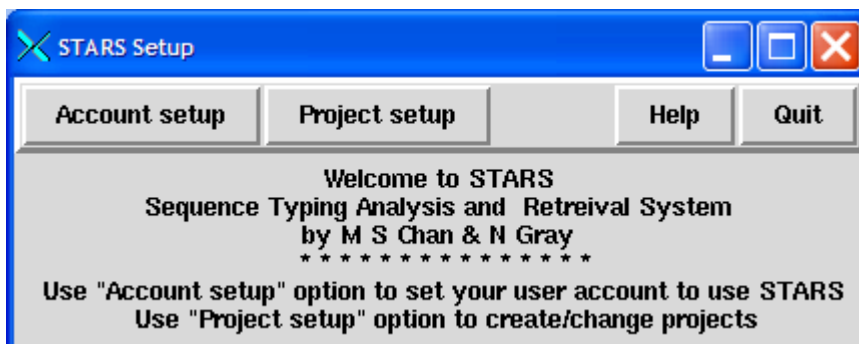
```
cp -r ~course/stars ~/stars_course/
```

#### I. Setting up your account to use STARS:

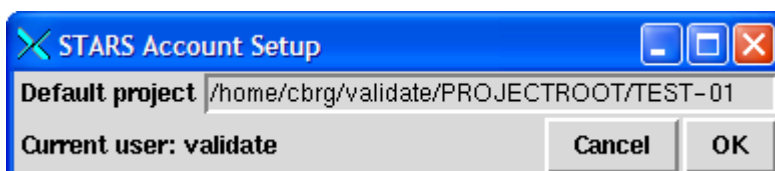
1. In the SSH window type the following command:

```
stars -s
```

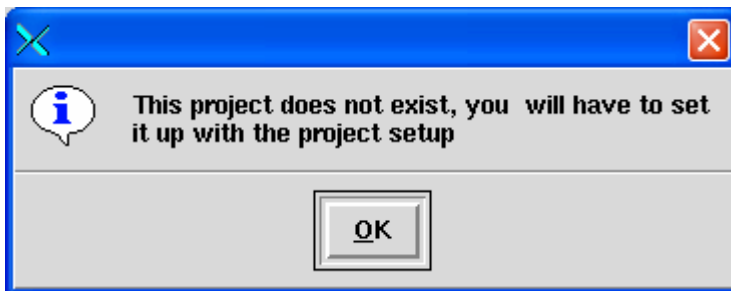
A small window saying "welcome to stars" will pop up. From here you can set up your account to use STARS (once, the first time you use STARS), set up new projects (once, for each project) and modify the setup of existing projects.



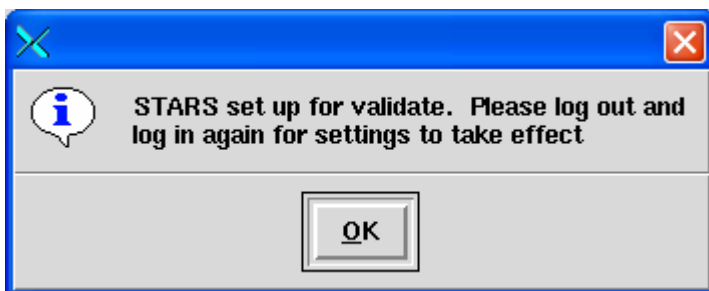
2. Click on 'Account setup'. A new window with some default account settings will be created:



3. It is recommended that you put all projects in one directory called PROJECTROOT, so we will not change the 'Default project' path. Accept these defaults by clicking 'OK'.
4. If you have never used STARS before you will see the following messages asking you to log out of your account and then to log back in again (this is to allow the new settings for your account to take effect):



- click 'OK'



- again, click 'OK'

5. in the STARS Setup window, press 'Quit'
6. log out of your account (type: `exit` and press the return key)
7. log back into your molbiol account again.

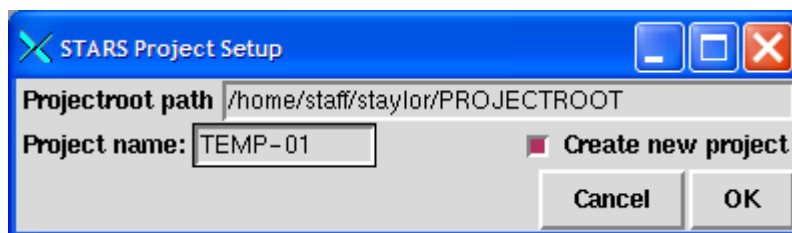
**Note:** If you have used STARS before, you will receive a message telling you that STARS is already set up for your username.

## II. Setting up a new STARS project:

You will need to create a project for this tutorial. A suggested naming scheme for projects is PROJECT-NUMBER. The NUMBER at the end of STARS projects allows sequential numbering to accommodate growing amounts of data in a 'real' project.

For each project you can sequence several loci (ie short gene regions sequenced by a pair of reads), each locus should be given a code name of four letters (eg abcZ, adk\_). The names are case sensitive and can accommodate "\_" characters to pad out shorter names.

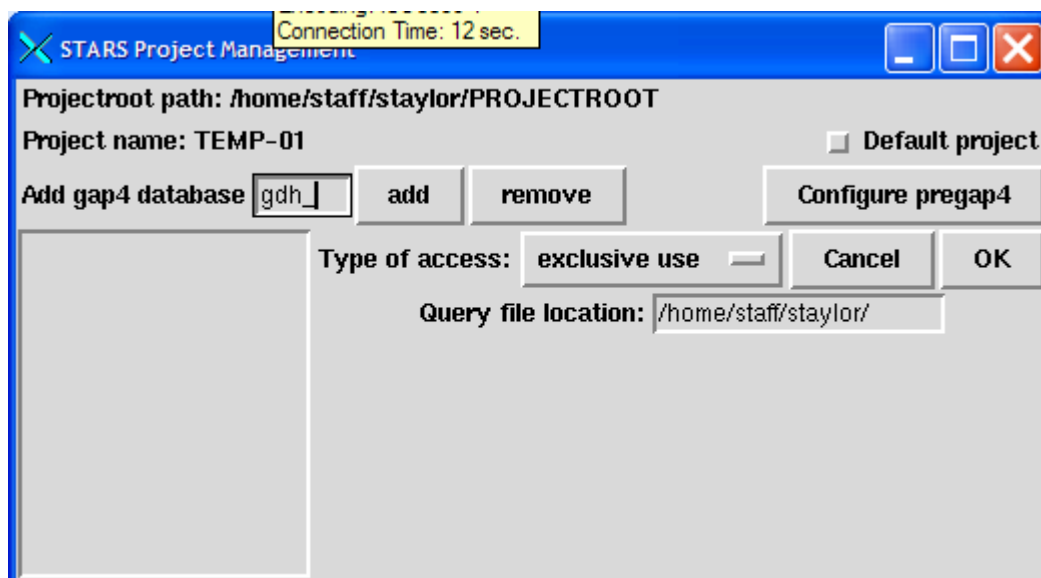
Click on 'Project setup' in the 'STARS Setup' window to create a new project:



In the new window, make the following changes:

- Call the example project 'TEMP-01' (following the suggested naming scheme)
- Click the box next to 'Create new project'
- As we saw earlier, all projects should be created in a directory called 'PROJECTROOT' so we can leave the default value for 'Projectroot path'.
- click 'OK'.

Another window will open to allow you to tell STARS about this new project:

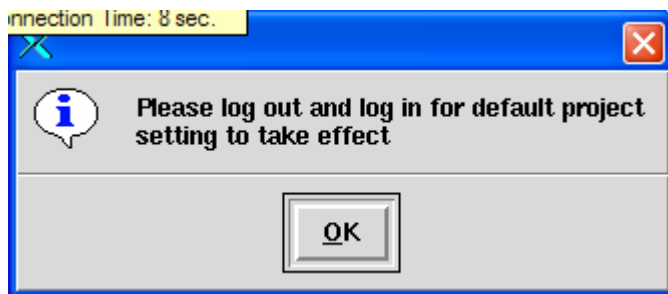


- After 'Add gap4 database', enter 'gdh\_'
- click 'add'
- make this the default project by clicking the box next to 'Default project'

Note: You can also directly configure pregap4 from this window. This will open a pregap4 window. Configure the modules as normal and save the changes in pregap4. Note that some parts of this config file are STARS variables and should not be changed, specifically DATABASE and VECTORDIRECTORY where these occur. We will not be altering these during the course of this practical.

- Click 'ok' to create the project.

You will receive another notice before the project is set up:

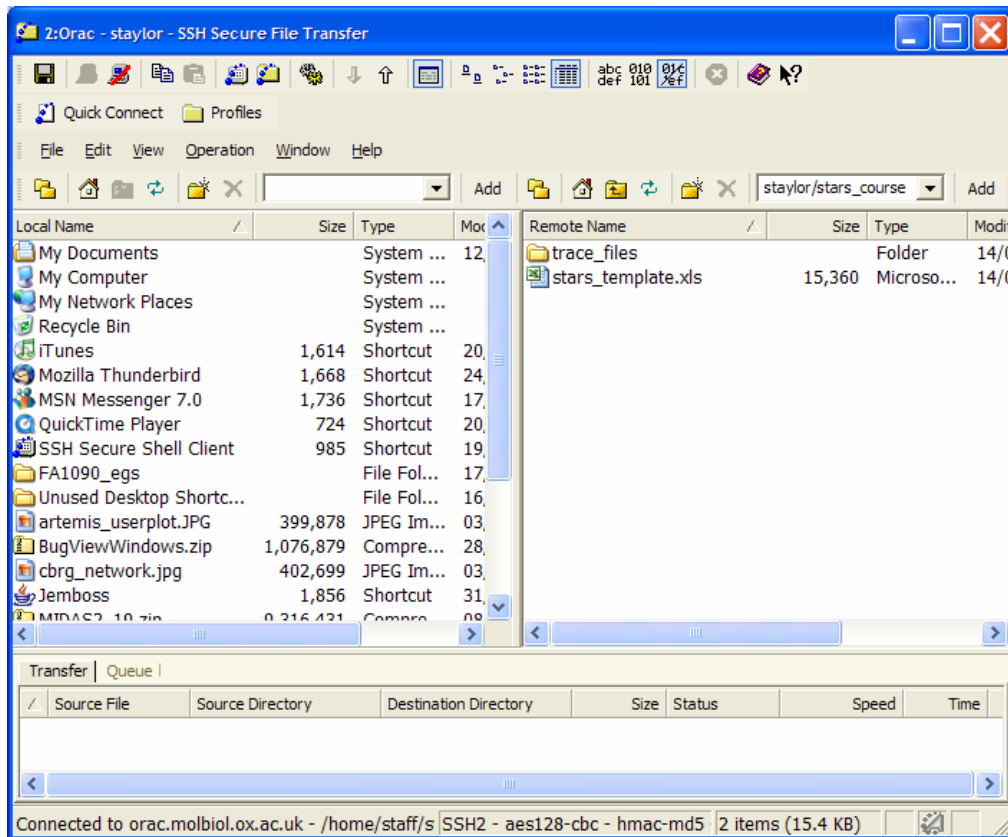


- click 'OK':
- log out of molbiol
- log back in to your account

You are now ready to use STARS.

### III. Adding data to the new project.

Open the Excel file 'stars\_template.xls' using the secure file transfer window of SSH (Click the SSH icon). The Excel file should be in the 'stars\_course' directory.



You will use this Excel file to create a 'list file' for renaming 96 sequence trace files.

- a. Important: this file is designed for use with sequences from an Applied Biosystems sequencer and has a format like this:

	1	2	3	4	5	6	7	8	9	10	11	12
A	1	2	3	4	5	6	1	2	3	4	5	6
B	7	8	9	10	11	12	7	8	9	10	11	12
C	13	14	15	16	17	18	13	14	15	16	17	18
D	19	20	21	22	23	24	19	20	21	22	23	24
E	25	26	27	28	29	30	25	26	27	28	29	30
F	31	32	33	34	35	36	31	32	33	34	35	36
G	37	38	39	40	41	42	37	38	39	40	41	42
H	43	44	45	46	47	neg	43	44	45	46	47	neg

Forward seqs

Reverse seqs

The sequence trace file called A1 pairs with trace file A7, A2 with A8, ..., B1 with B7, B2 with B8, ...etc. Using the Excel template will result in a text file

that is ordered such that the sequences are renamed and paired correctly in STARS.

b. STARS has a strict naming scheme: 'idno.gene1.abi' and 'idno.gene2.abi'.

The different parts of the name are separated by full stops.

idno = name of the strain being sequenced

gene = 4 character gene name – if the gene name is only 3 characters then an underscore must be used, ie. recP, aroE, spi\_, xpt\_

1 = forward sequence

2 = reverse sequence

.abi = abi files come off the ABI sequencer as .ab1 – the visual basic code in the Excel template will change this to .abi so you DO NOT need to add .abi to each name when using the Excel template.

c. Fill in the Excel spreadsheet with the strain id numbers as shown above in the diagram, but also include the gene name (gdh\_) and whether it is a forward or reverse trace, using the naming format as described above. (eg. in the above figure: cell A1 = 1.gdh\_1, A7 = 1.gdh\_2; B1 = 7.gdh\_1 and B7 = 7.gdh\_2).

Note: it saves time to name the forward traces in columns 1-6, and then copy and paste the block of text into columns 7-12 and replace gdh\_1 with gdh\_2.

The final spreadsheet should look like this when it has been filled in:

1.gdh_1	2.gdh_1	3.gdh_1	4.gdh_1	5.gdh_1	6.gdh_1	1.gdh_2	2.gdh_2	3.gdh_2	4.gdh_2	5.gdh_2	6.gdh_2
7.gdh_1	8.gdh_1	9.gdh_1	10.gdh_1	11.gdh_1	12.gdh_1	7.gdh_2	8.gdh_2	9.gdh_2	10.gdh_2	11.gdh_2	12.gdh_2
13.gdh_1	14.gdh_1	15.gdh_1	16.gdh_1	17.gdh_1	18.gdh_1	13.gdh_2	14.gdh_2	15.gdh_2	16.gdh_2	17.gdh_2	18.gdh_2
19.gdh_1	20.gdh_1	21.gdh_1	22.gdh_1	23.gdh_1	24.gdh_1	19.gdh_2	20.gdh_2	21.gdh_2	22.gdh_2	23.gdh_2	24.gdh_2
25.gdh_1	26.gdh_1	27.gdh_1	28.gdh_1	29.gdh_1	30.gdh_1	25.gdh_2	26.gdh_2	27.gdh_2	28.gdh_2	29.gdh_2	30.gdh_2
31.gdh_1	32.gdh_1	33.gdh_1	34.gdh_1	35.gdh_1	36.gdh_1	31.gdh_2	32.gdh_2	33.gdh_2	34.gdh_2	35.gdh_2	36.gdh_2
37.gdh_1	38.gdh_1	39.gdh_1	40.gdh_1	41.gdh_1	42.gdh_1	37.gdh_2	38.gdh_2	39.gdh_2	40.gdh_2	41.gdh_2	42.gdh_2
43.gdh_1	44.gdh_1	45.gdh_1	46.gdh_1	47.gdh_1	neg.gdh_1	43.gdh_2	44.gdh_2	45.gdh_2	46.gdh_2	47.gdh_2	neg.gdh_2

d. When all the sequence trace file names have been filled into the spreadsheet, press the 'Save' button at the bottom of the spreadsheet. Indicate the full computer path and a name for the text file eg. c:\temp\testfile.txt. Be sure the filename ends in .txt

#### IV. **Moving data into 'staden' directory.**

Using the SSH File Transfer utility, transfer the list file that you have just created into the 'my\_lists' folder in the staden folder in your molbiol account. Transfer 96 raw sequence trace .ab1 files into the 'new\_data' folder, using the following command:

```
mv ~/stars_course/trace_files/* ~/staden/new_data/
```

Note: Both the 'my\_lists' and 'new\_data' folders are subdirectories of the staden directory in your home directory and were created when you set up STARS.

## V. Running a session in STARS

- a. Load STARS by typing 'stars' on the command line in the SSH window
- b. Press the 'Browse' button and open the list file you just transferred into the 'my\_lists' folder
- c. Make sure the project you wish to use is indicated. It should be correct for this tutorial since you just created a new project. If in the future you have multiple STARS project databases you will have to select the one you wish to use by changing the name to the correct project and press 'Change project'.
- d. At the top of the window, select 'List', then 'Load/Rename'. After a few seconds your text file list will appear in the window. All of your sequences will have been renamed and ordered according to the names given in the list file you created. You may wish to look at some of the traces by selecting an item and choosing trace/view.
- e. Press the 'Run' button. A window will appear, indicating that this may take 10 minutes. It runs faster now with the orac server so it may take less than 10 min. Do not disturb STARS during this time. (Although you can minimise the screens and continue working outside your molbiol account without a problem.)
- f. When the run is finished, a log will appear in a new screen. It is important to read through this log as it indicates the steps STARS has performed on the sequences and whether any problems occurred (see example in APPENDIX):
  - i. The names of each sequence trace file are checked for the correct naming format.
  - ii. The percentage quality is calculated for each sequence trace file. (This is the old "eba" value rather than the current default "phred" value.)
  - iii. Forward and reverse sequences are assembled in pregap/gap4. Matches of forward and reverse trace files are made, but if this is not possible (eg. if one trace fails) then 'No match found' is indicated.
  - iv. A list of single files found is given (indicating that the other trace in the pair failed).
  - v. A list of all the assemblies is given.
  - vi. STARS cleans up the run.
- g. Close the log window from the upper left corner.
- h. Next, go to 'Window' and 'Data retrieval window'

- i. In the Data retrieval window, select 'Data source' and then 'Contigs list'. Press the 'Retrieve' button on the right side of the window. Your list of assembled sequences appears in the window.
- j. Highlight the first strain listed, then press the 'Edit' button. The pregap assembly will appear so that you can edit the sequence. Double click anywhere on the consensus sequence to bring up the sequence trace windows.
- k. For the purposes of this tutorial, edit each assembly by trimming the traces to this exact location and length:

```
>gdh_1 (460 bases)
```

```
AGAACACTTTATCCGTGGGCAATACCGCTCTGGTAAGATTGATGGCATGAAATACATCTCTTAT
CGTAGCGAGCCAAATGTGAATCCAGAATCAACAACCTTTACATCAGGTGCCTTCTTTG
TAGACAGCGATCGATTCCGTGGTGTTCCTTTCTTTTTCCGTACAGGTAAACGACTGACTGAAAA
AGGAACCCATGTCAACATCGTCTTTAAACAAATGGATTCTATCTTTGGAGAACCACTTGCTCCA
AATATTTTGACCATCTATATTCAACCAACAGAAGGCTTCTCTCTTAGCCTAAATGGGAAGCAAG
TAGGAGAAGAATTTAACTTGGCTCCTAACTCACTTGATTACCGTACAGATGCGACTGCAACTGG
TGCTTCTCCAGAACCATAACGAAAAATTGATTTATGATGTCCTAAATAACAACCTCAACTAACTTT
AGCCACTGGGAT
```

- l. To delete a sequence assembly at this point (e.g. if trace quality is not sufficient and the sequence(s) need to be repeated), then remove the assembly by highlighting the name of the assembly and press the 'Remove' button. A window will appear asking you to confirm – this will remove the assembly permanently.
- m. When all of the traces have been edited, go to 'Select window' and 'Data management window'.
- n. Press 'Calculate' and a list of consensus sequences in fasta format will appear. You may also do this periodically as you go through the session to check progress.
- o. Use the mouse to highlight the entire list of consensus sequences, move the mouse to the blue bar at the top of the window, right-click and select 'Edit', 'Copy X selection', 'To clipboard'.
- p. Go to the pneumococcal MLST webpage at <http://spneumoniae.mlst.net>
- q. Select 'Batch query' then 'Batch locus' and paste the fasta files into the window. Change the locus to 'gdh\_' .
- r. Press 'Submit' and a new window appears with allele assignments for each strain. For the purposes of this tutorial all the sequences are known alleles. Allele numbers have been assigned to each unique sequence in the order of

discovery. All alleles at this locus are the same length so if you find an error such as “wrong length”, “not a DNA sequence” or “new allele” you will need to examine the sequence again.

- s. Highlight the list of strain names and allele assignments with the mouse, right-click and select ‘copy’
- t. Go back to STARS, and select ‘Select window’, ‘Data retrieval window’, ‘Data source’ and then ‘Load from web’. Press the ‘Retrieve’ button on the right side of the Data retrieval window. A new window appears – click the wheel/middle button of the mouse to paste the list of strains and allele assignments from the web. Your list of assembled sequences appears in the window. Press the ‘retrieve’ button in the middle of the window. The window will close and return to the Data retrieval window. The list of strains and allele assignments should now be visible in this window.
- u. The STARS session can now be ended by pressing the ‘End session’ button at the top of the window. A window appears, asking whether or not to ‘Append data’. Click ‘yes’ and a new screen appears with the list of strains and allele assignments. (Note: STARS requires an allele assignment for every strain, so for non-MLST users of STARS, alleles should be assigned to 0.)
- v. Each strain reads: ‘xxx is allele n.’ Since the MLST website has changed since STARS was created and STARS only accepts ‘xxx allele 7’, all the ‘is’ have to be deleted. (Sorry!)
- w. Press the ‘Save’ button, a window appears with ‘all alleles assigned’, click ‘ok’.
- x. Another window appears asking whether you wish for all the failed files to be deleted. Say ‘yes’ in this case.
- y. Another window appears saying ‘Local copy of entered data has been saved to ~/staden/session/assigned\_alleles.txt’ Click ok. Transfer the file assigned\_alleles.txt back to your PC using the secure file transfer utility and save it with a name relevant to the plate. Open this file using Word. You will find that it shows the sample and assigned allele and also your user name and date. This is useful for tracking in large projects.
- z. Use the ‘Quit’ button in the upper right corner of each screen to close STARS before beginning a new session.

**Notes:**

1. Once a session is started by pressing 'Run', it must be ended using 'End session' before another session can be started.
2. If there are any problems during the run, there will often be files that need to be cleaned up before starting again. Usually the best thing to do is end a blank session, i.e. 'End session' with a blank screen and follow steps v. – y. above. That usually clears the problem.
3. If it does not, check for LOCK or BUSY files in your account and delete them – they will prevent a new session from running.
4. Never create a filename that includes spaces (use an underscore), hyphen ( - ), or other characters such as #, ?, £, etc. Keep it very simple and as short as possible.
5. Every strain name within a database must be unique.

**APPENDIX**  
*Example of STARS session log*

---

Program running please wait Mon Jul 11 10:37:25 BST 2005

aroE|gdh\_|gki\_|recP|spi\_|xpt\_|ddl\_

checking naming scheme

1.gdh\_1.abi  
2.gdh\_1.abi  
3.gdh\_1.abi  
4.gdh\_1.abi  
5.gdh\_1.abi  
6.gdh\_1.abi  
1.gdh\_2.abi  
2.gdh\_2.abi  
3.gdh\_2.abi  
4.gdh\_2.abi  
5.gdh\_2.abi  
6.gdh\_2.abi  
7.gdh\_1.abi  
8.gdh\_1.abi  
9.gdh\_1.abi  
10.gdh\_1.abi  
11.gdh\_1.abi  
12.gdh\_1.abi  
7.gdh\_2.abi  
8.gdh\_2.abi  
9.gdh\_2.abi  
10.gdh\_2.abi  
11.gdh\_2.abi  
12.gdh\_2.abi  
13.gdh\_1.abi  
14.gdh\_1.abi  
15.gdh\_1.abi  
16.gdh\_1.abi  
17.gdh\_1.abi  
18.gdh\_1.abi  
13.gdh\_2.abi  
14.gdh\_2.abi  
15.gdh\_2.abi  
16.gdh\_2.abi  
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18.gdh\_2.abi  
19.gdh\_1.abi  
20.gdh\_1.abi  
21.gdh\_1.abi  
22.gdh\_1.abi  
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24.gdh\_1.abi  
19.gdh\_2.abi  
20.gdh\_2.abi  
21.gdh\_2.abi  
22.gdh\_2.abi  
23.gdh\_2.abi

24.gdh\_2.abi  
25.gdh\_1.abi  
26.gdh\_1.abi  
27.gdh\_1.abi  
28.gdh\_1.abi  
29.gdh\_1.abi  
30.gdh\_1.abi  
25.gdh\_2.abi  
26.gdh\_2.abi  
27.gdh\_2.abi  
28.gdh\_2.abi  
29.gdh\_2.abi  
30.gdh\_2.abi  
31.gdh\_1.abi  
32.gdh\_1.abi  
33.gdh\_1.abi  
34.gdh\_1.abi  
35.gdh\_1.abi  
36.gdh\_1.abi  
31.gdh\_2.abi  
32.gdh\_2.abi  
33.gdh\_2.abi  
34.gdh\_2.abi  
35.gdh\_2.abi  
36.gdh\_2.abi  
37.gdh\_1.abi  
38.gdh\_1.abi  
39.gdh\_1.abi  
40.gdh\_1.abi  
41.gdh\_1.abi  
42.gdh\_1.abi  
37.gdh\_2.abi  
38.gdh\_2.abi  
39.gdh\_2.abi  
40.gdh\_2.abi  
41.gdh\_2.abi  
42.gdh\_2.abi  
43.gdh\_1.abi  
44.gdh\_1.abi  
45.gdh\_1.abi  
46.gdh\_1.abi  
47.gdh\_1.abi  
neg.gdh\_1.abi  
43.gdh\_2.abi  
44.gdh\_2.abi  
45.gdh\_2.abi  
46.gdh\_2.abi  
47.gdh\_2.abi  
neg.gdh\_2.abi

1.gdh\_1.abi 94.160000  
2.gdh\_1.abi 92.890000  
3.gdh\_1.abi 93.600000  
4.gdh\_1.abi 91.160000

5.gdh\_1.abi 91.340000  
6.gdh\_1.abi 92.150000  
1.gdh\_2.abi 93.960000  
2.gdh\_2.abi 92.480000  
3.gdh\_2.abi 93.590000  
4.gdh\_2.abi 91.250000  
5.gdh\_2.abi 90.830000  
6.gdh\_2.abi 91.440000  
7.gdh\_1.abi 92.330000  
8.gdh\_1.abi 92.930000  
9.gdh\_1.abi 92.410000  
10.gdh\_1.abi 91.800000  
11.gdh\_1.abi 91.390000  
12.gdh\_1.abi 91.770000  
7.gdh\_2.abi 91.670000  
8.gdh\_2.abi 91.980000  
9.gdh\_2.abi 91.410000  
10.gdh\_2.abi 90.690000  
11.gdh\_2.abi 90.460000  
12.gdh\_2.abi 89.470000  
13.gdh\_1.abi 92.890000  
14.gdh\_1.abi 92.720000  
15.gdh\_1.abi 91.920000  
16.gdh\_1.abi 91.710000  
17.gdh\_1.abi 91.570000  
18.gdh\_1.abi 92.280000  
13.gdh\_2.abi 91.840000  
14.gdh\_2.abi 92.070000  
15.gdh\_2.abi 91.850000  
16.gdh\_2.abi 91.720000  
17.gdh\_2.abi 91.060000  
18.gdh\_2.abi 91.400000  
19.gdh\_1.abi 92.660000  
20.gdh\_1.abi 93.030000  
21.gdh\_1.abi 91.350000  
22.gdh\_1.abi 92.750000  
23.gdh\_1.abi 91.740000  
24.gdh\_1.abi 93.410000  
19.gdh\_2.abi 91.130000  
20.gdh\_2.abi 91.810000  
21.gdh\_2.abi 89.570000  
22.gdh\_2.abi 91.550000  
23.gdh\_2.abi 90.200000  
24.gdh\_2.abi 91.280000  
25.gdh\_1.abi 92.360000  
26.gdh\_1.abi 93.100000  
27.gdh\_1.abi 93.260000  
28.gdh\_1.abi 91.920000  
29.gdh\_1.abi 93.280000  
30.gdh\_1.abi 92.130000  
25.gdh\_2.abi 92.320000  
26.gdh\_2.abi 91.850000  
27.gdh\_2.abi 90.790000

28.gdh\_2.abi 91.280000  
29.gdh\_2.abi 91.610000  
30.gdh\_2.abi 91.800000  
31.gdh\_1.abi 93.340000  
32.gdh\_1.abi 92.660000  
33.gdh\_1.abi 92.940000  
34.gdh\_1.abi 91.860000  
35.gdh\_1.abi 94.450000  
36.gdh\_1.abi 92.620000  
31.gdh\_2.abi 92.440000  
32.gdh\_2.abi 92.120000  
33.gdh\_2.abi 93.200000  
34.gdh\_2.abi 92.020000  
35.gdh\_2.abi 94.000000  
36.gdh\_2.abi 91.410000  
37.gdh\_1.abi 92.570000  
38.gdh\_1.abi 93.180000  
39.gdh\_1.abi 93.180000  
40.gdh\_1.abi 93.140000  
41.gdh\_1.abi 92.200000  
42.gdh\_1.abi 92.930000  
37.gdh\_2.abi 92.630000  
38.gdh\_2.abi 92.010000  
39.gdh\_2.abi 91.230000  
40.gdh\_2.abi 92.270000  
41.gdh\_2.abi 92.090000  
42.gdh\_2.abi 90.200000  
43.gdh\_1.abi 93.490000  
44.gdh\_1.abi 93.710000  
45.gdh\_1.abi 94.010000  
46.gdh\_1.abi 92.870000  
47.gdh\_1.abi 92.990000  
neg.gdh\_1.abi 43.470000  
43.gdh\_2.abi 92.740000  
44.gdh\_2.abi 91.770000  
45.gdh\_2.abi 93.280000  
46.gdh\_2.abi 92.570000  
47.gdh\_2.abi 91.970000  
neg.gdh\_2.abi 26.420000Sequences checked, now entering into pregap

Please wait

\*\*\*\*\*

Processing your sequence list

\*\*\*\*\*

\*\*\*\*\*

Finished making your files arrays.

\*\*\*\*\*

match found. 1.gdh\_1.abi 1.gdh\_2.abi  
match found. 2.gdh\_1.abi 2.gdh\_2.abi  
match found. 3.gdh\_1.abi 3.gdh\_2.abi  
match found. 4.gdh\_1.abi 4.gdh\_2.abi  
match found. 5.gdh\_1.abi 5.gdh\_2.abi  
match found. 6.gdh\_1.abi 6.gdh\_2.abi  
match found. 7.gdh\_1.abi 7.gdh\_2.abi

```
match found. 8.gdh_1.abi 8.gdh_2.abi
match found. 9.gdh_1.abi 9.gdh_2.abi
match found. 10.gdh_1.abi 10.gdh_2.abi
match found. 11.gdh_1.abi 11.gdh_2.abi
match found. 12.gdh_1.abi 12.gdh_2.abi
match found. 13.gdh_1.abi 13.gdh_2.abi
match found. 14.gdh_1.abi 14.gdh_2.abi
match found. 15.gdh_1.abi 15.gdh_2.abi
match found. 16.gdh_1.abi 16.gdh_2.abi
match found. 17.gdh_1.abi 17.gdh_2.abi
match found. 18.gdh_1.abi 18.gdh_2.abi
match found. 19.gdh_1.abi 19.gdh_2.abi
match found. 20.gdh_1.abi 20.gdh_2.abi
match found. 21.gdh_1.abi 21.gdh_2.abi
match found. 22.gdh_1.abi 22.gdh_2.abi
match found. 23.gdh_1.abi 23.gdh_2.abi
match found. 24.gdh_1.abi 24.gdh_2.abi
match found. 25.gdh_1.abi 25.gdh_2.abi
match found. 26.gdh_1.abi 26.gdh_2.abi
match found. 27.gdh_1.abi 27.gdh_2.abi
match found. 28.gdh_1.abi 28.gdh_2.abi
match found. 29.gdh_1.abi 29.gdh_2.abi
match found. 30.gdh_1.abi 30.gdh_2.abi
match found. 31.gdh_1.abi 31.gdh_2.abi
match found. 32.gdh_1.abi 32.gdh_2.abi
match found. 33.gdh_1.abi 33.gdh_2.abi
match found. 34.gdh_1.abi 34.gdh_2.abi
match found. 35.gdh_1.abi 35.gdh_2.abi
match found. 36.gdh_1.abi 36.gdh_2.abi
match found. 37.gdh_1.abi 37.gdh_2.abi
match found. 38.gdh_1.abi 38.gdh_2.abi
match found. 39.gdh_1.abi 39.gdh_2.abi
match found. 40.gdh_1.abi 40.gdh_2.abi
match found. 41.gdh_1.abi 41.gdh_2.abi
match found. 42.gdh_1.abi 42.gdh_2.abi
match found. 43.gdh_1.abi 43.gdh_2.abi
match found. 44.gdh_1.abi 44.gdh_2.abi
match found. 45.gdh_1.abi 45.gdh_2.abi
match found. 46.gdh_1.abi 46.gdh_2.abi
match found. 47.gdh_1.abi 47.gdh_2.abi
No single forward sequences found
No single reverse sequences found
```

```
Single reverse files found (0):
/proj/microid/PROJECTROOT/SPCUR-01/data
Mon Jul 11 10:37:50 BST 2005
```

```
This is your fofnfile array
fofn.gdh_.1 fofn.gdh_.10 fofn.gdh_.11 fofn.gdh_.12 fofn.gdh_.13 fofn.gdh_.14 fofn.gdh_.15 fofn.gdh_.16
fofn.gdh_.17 fofn.gdh_.18 fofn.gdh_.19 fofn.gdh_.2 fofn.gdh_.20 fofn.gdh_.21 fofn.gdh_.22 fofn.gdh_.23
fofn.gdh_.24 fofn.gdh_.25 fofn.gdh_.26 fofn.gdh_.27 fofn.gdh_.28 fofn.gdh_.29 fofn.gdh_.3 fofn.gdh_.30
fofn.gdh_.31 fofn.gdh_.32 fofn.gdh_.33 fofn.gdh_.34 fofn.gdh_.35 fofn.gdh_.36 fofn.gdh_.37 fofn.gdh_.38
fofn.gdh_.39 fofn.gdh_.4 fofn.gdh_.40 fofn.gdh_.41 fofn.gdh_.42 fofn.gdh_.43 fofn.gdh_.44 fofn.gdh_.45
fofn.gdh_.46 fofn.gdh_.47 fofn.gdh_.5 fofn.gdh_.6 fofn.gdh_.7 fofn.gdh_.8 fofn.gdh_.9
Mon Jul 11 10:37:50 BST 2005
```

fofn.gdh\_1 this is gdh\_db  
fofn.gdh\_10 this is gdh\_db  
fofn.gdh\_11 this is gdh\_db  
fofn.gdh\_12 this is gdh\_db  
fofn.gdh\_13 this is gdh\_db  
fofn.gdh\_14 this is gdh\_db  
fofn.gdh\_15 this is gdh\_db  
fofn.gdh\_16 this is gdh\_db  
fofn.gdh\_17 this is gdh\_db  
fofn.gdh\_18 this is gdh\_db  
fofn.gdh\_19 this is gdh\_db  
fofn.gdh\_2 this is gdh\_db  
fofn.gdh\_20 this is gdh\_db  
fofn.gdh\_21 this is gdh\_db  
fofn.gdh\_22 this is gdh\_db  
fofn.gdh\_23 this is gdh\_db  
fofn.gdh\_24 this is gdh\_db  
fofn.gdh\_25 this is gdh\_db  
fofn.gdh\_26 this is gdh\_db  
fofn.gdh\_27 this is gdh\_db  
fofn.gdh\_28 this is gdh\_db  
fofn.gdh\_29 this is gdh\_db  
fofn.gdh\_3 this is gdh\_db  
fofn.gdh\_30 this is gdh\_db  
fofn.gdh\_31 this is gdh\_db  
fofn.gdh\_32 this is gdh\_db  
fofn.gdh\_33 this is gdh\_db  
fofn.gdh\_34 this is gdh\_db  
fofn.gdh\_35 this is gdh\_db  
fofn.gdh\_36 this is gdh\_db  
fofn.gdh\_37 this is gdh\_db  
fofn.gdh\_38 this is gdh\_db  
fofn.gdh\_39 this is gdh\_db  
fofn.gdh\_4 this is gdh\_db  
fofn.gdh\_40 this is gdh\_db  
fofn.gdh\_41 this is gdh\_db  
fofn.gdh\_42 this is gdh\_db  
fofn.gdh\_43 this is gdh\_db  
fofn.gdh\_44 this is gdh\_db  
fofn.gdh\_45 this is gdh\_db  
fofn.gdh\_46 this is gdh\_db  
fofn.gdh\_47 this is gdh\_db  
fofn.gdh\_5 this is gdh\_db  
fofn.gdh\_6 this is gdh\_db  
fofn.gdh\_7 this is gdh\_db  
fofn.gdh\_8 this is gdh\_db  
fofn.gdh\_9 this is gdh\_dbSequences entered, now tidying up

Please wait  
gdh\_  
1.gdh\_2  
gdh\_  
2.gdh\_2  
gdh\_

3.gdh\_2  
gdh\_  
4.gdh\_2  
gdh\_  
5.gdh\_2  
gdh\_  
6.gdh\_2  
gdh\_  
7.gdh\_2  
gdh\_  
8.gdh\_2  
gdh\_  
9.gdh\_2  
gdh\_  
10.gdh\_2  
gdh\_  
11.gdh\_2  
gdh\_  
12.gdh\_2  
gdh\_  
13.gdh\_2  
gdh\_  
14.gdh\_2  
gdh\_  
15.gdh\_2  
gdh\_  
16.gdh\_2  
gdh\_  
17.gdh\_2  
gdh\_  
18.gdh\_2  
gdh\_  
19.gdh\_2  
gdh\_  
20.gdh\_2  
gdh\_  
21.gdh\_2  
gdh\_  
22.gdh\_2  
gdh\_  
23.gdh\_2  
gdh\_  
24.gdh\_2  
gdh\_  
25.gdh\_2  
gdh\_  
26.gdh\_2  
gdh\_  
27.gdh\_2  
gdh\_  
28.gdh\_2  
gdh\_  
29.gdh\_2

gdh\_  
30.gdh\_2  
gdh\_  
31.gdh\_2  
gdh\_  
32.gdh\_2  
gdh\_  
33.gdh\_2  
gdh\_  
34.gdh\_2  
gdh\_  
35.gdh\_2  
gdh\_  
36.gdh\_2  
gdh\_  
37.gdh\_2  
gdh\_  
38.gdh\_2  
gdh\_  
39.gdh\_2  
gdh\_  
40.gdh\_2  
gdh\_  
41.gdh\_2  
gdh\_  
42.gdh\_2  
gdh\_  
43.gdh\_2  
gdh\_  
44.gdh\_2  
gdh\_  
45.gdh\_2  
gdh\_  
46.gdh\_2  
gdh\_  
47.gdh\_2

moving single forwards  
moved single forwards  
moved textout files  
deleted fofn files  
moved sequence lists  
removed abi filesFINISHED  
Please close this window from the top left corner