Quick Tour of Consed

(modified for the BBSI, from CONSED 11.0 DOCUMENTATION)

What is it?

Consed is a graphical tool integrated with *Phred* and *Phrap* to aid in the finishing of genome sequencing projects.

To get started

1. Log on to your Watson account, open the X-window.

2. Create three folders for your sequence analysis:

```
> mkdir chromat_dir
> mkdir edit_dir
> mkdir phd_dir
```

3. Copy the ABI sequencer format sequences into your `chromat_dir` directory from /home/pingxu/SequenceAnalysis/standard/chromat_dir/ by typing:

```
> cp /home/pingxu/SequenceAnalysis/standard/chromat_dir/* chromat_dir/
```

4. Run *Phred* and *Phrap* by typing:

```
> cd edit_dir
> phredPhrap
```

   The perl script phredPhrap will run phred for basecalling and run phrap for sequence assembly. You will find file with *.ace1 after the program.

5. Start *Consed* by typing:

```
> consed
```

   Two windows will appear: the Consed Main Window and the Ace Files window. The Ace Files window will have the list of .ace files and say 'select assembly file to open' and 'standard.fasta.screen.ace.1'.

6. Double click on that name. Click “Yes”.
   The Ace Files window will go away, and you will now see a list of one contig and a list of reads. This is the 'Main Consed Window'.

7. Double click on 'Contig1'.
   The 'Aligned Reads Window' will appear.

8. Alternate ways of scrolling:
   - Drag the thumb of the scrollbar
   - (small amounts) Click on one of the four << < > >> buttons
   - (tiny amounts) Click on the arrows at either end of the scrollbar.
   - (huge amounts) Use the middle mouse button and click some location on the scrollbar
   - (to beginning or end of contig) Use the <<< or >>> buttons