Gap5 – A Database and Visualisation Tool for the Next-gen Data

Practice Session of Sequence Alignment and Genome Assembly

(1) Gap5 source

http://sourceforge.net/projects/staden/files/Gap5/1.2.2

(2) Installation
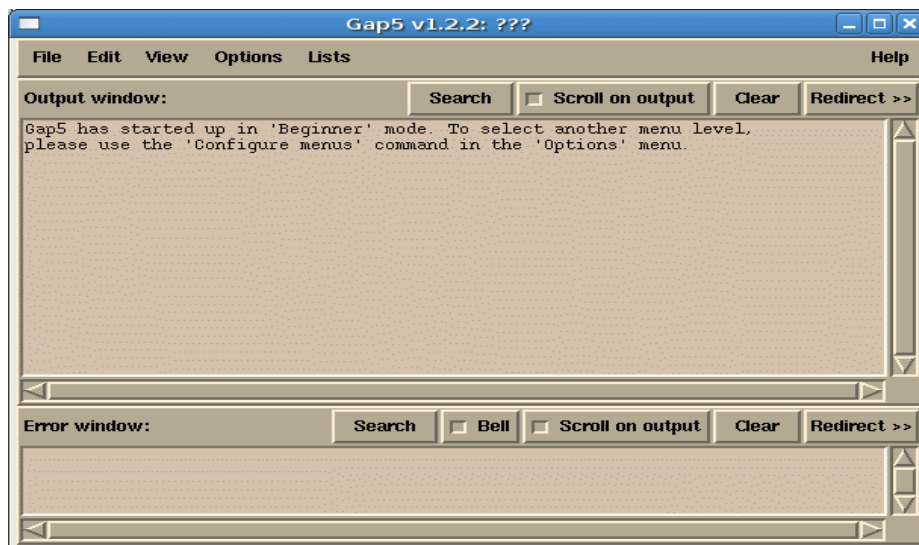
/home/dbxx/sbf/gap5/gap5-1.2.2-linux-x86_64/linux-x86_64-bin/

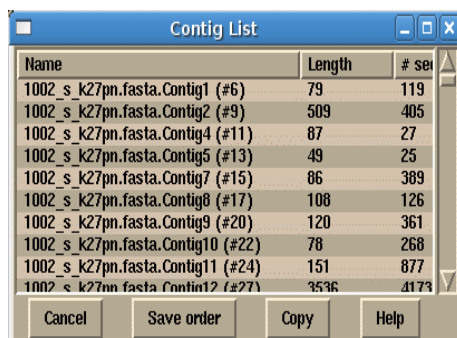cd /home/dbxx/sbf/gap5/gap5-1.2.2-linux-x86_64/linux-x86_64-bin/

(3) Running steps:

(a) Open a database file: maq.denovo

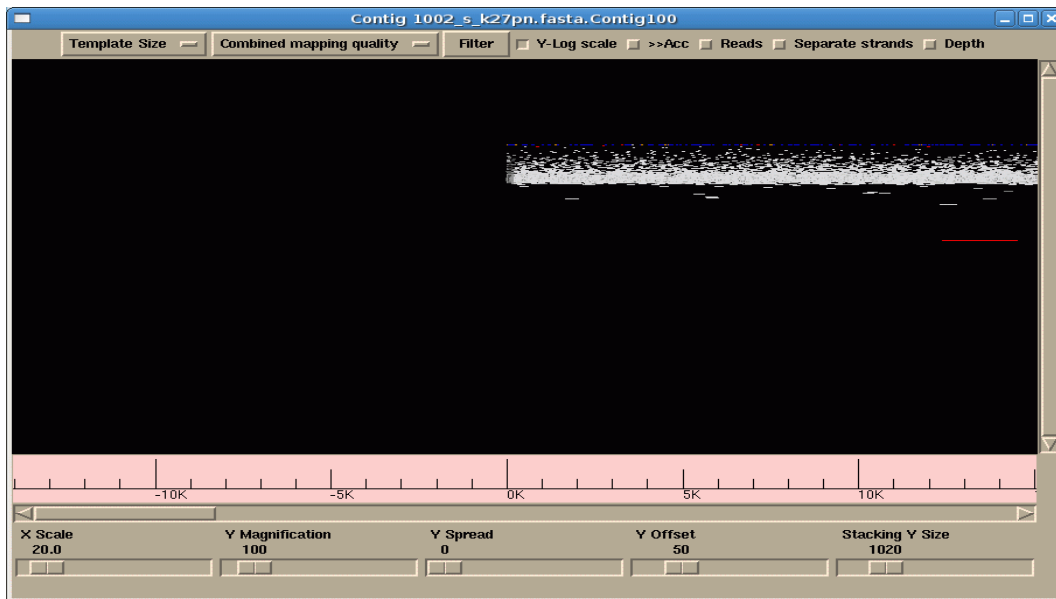./gap5 –ro maq.denovo

(b) Click "view" on the window gap5 v1.2.2:???

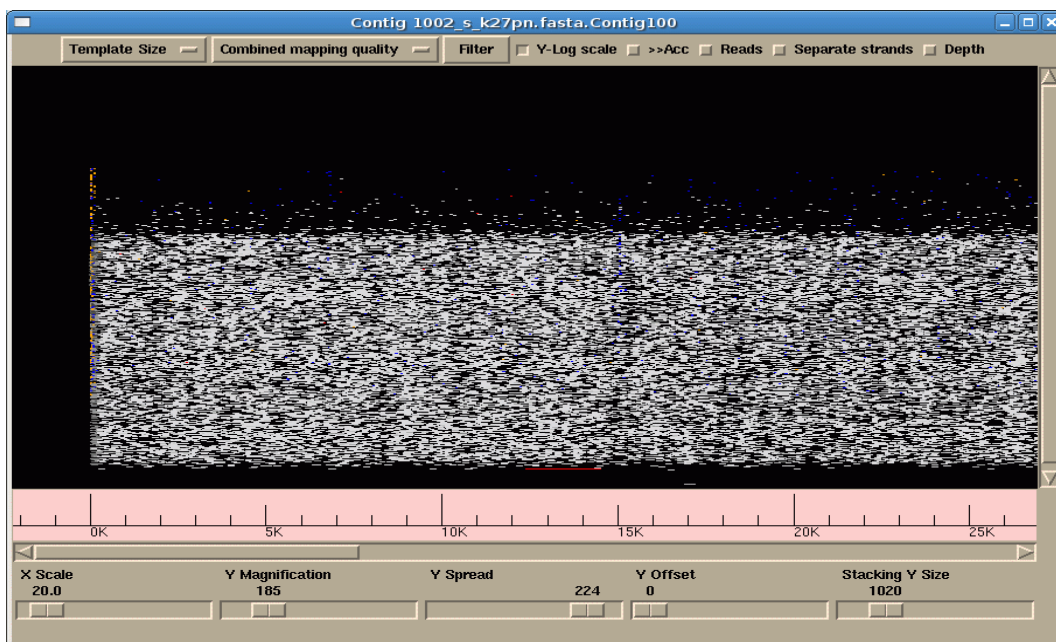(c) Click "Contig list" on "view" - get a window of contig list

(d) Select a contig from the contig list window, say
1002_s_k27pn.fasta.Contig100

Tip 1: point the cursor to the contig and click the right button of mouse to look for "Edit contig";

Tip 2: enlarge the window to see higher depth of data;

Tip 3: move to cursor to see reads at different regions.

(e) Click "Quality" on contig edit window to see base qualities

(f) Template display

Like (d), Point the cursor to a contig and click the right button of mouse to look for "Template Display".

(g) Adjust templates

You can adjust the viewing on X Scale, Y Magnification, Y Spread, Y Offset, etc.

(4) Repeat the above steps by opening another file, such as ssaha.denovo or ssaha.ref etc.