## 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:???

Gap5 v1.2.2: ???								
File Edit View Options Lists				Help				
Output window:	Search	🔲 🗖 Scroll on output	Clear	Redirect >>				
Gap5 has started up in 'Beginner' m please use the 'Configure menus' co	node. To se	lect another menu : he 'Options' menu.	Level,					
Error window: Sea	rch 🛛 🗖 Be	ll 🔲 Scroll on output	Clear	Redirect >>				

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

	Contig Lis	t	_ 🗆 🗙
Name		Length	# sei 🛆
1002_s_k27pn.fa	asta.Contig1 (#6)	79	119
1002_s_k27pn.fa	asta.Contig2 (#9)	509	405
1002_s_k27pn.fa	asta.Contig4 (#11)	)	27
1002_s_k27pn.fa	asta.Contig5 (#13)	) 49	25
1002_s_k27pn.fa	asta.Contig7 (#15)	)	389
1002_s_k27pn.fa	asta.Contig8 (#17)	) 108	126
1002_s_k27pn.fa	asta.Contig9 (#20)	) 120	361
1002_s_k27pn.fa	asta.Contig10 (#22	2) 78	268
1002_s_k27pn.fa	asta.Contig11 (#24	4) 151	877
1002 s k27nn f	asta Contin12 (#2)	7) 3536	4173
Cancel	Save order	Сору	Help

(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.

Edit: 1002_s_k27pn.fasta.Contig100									
File Settings									Help
Undo Redo	Search	🗆 Cutoffs 🗔	Quality						Save
Consensus	ТААТАТ	[CAGAAGCT]	<b>ICCATGCCO</b>	GCCGTATCTGGACT	TCCAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	
		10	20	30	40	50	60	70	80 🗆
>> < 1	гтаатат	[CAGAAGCT]	FCCATGCC	GCCGTATCTGGAC	CCAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCC	GACA
>> < 1	гтаатат	[CAGAAGCT]	FCCATGCC	GCCGTATCTGGAC	CCAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCC	GACA
>> < 1	TAATAT	FCAGAAGCTI	FCCATGCC	GCCGTATCAGGAC	CCAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCC	GACA
> > < 1	TAATAT	FCAGAAGCTI	ICCATGCC	GCCGTATCTGGACT	CAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCC	GACA
$\rangle \dots \rangle \dots \rangle 1$	ГТААТАТ	FCAGAAGCTI	ICCATGCC	GCCGTATCTGGACT	CAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCC	ACA
$\rangle \dots \rangle \dots \rangle 1$	ГТААТАТ	[CAGAAGCT]	ICCATGCCO	GCCGTATCTGGACT	CAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCA	ACA
$\rangle \dots \rangle \dots \rangle 1$	ГТААТАТ	FCAGAAGCTI	ICCATGCC	GCCGTATCTGGACT	CAGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCC	ACA
> > < 1	FTAATAT	FCAGAAGCT	ICCATGCC	GCCGTATCTGGCCT	- AGTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCG	ACA
> < < 1	FTAATAT	FCAGAAGCTI	ICCATTCA	GCCGTATATGGACT	. AATTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCG	CA
$\rangle \dots \rangle \dots \rangle 1$	[TAATA]	FCAGAAGCTI	ICCATGCC	GCCGTATCTGGACT	GTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	i A
$\rangle \dots \rangle \dots \rangle$	TAATAT	FCAGAAGCTI	ICCATGCC	GCCGTATCTGGACT	'T GTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	i A
$\rangle \dots \langle \dots \rangle$	TAATAT	FCAGAAGCTI	FCCATGCCO	GCCGTATCTGGACT	'T GTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	i A
$\rangle \dots \langle \dots \rangle$	TAATAT	FCAGAAGCTI	FCCATGCCO	GCCGTATCTGGACT	T GTTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	i A
$\rangle \dots \rangle \dots \langle$	AATAT	[CAGAAGCT]	FCCATGCC	GCCGTATCTGGACT	TC TTA	TAGTAGGTG	GCCTCAGAGA	TACCGGCCTCCCGG	iC A 🔽
	$\triangleleft$								
1									
Base confidence:3071	I.8 (Prob.	1.000000) A=-3	3076.5 C=-307	6.5 G=3071.8 T=-3076.	.5 *=-37449.9	Position 54			

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

				dit: 1002_s_k2	7pn. fast	a.Conti	g100				
File Settings											Help
Undo Redo	Search	🗆 Cutoffs	🗆 Quality								Save
Consensus	TAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACTTC	CAGTTA	ATAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCCCG	GCAGACA
		10	20	30	4	0	50		60	70	80 🗆
>> K	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GAC C	CAGTTA	ATAGTAGO	ITGGCCT	CAGAGA	FACCGGCCTCC	GACA
>> K	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GAC C	CAGTTA	TAGTAGE	ITGGCCT	CAGAGA	FACCGGCCTCC	GACA
>> K	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCAG	GA <mark>C</mark> C	CAGTTA	TAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCC	GACA
> > K	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACT	CAGTTA	TAGTAGO	ITGGCCT	CAGAGA	FACCGGCCTCCC	GACA
> > >	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACT	CAGTT	TAGTAGE	TGGCCT	CAGAGA	FACCGGCCTCCC	ACA
> > >	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACT	CAGTT	TAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCCA	ACA
> > >	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACT	CAGTTA	ATAGTAGE	TGGCCT	CAGAGA	FACCGGCCTCCC	ACA
> > K	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GCCT	AGTTA	ATAGTAG	TGGCCT	CAGAGA	FACCGGCCTCCCG	ACA
> < K	TTAATA	TCAGAAG <mark>C</mark>	TTCCAT	AGCCGTATATG	GACT	AATTA	ATAGTAG	TGGCCT	CAGAGA	FACCGGCCTCCCG	CA
>>	TTAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACT	GTT	TAGTAG	ITGGCCT	CAGAGA	FACCGGCCTCCCG	G A
>>	TAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACTT	GTT	TAGTAG	it <b>g</b> gcct	'CAG <mark>A</mark> GA'	FACCGGCCTCCCG	G A
> <>	TAATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACTT	GTT	TAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCCCG	G A
> <>	TAATA	TCAGAAG <mark>C</mark>	TTCCATGC	CGCCGTATCTG	GACTT	GTT	ATAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCCCG	G A
> >K	AATA	TCAGAAGC	TTCCATGC	CGCCGTATCTG	GACTTC	TT	ATAGTAGO	TGGCCT	CAGAGA	FACCGGCCTCCCG	GC A 🔽
1											
Base confidence:3071.8 (Prob. 1.000000) A=-3076.5 C=-3076.5 G=3071.8 T=-3076.5 *=-40048.5 Position 51											

(f) Template display

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

		Contig 10	002_s_k2	7pn.fasta.Contig100	
	Template Size 😑	Combined mapping quality	Filter	🗖 Y-Log scale 🔲 >>Acc 🗐 Reads 📄 Separate strands 🗐 Depth	
					$\nabla$
<u> </u>	-10K				
					$\geq$
X Sca	de	Y Magnification	Y Spread	Y Offset Stacking Y Size	
20.0					
			and and		

(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.