Adelaide_Nov2012

SurveyMonkey

1. Name (optional)

	Response Count
	16
answered question	**16**
skipped question	**10**

2. Email (optional)

	Response Count
	14
answered question	**14**
skipped question	**12**

3. Type of delegate

		Response Percent	Response Count
Academic		**50.0%**	**13**
Student		26.9%	7
Corporate		7.7%	2
Other (please specify)		15.4%	4
	answered question		**26**
	skipped question		**0**

4. How did you find out about this course?

		Response Percent	Response Count
From the Australian Bioplatforms website		11.5%	3
Other website (please specify below)		3.8%	1
From an email mailing list (please specify below)		38.5%	10
From a poster (please specify below)		0.0%	0
At a conference (please specify below)		0.0%	0
Word of mouth/recommendation		**42.3%**	**11**
Other (please specify)		3.8%	1
		Other (please specify)	10
		answered question	**26**
		skipped question	**0**

5. What aspect of the workshop/training prompted you to register?

	Response Count
	26
answered question	**26**
skipped question	**0**

6. How useful did you find the following sessions? Please use the text box below to provide specific comments on the programme.

	Not useful (please justify)	Indifferent	Useful	Essential	N/A	Rating Average	Response Count
Next generation sequencing overview	3.8% (1)	3.8% (1)	**53.8% (14)**	34.6% (9)	3.8% (1)	3.24	26
NGS quality control and sequence alignment	0.0% (0)	0.0% (0)	26.9% (7)	**69.2% (18)**	3.8% (1)	3.72	26
Introduction to ChIP-seq	3.8% (1)	26.9% (7)	**42.3% (11)**	23.1% (6)	3.8% (1)	2.88	26
ChIP-seq analysis - peak calling and annotation	3.8% (1)	15.4% (4)	**61.5% (16)**	15.4% (4)	3.8% (1)	2.92	26
ChIP-seq analysis - motif analysis	3.8% (1)	19.2% (5)	**53.8% (14)**	19.2% (5)	3.8% (1)	2.92	26
Introduction to RNA-seq	0.0% (0)	3.8% (1)	46.2% (12)	**50.0% (13)**	0.0% (0)	3.46	26
Alignment and slice junction identification	0.0% (0)	3.8% (1)	38.5% (10)	**57.7% (15)**	0.0% (0)	3.54	26
Transcriptome assembly	0.0% (0)	0.0% (0)	34.6% (9)	**65.4% (17)**	0.0% (0)	3.65	26
Differential expression analysis	0.0% (0)	3.8% (1)	30.8% (8)	**65.4% (17)**	0.0% (0)	3.62	26
Introduction to de novo assembly	0.0% (0)	0.0% (0)	46.2% (12)	**53.8% (14)**	0.0% (0)	3.54	26
De novo assembly using velvet	3.8% (1)	0.0% (0)	**57.7% (15)**	38.5% (10)	0.0% (0)	3.31	26
Review and discussion of Velvet de novo assembly exercises	0.0% (0)	7.7% (2)	**57.7% (15)**	34.6% (9)	0.0% (0)	3.27	26
					Specific comments on topics and the programme		13

answered question	**26**
skipped question	**0**

7. What other topics would you like to have seen covered and at what level would you like it to be set?

	Response Count
	26
answered question	**26**
skipped question	**0**

8. Overall organization of the workshop and training

	Response Percent	Response Count
Excellent	**46.2%**	**12**
Good	**46.2%**	**12**
Satisfactory	7.7%	2
Poor	0.0%	0
Very poor	0.0%	0
answered question		**26**
skipped question		**0**

9. Programme/format

	Response Percent	Response Count
Excellent	38.5%	10
Good	**46.2%**	**12**
Satisfactory	15.4%	4
Poor	0.0%	0
Very poor	0.0%	0
answered question		**26**
skipped question		**0**

10. Materials provided

		Response Percent	Response Count
Excellent		**50.0%**	**13**
Good		34.6%	9
Satisfactory		15.4%	4
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

11. Facilities provided

		Response Percent	Response Count
Excellent		**65.4%**	**17**
Good		26.9%	7
Satisfactory		7.7%	2
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

12. Contents of individual presentation sessions

		Response Percent	Response Count
Excellent		19.2%	5
Good		**76.9%**	**20**
Satisfactory		3.8%	1
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

13. Clarity of presentations

		Response Percent	Response Count
Excellent		15.4%	4
Good		**57.7%**	**15**
Satisfactory		26.9%	7
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

14. Knowledge of speakers

		Response Percent	Response Count
Excellent		**61.5%**	**16**
Good		34.6%	9
Satisfactory		3.8%	1
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

15. Contents of practical sessions

		Response Percent	Response Count
Excellent		34.6%	9
Good		**61.5%**	**16**
Satisfactory		3.8%	1
Poor		0.0%	0
Very poor		0.0%	0
		answered question	**26**
		skipped question	**0**

16. Duration of sessions

		Response Percent	Response Count
Too short		30.8%	8
About right		**57.7%**	**15**
A bit long		11.5%	3
Much too long		0.0%	0
		answered question	**26**
		skipped question	**0**

17. Level of scientific content in the tutorial

		Response Percent	Response Count
Too general		3.8%	1
About right		**73.1%**	**19**
A little specific		15.4%	4
Much too specific		7.7%	2
		answered question	**26**
		skipped question	**0**

18. How do you rate tis workshop compared to similar events you have attended previously?

		Response Percent	Response Count
much better		15.4%	4
better		**57.7%**	**15**
average		26.9%	7
poorer		0.0%	0
		please explain	10
		answered question	**26**
		skipped question	**0**

19. How would you rate the practical usefulness of the tutorials as applied to your work?

		Response Percent	Response Count
Not very useful		0.0%	0
Useful		**69.2%**	**18**
Extremely useful		30.8%	8
		answered question	**26**
		skipped question	**0**

20. Would you like further training?

	Response Percent	Response Count
Yes	**84.6%**	**22**
No	15.4%	4
if yes, what would you like to see covered?		20
answered question		**26**
skipped question		**0**

21. Would you recommend this training to colleagues?

	Response Percent	Response Count
Yes	**100.0%**	**26**
No	0.0%	0
answered question		**26**
skipped question		**0**

22. On this course there should have been more opportunities for... because...

	Response Count
	26
answered question	**26**
skipped question	**0**

23. What do you think you will remember most about this course...and why?

	Response Count
	26
answered question	26
skipped question	0

24. What did you think of the catering?

	Response Count
	19
answered question	19
skipped question	7

25. Please add any other comments here

	Response Count
	6
answered question	6
skipped question	20

Page 2, Q4. How did you find out about this course?		
1	email list of School of medicine, Flinders University	Nov 28, 2012 6:31 AM
2	Not entirely sure now. I got told about it from a collegue, got an email through the uni and might have also got one from BigSA.	Nov 28, 2012 6:29 AM
3	Bioinformatition fwd me email from somewhere...	Nov 28, 2012 6:27 AM
4	South Australian Museum	Nov 28, 2012 6:27 AM
5	BigSA email list	Nov 28, 2012 6:27 AM
6	BigSA mailing list.	Nov 28, 2012 6:27 AM
7	FCIC centre email mailing list	Nov 28, 2012 6:26 AM
8	BIG SA	Nov 28, 2012 6:26 AM
9	I think it was the BIG SA mailing list	Nov 28, 2012 6:26 AM
10	BIG SA	Nov 28, 2012 6:24 AM

Page 2, Q5. What aspect of the workshop/training prompted you to register?		
1	Practical side of the workshop, RNA-seq, Diff exp and general knowladge of bioinformatics.	Nov 28, 2012 6:31 AM
2	chance to learn bioinformatics analysis tools hands on, including the use of the line command in UNIX; I was especially interested in the RNA-seq analysis.	Nov 28, 2012 6:31 AM
3	The content and the target people	Nov 28, 2012 6:31 AM
4	De novo assembly - Hands-on to NGS data in general	Nov 28, 2012 6:30 AM
5	I'm particularly interested in denovo assembly and have attended a few theoretical information sessions (and a lot of seminars that have used NGS) but wanted some hands on as I'd reached a point where I was only going to understand more by actually doing something myself but was unsure where to actually start by myself. So I guess the hands on aspect (and the small class size).	Nov 28, 2012 6:29 AM
6	RNA- Seq	Nov 28, 2012 6:27 AM
7	hands on aspect	Nov 28, 2012 6:27 AM
8	general background for NGS analysis	Nov 28, 2012 6:27 AM
9	Hands-on demostrations/exercises	Nov 28, 2012 6:27 AM
10	RNAseq	Nov 28, 2012 6:27 AM
11	interest in hands on introduction to NGS etc	Nov 28, 2012 6:27 AM
12	RNA seq and de novo genome assembly information within the course Definitely the hands on experience available within the course	Nov 28, 2012 6:27 AM
13	The 'beginner' part!!!	Nov 28, 2012 6:27 AM
14	RNASeq workshop	Nov 28, 2012 6:26 AM
15	The course mentioned that it was for those with little or no bioinformatics experience. I also noticed that some of the topics that were covered were what I needed to learn about for my project.	Nov 28, 2012 6:26 AM
16	The aspects involved with new & better methods for analysing sequence data.	Nov 28, 2012 6:26 AM
17	De novo genome assembly	Nov 28, 2012 6:26 AM
18	The overall understanding of NGS.	Nov 28, 2012 6:26 AM
19	RNA Seq and basic bioinformatics workshop	Nov 28, 2012 6:26 AM
20	Hands on analysis of data and learning workflows Short (only two days)	Nov 28, 2012 6:26 AM
21	Strong interest in RNA-seq and ChIP-seq (we are using these techniques in our lab)	Nov 28, 2012 6:26 AM
22	Hands-on aspect	Nov 28, 2012 6:26 AM
23	The words 'NGS', as I needed to investigate this new technology	Nov 28, 2012 6:26 AM

Page 2, Q5. What aspect of the workshop/training prompted you to register?		
24	I wanted to get a basic understanding of NGS	Nov 28, 2012 6:25 AM
25	Specifically targeted at novices like myself	Nov 28, 2012 6:24 AM
26	RNA-seq component of the course and hands on practical focus	Nov 28, 2012 6:16 AM

Page 3, Q6. How useful did you find the following sessions? Please use the text box below to provide specific comments on the programme.

1	I found the whole program really intersting and useful. The only reason I haven't ticked essential for every session is I'm not sure if I'm likely to use ChIP and RNAseq. Probably more likely to use RNAseq than ChIP. Gaining an understadning of them though was definitely useful.	Nov 28, 2012 6:39 AM
2	good background information on methods of the lab procedures and also how to do the analysis; RNA-seq and ChIP-seq were very good and useful	Nov 28, 2012 6:38 AM
3	I feel like the de novo assembly section was rushed and I didn't get through the hands-on components in the time given. I think this section needs a whole day dedicated to it. The RNA Seq section was the section I most enjoyed and understood the easiest. Perhaps this could have been allocated at the end of the first day to leave the whole of the second day for de novo genome assembly. The Chip-Seq hands-on section was difficult to understand. It would be useful to have more time and information to dissect what we are actually asking the programs we are using to do. ie deciphering the command lines we are using	Nov 28, 2012 6:36 AM
4	Fantastic work!!!	Nov 28, 2012 6:34 AM
5	I got a bit lost in the de Novo paired ends session, this may be due to the fact we skipped the single-end session	Nov 28, 2012 6:33 AM
6	The de novo assembly isthe most complex and time consuming yet is squashed into a short amount of time and truncated in order to fit it in (which almost no one managed). Sems somewhat anti-thetical. Perhaps it deserved a whole day or a separate workshop? Whilst I understand the point of using a prokaryotic example and velvet, it has little relevance to those working with eukaryotic genomes.	Nov 28, 2012 6:32 AM
7	Although I found most of the course useful, I would have liked more time to be spent on RNA Seq & De Novo assembly, as they're the most relevent to my work, & the most conceptually difficult to grasp.	Nov 28, 2012 6:32 AM
8	I think the course was structured well and worked through a logical build up to more complex topics. The tutors were excellent and the ratio of tutors to students was great to see. Always some one to help and talk to.	Nov 28, 2012 6:32 AM
9	Overall an excellent workshop that I got a lot out of. Some suggestions: 1) ChIP-seq lecture: not enough focus on the actual bioinformatics (I wanted to hear about differences between peak calling tools), too much emphasis on wet-lab experiments 2) Some figures on slides too small to read/interpret. 3) Could provide extended exercises for people who finish early (especially in ChIP-seq and RNA-seq sections). 4) De novo genome assembly: processes/tasks took too long - spent a considerable time waiting.	Nov 28, 2012 6:31 AM
10	Not nearly enough time left to cover the exercises for the de novo assembly. Otherwise all other topics covered well with enough time.	Nov 28, 2012 6:30 AM
11	ChIP seq we went through it a bit to quickly for complete understanding also not very relevant to my personal work	Nov 28, 2012 6:30 AM
12	The de novo stuff was the most interesting to me, yet we spent the least time on it. Giving out the details that were removed from previous courses as advanced exercises would be good, so that those who are interested in this aspect could focus on this would have been great.	Nov 28, 2012 6:29 AM

Page 3, Q6. How useful did you find the following sessions? Please use the text box below to provide specific comments on the programme.

13	A professional bias, but a whole day on RNA-seq would be good	Nov 28, 2012 6:18 AM

Page 3, Q7. What other topics would you like to have seen covered and at what level would you like it to be set?		
1	I would have loved more time on the denovo assembly. A whole day or even a two day course just on the denovo would be useful for me. Maybe, more basic information of what the outputs meant might have been useful. Just as pictures int eh manual even.	Nov 28, 2012 6:39 AM
2	metagenomics; pyrosequencing data analysis	Nov 28, 2012 6:38 AM
3	NGS in small RNA, ie miRNA. Similar level would be good for me.	Nov 28, 2012 6:37 AM
4	I would like more time dedicated to particular sections.	Nov 28, 2012 6:36 AM
5	Metagenomics and more info and hands-on de novo assembly.	Nov 28, 2012 6:34 AM
6	RAD-sequencing	Nov 28, 2012 6:34 AM
7	I would have liked more on transcriptome assembly without a reference genome and perhaps more on the alternative programs available (including looking at 454 data). This information set at about the same level as this course would be good.	Nov 28, 2012 6:33 AM
8	SNP, variation and mutation calling	Nov 28, 2012 6:32 AM
9	I would have liked to have seen new methods for determining sequence diversity within heterogenous DNA extractions (such as environmental samples).	Nov 28, 2012 6:32 AM
10	The level was perfect for me considering that we only had two days	Nov 28, 2012 6:32 AM
11	The course provided a good overview of the main applications of NGS technology. I don't think much more should be added to the beginner course. Instead specific courses should be developed which cover each of the existing topics in greater detail and provide more advanced training.	Nov 28, 2012 6:32 AM
12	would be great to have a specific RNA-seq course with detailed experimental and bioinformatics topics	Nov 28, 2012 6:31 AM
13	More on RNA-seq	Nov 28, 2012 6:31 AM
14	-	Nov 28, 2012 6:30 AM
15	Level was appropriate - probably wouldn't have like it to have been aimed much higher	Nov 28, 2012 6:30 AM
16	R - at an introductory level	Nov 28, 2012 6:30 AM
17	Extended RNA seq including some info on experimental design, Programs for whole genome alignments. Extended de novo assembly section.	Nov 28, 2012 6:30 AM
18	None	Nov 28, 2012 6:29 AM
19	How to interprete the data and how to analyze the data.	Nov 28, 2012 6:29 AM
20	RAD-Seq, metagenomics	Nov 28, 2012 6:29 AM
21	more other applications	Nov 28, 2012 6:28 AM
22	Now that I have the overview provided by this great course I would like some	Nov 28, 2012 6:28 AM

Page 3, Q7. What other topics would you like to have seen covered and at what level would you like it to be set?		
	information of metagenomics.	
23	metagenomics	Nov 28, 2012 6:28 AM
24	RNA Seq starting a bit basic and finishing with in-depth analysis	Nov 28, 2012 6:28 AM
25	I am very new to NGS and I found myself lost quite often. I had hoped this would be more suited to a beginner but the jargon and complex nature of NGS meant I struggled to understand much of what was going on	Nov 28, 2012 6:28 AM
26	the impact of experimental design and library prep methods	Nov 28, 2012 6:18 AM

Page 3, Q18. How do you rate tis workshop compared to similar events you have attended previously?		
1	lots of helpful tutors on hand	Nov 28, 2012 6:39 AM
2	chance for hands on learning and also lots of support during the practicals from the tutors	Nov 28, 2012 6:38 AM
3	This is the first workshop of this type I have attended	Nov 28, 2012 6:36 AM
4	NA	Nov 28, 2012 6:34 AM
5	Not that I attend many things like this, but actually doing the exercises as you learn about the processes is very good	Nov 28, 2012 6:33 AM
6	not attended another, so this is the average (although n = 1)	Nov 28, 2012 6:32 AM
7	Most such events I've attended were far too theoretical, & had far too little focus on practical knowledge.	Nov 28, 2012 6:32 AM
8	It covered complex topics in a very structured and effective way in a short amount of time	Nov 28, 2012 6:32 AM
9	good hands on sessions with easy access to knowledgable leaders	Nov 28, 2012 6:31 AM
10	I haven't attended any previously	Nov 28, 2012 6:29 AM

Page 4, Q20. Would you like further training?		
1	use of command line in UNIX (learn all the commands and shortcuts) and more indepth and other programs for RNA-seq analysis (and other analyses too possibly)	Nov 28, 2012 6:50 AM
2	de novo assembly but after I've had more of a practice on my own	Nov 28, 2012 6:40 AM
3	NGS in small RNA	Nov 28, 2012 6:39 AM
4	metagenomics, RNA-Seq, de-novo assembly	Nov 28, 2012 6:38 AM
5	More detailed coverage of the same topics!	Nov 28, 2012 6:37 AM
6	I don't know yet!!	Nov 28, 2012 6:37 AM
7	de Novo transcriptome assembly and Amplicon sequencing and analysis	Nov 28, 2012 6:37 AM
8	sequence analyis compared to reference genomes (ie SNP/mutation/ insertion deletion calling on NGS data)	Nov 28, 2012 6:36 AM
9	Sequence diversity in environmental DNA samples	Nov 28, 2012 6:35 AM
10	Slightly more advanced de novo assembly. A basics in linux to increase understanding of what i am actually typing!	Nov 28, 2012 6:34 AM
11	RNA-seq, variant calling (especially for heterogeneous cancer samples)	Nov 28, 2012 6:33 AM
12	the same but with more practical time	Nov 28, 2012 6:32 AM
13	more in depth RNASeq and use of R	Nov 28, 2012 6:32 AM
14	How to interprete and analyze the data	Nov 28, 2012 6:32 AM
15	RAD-Seq, metagenomics	Nov 28, 2012 6:32 AM
16	Transcriptome and differential expression of genes and small RNA Seq	Nov 28, 2012 6:31 AM
17	RNA-seq	Nov 28, 2012 6:31 AM
18	Same but with way more guidence and a lot slower	Nov 28, 2012 6:31 AM
19	Metagenomics	Nov 28, 2012 6:30 AM
20	Statistical considerations and experimental design	Nov 28, 2012 6:20 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
1	learning the command line ahead of time (some training or workshop on that); the practicals would have gone faster for me	Nov 28, 2012 6:50 AM
2	probably about right.	Nov 28, 2012 6:40 AM
3	N/A	Nov 28, 2012 6:39 AM
4	metagenomics	Nov 28, 2012 6:38 AM
5	Just more time for asking more questions	Nov 28, 2012 6:37 AM
6	observing analysis in current real life scenarios. We worked with very simple data sets so some presentations showing the analysis workflow for more complex datasets using command line would have been interesting	Nov 28, 2012 6:37 AM
7	Not sure...would have liked more time to just chat to others, but felt like I was getting behind on the tutorial.	Nov 28, 2012 6:37 AM
8	NA	Nov 28, 2012 6:36 AM
9	To come to grips with the commands and processes. More of a discussion of the web based tools which, however flawed, are still likely to be places people will go to and use (Galaxy.org, Broad etc)	Nov 28, 2012 6:36 AM
10	working on practical examples-perhaps even ones randomly downloaded from online, because practice makes perfect.	Nov 28, 2012 6:35 AM
11	The sessions on the second dady should all have been longer to leave more time for understanding and questions	Nov 28, 2012 6:34 AM
12	.	Nov 28, 2012 6:34 AM
13	a longer course would have been good so that we can more thoroughly understand the tools	Nov 28, 2012 6:33 AM
14	..	Nov 28, 2012 6:32 AM
15	ran out of time on the de novo, otherwise very good. Lots of help from instructors was also good	Nov 28, 2012 6:32 AM
16	It would be better to send us some general and basic information about the background knowledge before the course.	Nov 28, 2012 6:32 AM
17	advanced exercises for those interested in specific parts, i.e. ChIP-Seq, or de novo assemblies	Nov 28, 2012 6:32 AM
18	-	Nov 28, 2012 6:31 AM
19	N/A	Nov 28, 2012 6:31 AM
20	NA	Nov 28, 2012 6:31 AM
21	I think instructor lead demonstrations that we follow would have been better	Nov 28, 2012 6:31 AM
22	na	Nov 28, 2012 6:30 AM
23	Other non-linux programs such as Seqman	Nov 28, 2012 6:30 AM

Page 4, Q22. On this course there should have been more opportunities for... because...		
24	NA	Nov 28, 2012 6:29 AM
25	-	Nov 28, 2012 6:29 AM
26	working with data relevant to your own work	Nov 28, 2012 6:20 AM

Page 4, Q23. What do you think you will remember most about this course...and why?		
1	the chance to use the cloud and analyse lots of cool data; also all the help received	Nov 28, 2012 6:50 AM
2	hopefully what's important for assemblies. Helpful tutors.	Nov 28, 2012 6:40 AM
3	Practical aspect	Nov 28, 2012 6:39 AM
4	de novo assembly	Nov 28, 2012 6:38 AM
5	The hands on component of trying computer programs that I haven't used before	Nov 28, 2012 6:37 AM
6	The conversations and people I met and information I found out about what people are doing and the bioinformatics challenges involved	Nov 28, 2012 6:37 AM
7	Chatting to the tutors about my own work, and finding some local people to bug now :)	Nov 28, 2012 6:37 AM
8	That it's a lot of information. Need to work closely with bioinformatic people	Nov 28, 2012 6:36 AM
9	First attempt at getting to grips with bioinformatics. Somewhat demystified but still a foreign language!	Nov 28, 2012 6:36 AM
10	RNA-Seq, because I think it will be the most relevent to my future work.	Nov 28, 2012 6:35 AM
11	RNA seq difference between -G and -g. How to visulise using IGV it was well explained and we practised it enough times to really understand	Nov 28, 2012 6:34 AM
12	Thanks to this course I now have the confidence to conduct an RNAseq experiment	Nov 28, 2012 6:34 AM
13	hopefully how to use ssh and RNA-seq analysis	Nov 28, 2012 6:33 AM
14	..	Nov 28, 2012 6:32 AM
15	Good material, access to training material & good help from tutors. Well run thank you	Nov 28, 2012 6:32 AM
16	How to use the command and basic understanding on the NGS.	Nov 28, 2012 6:32 AM
17	The tools I learnt about that I had no idea existed	Nov 28, 2012 6:32 AM
18	-	Nov 28, 2012 6:31 AM
19	Good course content for RNA Seq and helpful demonstrators	Nov 28, 2012 6:31 AM
20	RNA-seq bioinformatics - most relevant to my work	Nov 28, 2012 6:31 AM
21	That NGS is beyond me at this point	Nov 28, 2012 6:31 AM
22	The overview gave me a good perpestive about what can be done with sequence data. Very helpful when starting out but also when conversing with someone who is dealing with your data for you.	Nov 28, 2012 6:30 AM
23	RNA seq	Nov 28, 2012 6:30 AM
24	NA	Nov 28, 2012 6:29 AM

Page 4, Q23. What do you think you will remember most about this course...and why?		
25	-	Nov 28, 2012 6:29 AM
26	Some of the short cuts and teh use of unique tools. Insight into methods that I was unaware of	Nov 28, 2012 6:20 AM

Page 4, Q24. What did you think of the catering?		
1	excellent; great food	Nov 28, 2012 6:50 AM
2	good	Nov 28, 2012 6:40 AM
3	great	Nov 28, 2012 6:38 AM
4	Good	Nov 28, 2012 6:37 AM
5	Ordinary but acceptable	Nov 28, 2012 6:37 AM
6	I'm a bit hungry, not much lunch left when I got out there	Nov 28, 2012 6:37 AM
7	Good, Some water would have been good.	Nov 28, 2012 6:36 AM
8	Fine	Nov 28, 2012 6:36 AM
9	Very good.	Nov 28, 2012 6:35 AM
10	Good	Nov 28, 2012 6:34 AM
11	Good	Nov 28, 2012 6:34 AM
12	ok, more non-cake based snaks would have been good...	Nov 28, 2012 6:33 AM
13	Very good	Nov 28, 2012 6:32 AM
14	OK	Nov 28, 2012 6:32 AM
15	good.	Nov 28, 2012 6:31 AM
16	ok	Nov 28, 2012 6:30 AM
17	Could be improved	Nov 28, 2012 6:30 AM
18	ok	Nov 28, 2012 6:29 AM
19	Average	Nov 28, 2012 6:20 AM

Page 4, Q25. Please add any other comments here		
1	would be good to have printouts of the presentations to make notes on or a way to make notes digitally great tutoring during the practicals	Nov 28, 2012 6:50 AM
2	Great work. The tutros and local bioinformaticians were very gracious in giving their time for this and it was invaluable to have them here giving hands on advice and help. I really enjoyed meeting people and talking more about bioinformatics	Nov 28, 2012 6:37 AM
3	Thanks for the workshop :)	Nov 28, 2012 6:37 AM
4	Good if the paper workbook was up to date instead of reading off the electronic one,. Handy to ahve some copies of the presentations to help with note taking as the presentations occur. Bioinformatics team were Great in general and Thanks for taking time to help us out!!	Nov 28, 2012 6:34 AM
5	The hard copy of the manual needed to reflect the electronic copy more, plus there were a lot of spelling and grammar mistakes which sometimes made it confusing what we actually needed to do.	Nov 28, 2012 6:32 AM
6	If any jargon has to be used then it should be fully explained. I felt a little put off about asking questions as the group moved so fast and I didn't feel confident to do so	Nov 28, 2012 6:31 AM