Gene Expression profiling with HTS: RNA-Seq data analysis

Rome, 19-22 October 2015

Feedback questionnaire

1-10%	very bad/disagree completely
25%	bad/disagree
50%	nor good nor bad/no strong feelings
75%	good/agree
90-100%	excellent/agree completely

Nella tabella sottostante i valori in grassetto indicano la percentuale di voti mentre, tra parentesi, è indicato il numero assoluto di voti. In grigio, le caselle che hanno preso più voti.

		Don't know	0-10%	25%	50%	75%	90-100%
1	**Information about the course was...**			**5**(1)	**10**(2)	**29**(6)	**57**(12)
2	**The course website was...**			**5**(1)	**14**(3)	**24**(5)	**57**(12)
3	**Registration was...**				**5**(1)	**29**(6)	**67**(14)
4	**The venue was...**					**25**(5)	**76**(16)
5	**The IT support was...**				**5**(1)	**10**(2)	**86**(18)
6	**Catering was...**					**19**(4)	**81**(17)
7	**The overall organization was...**					**33**(7)	**67**(14)
8	**The topics were relevant for my work/research interests**	1				**29**(6)	**67**(14)
9	**I was inspired to new ways of thinking**				**5**(1)	**48**(10)	**48**(10)
10	**Did the course fulfill your expectations?**					**43**(9)	**57**(12)
11	**Overall, how would you rate this course?**					**43**(9)	**57**(12)
12	**The lectures were clearly presented and comprehensible**						
	Introduction to HTS data and tools (T. Colombo)					**19**(4)	**81**(17)
	Unix/Linux command line (A. Via)					**5**(1)	**95**(20)
	CINECA command line (T. Castrignanò &C. Padrin)			**14**(3)	**10**(2)	**48**(10)	**29**(6)
	RNA-Seq data analysis (F. Ferrè)					**19**(4)	**81**(17)
	RNA-Seq CINECA pipelines (G. Chillemi/M. D'Antonio)	1			**10**(2)	**24**(5)	**62**(13)
13	**The pace of teaching was right**						
	Introduction to HTS data and tools (T. Colombo)					**24**(5)	**76**(16)
	Unix/Linux command line (A. Via)					**14**(3)	**86**(18)
	CINECA command line (T. Castrignanò &C. Padrin)			**5**(1)	**14**(3)	**48**(10)	**33**(7)

#	Lecture / Statement							
	RNA-Seq data analysis (F. Ferrè)					**5**(1)	**24**(5)	**71**(15)
	RNA-Seq CINECA pipelines (G. Chillemi/M. D'Antonio)					**5**(1)	**24**(5)	**71**(15)
14	**Teaching aids used (e.g. slides) were well prepared**							
	Introduction to HTS data and tools (T. Colombo)						**29**(6)	**71**(15)
	Unix/Linux command line (A. Via)						**14**(3)	**86**(18)
	CINECA command line (T. Castrignanò &C. Padrin)				**10**(2)	**5**(1)	**43**(9)	**43**(9)
	RNA-Seq data analysis (F. Ferrè)					**10**(2)	**14**(3)	**76**(16)
	RNA-Seq CINECA pipelines (G. Chillemi/M. D'Antonio)					**14**(3)	**5**(1)	**81**(17)
15	**Hands-on exercises and demonstrations were a valuable contribution to the course**							
	Introduction to HTS data and tools (T. Colombo)	2					**33**(7)	**57**(12)
	Unix/Linux command line (A. Via)						**14**(3)	**86**(18)
	CINECA command line (T. Castrignanò &C. Padrin)	1			**10**(2)	**10**(2)	**19**(4)	**57**(12)
	RNA-Seq data analysis (F. Ferrè)						**10**(2)	**91**(19)
	RNA-Seq CINECA pipelines (G. Chillemi/M. D'Antonio)				**5**(1))	**14**(3)	**24**(5)	**57**(12)

16	**Would you suggest this course to a friend/colleague?**

21: yes
0: no

17	**What did you like most about the course?**

14: Practical sessions, hands-on, interactivity, teachers' attitude
4: RNA-Seq data analysis session
1: Discovering job submission to CINECA
1: The command line session

18	**What did you like least about the course?**

13: Nothing
2: Some lectures have been repetitive
2: CINECA command line need to be better explained
1: Sometimes too difficult language for people with no bioinformatics background
1: Little detail on biological framework
1: Need for more lessons on the command line
1: Some teachers spoke too fast

19	**Additional comments and suggestions on the content, specific lectures, etc.**

13: None
2: add one day course
1: add intro lecture about biology
1: first day should be more "compact" (??)
1: more Unix command line for beginners
1: more on CINECA pipeline with more practical examples
1: organise evening networking events
1: link to Unix command line courses
1: expand your fame