

BGRS'04 Tutorial-Evaluation Results

High Performance Computing in Bioinformatics

Calculation of result values	value=1 ⇒	<input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>	⇐ value=5
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PART I: High Performance Computing Thomas Ludwig

1.	I found the contents	too difficult	3.4	too easy
2.	I found the contents	boring	4.7	interesting
3.	In relation to my research this part is	not helpful	3.8	helpful
4.	The number of issues presented is	too low	3.2	to high
5.	This part of the tutorial is	unstructured	4.8	well-structured
6.	The number of slides is	too low	3.1	too high
7.	The slide layout is	poor	4.6	excellent
8.	The oral presentation quality is	poor	4.8	excellent
9.	Would you recommend this part?	no	4.9	yes

PART II: High Performance Bioinformatics Alexandros Stamatakis

1.	I found the contents	too difficult	2.5	too easy
2.	I found the contents	boring	4.1	interesting
3.	In relation to my research this part is	not helpful	3.3	helpful
4.	The number of issues presented is	too low	3.3	to high
5.	This part of the tutorial is	unstructured	4.7	well-structured
6.	The number of slides is	too low	3.4	too high
7.	The slide layout is	poor	4.6	excellent
8.	The oral presentation quality is	poor	4.6	excellent
9.	Would you recommend this part?	no	4.8	yes

Which aspects of the tutorial did you find most interesting?

General aspects; too much details are difficult to follow // about phylogeny inference // Overview of HPC is very interesting; detailed explanation and RaxML for phylotrees: comparison is useful for me // Biological aplices // Part I: would be cool to include photos of Earth Simulator // Practical examples of using HPC // The actual algorithms // Multiple alignment // parallel features to help working // parallel programming

Which aspects of the tutorial did you find least interesting?

Deep algorithms explanations // Technical aspects // The details of comparative tests between RaxML and other software // The HPC introduction since I'm already familiar with these things // Top500 computers, not clearly all informations about this // Some details in realization technique // The very last part of part II (about shared memory parallelism) seems to be slightly "not in place"; or maybe I just don't catch the meaning

Which aspects would you like to see covered additionally in such a tutorial?

Some specific aspects taken out and done thoroughly in greater detail without much prior assumption about the participants // maybe more detailed about programs which are used for phylogenetic reconstruction, about their principles // more results of concrete phylo-trees // Part I: parallel processors and motherboards, programs for automatical parallelism, what features of programs for parallel use? // more data of real calculation experiment; data of scientific application (climate, phylogeny etc.) // I would like to see some coverage on transputers in the first part

Additional comments:

Very good tutorial // First part was absolutely excellent. In the second part, I would prefer to see wider range of bioinformatic issues covered: parallelization and alignment tools, etc. // A short break in the middle would be helpful // Well-done // Excellent tutorial // [A longer comment on Amdahl's Law] // Presentations have some new interesting points for me // 5x thank you [very polite people ☺]