



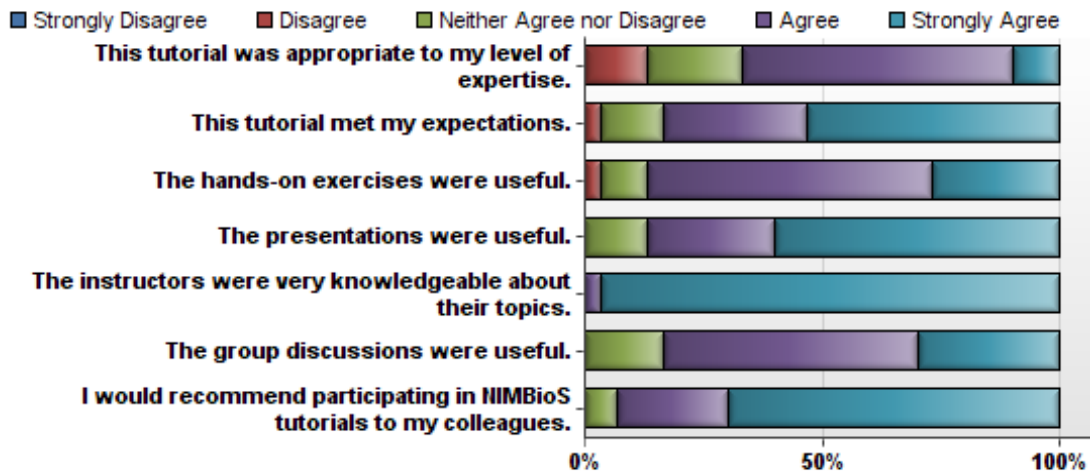
Evaluation Summary Report

Tutorial: *Evolutionary Quantitative Genetics 2015*

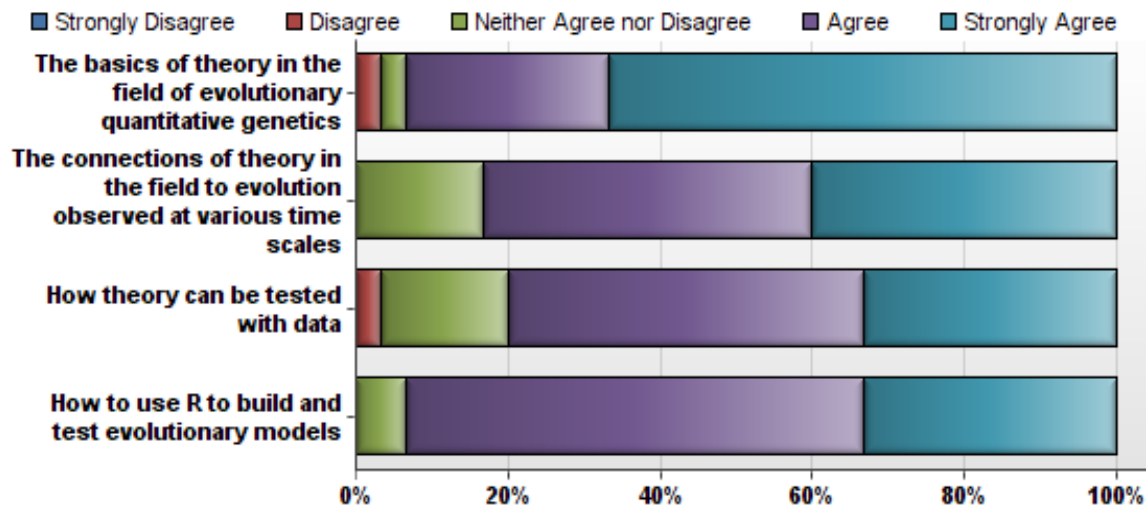
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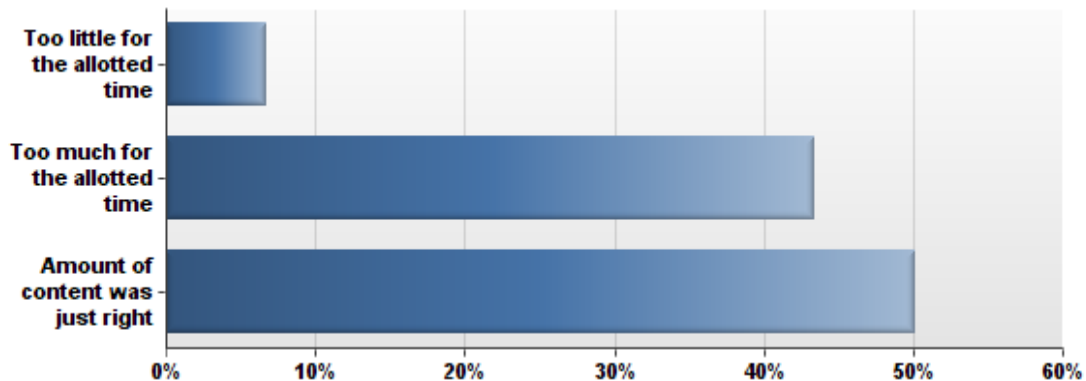
Please indicate your level of agreement with the following statements about this tutorial:



As a result of participating in this tutorial, I have a better understanding of:



How do you feel about the amount of content offered during the tutorial?



The annotated code will definitely be useful

The time given for discussion.

Explanation and insights from lecturers

The connection between lecture subject matter to real world implementation in R was useful for cementing tricky or unfamiliar ideas in my brain.

Having the R scripts available to work through many of these complex analyses. Although I may not have always understood them, I consider it much more likely that I can modify these scripts to my own needs than come up with the code from scratch.

I thought both the lectures and computer exercises to be essential to the course. I found the lectures to be extremely helpful, as the instructors were able to effectively communicate conceptually challenging ideas in a way that increased my level of understanding. I also found to discussions following the lectures to be extremely productive.

I think it's hard to say a 'most useful' aspect, because everything ties together so well. Long term, probably the R code is most useful. Currently, the lectures are probably most useful.

To me it was being able to connect the analytical and conceptual features of models in quantitative genetics. All the instructors used their own metaphors to make the models and their assumptions intuitive. I found this to be most important in clarifying things.

The combination of discussion that occurred during each lecture. Many of the questions asked as we went through each topic made the content easier to digest.

I liked the hands-on exercises, but I felt the interpretations of the results were not given enough priority, especially for those with less biological background

Theory integrated with the practicals immediately after the lectures. Interaction with the instructors.

Connection between macro and micro processes. Demonstrations of concepts in R.

2 things: 1) hearing more about the theories. I was familiar with some of the work and completely new to other parts. Learning about the theory that goes into evolutionary thinking was very eye-opening. 2) Getting to hear how the instructors developed their models. I have been curious about modeling for a long time and learning how people go about modeling and learning about some of the tools (e.g. OUwie, Brownian motion models, Matrix models etc.) gave me a deeper understanding and more confidence in trying to pursue modeling on my own.

The most useful aspect was seeing a broad range of computing options for testing hypothesis in evolutionary quantitative genetics. This came on top of a thorough coverage of basic theory in the discipline.

Clear biological examples linked to the theoretical components during lectures

The comparative method, ancestral trait state reconstructions and the adaptive landscape

The hands-on experience of performing the statistical analyses.

Good balance of theory and practice, ample time for interacting with instructors

The balance between lectures and exercises was fantastic.

R code and the presence of its coders. Seminal paper and techniques dissected by their authors. The occasional undeserving postdoc who got a deep hold of a complex technique and is ready to share his knowledge with a roomful of avid users... my hat goes to Liam.

The R scripts and various R exercises were very good.

Collaborating with biologists and finding useful problems at the intersection of mathematics and biology. Also learning to use R for data-driven models.

but for those wanting additional instruction in various topics, the possibility to perform these exercises on their own time would really be valuable.

I would have liked more of the exercises to be completed in a group setting, because I found that when I was discussing what we were doing with the exercises with my neighbors I got more out of them. Possible fewer exercises with more time allotted to each.

I would suggest that bigger blocks of time be set aside for exercises in R. I speak for myself here, but I learn better by figuring things out on my own, by making mistakes and fixing it. While it was nice to have the code, it was disruptive to follow along, and just execute code without having the time to deconstruct the code and understand the variables and data structure. I also think that if possible participants should be encouraged to bring their own data, because we usually have the best idea about what the data is and what biological questions we are asking with the data. I think that would provide much better context when running exercises in R. Additionally, I think the course would benefit greatly by having learning objectives outlined. For example "1. If you have trait measurements for two traits from 20 closely related species, at the end of this course, you would have learned how do x, y and z.." and so on.

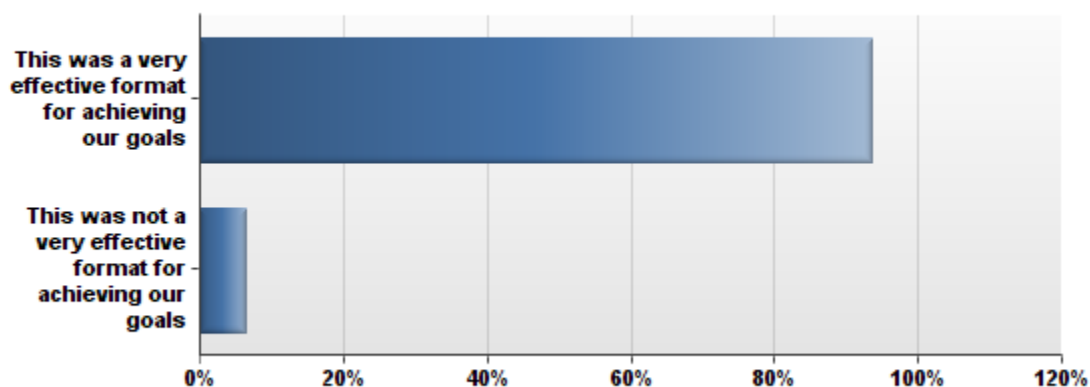
Instead of having everyone run the R tutorials on their own machines during the class, provide the script but only have the instructor run the code and allow participants to annotate and ask questions as we move through the code. If people want to run the code on their own and ask questions maybe have an hour at the end of the day were those who wish to learn more about a particular package or analysis can ask more in depth questions without wasting so much time solving mac/pc/linux conversion issues.

More breaks during the day smaller discussion groups during discussion time and during R programming recommended background reading prior to the tutorial being made available

May be try to put students to work in common interest groups and people with complementary skills instead of random groups.

A little more time to discuss the findings from the labs.

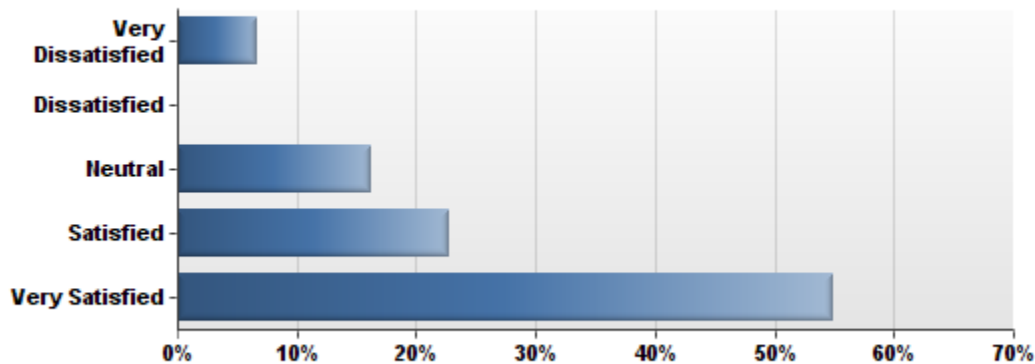
How do you feel about the format of the tutorial?



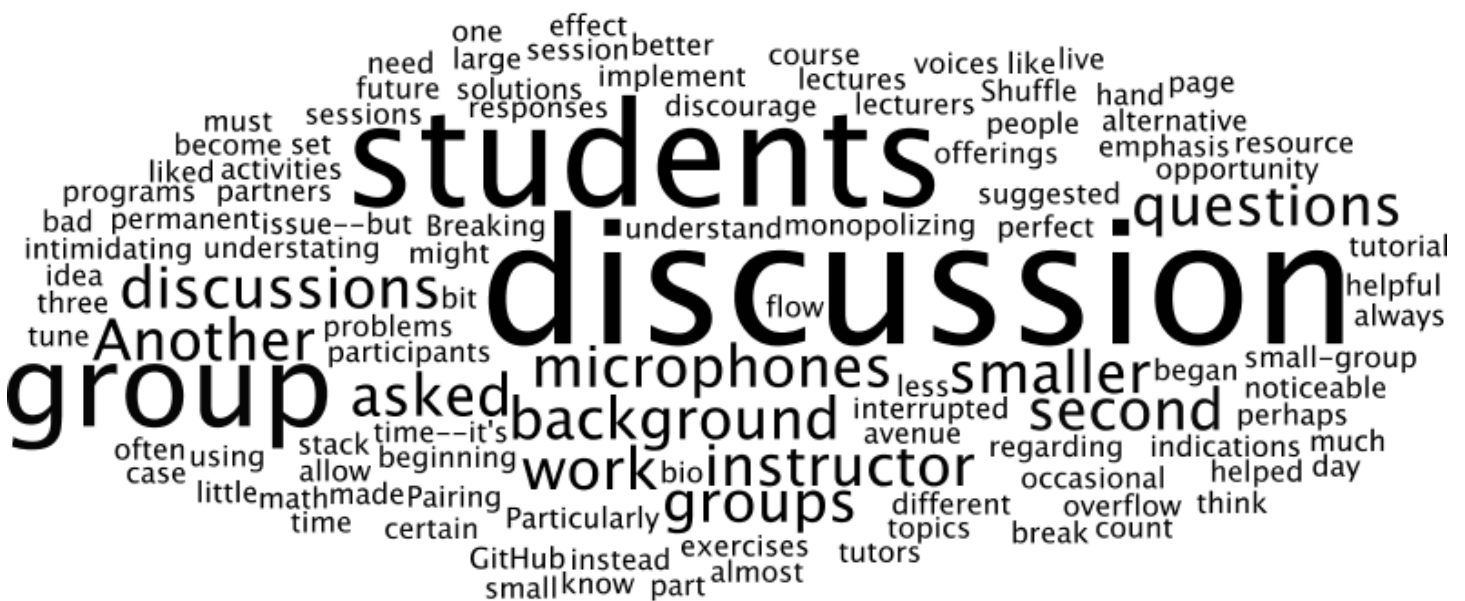
The tutorial format would have been more effective if:

No comments

How satisfied were you with the opportunities provided during tutorial presentations and discussions to ask questions and/or make comments?



Please indicate any suggestions you have for facilitating communication among participants during the tutorial:



Pairing students with math background with students with bio background from the beginning.

More group activities and discussion.

I wouldn't implement too much of this, but the occasional small-group discussion might not be a bad idea. Particularly regarding the R programs (I think the lectures were more or less perfect, and the lecturers made certain that questions could be asked at any time).

A GitHub page was suggested as a live Q & A session. I second that. Another alternative would be like stack overflow, where the problems and solutions can become part of a permanent resource for future course offerings.

The emphasis on using the microphones interrupted the flow of the discussion, but I understand the need for the microphones.

On the whole this was an extremely positive experience for me. I learned a lot and was introduced to many topics that were new to me. I came from an empirical genetics background and the tutorial was very useful for me as a way to start thinking about questions in a different way. I also want to add a note of thanks to/about the instructors. They were all great - very friendly, approachable and helpful, and highly effective in what they were doing. It was a great team of instructors (including Tyler). I personally enjoyed learning from Joe Felsenstein and Stevan Arnold - with whom we also spent a great deal of time because they were around the whole week. They made a terrific impact on me with the depth of their knowledge and the clarity of their thoughts on this topic. Thank you very much for the opportunity to learn from all of you.

Thank you!

Providing key literature before the start of the tutorial would be good and help to be more prepared for the lectures. To keep discussion groups via virtual tools to keep in touch and help to understand better the information treated during the tutorial.

Thanks to the people at NIMBioS and the other organizers for putting on such a great tutorial. I had a great time and learned a lot.

In a lot of ways, this was a wonderful opportunity. I am VERY thankful for NIMBioS and all of the instructors. You opened my eyes to a lot of wonderful perspectives that I hope to use in my own research. Also, I will tell my peers about this opportunity. Thank you again. At times I was frustrated at the speed of the R exercises. I am new to coding in R and I felt that the exercises were often wasted on me because I was too slow to catch up. Also, I think it might be beneficial to do more work on these theories and (R) models on our own, perhaps in small groups.

I really enjoyed participating in this tutorial this year. I thought the students were excellent, and I had a great time interacting with them during class time and afterwards. I hope to do it again next year!

It was great! :)

I like the format, which managed to get most people to a full degree of immersion in the matter and tools.

I'm going to emphasize a third time that I think there needs to be a focus on molecular data. So many of us are working with genomes, high throughput genotype data, etc. and using this to study quantitative genetic questions that it would have been helpful to discuss methodologies and learn some new tools.

I would like to say that I am really thankful for to be part of this amazing tutorial and rich opportunity.

Participating in this tutorial was a unique opportunity! It was amazing to be in contact with very experienced professors. And one great thing was how accessible they were, making everybody comfortable for questions and discussions!

This was a great tutorial!!!! I would definitely come back and take another course!! Thanks for all your hard work and dedication in making this tutorial happen this year, and thank you so much for having me!