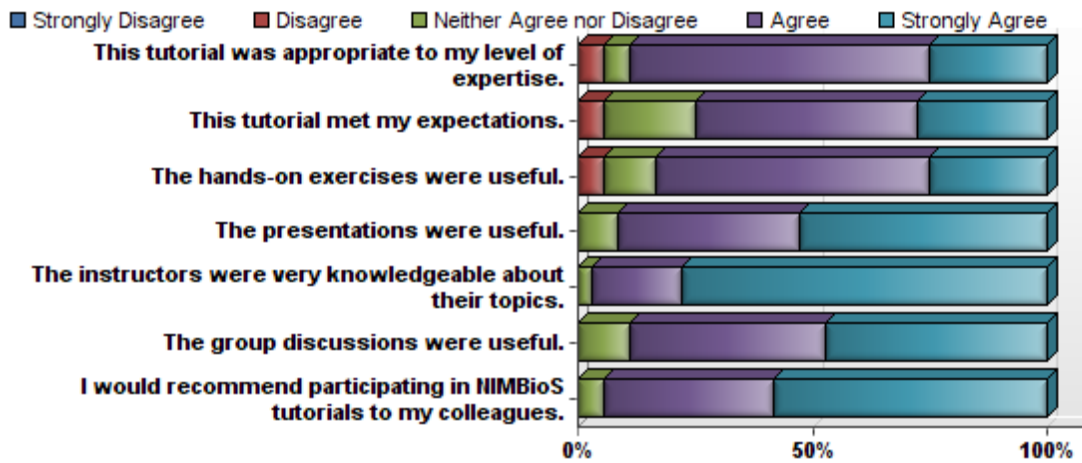NIMBioS

Evaluation Summary Report
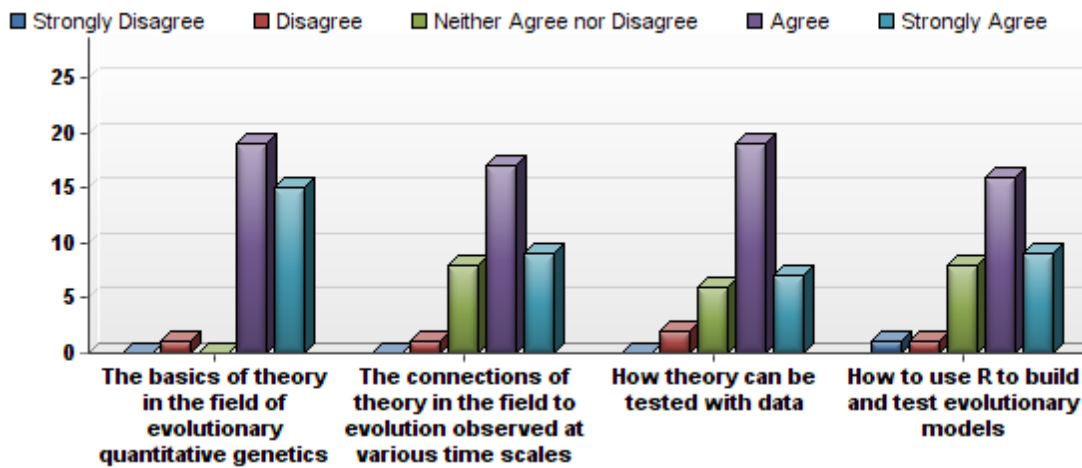
Tutorial: Evolutionary Quantitative Genetics
August 4-9, 2014

Pamela Bishop
Evaluation Manager
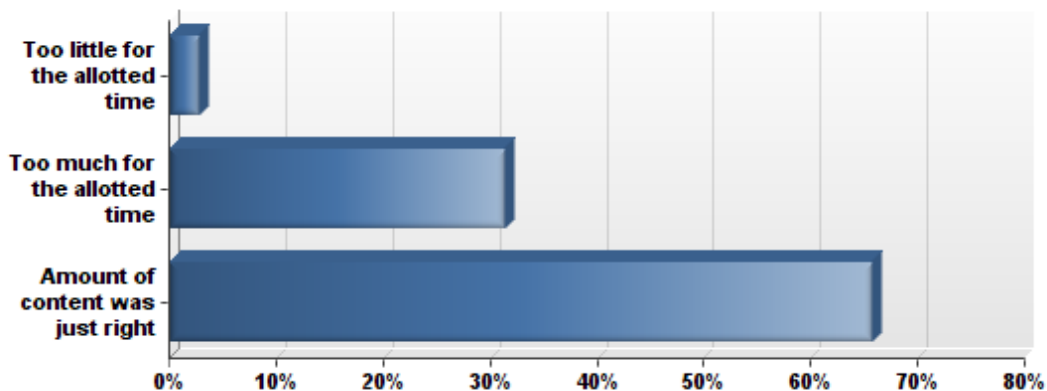National Institute for Mathematical and Biological Synthesis

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

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

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

4. What topics would you have liked to have covered in this tutorial if given more time?

A short lecture about QTLs

Molecular evolution. Epigenetics. Epistasis. Environmental effects. More biological realities. More criticism of models and time to come up with better ways.

As someone interested in quantifying selection on microevolutionary timescales, I would have liked to see an extension of what Stevan Arnold covered on selection analysis, with coverage of some more complex ways of measuring selection (e.g. path analysis, contextual selection analysis).

We were not really given the opportunity to develop our own R scripts. More coverage of matrix algebra in R would have been nice.

I don't know enough about the field to complain about topics not covered. Perhaps a lecture that bettered surveyed the field would have helped. The survey could answer: Who are the current major theorists, what are the leading institutions and journals, and what are the dozen or so main theories of the field? Felsenstein gave a brief introduction, but a full length lecture on those questions would be good.

More information of the animal model, QTL mapping, and GWAS.

Estimating genetic variation, environmental variation, and heritability with R. This is a freely to use program that everyone had on their computer before the course. However, none of the exercises taught us how to use this tool to extract these basic parameters. This was the skill that I was hoping to come away from the course.

I found the first three days of the tutorial extremely useful and valuable, but there was a disconnect with the latter 3 days that required a certain expertise that I didn't have, nor was it really in my field of interest and while valuable, I would have liked more time focusing on ideas/methods/models from the first 3 days of the workshop over the focus on deep time phylogenetics which is a bit more of a niche than quantitative genetics

Would have liked to have covered common tests of selection such as GWAS studies and how those fit in the context of quantitative traits. Would have liked more time on the fundamentals (one more day)

Using R to test animal models.

I wish we actually could have gotten into more detail in the topics that were already covered. I would have preferred presentations like Marguerite's where we got to see the story unfold about a research question. The other lectures were fantastic, but it was really helpful to not only understand the study system, but then spend a good amount of time figuring out how we would test the hypotheses, and then interpret our results. I personally would have liked to get into some of the computational challenges of conducting selection analyses.

More about the modelling of the G-matrix Statistical analysis of the causal relationships between traits (e.g., path analysis, structural equation modelling).

Matrix comparisons. Slightly longer spent on the G-matrix and adaptive landscapes

Comparative methods

QTL mappings and connections with population genetics.

Comparing G-matrices, but I heard that I was just in the wrong session.

Estimation of parameters of the animal model more in depth

Breeding Design

Some inclusion of selection theory using quantitative genetics and how that connects to the adaptive evolution models in the macroevolutionary topics

More on experimental design and sampling for heritability studies.

I was happy with the topics covered.

I would have liked to spend more time on the animal model and how to compare heritability estimates across populations

I would have enjoyed discussing how genomics will affect or change the field of evolutionary quantitative genetics.

I would have gained more from a more thorough discussion of the topics covered in the first three days. However, that is probably due to my lack of interest in interspecific comparisons (evolution over more than one or a few generations).

Lectures on the current state of ecological niche theory would be helpful, to broaden the perspective on attempts to reconstruct adaptive landscapes.

Morphometrics

More about morphometrics.

I don't have any suggestion for this. Maybe a repository of the current presentation given at the tutorial.

5. What do you feel was the most useful aspect of the tutorial?

It was good for networking. I enjoyed meeting so many new people.

Talking to people, learning about teaching styles, comedic aspects of watching scientists wave their hands wildly.

The hands-on tutorials were the most useful part. In fact, I think we could have spent more time on those and less time on the lectures. Some of the lectures were too detailed and the information wasn't used in the tutorials.

G-matrices

The most useful aspect of the tutorial was the collection of tutorials, especially those that showed how to use programs in R. I wouldn't add more tutorials, as the lectures were good and necessary to get the students from getting buried in tutorials. Also, the time spent on the G matrix was awesome.

The first two days on the animal model and G matrix.

Making connections with other participants.   The accessibility of the instructors was unparalleled.

The exercises and discussion were extremely useful - and the long lunch hour was actually really good to sit down and chat with people and find common interests and think of things in new ways. The lectures were all very good.

The first three days were highly useful.

Putting it all together/the synthesis: we need to understand ecology to understand patterns of macro-evolution, and that G and short-term selection don't seem to be important at macro-evolutionary timescales.   A synthesis or discussion of this sort would be very useful in subsequent workshops.

The opportunity to interpret with the instructors on a more personal level, and then access and training for the computer codes. They were extremely helpful, and gave me some great resources to improve my research.

Theory and practice around the G-matrix

The opportunities for discussion, both the formal times allocated during the tutorial and those that happened during breaks and in the evenings.

The use of R in solving problems

The lectures and some exercises.

I found it very useful that R scripts were given to us, so we could see how you can code evolutionary problems and adapt the scripts to your own data.

The presentations and tutorials

Everything except the last two days, too much into phylogeny.

G-Matrix Evolution

Introduction to models and exercises exploring the use of these models

The material from M-W was the most useful to me.

The interactions between the audience and the presenters were very interesting and useful.

The hands-on exercises

I was unfamiliar with many of the topics in the tutorial and found the background info very useful. Going over the equations (particularly animal model based) and the basics was very helpful for me.   I also benefited from the computer exercises and learning about programs to utilize for quantitative genetics.

Collaboration with other students, fill-in-the-blanks R coding

Due to my lack of prior knowledge in the field, the first two days were the most useful.

Lectures and observing the infighting between instructors.

This kind of course, with this coverage is not available elsewhere, so it was very productive to think about my data and the lectures.

It was very good to have lectures and exercises about it. All the topics were very important to understand quantitative genetics field and we had a good historical and very new data discussed. The organizers and professors were the best!

Everything was useful. In fact I learn new material that I would like to implement in my research.

6. What would you change about the tutorial?

Regular bathroom/water breaks should be built into the schedule. Also, I would make it 5 days long instead of 6 days--which last day was pretty rough, and it would have been helpful to have that Saturday to travel home. Also, I apparently was very misinformed about what this workshop was going to teach. I said in my application that I don't have any experience with R, but wanted to learn the basics from the workshop. I shouldn't have been accepted into the workshop, because it was not at all designed for people with no background in R. I was very lost and frustrated a lot of the time. In the future, it might be helpful if there was an optional "working lunch" the first day for R beginners, just to teach them a few basic things like how to load data into R and how to open the data file (while everyone else who is experienced with R can go have lunch).

First experience, don't have too much to criticize.

I feel we could have used more breaks here and there. Additionally, I would consider breaking it up into two tutorials- there seemed to be a divide among the participants' interests between micro- and macroevolutionary timescales. I found the macroevolutionary time scale stuff (phylogenetics) well-explained and interesting, but if given the option of stopping the tutorial after the first three days vs. completing the full course, I probably would have stopped after the first three days.

In the course description there was a lot of talk of using R, and we were encouraged to be proficient in R before coming to the course. As an avid R user, I found the incorporation of R coding into the course extremely weak. Much of the coding/modeling was done in other platforms (e.g. Wombat), which are really superfluous and obsolete. R can do everything Wombat and really all of the other software we used can do, and is more intuitive to use. Furthermore, the R exercises we did do were canned and did not allow for much skill development. Finally, we spent over half of the first day just trying to get the Windows partition running on our computers. I finally resorted to some "questionable" methods to acquire Virtual Box and make it work. If we had been given very explicit instructions a week ahead of time, much time would have been saved. For that matter, if we hadn't been futzing around with software that only ran on Windows, this would not have been an issue. Just make people write their own R scripts in the future.

The tutorial focused too much on how quantitative genetic models integrate with phylogenies. The intersection of the two is super interesting, but we spent three days on the topic, when a day and a half would have been enough. Furthermore, we needed more time to learn the basics of quantitative genetics, before we could ably apply it to phylogenies. If I were to alter the course, I would spend at least four and a half days on topics from quantitative genetics proper, and then I would introduce its connections to phylogenetics. Also, i would have a brief R review session in the hotel the day before the workshop started.   Also, Liam Revell is an awesome

person to work with in small groups, but lectures are the wrong way to use his skills. Perhaps have him develop more exercises, but fewer lectures.

The length...after Day 4 it seemed like most students and post-docs were eager to get back to their own research. I'm not sure the full 6 days are beneficial.

I think the length of the tutorial is too long to do full days. Three-four full days of a tutorial or a 5 day workshop with 6 hours each day would be better. I also think it would be really nice to leave a full day for small group work actually implementing an analysis that encompasses all the previous lecture topics would be really helpful. The short computer exercises were useful, but they did not allow much time for trouble shooting and writing code for ourselves. Ultimately we want to leave the tutorial empowered to address these sorts of questions for ourselves.   I also think that all exercises should use the same programming platform as was advertised for the course. Compatibility of additional programs took lots of time in our course and reduced the effectiveness of the exercises in terms of understanding and implementing concepts.   It would be cool if participants could have the opportunity to use and talk about their own data and specific questions and challenges concerning quantitative genetics in small groups.

Less focus on deep time phylogenetics Use R instead of Wombat for exercise in quantitative genetics Focus more time on quantitative genetics - the course spent surprisingly little time really hammering this topic home given the title of the course. And given the lack of really comprehensive courses on this subject I think you could dedicate the entire week to this subject.

I felt the last three days were decreasingly useful. The topics were too specific and also drifted far from my expectation based on the tutorial description. Too much phylogenetic work. And the computer exercises were mostly not useful- primarily they were much too hand holding (not learning much) or too vague (go do something). The last day, morphometrics, seemed only useful to a very few participants. I know many participants tuned out the last two days.

I would add some group work projects. Maybe some of the computer workshops could have been set up at mini assignments and the students would divide into small groups and spend a few hours working on them during the day or in the evening. Maybe they could even use their own data - of someone in the small group has some data to look at. Then small informal presentations or just informal small write-ups could be done/collected on the last day. I know it was already super busy - maybe this would add another day on the tutorial. It would be a really helpful exercise though.

The Wombat instructor was fantastic, but Wombat seems dated. MCMCglmm in R can be used to fit animal models, and is more relevant to emerging professionals.

I would have preferred to have gone into more detail for each topic, and/or if we had some documentation that helped to tie everything together. For instance, it was a bit confusing that the first third of the lectures used similar symbols, but those symbols all meant different things in those lectures. This happens a lot in the literature, but we had so much less time to internalize the information. It would have also been nice if there was more instruction prior to the course. Pat Carter was really great about providing instructions for installing the computer software ahead of time, but it would have been more helpful for the attendees to have a list of responsibilities that they needed to complete before the tutorial so there was a better chance of having the attendees on the same level of understanding. The people sitting next to me didn't know how to code in R, so a good proportion of my time was spent teaching them how to use R, and I missed out on some good discussion. Luckily the discussions were recorded, but it impeded my ability to stage engaged in the

discussion. Perhaps it also would have been helpful for NIMBioS/instructors to poll the attendees to determine what they hoped to gain out of the tutorial (e.g., what specific research area they were interested in), and then add that to the contact info list that was handed out. Although I met a ton of people of like interest, I missed out on some good opportunities to meet some people because there were so many people in the tutorial and only so much time.

Too much time spent on the Brownian motion model and phylogenies. These topics are interesting but may have been covered only on 1 or 2 days instead of 4 days. I also think that Bayesian inference is not necessary to the tutorial, which would make more time for going deeper in other topics (linear mixed-effects models, G-matrix, how to include non-additive genetic effects into quantitative genetic analysis of single and multiple traits)

I would have preferred a slightly different balance between the quantitative genetic and comparative components, with these given 4 days and 2 days respectively, rather than 3 days and 3 days to allow for more time to be spent on quantitative genetic theory and practice. I also feel that the computer exercises would have been more useful if there had been more communication ahead of time about the purpose of each one and the software required so everyone could ensure it was installed and working. There were quite a few compatibility issues with the software used, which the organizers found solutions to, however solving these issues ahead of time would have been helpful.

There were too many people, which I think is not the best for discussion in general. I would probably also add some "homework" assignment, or project, just to allow the opportunity to use the concepts taught. That would probably imply having less theory, but that could be more useful, I think.

I found it very well organised, and wouldn't change anything. Except for the last days, the theory was more difficult (because I never use phylogenies) and also people are already more tired because it's the end of the week, then it is harder to pay attention for the difficult parts. Maybe they should have started with more basic phylogeny and then built up.

Lectures in the morning, exercises in afternoon. More hands-on. More reading beforehand

Separate sections for theoretical and applied

A concise list of "computer software to download/install" beforehand. To avoid issues of software incompatibility encountered during the computer exercises.

The phylogenetic material presented from Th-Sat was a bit too much. I would have liked to spend more time on fewer models and really understand them.

Maybe there should be more social opportunities -- something like an optional poster session one night for the participants might be nice.

It would have been nice to have a bit more communication from the organizers, particularly about the computer programs we would need for the computer exercises.

I would have liked more information before the tutorial, particularly computer programs we would be using. It would have been nice to be able to install and get everything working beforehand on the computer. I think that I would have also benefitted from background readings in advance and exercises to do on my own after class. I understand things better when I have to work through problems on my own after a class or lecture.

Mini research project about G matrix movement under selection was good useful exercise, but would have been more interesting if we hadn't already been told the answers to all the proposed hypotheses during the lecture. I suggest performing that exercise before the last part of the lecture.

I would have appreciated more discussion and lecture on designing breeding experiments to best partition variance into different components. I also would have appreciated more discussion of the applications of the theory that we were learning, and the limitations of the theory.

Not much, except using R instead of wombat

1 . The exercises with R.   I think that will be better to have time to explore the R exercises (maybe with homeworks). 2. Another thing that would be interesting is to provide reading material (papers and lectures) in advance.

The tutorial was really fast. I would change the time. It was a lot of new information in a few hours.

## 7. How do you feel about the format of the tutorial?
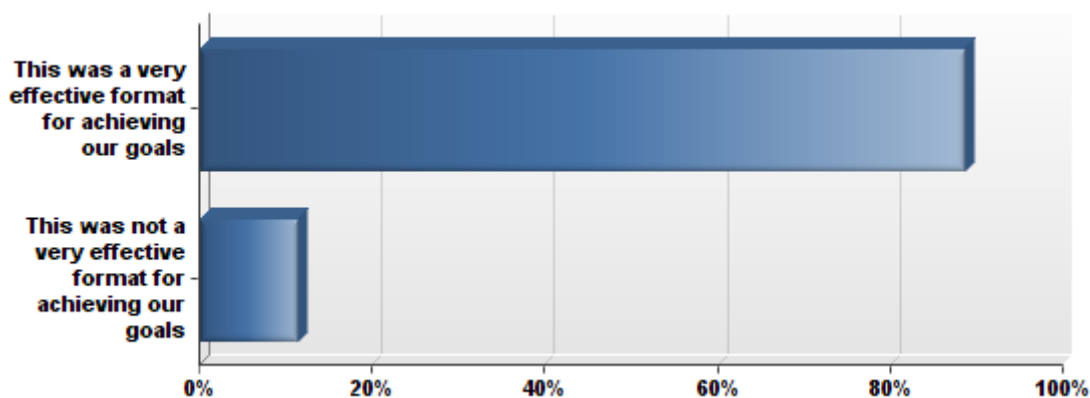
8. The tutorial format would have been more effective if:

Lectures in the morning, exercises in the afternoon.

One of the goals of the workshop is to encourage collaborations, however nothing was done to encourage or facilitate collaboration. At least, small group discussion or problem solving could set up a more collaborative environment.   Exercises felt largely like cookbook experiments. Get data and program, spend time making program runnable, run it with given parameters, look at output, after that have the purpose of the program explained. This format is not conducive to learning for most people

9. Please indicate your level of satisfaction with the tutorial accommodations:
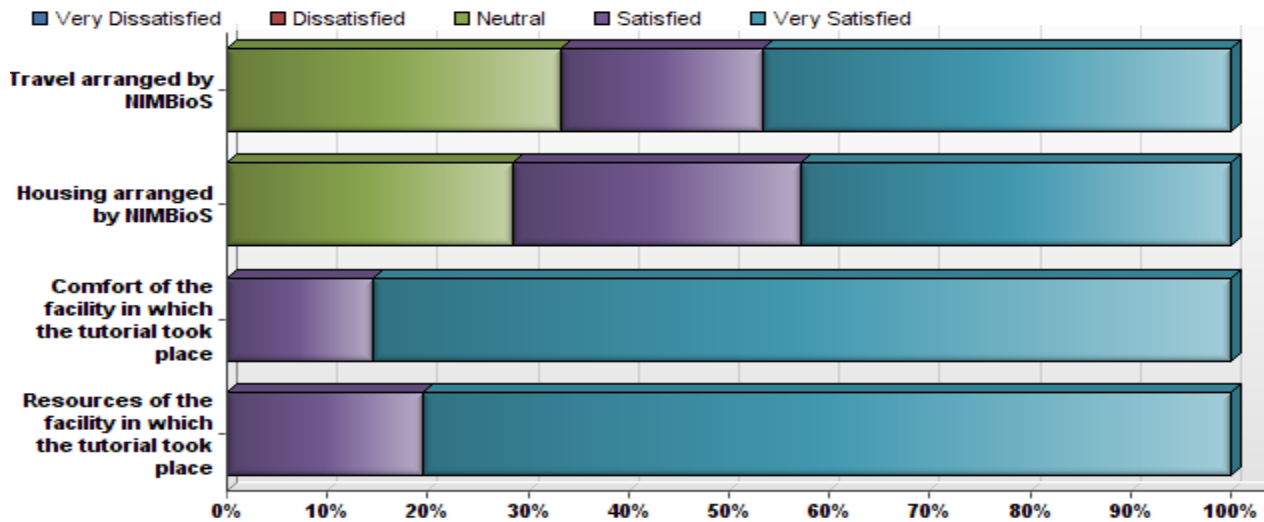
10. Comments about accommodations:

The Sheraton is just way too expensive. I opted for alternative lodging.

Great food, comfortable seating areas, love the compostable options.

The room where lectures took place was very comfortable and perfectly equipped for this purpose. Meals provided were all very good, and layout of the room in which we ate these meals was great for facilitating discussion with other participants and instructors.

I had a multi-city trip and the travel agent wouldn't book it for me. Neither would they reimburse me until after the course. I had to pay out of pocket for months in order to get a reasonable fare, but had to carry this bill on my credit card. Not very happy about this.

Only minor quibble was sometimes running out of hot water for tea. Everything else was superb.

Great

We rented a house by ourselves at Knoxville.

Internet was wimpy, and I could not get TV to show actual TV instead of pay-for-content. The blackout shades for the room seemed not to work either. But aside from these it was fine.

11. How satisfied were you with the opportunities provided during tutorial presentations and discussions to ask questions and/or make comments?
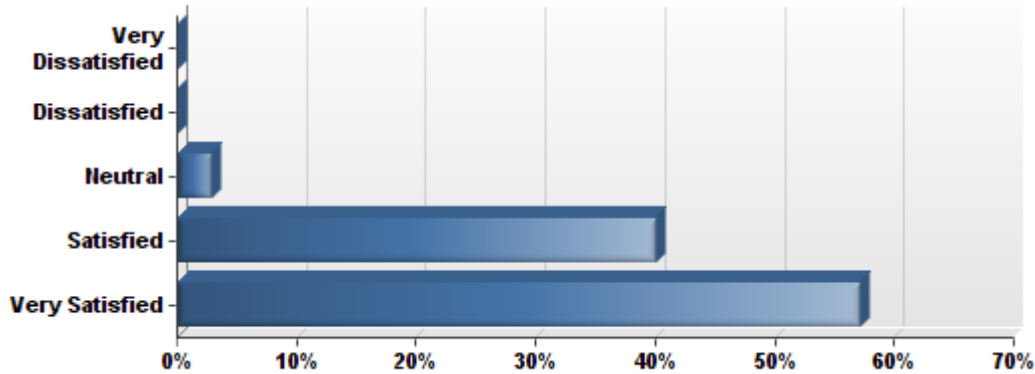
12. Please indicate any suggestions you have for facilitating communication among participants during the tutorial:

Google Doc? Chat room? Better usage of the WordPress site.

We only had one opportunity to conduct and present group projects. We were given a rather glitchy software package to use and then given 20 minutes to come up with a question, test it, and present it. This was an utterly ineffective teaching tool. Hours should be allocated to group projects, and groups should be allowed to explore using R or other coding languages.

More mini-break times.

Many presentations were too rushed, pressed up against "Discussion" or lunch and some questions were passed over. But other lectures questions were very welcome

Make sure to use the Mic.

Not really something that NIMBioS is responsible for, but it would have been more enriching if more people participated in the WordPress site or even Twitter. That might help spur more active discussion, and potentially recruit more people to tweet into the discussion if they were watching from the live stream.

In general opportunities for communication were excellent. I think that some of the practical exercises may have been more useful if they were done in small groups rather than individually, and with more time allocated, to enable discussion between participants.

Encourage posting more questions online and answering during tutorial

More small group discussions could have helped facilitate communication.

Especially during exercises, instructor should do assessment (asking for shows of hands, asking questions/problems with short responses to be collected on notecards, many possibilities) of students to see what is understood, what isn't understood, what's working, what isn't   the institute was very much asking students to sit and listen to white men talk, especially days 1,2,3. Nothing was done to make people outside

white men feel welcome/valued/seen, which means they weren't.   Nametags worn down on the belly which have 'NIMBioS' in larger font than individuals' names are ineffective. Also contributes to a non-collaborative environment.

Maybe will be good to have group exercises after lectures. It was very productive when we did that once after a lecture.

Everything was very good.

13. Additional comments:

Thank you for the course. Happy a happy day in Knoxville :)

This was a great experience! I will definitely recommend it to my peers.

The organizers and lecturers did an excellent job of setting the intellectual and social climate for the workshop. They were amiable, inclusive, fallible, and never rude, mean, or dismissive. Those behaviors then extended to all of the participants in the workshop, and they made for an enjoyable and fruitful workshop.

I think certain tutorials without some sort of basic instruction were very difficult to use from. Also, it would be beneficial if the presenters pretended that all participants had no knowledge about DOS, Linux, patches, C++ coding, etc...Since they often used advanced computing knowledge when talking about how to download needed software. Those who have little knowledge about computing had great difficulty during those times which were fairly often throughout the tutorial.

Great course!!

I think we should have had a break after day three to enjoy a hike or something, then back to the tutorial. A break would have helped people avoid fatigue by week's end

Great job - This tutorial offered a very unique and educational experience.

NIMBioS hosted an amazing workshop. Frankly, I'm floored by the entire event. I still can't believe that Stevan A. and Joe F. and many other outstanding researchers were flown in to teach us. Thanks NIMBioS!!   Ps. Even the food was excellent!

Thank you for hosting such an amazing tutorial. It was very impressive that we were able to learn from the top evolutionary biologists from our field. The tutorial was one of the most satisfying, enriching, enlightening experiences I've ever had, and I learned so much. I know some people said that they didn't like the Macroevolutionary portions of the tutorial, but I loved it. It's an area that I am hoping to pursue, and it provided some much needed context for how you can link microevolution with macroevolution and how you can ask evolutionary questions in a very broad sense. It was very exhausting since we didn't have dedicated breaks, but it was very helpful to have longer lunches and I appreciated being able to maximize our time with the instructors.

On the whole a great tutorial and a very valuable experience, which I would highly recommend to anyone interested in evolutionary quantitative genetics!

I am very grateful for NIMBioS for the opportunity for taking this workshop and for the instructors for their time.

I really would have liked to spend more time on how we can link results from transitional quantitative genetics models to genome scans, rather than on phylogenetics.

Often a student will ask one question, and a different one is answered. This was sometimes followed by an extensive back-and-forth and sometimes just called a failure. This pattern does not encourage students to ask questions. Communication would be smoother if instructors took time (including asking back clarifying questions) to understand students' questions.

I had a great experience teaching in this tutorial and hope I can do it again in the future!

This tutorial was a wonderful moment for learning and knows very good people. Thanks for offering it!   It was very good to have more contact with people during the tutorial. We had lot of people to interact in small amount of time. To promote more interaction maybe it will be good ask people to put their names, affiliation and research with their pictures before the tutorial starts. This can help us to remember each person and promote more interactions. This is an example: http://bie5782.138098.n3.nabble.com/Curso-IB-2014-td4025931.html (sorry, this is a Brazilian site but I think that can help to illustrate my suggestion).   Thanks a lot for this opportunity! Hope to come back more!

I was very happy with the support we got from NIMBioS staff, who were much more capable and available than the people at our previous location.   We hope to do it again next year.