

NIMBioS

National Institute for Mathematical
and Biological Synthesis

TUTORIAL: EVOLUTIONARY QUANTITATIVE GENETICS 2016

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Evaluation Report

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Figure 1. Agreement with the following statements about this tutorial:

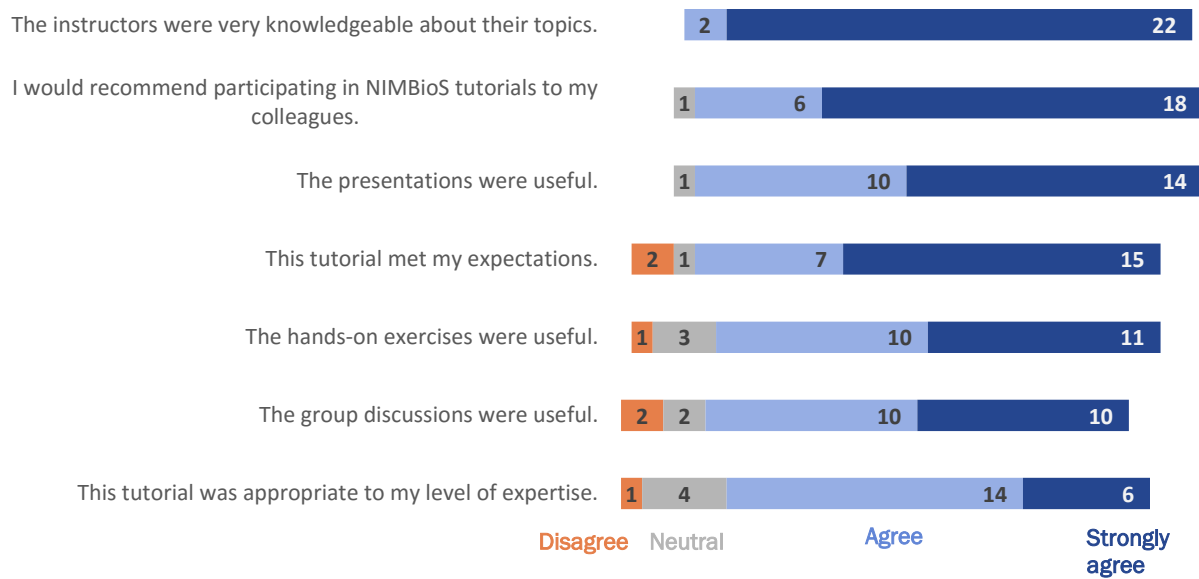
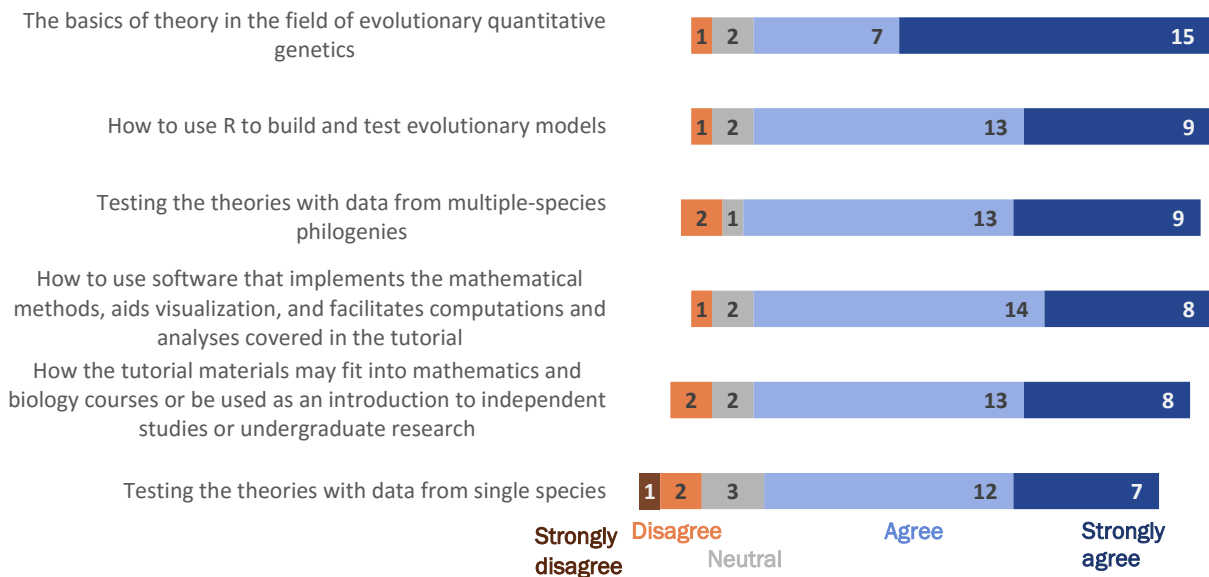
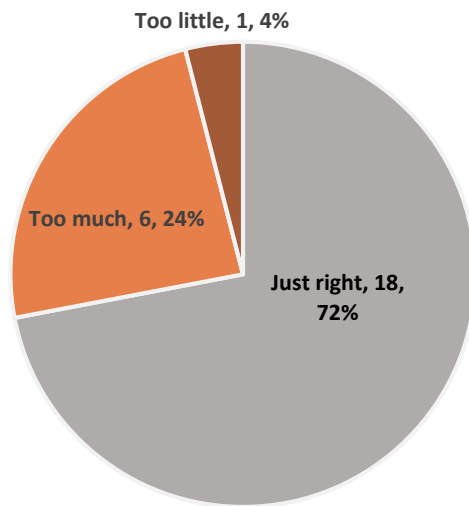


Figure 2. Agreement with “As a result of participating in this tutorial, I have a better understanding of...”



100% of survey participants indicated the tutorial was a very effective format for achieving their goals.

Figure 3. Feelings towards the amount of content offered during the tutorial



Open-ended feedback: “What topics would you have liked to have covered in this tutorial if given more time?”



- Testing for adaptation, ancestral state reconstructions
- Trait dependent diversification, as well as trait evolution along a tree.
- G matrix evolution, discussion around BAMM
- More single species examples, and a bit more about microevolutionary quantitative genetics.
- A more detailed exploration of the underlying mathematics.
- More empirical comparison of g-matrices, more discussion about projecting evolutionary responses.
- More time allocated to specific programs in R.

Multivariate OU modeling would have been a great addition. More discussion of the problems associated with interpretation of model fits, and not the evaluation of the tests alone would have been welcome.

I had an interest in comparative methods and would have appreciated more time learning and working through R tutorials, but that is my own research bias.

I think more time on comparative methods would be beneficial. We went over those, but I feel that some of the computer exercises were a little rushed and more time to go through those more slowly would be helpful.

Lecture and tutorials in multivariate statistical methods in general would have been extremely relevant to the rest of the contents. These topics may further include rather specific topics such as geometric

morphometrics and matrix comparison techniques.

integration of micro and macro evolution - more advanced material on the g-matrix (example studies, constraints, evolution of etc) - more on opportunities to test theory offered by the generally loosening bottleneck on acquisition of trait and genetic data.

How to input next generation sequence data into mcmcgmm as an A matrix. How to deal with other types of artificially structured genetic populations (RIL, NAM, etc.)

How rapidly increasing amounts of genomic data improve our ability to carry out quantitative-genetics analyses to investigate the genotype-phenotype relationship. Also, I wanted to learn concepts of QTL mapping.

A more extended treatment of different designs for quantitative genetics and perhaps a more step-by-step explanation for some R-packages

1. More in-depth coverage of the animal model (e.g., maternal effects, cross-sex genetic correlations), and perhaps detecting selection on genes (e.g., gene-dropping simulations)
2. Some more coverage on QTL/GWAS methods would perhaps be interesting

I only realized after Day 1 that the lion's share of the focus would be on phenotypic evolution with almost no coverage of molecular evolution, but both are useful to me, so that's okay

I don't think it would be good to add additional topics to this course, and I wouldn't remove any of the ones that are in there.

Figure 4. Satisfaction with the opportunities provided during tutorial presentations and discussions to ask questions and/or make comments



Open-ended feedback: “Please indicate any suggestions you have for facilitating communication among participants during the tutorial:”

More group activities

Encouraging discussions before the tutorial among participants would help, as it might identify areas that the tutorial may want to focus on, as well as give participants an opportunity to network before the event.

One solution might be to install parabolic microphones; this way comments don't have to wait for a microphone?

Distribute an email list.

Already indicated: another group exercise, or 2. Longer introductions so we have more of a handle. Nightly dinners are great.

Maybe have people write down questions on paper. At the end of a session the discussion leader can read some of the aloud anonymously. Might encourage shy people to get their questions answered better.

It was better if the participants asked frank questions to understand the topics of the tutorials instead of trying to discuss the topics before fully understanding them.

More group work

The tutorials and exercises helped the students to focus their questions. Although, the levels of difficulty changed a lot from script to script.

Open-ended feedback: “*What do you feel was the most useful aspect of the tutorial?*”

I was watching remotely as I couldn't get there (cancelled flights), but for me the lectures/background material were very useful as context for the tutorials and code.

The resources we were given (scripts, lecture slides, notes, references, etc.) are extremely useful. Having access to these enables me to continue utilizing the information I learned in the tutorial.

For my interests, the latter half of the course on comparative methods provided me exactly the background understanding I needed to move forward in my studies with a more synthesized understanding of the fundamentals.

The tutorials of using the packages in R was especially useful. Brian O'Meara's R examples were a good example of how to implement these in a meaningful manner.

The most useful aspect of the tutorial was going through exercises in R. When reading the manuals for some of the packages out there for comparative methods it can be difficult to navigate through, so working through exercises was incredibly useful.

The hands-on R practicals where we were walked through how to use the packages and shown how different parameters affected the analysis.

Learning theoretical implications of evolutionary quantitative genetics and seeing it applied to real questions and data.

The discussion, being able to ask questions, the redundancy of some of the more difficult topics.

1: How to run and specify parameters in MCMCglmm package

2: How to run bayou package

3: Lecture of sexual selection in birds of paradise. Especially, the idea of interpreting parameters derived from OUwie by means of quantitative genetic parameters was very inspiring.

The structure was almost perfect - interspersed lectures and exercises, with regular short breaks and bottomless coffee. All of the topics covered were of interest to me, and were generally very well presented.

Rigorous development of theory. Illustrative examples. Practical exercises. I think by attending this tutorial I went from have a vague understanding of the concepts to being able to perform some basic investigations independently.

Learning how to use R to carry out quantitative-genetic analyses.

To have the opportunity to discuss such interesting topics with this incredibly good professors.

Being introduced to a wide variety of techniques and theories, from micro- to macroevolution.

The R tutorials can be easily applied to my own dataset.

Group activity

The R scripting tutorials.

1. Simulations (e.g., simulating the evolution of the G-matrix, simulating OU and BM)
2. Extended time to accomplish tasks in R (i.e., Brian's exercise in which we coded in R to test if there was substantial power to differentiate between two OU/BM models)

Open-ended feedback: *“What would you change about the tutorial?”*

A few of the later exercises seemed a bit rushed- particularly those working with bayou in R. I didn't feel like we had a sufficient amount of time to go through the more complicated coding sessions. It would have been more effective if the exercises were a bit simpler, or we had more time to go through them.

I don't have specific recommendations, but I would say that it seemed as though the transition from studying single organisms (g matrix, etc) for the comparative methods was a bit abrupt. the OU and brownian models were introduced during the comparative portion of the course, although I think they could have been introduced earlier.

Add more days if possible. Some of the software tutorials were a bit rushed, or were formulaic without getting at the nuances of implementation. More time would allow for the participants to learn about these details, as well as have more opportunity to work through the packages.

I don't have a strong opinion on what should be changed about this tutorial, I enjoyed it.

More time for the computer exercises we did at the end of the week. I think adding at least a half day would help alleviate the rushed feeling towards the end.

Organized group time for the tutorials outside of class time (i.e. working dinner, happy hour, etc.)

In an exercise of G-matrix comparison, the entire class was divided into groups and we made a group work. I think it was a great idea, but the time provided to work in a group was way too small to make a fusion of thoughts to occur. What would have been very nice is to first provided with some materials

(how-to-use some softwares), then each group are given respective questions regarding evolutionary quantitative genetics. We then have a half-day-off, where groups have time to gather and think as they wish. The following day or towards the end of the course, there is a slot where groups have relatively longer time (i.e. 15 min including questions) to present what they have done. Finally, a follow up lecture will be given in relation to the assignments.

Other than that, I think the tutorial was very well prepared so that participants can learn maximally within 5 working days.

1. More opportunity for interaction among students - e.g. group exercises, and I would suggest extending the initial introductions to talk in more detail about the questions that we're studying, the species we work with, the kind of data we have, and how we're using it.
 2. For what it's worth, I would be in favor of 6 days (or 16). Sorry
 3. Scale back some of the macroevolutionary software exploration in favor of more advanced quant gen, stat gen.
 4. The sessions I liked least were (A) Adam Jones' parameter sweep. Partly this was frustration at the annoying GUI - seemed like more button pressing, less learning. (B) I liked Josef's stuff, but the bayou exercise seemed a little rushed, unfocused and unpolished. Perhaps it's just bleeding edge, and will have matured by next year.
 5. The presenters should get on the same page as to the expected level of R familiarity, and therefore the pace they will take through their sessions. Personally, there was a lot of time wasted (or available for thought ;-)) on this, though as a post-doc I guess I'm not the point estimate of the target audience. Yes, it's always going to be patchy, but I think a clear expectation should be set before starting the course - there's no shortage of good beginners tutorials out there, and really, this is 2016. Also, quit the copy and paste and just switch to Rstudio!
 6. I would love to see more along the lines of Steve's final session. It was nice to have real data to play with throughout the course, but it's even better to see how published analyses were actually done.
- Quibbles:
7. Patrick Carter: Pedigrees are useful, but genetic data is better and more widely available now.
 8. Brian O'Meara: don't ask questions and stand there insistently waiting when you have the answer on the slide (maybe 3 times)! Not much of an inducement to vocalize.
 9. In general: better integration of theory/units/variables across topics.

Maybe add another day. There was a lot of information presented.

The schedule was too tight and the participants appeared exhausted toward the end of the tutorial. I would reduce the number of lectures/computer exercises and make tutorial topics more closely related to each other.

Some of the exercises were explained too fast. I would simplify them and ask the teachers to practice explaining slowly

More balanced micro and macro, less narrow focus on OU and BM model specifics and more on how they matter for real biological questions.

more encouragement to apply some of the methods to our own data and use it as short presentation on the last day

I would spend more time on morphometrics (perhaps one full lecture).

1. I think the most successful parts of the tutorial were the ones that combined lecture with exercise. I would reduce the amount of material covered in lecture, and instead use simulations to give students a feel for the models (very helpful) and increase the time students spend thinking about problems and trying to address them on their own (i.e., Brian's coding exercise).
2. Josef's exercises in particular had far too much material in them. I think this led to a lot of simple copying and pasting with little real understanding of what we were doing or why. Less material, more well focused, with more required interaction from students would be helpful.

Open-ended feedback: “Please use this space for any additional comments.”

My experience at the NIMBioS tutorial was positive. I was able to interact with researchers in the field that I might not otherwise approach on my own at a conference for example. Everyone was incredibly kind and supportive and I really enjoyed myself, learned quite a bit, and am considering my research with a different perspective.

Everything went great again this year! The facility and staff are excellent, and the students were interested and engaged.

I am extremely happy about the tutorial. Course contents were exactly what I was expected to learn, and the level of these contents were among the highest I could imagine. There are only a couple of ideas how to improve the course further: 1) the way group work was implemented during the course would have been improved as written in the previous section of this questionnaire, 2) the connection between quantitative genetics and phylogenetic comparative studies would have been explained more, 3) lecture room should be warmer, 4) the tutorial venue would have been a better accessible place by participants from outside of the US.

Even though the amount of the tutorial was just right for 5 working days, I think it is too short to experience a full implication of evolutionary quantitative genetics. It would be really great if there would be a follow-up course for those who take the first tutorial, to learn more advanced methods like multivariate statistics and geometric morphometrics in evolutionary quantitative genetics studies.

Overall, I really think the tutorial was extremely well prepared with extremely high level lectures and workshops. Not only to learn the scientific contents, it was an excellent tutorial for how to teach as well. I thank all lecturers and staffs for the wonderful experience.

This was a fantastic, stimulating experience, all things considered. How about part II?

Attending by videoconference was not easy because of sound quality in the connection. Eric Carr struggled heroically with this and did the best he could, so the NIMBioS part of this was handled well.

The other unanticipated issue with video connection was "jet lag". Sessions started at 9am, and that is 6am in Seattle. So every day I had to get up at 5:30am. That was a sort of "jet lag" that didn't go away with time!

As someone else mentioned during our roundtable discussion the periods we spent doing independent coding exercises was very illustrative.

It builds confidence that you can actually do this stuff on your own.

It was also nice to have one, independent group exercise where participants worked in small teams to answer questions for the entire group.

Overall, the organizers did a good job in organizing the tutorial.

The tutorial was an excellent experience. Professor and attendant were very nice, discussion was at a high level and the level was very high