

**To: Dr. Titus Brown**  
**From: STEM E.D., LLC**  
**Re: NGS Summer Workshop Evaluation**  
**Date: September 20, 2013. FINAL.**

A pre-workshop evaluation of the NGS Summer Workshop 2013 - Analyzing Next-Generation Sequencing Data was conducted on June 10, with a post-workshop evaluation occurring June 20, 2013. Observations were also conducted at the start, middle, and end of the workshop. In all, 22 participants completed at least one scale on the pre-survey and 22 participants completed at least one scale on the post-surveys. This response rate is in alignment with a similar assessment conducted in Summer 2012 (see appended report).

### ***Demographics***

Demographic data are reported for pre-workshop respondents. One participant declined to respond to any demographic questions and one additional participant declined to respond to the race/ethnicity question. 22 remaining respondents completed all demographic questions. Participants ranged in age from 24-53, with an average age of  $34.5 \pm 11.6$  years. Participants were 59% male (n=13), with the remainder female (n=9) and no transgendered participants. Participants were also 86% Caucasian (n=19), with one Asian/Asian-American participant and one mixed race participant (African/African American/Black, Asian/Asian American, Caucasian/White). Finally, the academic status of participants included staff (n=1), undergraduates (n=1), graduate students (n=7), M.S.-holding professionals (n=1), and Ph.D.-holding professionals (n=12).

### **EXECUTIVE SUMMARY OF RESULTS**

We summarize evaluation results below. Following this summary, we provide: 1) A description of scales used to measure participant characteristics, including overall scores, and 2) results for qualitative and close-ended questions related to participant impressions of the workshop. In summary, we found that:

1. *Many participants attended the workshop with specific programming or data analysis needs, and with a range of programming experience (from none to significant).*
2. Scores on the Computational Understanding – Sequencing Data scale were calculated for both the pre- and post-workshop surveys. Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.924$ ,  $p \leq 0.001$ ), with higher post-workshop scores. *This indicates that participants perceived greater understanding after engagement in the workshop.*
3. Scores on the Perception of Computational Ability scale were calculated for both the pre- and post-workshop surveys. Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.922$ ,  $p \leq 0.001$ ), with higher post-workshop scores. *This indicates that participants perceived greater computational ability after engagement in the workshop.*
4. Scores on the Python Coding Ability scale were calculated for both the pre- and post-workshop surveys. Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.623$ ,  $p \leq 0.001$ ), with higher post-workshop scores. *This indicates that participants perceived greater coding ability after engagement in the workshop.*

5. *Participants were generally very satisfied with the workshop, felt the workshop met their needs, and would overwhelmingly recommend it to others.* On average, participants rated the workshop components as Good-Very Good. 100% of respondents indicated that they would recommend the workshop to others.
6. *Participants were generally positive about the workshop in their open-ended comments.* Suggestions for improvement include providing more introduction for those new to scripting, limiting lectures to one hour or less, and providing more opportunity to engage in hands-on tutorials. See end of report for more suggestions.

## WORKSHOP EVALUATION SCALES AND RESULTS

Scales used for the NGS Summer Workshop were identical to scales used in Summer 2012, except as noted; validity and reliability of scales is assumed based on Summer 2012 results. Participants completed identical pre- and post-workshop surveys containing three scales: *Perception of Computational Ability – Sequencing Data*, *Computational Understanding*, and *Python Coding Ability*. The post-survey also contained questions about overall perceptions of the workshop. Respondents also completed several demographic questions, responded to two open-ended questions covering workshop content, and completed one box-and-arrow diagram.

**Table 1. Pre- and Post-Workshop Scale Averages**

Scale	Pre	Post
Perception of Computational Ability – Sequencing Data	1.47 ± 0.45	2.65 ± 0.36
Computational Understanding	2.22 ± 0.71	3.34 ± 0.34
Python Coding Ability	2.04 ± 0.67	2.69 ± 0.54

### ***Perception of Computational Ability – Sequencing Data***

Eight Likert-type items correspond to the various data sequencing abilities taught in the workshop. Participants were asked to rate their ability in each on a No Ability-Low Ability-Intermediate Ability-High Ability rating scale. A score of 1 implies No Ability, while a score of 4 implies High Ability.

Scores on the *Perception of Computational Ability – Sequencing Data* scale were calculated for the pre- and post-workshop survey. Overall scale scores were calculated as averages across all eight items. Data were inappropriate for parametric tests, so related samples nonparametric tests were run on matched data (n=20). Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.924$ ,  $p \leq 0.001$ ). Statistical significance and mean results (Table 1) indicate that perceptions of computational ability increased as a result of instruction.

### ***Computational Understanding***

Participants were asked to indicate the extent to which they understood specific concepts related to computation, with ratings of Strongly Disagree, Disagree, Agree, and Strongly Agree. A score of 1 implies low understanding (Strong Disagreement), while a score of 4 implies high understanding (Strong Agreement).

Scores on the *Computational Understanding* scale were calculated for both the pre- and post-workshop surveys. Overall scale scores were calculated as averages across all 11 items. Data were inappropriate for parametric tests, so related samples nonparametric tests were run on matched data (n=20). Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.922$ ,  $p \leq 0.001$ ). Statistical significance and mean results (Table 1) indicate that computational understanding increased as a result of instruction.

### ***Python Coding Ability***

Participants were asked to indicate the extent to which they agreed with statements about their Python coding ability, with ratings of Strongly Disagree, Disagree, Agree, and Strongly Agree. A score of 1 implies low ability (Strong Disagreement), while a score of 4 implies high ability (Strong Agreement).

Scores on the *Python Coding Ability* scale were calculated for both the pre- and post-workshop surveys. Overall scale scores were calculated as averages across all 20 items. Data were inappropriate for parametric tests, so related samples nonparametric tests were run on matched data (n=17). Results from the Wilcoxon Signed Ranks Test indicate that pre- and post-workshop results are statistically different ( $Z = -3.623$ ,  $p \leq 0.001$ ). Statistical significance and mean results (Table 1) indicate that Python coding ability increased as a result of instruction.

### ***Open-Ended Questions and Box-and-Arrow Diagram***

Two open-ended questions related to the concepts covered in the workshop were completed pre- and post-workshop (Table 2). These questions were analyzed for evidence of increased understanding of workshop concepts, specifically as reflected in the complexity of participant responses. Response rates were much higher post-workshop for individual questions, suggesting greater ability to respond to questions; as one participant put it pre-workshop, “*I have no idea how to answer this question.*” In general, complexity of responses increased from pre- to post-workshop. Further analysis of open-ended responses for accuracy is possible with collaboration between evaluators and workshop facilitators. The box-and arrow diagram asked participants to draw a diagram illustrating the process of moving raw sequencing data to a final “answer”. In general, pre-workshop diagrams were much simpler than post-workshop.

**Table 2. Open-Ended Response Rates**

Open-Ended	Pre Response Rate*	Post Response Rate*
Suppose that you are using Illumina to sequence DNA from a mouse sample that should have genetic differences from the mouse reference genome. Discuss one or more approaches you would take to analyze the data, as well as your expected sensitivity and specificity to SNPs and indels. Include in your discussion how much you will miss, and how much you find that will be wrong.	52%	77%

Suppose that you are doing a transcriptome expression analysis of a non-model system for which you do not have a good reference genome. Discuss a sequencing strategy, challenges you expect to face, the expected sensitivity and specificity of your analysis, and what kinds of additional large-scale and/or computational data sets you could use to help explore your transcriptome data set.	43%	77%
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\*Response rates are for participants completing surveys only; “no idea” or similar responses are not included in response rate.

### ***Observations***

The workshop was observed three for one to two hour periods. Observations indicate that facilitators generally struck a good balance between lecture and student engagement in actual programming, although students became distracted towards the end of one lecture. During observations, little connection was made between computational science and biological science, although this may reflect the limited number of observations.

### ***Overall Workshop Impressions***

Participants were asked to respond to close-ended questions related to overall impressions of the workshop (Table 3). Participants also responded to open-ended questions about their expectations for the workshop (pre-survey) and their perceptions of the workshop (post-survey).

*Close-Ended Questions.* Eleven questions asked participants to rate components of the workshop, as well as the overall workshop, on a 5-point Likert scale of Very Poor-Poor-Adequate-Good-Very Good. A 1 corresponds to a Very Poor rating and a 5 corresponds to a Very Good Rating. Participants were also asked if the workshop met their needs on a 4-point scale (4 = Very Well), if they learned as expected from the workshop, if understanding of computational science changed, and if they would recommend the workshop (Table 3).

**Table 3. Overall Workshop Impressions**

<b>Workshop Components</b>	<b>Average Score</b>	<b>% Yes</b>
Day 1: EC2, UNIX, and BLAST	4.14 (5)	NA
Day 2: Mapping	4.09 (5)	NA
Day 3: Assembly	4.23 (5)	NA
Day 4: ChIP-Seq	2.00 (5)	NA
Day 5: Statistics and Plotting	3.50 (5)	NA
Day 6, part a: More ChIP-Seq	2.67 (5)	NA
Day 6, part b: Genome Assembly and Annotation	3.89 (5)	NA
Day 6, part c: Current and Future Sequencing Technology	3.70 (5)	NA
Day 7: mRNAseq and Alternative Splicing	3.86 (5)	NA

Day 8: STACKS and Reduced Representation Sequencing	2.27 (5)	NA
Overall Workshop Rating	4.50 (5)	NA
Meet Needs?	3.3 (4)	NA
Learn What Hoped to Learn?	NA	95%
Computational Understanding Change?	NA	86%
Recommend Workshop?	NA	100%

*Results.* Post-workshop responses to questions about the efficacy of the workshop indicate that participants were generally very satisfied with the workshop (Table 3). In general, participants rated the workshop components as Good-Very Good. Chip-SEQ from Days 4 and 6, as well as STACKS and Reduced Representation Sequencing (Day 8), were rated as Adequate-Good. This may reflect a misalignment between the survey and actual content coverage, although workshop leaders should consider reducing content coverage to increase retention.

Participants generally felt the workshop met their needs and would overwhelmingly recommend it to others. Participants gave the workshop an overall rating of 4.5 out of 5 and indicated that the workshop met their needs well or very well. Eighty-six percent (n=20) of participants felt their computational understanding changed, 95% felt they learned what they hoped to learn, and 100% of respondents indicated they would recommend the workshop to others.

*Qualitative Data: Participant Expectations and Perceptions.* On the pre-survey, participants responded to a prompt: “Please provide any additional comments about your expectations for the workshop below.” Participants also responded to a similar post-survey question: “Please provide any additional suggestions or comments about the workshop below.”, and were given opportunities to comment to each of the three yes-no questions in Table 3.

*Results.* Twelve participants provided comments about expectations on the pre-survey (Table 4). These comments related to interest in analyzing sequencing data, use of multiple data sets, and increasing understanding of tools. Selected pre-workshop expectations are provided below. Analysis of these expectations indicates that the workshop, as anticipated from prior work, was comprised of people completely new to programming and those with significant programming experience. Many participants attended the workshop with specific programming or data analysis needs. All quotes are provided verbatim, unless noted:

- *I am hoping to learn how to detect snps and other things from sequenced data and get some familiarity with python and other scripting languages*
- *Basic introduction to Python and NGS analysis pipelines to point I can explore public datasets and extract biological insights*
- *I hope to learn how to assemble short reads (from RNAseq, for example) to a (non-annotated) genome, and [] to analyze differential expression levels from RNA seq.*
- *I have used various software tools to analyze raw ngs exome data, from the fastq files to vcf files. However, I'm not clear on how the software works. Also, I'm not sure how to filter variants based on quality control values. I have both exome and*

- transcriptome data with me to analyze. I would like to become familiar with analyzing both.*
- I am starting from zero with programming. I hope I will start to learn how to handle genome sequence data sets when they first come back from the sequencer. I need to learn how to quality control what I get back, how to analyze it, and what it means. I would like to know what limitations a data set has and what uses it can have.*
  - Hopefully we can deal with de novo assemblies for non model organisms, and how to upgrade the analysis with a reference genome."*
  - Broaden my understanding of NGS in general.*
  - I would expect know the basic workflow for ngs data analysis, from raw reads to variant calls. Also to learn about RNAseq analysis, since I've never done it before.*
  - I'm a newbie*

Workshop responses were very positive on all open-ended questions. For examples:

- I think this is a really useful place to start if you have some data and need help getting it analyzed. The tutorials provide a low risk way of learning the commands, and the little assignments of making pipelines were especially useful*
- [My computational science] is an order of magnitude higher now.*
- Excellent, hard-working instructors and TAs! Lots of fun both in and out of class. Superb venue!*
- The course was above my expectations.*

Participants made a number of suggestions for improving the workshop, summarized here:

- Keep lectures to one hour or less, followed by hands-on tutorials. Multiple respondents indicated that they had difficulty keeping focused on multi-hour lectures.*
- In general, participants wanted more time to engage in tutorials and hands-on work while faculty and teaching assistants were available.*
- Make sure all groups complete tutorials so everyone has an opportunity to work through the code.*
- Provide a concept map of the workshop that participants can refer to throughout workshop.*
- Possibly do more work in the first week to allow more time for reflection and hands-on work in the second week. This includes balancing evening free time between first and second weeks – the second week seemed heavier in workload.*
- Provide a more thorough introduction on the first day for those new to programming. This would include shell scripting, file movement, and similar basic concepts.*
- Provide suggestions before the workshop for how participants can organize their data in order to be able to analyze it during the workshop.*

**Table 4. Perception and Expectations Response Rates**

<b>Prompt/Question</b>	<b>N responses</b>
Please provide any additional comments about your expectations for the workshop. (pre)	12
Please provide any additional suggestions or comments about the workshop. (post)	15