Incorporating a commercial biology cloud lab into online education

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1 Abstract

Traditional biology classes include lab experiments, which are missing from online education. Key challenges include the development of online tools to interface with laboratory resources, back-end logistics, cost, and scale-up. The recent emergence of biology cloud lab companies offers a promising, unexplored opportunity to integrate such labs into online education. We partnered with a cloud lab company to develop a customized prototype platform for graduate biology education based on bacterial growth measurements under antibiotic stress. We evaluated the platform in terms of (i) reliability, cost, and throughput; (ii) its ease of integration into general course content; and (iii) the flexibility and appeal of available experiment types. We were successful in delivering the lab; students designed and ran their own experiments, and analyzed their own data. However, the biological variability and reproducibility of these online experiments posed some challenges. Overall, this approach is very promising, but not yet ready for large-scale deployment in its present form; general advancements in relevant technologies should change this situation soon. We also deduce general lessons for the deployment of other (biology and non-biology) cloud labs.

2 Introduction

A new paradigm has recently emerged for providing access to biology experimentation through a distributed online platform known as cloud biology labs (Hossain et al., 2015), (Hossain et al., 2016), (Hossain et al., 2015), (J. Lee et al., 2014), (Hayden, 2014). The notion is similar to the well-established framework of cloud computing (Fox, 2011) and complements ongoing advances in life-science technology (Kong, Yuan, Zheng, & Chen, 2012), (Melin & Quake, 2007), which have focused mainly on automation and parallelization but have largely ignored issues related to remote or shared access. This cloud lab technology reduces access barriers to costly biological lab equipment and also abates the need for maintenance and hands-on preparation, allowing users to concentrate on experimental design and data analysis. Further advantages include reduced training needs, improved biosafety, facilitated data tracking, and increased standardization (Sia & Owens, 2015).

Two of these biology cloud labs have been successfully deployed recently in academic settings for educational purposes: interactive chemotaxis experiments with
the slime mold physarum over the course of a day (Hossain et al., 2015), and real-time interactive phototaxis experiments with the protist Euglena over the course of one minute (Hossain et al., 2016); the latter lab in particular promises to scale at low cost to massive user numbers (millions of students per year with a cost of less than 1 cent per experiment). Recent years have also seen the emergence of dedicated biology cloud lab companies with initial efforts largely focused on industrial applications (Hayden, 2014); however, there is an opportunity for partnership between commercial cloud lab providers and biology educators to teach lab biology via the web, which has not yet been achieved.

There is a growing literature regarding the utility of educational online experiments and how such remote labs should be designed (Lowe, Newcombe, & Stumpers, 2012), (de Jong, Linn, & Zacharia, 2013), (Heradio et al., 2016), (Wieman, Adams, & Perkins, 2008), (Bonde, Makransky, Wandall, & Larsen, 2014), (Sauter, Uttal, Rapp, Downing, & Jona, 2013). Key design principles include that students feel a real presence (such as via a live video) and that the user interface is intuitive enough to effectively abstract the logistics of preparation so that students can focus on experimental designs and strategies. The development of large-scale cloud biology platforms could be instrumental in bringing true laboratories into online education. The above cited research also compares real labs (remote or local) to simulations (virtual labs), with the conclusion that both have their situation-dependent advantages, and

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**Fig 1:** Commercial biology cloud labs supported by robotics allow remote and controlled execution of cellular and molecular biology experiments. **A)** Workcell (Transcriptic) automates the execution of life-science experiments in order to increase speed, ease, accuracy, and reproducibility. This Workcell contains several instruments and a robot that moves the sample plates among instruments. Image adapted from https://www.transcriptic.com/. **B)** Top, electron micrograph of bacteria. Bottom, schematic of a typical bacterial growth curve in which optical density is measured as a proxy for bacterial concentration. Generally, four phases of growth can be distinguished: lag phase, exponential phase, stationary phase, and decay phase. (Image: Public Domain, Credit Rocky Mountain Laboratories, NIAID, NIH; Scale: individual bacterium ~2μm in length.)
that ideally both are used synergistically.

The goal of the presented work is to assess whether and how commercial biology cloud labs could be utilized for education. We partnered with the start-up company Transcriptic (https://www.transcriptic.com/) to develop a customized cloud-based biological experimentation activity for educational use. Transcriptic has been developing the Workcell platform (Fig. 1), in which a robot shuttles biological specimens in 96-well plates between experimental instruments such as liquid-handling robots, imaging devices, and incubators. Experiments can be fully programmed in Python. This overall framework is under constant development; for example, some experimental steps are still executed by hand, but will eventually be automated. The vision and roadmap to full and flexible automation of cloud experiments is clear. To assess the affordance for future scale-up in educational settings, we deployed this platform in a graduate class user study where students designed and analyzed their own experiments to model the effects of antibiotics on bacterial growth curves. The main categories in which we evaluated the system were (1) logistical feasibility and cost and (2) student responses and potential educational outcomes.

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Fig. 2: User interface, cloud lab technology, and experimental data on bacterial growth. A) Website displayed to students after login. On the left, six different amounts of Kan can be entered. On the right, the currently selected batch of data is displayed, updated every ~40 min during the experiment to generate a new recorded data point. Current and previous batch data can be selected for display. B) Top: Plate reader used by the collaborating company; a robotic platform shuttles the plate between the incubator and spectrophotometer. Bottom, transparent 96-well plates in which experiments are executed. Each student is assigned to six wells during each run, enabling up to 16 students to execute experiments in parallel. (Images: Thermo Fischer Scientific)
3 Methods

All experiments were handled off-site by our commercial partner (Transcriptic, Inc., Menlo Park, CA). Transcriptics has developed a Workcell that automatically executes all experiments (Fig. 1A). These experiments are executed in disposable, standard 96-well plates. A liquid handling robot mixes the corresponding solutions and distributes them among the individual wells, achieving the specific antibiotic concentrations requested by the remote users. The Workcell shuttles these plates between incubators and a plate reader that executes the measurements. This platform is controlled via a Python-based framework. In order to enable student access, we developed a Python-based user interface that enabled students to enter their experimental instructions, read-off their results in graphical form, and download their experimental data in csv format (Fig. 2A).

Bacterial growth experiments were performed in 96-well plates (Fig. 2B). At the beginning of an experiment, a robotic pipetting assembly was programmed to load each well with 150 µL of a suspension of *Escherichia coli*. The *E. coli* suspension was prepared by diluting an *E. coli* stock (optical density at 600 nm (OD$_{600}$) = 0.9) into Miller’s Luria Broth (LB) at a 1:150 ratio. To generate the stock, the DH5α strain of *E. coli* (Zymo Research Corp, US) was transformed with pUC19 plasmid. The robotic pipettor then added the user-specified amount (0–50 µL) of the antibiotic kanamycin (Kan; 40 µg/mL in LB). Each well was then filled to 200 µL with LB, yielding final Kan concentrations of 0-10 µg/mL. A robotic setup then shuttled the plate to a spectrophotometer (Figs. 1,2) to measure and record the bacterial concentration of each well using OD$_{600}$. The plate was covered and placed in an incubator at 37 °C, with shaking at 180 rpm. Every 47 min, the plate was shuttled back to the plate reader and new OD measurements were recorded. This cycle was repeated continually overnight for a total of 20 times to generate a full bacterial growth curve (Figs. 1,2,3).

These activities were deployed in a graduate-level, lecture-based class on the biophysics of multicellular systems. Students used the Transcriptic web interface from home. Students handed in a homework report, and later were given a post-questionnaire. Students were asked to provide written consent to have their homework and questionnaires analyzed for this study; all students gave permission to do so.

4 Results

Among the many possible experiments available on this platform, we chose bacterial growth in the presence of different antibiotic concentrations, as it suited the content of a college-level class (and was likely suitable for middle and high school) and had the potential for easy adaptation on the existing Transcriptic platform. We developed a custom web interface (Fig. 2A) that allowed students to run and evalu-
ate experiments to test the effects of antibiotic concentration on the growth of bacterial populations. Each user accessed six wells; wells from up to 16 users could be combined for a parallel run on a 96-well. For each of the six wells, the user specified varying amounts of an antibiotic to add to the medium (from 0 to 10 µg/L Kan), which affected growth, primarily leading to delayed onset of growth, slower growth, and lower maximal OD$_{600}$ (Methods). Experiments ran overnight; the next day, users logged on to the web interface to view and download the resultant bacterial growth curves (Fig. 2A).

Prior to the user study, we performed approximately 10 test runs. Overall, these initial test experiments were stable and satisfactory, with the typical experimental outcome leading to Hill-type functions (Figs. 1B,2A,3A). The OD$_{600}$ began at a low and reasonably steady value (OD$_{600}=0.2$; lag phase), increased over time (5-10 h; exponential phase), and eventually plateaued (OD$_{600}=0.2$; stationary phase), yielding

![Fig. 3: Examples of experimental growth curves and experimental encountered during study. A) Example of an experimental recording showing a linear sweep from 0 to 50 µL Kan (the maximal amount). We see the expected growth behavior as in Fig. 1B, with increasing Kan resulting in a slower or delayed exponential phase and lower plateau phase; decay phases are partially visible. B) Different types of errors occurred during some experiments: (i) systematic shifts of individual data points (according to the company this was due to condensation on the lids); (ii) one of the samples had a significantly shorter lag phase than the others; (iii) one sample still grew but was much delayed, even with saturating Kan levels (likely due to a spontaneous mutation in the sample); and (iv) same Kan concentration plateaus at different levels. (Legends on the right indicate Kan concentrations)](image-url)
the familiar sigmoidal curve associated with bacterial growth. The somewhat high initial OD$_{600}$ reading of 0.2 reflects the initial bacterial starting concentration as well as the fact that reading were not normalized against initial readings or blanks. Maximal OD$_{600}$ is dependent on the total volume of media in the plate, the well size, culture aeration during growth, and the bacterial strain. In the presence of Kan, the entry into exponential phase was delayed, leading to a lower maximal OD$_{600}$ consistent with the literature (Faraji, Parsa, Torabi, & Withrow, 2006), (Lin, Lee, Lee, & Koo, 2000). At the maximum Kan concentration (10 $\mu$g/mL), growth was completely inhibited, yielding a flat growth curve at OD=0.2.

The platform was deployed in an advanced undergraduate/graduate-level class on modeling multicellular systems. Thirteen students of both genders with various backgrounds related to engineering, physics, and biology took the class. Some of the students did not have any hands-on biology lab experience beyond what is standard in high schools, while others had taken extensive biology lab courses or had previously worked in wet labs including performing equivalent bacteria sample preparation and OD measurements on bacterial growth.

As part of a lecture module on biological growth and competition, students were provided with the theoretical background and pointed to review papers on how to model bacterial growth under the influence of antibiotics. The students were then introduced to the commercial cloud platform and given an open-ended homework assignment to model the growth of bacteria in the presence of antibiotics. Students were responsible for designing their experiment to generate data on the cloud platform. Each student had a total of six overnight experimental rounds with six wells per round. In addition, students were asked to develop models to analyze and fit the data collected, and to write a short 1–2 page report detailing their conclusions on the effects of antibiotics on bacterial growth. In their reports, students were required to explain the rationale behind their experimental strategy and encouraged to explore multiple models to explain their results. Throughout the process, experimental design, hypothesis testing, and data fitting were largely left open to students,

<table>
<thead>
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<th>Strategy</th>
<th>Description</th>
<th>Examples</th>
<th># students</th>
<th># students</th>
<th>Incl.</th>
<th>Incl.</th>
<th>Sweep</th>
<th>Sweep</th>
<th>Replicate</th>
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<tr>
<td>1a</td>
<td>Linear sweep through all parameter ranges</td>
<td>[0 10 20 30 40 50]</td>
<td>5</td>
<td>5</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>1b</td>
<td>A logarithmic sweep through all parameter ranges</td>
<td>[0 1 2 3 5 7 9 50]</td>
<td>3</td>
<td>1</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>1c</td>
<td>A single logarithmic sweep (log 0.5)</td>
<td>[0 0.5 1 2 4 8 16 32 50]</td>
<td>1</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1d</td>
<td>2 Trips at 5 levels</td>
<td>[0 0 10 20 30 50]</td>
<td>1</td>
<td>1</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>2b</td>
<td>2 Trips at 5 levels and one low level</td>
<td>[0 0 10 10 10]</td>
<td>1</td>
<td>0</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2c</td>
<td>Low control and spanning the space</td>
<td>[0 0 0 0 0 0 0 0 0]</td>
<td>1</td>
<td>1</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>6 trips, same average</td>
<td>[10 30 50 20 30 20]</td>
<td>1</td>
<td>0</td>
<td>X</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>4b</td>
<td>All levels alternate</td>
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<td>0</td>
<td>3</td>
<td>X</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

Table 1: Distinct initial experimental strategies and answers from the post questionnaire.
was fully functional and returned the expected growth curves (Fig. 3A). The second experimental results varied and ultimately deteriorated between runs. The first run was also fully functional for most of the students. However, in some cases (Fig. 3B), we observed that at certain time points, all OD 600 readings systematically increased, the variability between replicates increased, and bacteria grew even under high Kan concentrations. There were at least two main reasons for these inconsistent results, as clarified later with Transcriptic. (1) The robot handling logistics had some issues: the lid collected condensation due to delayed shutting of the plate between the incubator and the reader, because Transcriptic’s robot was executing many other experiments in parallel. (2) Bacterial cultures were taken from a stock generated specifically for this study and stored at 4 °C instead of freshly prepared every time in order to reduce costs. Thus, although batch-to-batch variations due to stock preparation were eliminated, the time in storage likely led to the emergence of resistant strains in the starter culture. None of these issues had arisen during our pre-tests prior to classroom use. As a result of these issues, several students obtained variable, unexpected results from their runs. While it would have been feasible to restart the entire set of runs with fresh bacterial cultures at a later time in the course, we ultimately decided, in conjunction with student feedback, to continue the experimental runs as they were. Students had the option to either use their own data or to use pre-recorded data sets of higher quality that had been obtained when the protocols were developed (about half of the students did, the others did not).

Student used a variety of models for fitting their growth curves to explain the results in their reports. Roughly half (7/13 students) applied growth models from review papers (Buchanan, 1997), (Faraji et al., 2006), (Lin et al., 2000), (SWINNEN, 2004), (Zwietering, de Koos, Hasenack, de Witt, & van ’t Riet, 1991) that we provided...
in the assignment handout, whereas the rest of the class developed novel models or sought other models from the literature (Fig. 4). Depending on the model, students needed to deduce 5-7 parameters; the quality of the match depended on the chosen model. Some students chose global fitting strategies for all data at once, while others (Fig. 4) systematically determined individual parameters from subsets of their data.

Although these data could have been subjected to error analysis, we did not request the students to do so, given that error analysis was not the focus of the class and given the technical challenges experienced during some of the experiments. More than half of the students (7/13) nevertheless presented some analysis of uncertainty in their fit parameters, computed statistical errors, or otherwise made comments on error and noise with regard to their results.

In the discussion, all students critiqued their own modeling and experimental strategies, as instructed. More than half of the students (7/13) responded that they could have improved their reports with less variable data, while 7/13 students proposed variations on the growth model to test in the future. Notably, 5/13 students explicitly suggested improvements to their experimental strategy. Overall, students self-reported that they spent an average of 10 h (min/max: 5/20 h) on all activities (planning, experiment, data analysis, and reporting). The most time was spent developing models, analyzing data, and writing reports, with much less time spent per-

![Fig. 4: Example data set and fitting approach from one student.](Image)

**Left** Data for six Kan amounts (dots) with fitting curves (solid) superimposed. For the 0 µL Kan condition, multiple data repeats were collected; for 25 µL Kan, two were recorded; all others are single runs. **Right** The student chose a sigmoidal model with four independent parameters—note that these four parameters could have been defined differently by using a different notation for the sigmoidal curve. The table shows the fit parameters for each condition. A linear dependency on Kan amount is assumed (fitted) for each of these four parameters, leading to eight parameters shown in the table in panel D. One component is found to be zero, leaving the student with a 7-parameter fit to explain bacterial growth under the influence of Kan, which leads to the fit curves in A.
forming the actual experiments.

In order to assess whether students gained experience or changed their approach to the task after using the cloud lab, the post-assignment questionnaire included a question about how they would design their first experimental run if they were to repeat the assignment. We again categorized the experimental strategies (Table 1) and observed that the number of students choosing a sweep strategy diminished from 9/13 to 6/13. Those six students used the replicate strategy, including three students who suggested a full blank control \([0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0] \ \mu L\), as well as a single student who used the hybrid strategy. All students now included at least one negative control well \((0 \ \mu L \ \text{Kan})\), which had not been the case during the original experiment. More students now also proposed a full parameter exploration. We cannot resolve these transitions on the individual student level, as the questionnaires were anonymous.

In order to assess the potential learning benefit from this type of activity, we

<table>
<thead>
<tr>
<th>Question</th>
<th>Disagree (1-3)</th>
<th>Neutral (4-6)</th>
<th>Agree (7-9)</th>
<th>mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>15 I enjoyed this activity.</td>
<td>2</td>
<td>0</td>
<td>5</td>
<td>6</td>
</tr>
<tr>
<td>6 The activity reinforced concepts in class.</td>
<td>0</td>
<td>2</td>
<td>4</td>
<td>7</td>
</tr>
<tr>
<td>2 The activity was worth the time and effort.</td>
<td>2</td>
<td>6</td>
<td>5</td>
<td>5.4</td>
</tr>
<tr>
<td>7 The experiments were too simple to be useful in a graduate level class.</td>
<td>3</td>
<td>6</td>
<td>4</td>
<td>5.2</td>
</tr>
<tr>
<td>10 The experiments were too simple – this activity needs more degrees of freedom.</td>
<td>0</td>
<td>5</td>
<td>8</td>
<td>7.2</td>
</tr>
<tr>
<td>13 It was good that I could change only one experimental variable as the activity overall had much complexity.</td>
<td>4</td>
<td>1</td>
<td>8</td>
<td>4.8</td>
</tr>
<tr>
<td>16 Submitting with pre-recorded data would have had the same learning outcome.</td>
<td>4</td>
<td>1</td>
<td>8</td>
<td>4.1</td>
</tr>
<tr>
<td>11 The fact that these were real experiments executed in real time made it more interesting for me.</td>
<td>2</td>
<td>3</td>
<td>8</td>
<td>6.6</td>
</tr>
<tr>
<td>2 The fact that the data was noisy made me think deeper and therefore was actually a good thing.</td>
<td>4</td>
<td>4</td>
<td>5</td>
<td>5.5</td>
</tr>
<tr>
<td>17 It was nice that there was freedom of what model to choose and to deal with the ambiguity of the data.</td>
<td>0</td>
<td>3</td>
<td>10</td>
<td>7.0</td>
</tr>
<tr>
<td>10 Pre to the first experiment I strongly trusted the reliability of the system.</td>
<td>0</td>
<td>6</td>
<td>7</td>
<td>6.6</td>
</tr>
<tr>
<td>12 The data was noisy because of instrumentation issues.</td>
<td>0</td>
<td>3</td>
<td>9</td>
<td>7.1</td>
</tr>
<tr>
<td>8 The data was primarily noisy because of biological effects.</td>
<td>6</td>
<td>5</td>
<td>1</td>
<td>3.7</td>
</tr>
<tr>
<td>14 The data was noisy due to a combination of instrumentation issues and biological effects.</td>
<td>1</td>
<td>4</td>
<td>7</td>
<td>6.5</td>
</tr>
</tbody>
</table>

* one student did not answer these questions

Table 2: Overview of the post-activity questionnaire. Questions were grouped according to topic; the first column indicates the order in which questions were initially presented to the students (1, “strongly disagree”; 9, “strongly agree”).
asked the students to “State up to 3 things that you feel you have learned / gained / benefited from this activity.” We categorized the student responses, with some answers appearing in multiple categories (numbers in parentheses are the number of answers in that category with one example): (i) Biological content about bacterial growth (6, “I learned more about bacterial growth”); (ii) Biology cloud lab technology (4, “learned what a cloud lab is”); (iii) Insights into experimentation (2, “I learned experimental design”); (iv) Experimental noise and errors (6, “I learned more about experimental noise”); (v) How to develop and evaluate models (8, “learned about growth curve model types”); (vi) Data fitting (5, “Data fitting and analysis”). Two answers did not fit into these categories (“remembered why I don’t like experimental research”, “freedom of modeling framework as proposed to the other homework”). Hence, the students reported learning advances on a variety of issues relating to biological content, experimentation, modeling, and data fitting. Future controlled studies would evaluate the extent to which these outcomes are met.

This post-questionnaire also solicited general student feedback via 17 questions summarized in Table 2. These questions can be loosely clustered into five aspects. The first three aspects targeted general student impressions of whether they thought the activity was useful/appropriate/engaging. The last two aspects focused on whether there was substantive value in having run real experiments with real noise.

The majority of the class was neutral or positive as to whether they liked the assignment, and also in whether they felt it was a valuable addition to the class and reinforced course concepts. Students clearly found the web interface to be intuitive. Overall, students were neutral in whether this activity was appropriate for the class level, with many believing that the activity was too simple and lacked experimental freedom. Some students reported that the noisiness of the real data provided an added benefit, while others did not. Students preferred the freedom in model choices and the ambiguity of the data. Students had high trust in the system before starting the experiment, but became more critical about the instrument throughout the assignment, which is an important lesson for any experimentalist. Overall, students interpreted the variability in their data as stemming primarily from issues with instrumentation rather than biological noise. Overall, we conclude a subpopulation of students appreciated this online lab and had a positive educational outcome.

5 Discussion

In this proof-of-concept project, we explored the feasibility and utility of using a commercial biology cloud lab in (college) education. We found that such platforms can be integrated into classes in an enjoyable and useful manner for students. Overall, a significant portion of the students appreciated the open-endedness of exploring a real experimental environment without having to do the experiments manually. Some of the challenges we experienced during this first deployment revealed that
these automated biology cloud labs are still in their early days, but these technologies are advancing very rapidly.

We learned multiple lessons for what would make biology cloud labs useful for education and possibly for research as well. (1) Both stimulus and response spaces should be large enough to be interesting, but not too large to become unmanageable for the students, depending on the student audience and educational goals. For example, having three chemicals at ten concentrations that can be added at multiple time points during the experiment provides a stimulus space that is difficult to test exhaustively. In terms of response space, the individual growth curves are rather low dimensional, as they can be described with 5–7 parameters based on the students’ projects, with experimental variability providing additional information. (2) The instruments, as well as the biological responses, should be within desired, pre-specified parameters regarding variability, noise, and measurement uncertainty. It would be good practice to run standards alongside each experiment and to provide that information to the user. Standards would reveal the quality of execution and could be used to normalize raw data in certain scenarios. This variability can be enriching or disruptive to the educational outcome depending on its extent and how well it is embedded into the educational context. (3) Ideally, the setup is interactive in that the stimulus can be changed while the experiment is running, which was not the case for the present lab. Experiments should be chosen where automation also enables experiments that no student would be able to do in a lab by hand, such as adding a stimulus every 20 s over the course of hours to days. (4) When going through the effort of running real experiments, there should be an added benefit to the students versus running a simulation or using pre-recorded data. Hence, students should be aided in feeling the reality (such as providing a live webcam to see the machine operating), or be empowered to make interactive choices throughout the run, which counters arguments for pre-recorded data, or be able to experience biological variability.

Who is the target audience for this particular biology experiment? There was some a priori debate among instructors whether the activity was too simple for a graduate-level class, which was also indicated by student feedback. There was essentially only one variable that students could choose: the amount of antibiotic. Students would have preferred more experimental freedom. We therefore believe that this set of activities would be better suited to more introductory research-focused classes, perhaps at advanced high-school or introductory college levels, to train students on experimental design and data analysis while taking away the time consuming efforts for a hands-on lab.

Overall, the Transcriptic platform enables much more complex experiments for future deployments given its professional target audience. These experiments could be made more interactive and versatile, such as being able to choose from multiple antibiotics or adding liquids to the sample at multiple times during the experimental run. Many other experiments are possible, given that the ultimate vision of these cloud lab companies is to enable (nearly) every possible experiment in the molecular
and cellular research domain. Finally, another interesting aspect is that students can access research-grade equipment over the web.

Based on Transcriptic’s business model, the current cost of these of experiments is ~$70 per 96-well plate. This cost depends on the experiment type and is likely to decrease in the future given advancements in the technology. Hence, running five successive experiments of six wells per student might be considered reasonable for this activity, which would cost ~$20 per student, a price point that can be considered reasonable in comparison to advanced hands-on lab classes in colleges, but is potentially at the upper limit for K-12 education. One of the major advantages of such a commercial cloud lab approach is that all the costs are already factored in, with no additional logistics for the instructor. The 96-well experiment also demonstrates how high-throughput experiments in general can be virtually partitioned among many users. Given the size of the educational market, with millions of students in the US alone going through the same curriculum each year, offering cloud biological experiments could be of interest to commercial cloud lab companies.

We asked our collaborators at Transcriptic for their evaluation of the project. They indicated that it was an important educational experience for them as well, especially as the Workcell had just gone operational and was still in the debugging phase. The variability that had emerged during the experiments was unintended, but also provided valuable insights into where the system and the protocols needed improvements. These issues were subsequently resolved through a combination of improved hardware and specimen-handling protocols, such as purchasing more advanced liquid handling robots and avoiding condensation on the plates.

It is also important and insightful to compare these results to the two other biology cloud labs that were deployed in educational settings previously (Hossain & Chung, 2015), where students performed chemotaxis experiments with the slime mold physarum over the course of one day (Hossain et al., 2015) or phototaxis experiments with Euglena cells over the course of one minute (Hossain et al., 2016). The bacterial growth experiment investigated here provided the students with a significantly smaller design space for their experiments (exhaustive exploration within five experiments vs. effectively having an infinite space in the other two cases). Similarly, the result space was much more limited (discrete data curves vs. rich image data, although the biological variability in the growth curves added interesting elements). The Workcell approach of shuttling experiments between different types of instruments provides a tremendous opportunity for effectively executing an unlimited number of experimental designs (these experiments could even be research grade), and therefore this approach should ultimately have an even higher design and discovery space than the previous two labs (Hossain et al., 2015), (Hossain et al., 2016). The experimental duration of one day was similar to the physarum lab, but was much longer than the Euglena lab. A major advantage of any commercial cloud lab is the sustained business model, which is in stark contrast to many academic initiatives, which often become non-operational when research funding ceases.
Regarding comparable virtual labs, the Labster platform (https://www.labster.com/) (Bonde:2014wk) enables the execution of a variety of simulated experiments typical of the life sciences, including the type that we presented here as well as what Transcriptics offers in general. Due to various animations, the current Labster user interface provides a much more realistic laboratory feel than the students experienced in the current study. In the future, it will be important to compare and implement both approaches side by side, as virtual and real experiments have their own standout features and are likely best used synergistically (see references in introduction). Another aspect to consider is the integration of this cloud lab into learning management systems (LMS) (Heradio et al., 2016). Given the currently dynamic development for both biology cloud labs as well as LMSs, we suggest that a tight integration should not be the foremost goal. Rather, a more flexible, modular approach with simple data transfer between the platforms is recommended, e.g., accessing the cloud lab via a simple web link inside the LMS and bringing the data from the cloud lab to the LMS via intermediate file download onto a local hard drive.

Overall, our work demonstrates that commercial biology cloud labs can be integrated into education and that they offer potential for developing enjoyable and useful online learning platforms to teach essential scientific skills such as experimental design and data analysis. Although the technology is at the cusp of being mature enough to deploy in educational settings, more interesting research and development should be carried out regarding technology, user interface design, and educational framing. We encourage other stakeholders from educators and industry to join the effort.

Acknowledgements: We would like to thank M. Hodak, the transcriptics team, Z. Hossain, X. Jin, H. Kim, M. Head, and the students in the class.

6 References


