Emily Liu el545 Haonan Kuang hk876

Nutrient Removal in a Batch Reactor

Introduction and Objectives

Nutrient pollution is one of the most widespread and costly environmental problems around the world. Nutrients such as nitrogen and phosphorus are essential for the growth of all living creatures. However, excessive amounts of nutrients released to the environment by human activities can harm ecosystems and impact human health, for example, eutrophication due to algal blooms and dense wastewater discharged into water resource. For our research, we focused on biological nitrogen removal, using aerobic bacteria to consume nitrogen. The mechanism is the two-step combination of nitrification and denitrification. First, nitrification is achieved when aerobic bacteria converts ammonia to nitrate:

$$2NH_4^+ + 3O_2 \rightarrow 2NO_2^- + 4H^+ + 2H_2O$$

$$2NO_2^- + O_2 \rightarrow 2NO_3^-$$

Second, denitrification takes place under anoxic conditions and convert nitrate to nitrogen, releasing to atmosphere:

$$2NO_3^- + 10e^- + 12H^+ \rightarrow N_2 + 6H_2O$$

However, continuously aeration is very expensive. Thus, we want to see if discontinuous aeration could also sufficiently removal nitrogen in the wastewater.

Our schematic was composed of a batch reactor, a Dissolved Oxygen (DO) probe, an accumulator, two needle valves, 2 pressure sensors, 2 pumps and a stirrer. The system was well controlled by an automated program we made in ProCoDA. In the tank, we added the synthetic feed composition and bacteria. The synthetic feed composition was 100 times the concentration we need and was made up of organic carbon, nitrogen, and phosphate. Bacteria was collected from Fall Creek behind Risley Hall.

We hope with this setup we could observe sufficient nitrogen removal with expected patterns. In order to reach the objectives, we learned to program ProCoDA and brainstormed to solve problems, for example how to keep bacteria away from the DO probe. This research provided us with a real life experience of what we might meet in our future career.

Procedures

This lab's methodology was based off the Gas Transfer lab (https://monroews.github.io/EnvEngLabTextbook/Gas_Transfer/Gas_Transfer.html), with the following modifications: The batch reactor was a 6 L rubbermaid square reactor with three inlets/outlets,

consisting of the aeration stone, an additional pressure sensor used to measure the volume of liquid in the reactor, and plastic tubing connected to a peristaltic pump leading to the sink that was used to drain the reactor after experiment completion. Additionally, there was plastic tubing leading to another peristaltic pump used to pump distilled water from a 20 L jerrican. Both peristaltic pumps were connected to ProCoDA so that we could program ProCoda to add water and empty the reactor, which we did so. We also programmed more states into ProCoda: when the DO probe read that the DO level in the reactor as less than 1 mg/L, it would begin aeration; when it read a level greater than 6 mg/L, it would stop aeration. The reactor was placed on top of a stirrer and a medium sized stir bar was placed within. We used ProCoDA Our setup looked like the following:

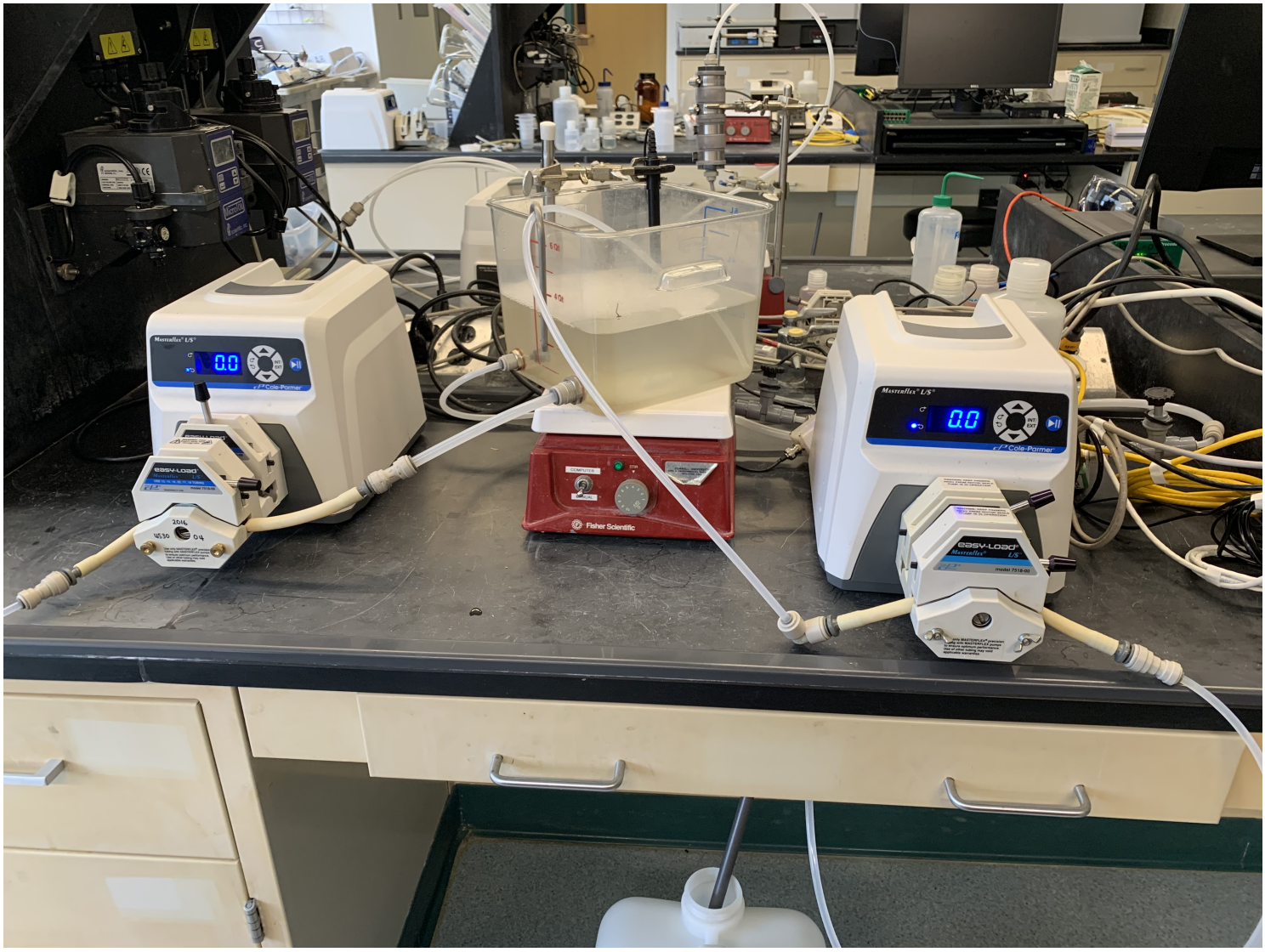

Figure 1. Reactor setup

In each trial, we used 3 L of DO water and 30 mL of the synthetic feed. While we used bacteria from Fall Creek in our reactor, rotting food can also be used. After adding bacteria, we let the reactor run, cycling between aeration and non-aeration. During the cycling, the stirrer was on. We aerated at a rate of $100 \mu M/s$. In our first trial, we only ran one cycle of aeration and non-aeration. The rest of the trials we

cycled indefinitely. In the later trials, enough bacteria had grown in the tank that we did not need to add new samples of Fall Creek bacteria to the reactor.

Results and Discussion

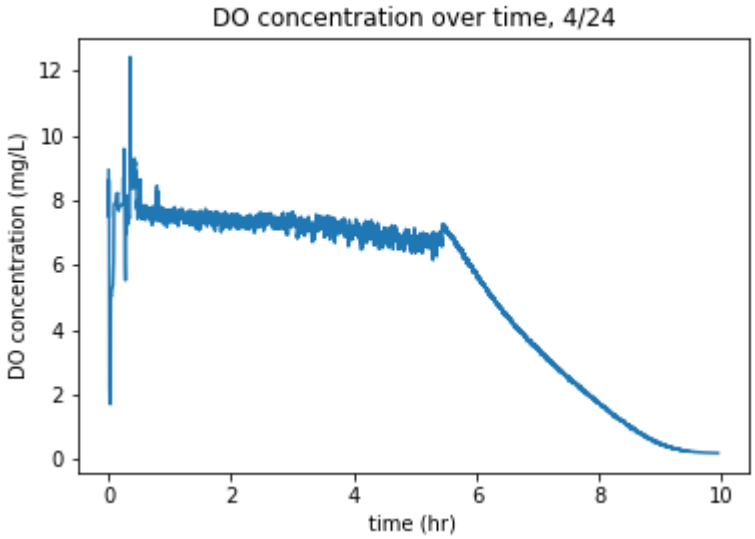

Figure 2. Dissolved oxygen over time, 4/24

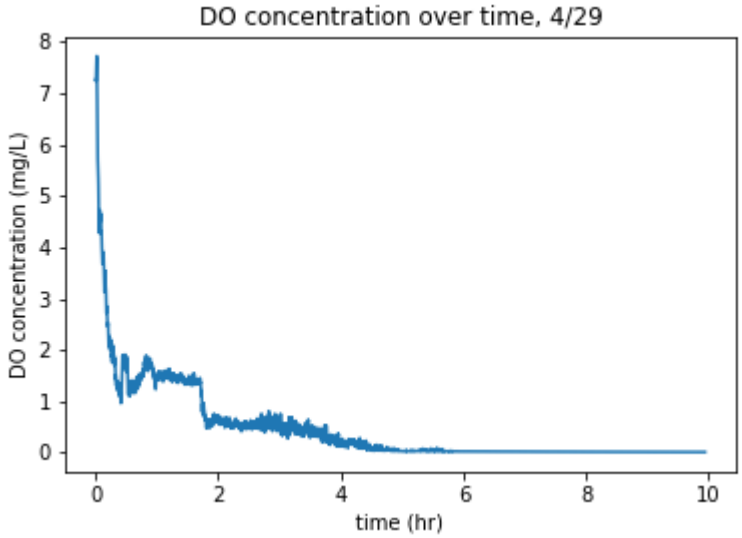

Figure 3. Dissolved oxygen over time, 4/29

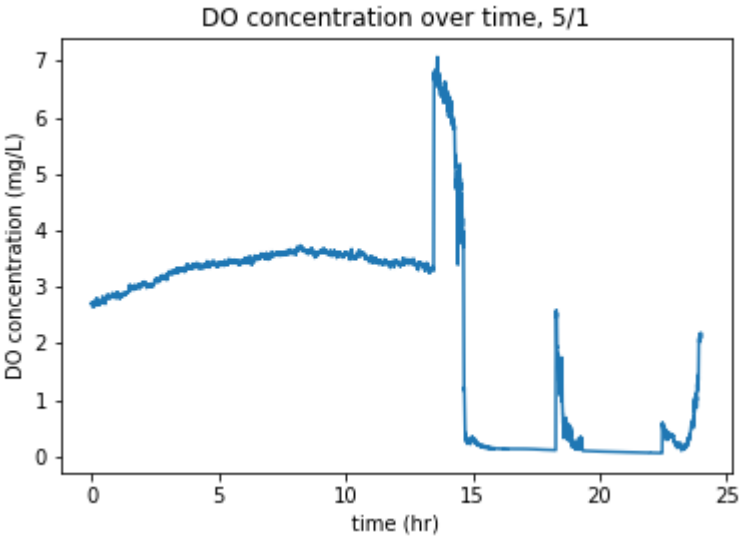

Figure 4. Dissolved oxygen over time, 5/1

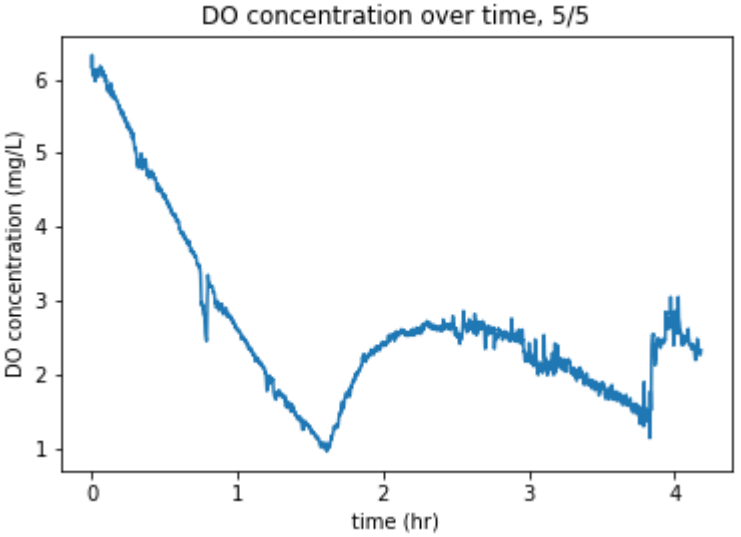

Figure 5. Dissolved oxygen over time, 5/5

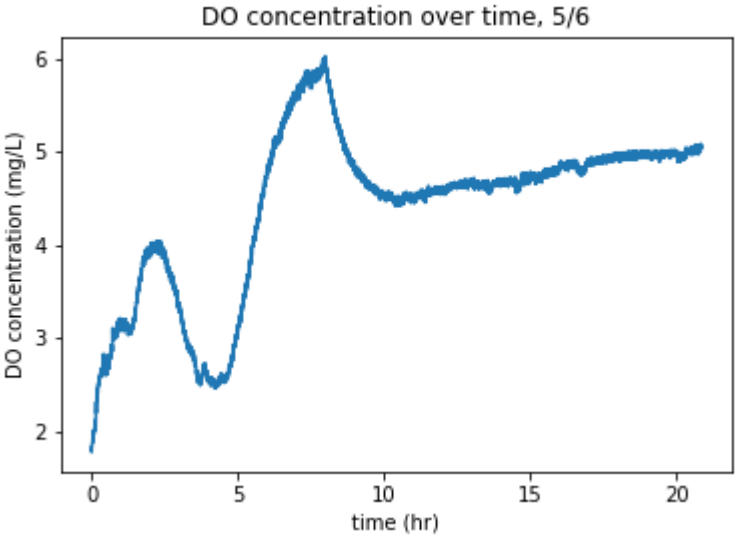

Figure 6. Dissolved oxygen over time, 5/6

In Figure 2, one can see our results for the first trial. We aerated for 5 hours and allowed the bacteria to grow for 15 hours. This was done to see if the bacteria we had found would deplete the oxygen, which it did.

Figures 3 and 4 are some of many failed trials. In each of the failed trials, bacteria grew to cover the DO probe such that no wastewater could enter. As a result, the DO probe read values that were lower than 1 mg/L even as aeration was occurring.

Figures 5 and 6 are from the same trial --our last and only successful trial. In this trial, the oscillating behavior that we expected occurred, with a DO level that eventually plateaued. Given that the DO level during aeration did not go up very quickly and instead bounced between 1 mg/L and 3 mg/L, we suspect that the rate of oxygen depletion from the bacteria outstrips the rate at which oxygen is being added. To test that, we attempted another trial after that with a faster aeration rate of 200 $\mu M/s$, but it failed as the tank began leaking.

Conclusions

After many failed trials, we were able to successfully deplete the nitrogen in the wastewater in a batch reactor, as can be seen in Figure 6. We did so with discontinuous aeration through ProCoDA, and in the process of doing so became comfortable with programming ProCoDA. We were unable to run trials with different aeration rates, but in the future this may be an avenue of exploration.

Suggestions

We were unable to figure out a way for ProCoda to automatically run the experiment without some manual state changes. In particular, we did not know how to switch from the cycling between aeration and non-aeration states to the reactor draining after experiment completion. Perhaps with another peristaltic pump, we would be able to automatically add the concentrated synthetic feed. Excluding that, our main problem lied in the fact that the bacteria would cover the DO probe. To alleviate that, we increased the speed of the stirrer and angled the DO probe as close to the center of the tank (and thus the stir bar) as possible with the hopes that the contents of the tank were moving too fast for bacteria to grow on the probe. This was successful for the most part, so if we had more time to run this lab, we would run further trials. It was our intention to explore how the air flow rate affected bacterial growth and consumption of DO, but we ran out of time and could not do so.

Appendix

```
from aguaclara.core.units import unit_registry as u
import aguaclara.research.environmental_processes_analysis as epa
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt


DO_column = 3 #index of DO column

###Trial 1 4/24
DO_first_row_t1 = 179
dirpath_trial1 = 'https://raw.githubusercontent.com/el545/el545-4530/master/Final%20project/datalc
DO_data_t1=epa.column_of_data(dirpath_trial1, DO_first_row_t1, 3, -1, 'mg/L')
DO_time_data_t1 = (epa.column_of_time(dirpath_trial1,DO_first_row_t1,-1)).to(u.hr)
# Plot the raw data
plt.plot(DO_time_data_t1, DO_data_t1, '-')
plt.title('DO concentration over time, 4/24')
plt.xlabel('time (hr)')
plt.ylabel('DO concentration (mg/L)')
plt.savefig('/Users/Emily/Desktop/4530/Final project/4-24_data.png')
plt.show()

#Trial 2 4/29
dirpath_trial2 = 'https://raw.githubusercontent.com/el545/el545-4530/master/Final%20project/datalc

DO_first_row_t2 = 10

DO_data_t2=epa.column_of_data(dirpath_trial2, DO_first_row_t2, 3, -1, 'mg/L')
DO_time_data_t2 = (epa.column_of_time(dirpath_trial2,DO_first_row_t2,-1)).to(u.hr)
# Plot the raw data
plt.plot(DO_time_data_t2, DO_data_t2, '-')
plt.title('DO concentration over time, 4/29')
plt.xlabel('time (hr)')
plt.ylabel('DO concentration (mg/L)')
plt.savefig('/Users/Emily/Desktop/4530/Final project/4-29_data.png')
plt.show()

###Trial 3 5/1
DO_first_row_t3 = 10
dirpath_trial3 = 'https://raw.githubusercontent.com/el545/el545-4530/master/Final%20project/datalc
DO_data_t3=epa.column_of_data(dirpath_trial3, DO_first_row_t3, 3, -1, 'mg/L')
DO_time_data_t3 = (epa.column_of_time(dirpath_trial3,DO_first_row_t3,-1)).to(u.hr)
# Plot the raw data
plt.plot(DO_time_data_t3, DO_data_t3, '-')
plt.title('DO concentration over time, 5/1')
plt.xlabel('time (hr)')
plt.ylabel('DO concentration (mg/L)')
plt.savefig('/Users/Emily/Desktop/4530/Final project/5-1_data.png')
plt.show()
```

```
##Trial 4 5/5
DO_first_row_t4 = 10
dirpath_trial4 = 'https://raw.githubusercontent.com/el545/el545-4530/master/Final%20project/datalc
DO_data_t4=epa.column_of_data(dirpath_trial4, DO_first_row_t4, 3, -1, 'mg/L')
DO_time_data_t4 = (epa.column_of_time(dirpath_trial4,DO_first_row_t4,-1)).to(u.hr)
# Plot the raw data
plt.plot(DO_time_data_t4, DO_data_t4, '-')
plt.title('DO concentration over time, 5/5')
plt.xlabel('time (hr)')
plt.ylabel('DO concentration (mg/L)')
plt.savefig('/Users/Emily/Desktop/4530/Final project/5-5_data.png')
plt.show()


##Trial 5 5/5
DO_first_row_t5 = 400
dirpath_trial5 = 'https://raw.githubusercontent.com/el545/el545-4530/master/Final%20project/datalc
DO_data_t5=epa.column_of_data(dirpath_trial5, DO_first_row_t5, 3, -1, 'mg/L')
DO_time_data_t5 = (epa.column_of_time(dirpath_trial5,DO_first_row_t5,-1)).to(u.hr)
# Plot the raw data
plt.plot(DO_time_data_t5, DO_data_t5, '-')
plt.title('DO concentration over time, 5/6')
plt.xlabel('time (hr)')
plt.ylabel('DO concentration (mg/L)')
plt.savefig('/Users/Emily/Desktop/4530/Final project/5-6_data.png')
plt.show()
```