

week2_data_analysis

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1 E164: Introduction to Biological System Design

1.1 Introduction to Biological Data Analysis

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If you have not setup your computer to run this notebook, make sure to follow steps here: <https://docs.google.com/document/d/1js7XQbjorU5LCIoWfrzkUCXjjQkVcITkT0N8osiy4Go/edit?usp=sharing>

The purpose of this interactive Python notebook is to introduce basic data analysis tools available in Python with the help of biological data examples.

If you have installed numpy, scipy, matplotlib, and pandas already, then you are all set to run this notebook.

2 Data Analysis with Python

2.1 Introduction to Pandas

You can think of Pandas as the Python data-management library. It can be used to manage large quantities of data in a structured way so you don't get lost and provides functions to retrieve/store/edit your data so that it is easily interfaced with numerical, scientific, and plotting libraries.

More information on Pandas here: <https://pandas.pydata.org/pandas-docs/stable/>

Data is often stored as .csv files. Here's how to import a CSV file with Pandas and structure the data as desired.

```
[1]: import pandas as pd

url = 'https://raw.githubusercontent.com/biocircuits/bioscrape/master/
↳inference%20examples/data/od_data.csv'
# To import a CSV file, you can use the `read_csv` function.
# Either provide a URL as its input or a string of address to the CSV file on
↳your local machine.
df = pd.read_csv(url)
# You get a "dataframe" object out that contains all of the data in the CSV file
```

2.1.1 In an IPYNB (like this one), the Pandas dataframes are nicely formatted:

```
[31]: df
```

```
[31]:
```

	Time	t	A1	A2	A3	A4	A5	A6	A7	A8	\
0	0:09:19	9.32	0.086	0.087	0.088	0.095	0.091	0.089	0.090	0.085	
1	0:19:19	19.32	0.086	0.090	0.089	0.090	0.091	0.092	0.091	0.086	
2	0:29:19	29.32	0.086	0.088	0.090	0.089	0.089	0.092	0.093	0.087	
3	0:39:19	39.32	0.088	0.090	0.091	0.090	0.092	0.093	0.096	0.088	
4	0:49:19	49.32	0.089	0.092	0.093	0.092	0.094	0.096	0.099	0.091	
..	
68	11:29:19	689.32	0.543	0.562	0.614	0.604	0.573	0.566	0.615	0.572	
69	11:39:19	699.32	0.543	0.563	0.615	0.605	0.574	0.568	0.616	0.572	
70	11:49:19	709.32	0.545	0.564	0.616	0.606	0.574	0.569	0.617	0.575	
71	11:59:19	719.32	0.544	0.565	0.617	0.607	0.575	0.570	0.618	0.576	
72	12:09:19	729.32	0.544	0.566	0.618	0.608	0.576	0.571	0.619	0.577	

	A9	A10	A11	A12
0	0.090	0.090	0.088	0.091
1	0.092	0.092	0.088	0.090
2	0.089	0.093	0.089	0.092
3	0.091	0.093	0.090	0.094
4	0.093	0.094	0.094	0.096
..
68	0.570	0.566	0.568	0.606
69	0.570	0.568	0.569	0.607
70	0.572	0.568	0.570	0.608
71	0.573	0.570	0.570	0.609
72	0.574	0.570	0.571	0.610

```
[73 rows x 14 columns]
```

2.1.2 Accessing the dataframe in arrays:

```
[3]: import numpy as np
time_array = np.array(df['t'])
```

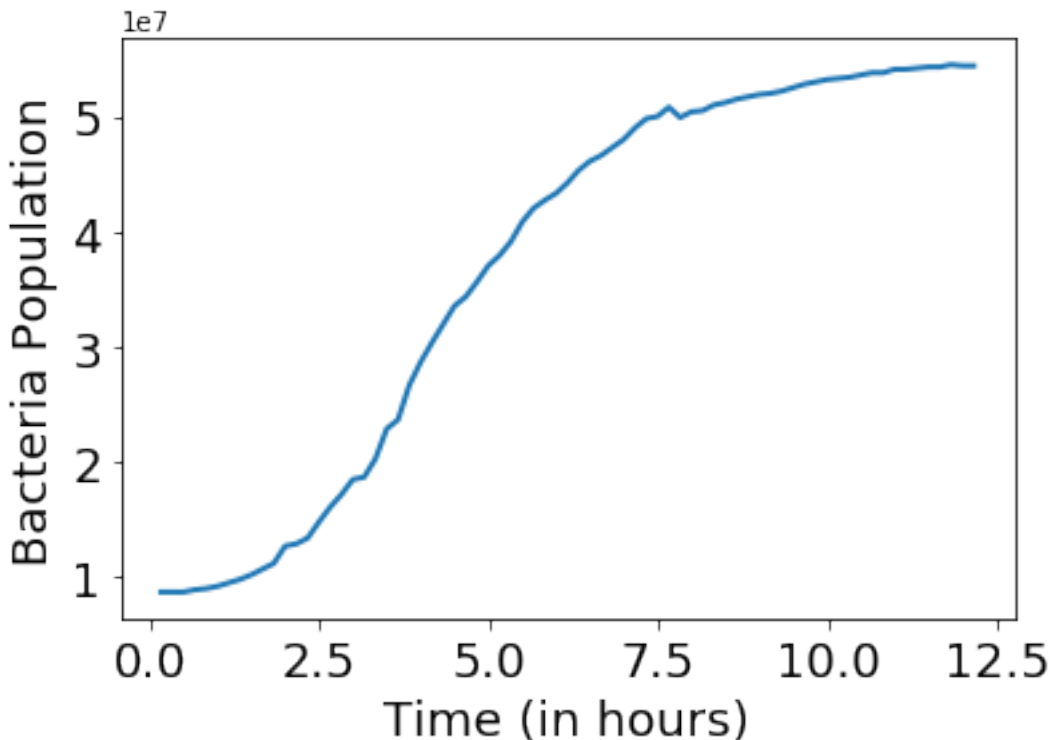
```
[4]: # Here's the time in minutes from the dataset:
time_array
```

```
[4]: array([ 9.32, 19.32, 29.32, 39.32, 49.32, 59.32, 69.32, 79.32,
          89.32, 99.32, 109.32, 119.32, 129.32, 139.32, 149.32, 159.32,
          169.32, 179.32, 189.32, 199.32, 209.32, 219.32, 229.32, 239.32,
          249.32, 259.32, 269.32, 279.32, 289.32, 299.32, 309.32, 319.32,
          329.32, 339.32, 349.32, 359.32, 369.32, 379.32, 389.32, 399.32,
          409.32, 419.32, 429.32, 439.32, 449.32, 459.32, 469.32, 479.32,
          489.32, 499.32, 509.32, 519.32, 529.32, 539.32, 549.32, 559.32,
          569.32, 579.32, 589.32, 599.32, 609.32, 619.32, 629.32, 639.32,
```

```
649.32, 659.32, 669.32, 679.32, 689.32, 699.32, 709.32, 719.32,
729.32])
```

2.1.3 Plotting dataframe using matplotlib:

```
[5]: import matplotlib.pyplot as plt
fig, ax = plt.subplots()
# Plot the data for the container A1 against time:
# Convert time to hours and "A1" density data to cell counts.
ax.plot(df['t']/60, df['A1']*1e8, lw = 2)
ax.set_xlabel('Time (in hours)', fontsize = 18)
ax.set_ylabel('Bacteria Population', fontsize = 18)
ax.tick_params(labelsize = 18)
```



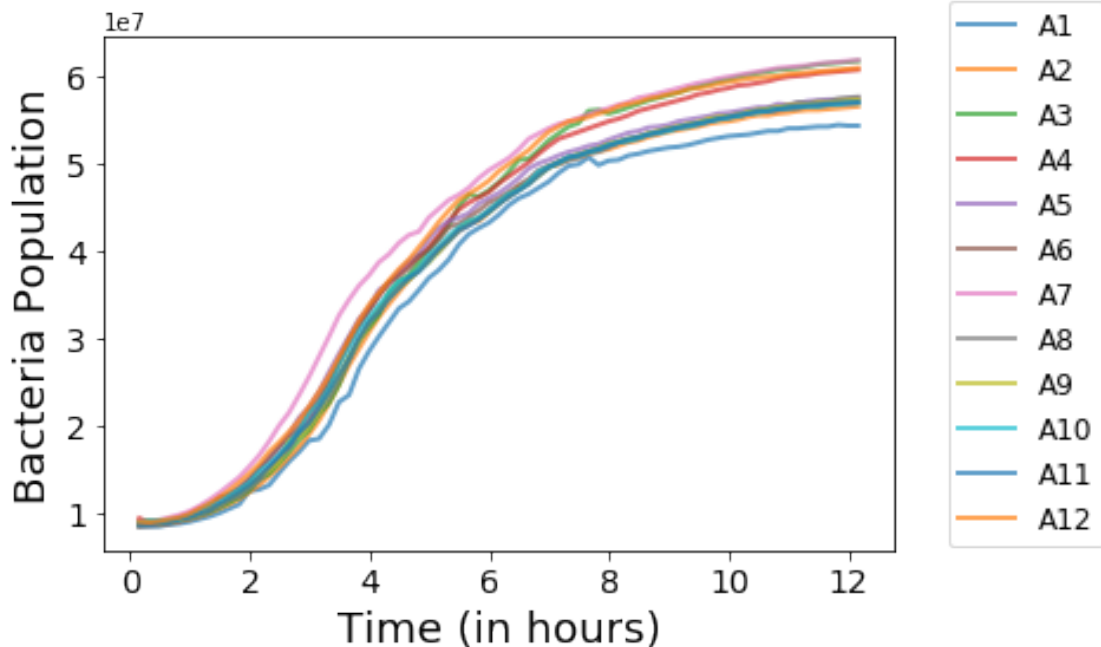
2.1.4 Now plot all data together:

```
[6]: fig, ax = plt.subplots()
for column_title in df:
    # the first two columns are not data, they are time columns, so we ignore
    # those:
    if column_title == 't' or column_title == "Time":
        # Skip this and continue to iterate
```

```

        continue
    ax.plot(df['t']/60, df[column_title]*1e8, alpha = 0.7, lw = 2, label = _
↪column_title)
ax.set_xlabel('Time (in hours)', fontsize = 18)
ax.set_ylabel('Bacteria Population', fontsize = 18)
ax.tick_params(labelsize = 14)
# bbox_to_anchor command is used to set the position of the legend box
ax.legend(fontsize = 12, bbox_to_anchor = (1.05,1.1), loc = "best");

```



2.2 Manually fit logistic growth to the OD data

```

[53]: import numpy as np
def logistical_growth(t, x, k, C):
    return k*x*(1 - x/C)

timepoints = np.array(df['t']/60) # time array in hours
from my_numerical_integrators import integrate

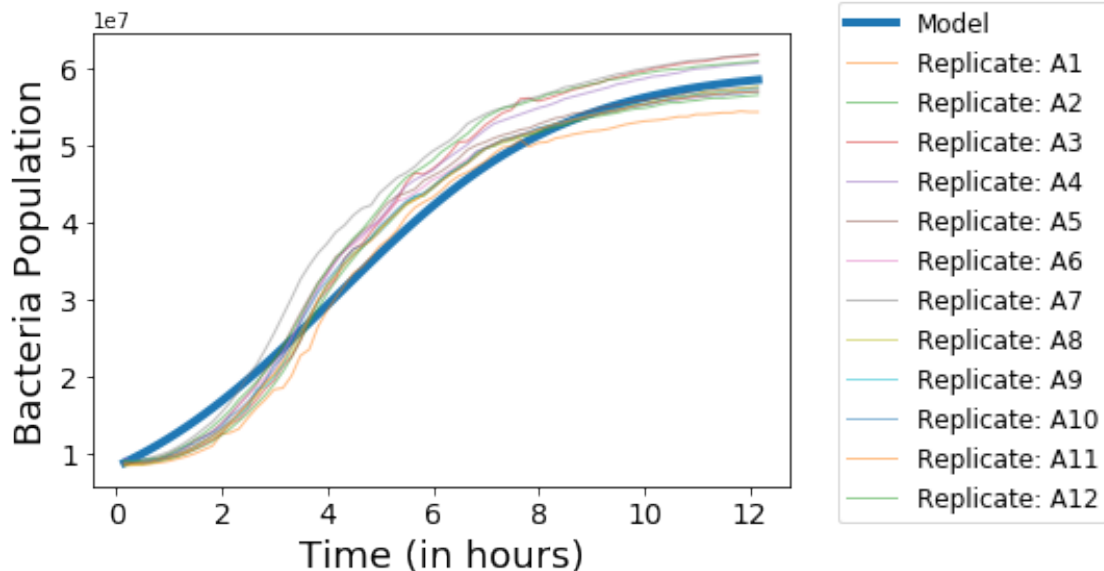
x0 = np.mean(df.iloc[0][2:])*1e8 # Initial condition = Get from data
k = 0.45 # growth rate in 1/hour unit
C = 6e7 # maximum capacity
x = integrate(logistical_growth, timepoints, x0, k, C)
fig, ax = plt.subplots()
# Plot model simulation
ax.plot(timepoints, x, linewidth = 4, label = 'Model')

```

```

# Plot experimental data
for column_title in df:
    # the first two columns are not data, they are time columns, so we ignore
    those:
    if column_title == 't' or column_title == "Time":
        # Skip this and continue to iterate
        continue
    ax.plot(timepoints, df[column_title]*1e8, alpha = 0.5, lw = 1, label =
    'Replicate: '+column_title)
ax.set_xlabel('Time (in hours)', fontsize = 18)
ax.set_ylabel('Bacteria Population', fontsize = 18)
ax.tick_params(labelsize = 14)
# bbox_to_anchor command is used to set the position of the legend box
ax.legend(fontsize = 12, bbox_to_anchor = (1.05,1.1), loc = "best");

```



2.3 Data Analysis:

1. Steady state analysis (Week 7)
2. Growth rate computation (Week 2)
3. State-space exploration (Week 9)
4. Asymptotic analysis

[]: