



BIOENGINEERING  
UNIVERSITY *of* WASHINGTON

# Photosimulator

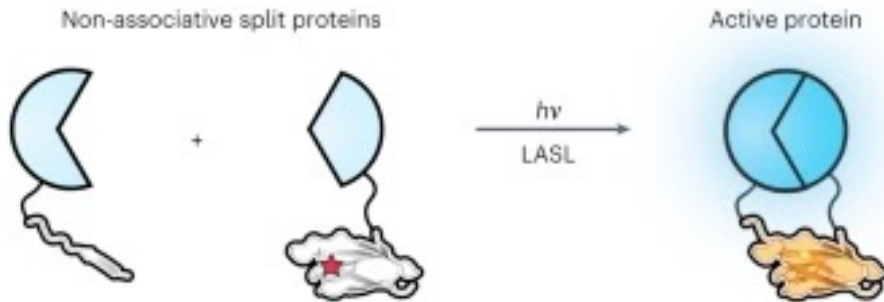
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Brizzia G. Munoz Robles

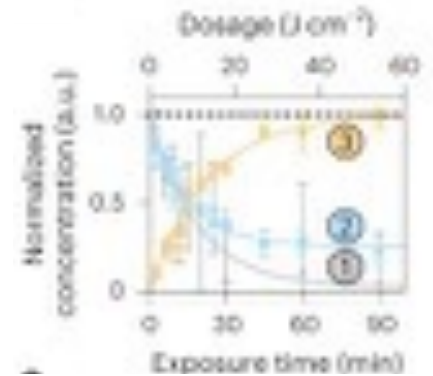
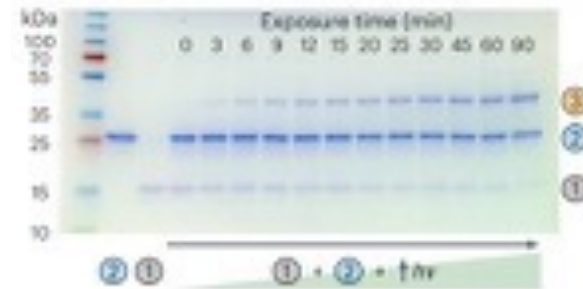
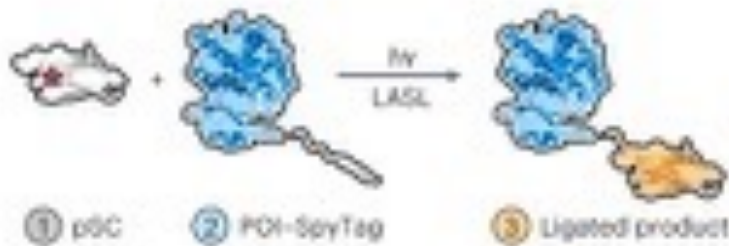
Graduate Student Software Project

BIOEN 537

# Background: Modeling Photokinetics

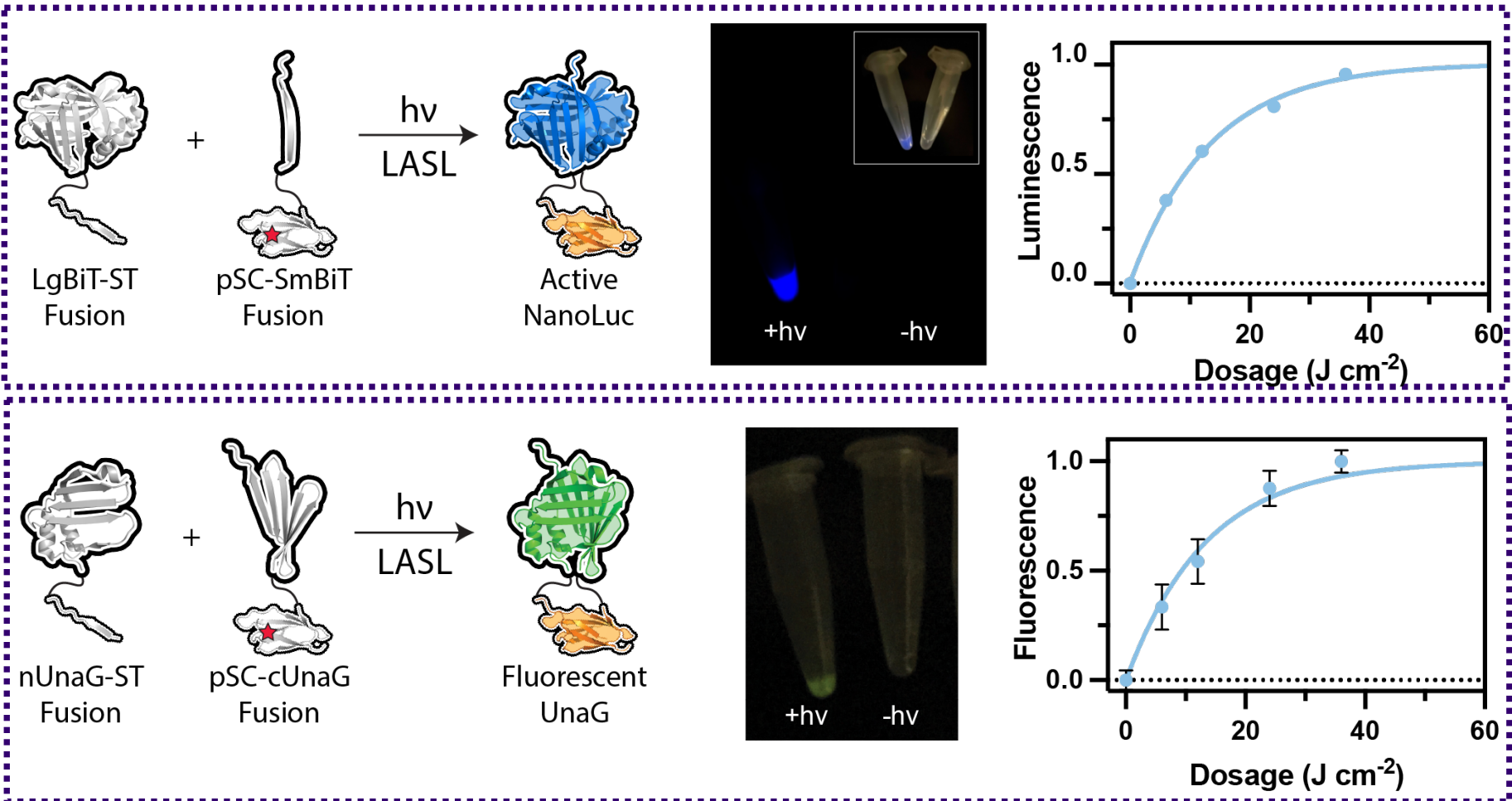


- ✓ Genetically encoded
- ✓ Functional protein activation in living cells
- ✓ Micrometre-scale patterning resolution in four dimensions
- ✓ Rapid and irreversible activation
- ✓ Covalent and stable product
- ✓ Versatile plug-and-play approach



Munoz-Robles, B.G.\*, Ruskowitz, E.R.\*, Strange, A.C., Butcher, C.H., Kurniawan, S., Filteau, J.R. & DeForest, C.A. Spatiotemporal Functional Assembly of Split Protein Pairs through a Light-Activated SpyLigation. *Nature Chemistry* (2023) \*Equal contribution

# Background: Modeling Photokinetics



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# Use Case I: PhotokineticAnalysis()

**Use Case I:** Theoretical photokinetic data:

- The user can input theoretical x values (in any units) and kinetic rate constant (unit must match x value unit) to obtain expected y values when input into the equation:

## Design:

- **PhotokineticAnalysis.check()**
  - a. **Purpose:** checks that the inputs for the calculate\_theoretical function are correct
- **PhotokineticAnalysis.calculate\_theoretical()**
  - a. **Purpose:** Calculates theoretical photouncaging values using the following first order kinetic equation for photouncaging:  

$$Y = Y_o + (\textit{plateau} - Y_o)(1 - \exp(-k * x))$$
  - a. **Input:**
    - i. x values
    - ii. Kinetic constant
  - b. **Output:**
    - i. Kinetic rate constant with standard deviation
    - ii. Table of x and corresponding y values (normalized to 1)
    - iii. Graph of theoretical data

# PhotokineticAnalysis.calculating\_theoretical()

```
def calculate_theoretical(self, display = False):
    """
    Calculates theoretical photokinetics

    Args:
    -----
    x: x-values to be calculated
    k: photokinetic rate constant

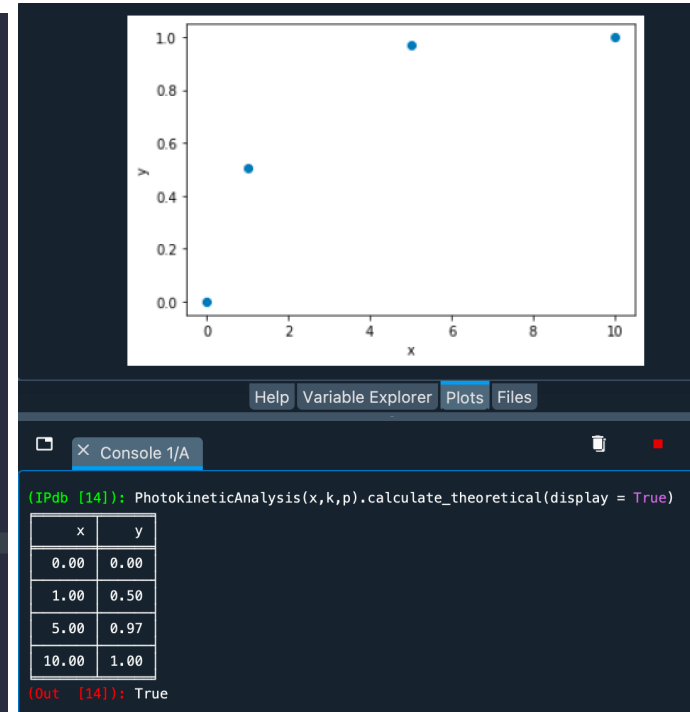
    Returns:
    -----
    A scatter plot of the values plotted as well as the output data in a table.

    """
    if all([isinstance(item, np.int64) for item in self.x_value]) and type(self.k_value) == float:
        column_headers = ["x", "y"]

        y = 1 - np.exp(-self.k_value*self.x_value)

        merged_array = np.array([self.x_value,y]).T

        output = tabulate(merged_array , column_headers, tablefmt="fancy_grid", floatfmt = ".2f")
        if display == True:
            Displayed = True
            figure1, axis1 = plt.subplots(1, 1)
            plt.scatter(self.x_value,y)
            plt.xlabel("x")
            plt.ylabel("y")
            print(output)
        else:
            Displayed = None
        return Displayed
```



This is very useful to see what the expected curve/data should look like prior to running an experiment. Sometimes in the DeForest lab we run two to three time points instead of a larger range and it is good to anticipate what the next value should be, and if the experimental data does not match, typically this indicates there is a problem with the experimental set up.

# TestPhotokineticAnalysis

```
class TestPhotokineticAnalysis(unittest.TestCase):

    def setUp(self):
        #Correct x and k input
        x = np.array([0,1,5,10])
        k = 0.7

        #Incorrect x input
        x1 = np.array([0,1,'hello',10])
        k1 = 0.7

        #Incorrect kinetic input
        k2 = 1

        #excel sheet containing experimental data
        p = "example_2.xlsx"

        self.entry = PhotokineticAnalysis(x,k,p)
        self.entry1 = PhotokineticAnalysis(x1,k1,p)
        self.entry2 = PhotokineticAnalysis(x, k2,p)
        self.entry3 = PhotokineticAnalysis(x1,k2,p)

    def test_check(self):
        result = self.entry.check()
        result1 = self.entry1.check()
        result2 = self.entry2.check()
        result3 = self.entry3.check()
        self.assertEqual(result, "Valid input")
        self.assertEqual(result1, "Invalid x input")
        self.assertEqual(result2, "Invalid k input")
        self.assertEqual(result3, "Invalid x input and k input")

    def test_theoretical(self):
        result_theoretical = self.entry.calculate_theoretical(display = True)
        result_theoretical2 = self.entry.calculate_theoretical(display = False)
        self.assertTrue(result_theoretical)
        self.assertIsNone(result_theoretical2)

    def test_experimental(self):
        result_experimental = self.entry.calculate_experimental(graph = True)
        result_experimental1 = self.entry.calculate_experimental(graph = False)
        self.assertTrue(result_experimental)
        self.assertIsNone(result_experimental1)
```

## Use Case II: PhotokineticAnalysis()

**Use Case II:** Experimental photokinetic data:

- If the user wants to obtain a graph and kinetic rate constant for their experimental data, the user can input their experimental time or light dosage conditions and corresponding y-values. This is useful as the calculation can be done very quickly and does not require the user to know how to interface with GraphPad, which can be tricky, or if they do not have access to the computer with GraphPad this is an alternative.

### Design:

- **PhotokineticAnalysis.calculate\_experimental()**
  - a. **Purpose:** Calculates the photouncaging constant  $k$  using the first order equation from above using raw data inputted from user as an excel file. It uses `scipy.optimize.curve_fit` to calculate the  $k$  value.
  - b. **Input:**
    - i. Excel file, formatted such that the first column is labelled with the x value and the corresponding y values titles labelled value
  - c. **Output:**
    - i. Table of x and y values
    - ii. Kinetic constant
    - iii. Data normalized and plotted in a scatter plot

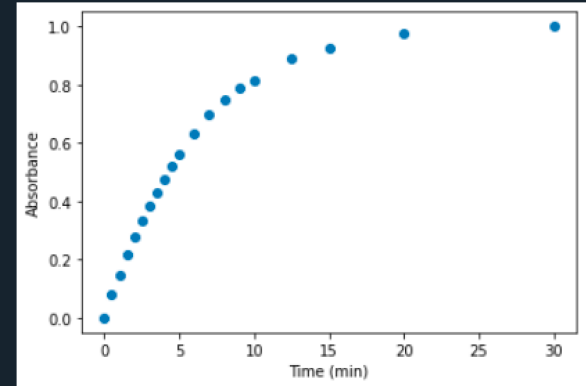
# PhotokineticAnalysis.calculating\_experimental

```
def calculate_experimental(self, graph = False):
    """
    Calculates the kinetic rate constant from experimental photokinetic data

    Args:
    -----
    x: excel sheet containing initial x and y data with headers
    k: estimated photokinetic rate constant

    Returns:
    -----
    A scatter plot of the values plotted as well as the output data in a table.
    """
def exp_association(xx, k):
    """
    exponential association equation used to fit the data
    """
    return 1-np.exp(-k*xx)
try:
    df = pd.read_excel(self.file_name)
    labels = list(df.columns.values)
    x_array = df[labels[0]]
    y_array = df[labels[1]]
    column_headers = [labels[0], labels[1]]
    popt, pcov = scipy.optimize.curve_fit(exp_association, x_array, y_array)
    k_rate = '%5.3f' %tuple(popt)
    perr = np.sqrt(np.diag(pcov))
    merged_array2 = np.array([x_array,y_array]).T
    output2 = tabulate(merged_array2, column_headers, tablefmt="fancy_grid", floatfmt = ".2f")
    print("The kinetic constant is ", k_rate, u"\u00B1", '%5.3f' %perr)
    if graph == True:
        Data = True
        print(output2)
        figure, axis = plt.subplots(1, 1)
        plt.scatter(x_array,y_array)
        plt.xlabel(labels[0])
        plt.ylabel(labels[1])
    else:
        Data = None
except FileNotFoundError:
    print('File does not exist or the title is incorrect. Verify file is in the format: title.xlsx')
    Data=None

return Data
```



Help Variable Explorer Plots Files

Console 1/A

```
(IPdb [13]): PhotokineticAnalysis(x,k,p).calculate_experimental(graph = True)
The kinetic constant is 0.167 ± 0.001
```

Time (min)	Absorbance
0.00	0.00
0.50	0.08
1.00	0.15
1.50	0.22
2.00	0.28
2.50	0.33
3.00	0.39
3.50	0.43
4.00	0.47

IPython Console History



## Use Case III: ChemotaxisSimulation()

**Use Case III:** Modeling 2D cell migration in response to a stimulus:

- If the user wants to visualize 2D cell migration in response to different conditions such as cell type (cell types have varying characteristics, which can be modeled by changing the cell proliferation, death, movement rate inputs), size of the experiment, number of cells they are starting with and their orientation (e.g. for an experimental scratch assay usually cells are confluent on two sides of 2D area with no cells at the center, and their migration into the center is tracked. Another example are transwell migration assays.

### Design:

- **ChemotaxisSimulation.cell\_movement()**
  - Purpose:** Simulates cell migration using a stochastic agent based model designed by Fadai et al. 2019.
    - Input:**  $n, m, CC, V, rm, rp, rd, tf, C\_start, C\_end, rho_x$
    - Output:** Matrix consisting of cell location using a heat map, where yellow equates to occupancy by a cell and purple equates to an empty compartment
- **ChemotaxisSimulation.()**
  - Purpose:** Calculates the photouncaging constant  $k$  using the first order equation from above using raw data inputted from user as an excel file. It uses `scipy.optimize.curve_fit` to calculate the  $k$  value.
  - Input:**
    - Title of the video generated
  - Output:**
    - Movie of cell migration over time

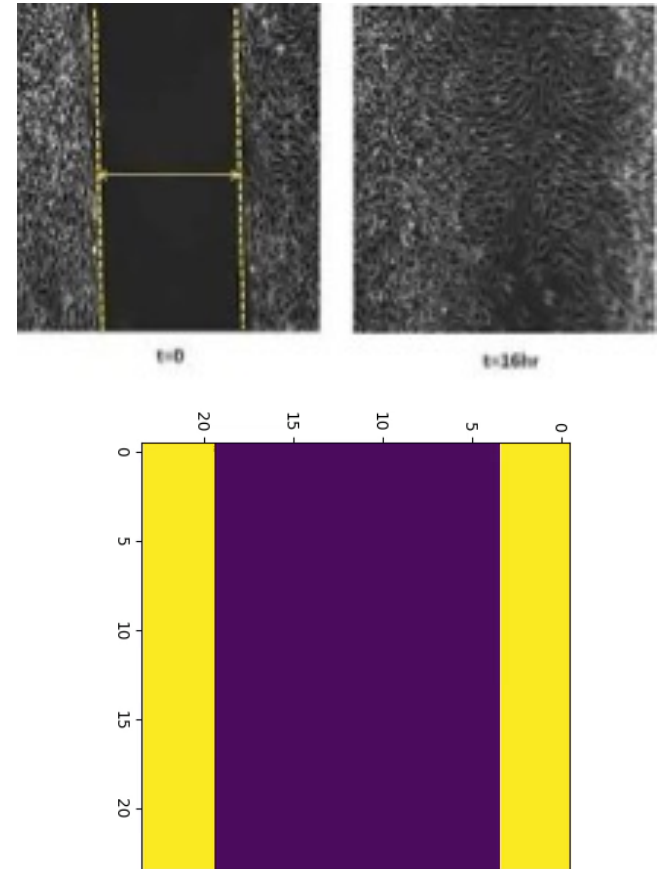
# ChemotaxisSimulation.simulate()

## Input:

- V: compartment size
- rm: motility rate between 0-1, where 1 equates to faster cells
- rp: proliferation rate between 0-1, where 1 equates to max proliferation
- rd: death rate between 0-1, where 1 equates to max death rate
- tf: final dimensionless time
- C\_start: if there is a chemotactic variable applied, when is it applied.
- C\_end: if there is a chemotactic variable applied, when does it end.
- rhox: how the chemotactic variable is applied over space (i.e gradient, etc)

## Output:

- Graph of cell position



# TestChemotaxisSimulation

```

class TestChemotaxisSimulation(unittest.TestCase):

    def setUp(self):

        #correct inputs
        n=24 #lattice nodes in x-direction
        m=24 #lattice nodes in y-direction
        CC=np.zeros((m,n)) #inital array of the area
        CC[:,0:4]=1 #Initial condition of scratch assay
        CC[:,20:24]=1 #Initial condition of scratch assay
        V=1 #one cell per compartment
        rm=1 #motility
        rp=0.4 #proilferation
        rd=rp*.01 #death
        tf=10 #unntiless time
        C_start = 0
        C_end = tf
        rhox=np.zeros((m,n)) #no bias

        #no cells
        self.CC2=np.zeros((m,n)) #inital array of the area

        self.entry = ChemotaxisSimulation(n,m,CC,V,rm,rp,rd,tf,C_start,C_end,rhox)
        self.entry1 = ChemotaxisSimulation(n,m,self.CC2,V,rm,rp,rd,tf,C_start,C_end,rhox)

    def test_cell_movment(self):
        result = self.entry.cell_movement()
        result1 = self.entry1.cell_movement()
        self.assertIsNotNone(result)
        #self.assert_array_equal(result1==self.CC2)

    def test_simulate(self):
        result = self.entry.simulate("fig1.gif")
        file_exists = os.path.isfile('fig1.gif')
        self.assertIsNone(result)
        self.assertTrue(file_exists)
        os.remove('fig1.gif')

if __name__ == '__main__':
    unittest.main()

```

# Project Structure



Photosimulator

Public



Pin



Unwatch 1



main



1 Branch



0 Tags



Go to file

t

Add file

<> Code



**bmunozro1** [Update README.md](#)

9f8c2c1 · 11 hours ago



15 Commits



docs

Create \_\_init\_\_.py

11 hours ago



src

Add files via upload

11 hours ago



test

[Add files via upload](#)

11 hours ago



.gitignore

Initial commit

11 hours ago



LICENSE

Initial commit

11 hours ago



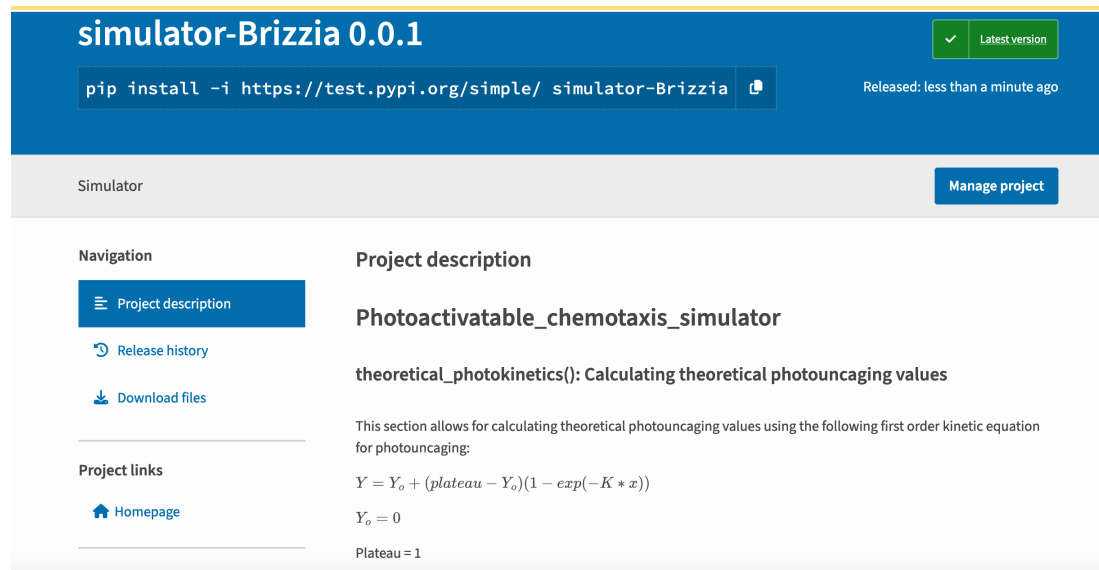
README.md

Update README.md

11 hours ago

# Lessons Learned/Future Outlook

- I can download github repository but not push changes,
- Make package of final products (used test.pypi to test one of the components and it did work. Unittest does run but need to verify that it runs properly when placed in a different folder)



The screenshot shows the PyPI page for the package **simulator-Brizzia 0.0.1**. At the top, there is a blue header with the package name and version. To the right of the header, there is a green button labeled "Latest version" and a status "Released: less than a minute ago". Below the header, there is a search bar containing the command `pip install -i https://test.pypi.org/simple/ simulator-Brizzia`. The main content area is divided into two columns. The left column contains a "Navigation" section with links to "Project description", "Release history", and "Download files", and a "Project links" section with a link to the "Homepage". The right column contains a "Project description" section with the title **Photoactivatable\_chemotaxis\_simulator** and a description of the `theoretical_photokinetics()` function, which calculates theoretical photouncaging values using a first-order kinetic equation. The equation is 
$$Y = Y_o + (plateau - Y_o)(1 - \exp(-K * x))$$
 with initial conditions  $Y_o = 0$  and  $Plateau = 1$ .