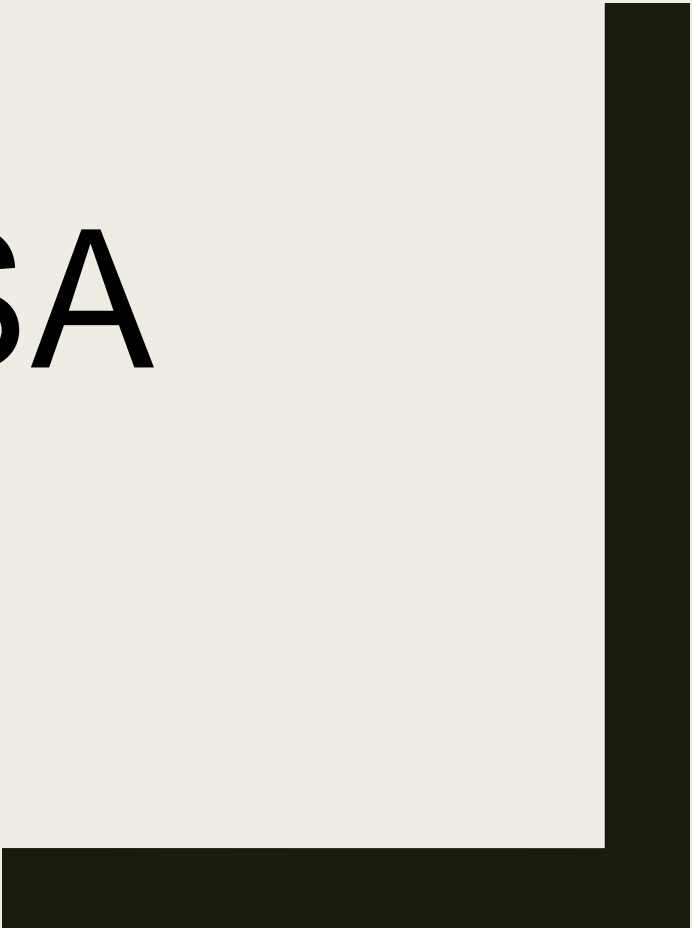


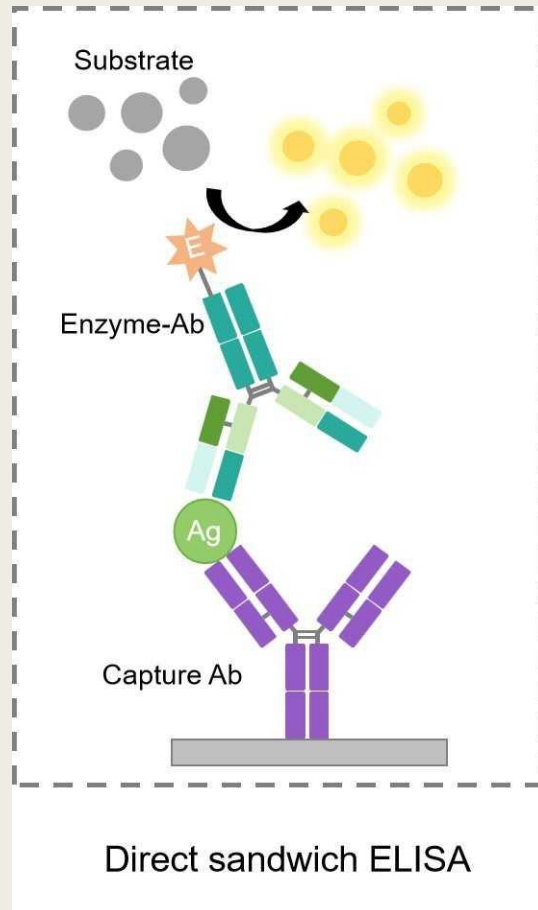


# model\_ELISA

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BIOEN 537



# Background



<https://www.antibody-creativebiolabs.com/sandwich-elisa-with-streptavidin-biotin-detection.htm>

- An **enzyme-linked immunosorbent assay** or ELISA is used to identify and/or quantify proteins.
- There are multiple different varieties of ELISAs, however one of the most commonly used is the **direct sandwich ELISA**.
- Given its detection abilities, it is highly useful for diagnosing various diseases from immune system disorders to infections.

ELISA development and optimization requires researchers to perform benchtop experiments that are often cumbersome and necessitate many experiments

Problem

This tool allows the user to mimic sandwich ELISA component relationships with ease

Solution

# User cases:

## Use case #1

Identifying which components are in excess

## Use case #2

Seeing how temperature changes affect each step by altering kinetic constants

## Use case #3

Determining when steady state occurs to find minimum reaction time

# Users:

## Users #1

### For lab use:

Researchers with a general knowledge of sandwich ELISAs and assay development.

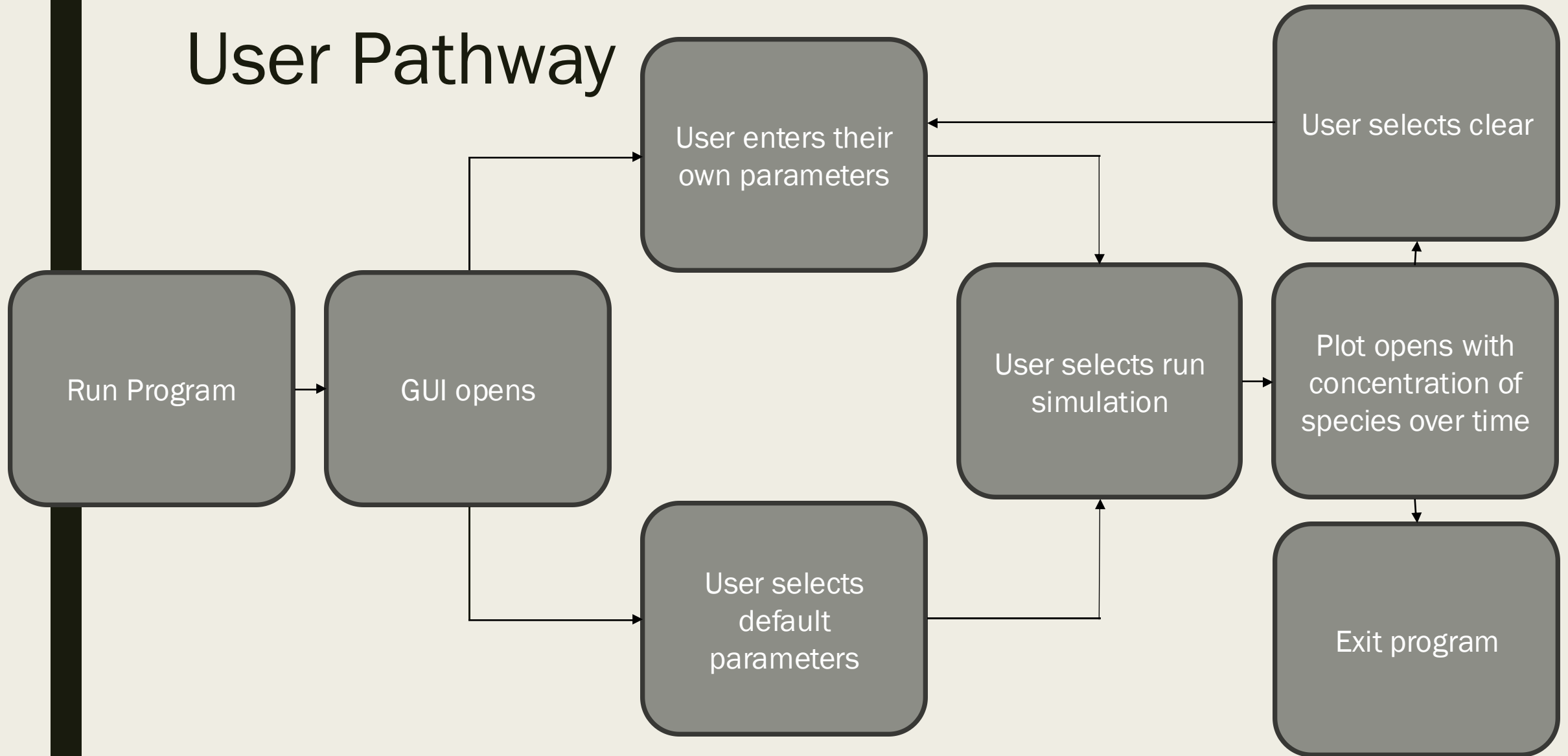
Generally, these users are predicted to have programming experience in python.

## User #2

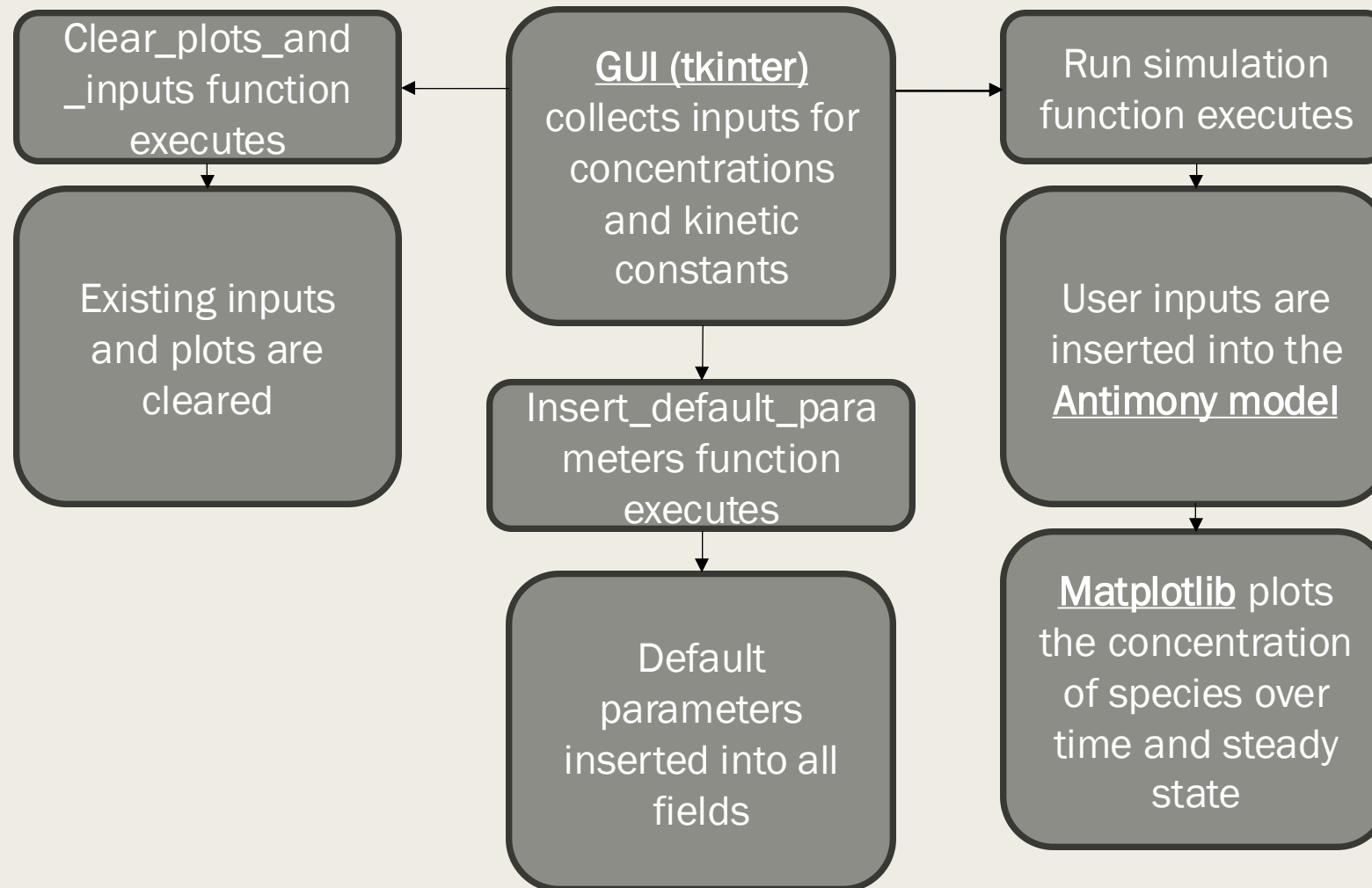
### For education purposes:

Users with minimal python knowledge who want to use the package to learn more about how an ELISA works.

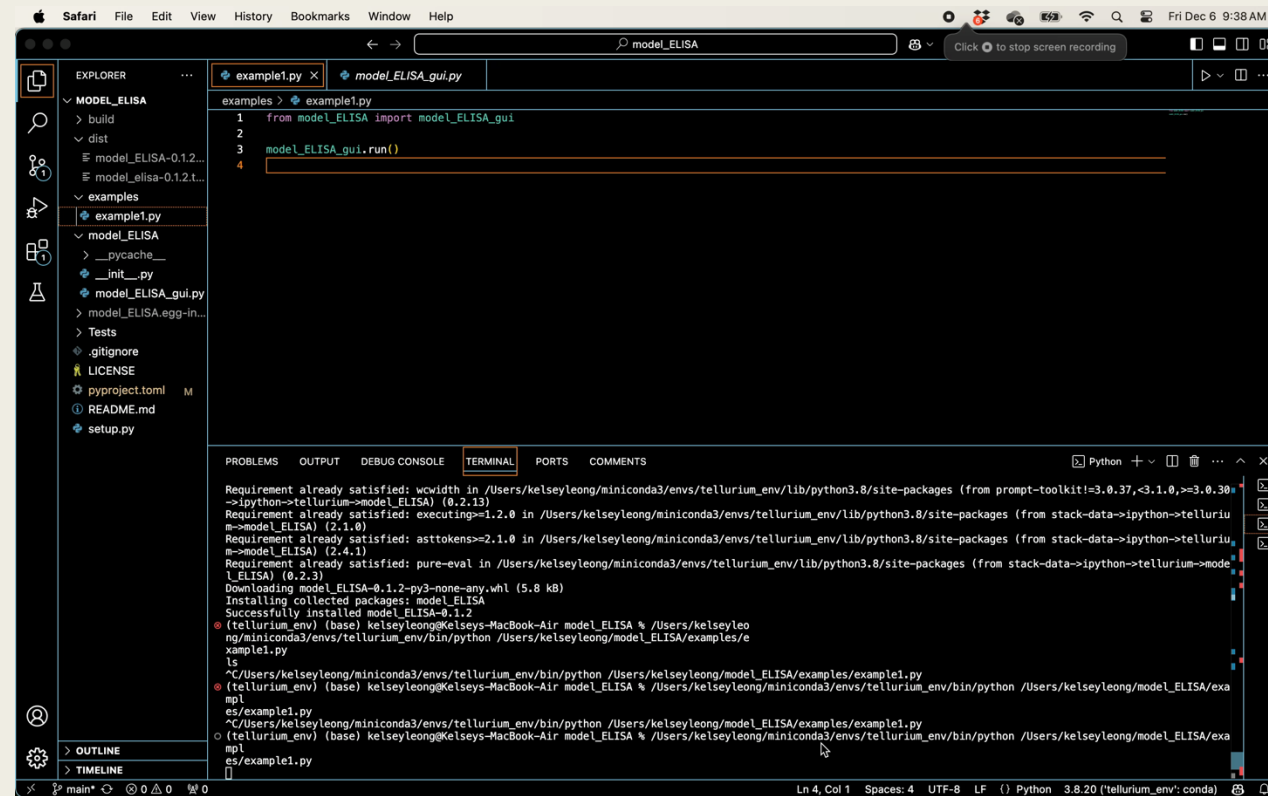
# User Pathway



# Design



# Demo



The screenshot shows a web browser window with the address bar displaying "model\_ELISA". The browser's address bar also shows a "Click to stop screen recording" button. The main content area displays a JupyterLab interface. On the left, the "EXPLORER" sidebar shows a file tree with the following structure:

- MODEL\_ELISA
  - build
  - dist
  - model\_ELISA-0.1.2...
  - model\_elisa-0.1.2.t...
  - examples
    - example1.py
  - model\_ELISA
    - \_\_pycache\_\_
    - \_\_init\_\_.py
    - model\_ELISA\_gui.py
  - model\_ELISA.egg-in...
  - Tests
  - .gitignore
  - LICENSE
  - pyproject.toml
  - README.md
  - setup.py

The main editor area shows the code for "example1.py":1 from model\_ELISA import model\_ELISA\_gui
2
3 model\_ELISA\_gui.run()
4

Below the code editor, the "TERMINAL" tab is active, displaying the following output:

```
Requirement already satisfied: wcwidth in /Users/kelseyleong/miniconda3/envs/tellurium_env/lib/python3.8/site-packages (from prompt-toolkit!=3.0.37,<3.1.0,>=3.0.30
->ipython->tellurium->model_ELISA) (0.2.13)
Requirement already satisfied: executing>=1.2.0 in /Users/kelseyleong/miniconda3/envs/tellurium_env/lib/python3.8/site-packages (from stack-data->ipython->telluriu
m->model_ELISA) (2.1.0)
Requirement already satisfied: asttokens>=2.1.0 in /Users/kelseyleong/miniconda3/envs/tellurium_env/lib/python3.8/site-packages (from stack-data->ipython->telluriu
m->model_ELISA) (2.4.1)
Requirement already satisfied: pure-eval in /Users/kelseyleong/miniconda3/envs/tellurium_env/lib/python3.8/site-packages (from stack-data->ipython->tellurium->mode
l_ELISA) (0.2.3)
Downloading model_ELISA-0.1.2-py3-none-any.whl (5.8 kB)
Installing collected packages: model_ELISA
Successfully installed model_ELISA-0.1.2
(tellurium_env) (base) kelseyleong@Kelseys-MacBook-Air model_ELISA % /Users/kelseyleo
ng/miniconda3/envs/tellurium_env/bin/python /Users/kelseyleong/model_ELISA/examples/e
xample1.py
ls
^C/Users/kelseyleong/miniconda3/envs/tellurium_env/bin/python /Users/kelseyleong/model_ELISA/examples/example1.py
(tellurium_env) (base) kelseyleong@Kelseys-MacBook-Air model_ELISA % /Users/kelseyleong/miniconda3/envs/tellurium_env/bin/python /Users/kelseyleong/model_ELISA/exa
mple1.py
^C/Users/kelseyleong/miniconda3/envs/tellurium_env/bin/python /Users/kelseyleong/model_ELISA/examples/example1.py
(tellurium_env) (base) kelseyleong@Kelseys-MacBook-Air model_ELISA % /Users/kelseyleong/miniconda3/envs/tellurium_env/bin/python /Users/kelseyleong/model_ELISA/exa
mple1.py
```

The status bar at the bottom indicates the current file is "main\*", the cursor is at line 4, column 1, and the file is encoded in UTF-8.

Github repo: [https://github.com/kml5gb/model\\_ELISA.git](https://github.com/kml5gb/model_ELISA.git)

The screenshot shows the GitHub repository page for **model\_ELISA** by user **kml5gb**. The repository is public and has 1 branch and 0 tags. It has 0 forks and 0 stars. The repository description is: "Creates a GUI which simulates the mechanisms of a direct Sandwich ELISA".

The file list shows the following files and their commit history:

File	Commit Message	Time Ago
Tests	Updates to create package	4 hours ago
docs	Add files via upload	3 hours ago
examples	Updates to create package	4 hours ago
model_ELISA	Updates to create package	4 hours ago
.gitignore	Initial commit	8 hours ago
LICENSE	Initial commit	8 hours ago
README.md	Update README.md	5 hours ago
pyproject.toml	Updates to create package	4 hours ago
setup.py	Updates to create package	4 hours ago

The README section is visible, showing the title **model\_ELISA** and the description: "Creates a GUI which simulates the mechanisms of a direct Sandwich ELISA". Below this, it states: "An enzyme-linked immunosorbant assay or ELISA is used to identify and/or quantify proteins. Given its detection capability, it is highly useful for diagnosing various diseases from immu-".

The right sidebar shows the repository's activity and statistics:

- About:** Creates a GUI which simulates the mechanisms of a direct Sandwich ELISA. Includes links to Readme, MIT license, and Activity.
- Releases:** No releases published. Link: [Create a new release](#).
- Packages:** No packages published. Link: [Publish your first package](#).
- Languages:** Python 100.0%.



# Lessons learned and future work

## Lessons learned

- First time creating a GUI -> tkinter
- Gained more experience working with Tellurium
- First time using unittest to test a program
- Learned proper code documentation
- Gained more experience debugging

## Future work

- Add more advanced kinetics/variables to more closely mimic the relationships
- Expand the simulation to more types of ELISAs
- Add additional functionality to the GUI as I continue to use it in my lab
- Add more functionality in case of user errors