

Python Hackathon

UCLA QCBio
Collaboratory

Thiago Mosqueiro
Renaud Dessalles
Simon Mitchell

Our goal for today

- Use this time to **code together** and **exchange ideas and experiences** among the participants
- Learn more about **how Python is used in real-life projects** applied to bio-related fields
- **Collectively solve a set of projects** of interest to the QCBio community
- Collaboratory fellows will be available to help during the development of the projects

Schedule for today

Time	Event
9:00 - 9:30	Initial set ups and chat
9:30 - 10:00	Quick presentation about the Hackathon and overview of the problems
10:00 - 12:30	First coding session
12:30 - 2:00pm	Lunch while coding
2:00 - 4:00	Second coding session
4:00 - 4:30	Final remarks and discussions about the future
4:30 - 5:00	Summary of what was done in each project

Schedule for today

Time	Event
9:00 - 9:30	Initial set ups and chat
9:30 - 10:00	Quick presentation about the Hackathon and overview of the problems
10:00 - 12:30	First coding session
12:30 - 2:00pm	Lunch while coding
2:00 - 4:00	Second coding session
4:00 - 4:30	Final remarks and discussions about the future
4:30 - 5:00	Summary of what was done in each project

The material is currently available on
https://github.com/thmosqueiro/UCLA-Collaboratory_Hackathon/

or <https://goo.gl/c4LtW6>

Python Hackathon

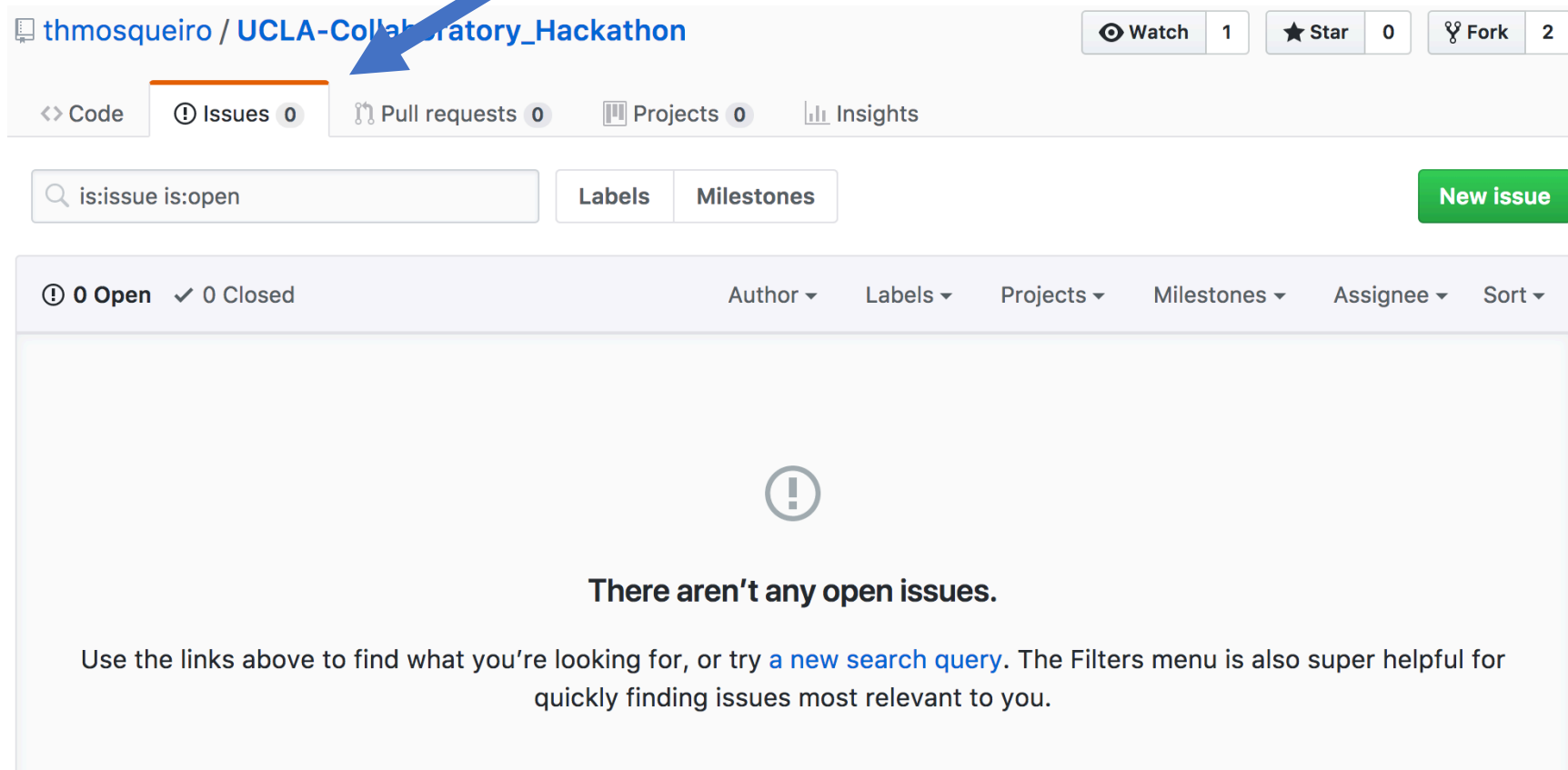
UCLA QCBio
Collaboratory

Many of you who enjoyed the Collaboratory workshops have requested the opportunity to continue improving your computational skills beyond the workshop. We're pleased to announce a new event for those with interest in computational and quantitative methods in biology: **a Hackathon dedicated to solving problems of interest to our community**, using Python.

Table of contents

- [Where? When?](#)
- [Registration and contact](#)
- [Schedule](#)
- [Coding problems](#)
- [Who is this Hackathon intended for?](#)
- [Frequently asked questions](#)

If you have some material you want to share with everyone else, use the **Issues** page on the GitHub.



The screenshot shows the GitHub interface for the repository **thmosqueiro / UCLA-Collaboratory_Hackathon**. The repository has 1 Watch, 0 Stars, and 2 Forks. The navigation bar includes links for Code, Issues (0), Pull requests (0), Projects (0), and Insights. The 'Issues' tab is selected and highlighted with a blue arrow. Below the navigation bar, there is a search bar with the query 'is:issue is:open', buttons for 'Labels' and 'Milestones', and a green 'New issue' button. The main content area shows a summary of issues: '0 Open' and '0 Closed'. Below this, there is a large exclamation mark icon and the text 'There aren't any open issues.' followed by a helpful message: 'Use the links above to find what you're looking for, or try a new search query. The Filters menu is also super helpful for quickly finding issues most relevant to you.'

Projects

1- Analysis of calcium imaging

- **Goal:**

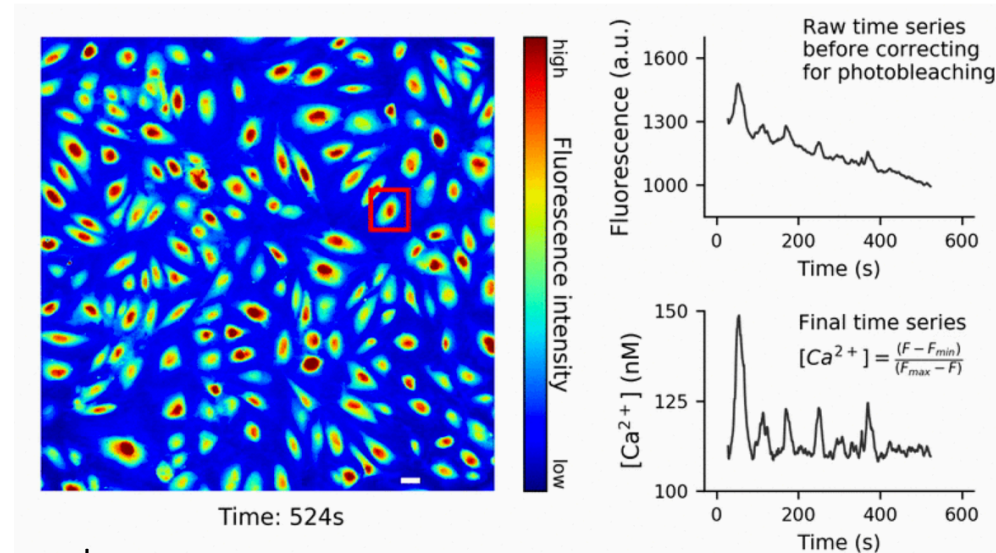
A Jupyter notebook that summarizes how we extracted calcium time series

- **Technical Challenges:**

- Handling images and videos with python
- Dealing with photobleaching and estimating calcium concentration
- Applying regression on a set of time series
- Extracting statistics based on a set of cells

- **Dataset:**

- We will use a dataset used in a recent publication by Julia Mack @ Arispe Lab



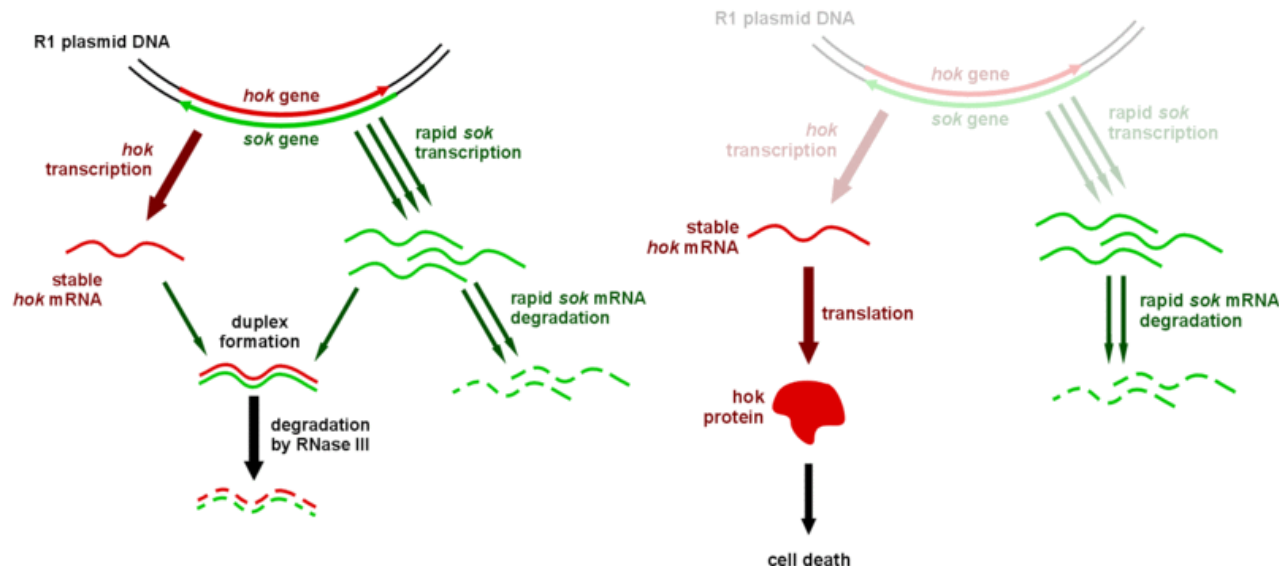
2- Gene expression with Gillespie algorithm

- **Goal:**

Using the Hok/Sok system as an example, we will explore the Gillespie algorithm

- **Technical Challenges:**

- Create a model that represents a real biological system.
- Learn how to implement the Gillespie algorithm
- Determine the parameters for the simulation



3- Automation of pipeline

- **Goal:**

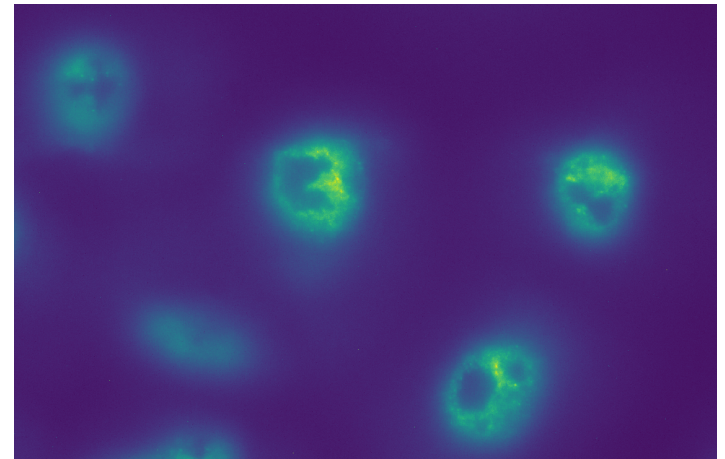
Automate a pipeline for image processing using efficient use of parallel resources and memory management.

- **Technical Challenges:**

- Basics of parallel processing in Python
- Automating the analysis of batches of large images
- Good practices for a memory efficient implementation of parallel processing in Python

- **Dataset:**

- We will use a dataset currently being developed by Rob Foreman @ Wollman Lab



4- Automated job submissions

- **Goal:**

Write a script that prepares and sends sequences to SignalP server, an online service that predicts cleavage sites of signal peptides.

- **Technical Challenges:**

- Automating genomics analyses based on online applications
- Dealing with a bottleneck when analyzing a large dataset
- Learning how to construct web crawlers

- **Dataset:**

- *Chlamydomonas reinhardtii*'s
- proteome, available on the Genome Portal hosted by the Joint Genome Institute

SignalP 4.1 Server

SignalP 4.1 server predicts the presence and location of signal peptide cleavage sites in Gram-positive prokaryotes, Gram-negative prokaryotes, and eukaryotes. The server also provides a signal peptide/non-signal peptide prediction based on a combination of several algorithms.

View the [version history](#) of this server. All the previous versions are available on line, for comparison.

NEW (August 2017): A book chapter on SignalP 4.1 has been published:

Predicting Secretory Proteins with SignalP

Henrik Nielsen

In Kihara, D (ed): *Protein Function Prediction* (Methods in Molecular Biology vol. 161)

doi: [10.1007/978-1-4939-7015-5_6](#)

PMID: [28451972](#)

5- Integrating camera and arduino

- **Goal:**

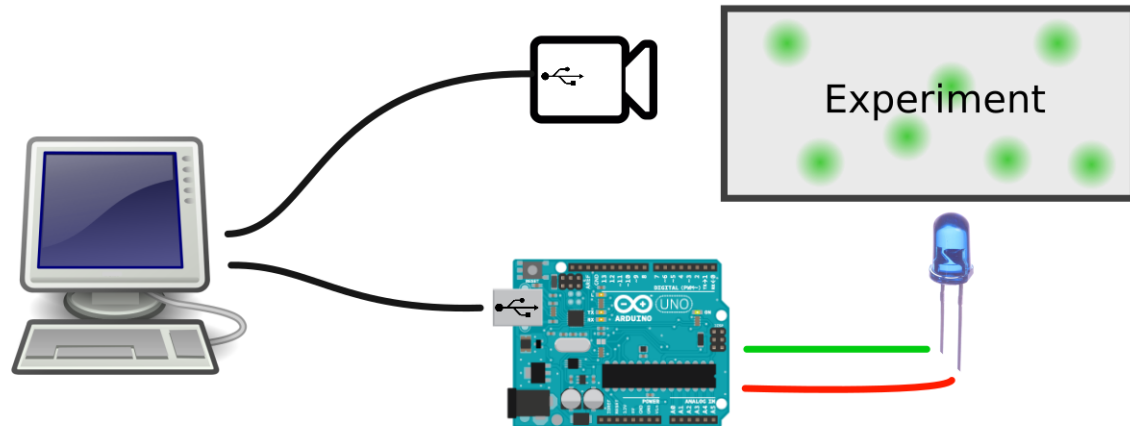
Construct an acquisition system that integrates a camera with an LED array controlled by an arduino.

- **Technical Challenges:**

- Use Python to synchronize an LED array and a camera
- Writing very simple code for arduino
- Control a camera from Python

- **Dataset:**

- We will use the camera and arduino to capture data during the Hackathon



Let's get started!