

GUI for PluMA: Plugin-Based Microbiome Analysis

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Problem

Many of PluMA's users aren't developers, therefore it can be a difficult process to download plugins from the pool and forming the pipeline. The GUI for PluMA was developed in order to facilitate this process, and make the user experience as easy as possible, for both skilled and unskilled users. My project's goal was to establish a Graphical User Interface, where users did not have to code anything at all from the start to finish of installing plugins to forming the pipeline.

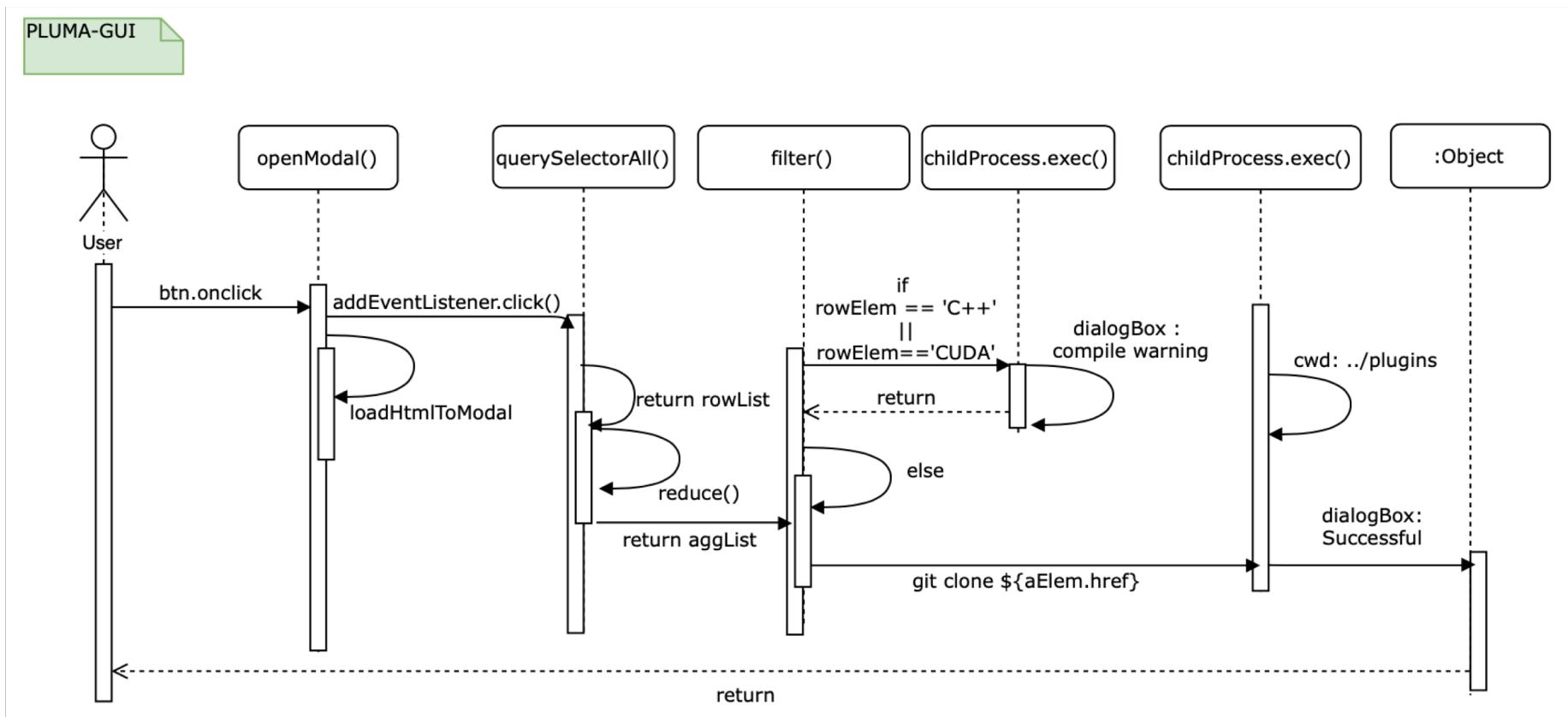
My goal as a developer was to display the plugins that have been installed, and scrape the whole plugin pool and make it accessible for users to install more plugins without ever using the command line. I also helped with the UX of the pipeline format.

Implementation

Sequence Diagram for user story #30

*As a user, I want to git clone the repo of a selected plugin inside my plugin folder in the background of my webscraping.

SEQUENCE UML DIAGRAM

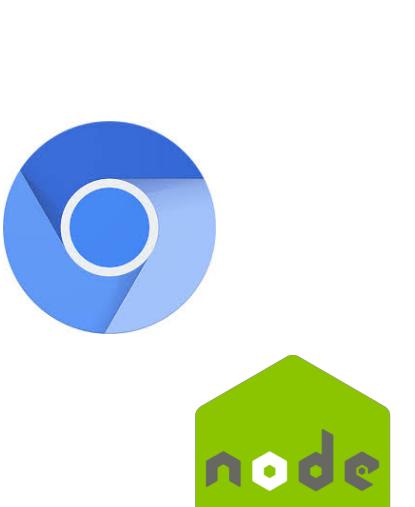


Verification

Manual Testing was performed with PluMA

Test Case ID:	When not C++ or CUDA
PluMA_30	
Purpose	To test the functionality when a user was clicking a plugin from the plugin pool to install, the plugin would not need recompiling therefore it could not be C++ or CUDA
Preconditions	The user should have a plugins folder The user should have git installed The user should have cheerio installed The user should have electron js installed
Input	Click -> git clone <plugin name> cwd: './plugins'
Expected Output	If the plugin had already be downloaded previously, a dialog box will let them know it exists already in the plugin folder. If the plugin was downloaded for the first time in the plugins folder, a dialog box well let the user know it was successful.

Technologies



HTML

5

JS

cheerio

Current System

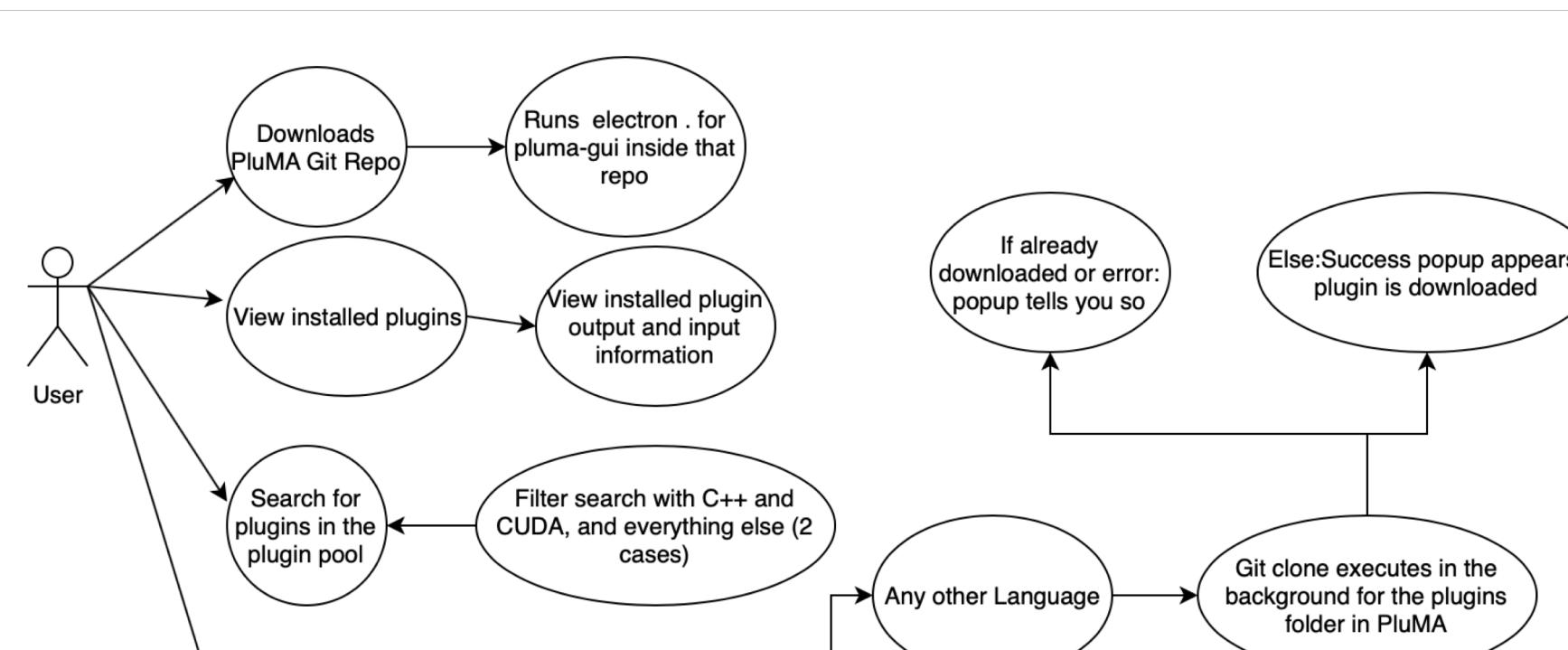
Currently, Users have to go to the BioRG website to access the plugin pool. They must also go to each plugin's GitHub and download using the terminal. It is difficult for users if they have not used the terminal or don't know any git. Users also have to form the pipelines through the terminal.

Object Design

User Story Diagram for User Story #27 & #30

- As a user, I should able to view all plugins from the pool in a popup window
- As a user, I want to git clone the repo of a selected plugin inside my plugin folder in the background of my webscraping.

USER STORY DIAGRAM



Screenshots

Installed Plugins

BIOM2CSV	Input: BIOM file,Output: CSV file
CSV2GML	Input: CSV (file to convert),Output: GML (converted file)
CSV2Tab	Input: CSV file,Output: CSV tab-delimited file
CSVAvgDeg	Input: CSV (edge weights),Output: none (average degree printed to screen)
CSVMax	Input: CSV (samples),Output: screen
CytoViz	Input: GML (network),Output: none (Cytoscape visualizes network)
Horn	Input: CSV (abundances),Output: CSV (dissimilarities)
Raup	Input: CSV (abundances),Output: CSV (dissimilarities)

Add and Install more Plugins

Search Plugin Pool			
Installed Plugins			
Name	Short Description	Language	
BIOM2CSV	Convert BIOM file to CSV	Python	AffinityPropagation
ClusterCSV2NOA	Convert CSV File to NOA	Python	CKMeans
CountTableProcessing	Converts Matrix Counts To	R	Locuster
CSV2EDTA	Converter from CSV to EDTA format	Python	MCL
CSV2GML	CSV To GML Converter	Python	
CSV2Viz	Converter from comma-separated-to-tab-delimited	Python	
CSVMerge	Merge Multiple CSV Files	Python	
CSVPad	CSV Padding	Python	
CSVPad	GML To CSV Converter	Python	
PCLC2SV	PCL To CSV (File Conversion)	Python	

PluMA	Phenotypically Central Metabolites	Python
plugins	Central Centrality (Freeman, 1979)	C++
DickeyFuller	Central Centrality (Benzl, Klymko, 2013)	Python
Raup	GPUATria (ATria, on the GPU)	CUDA
Horn	Katz	C++
CytoViz	Katz Prestige Centrality (Katz, 1953)	C++
CSVAvgDeg		
CSV2Tab		
CSVMax		
BIOM2CSV		

Requirements

Development of the project goes as following:

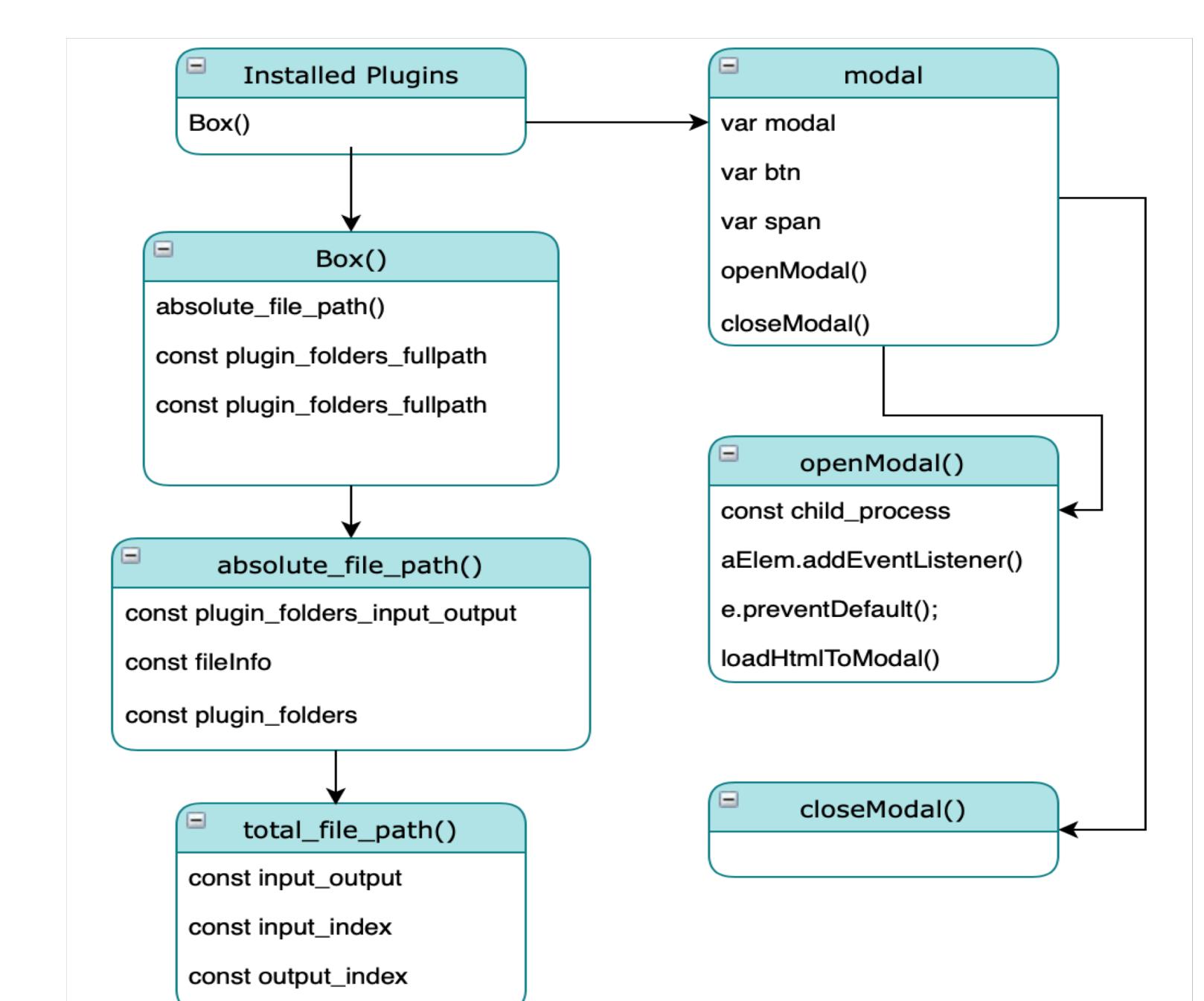
- Setting and creating the project using git and electron
- Conversion from static to dynamic interface
- Building and compiling webscraping of plugins and having the pipelines be dynamic

Integration of webscraping and installing pipelines required the following:

- Dynamically read the html from the plugins folder, in order to let the user know what pipeline has been installed
- Dynamically webscraping the BioOrg pipeline pool using cheerio
- Dynamically letting users click on plugin, if they wish to install it, and writing scripts as child processes of the event in order to execute git clone commands in the background
- Displaying a warning box if the plugin has already been installed
- Displaying a warning box should the user want to git clone a plugin written in C++ or CUDA, since the whole system of PluMA would have to be recompiled

System Design

UML CLASS DIAGRAM



Summary

- Users can use the GUI in order to view their downloaded plugins in their plugins folder
- Users can view the input and output files needed for each plugin in order to form a plugin
- Users can search the plugin pool dynamically by web scraping the website (it can be updated dynamically)
- Users can choose to download plugins without having to execute commands on the terminal

Acknowledgement

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