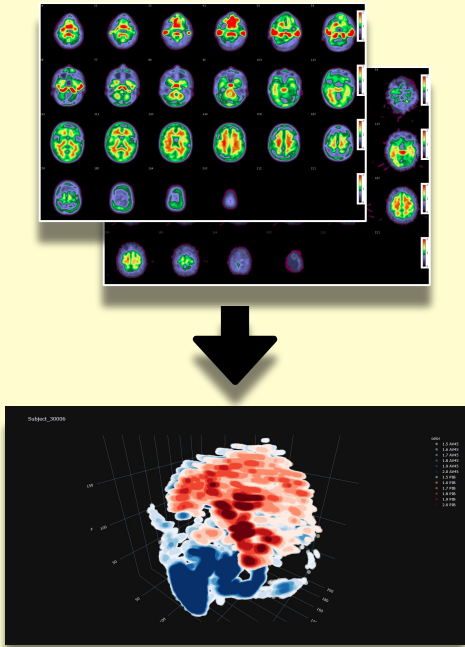


# NeuroPET-M: A Multimodal PET Scan Platform as a Novel Diagnostic Tool for Neurodegenerative Diseases

## Q1: Engineering Problem & Objectives

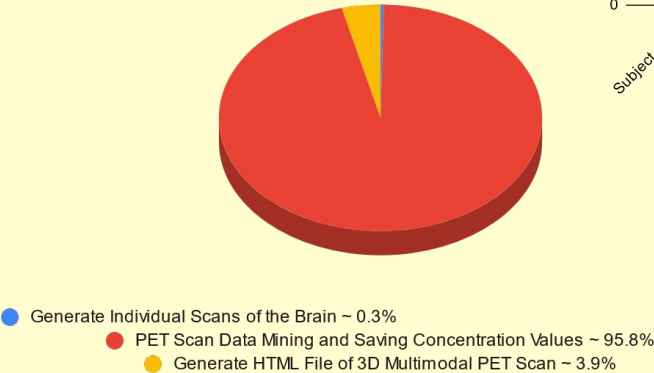
- current PET-based neuroimaging is limited to a **unimodal** technique, which prohibits the ability to diagnose complex brain conditions with multiple biomarkers, such as **bipolar disorder**
- the current medical diagnosis procedure of a complex disorder, such as bipolar disorder, can be **biased** or **inaccurate**
- NeuroPET-M* objective is to solve this problem so there is **less of a margin of error** and **earlier accurate diagnosis**
- there is little to no work reported on combining PET scans, thus my project will open a up chapter in medical diagnostic procedures
- this project's goal is: to **visualize** the location of multiple (two or more) **biomarkers** in the brain through a **software application** that takes a set of patient's **PET images** as input and relays a widget consisting of a **3D interactive brain output**



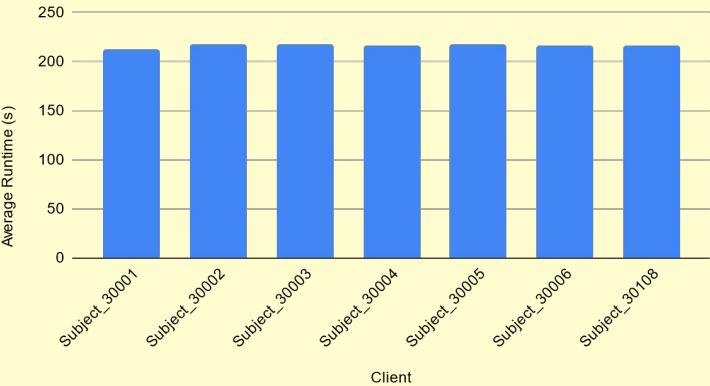
## Q3: Data Analysis & Results

- average runtime is  $\approx 216$  seconds, 108 seconds per biomarker
- standard deviation  $\approx 3.9$  seconds

Average Runtime Distribution



Average Runtime of 7 Unique Subjects



Hyperlinks to produced PET Scans

- [Subject 30001](#)
- [Subject 30002](#)
- [Subject 30003](#)
- [Subject 30004](#)
- [Subject 30005](#)
- [Subject 30006](#)
- [Subject 30108](#)

## Q2: Project Design

- Design criteria: modularized, lightweight, object-oriented, and user-friendly
- Concepts utilized:
  - 1) Multithreading - allows the program to performs multiple tasks concurrently
  - 2) Cython - superset of Python, was used to attain more than 30x speedup
  - 3) Image Processing - has the ability to extract RGB values out of the PET scan
  - 4) Data Visualization - allows us to plot the points onto the 3D coordinate system
  - 5) Colour Difference - calculate the concentration of a biomarker given a RGB value
- Optimization: 99% faster compared to the naive approach
- Procedure:
  - 1) Setup environment (initialize directory & config files)
  - 2) Input PET scans as snapshots in their according folders
  - 3) Edit thresholds of concentration for each biomarker and create a title
  - 4) Produce a NeuroPET-M Scan
    - a) Concurrent image data mining
      - i) Crop PET scans into individual scans of the brain
      - ii) Concurrently data mine each image and save concentration values
    - b) Use data visualization to create an HTML file that produces a widget
  - 5) Access scan through your respective browser

## Q4: Interpretation & Conclusions

- Improvements:
  - currently, diagnosis of neurodegenerative highly depends on PET scans and the ability for the client to visualize multiple 2D PET scans
  - due to the novelty of NeuroPET-M, clients no longer need to depend on their visualization skills, but can view the localization of biomarkers on this novel platform
- Final Takeaways:
  - NeuroPET-M* has exceeded most expectations made four months ago
  - Software is efficient, user-friendly, and visually accurate
- Next Steps:
  - Self-diagnosis tool which predicts the chances of a specific disease to occur

### Applications

Allows researchers to study and create biomarkers for complex conditions such as bipolar disorder.

Enable the development of open access PET scans used to the location of multiple biomarkers.

Practical usage at hospitals for an earlier and more accurate diagnosis to aid lives suffering from neurodegenerative diseases.