



AUTOMATED MRI DATA ANALYSIS

Mentor: Dr. Andrew Bender
Author: Garrett Collier

MSU Departments of Neurology and CMSE

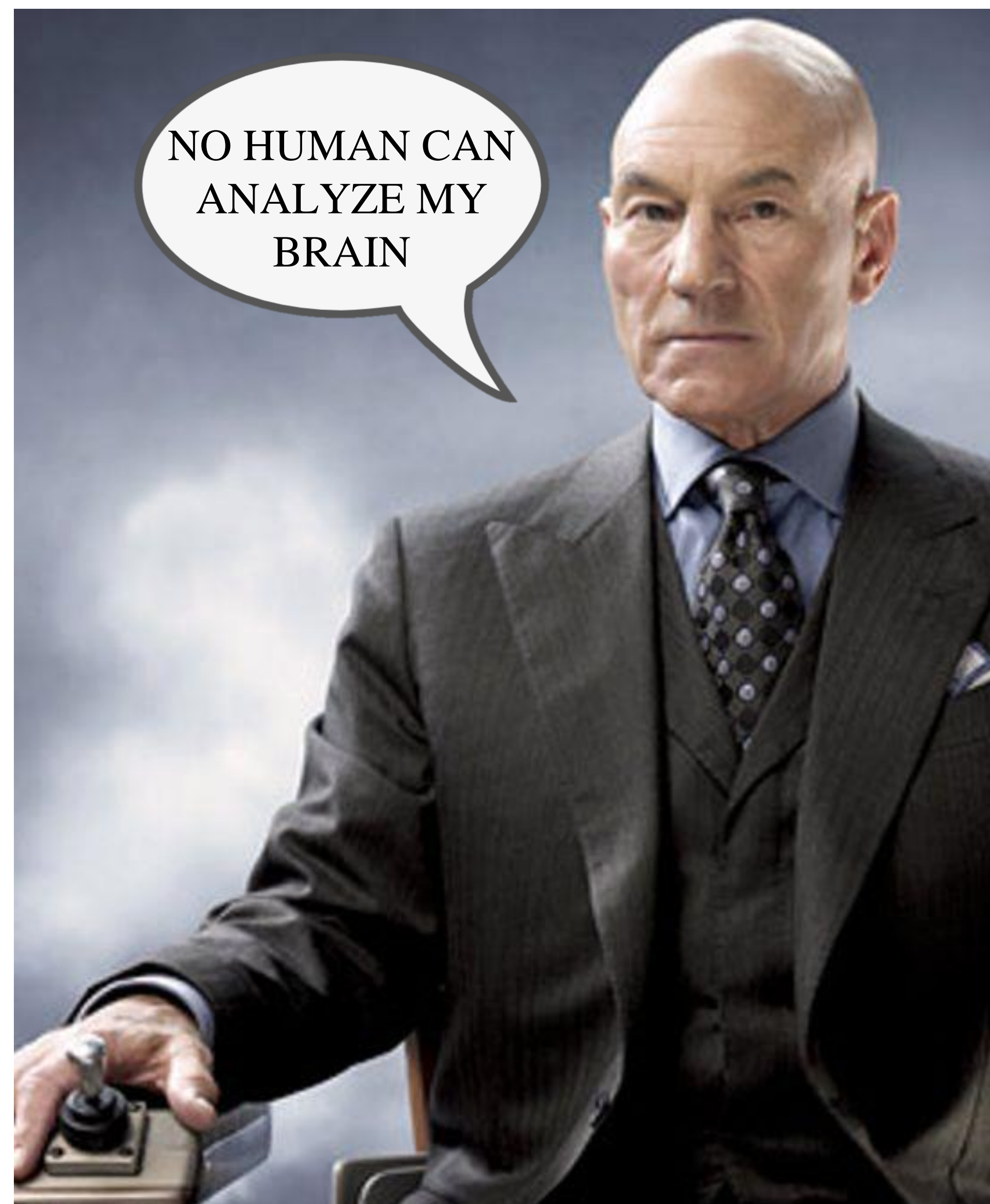


Background

With MRI Data becoming more complex and the world continuing to rely heavily on data and programming, it makes sense to **automate the process of MRI Data Analysis** using computers.

Dr. Bender, roughly 2 years ago, began the process of this automation through his creation of two **BASH** scripts.

I was tasked with creating a much more **effective** and **efficient** model of this automation, while promoting **voxel-wise throughput imaging** using **Python**.



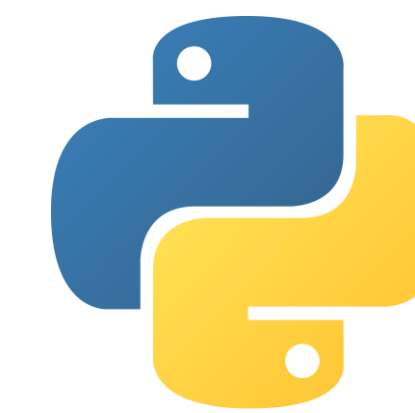
NOW WE CAN!

Objectives

Promote high **throughput voxel-wise analysis**

Enhance **Functionality** through:

- o Flexible Setup of MRI Variables
- o HPC Script Updates:
 - **Configuration file**
 - File linking



Establish **Error Checking**

Improve Output Files by **adding:**

- o **Parallel** Comparisons
- o Post Hoc Testing
- o Enhancements to Contrast Matrix
 - **Regressor and Covariates**

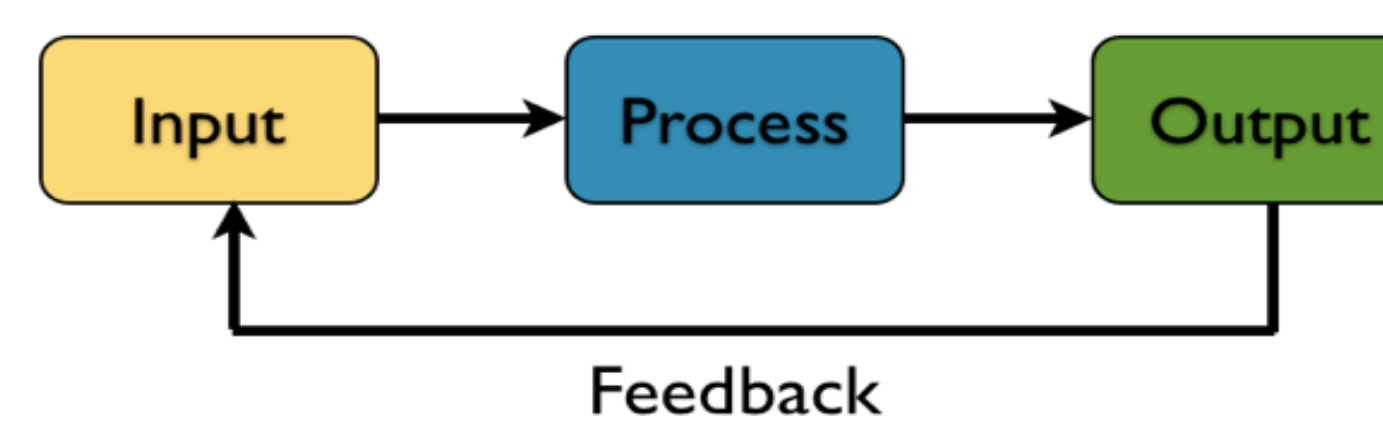


Improve **Transparency** of Reporting Data and Effects

Provide a **Universal Foundation** for Automated Data Analysis

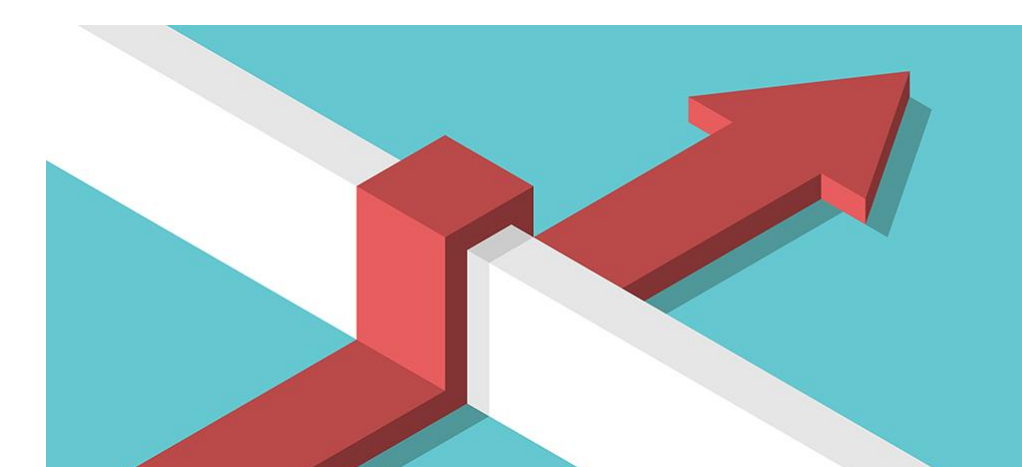
Methods

- o **Evaluate** initial BASH script methods
- o Translate **BASH** commands to **Python**
- o New **feature development** in consultation
- o Test and **bug fixing** with user feedback
- o **Deploy** to Research Group for **Testing**
- o **Maintain** scripts and **Develop** Documentation



Challenges Overcome

- o **Limited knowledge** in:
 - MRI Data/Neuroscience
 - BASH coding language
- o **Different versions** of:
 - Python
 - HPC modules



Conclusion

I **created** two **Python** scripts, and they have been **updated**, **tested**, and **deployed** for use in our research group and they will be made available on a public repository to allow for **enhanced flexibility** and **reproducibility** and **reduction** of potential user error. All objectives were met.

```

Data after limiting by user input variables...
0 0 2 4 7 55 60
1 0700_06072 1 1 2 -1 740.7718 -1
3 0766_06138 -1 1 -1 25.0478 -1
4 0768_04114 1 1 -1 40.0898 -1
5 0773_03440 1 1 -1 -66.5882 -1
...
211 1809_08303 ... -725.4902 ...
212 2001_07553 1 2 -1 -1270.4942 1
215 2017_07916 1 1 -1 -1019.4912 -1
216 2019_07829 -1 1 -1 425.6638 -1
217 2021_08048 1 1 1 844.6478 -1

[105 rows x 6 columns]

What type of subgroup analysis are you trying to run?
[1] all (include all cases in the grouping)
[2] separate (run independent models by subgroup)
[3] single (run on only 1 subgroup)
1

Running subset type all...

Data with both subgroups...
0 1 SEX CODED_DX FH-1 TOT_PUTAM NLVaMCI 55 60
1 1 1 2 -1 740.7718 -1
3 1 -1 1 -1 25.0478 -1
4 1 1 1 -1 40.0898 -1
5 1 1 1 -1 -66.5882 -1
...
211 1 1 2 -1 -725.4902 1
212 1 1 2 -1 -1270.4942 1
215 1 1 1 -1 -1019.4912 -1
216 1 -1 1 -1 425.6638 -1
217 1 1 1 1 844.6478 -1

[105 rows x 6 columns]

Running FBA...
Enter FBA parameters of interest separated by spaces:
FD FC all
all

These are the parameters that will be used for your FBA: FD, FC, FDC

Writing relative paths to _files text file FC_FBA_files.txt
Writing relative paths to _files text file FD_FBA_files.txt
Writing relative paths to _files text file FDC_FBA_files.txt
Adding fixelcfeStats -negative statements to SLURM FBA script...

Submit jobs to cluster? (0=no 1=MRClusterStats 2=FixelCFEStats 3=All)
0

No submissions to cluster have been made
Would you like to run another analysis? y/n
n

Thank you for using SAVANT

Contrast is...
0 0 1 0
0 0 0 -1 0

Would you like to model a covariate interaction? y/n
y

These are the variables you chose initially 2, 4, 7, 55, 60
These correlate to variables SEX, CODED_DX, FH-1, TOT_PUTAM, NLVaMCI

Your regressor variable is 55 : TOT_PUTAM
Contrast matrix variables 2, 4, 7, 55, 60

Enter a variable number for covariate:
4
  
```

Next Steps

- Future development will include:
- o Promoting **flexibility** to other **voxel-based analysis** software frameworks
 - o Improving **data visualization** for analysis and reporting
 - o Defining a **broader scope** for future project aspirations beyond **Alzheimer's disease** and **related dementias**

References

Michigan State University. "User Documentation." *ICER HPC Documentation*, docs.icer.msu.edu

Bender, Dr. Andrew and Bender Lab Research Group. "OSF Wiki." *Bender Lab*, osf.io/m8s7q/wiki/home

GNU. "Bash Reference." *BASH Manual*, www.gnu.org/software/bash/manual/bash.html

Python Software Foundation. "3.10.5 Documentation." *Python Manual*, docs.python.org/3

Acknowledgements

NSF ACRES REU – OAC1949912
Bender Lab Research Group



AUTOMATED MRI DATA ANALYSIS

Mentor: Dr. Andrew Bender
Author: Garrett Collier

MSU Departments of Neurology and CMSE

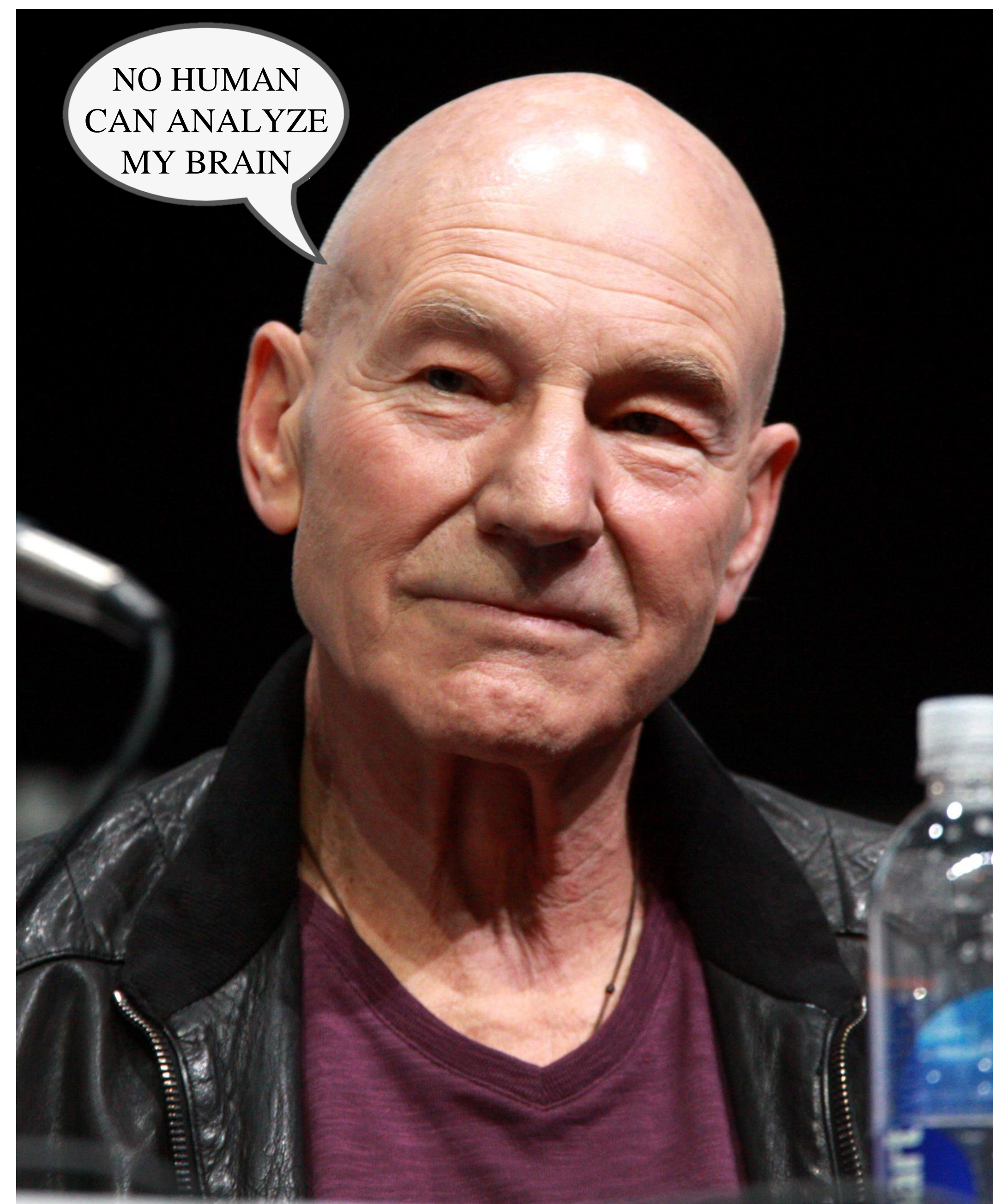


Background

With MRI Data becoming more complex and the world continuing to rely heavily on data and programming, it makes sense to **automate the process of MRI Data Analysis** using computers.

Dr. Bender, roughly 2 years ago, began the process of this automation through his creation of two **BASH scripts**.

I was tasked with creating a much more **effective and efficient** model of this automation, while promoting **voxel-wise throughput imaging using Python**.



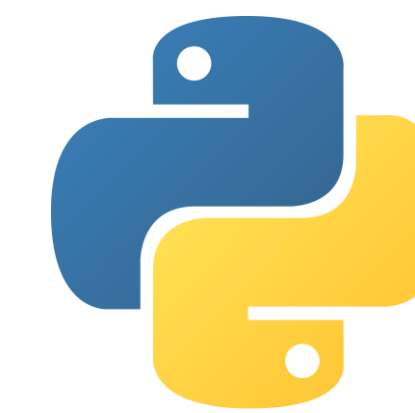
NOW WE CAN!

Objectives

Promote high **throughput voxel-wise analysis**

Enhance **Functionality** through:

- o Flexible Setup of MRI Variables
- o HPC Script Updates:
 - **Configuration file**
 - File linking



Establish **Error Checking**

Improve Output Files by **adding:**

- o **Parallel Comparisons**
- o Post Hoc Testing
- o Enhancements to Contrast Matrix
 - **Regressor and Covariates**

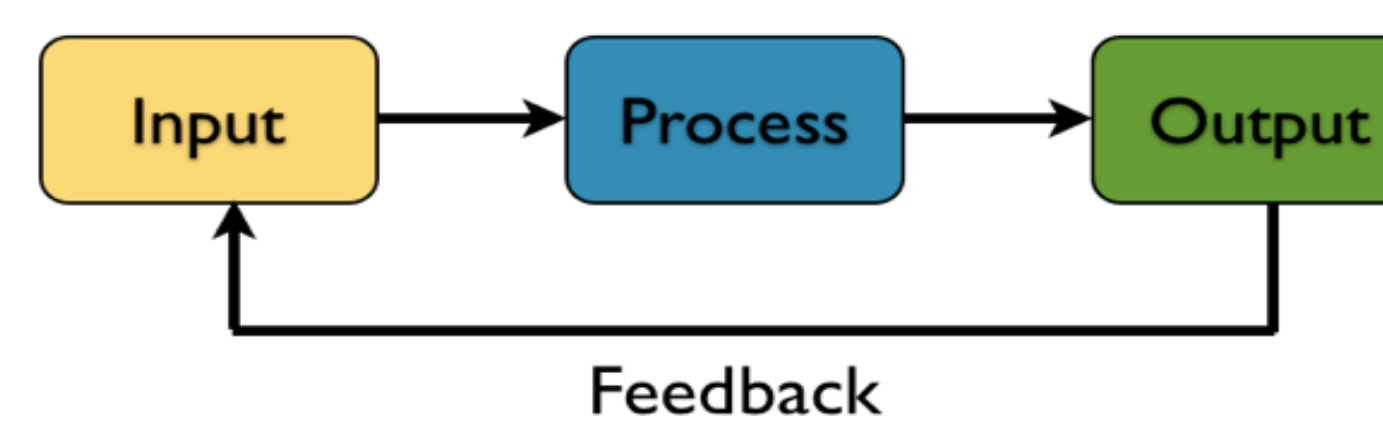


Improve **Transparency** of Reporting Data and Effects

Provide a **Universal Foundation** for Automated Data Analysis

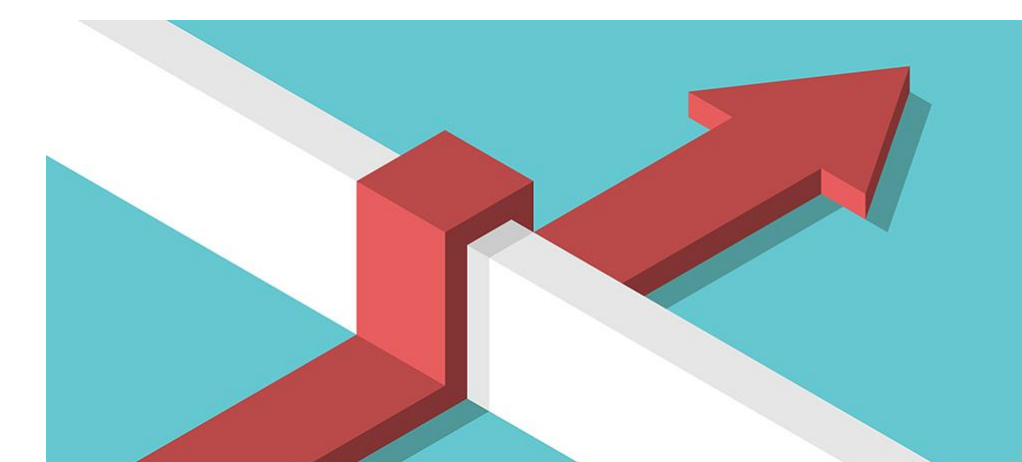
Methods

- o **Evaluate** initial BASH script methods
- o Translate **BASH** commands to **Python**
- o New **feature development** in consultation
- o Test and **bug fixing** with user feedback
- o **Deploy** to Research Group for **Testing**
- o **Maintain** scripts and **Develop** Documentation



Challenges Overcome

- o **Limited knowledge** in:
 - MRI Data/Neuroscience
 - BASH coding language
- o **Different versions** of:
 - Python
 - HPC modules



Conclusion

I **created two Python scripts**, and they have been **updated, tested, and deployed** for use in our research group and they will be made available on a public repository to allow for **enhanced flexibility and reproducibility** and **reduction** of potential user error. All objectives were met.

```

Data after limiting by user input variables...
0 0 2 4 7 55 60
1 0700_06072 1 1 2 -1 740.7718 -1
3 0766_06138 -1 1 -1 25.0478 -1
4 0768_04114 1 1 -1 40.0898 -1
5 0773_03440 1 1 -1 -66.5882 -1
...
211 1809_08303 ... -725.4902 ...
212 2001_07553 1 2 -1 -1270.4942 1
215 2017_07916 1 1 -1 -1019.4912 -1
216 2019_07829 -1 1 -1 425.6638 -1
217 2021_08048 1 1 1 844.6478 -1

[105 rows x 6 columns]

What type of subgroup analysis are you trying to run?
[1] all (include all cases in the grouping)
[2] separate (run independent models by subgroup)
[3] single (run on only 1 subgroup)
1

Running subset type all...

Data with both subgroups...
0 1 SEX CODED_DX FH-1 TOT_PUTAM NLVaMCI 55 60
1 1 1 2 -1 740.7718 -1
3 1 -1 1 -1 25.0478 -1
4 1 1 1 -1 40.0898 -1
5 1 1 1 -1 -66.5882 -1
...
211 1 1 2 -1 -725.4902 1
212 1 1 2 -1 -1270.4942 1
215 1 1 1 -1 -1019.4912 -1
216 1 -1 1 -1 425.6638 -1
217 1 1 1 1 844.6478 -1

[105 rows x 6 columns]

Running FBA...
Enter FBA parameters of interest separated by spaces:
FD FC all
all

These are the parameters that will be used for your FBA: FD, FC, FDC

Writing relative paths to _files text file FC_FBA_files.txt
Writing relative paths to _files text file FD_FBA_files.txt
Writing relative paths to _files text file FDC_FBA_files.txt
Adding fixelcfestats -negative statements to SLURM FBA script...

Submit jobs to cluster? (0=no 1=MRClusterstats 2=FixelCFEstats 3=All)
0

No submissions to cluster have been made
Would you like to run another analysis? y/n
n

Thank you for using SAVANT

Contrast is...
0 0 1 0
0 0 0 -1 0

Would you like to model a covariate interaction? y/n
y

These are the variables you chose initially 2, 4, 7, 55, 60
These correlate to variables SEX, CODED_DX, FH-1, TOT_PUTAM, NLVaMCI

Your regressor variable is 55 : TOT_PUTAM
Contrast matrix variables 2, 4, 7, 55, 60

Enter a variable number for covariate:
4
  
```

Next Steps

- Future development will include:
- o Promoting **flexibility** to other **voxel-based analysis** software frameworks
 - o Improving **data visualization** for analysis and reporting
 - o Defining a **broader scope** for future project aspirations beyond **Alzheimer's disease and related dementias**

References

Michigan State University. "User Documentation." *ICER HPC Documentation*, docs.icer.msu.edu

Bender, Dr. Andrew and Bender Lab Research Group. "OSF Wiki." *Bender Lab*, osf.io/m8s7q/wiki/home

GNU. "Bash Reference." *BASH Manual*, www.gnu.org/software/bash/manual/bash.html

Python Software Foundation. "3.10.5 Documentation." *Python Manual*, docs.python.org/3

Acknowledgements

NSF ACRES REU – OAC1949912
Bender Lab Research Group

