Executable Notebooks
(whats, whys, & hows)

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What

Jupyter Notebooks

What

Jupyter Notebooks are open source web applications

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Why

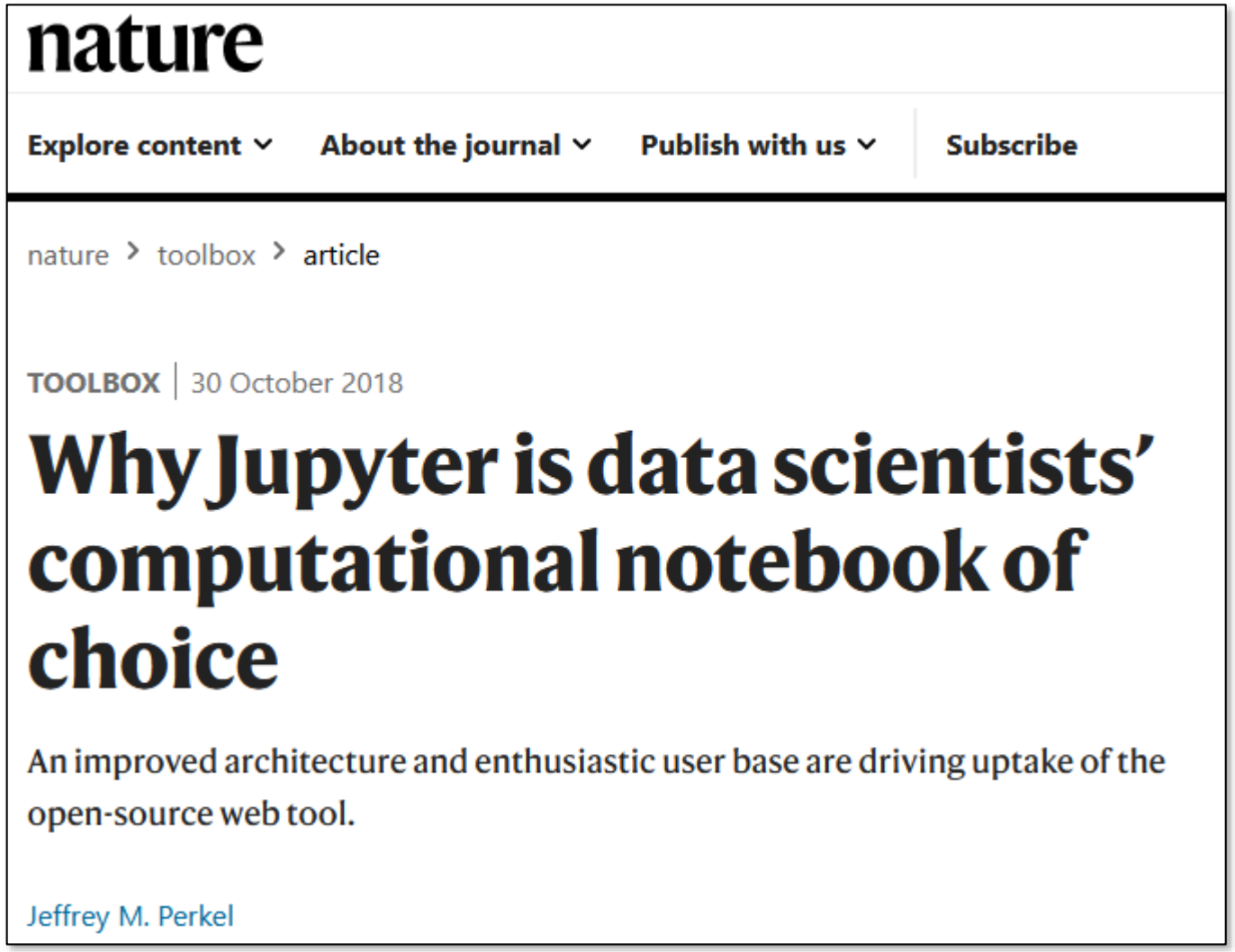
Boost your research productivity

Why

Boost your research productivity while simultaneously helping make science more open, accessible, and reproducible!

Why

More **than 2.5 million public Jupyter notebooks in September 2018 on GitHub**, up from 200,000 or so in 2015.



nature

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nature › toolbox › article

TOOLBOX | 30 October 2018

Why Jupyter is data scientists' computational notebook of choice

An improved architecture and enthusiastic user base are driving uptake of the open-source web tool.

Jeffrey M. Perkel

https://www.nature.com/articles/d41586-018-07196-1

How

Running notebooks

- Anaconda + Web Browser
- Base Python + Web Browser
- Anaconda + VS Code
- Base Python + VS Code
- Google Colaboratory
- Binder
- Jupyter Lab

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- Data processing, modeling/analysis, visualization

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- Sharing code + collaborating with others

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- Sharing code + collaborating with others
- Learning new skills
- Teaching others
- Publishing work and/or supplemental materials

Use cases

Data processing, analysis, visualization

fMRIPrep

All preprocessing was implemented using **fMRIPrep** (Esteban et al., 2018), which includes anatomical T1-weighted brain extraction, anatomical surface extraction, head-motion estimation and correction, susceptibility-derived distortion estimation and unwarping, intrasubject registration, and spatial normalization (intersubject registration). All volumes were registered to the MNI (Montreal Neurological Institute) standard template. Automatic removal of motion artifacts using independent component analysis (ICA-AROMA) was performed on the preprocessed BOLD time series in MNI space and the resulting data was smoothed using a 6.0 mm^3 FWHM Gaussian kernel and the time series was scaled within voxels to represent percent signal change.

We used the following `bash` command with `singularity` to run `fmriprep`:

```
SUBID=1234
singularity run --bind /mnt:/mnt --cleanenv /mnt/data/singularity/fmriprep-20.2.3.simg /mnt/
data/study/subjects /mnt/data/study/subjects/derivatives participant \
--work-dir /mnt/data/study/fmriprep-20.2.3_work \
--participant_label $SUBID \
--bold2t1w-dof 9 \
--output-spaces T1w:res-native MNI152NLin2009cAsym:res-native MNI152NLin6Asym:res-2 fsaverag
e:res-native \
--skull-strip-t1w force \
--ignore slicetiming \
--use-aroma \
--dummy-scans 0 \
--fs-license-file /mnt/data/freesurfer/license.txt \
--no-submm-recon \
--write-graph \
--fd-spike-threshold 0.5 \
--random-seed 2021
```

For group-level statistical inference, we ran a sign permutation test using the following `bash` command with `AFNI` to run `3dttest++` with `-Clustsim`:

```
dirA=mnt/data/study/firstlevel_glm/
3dttest++ -prefix /mnt/data/study/results/Condition_A.nii.gz \
          -mask /mnt/data/study/code/modeling/MNI152-graymatter-thr50-2mm.nii.gz \
          -Clustsim \
          -setA Condition_A \
             101 "$dirA/sub-101_stats.nii.gz[0]" \
             102 "$dirA/sub-102_stats.nii.gz[0]" \
             103 "$dirA/sub-103_stats.nii.gz[0]" \
             104 "$dirA/sub-104_stats.nii.gz[0]" \
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             106 "$dirA/sub-106_stats.nii.gz[0]" \
             107 "$dirA/sub-107_stats.nii.gz[0]" \
```

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             106 "$dirA/sub-106_stats.nii.gz[0]" \
             107 "$dirA/sub-107_stats.nii.gz[0]" \
```

In [14]:

```
print("Begin Searchlight\n")
sl_result = sl.run_searchlight(calc_svm, pool_size=pool_size)
print("End Searchlight\n")

end_time = time.time()

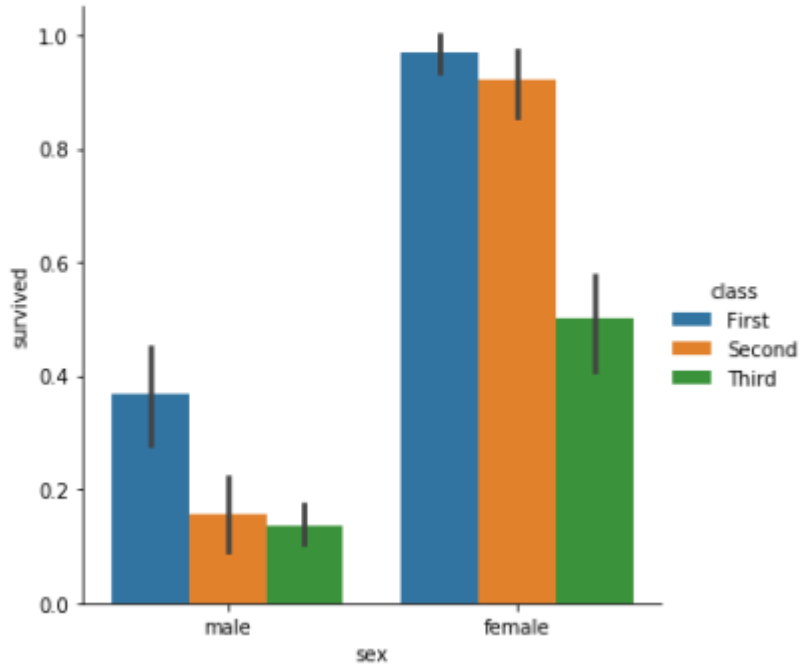
# Print outputs
print("Summarize searchlight results")
print("Number of searchlights run: " + str(len(sl_result[mask==1])))
print("Accuracy for each kernel function: " +str(sl_result[mask==1].astype('do
uble')))
print('Total searchlight duration (including start up time): %.2f' % (end_time
- begin_time))

# Save the results to a .nii file
output_name = os.path.join(output_dir, ('subj%s_SL_result.nii.gz' % (sub_id)))
sl_result = sl_result.astype('double')  # Convert the output into a precision
format that can be used by other applications
sl_result[np.isnan(sl_result)] = 0  # Exchange nans with zero to ensure compat
ibility with other applications
sl_nii = nib.Nifti1Image(sl_result, affine_mat)  # create the volume image
hdr = sl_nii.header  # get a handle of the .nii file's header
hdr.set_zooms((dimsize[0], dimsize[1], dimsize[2]))
nib.save(sl_nii, output_name)  # Save the volume
```

Data processing, analysis, visualization

Supplemental Figure 1

In [2]:
```
1 sns.catplot(x="sex", y="survived", hue="class",
  kind="bar", data=titanic)
2 plt.show()
```



Data processing, analysis, visualization

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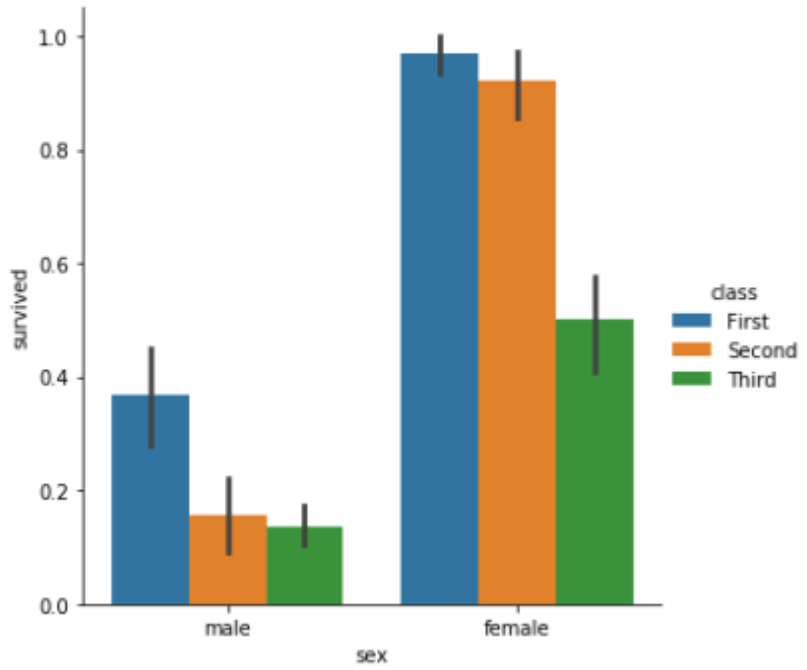
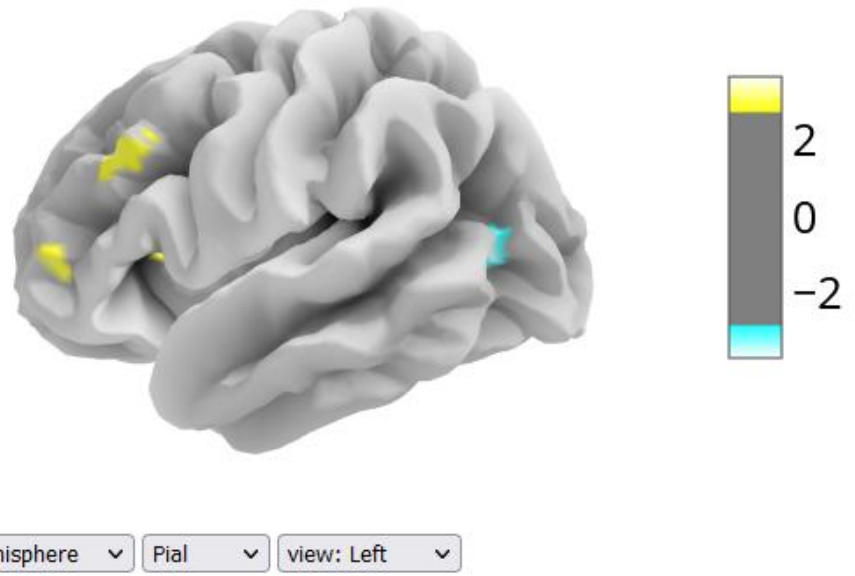


Supplemental Figure 3

```
In [2]:
1  from nilearn.plotting import view_img_on_surf
2
3  view_img_on_surf(zmap,threshold=2.8)
```

Out[2]:



Sharing your work!

- Lab mates

Sharing your work!

- Lab mates
- Collaborators

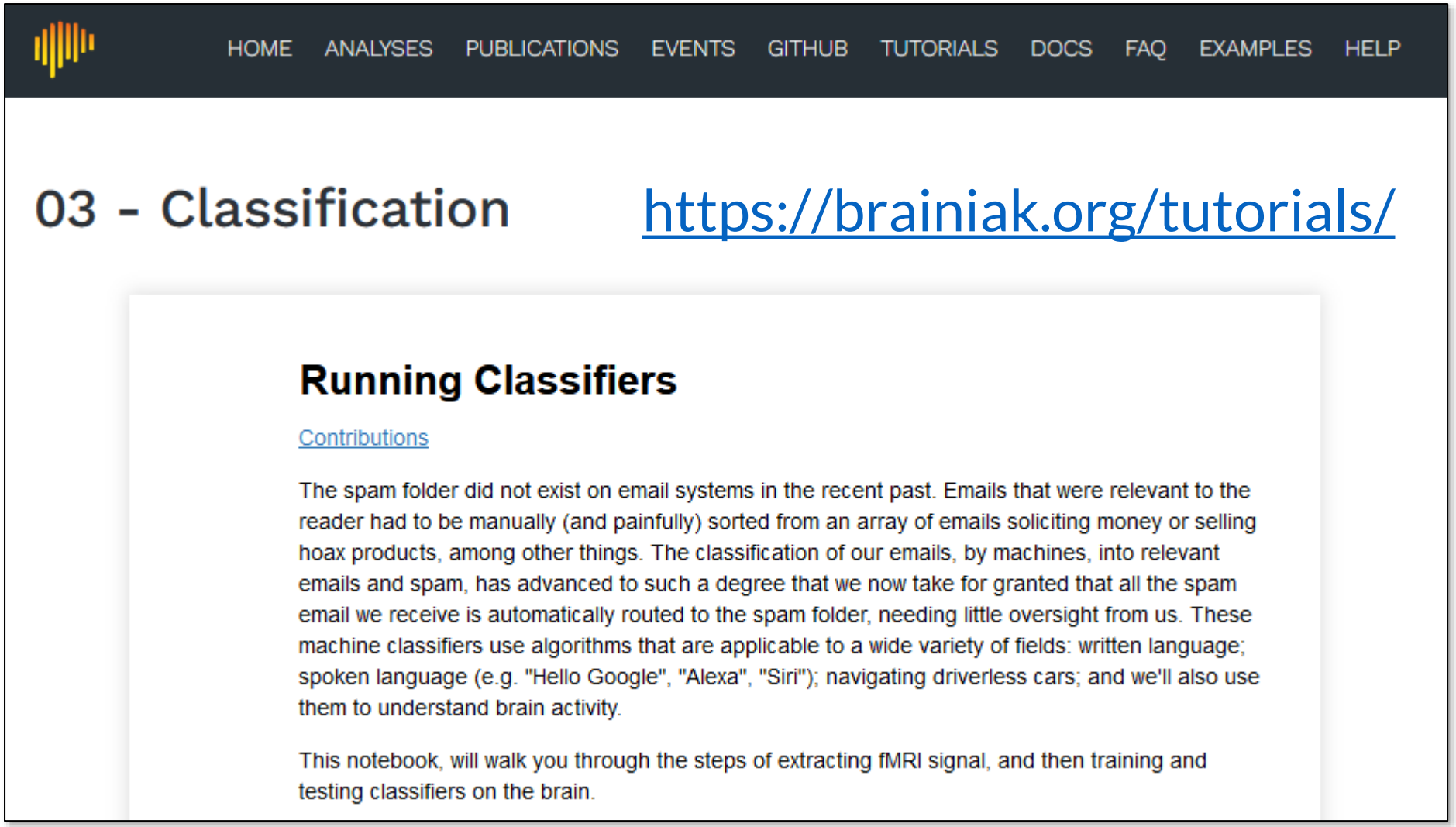
Sharing your work!

- Lab mates
- Collaborators
- Reviewers

Sharing your work!

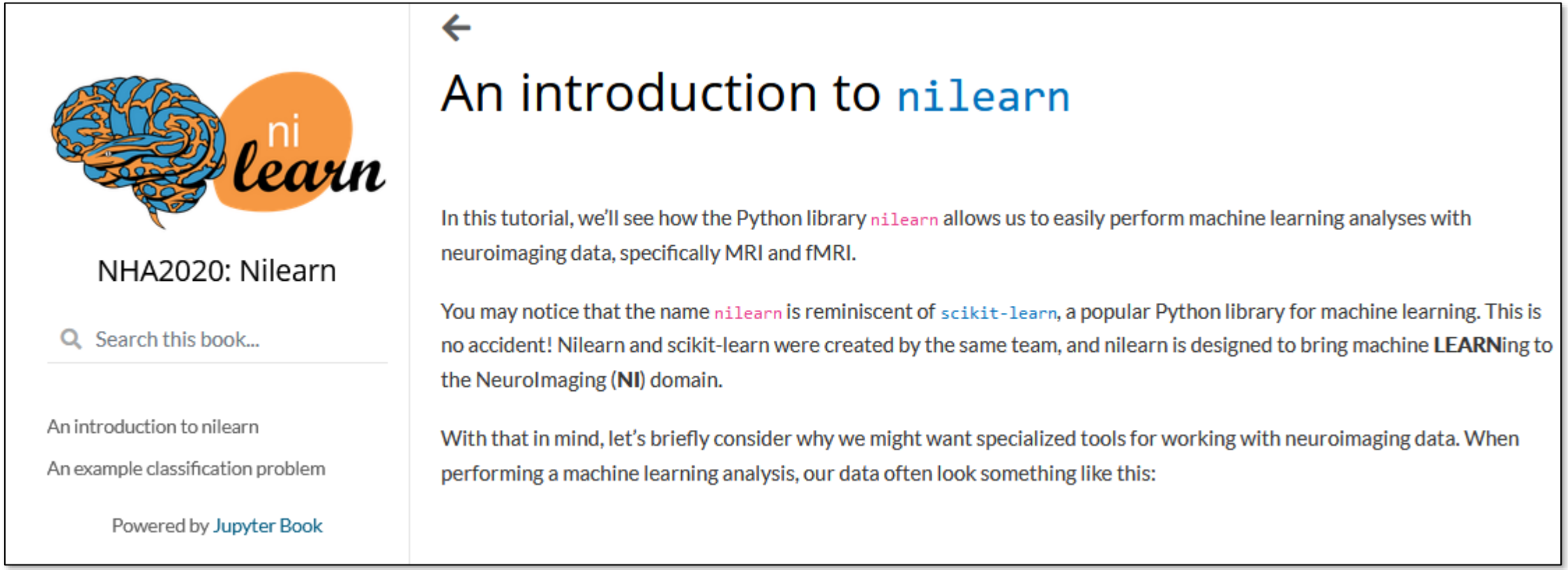
- Lab mates
- Collaborators
- Reviewers
- Yourself!

Learning


HOME ANALYSES PUBLICATIONS EVENTS GITHUB TUTORIALS DOCS FAQ EXAMPLES HELP
03 - Classification
https://brainiak.org/tutorials/
Running Classifiers
Contributions
The spam folder did not exist on email systems in the recent past. Emails that were relevant to the reader had to be manually (and painfully) sorted from an array of emails soliciting money or selling hoax products, among other things. The classification of our emails, by machines, into relevant emails and spam, has advanced to such a degree that we now take for granted that all the spam email we receive is automatically routed to the spam folder, needing little oversight from us. These machine classifiers use algorithms that are applicable to a wide variety of fields: written language; spoken language (e.g. "Hello Google", "Alexa", "Siri"); navigating driverless cars; and we'll also use them to understand brain activity.
This notebook, will walk you through the steps of extracting fMRI signal, and then training and testing classifiers on the brain.

Learning

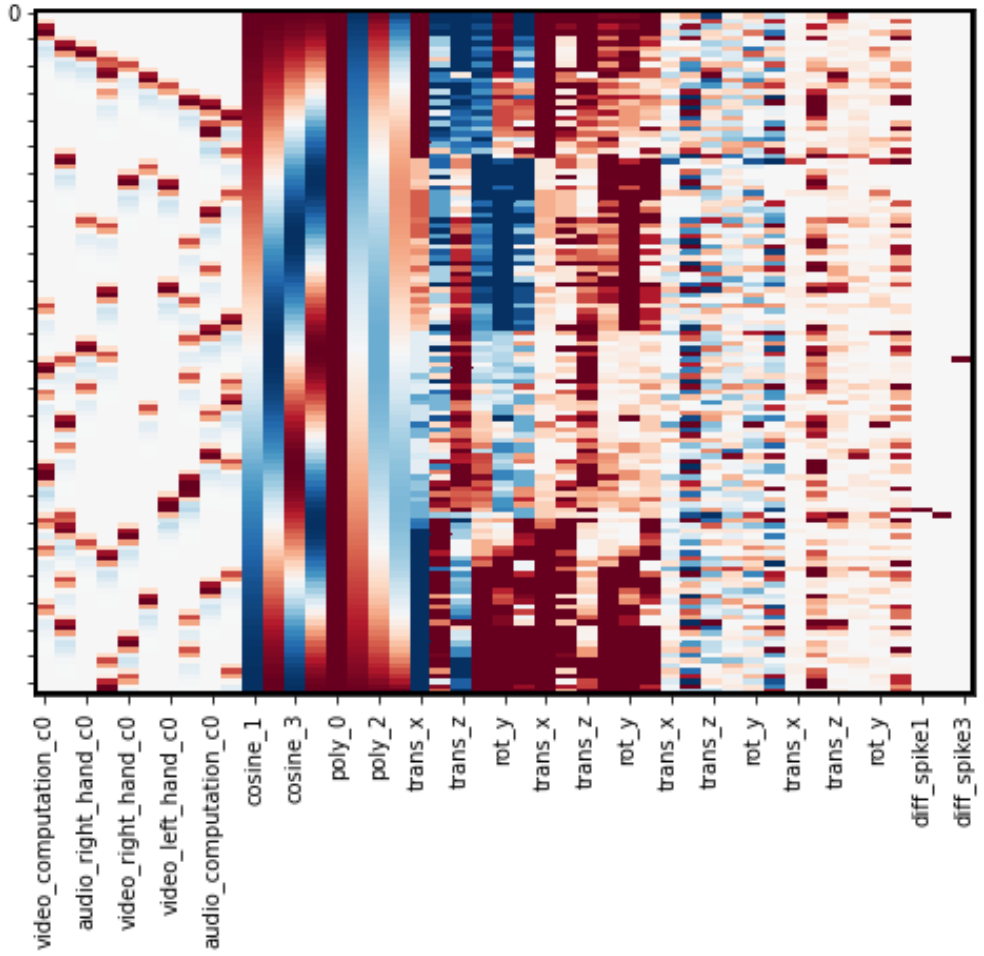
https://emdupre.github.io/nha2020-nilearn



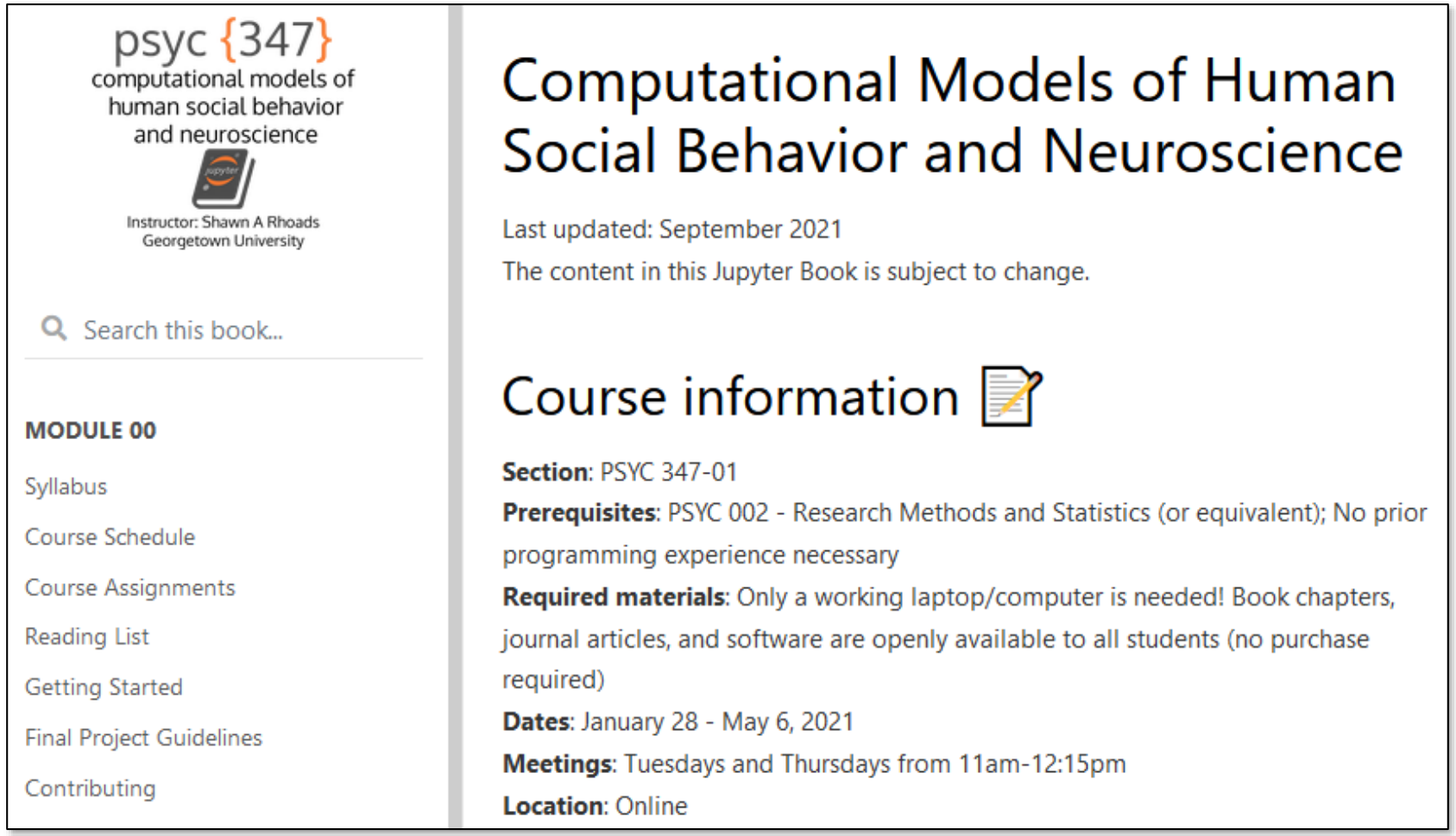
Learning

https://dartbrains.org/content/GLM_Single_Subject_Model.html

```
dm_conv_filt_poly_cov = pd.concat([dm_conv_filt_poly, mc_cov, spikes], axis=1)
dm_conv_filt_poly_cov.heatmap(cmap='RdBu_r', vmin=-1,vmax=1)
```

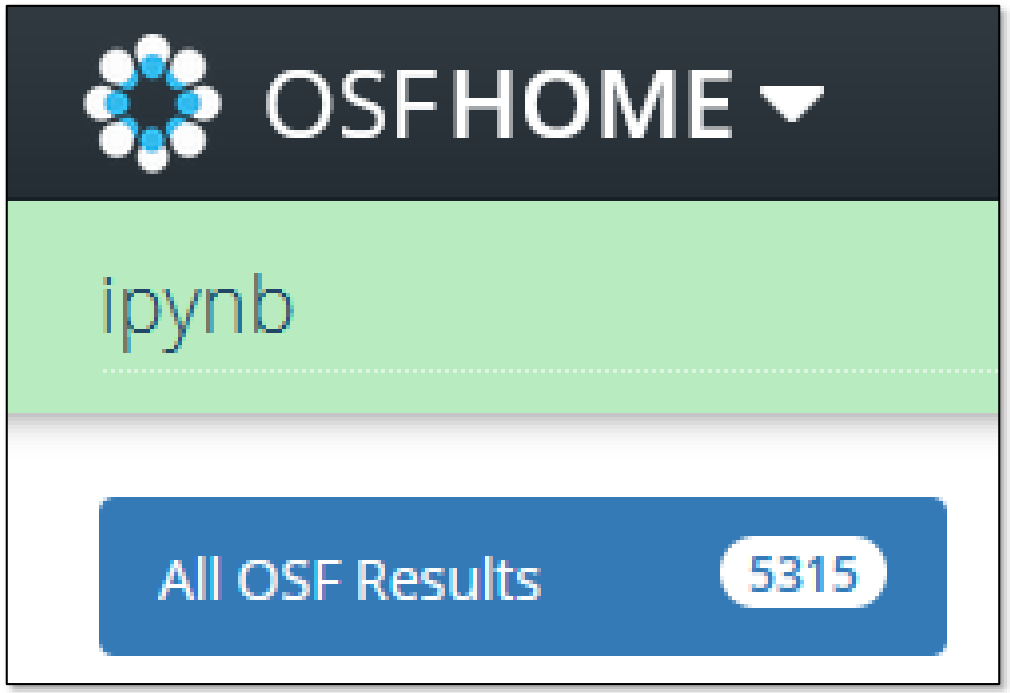


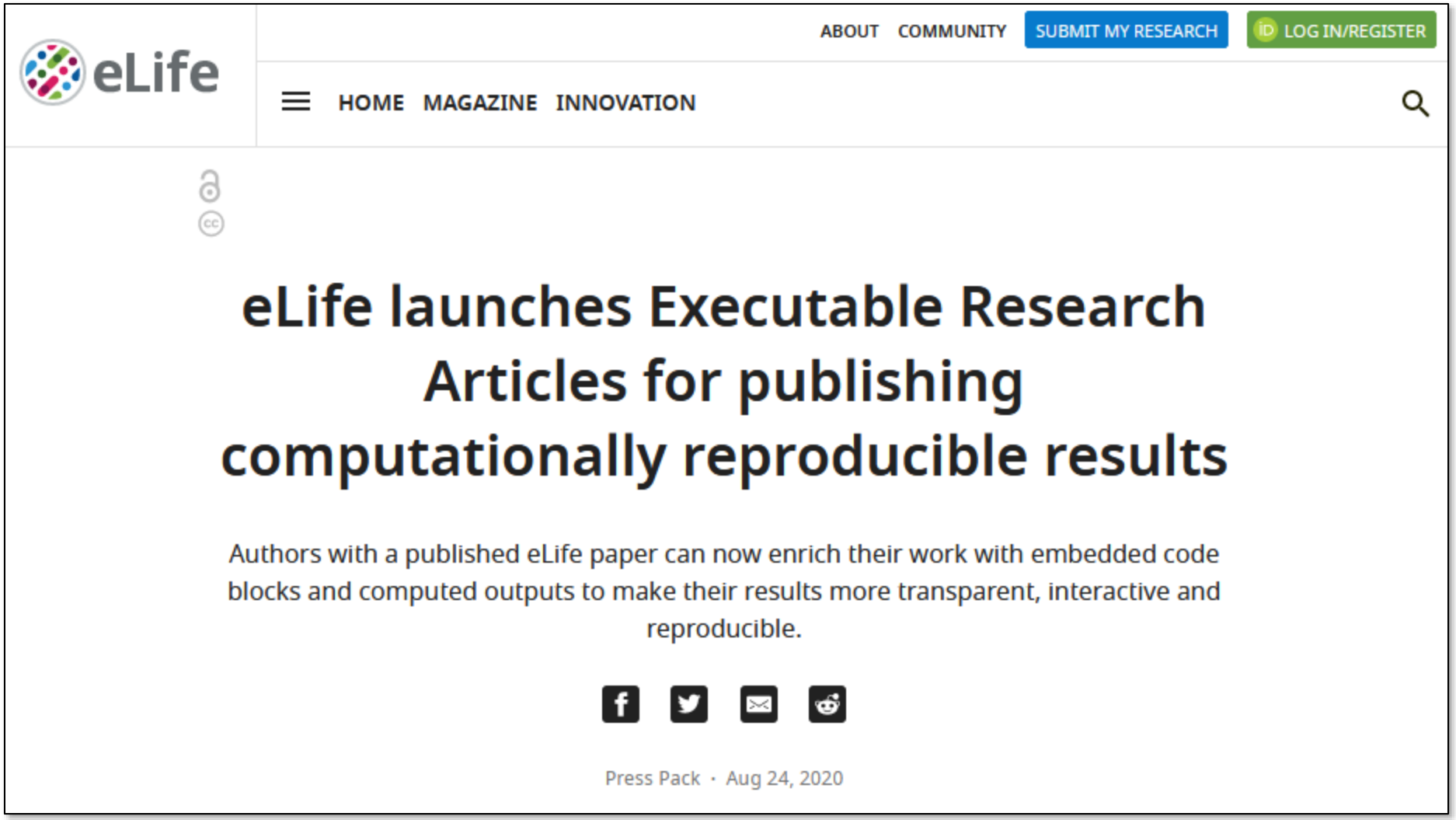
Teaching



https://shawnrhoads.github.io/gu-psyc-347

Publishing

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Authors with a published eLife paper can now enrich their work with embedded code blocks and computed outputs to make their results more transparent, interactive and reproducible.
Press Pack · Aug 24, 2020

An interactive meta-analysis of MRI biomarkers of myelin

Matteo Mancini, Agah Karakuzu, Julien Cohen-Adad, Mara Cercignani, Thomas E Nichols, Nikola Stikov

Department of Neuroscience, Brighton and Sussex Medical School, University of Sussex, Brighton, United Kingdom; NeuroPoly Lab, Polytechnique Montreal, Montreal, Canada; CUBRIC, Cardiff University, Cardiff, United Kingdom; Functional Neuroimaging Unit, CRIUGM, Université de Montréal, Montreal, Canada; Neuroimaging Laboratory, Fondazione Santa Lucia, Rome, Italy; Wellcome Centre for Integrative Neuroimaging (WIN FMRIB), University of Oxford, Oxford, United Kingdom; Big Data Institute, University of Oxford, Oxford, United Kingdom; Montreal Heart Institute, Université de Montréal, Montreal, Canada

https://elifesciences.org/articles/61523/executable

Notebooks of the Future

Notebooks of ~~the Future~~ Now

Outline

- Starting from scratch
- Running Jupyter Notebooks locally
  - Using typical method
  - Using VSCode
- Tutorial with Jupyter (Markdown, R, Python)
- Google Colaboratory
- Using GitHub + JupyterBook to publish your work online