



BIANCA

Brain Intensity AbNormality Classification Algorithm

Ludovica Griffanti, PhD

WIN, FMRIB, University of Oxford

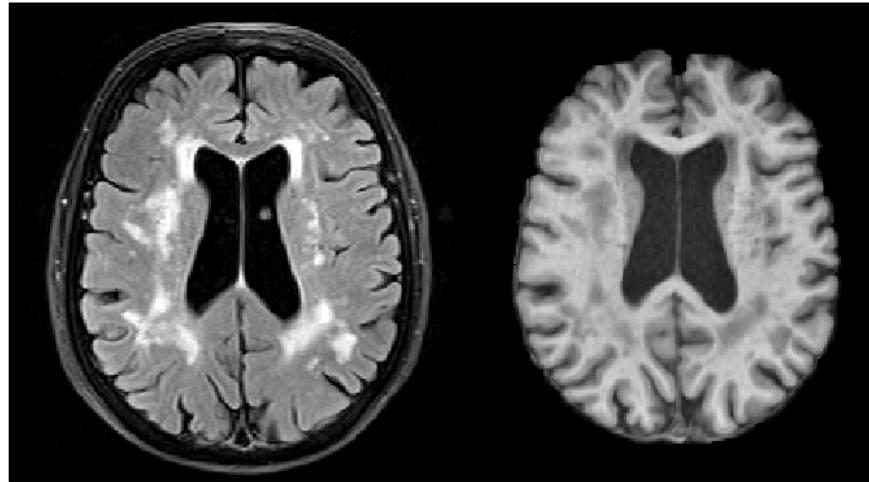
OHBM 2018 - OpenScienceRoom

18th June 2018



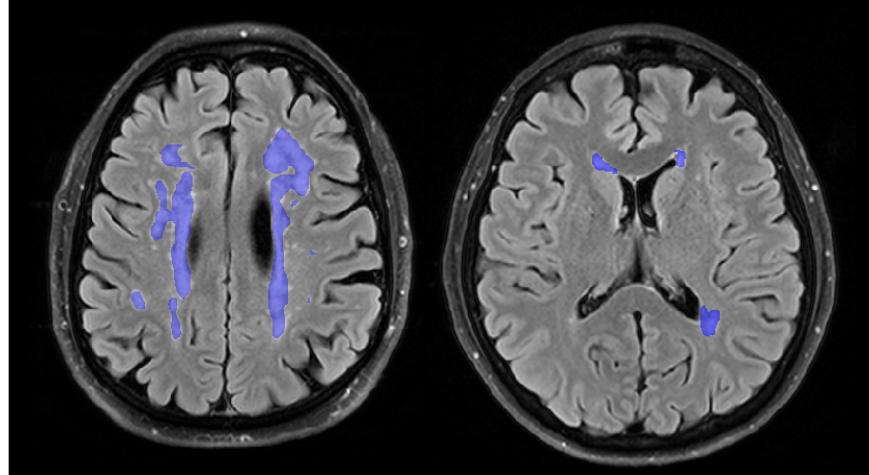
BIANCA - Overview

Lesion probability map

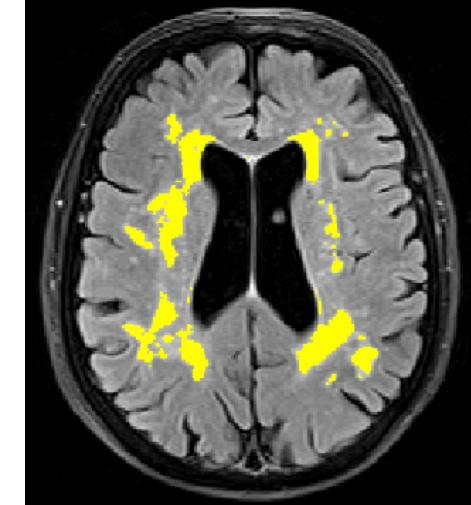
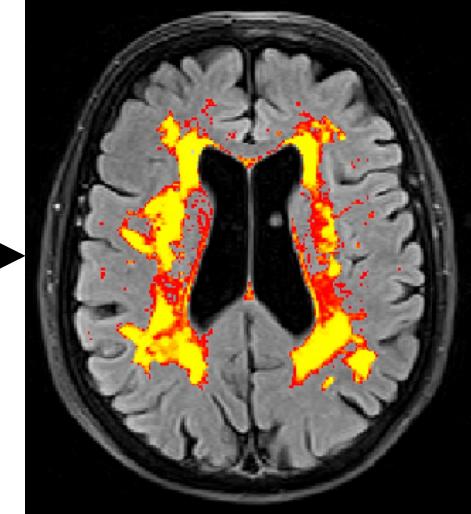


Features

K-NN Classifier



*Features
Labels*



BIANCA - Overview

Included in FSL 5.0.10



Contents

- 1. Introduction
 - 1.1. Research overview - BIANCA (Brain Intensity AbNormality Classification Algorithm)
 - 1.2. Referencing
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Research overview - BIANCA (Brain Intensity AbNormality Classification Algorithm)

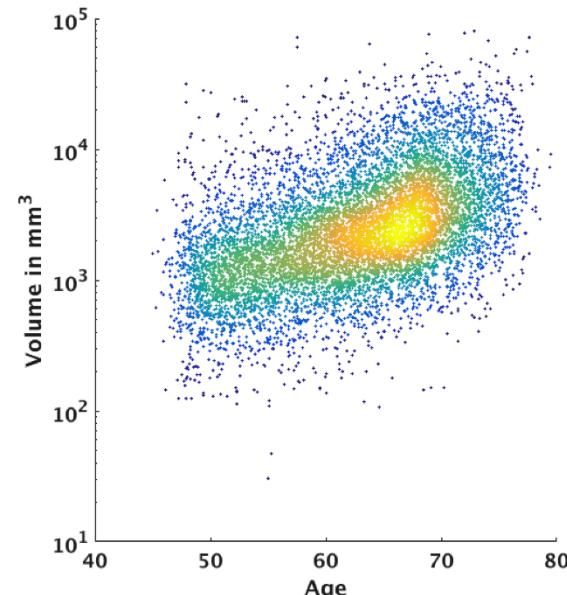
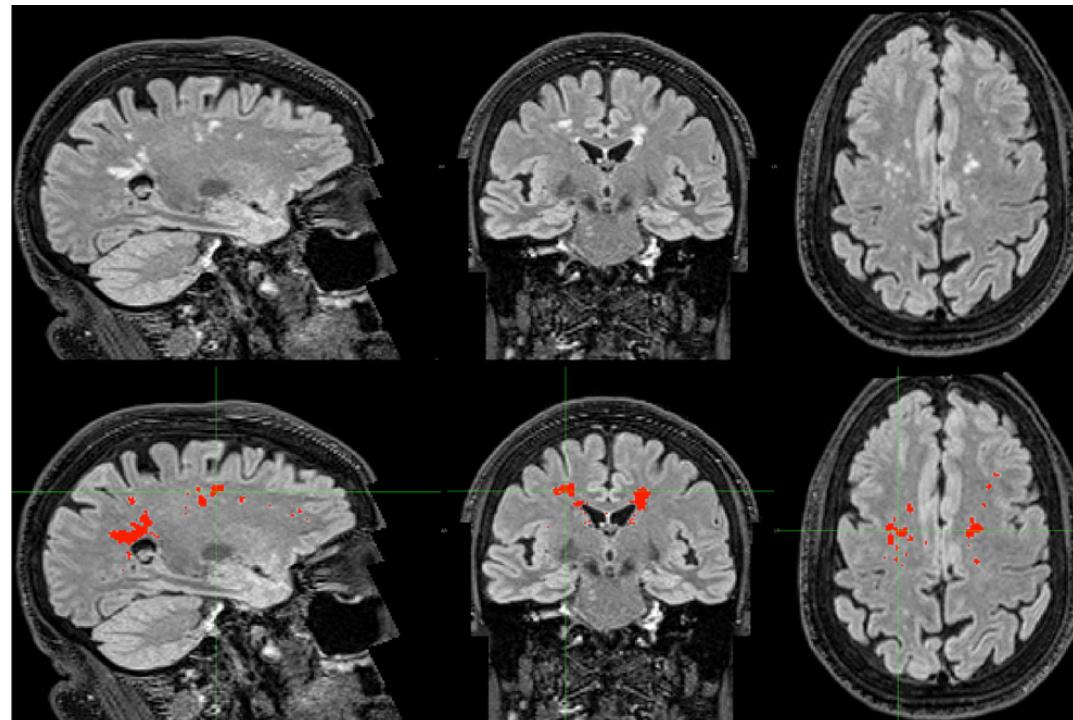
FMRIB's tool for automated segmentation of white matter hyperintensities

BIANCA is a fully automated, supervised method for white matter hyperintensities (WMH) detection, based on the k-nearest neighbour (k-NN) algorithm. BIANCA classifies the image's voxels based on their intensity and spatial features, and the output image represents the probability per voxel of being WMH. BIANCA is very flexible in terms of MRI modalities to use and offers different options for weighting the spatial information, local spatial intensity averaging, and different options for the choice of the number and location of the training points (see user guide for details).



BETA RELEASE

BIANCA is currently considered to be in testing, meaning that you will need to inspect its output a bit more carefully to see if you are happy with it. The output will depend critically on the choice of options and the quality of the training data and manual segmentations. Further recommendations and automated tuning methods, will be supported in an upcoming release.





BIANCA

BIANCA - Usage

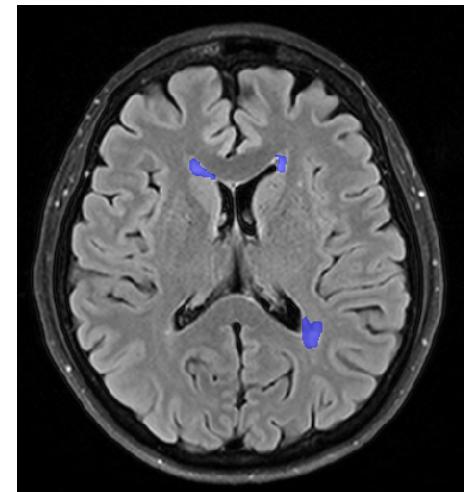
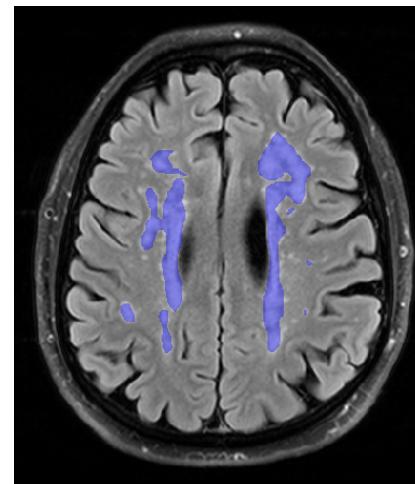
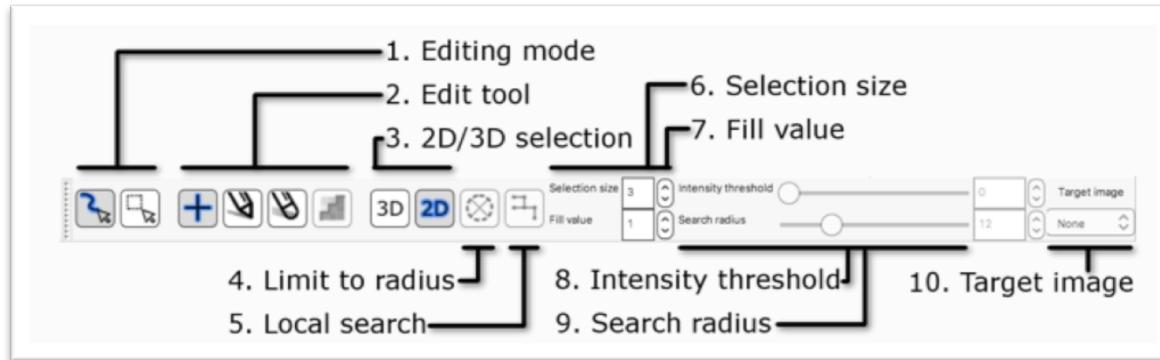
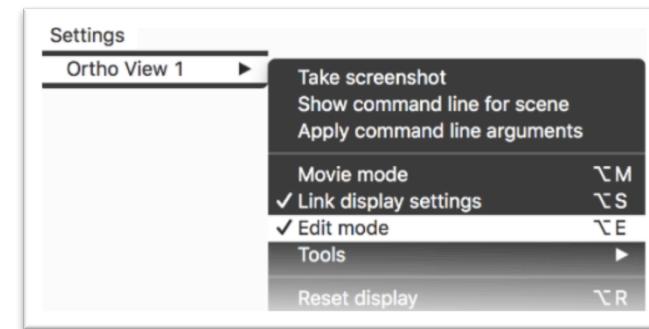
1. Prepare your **training dataset**
2. Prepare your **data**
3. **Usage** cases
 - A. Train and test
 - B. Create a training dataset
 - C. Testing using existing training dataset
4. **Post-processing**

1. Prepare your training file

- a. Manually segment lesions on 10-20 subjects (high lesion load)
- b. Save manual mask as binary image (1=lesion, 0=non-lesion)

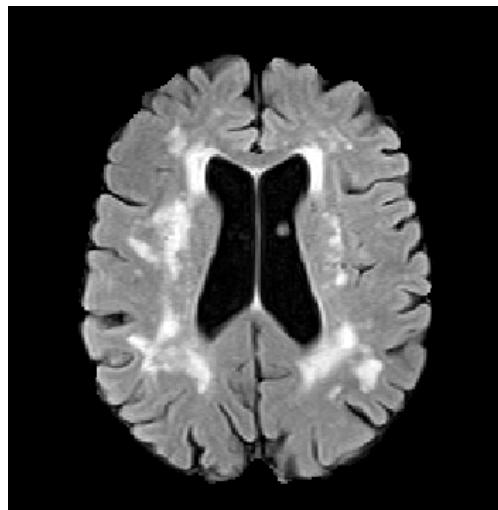


FSLEYES edit mode



2. Prepare your data

- a. Choose your base modality (reference for input/output)
- b. For each subject, register all other modalities to your base (including manual mask, if applicable)
- c. Brain-extract (at least) one modality
- d. For each subject, calculate the linear registration transform from base to MNI



FLAIR_brain



T1_2FLAIR



COMING SOON:
will support non-linear
registration



BIANCA

3. Usage case A) Train and test

Master file preparation

Masterfile.txt

sub01/FLAIR_brain.nii.gz
sub02/FLAIR_brain.nii.gz
sub03/FLAIR_brain.nii.gz
sub04/FLAIR_brain.nii.gz
sub05/FLAIR_brain.nii.gz
sub06/FLAIR_brain.nii.gz

...
subN/FLAIR_brain.nii.gz

sub01/T1_toFLAIR.nii.gz
sub02/T1_toFLAIR.nii.gz
sub03/T1_toFLAIR.nii.gz
sub04/T1_toFLAIR.nii.gz
sub05/T1_toFLAIR.nii.gz
sub06/T1_toFLAIR.nii.gz

sub01/FLAIR_toMNI.mat
sub02/FLAIR_toMNI.mat
sub03/FLAIR_toMNI.mat
sub04/FLAIR_toMNI.mat
sub05/FLAIR_toMNI.mat
sub06/FLAIR_toMNI.mat

sub01/WMHmask.nii.gz
sub02/WMHmask.nii.gz
sub03/WMHmask.nii.gz
sub04/WMHmask.nii.gz
placeholder
placeholder

subN/T1_toFLAIR.nii.gz subN/FLAIR_toMNI.mat subN/placeholder

One row per subject

All modalities registered to the base

One modality brain extracted

Registration matrix
from the base to MNI

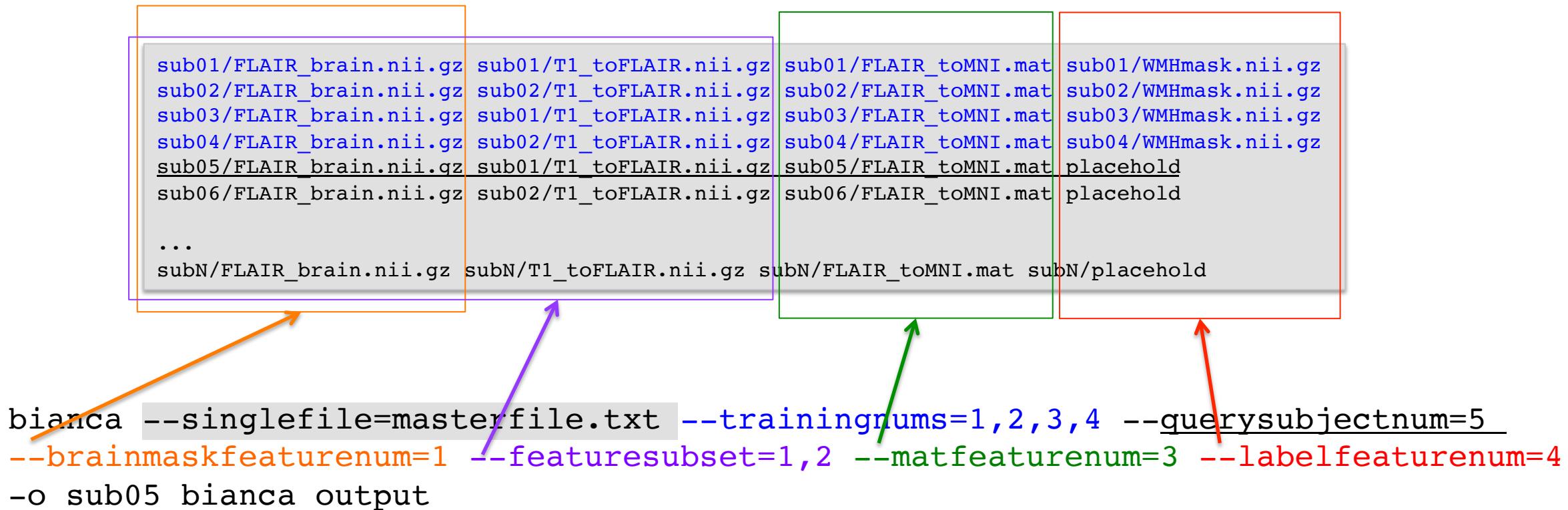
Manual masks
(for training subjects.
Use any “placeholder
text” for others)



3. Usage case A) Train and test

BIANCA

Command line (main options)



Automatic Leave-One-Out if query subject is one of the training subjects



BIANCA

3. Usage case B) Create a training dataset

Master file preparation

```
sub01/FLAIR_brain.nii.gz sub01/T1_toFLAIR.nii.gz sub01/FLAIR_toMNI.mat  
sub02/FLAIR_brain.nii.gz sub02/T1_toFLAIR.nii.gz sub02/FLAIR_toMNI.mat  
sub03/FLAIR_brain.nii.gz sub03/T1_toFLAIR.nii.gz sub03/FLAIR_toMNI.mat  
sub04/FLAIR_brain.nii.gz sub04/T1_toFLAIR.nii.gz sub04/FLAIR_toMNI.mat  
...  
subN/FLAIR_brain.nii.gz subN/T1_toFLAIR.nii.gz subN/FLAIR_toMNI.mat subN/WMHmask.nii.gz
```

```
sub01/WMHmask.nii.gz  
sub02/WMHmask.nii.gz  
sub03/WMHmask.nii.gz  
sub04/WMHmask.nii.gz
```

Command line (main options)

```
bianca --singlefile=masterfile.txt --trainingnums=1,2,3,4...N  
--querysubjectnum=1 --brainmaskfeaturenum=1 --featuresubset=1,2  
--matfeaturenum=3 --labelfeaturenum=4  
--saveclassifierdata=MyTraining
```

Output files:
MyTraining
MyTraining_labels



BIANCA

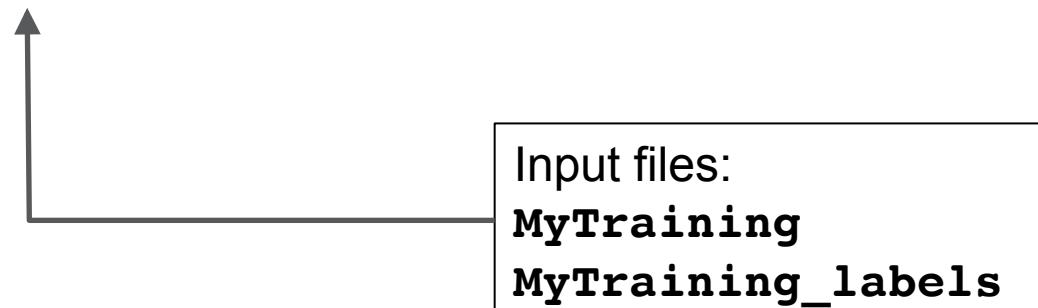
3. Usage case C) Test with existing training dataset

Master file preparation

```
subT01/FLAIR_brain.nii.gz subT01/T1_toFLAIR.nii.gz subT01/FLAIR_toMNI.mat placeholder  
subT02/FLAIR_brain.nii.gz subT02/T1_toFLAIR.nii.gz subT02/FLAIR_toMNI.mat placeholder  
subT03/FLAIR_brain.nii.gz subT03/T1_toFLAIR.nii.gz subT03/FLAIR_toMNI.mat placeholder  
subT04/FLAIR_brain.nii.gz subT04/T1_toFLAIR.nii.gz subT04/FLAIR_toMNI.mat placeholder  
...  
subTN/FLAIR_brain.nii.gz subTN/T1_toFLAIR.nii.gz subTN/FLAIR_toMNI.mat placeholder
```

Command line (main options)

```
bianca --singlefile=masterfile.txt --querysubjectnum=1  
--brainmaskfeaturenum=1 --featuresubset=1,2 --matfeaturenum=3  
--loadclassifierdata=MyTraining -o sub01_bianca_output
```



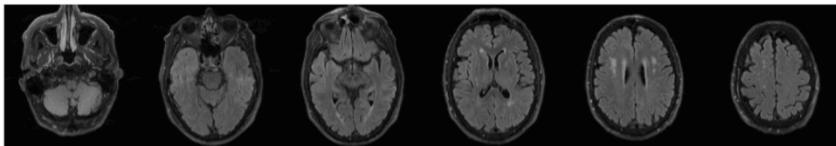


Coming soon: HTML reports

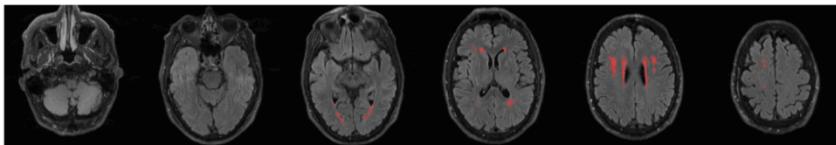
BIANCA report for subject : WH_092

/Users/ludovica/Documents/Projects/REPORT/TEST_DATA/WH_092/WH_092_biancathr09.nii.g

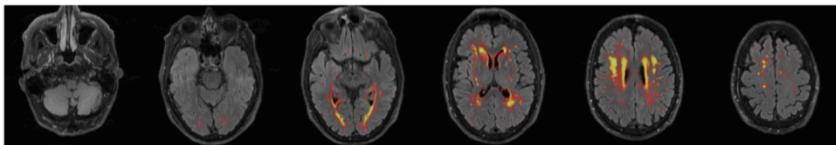
Original image



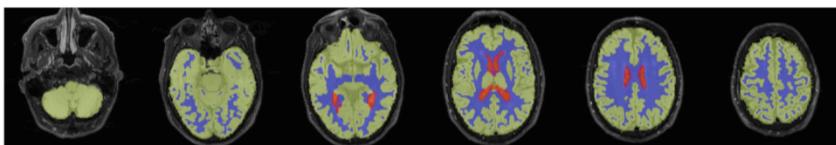
BIANCA output (thresholded)



BIANCA output (unthresholded)



Masks



Measures

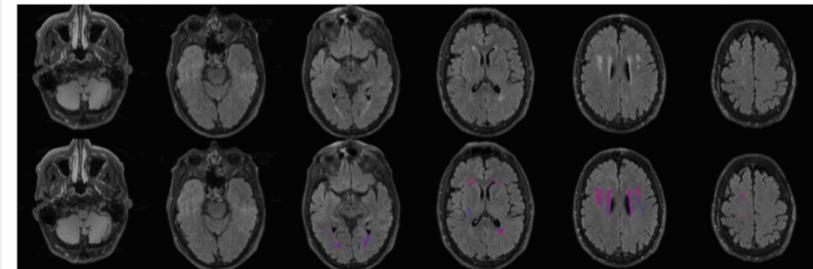
Metric	Absolute value (mm ³)	Normalised (% of brain volume)
Total lesion volume (mm ³)	13937.532	0.889
Total lesion count	154	-
Average lesion volume (mm ³)	90.503	0.006
Stdev lesion volume (mm ³)	373.783	0.024
Min lesion volume (mm ³)	0.554	0.0
Max lesion volume (mm ³)	2513.498	0.16

BIANCA training report

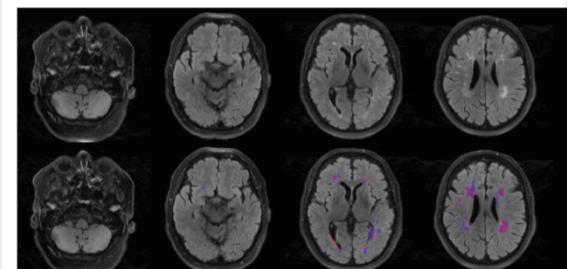
TRAINING SUBJECTS FILE:

/Users/ludovica/Documents/Projects/REPORT/training_list.txt

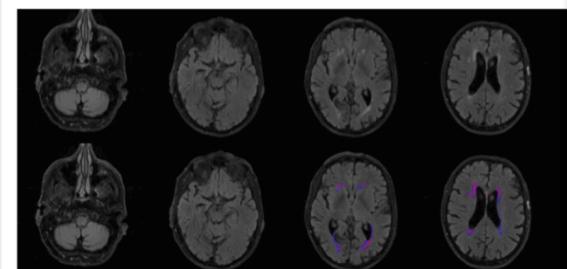
subject1: BIANCA vs Ground truth



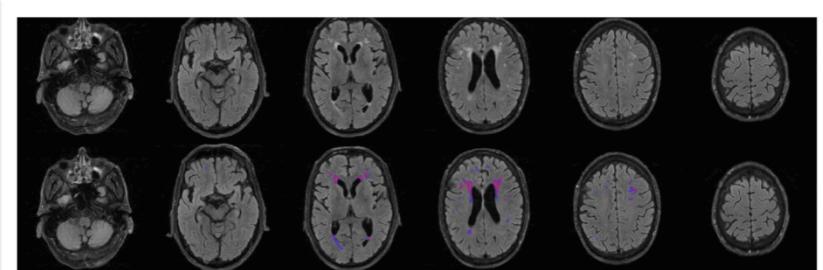
subject2: BIANCA vs Ground truth



subject3: BIANCA vs Ground truth



subject4: BIANCA vs Ground truth



Overlap measures

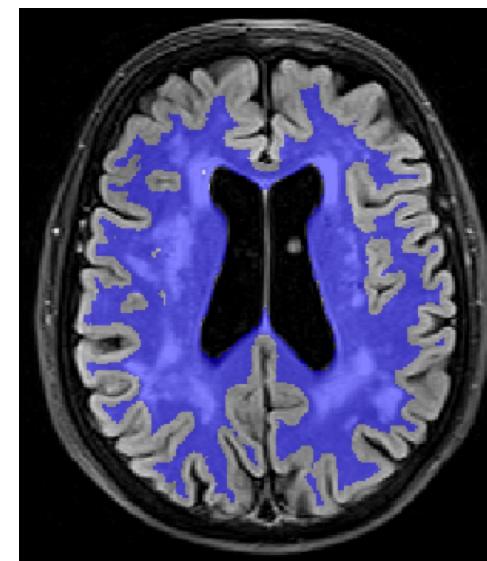
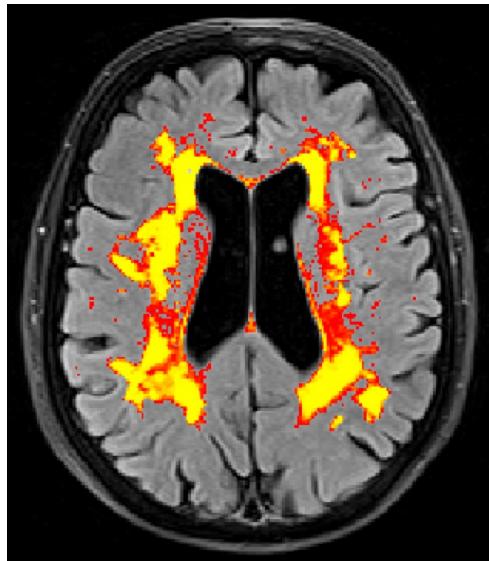
Subject	Total Volume (mm ³)	Ground truth (GT) volume (mm ³)	Diff. volume (BIANCA - GT) (mm ³)	Dice index
subject1	13937.532	16486.486	-15821.468	0.777756
subject2	11502.702	17478.7	-20047.298	0.696347
subject3	9718.268	19207.18	-24951.732	0.634567
subject4	15346.908	24271.294	-28464.092	0.739782

Summary Overlap Measures

Subject	Total Volume (mm ³)	Ground truth (GT) volume (mm ³)	Diff. volume (BIANCA - GT) (mm ³)	Dice index
Average	12626.3525	19360.915	-22321.1475	0.712113

BIANCA

4 Post-processing



Masking

`make_bianca_mask`



Thresholding

- How to decide the best threshold?
- Is one threshold enough?

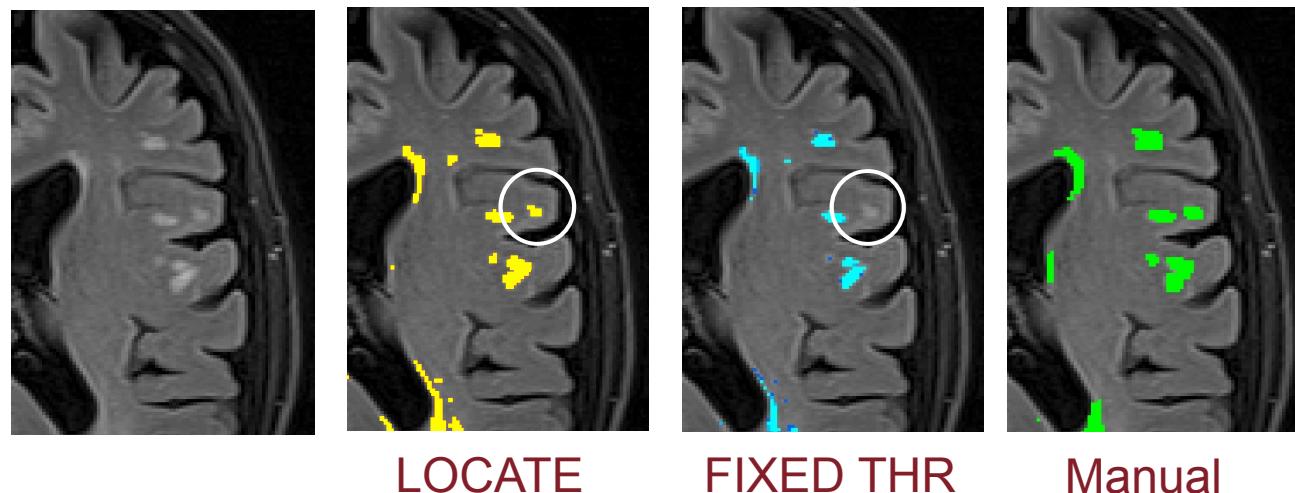
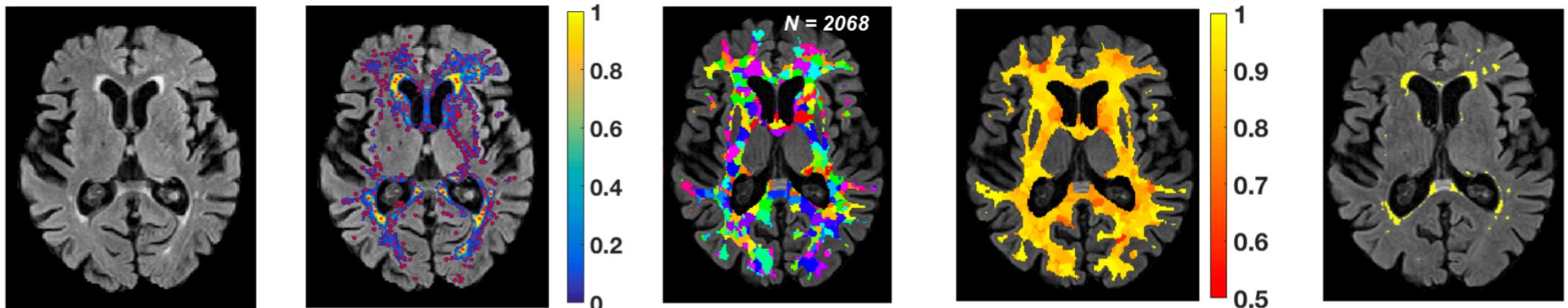




Coming soon: LOCALLy Adaptive Thresholds Estimation (LOCATE)



BIANCA



Sundaresan et al., in prep.

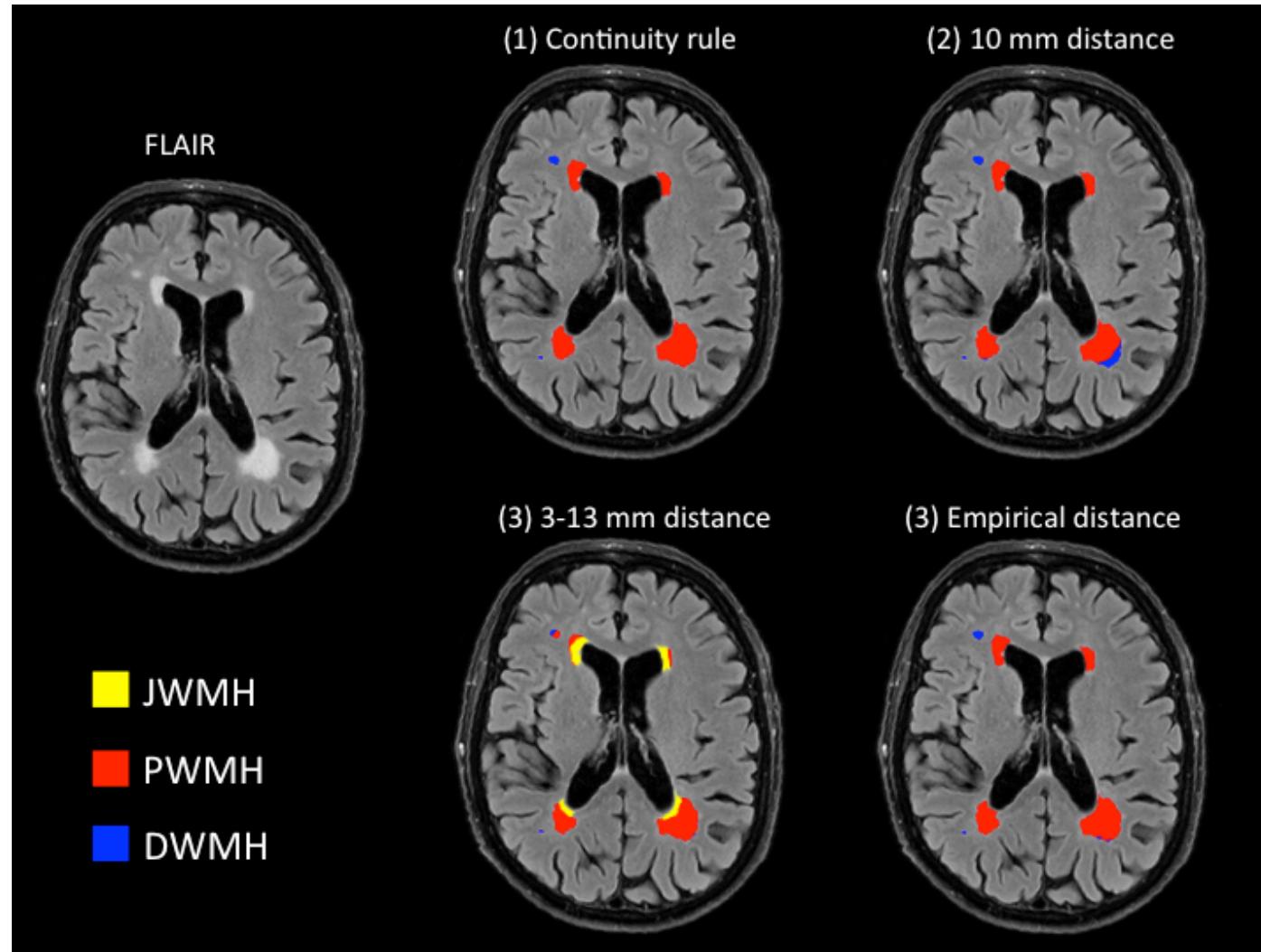
Poster n. 2587



Coming soon: WMH sub-classification



BIANCA



Griffanti et al., 2017
Neuroimage



BIANCA

Thank you

University of Oxford

Prof. Mark Jenkinson

Vaanathi Sundaresan

WIN-FMRIB Analysis Group

Poster n. 2587

USER GUIDE

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/BIANCA>

SUPPORT

<https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Support>



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centre
integrative
neuroimaging