Identification of Autism Spectrum Disorders on Brain Structural MRI with Variational Autoencoders

Melanie Garcia, Annabelle Blangero, Jean-Marc Orgogozo
Institut Hypercube, Paris, France
melanie.garcia@institut-hypercube.org, ablangero@octo.com, jean-marc.orgogozo@institut-hypercube.org

The study

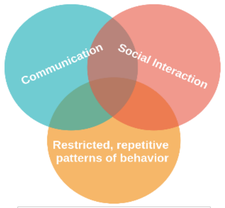
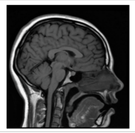


Figure on the evaluation of Autism



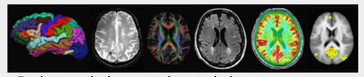
Example of sagittal section of a sMRI image

Autism Spectrum Disorders (ASD)

- Affects about 1 % of the global population
- Diagnostic based on behavioral observation
- **Evaluation very long** (about 1-3 years)

Neuroimaging

- Autism = neurodevelopmental disorder
- Brain imaging enables discoveries on neurological patterns associated with ASD



- Brain morphology can be study by Structural Magnetic Resonnance Imaging (sMRI)

Objective :
Compress sMRI data with deep autoencoder into relevant and interpretable features for Autism

Data

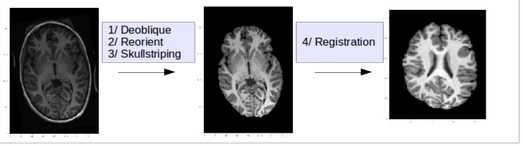
- Autism Brain Imaging Data Exchange I (ABIDE I)
- From 17 international sites
- Type of data :
  - Functional and Structural MRI
  - Preprocessing results on MRI
  - Results of diagnosis psychomotor tests
  - Age, sex, handedness
- Our study : **structural MRI** (sMRI)
- Preprocessing with C-PAC*

*Configurable Pipeline for the Analysis of Connectomes

Our work focus on structural MRI processing : **Comparison of preprocessed ABIDE 1 data from usual neuroimaging tools with our preprocessing method**

Examples of softwares used to extract neuroimaging features in ABIDE I:
- *Freesurfer*
- *SPM*
- *CIVET*
- *ANTS*

SMRI preprocessing transformations with C-PAC :



Tools

Mutual Information (MI)

Discrete MI I between two random variables X, Y :

$$I(X,Y)=\sum_{(x,y)} P(x,y)\log\frac{P(x,y)}{P(x)P(y)}$$

Recursive Feature Elimination (RFE)

- random sampling of k features to remove from X at each step
- fit an estimator on reduced X and get a performance score
- keep or remove features according to the score increase

ROC AUC Score

- area under the receiving operating characteristics curve

$$score=\int_{\infty} TPR(T)\,FPR'(T)\,dT$$

Logistic Regression (LogReg)

$$\hat{y}=logit\,P(Y=1|X=(x_{ij})_{i\in[1,n],\,j\in[1,p]})=w_0+\sum_{i=1}^{n}\sum_{j=1}^{p} w_i x_{ij}$$

Objective function :
- With L1 regularization :

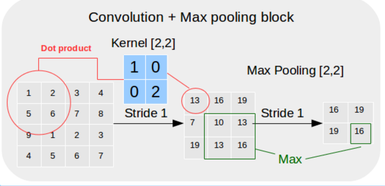
$$min_{w,w_0}\|w\|_1+C\sum_{i=1}^{n}\log(\exp(-y_i(X_i^T w+w_0))+1)$$

- With L2 regularization :

$$min_{w,w_0}\frac{1}{2}w^T w+C\sum_{i=1}^{n}\log(\exp(-y_i(X_i^T w+w_0))+1)$$

With :
$Y=(y_i)_{i\in[1,n]}$ the target variable,
$X=(x_{ij})_{i\in[1,n],j\in[1,p]}$ the explanatory variables
$w=(w_i)_{i\in[1,n]}$ the weights variable
C the regularization coefficient

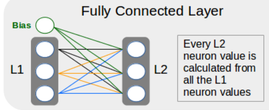
Convolution + Max pooling block



SeLu Activation Function

$$\text{selu}(x)=\lambda\begin{cases}x & \text{if } x>0\\ \alpha e^x-\alpha & \text{if } x\leqslant 0\end{cases}$$

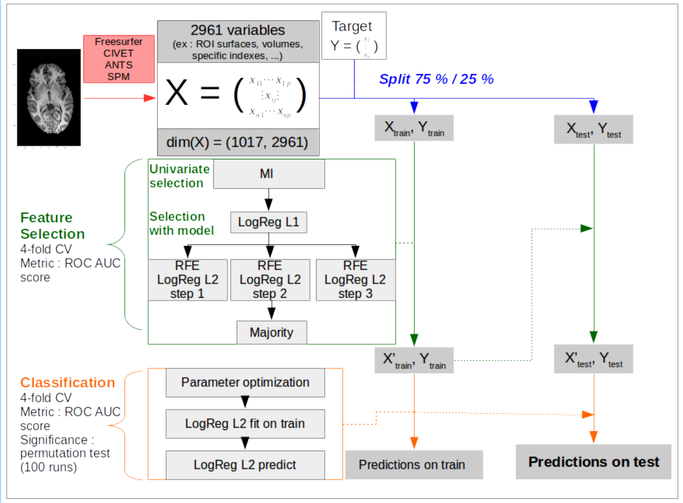
Fully Connected Layer



Every L2 neuron value is calculated from all the L1 neuron values

Methods and Results

Method 1 : Features extraction with brain imaging softwares, feature selection, classification autist / non autist



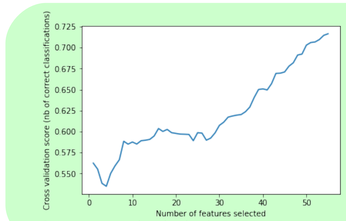
Results

dim(X) = (1017, 2436) after removing high correlated columns (Pearson's correlation coefficient > 0,9)

68 selected variables

Classification score : 0,67 (p_value = 0,01)

2 highest LogReg L2 coefficients :
- Folding index of banks of superior temporal sulcus
- Folding index of superior temporal gyrus



CV score at each selection in RFE LogReg L2 step 1

Method 2 : Features extraction with Variational Autoencoder, feature selection, classification autist / non autist

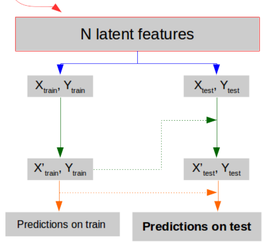
To evaluate the input distribution :

$$\log p_\theta(x)=KL(q_\phi(z|x)||p_\theta(z|x))+L(\theta,\phi;x)$$

Loss function :

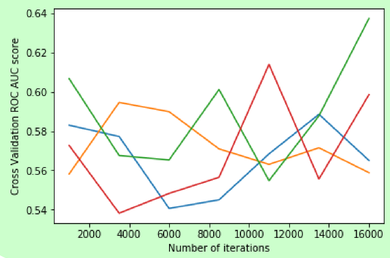
$$L(\theta,\phi;x)=\underbrace{E_{q_\phi(z|x)}\log p_\theta(x|z)}_{\text{Reconstruction Loss}}-\underbrace{KL(q_\phi(z|x)||p_\theta(z))}_{\text{Kullback-Leibler Divergence between the prior and the posterior (we guess Gaussian)}}$$

Conv. = (Convolution + Max pooling) blocks
DeConv. = Transpose (Convolution + Max pooling) blocks
FC = Fully-connected layers

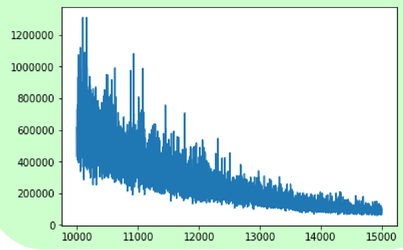


Results

Curve on the evolution of ROC AUC score according to iterations – Comparison on 4 models



Reconstruction loss during training (between 10000 and 15000 iteratons) :

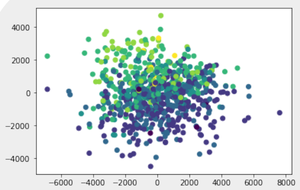


Hidden Layers	Number of encoded features	Score	Number of selected features
[512, 256]	128	0,59 (p_val = 0,01)	10
[1024, 512]	256	0,59 (p_val = 0,01)	26
[2048, 1024]	**512**	**0,65 (p_val = 0,01)**	**43**
[2048, 1024, 512]	256	0,61 (p_val = 0,01)	48

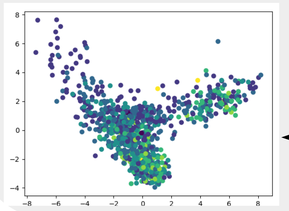
Discussion

Comparison between method 1 and method 2 extracted features

Data visualization with PCA

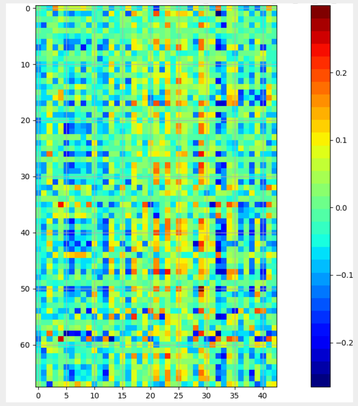


PCA on X'_{train}, coloration on age category



PCA on VAE features selected

Correlations between features selected from VAE encoding and method 1 selected features



Selected features are mostly correlated with :

Positive correlation	Negative correlation
- Right Hem. entorhinal cortex gray matter volume - Pole occipital gray matter volume	- left ventral diencephalon volume

Conclusion

- **ASD is associated with many neurological patterns which makes classification complex**
- **VAE are able to extract interesting features related to ASD from sMRI**
- **Method 2 processing time (~1 minute) < Method 1 processing time (~1 hour)**

Next steps:
- Validate the approach with another database (ABIDE 2)
- Increase the target number of modalities (to consider various modalities in ASD)
- Regularized VAE (β_VAE)

References

- Craddock, C., et al., *The Neuro Bureau Preprocessing Initiative: open sharing of preprocessed neuroimaging data and derivatives*, Neuroinformatics 2013.
- Kingma, DP., Welling, M., *Auto-Encoding Variational Bayes*, ICLR14, 2014.
- B. C. Ross "Mutual Information between Discrete and Continuous Data Sets". PLoS ONE 9(2), 2014.
- Guyon, I., Weston, J., Barnhill, S., & Vapnik, V., "Gene selection for cancer classification using support vector machines", Mach. Learn., 46(1-3), 389–422, 2002.