Support vector classification and prediction of resting-state functional connectivity over the lifespan

Scott James Peltier[1,2], Jillian Wiggins[3], Laura Jelsone-Swain[4], Christopher Monk[3], Rachael Seidler[3,5], and Robert Cary Welsh[4,6]

[1]*Functional MRI Laboratory, University of Michigan, Ann Arbor, MI, United States,* [2]*Biomedical Engineering, University of Michigan, Ann Arbor, MI, United States,* [3]*Psychology, University of Michigan, Ann Arbor, MI, United States,* [4]*Radiology, University of Michigan, Ann Arbor, MI, United States,* [5]*Kinesiology, University of Michigan, Ann Arbor, MI, United States,* [6]*Psychiatry, University of Michigan, Ann Arbor, MI, United States*

INTRODUCTION

Resting-state functional connectivity has the potential to characterize normal development and aging in brain networks. Multivariate pattern classification and prediction offers an alternative to standard univariate analysis techniques, and has recently been applied in MR imaging using support vector machines (SVM) [1].

Previous work using multivariate techniques to characterize brain maturity from resting-state scans [2,3] either did not look at an extended age range, or combined disparate data sets from multiple sites. This study extends the investigation of predicting brain age using resting-state scans to the entire lifespan, using a large matched sample from one site.

METHODS

Data were acquired on a 3.0 T GE scanner. T2*-weighted data was acquired using a spiral-in sequence (TR/TE/FA/FOV=2s/30ms/90/22cm, 64x64 matrix, 3mm slice thickness, 40 slices). Anatomical T1 overlays matching the prescription of the functional data and whole-brain T1 SPGRs were also collected. 188 subjects in total were scanned: <18 years old (n = 73, 16 F), 18-50 years old (n = 38, 13 F), > 50 years old, (n = 77, 34 F). Subjects were instructed to keep their eyes open using a fixation cross during the resting state acquisition (8 min duration, 240 timeframes).

All data was preprocessed using SPM8, including slice timing correction and realignment, anatomical coregistration and segmentation, normalization to MNI space, and spatial smoothing (5mm FWHM). Nuisance regressors (white matter, CSF, and motion) were removed prior to band-pass filtering. Timecourses were extracted using the 160 ROIs defined in [1], and correlation matrices were formed.

Support vector machine learning was performed using the 3dsvm toolbox [1] in AFNI [4], using the correlation matrices for each subject, labeled by age. Binary SVM classification was performed using a linear kernel and multistate classification, using young (<18), middle (18-50), and old age (>50) as labels. Support vector regression was performed using a linear kernel and epsilon width of 0.1. Leave-one-out cross-validation (LOOCV) was used to calculate classification accuracies and predicted values. Regression model weights were averaged across all LOOCV permutations, absolute value taken, and summed for all ROIs.

RESULTS

SVM multistate classification results in 87% accuracy in classifying young vs. old, 75% for middle vs. old, and 68% for young vs. middle.

Support vector regression resulted in a predicted brain age that tracked well with chronological age (see Figure 1). The top weights in the regression model were located in the cingulo-opercular and default mode networks (Table 1 and Figure 2).

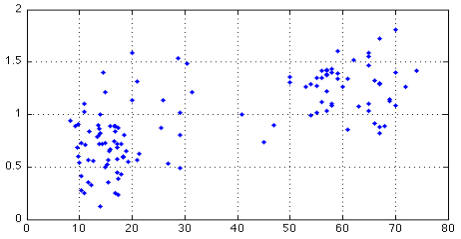

Figure 1. Chronological age vs predicted brain maturity. Maturity values are normalized to predicted value at 40 years of age.

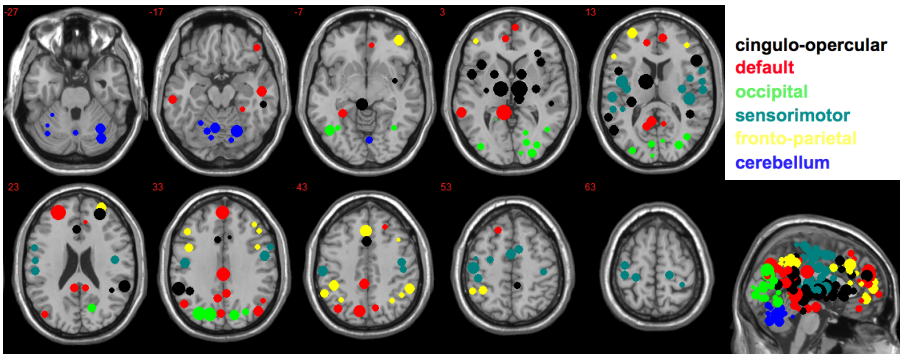

Figure 2. Summed absolute regression weights for each ROI, overlaid on standard MNI anatomy. The size of each circle is scaled to the maximum weight, and color corresponds to its network identity, defined in [1]. MNI z coordinate is displayed for each slice.

MNI coordinates x	y	z	Relative weight	Label	Network
11	-12	6	1	thalamus	cingulo-opercular
-12	-3	13	0.9	thalamus	cingulo-opercular
-8	-41	3	0.87	Posterior cingulate	default
-12	-12	6	0.86	thalamus	cingulo-opercular
-25	51	27	0.84	aPFC	default
-55	-44	30	0.82	parietal	cingulo-opercular
0	51	32	0.81	mPFC	default
-16	-76	33	0.8	occipital	occipital
-29	-75	28	0.76	occipital	occipital
1	-26	31	0.74	Posterior cingulate	default

Table 1. Top ten nodes having the highest summed absolute average weights in the regression model.

DISCUSSION

Thalamic and default mode network nodes were implicated in being important in the aging process, agreeing with previous studies [2,3]. This work demonstrates that aging can be investigated across the lifespan, which can form the basis for examining age-dependent pathologies, such as autism or Alzheimer's Disease. Alternate kernels and feature selection will also be investigated.

References: [1] LaConte et al., NeuroImage, 26:317 (2005). [2] Dosenbach et al., Science 329:1358 (2010). [3] Wang, et al., PLOS One, 7:1 (2012). [4] Cox. Comp. Biomed. Res, 29:162 (1996).