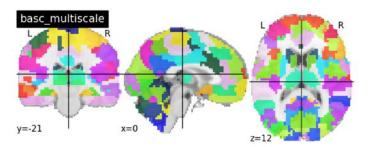
Supplementary Table 1: Description of studies that provided machine learning model for predicting schizophrenia using resting-state brain patterns (SCZ: Schizophrenia, HC: Healthy controls; AH: Auditory Hallucinations, FE: First episode, MDD: Major Depression, CV: Cross-validation, LOO: leave one out)

Study	Year	Sample size	Multi/Single Site	Data Acquisition	Feature selection/reduction	Classifier	CV	Accuracy	Reference
Shen	2010	32 SCZ, 20 HC	single-site (Second Xiangya Hospital of Central South University in Changsha, China)	Resting state	Kendall tau correlation - low-dimensional embedding	C-Means clustering	LOO	86.50%	Shen, H., Wang, L., Liu, Y., & Hu, D. (2010). Discriminative analysis of resting-state functional connectivity patterns of schizophrenia using low dimensional embedding of fMRI. NeuroImage, 49(4), 3110–3121. https://doi.org/10.1016/j.neuroImage.2009.11.011
Fan	2011	31 SCZ, 31 HC	Single-site (Institute of Mental Health, Second Xiangya Hospital, China)	Resting state	ICA + Grassmann manifold	SVM - various kernels	LOO	upto 87.1%	Fan, Y., Liu, Y., Wu, H., Hao, Y., Liu, H., Liu, Z., & Jiang, T. (2011). Discriminant analysis of functional connectivity patterns on Grassmann manifold. NeuroImage, 56(4), 2058–2067. https://doi.org/10.1016/j.neuroImage.2011.03.051
Anderson	2013	74 SCZ, 72 HC	single-site (COBRE dataset -multiple studies from University of New Mexico)	Resting state	ICA, graph-theoretic connectivity measures such as graph density, average path length, and small-worldness.	SVM	10-fold	65%	Anderson A, & Cohen MS. (2013). Decreased small-world functional network connectivity and clustering across resting state networks in schizophrenia: an fMRI classification tutorial. Frontiers in human neuroscience, 7, 520-520. doi: 10.3389/fnhum.2013.00520
Arbabshirani	2013	28 SCZ, 28 HC	single-site (Hartford hospital and Yale)	Resting state	ICA	Multiple Learners	LOO	upto 96%	Arbabshirani, M., Kiehl, K., Pearlson, G., & Calhoun, V. (2013). Classification of schizophrenia patients based on resting-state functional network connectivity . <i>Frontiers in Neuroscience</i> . Retrieved from http://journal.frontiersin.org/article/10.3389/fnins.2013.00133
Yu	2013	24 SCZ, 25 healthy siblings of SCZ, 22 HC	single-site (Second Xiangya Hospital of Central South University)	Resting state	PCA	SVM	LOO	62.00%	Yu, Y., Shen, H., Zhang, H., Zeng, LL., Xue, Z., & Hu, D. (2013). Functional connectivity-based signatures of schizophrenia revealed by multiclass pattern analysis of resting-state fMRI from schizophrenic patients and their healthy siblings. <i>Biomedical Engineering Online</i> , 12, 10. https://doi.org/10.1186/1475-925X-12-10
Yu	2013	32 SCZ, 38 HC (+19 MDD)	Single-site (Second Xiangya Hospital of Central South University)	Resting state	intrinsic discriminant analysis	SVM	LOO	80.9%	Yu, Y., Shen, H., Zeng, LL., Ma, Q., & Hu, D. (2013). Convergent and divergent functional connectivity patterns in schizophrenia and depression. PloS One, 8(7), e68250. https://doi.org/10.1371/journal.pone.0068250
Anticevic	2014	90 SCZ, 90 HC	single-site (outpatient clinics and community mental health facilities in the Hartford area)	Resting state	MVPA	linear SVM	LOO	73.9%	Anticevic, A., Cole, M. W., Repovs, G., Murray, J. D., Brumbaugh, M. S., Winkler, A. M., Glahn, D. C. (2014). Characterizing thalamo-cortical disturbances in schizophrenia and bipolar illness. Cerebral Cortex (New York, N.Y.: 1991), 24(12), 3116–3130. https://doi.org/10.1093/cercor/bht165

Watanabe	2014	54 SCZ, 67 HC	single-site (COBRE dataset -multiple studies from University of New Mexico)	Resting state	Fused Lasso or the GraphNet regularizer.	SVM	10-fold	73.50%	Watanabe, T., Kessler, D., Scott, C., Angstadt, M., & Sripada, C. (2014). Disease prediction based on functional connectomes using a scalable and spatially-informed support vector machine. NeuroImage, 96, 183–202. https://doi.org/10.1016/j.neuroImage.2014.03.067
Guo S	2014	69 SCZ, 62 HC	Single-site (National Taiwan University Hospital)	Resting state	FC link effect	SVM	LOO	80%	Guo, S., Kendrick, K. M., Yu, R., Wang, HL. S., & Feng, J. (2014). Key functional circuitry altered in schizophrenia involves parietal regions associated with sense of self. Human Brain Mapping, 35(1), 123–139. https://doi.org/10.1002/hbm.22162
Brodersen	2014	41 SCZ, 42 HC	Single-site (Department of Psychiatry and Psychotherapy (Campus Charité Mitte) of the Charité Universitätsmedizin)	n- back working- memory task	dynamic causal model (DCM), FC & regional activity	linear SVM, variational Bayesian Gaussian mixture model	5 fold CV	upto 78%	Brodersen, K. H., Deserno, L., Schlagenhauf, F., Lin, Z., Penny, W. D., Buhmann, J. M., & Stephan, K. E. (2014). Dissecting psychiatric spectrum disorders by generative embedding. NeuroImage. Clinical, 4, 98–111. https://doi.org/10.1016/j.nicl.2013.11.002
Arbabshirani	2014	195 SCZ, 175 HC	multi-site (7 sites)	Resting state	GICA + FC / Autoconnectivity (AR1) + minimum redundancy maximum relevancy	SVM (various kernels)	10 fold CV ?? (not clear)	85% ? (table says 88.2%)	Arbabshirani, M. R., Castro, E., & Calhoun, V. D. (2014). Accurate classification of schizophrenia patients based on novel resting-state fMRI features. Conference Proceedings: Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Annual Conference, 2014, 6691–6694. https://doi.org/10.1109/EMBC.2014.6945163
Chyzhyk	2015	26 SCZ with history of without a history of		Resting state	Heschl's gyrus seed based FC computed by lattice auto-associative memories	SVM	10-fold	upto 97.1%	Chyzhyk, D., Grana, M., Ongur, D., & Shinn, A. K. (2015). Discrimination of schizophrenia auditory hallucinators by machine learning of resting-state functional MRI. <i>International Journal of Neural Systems</i> , <i>25</i> (3), 1550007. https://doi.org/10.1142/S0129065715500070
Cheng	2015	19 SCZ, 29 HC	single-site (Indiana University)	Resting state	Betweenness centrality	Linear SVM	LOO	79%	Cheng, H., Newman, S., Goni, J., Kent, J. S., Howell, J., Bolbecker, A., Hetrick, W. P. (2015). Nodal centrality of functional network in the differentiation of schizophrenia. <i>Schizophrenia Research</i> , 168(1–2), 345–352. https://doi.org/10.1016/j.schres.2015.08.011
Cheng	2015	415 SCZ, 405 HC	multi-site (UK, USA, Taiwan, and China)	Resting state	region and voxel-based brain-wide association	SVM	LOO	75.81 (overall)	Cheng, W., Palaniyappan, L., Li, M., Kendrick, K. M., Zhang, J., Luo, Q., Feng, J. (2015). Voxel-based, brain-wide association study of aberrant functional connectivity in schizophrenia implicates thalamocortical circuitry. NPJ Schizophrenia, 1, 15016. https://doi.org/10.1038/npjschz.2015.16

Peters	2016	18 SCZ, 18 HC	single-site (Department of Psychiatry, Klinikum Rechts der Isar, TU München)	Resting state	Network and ROI FC	SVM	LOO	91% with allROIs- NWs	Peters, H., Shao, J., Scherr, M., Schwerthoffer, D., Zimmer, C., Forstl, H., Sorg, C. (2016). More Consistently Altered Connectivity Patterns for Cerebellum and Medial Temporal Lobes than for Amygdala and Striatum in Schizophrenia. Frontiers in Human Neuroscience, 10, 55. https://doi.org/10.3389/fnhum.2016.00055
Mikolas	2016	63 SCZ with FES, 63 HC	single-site (Bohnice Psychiatric Hospital, Prague)	Resting state	seed-based connectivity	Linear SVM	LOO	73.00%	Mikolas, P., Melicher, T., Skoch, A., Matejka, M., Slovakova, A., Bakstein, E., Spaniel, F. (2016). Connectivity of the anterior insula differentiates participants with first-episode schizophrenia spectrum disorders from controls: a machine-learning study. Psychological Medicine, 46(13), 2695–2704. https://doi.org/10.1017/S0033291716000878
Cabral	2016	66 SCZ, 66 HC	single-site (COBRE dataset -multiple studies from University of New Mexico)	Resting state (+ Structural MRI)	mutual Information + PCA	L2-regularized Logistic Regression	20 x 20 repeated double CV framework	70.5% (75% when combined with structural)	Cabral, C., Kambeitz-Ilankovic, L., Kambeitz, J., Calhoun, V. D., Dwyer, D. B., von Saldern, S., Koutsouleris, N. (2016). Classifying Schizophrenia Using Multimodal Multivariate Pattern Recognition Analysis: Evaluating the Impact of Individual Clinical Profiles on the Neurodiagnostic Performance. <i>Schizophrenia Bulletin</i> , <i>42 Suppl 1</i> , S110-7. https://doi.org/10.1093/schbul/sbw053
Skåtun	2016	182 SCZ spectrum, 348 HC	multi-site (1 from the University of Oslo, Norway and 2 from Karolinska Institutet, Stockholm, Sweden)	Resting state	ICA	regularized linea discriminant ana		upto 78.3%	Skatun, K. C., Kaufmann, T., Doan, N. T., Alnaes, D., Cordova-Palomera, A., Jonsson, E. G., Westlye, L. T. (2016). Consistent Functional Connectivity Alterations in Schizophrenia Spectrum Disorder: A Multisite Study. Schizophrenia Bulletin. https://doi.org/10.1093/schbul/sbw145
Yang	2016	40 SCZ, 46 HC	single-site (University of New Mexico, USA.)	Resting state(+ Structural MRI)	GICA	SVM, Maximum- linear discrimina	•	77·91% (combined)	Yang, H., He, H., & Zhong, J. (2016). Multimodal MRI characterisation of schizophrenia: a discriminative analysis. Lancet (London, England), 388 Suppl, S36. https://doi.org/10.1016/S0140-6736(16)31963-8
Iwabuchi	2017	62 SCZ, 71 HC	single-site (COBRE dataset -multiple studies from University of New Mexico)	Resting state	seed-based Granger causality analysis	SVM-multiple kernel learning classifier	LOO	78.04% (ReHO) - combined was lesser	Iwabuchi, S. J., & Palaniyappan, L. (2017). Abnormalities in the effective connectivity of visuothalamic circuitry in schizophrenia. Psychological Medicine, 1–11. https://doi.org/10.1017/S0033291716003469
Lottman	2017	34 unmedicated (17 drug-naïve) SCZ + follow-up post-treatment, 35 HC	single-site (University of Alabama at Birmingham)	Resting state	GICA -Static & Dynamic FC	linear SVM	LOO	83.8% (combined static & Dynamic FC) - static only:	Lottman, K. K., Kraguljac, N. V, White, D. M., Morgan, C. J., Calhoun, V. D., Butt, A., & Lahti, A. C. (2017). Risperidone Effects on Brain Dynamic Connectivity-A Prospective Resting-State fMRI Study in Schizophrenia. Frontiers in Psychiatry, 8, 14. https://doi.org/10.3389/fpsyt.2017.00014

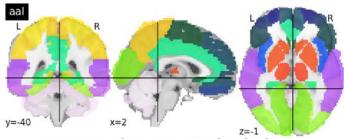
								73.5%	
Guo W	2017	28 FE drug- naive SCZ, 28 family-based controls, 40 HC	single-site (Mental Health Center of the First Affiliated Hospital, Guangxi Medical University in China)	Resting state	Voxel-mirrored homotopic connectivity	rbf SVM	LOO	92.86% (overfitting ??)	Guo, W., Liu, F., Chen, J., Wu, R., Li, L., Zhang, Z., & Zhao, J. (2017). Family-based case-control study of homotopic connectivity in first-episode, drug-naive schizophrenia at rest. <i>Scientific Reports</i> , 7, 43312. https://doi.org/10.1038/srep43312

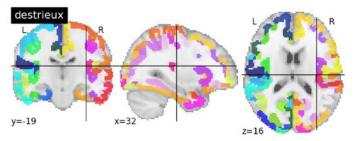


yeo L R R X=-1 Z=9

Multi-level bootstrap analysis of stable clusters







Automated Anatomical Labeling

Sulcal depth-based anatomical parcellation

Supplementary Figure 1: MRI overlay of representative atlases that were used for parcellation in the study.

The coordinate mapping information used to these create figures comes from public data made available by the studies cited in the manuscript. Here, the basic boundaries of 3D areas from the schematic atlases is redrawn on one of our study subjects.

Supplementary Table 2. Demographic and clinical profile of study subjects

Characteristic	Schizophrenia	Control	Stat	р
N	81	93		
Sex [M:F]	53:28	60:33	0.001 ¶	0.97
Age	30.72 ± 6.16	29.41 ± 5.71	1.45 ^{\$}	0.15
Total Intracranial Volume (TICV, mL)	1400 ± 135	1480 ± 144	3.76 ^{\$}	<0.001
Age at onset	26.6 ± 6.17	-	-	-
Duration of untreated illness (months)	36.95 ± 51.08	-	-	-
Total positive symptoms (SAPS)	27.65 ± 12.22	-	-	-
Total negative symptoms (SANS)	32.11 ± 27.79	-	-	-

^{\$} Independent Samples Test [t]

Men had significantly greater TICV than women ($Stat^{\$} = 6.7$, p < 0.001), and age showed significant negative correlation with TICV (pearson r = -0.24, p = 0.001)

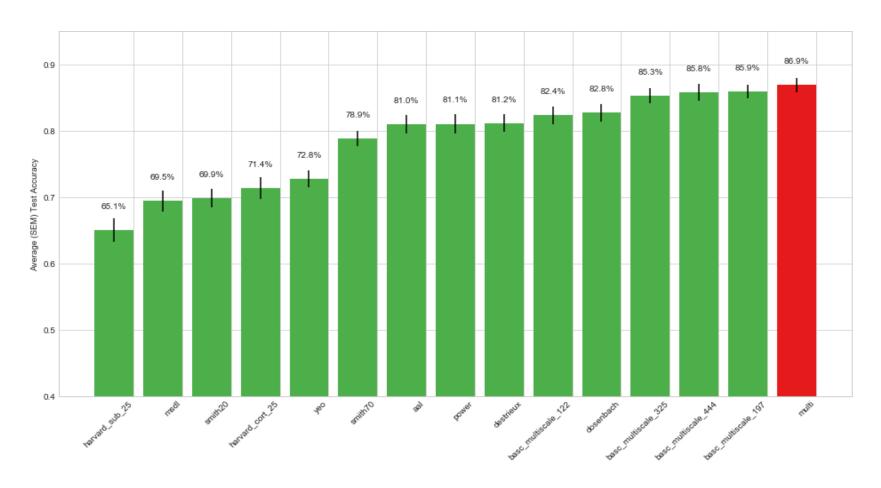
[¶] Chi-Square test $[\chi^2]$

Supplementary Table 3. Performance accuracy in percentage of single-source and stacked models for various feature-type and parcellations

	FC_c	orr	FC_p	art	FC_p	rec	AL	FF	Re	Но	fAL	.FF
	Mean	Stdev	Mean	Stdev	Mean	Stdev	Mean	Stdev	Mean	Stdev	Mean	Stdev
harvard_sub_25	0.67	0.12	0.55	0.12	0.52	0.10	0.67	0.10	0.69	0.10	0.61	0.11
smith20	0.68	0.12	0.63	0.11	0.65	0.10	0.64	0.12	0.67	0.12	0.67	0.12
msdl	0.72	0.12	0.59	0.11	0.59	0.11	0.67	0.09	0.71	0.10	0.70	0.11
harvard_cort_25	0.67	0.12	0.67	0.10	0.70	0.11	0.70	0.11	0.70	0.12	0.73	0.12
yeo	0.67	0.11	0.71	0.10	0.71	0.09	0.69	0.11	0.71	0.10	0.72	0.10
smith70	0.79	0.11	0.73	0.12	0.76	0.09	0.69	0.11	0.73	0.10	0.70	0.11
aal	0.71	0.09	0.75	0.11	0.78	0.12	0.72	0.11	0.72	0.11	0.73	0.10
destrieux	0.73	0.11	0.74	0.09	0.75	0.09	0.74	0.10	0.75	0.11	0.72	0.11
dosenbach	0.75	0.09	0.74	0.10	0.75	0.10	0.73	0.10	0.74	0.11	0.75	0.11
basc_multiscale_122	0.76	0.09	0.78	0.09	0.78	0.09	0.74	0.10	0.73	0.11	0.75	0.10
power	0.75	0.11	0.75	0.08	0.77	0.10	0.79	0.10	0.76	0.10	0.75	0.11
basc_multiscale_197	0.82	0.11	0.80	0.08	0.82	0.09	0.77	0.10	0.76	0.11	0.72	0.11
basc_multiscale_325	0.81	0.10	0.79	0.09	0.81	0.09	0.78	0.09	0.76	0.10	0.75	0.11
basc_multiscale_444	0.81	0.09	0.77	0.08	0.83	0.10	0.77	0.10	0.77	0.11	0.78	0.08
							! !					
stack_*	0.82	0.09	0.79	0.10	0.84	0.08	0.76	0.10	0.74	0.11	0.75	0.10

Supplementary Table 4. Model performance (in percentage) of the various parcellation-wise stacked learners: average (standard errors). All results are 10-fold CV.

	Accuracy	Precision	Sensitivity	Specificity
stacked-multi	86.9 (1.1)	91.9 (1.4)	79.8 (1.8)	93.1 (1.2)
stacked-aal	81.0 (1.4)	83.1 (1.9)	76.1 (2.1)	85.3 (1.6)
stacked-basc_multiscale_122	82.4 (1.3)	86.0 (1.8)	76.1 (1.6)	87.9 (1.7)
stacked-basc_multiscale_197	85.9 (1.0)	89.9 (1.3)	79.9 (1.8)	91.1 (1.3)
stacked-basc_multiscale_325	85.3 (1.1)	89.6 (1.4)	78.2 (1.8)	91.5 (1.2)
stacked-basc_multiscale_444	85.8 (1.3)	89.8 (1.6)	80.2 (2.3)	90.7 (1.6)
stacked-destrieux	81.2 (1.3)	86.2 (1.8)	72.7 (2.2)	88.6 (1.6)
stacked-dosenbach	82.8 (1.4)	87.3 (1.7)	76.1 (2.2)	88.6 (1.8)
stacked-harvard_cort_25	71.4 (1.7)	74.7 (2.3)	61.9 (2.7)	79.7 (2.2)
stacked-harvard_sub_25	65.1 (1.8)	64.5 (2.4)	58.8 (2.7)	70.5 (2.2)
stacked-msdl	69.5 (1.6)	69.7 (1.9)	62.1 (2.5)	75.9 (1.9)
stacked-power	81.1 (1.5)	82.3 (1.9)	77.8 (2.3)	84.0 (1.9)
stacked-smith20	69.9 (1.4)	71.8 (2.2)	62.5 (2.1)	76.4 (2.0)
stacked-smith70	78.9 (1.2)	83.8 (1.8)	70.8 (2.2)	85.9 (1.8)
stacked-yeo	72.8 (1.3)	71.8 (1.5)	69.9 (2.2)	75.3 (1.6)



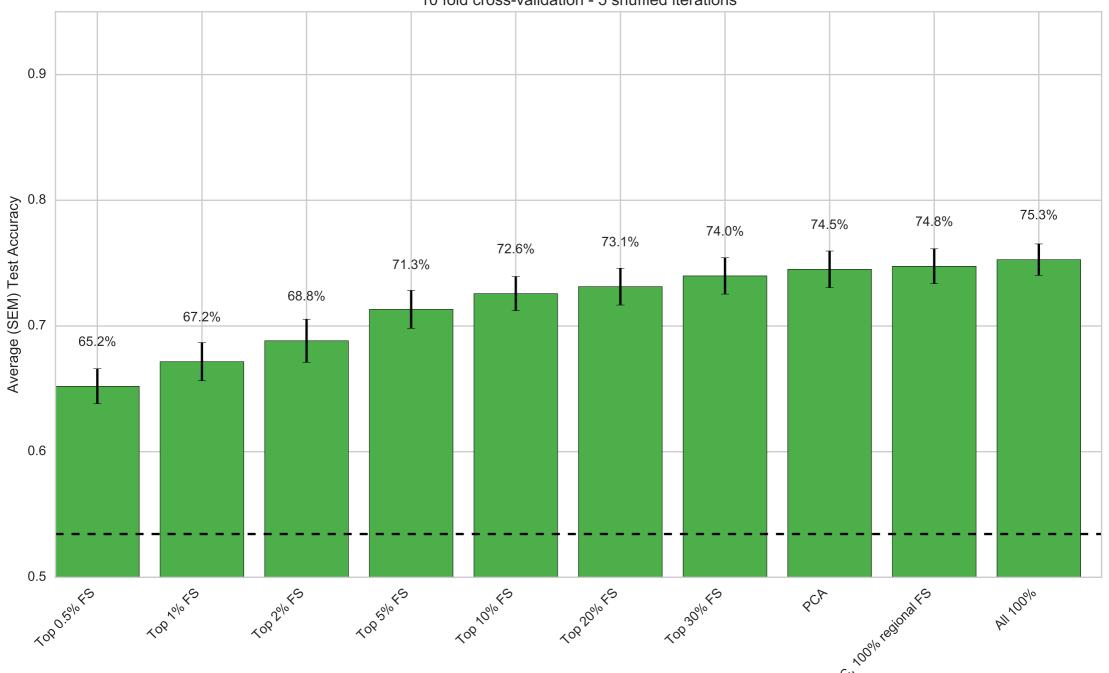
Supplementary Figure 2. Comparison of 10-fold cross-validation prediction accuracies for parcellation-wise stacked learners.

Supplementary Table 5. Performance in percentage of multi-source ensemble models with various feature selection (FS) / reduction criteria (Average and standard errors)

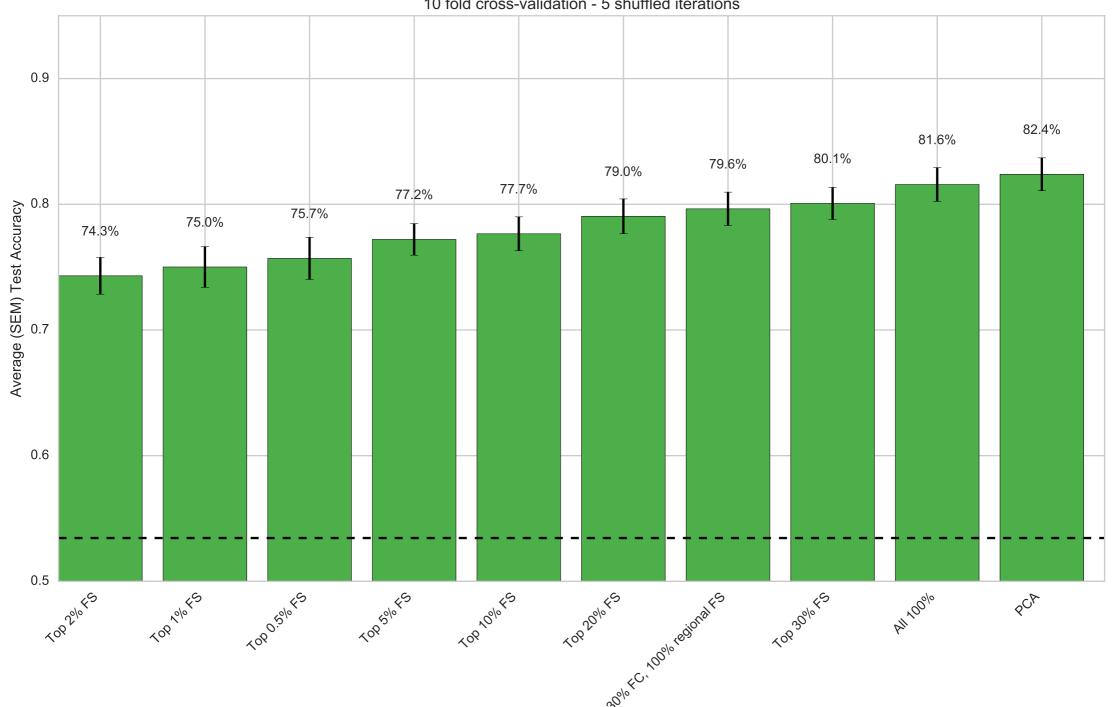
	Accuracy	Precision	Sensitivity	Specificity
PCA	0.87 (0.01)	0.92 (0.01)	0.8 (0.02)	0.93 (0.01)
Top 0.5 % FS	0.82 (0.01)	0.92 (0.01)	0.67 (0.02)	0.95 (0.01)
Top 1 % FS	0.82 (0.01)	0.92 (0.01)	0.69 (0.02)	0.94 (0.01)
Top 2 % FS	0.83 (0.01)	0.93 (0.01)	0.69 (0.02)	0.95 (0.01)
Top 5 % FS	0.83 (0.01)	0.93 (0.01)	0.69 (0.02)	0.95 (0.01)
Top 10 % FS	0.83 (0.01)	0.93 (0.01)	0.69 (0.02)	0.95 (0.01)
Top 20 % FS	0.82 (0.01)	0.91 (0.01)	0.7 (0.02)	0.94 (0.01)
Top 30 % FS	0.83 (0.01)	0.93 (0.02)	0.69 (0.02)	0.95 (0.01)
Top 30 % FC, 100 % Regional FS	0.84 (0.01)	0.92 (0.01)	0.72 (0.02)	0.94 (0.01)
All 100 % FS (No FS)	0.85 (0.01)	0.93 (0.01)	0.73 (0.02)	0.95 (0.01)

Comparison of prediction accurac	cy for stacked models with various featu Final ensemble model shown in red.	ure selection/reduction methods.

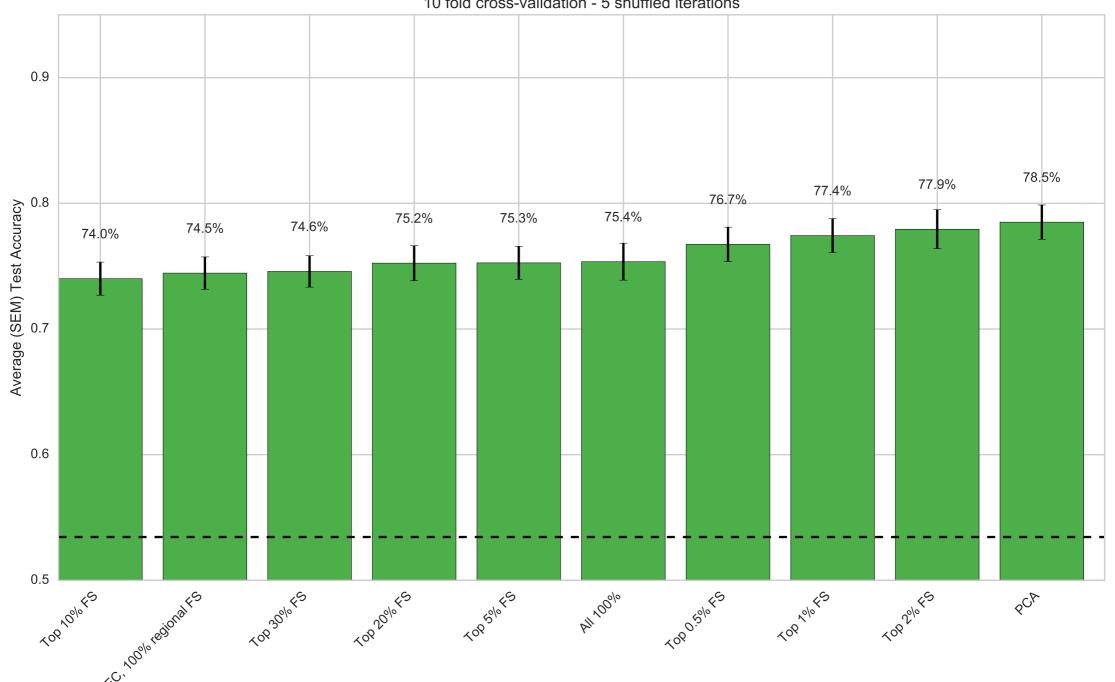
fALFF
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations



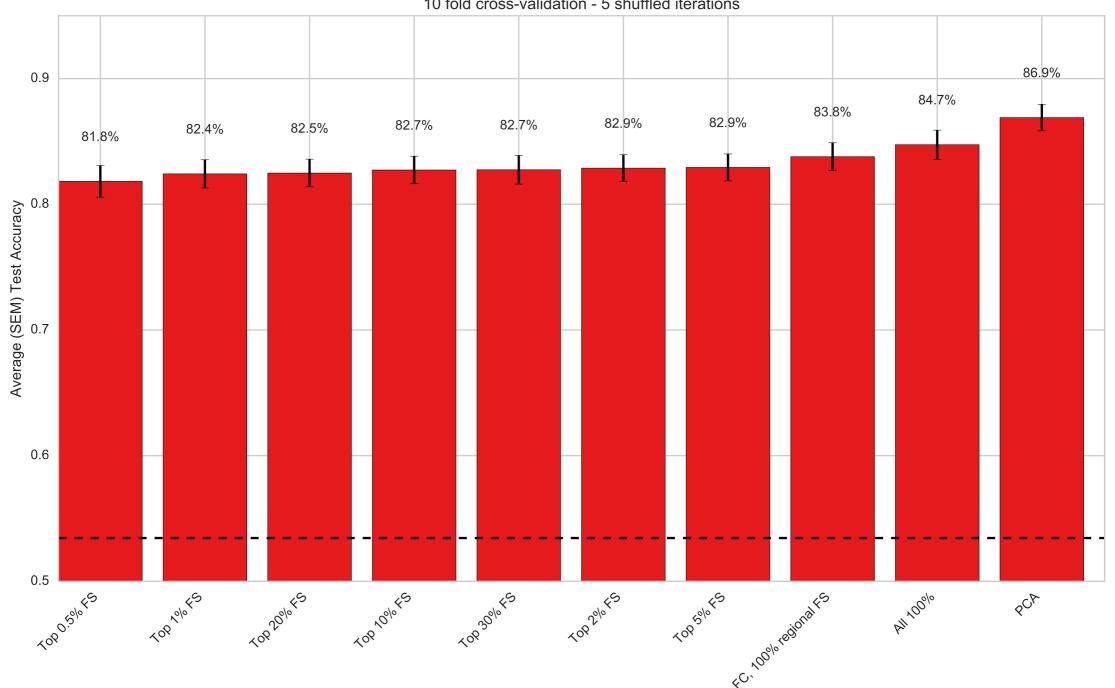
FC_corr
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations



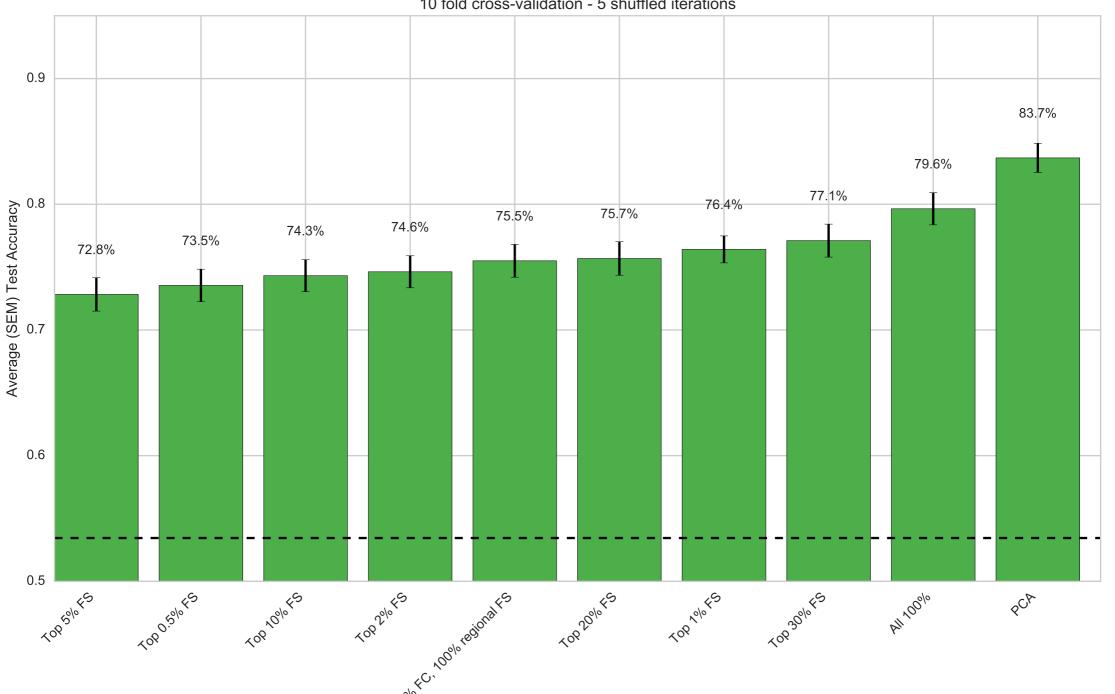
FC_part
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations



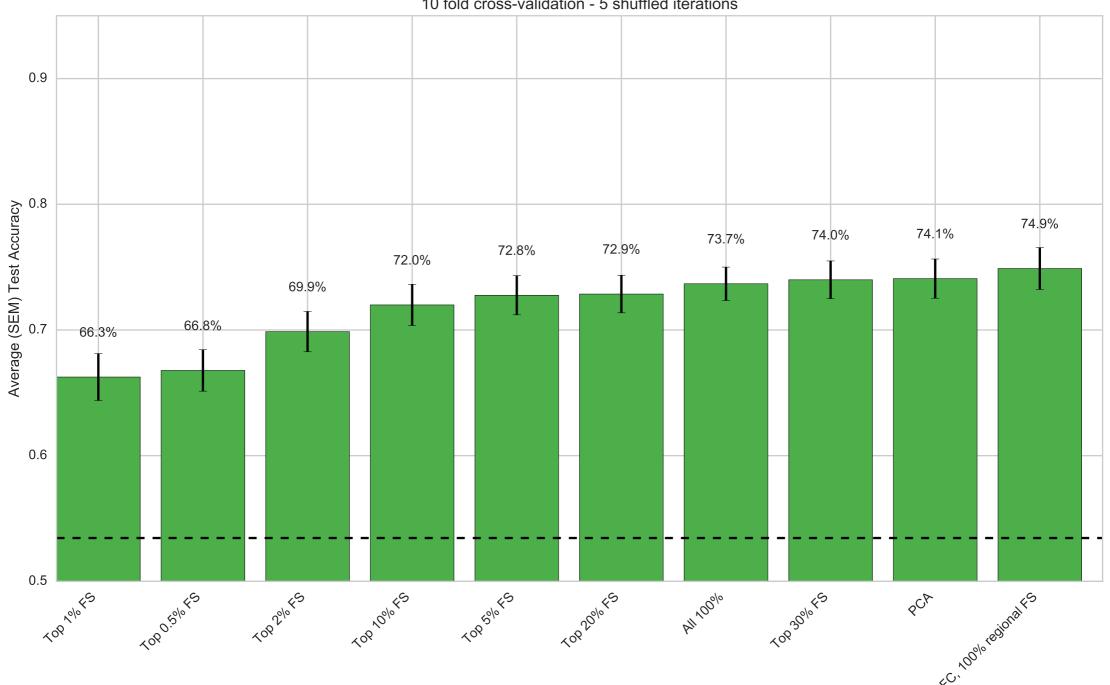
multi
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations



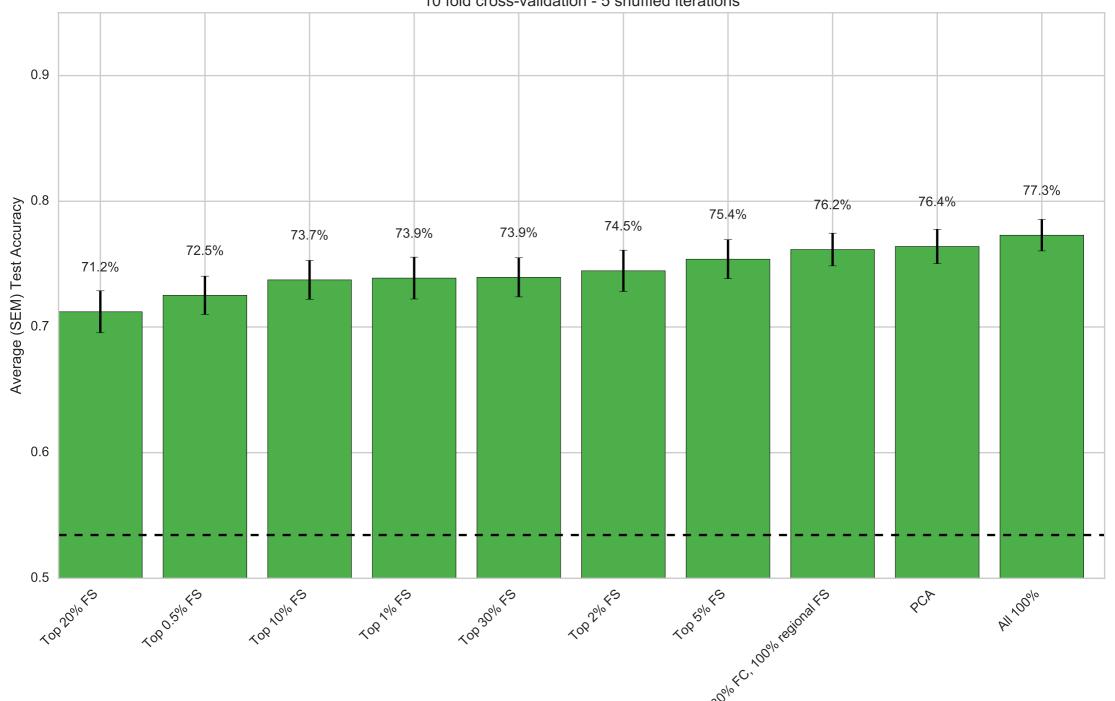
FC_prec
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations



ReHo
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations

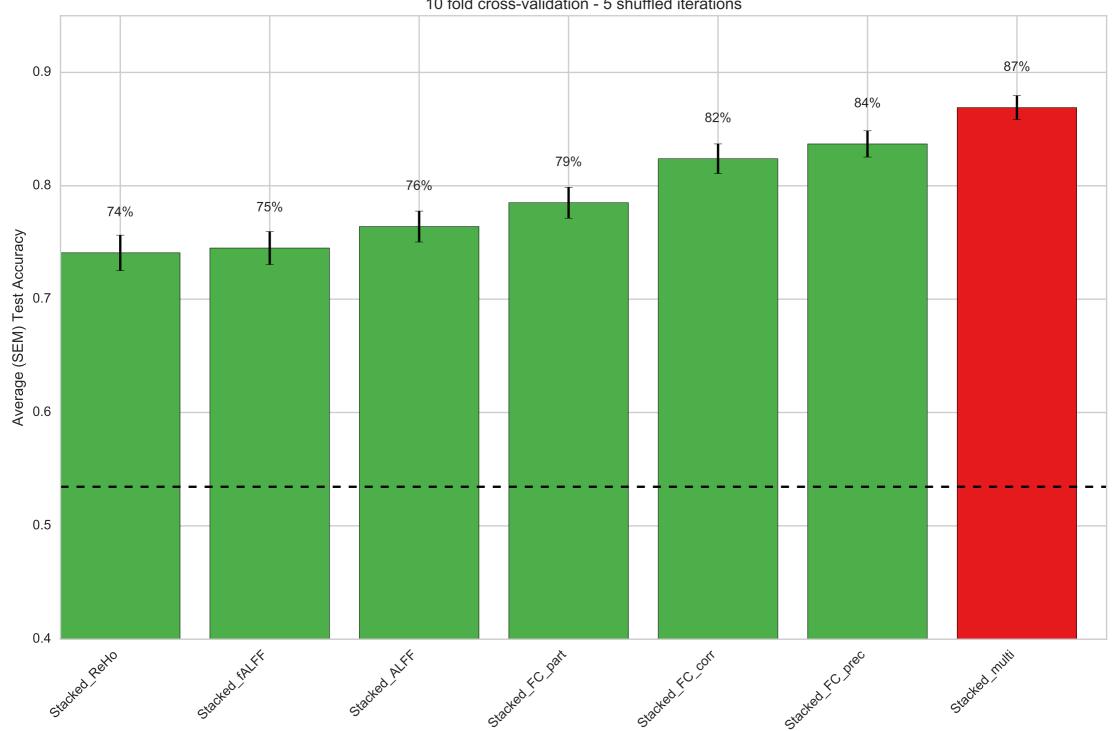


ALFF
Comparison across various feature selection / reduction methods
10 fold cross-validation - 5 shuffled iterations

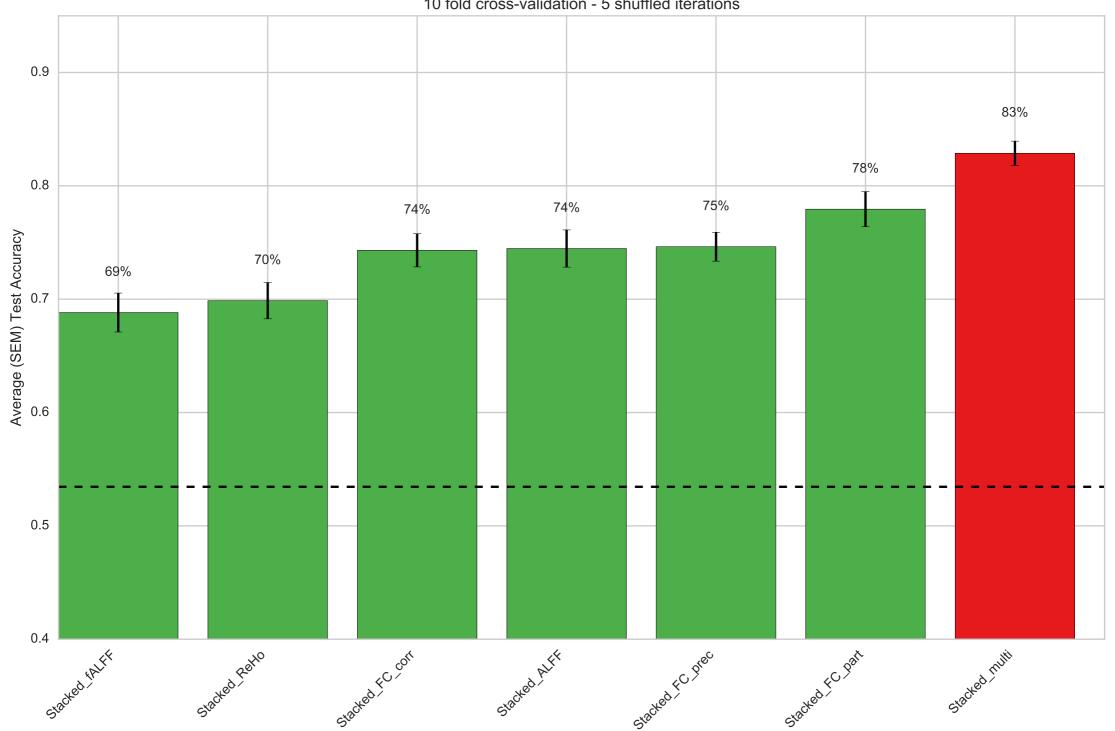


Comparison of prediction accuracy for stacked models of various feature types. Final ensemble model shown in red.

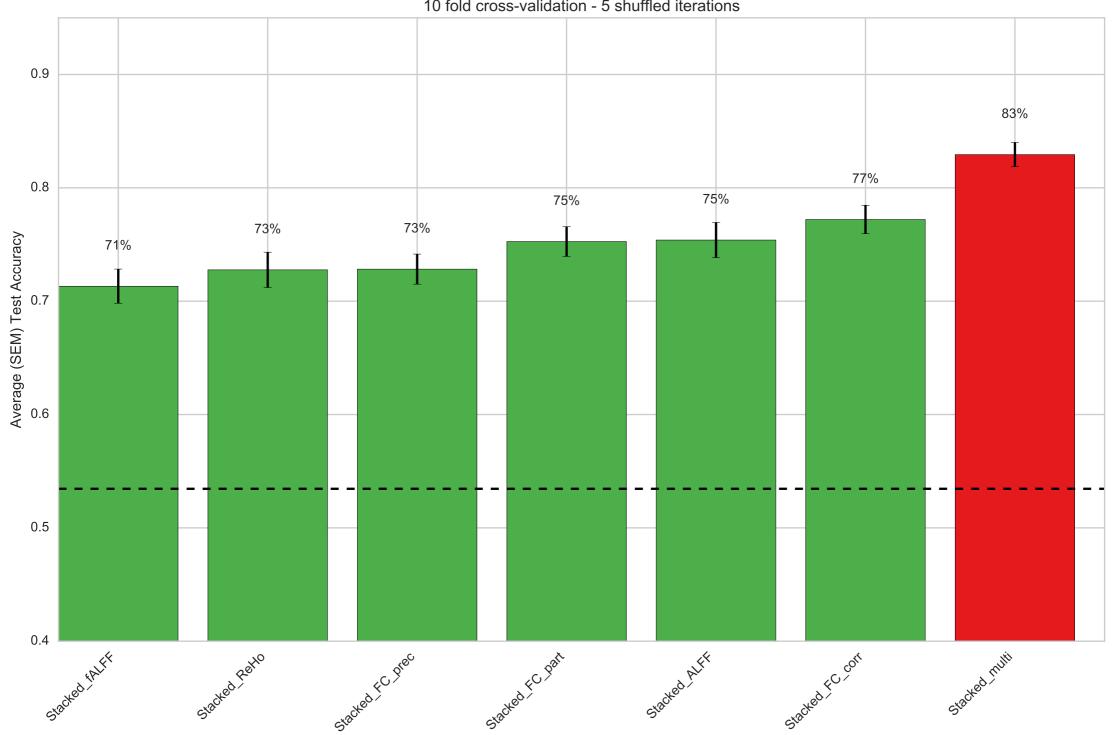
PCA - Dimensional Reduction
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



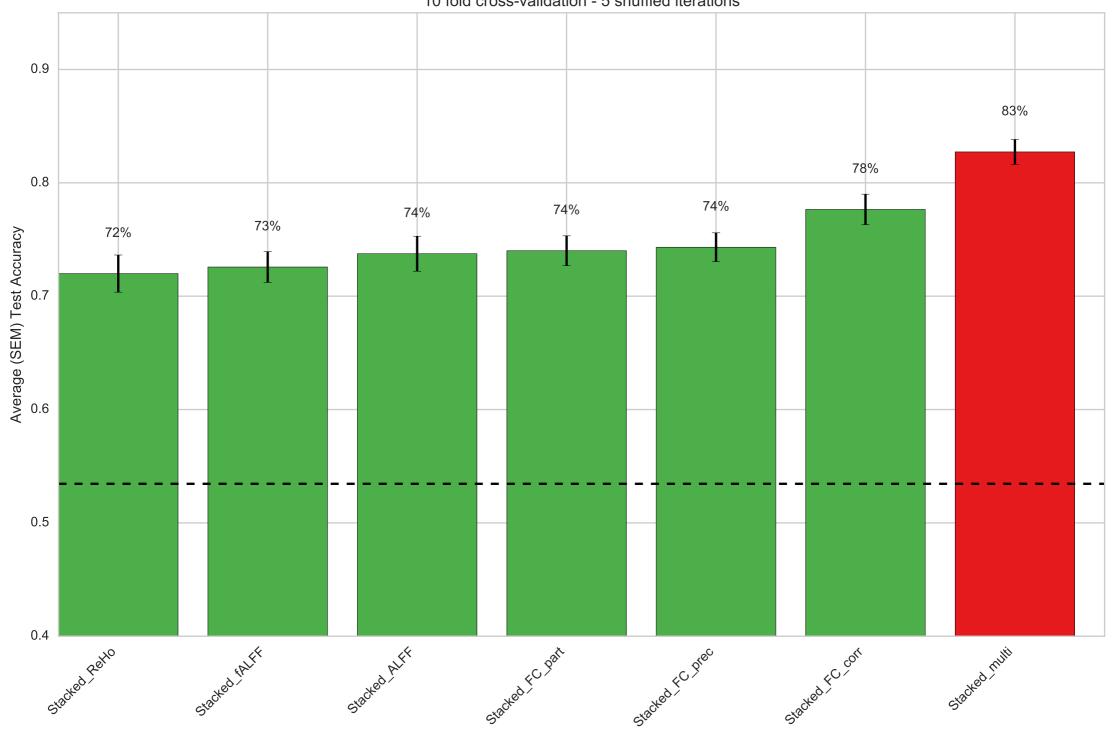
Top 2% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



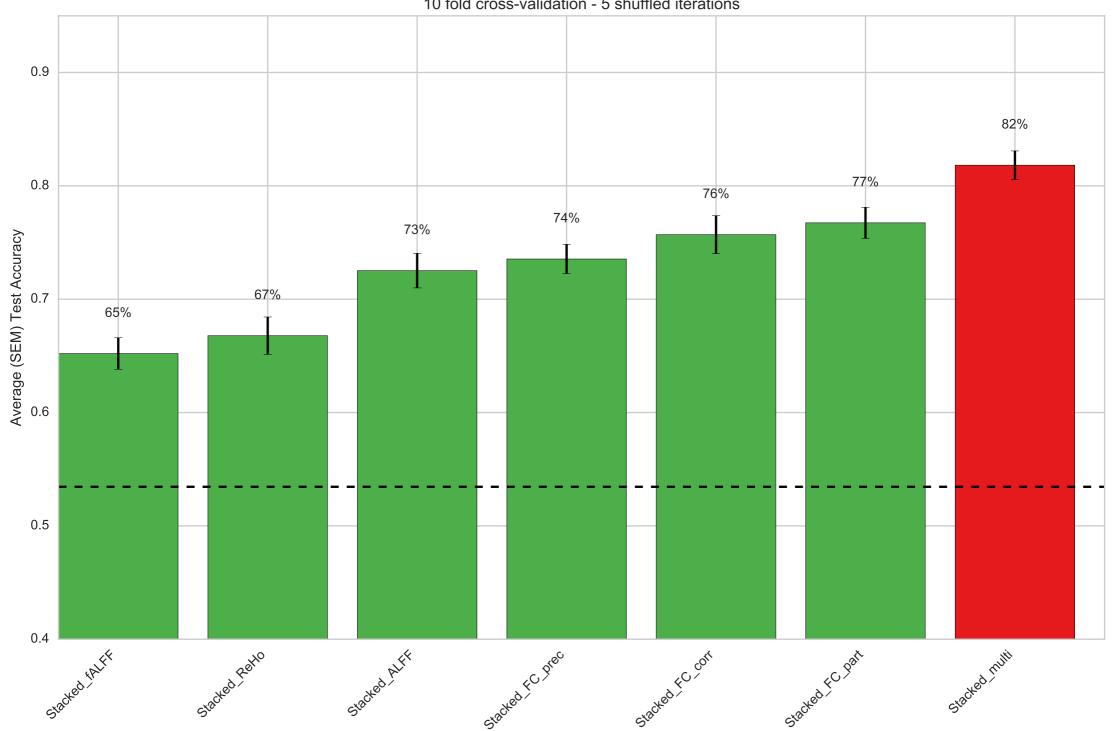
Top 5% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



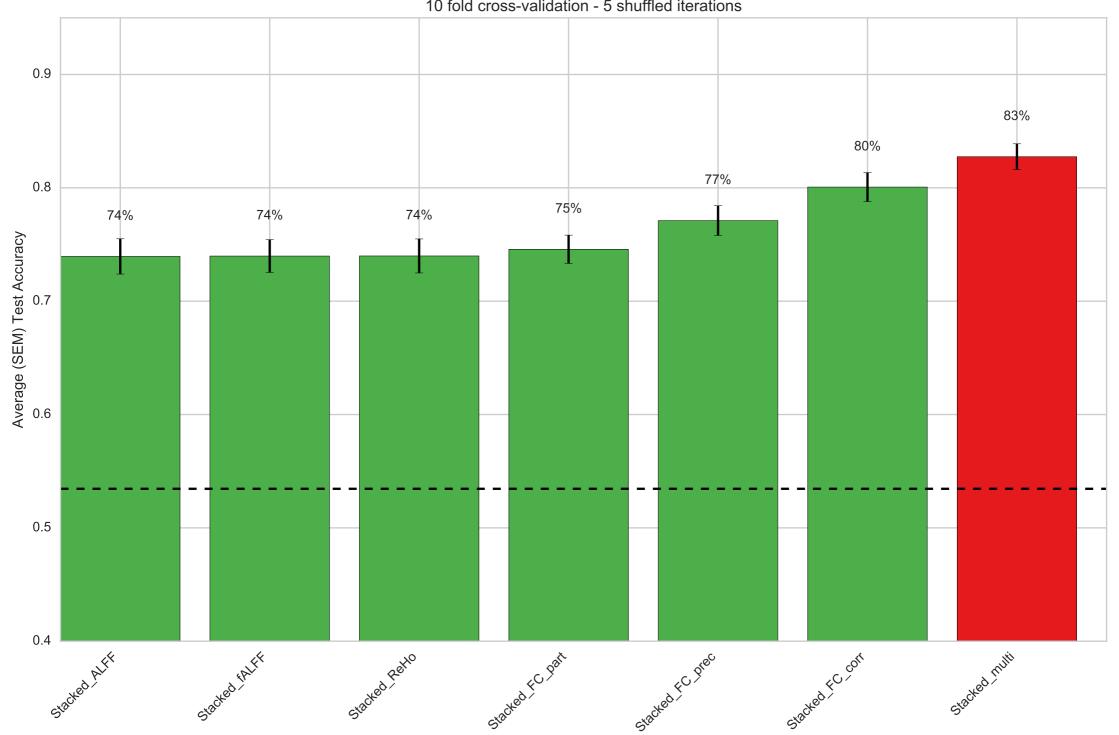
Top 10% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



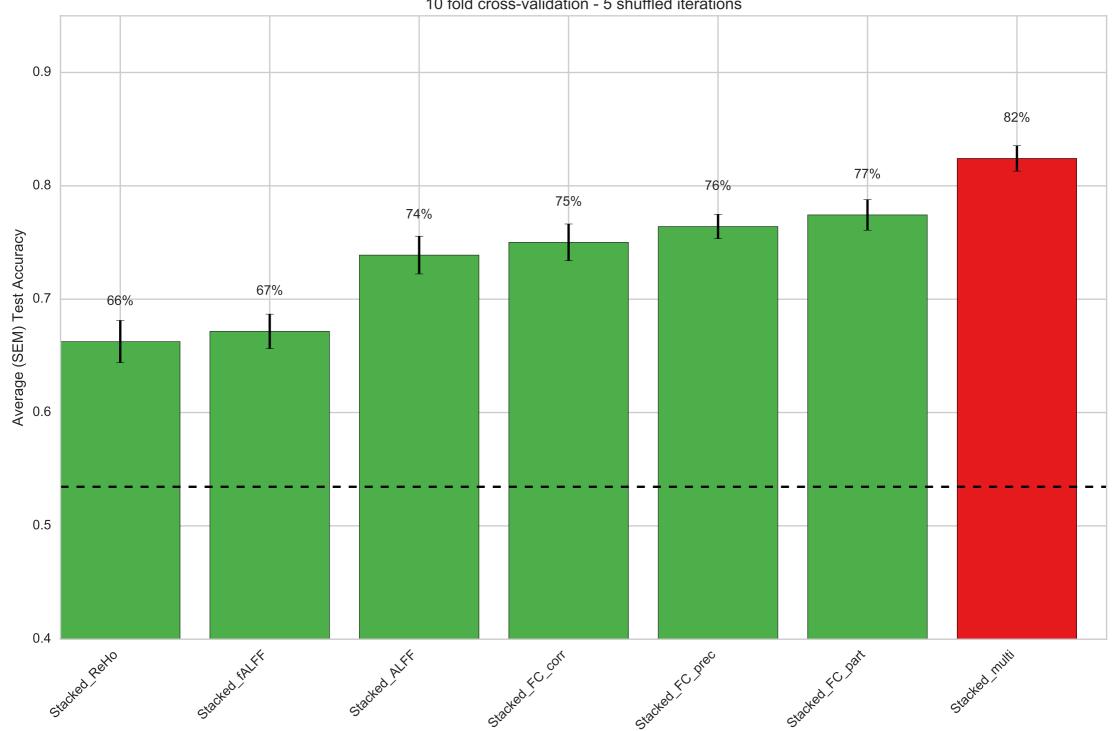
Top 0.5% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



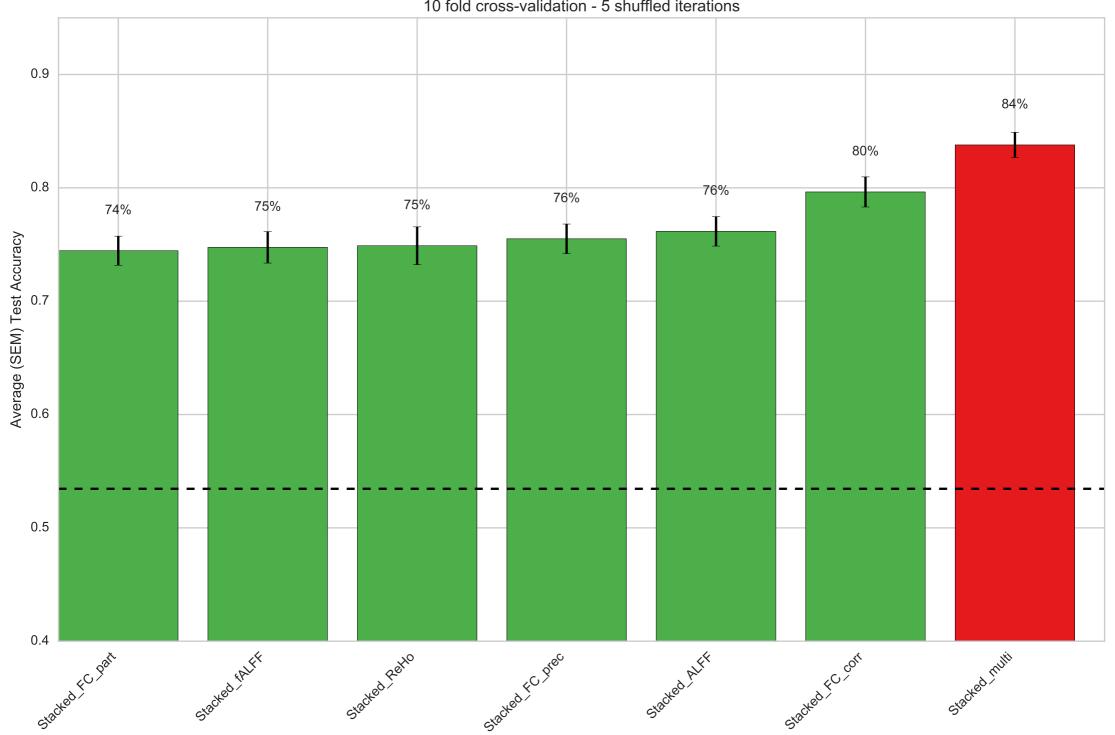
Top 30% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



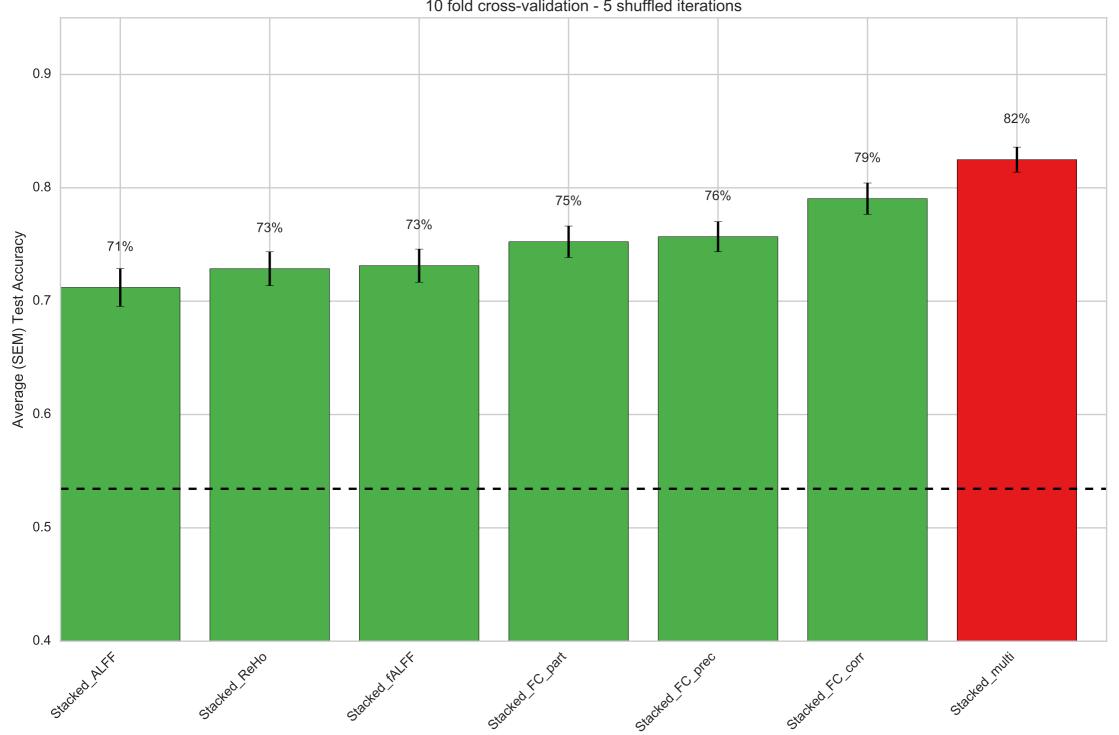
Top 1% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



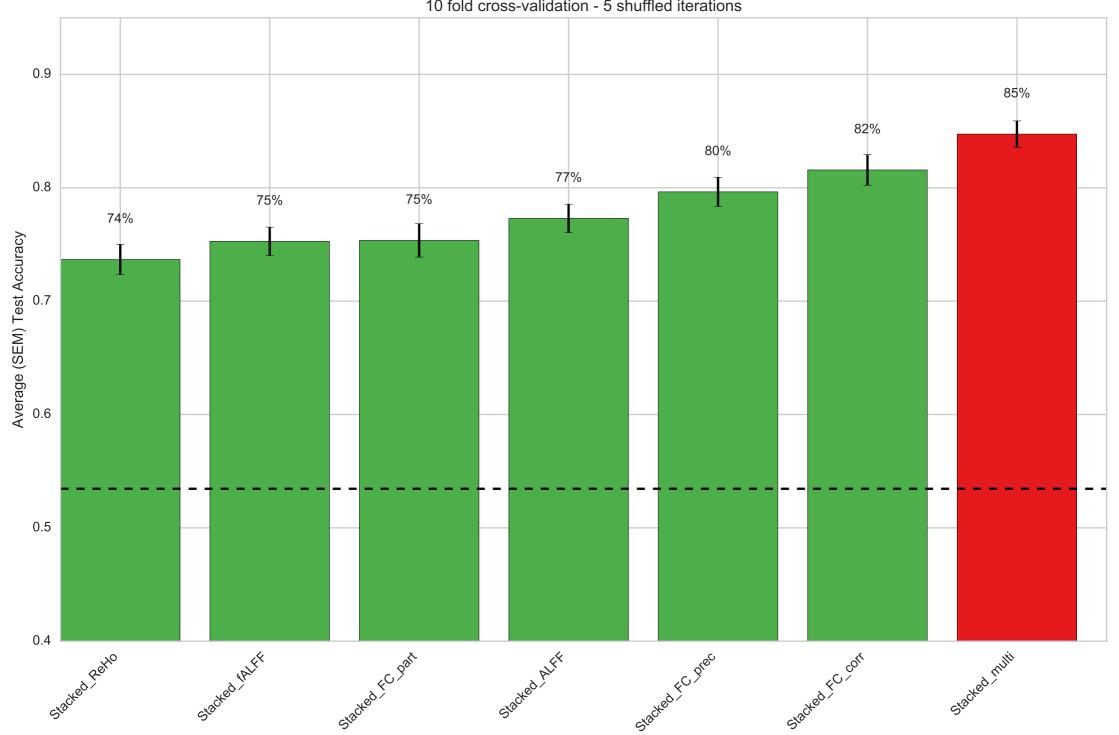
Top 30% FC, 100% regional Feature Selection Comparison across stacked predictions for various feature types 10 fold cross-validation - 5 shuffled iterations



Top 20% Feature Selection
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



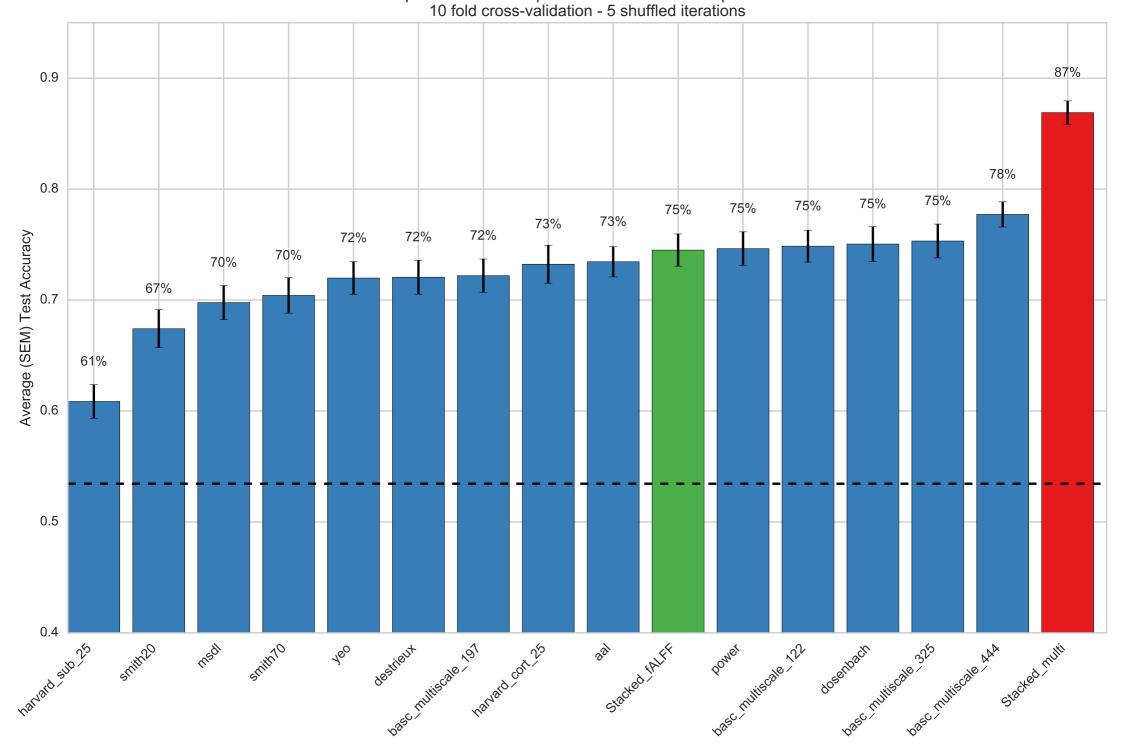
100% Features
Comparison across stacked predictions for various feature types
10 fold cross-validation - 5 shuffled iterations



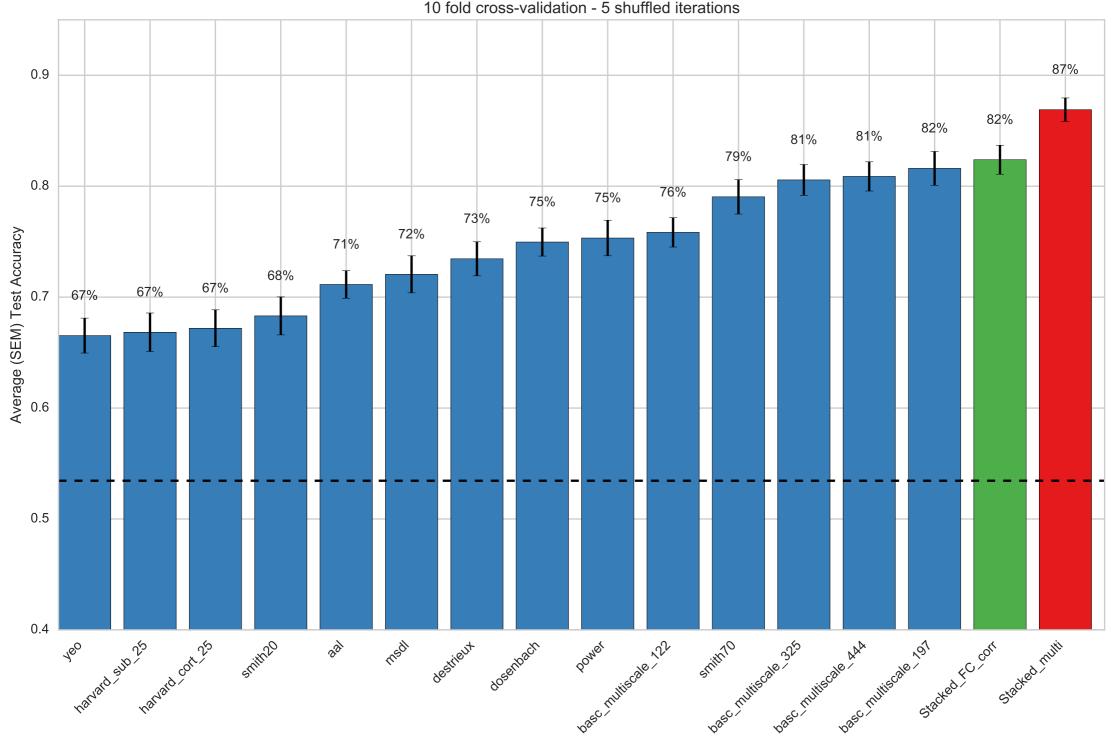
Comparison of prediction accuracy for	r single-source models (blue) and stacke Final ensemble model shown in red	ed model (green) for a feature type.



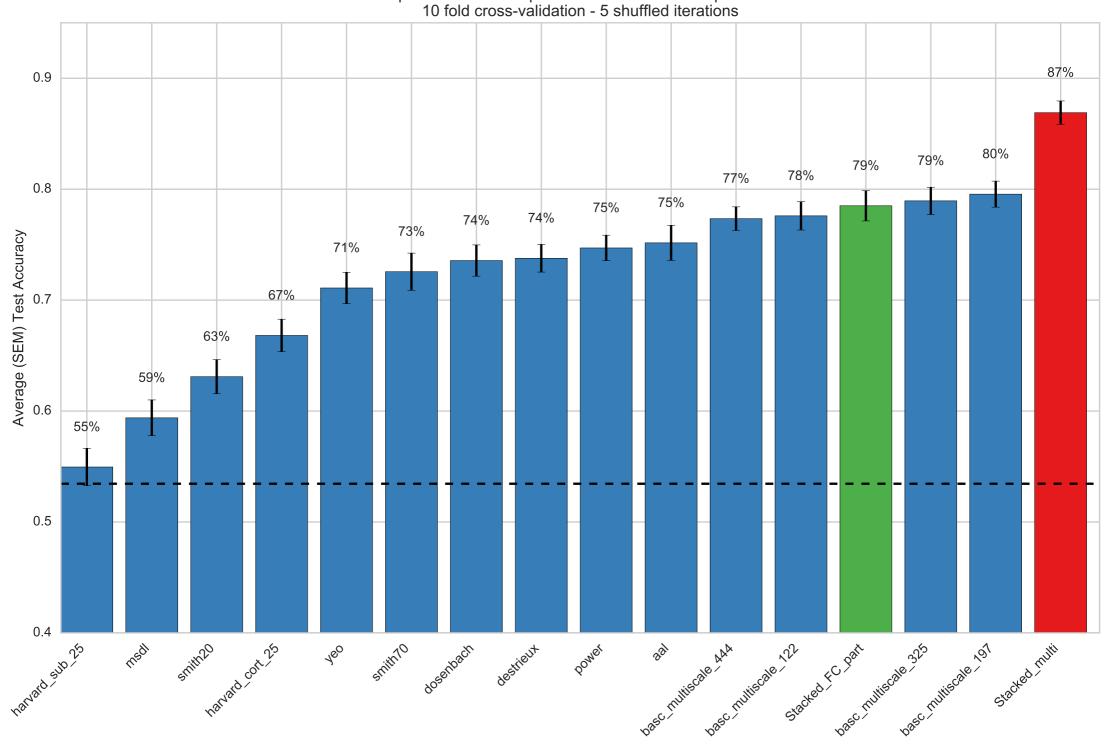
fALFF: PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



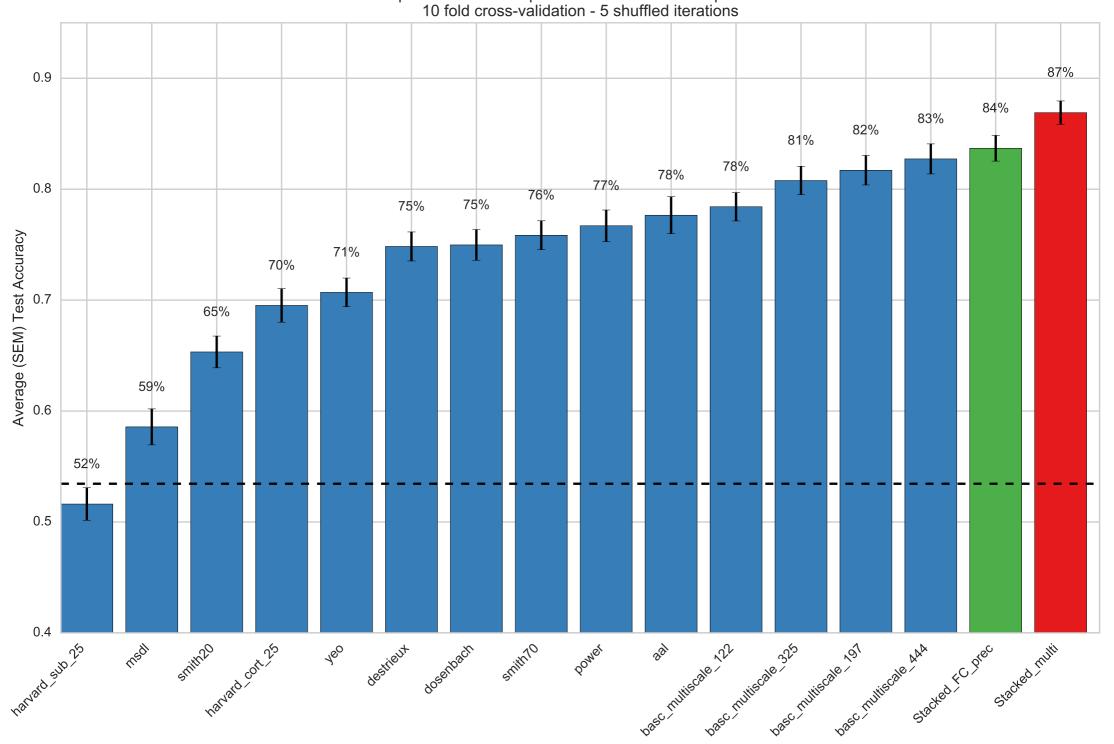
FC_corr : PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



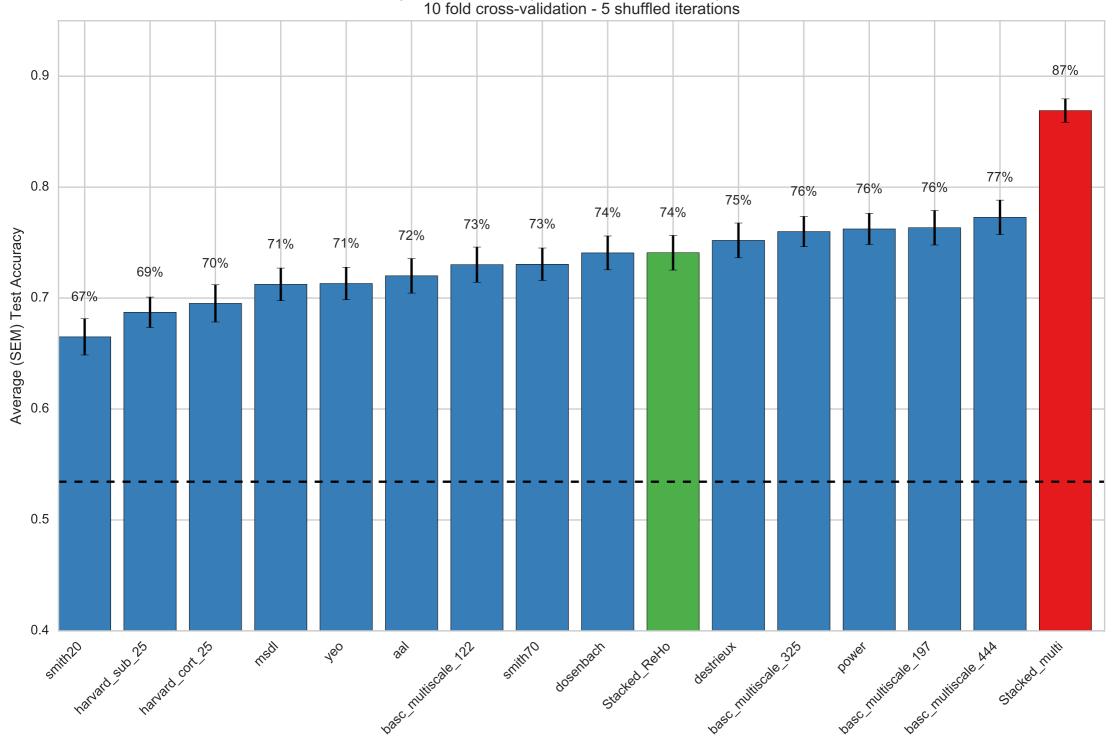
FC_part : PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



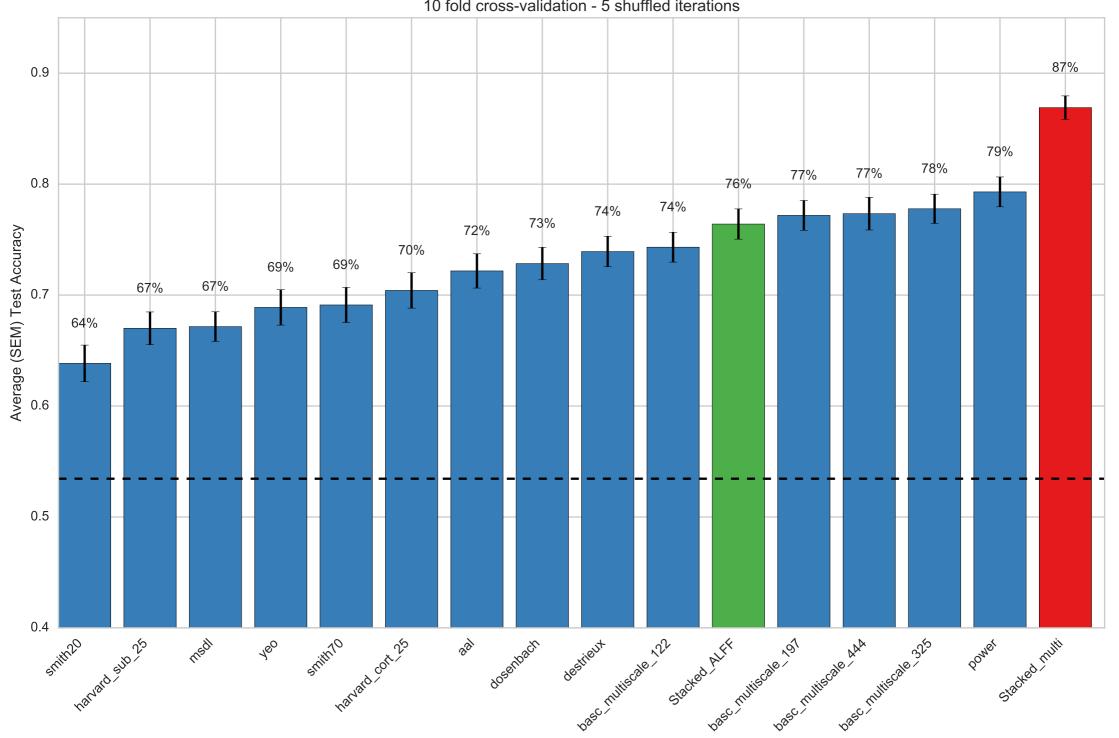
FC_prec : PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

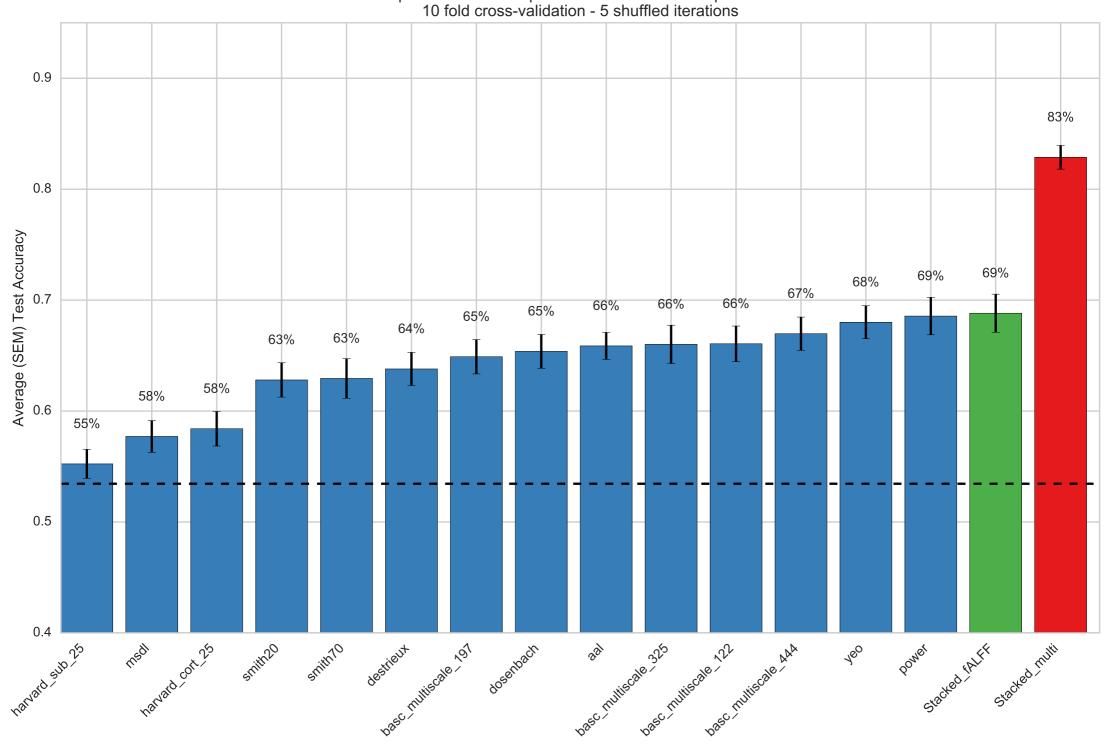


ALFF: PCA - Dimensional Reduction Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

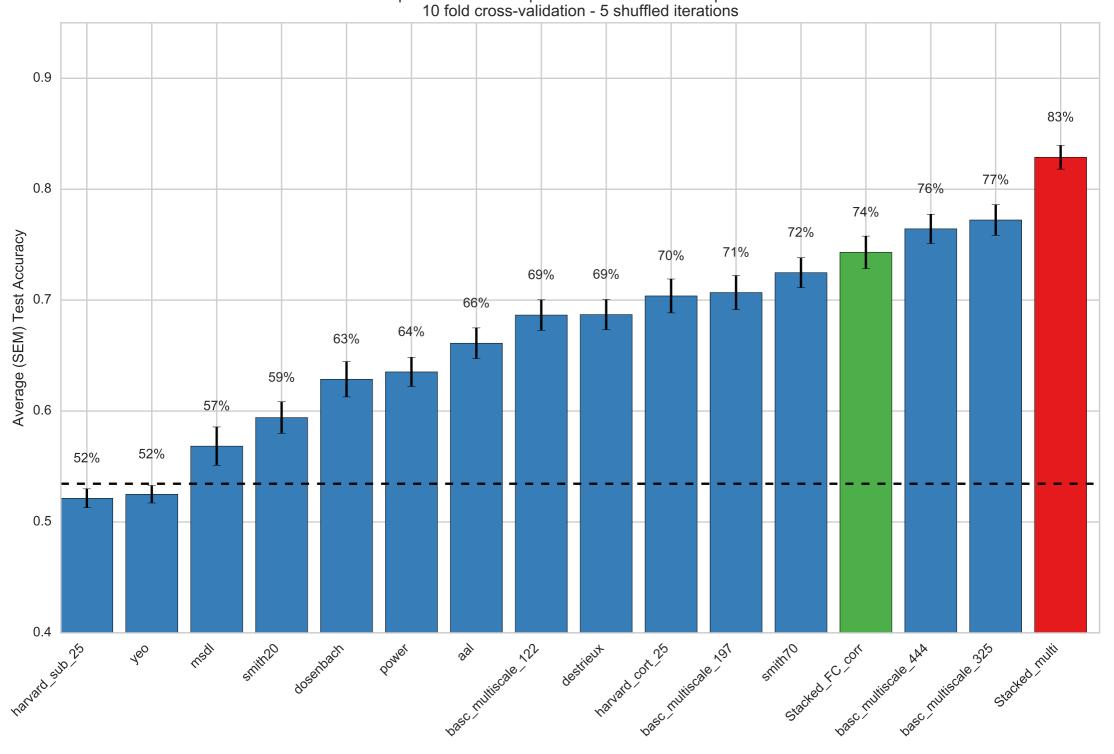




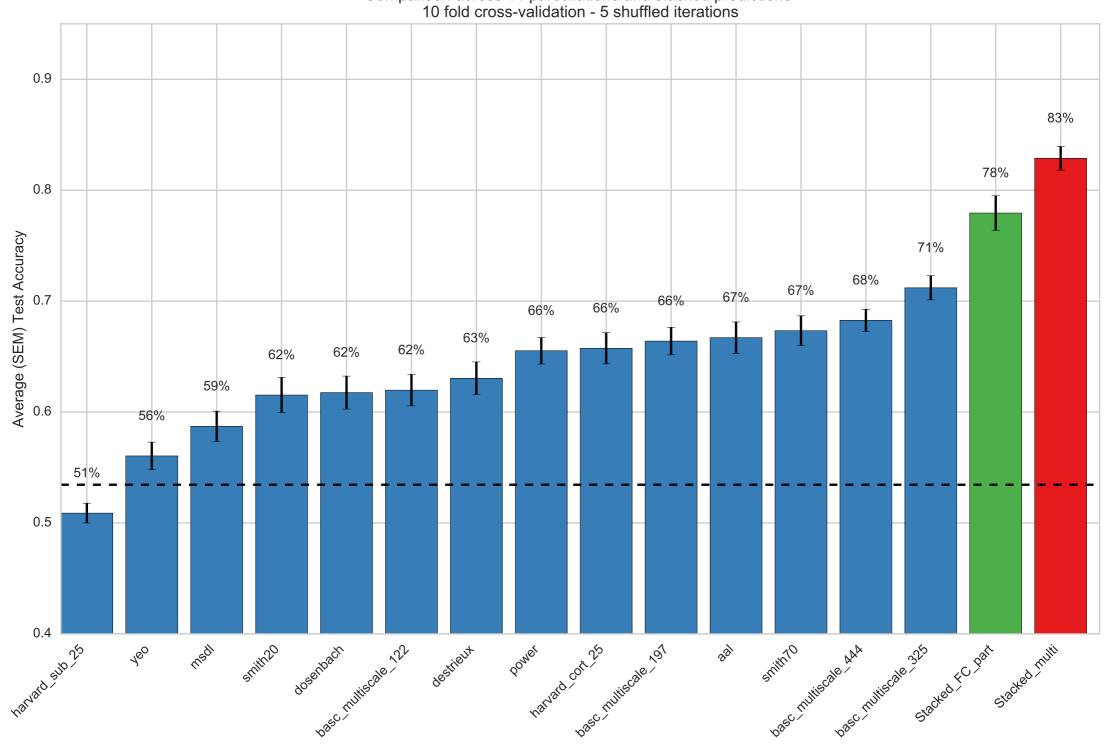
fALFF: Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



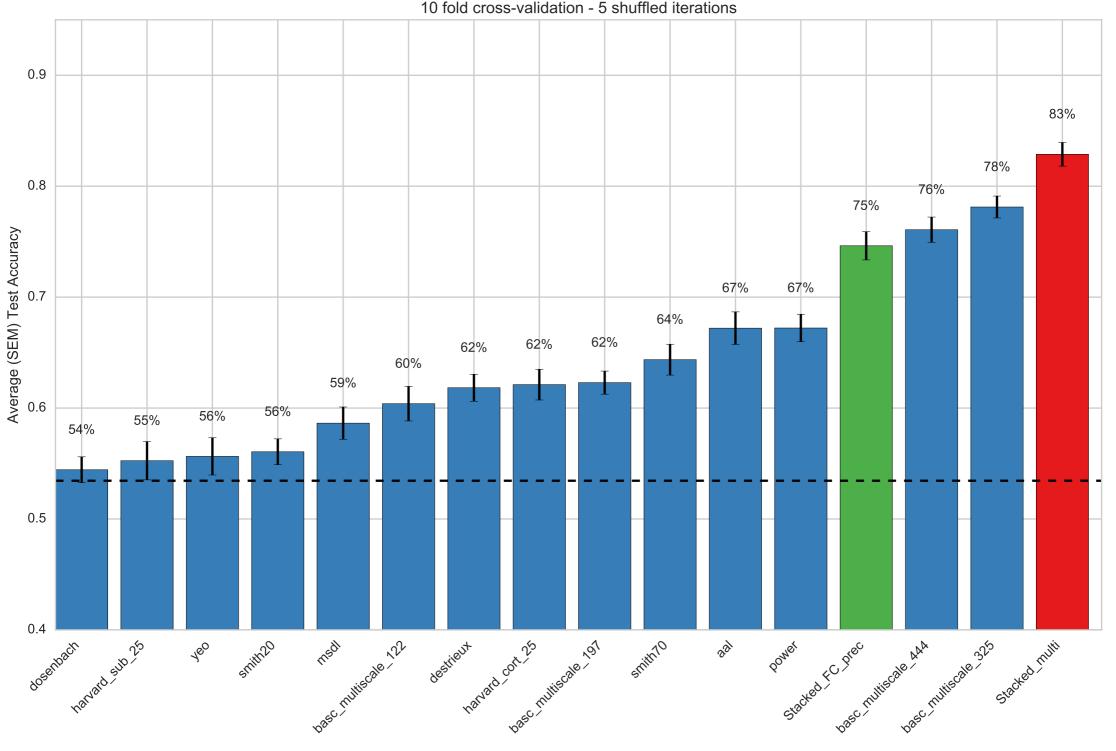
FC_corr : Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



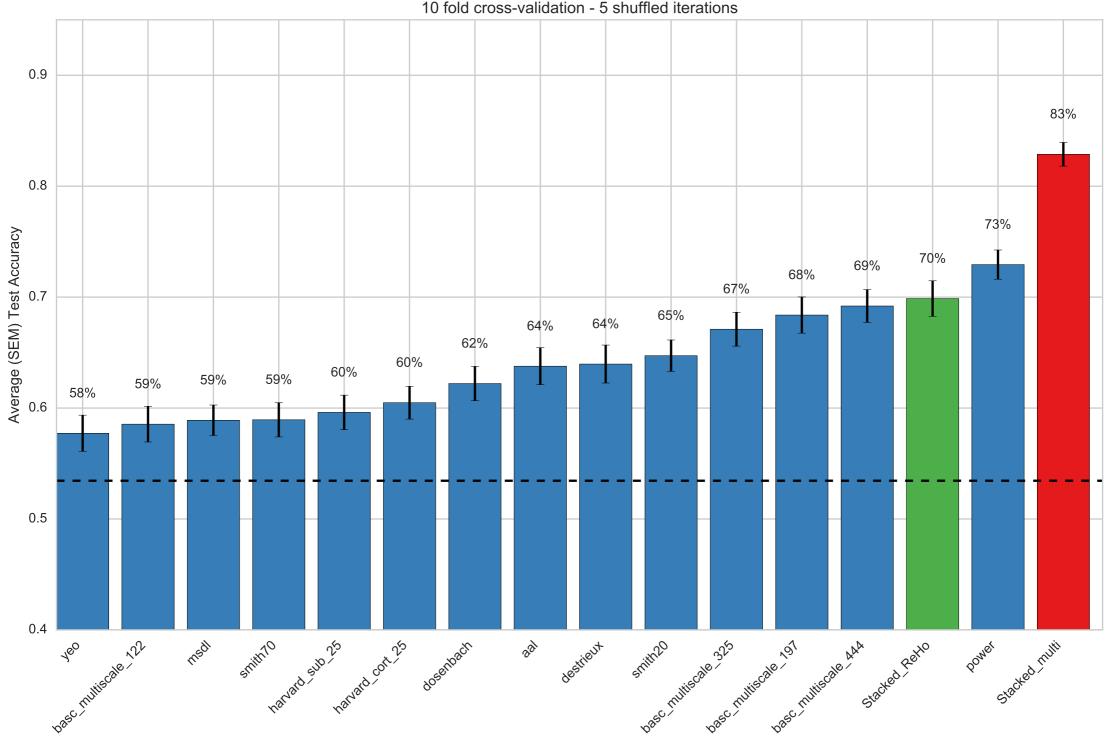
FC_part : Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



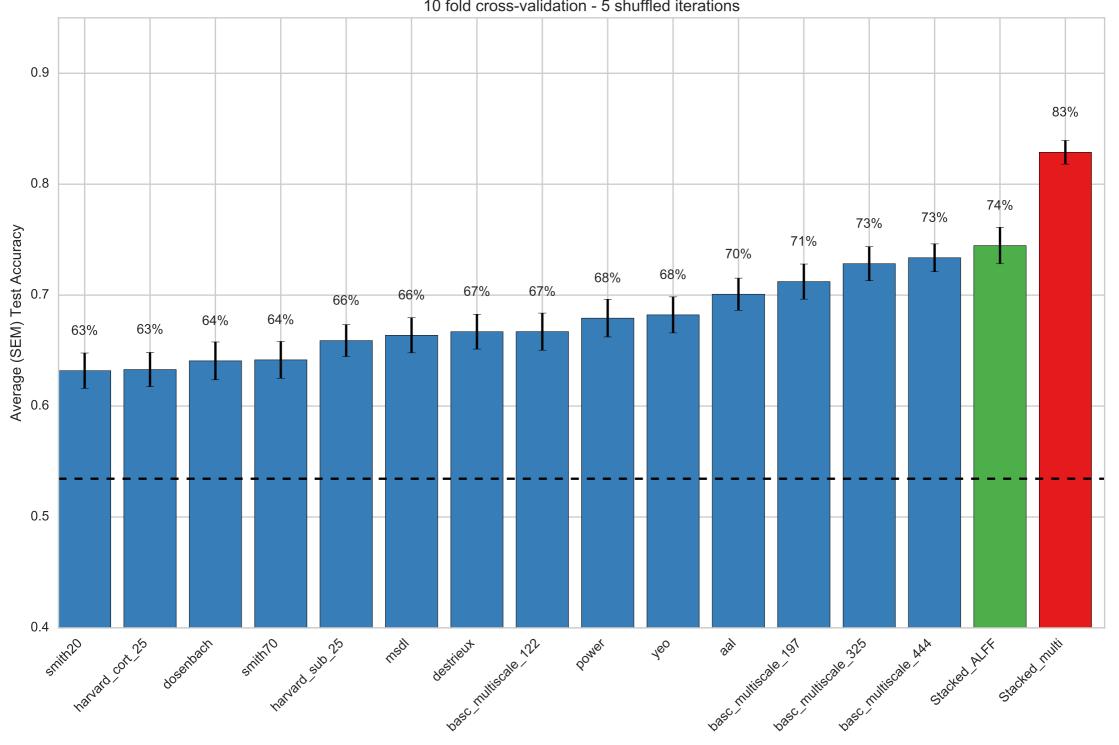
FC_prec : Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

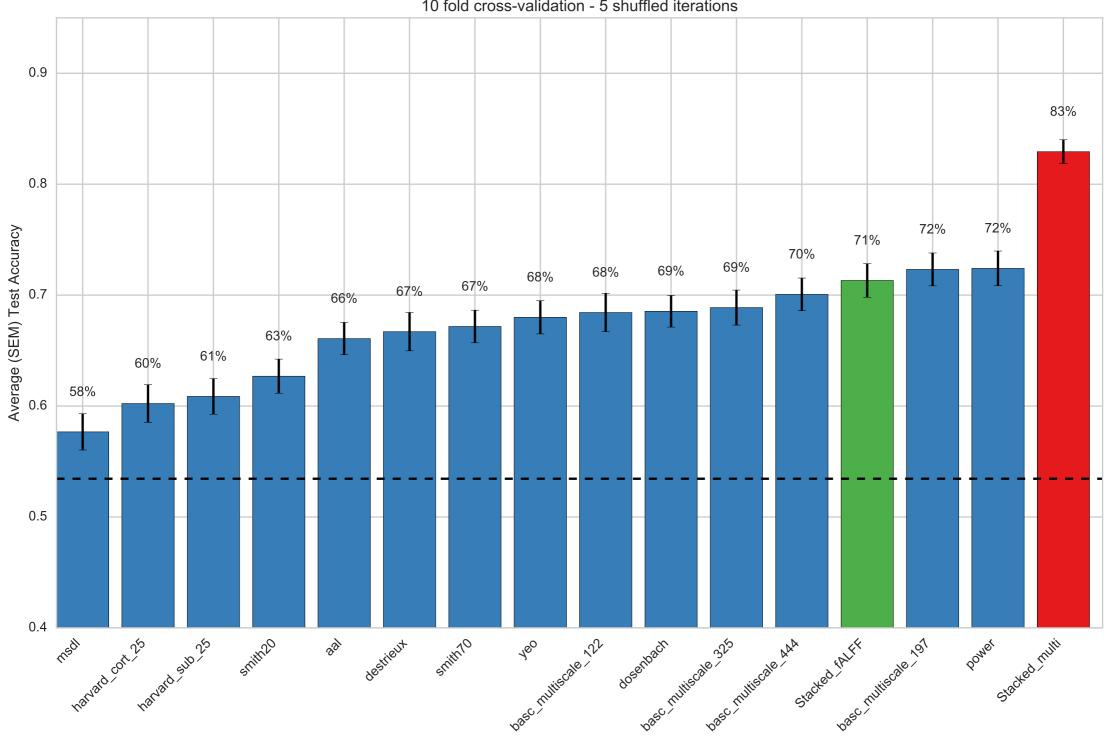


ALFF: Top 2% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

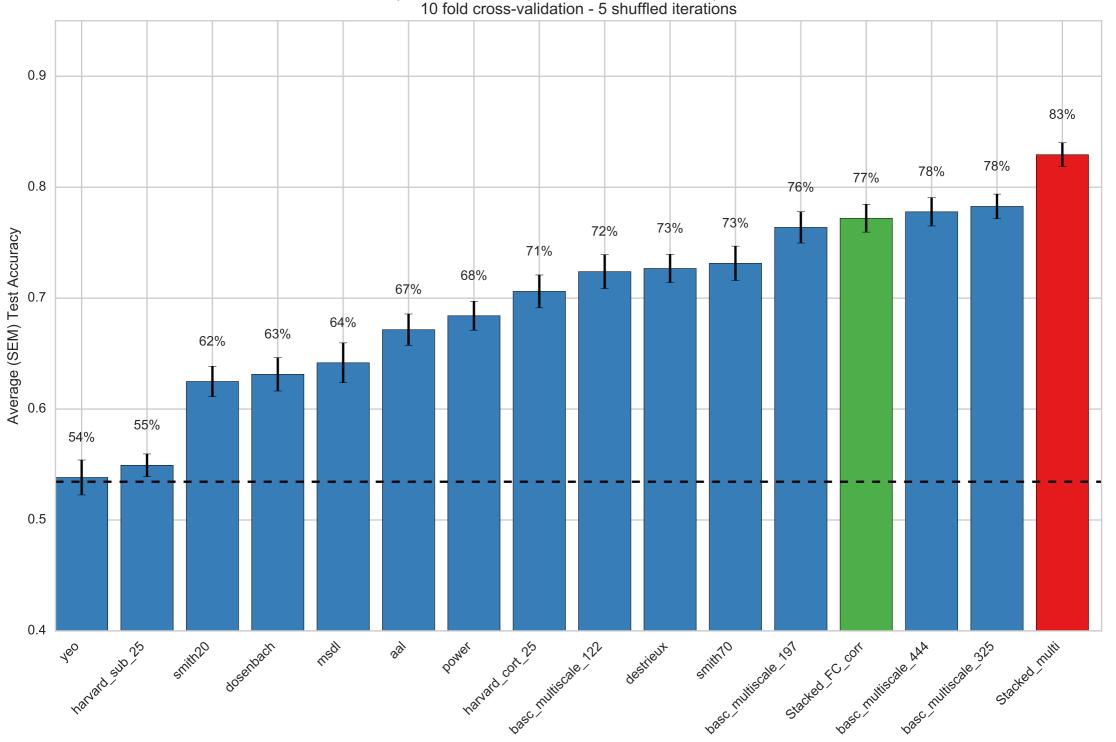




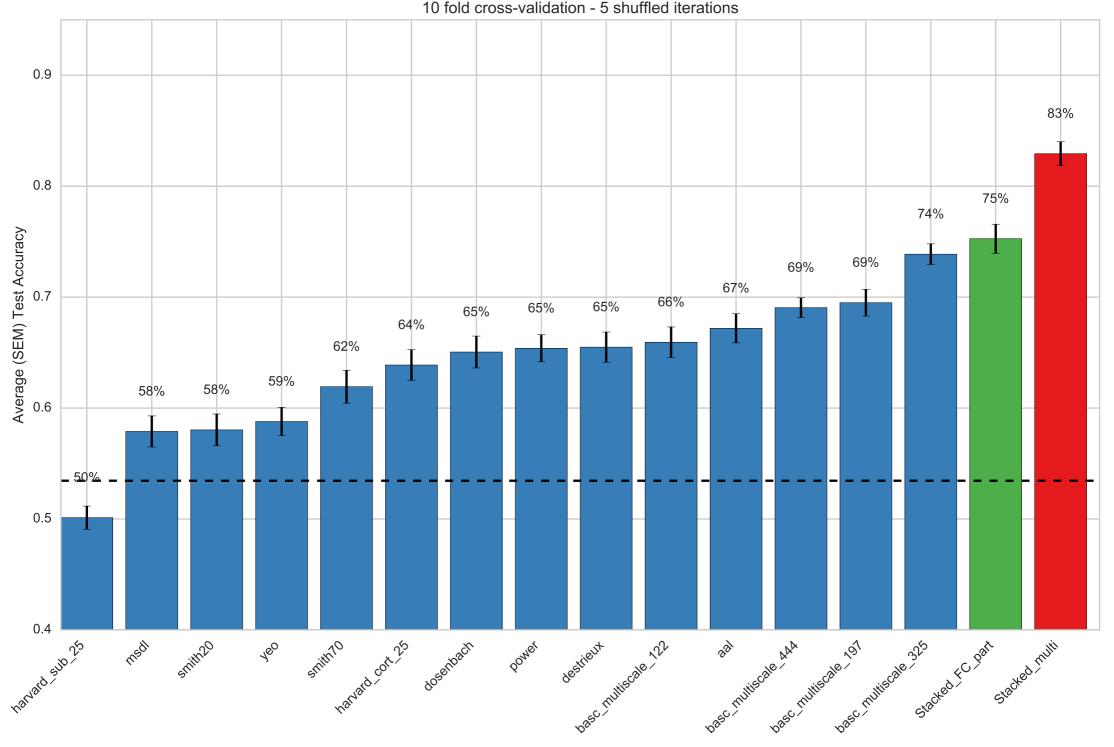
fALFF: Top 5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



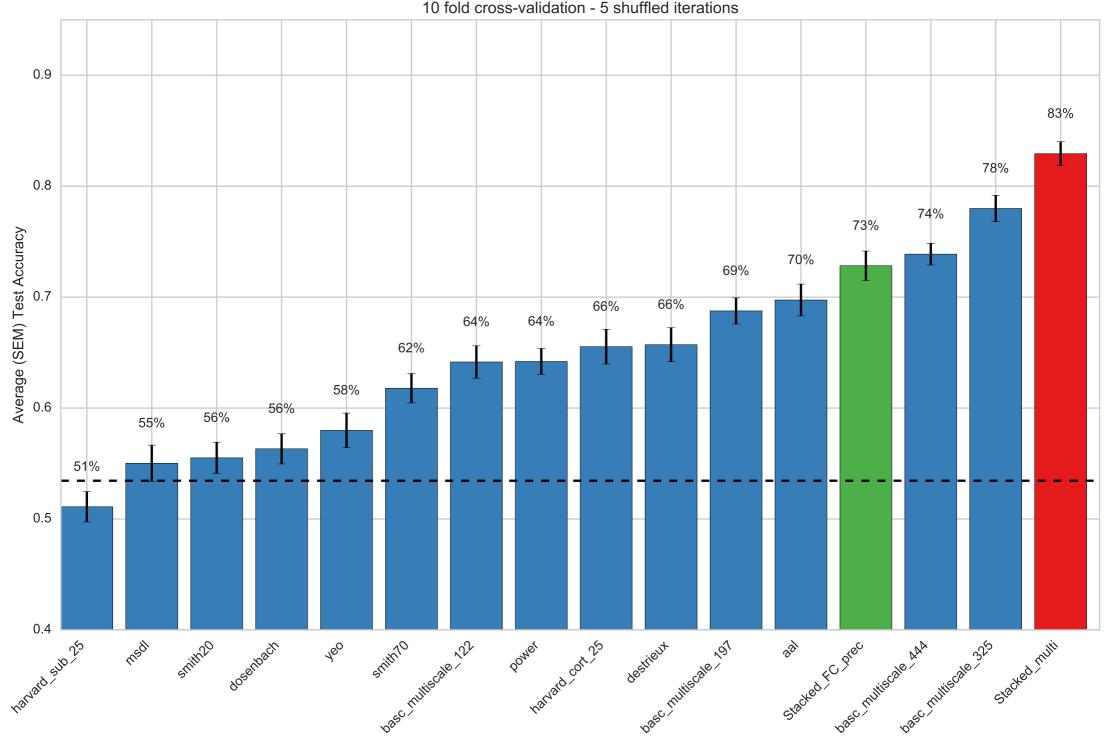
FC_corr: Top 5% Feature Selection
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



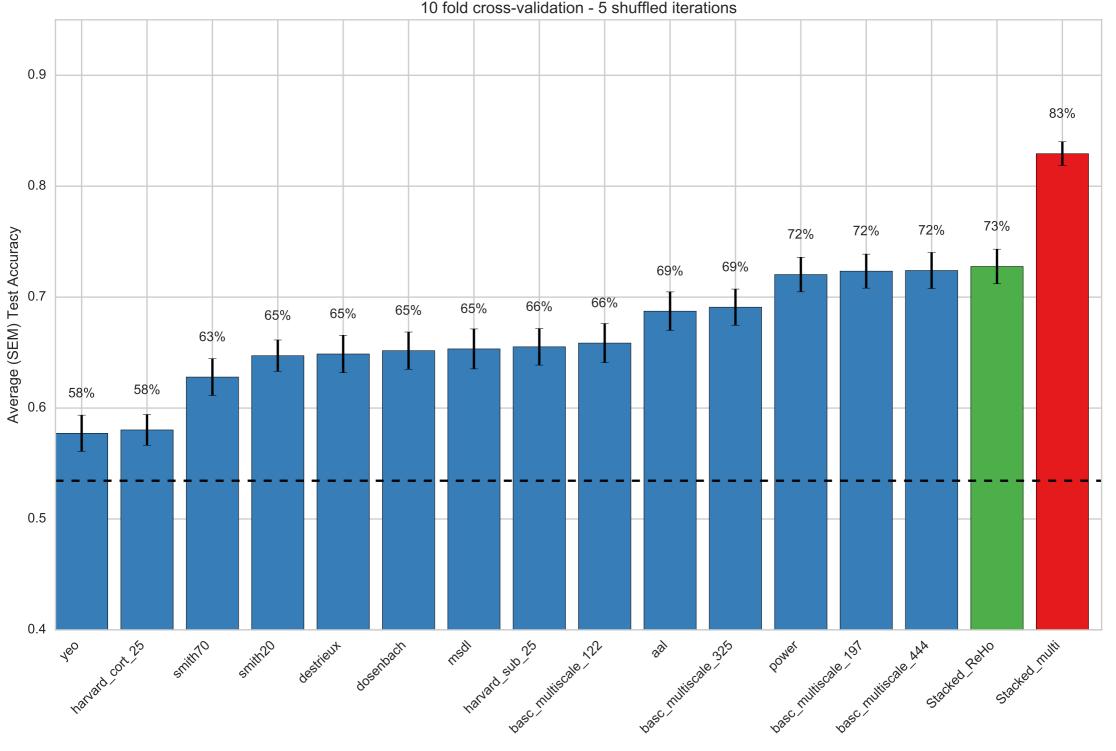
FC_part: Top 5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



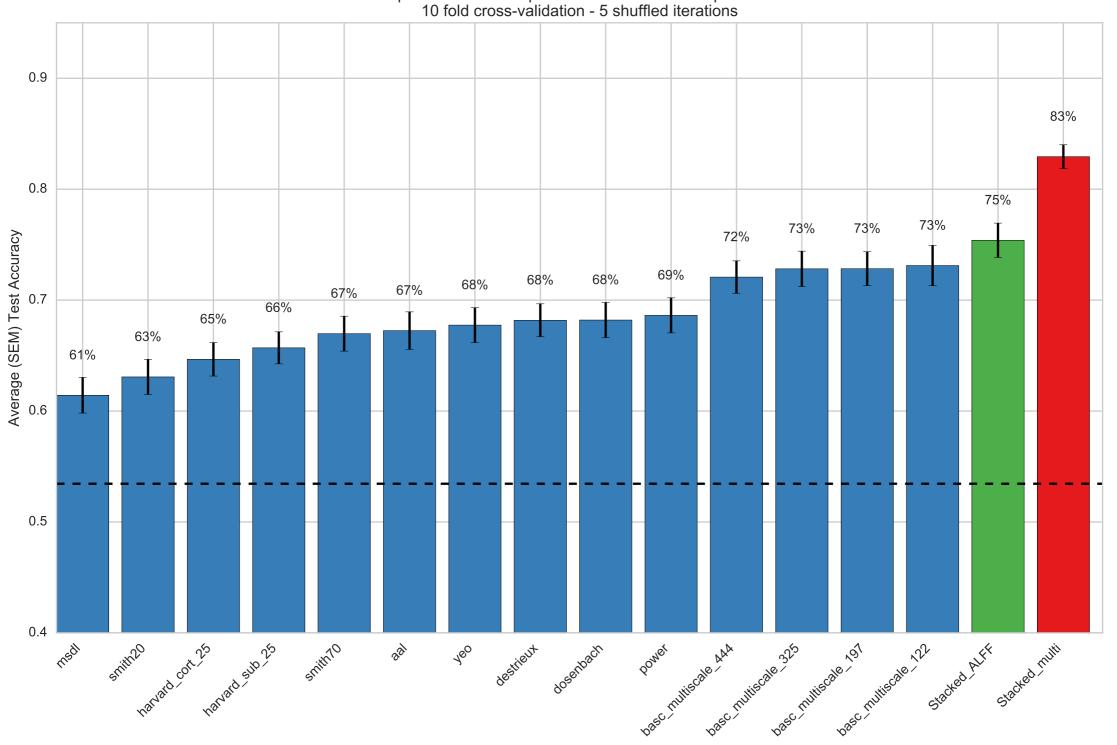
FC_prec : Top 5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

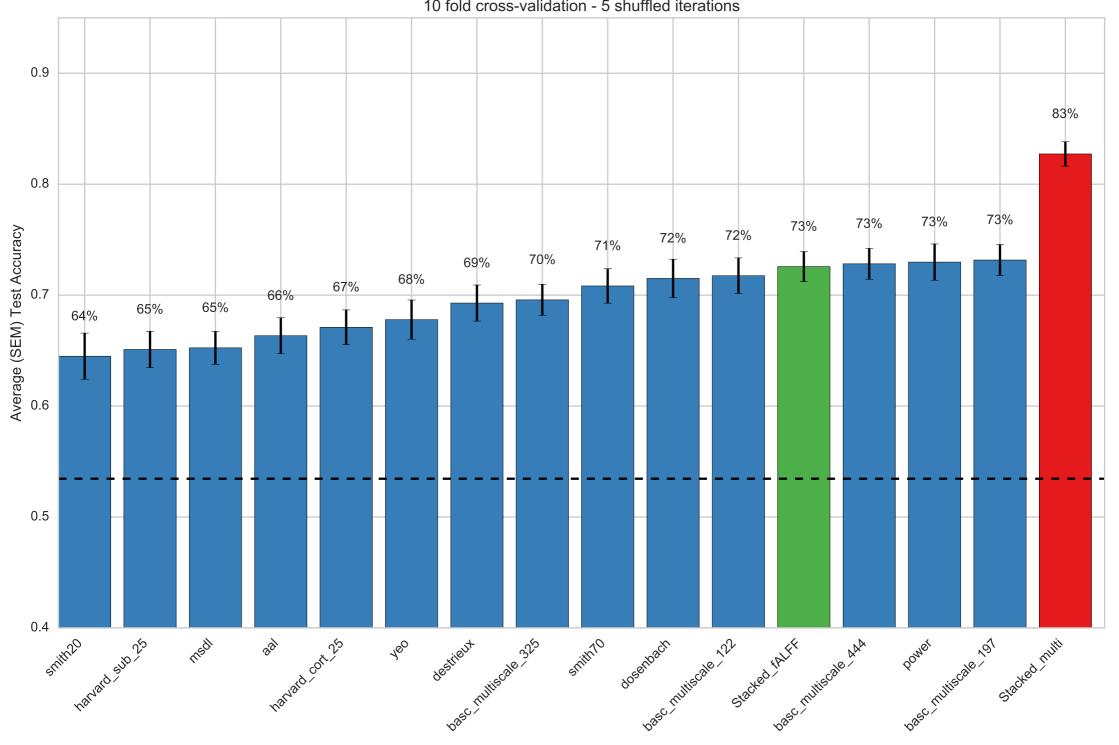


ALFF: Top 5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

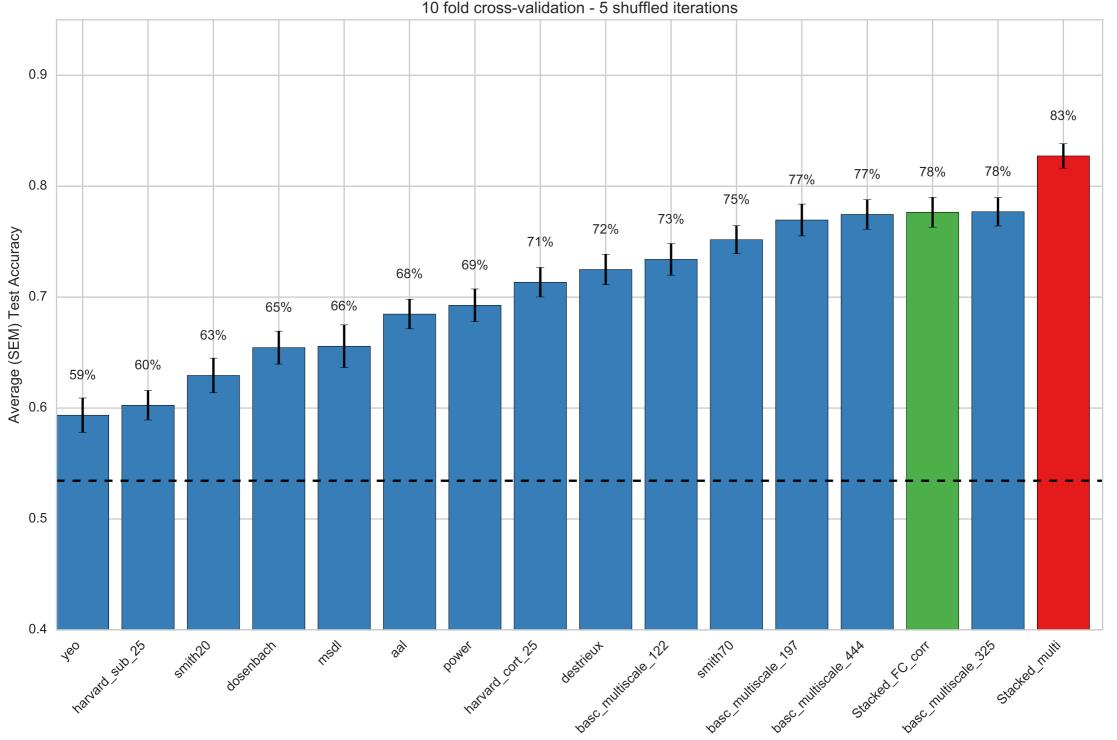




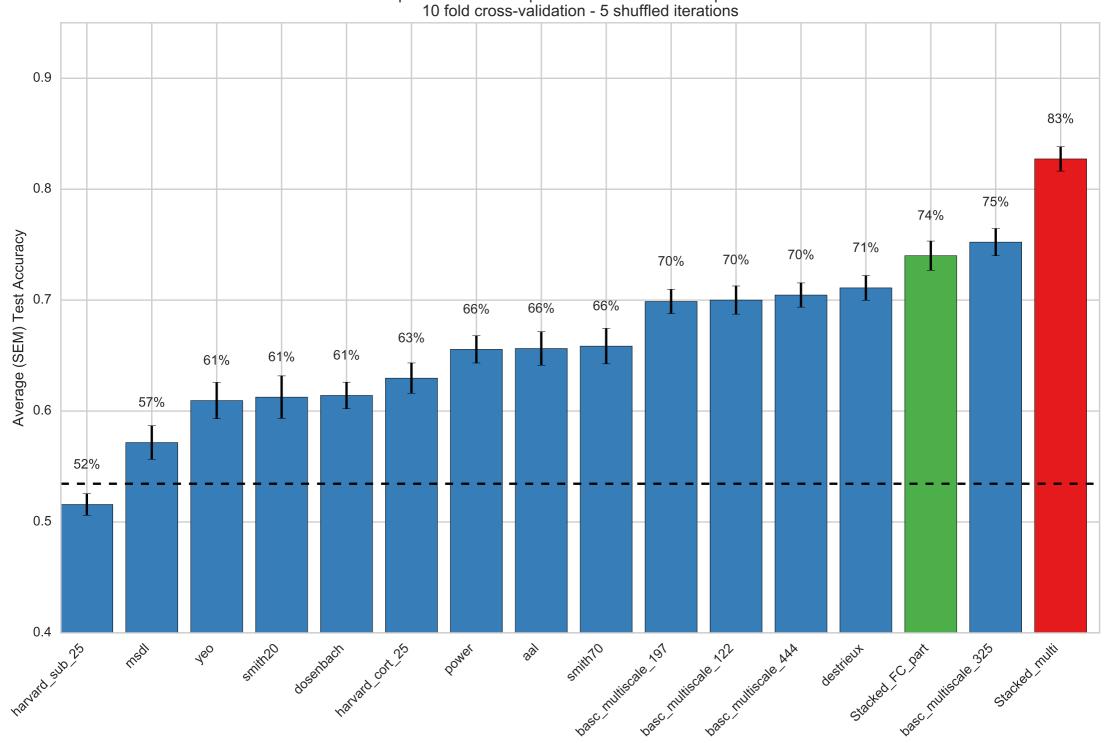
fALFF: Top 10% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



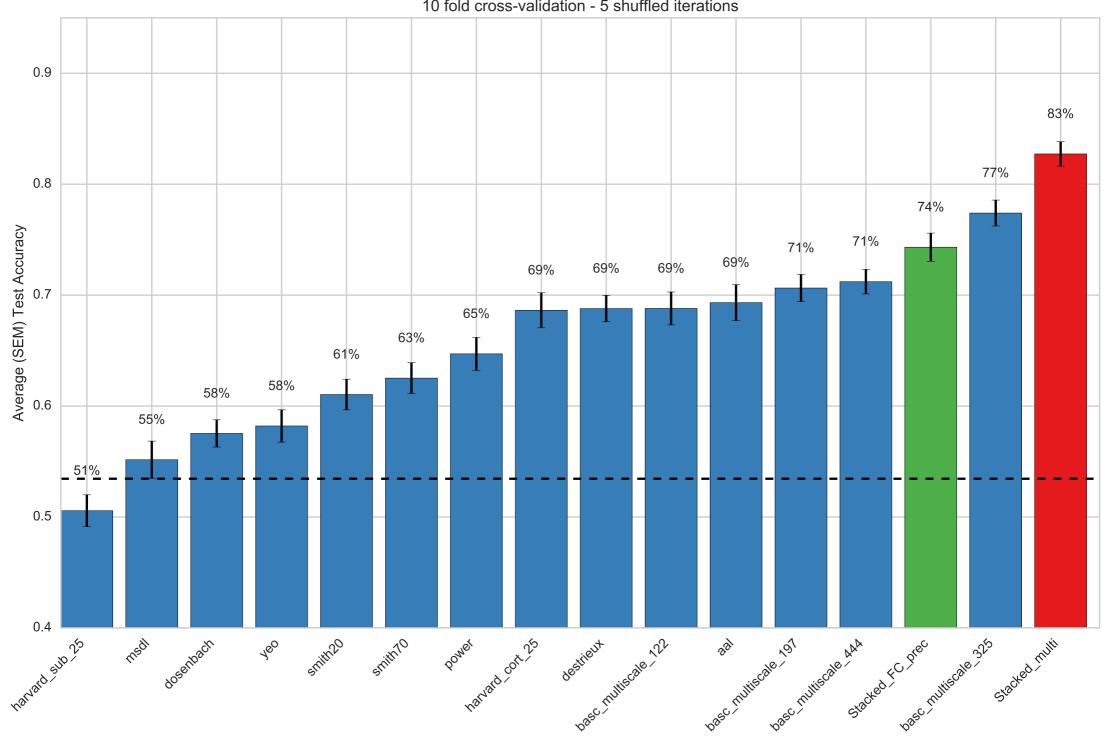
FC_corr: Top 10% Feature Selection
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



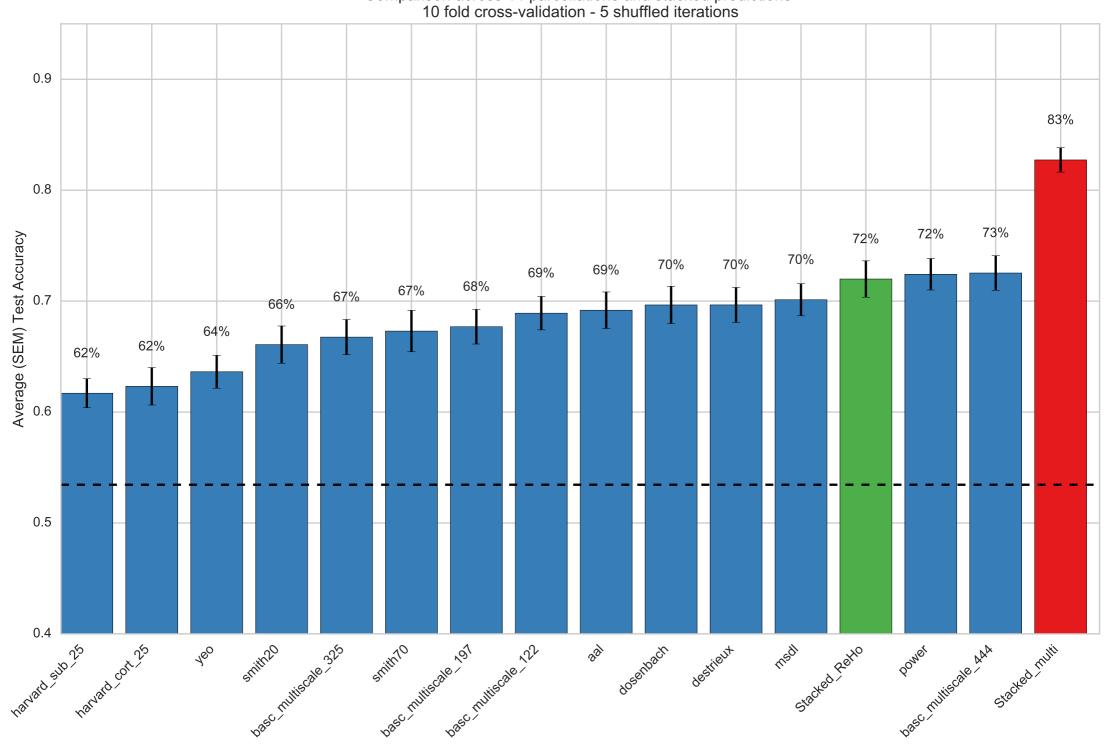
FC_part : Top 10% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



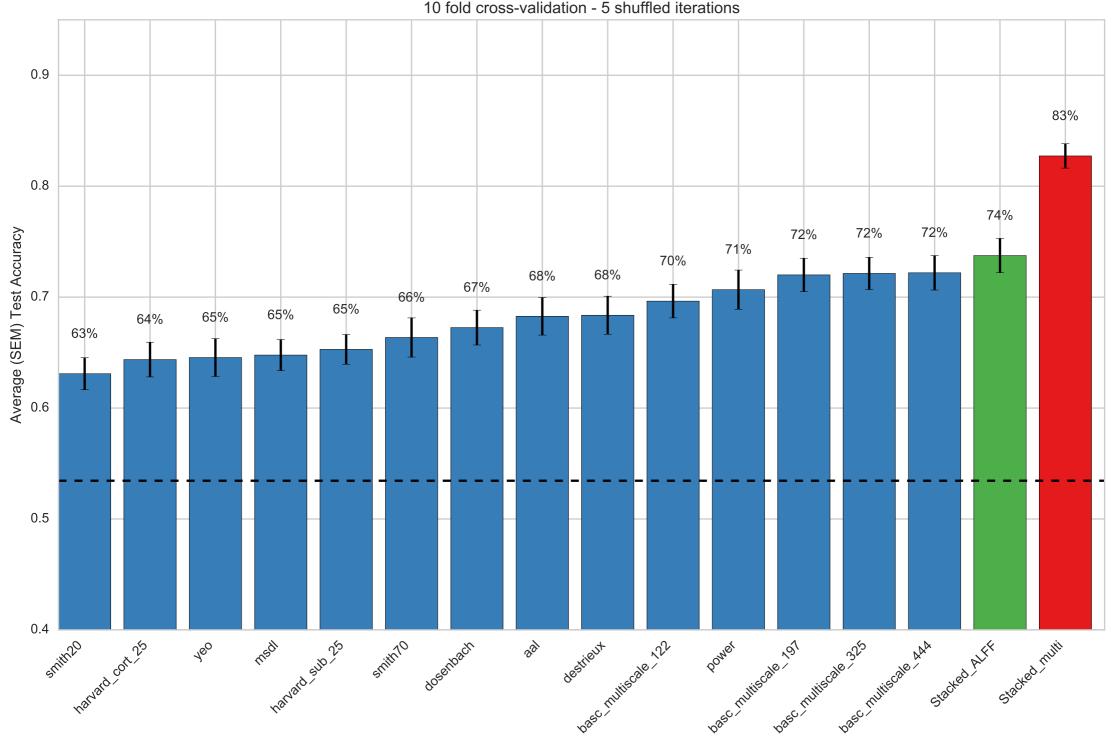
FC_prec : Top 10% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 10% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

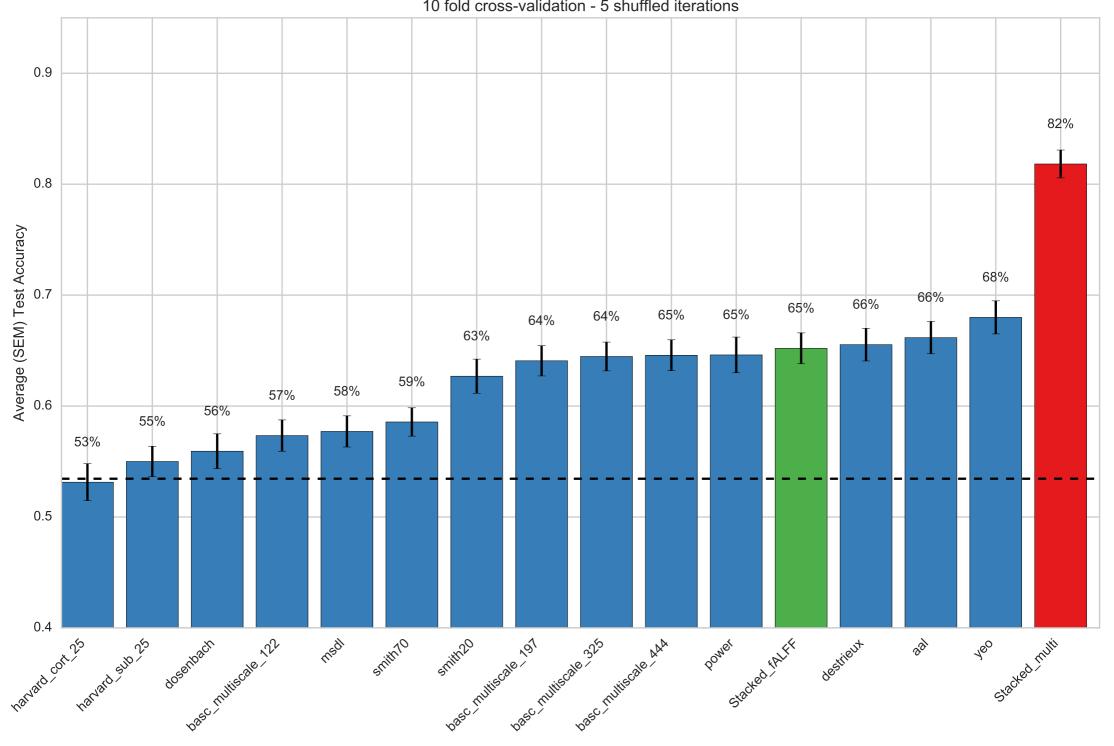


ALFF: Top 10% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

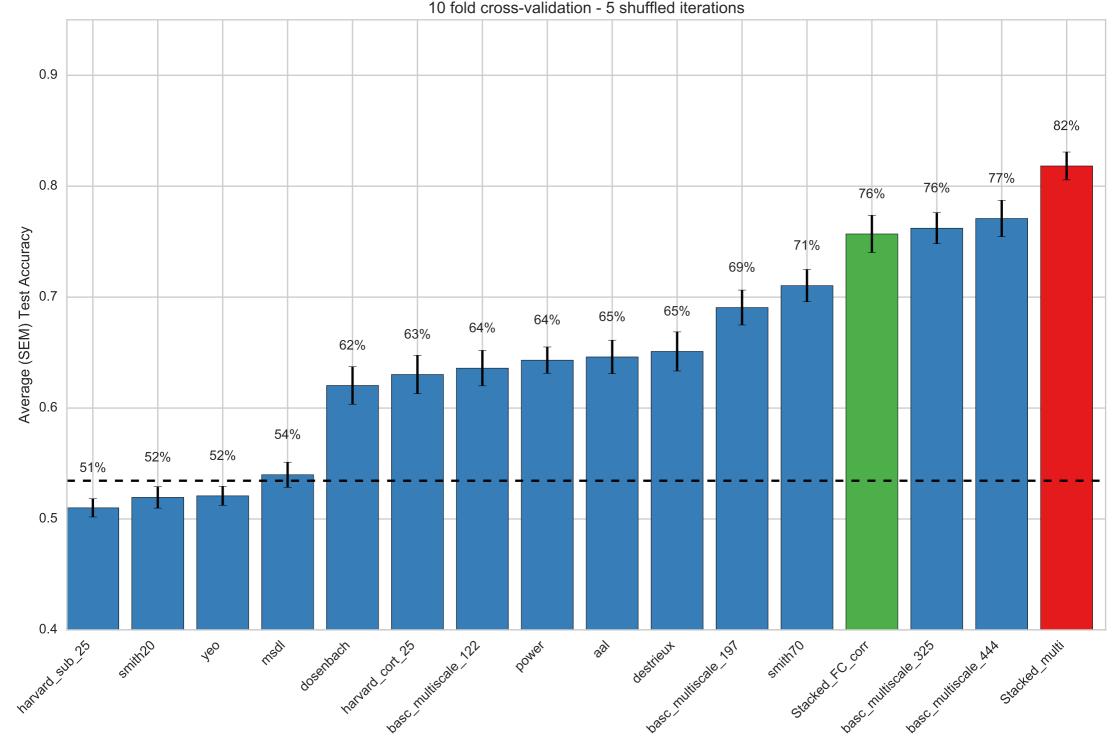




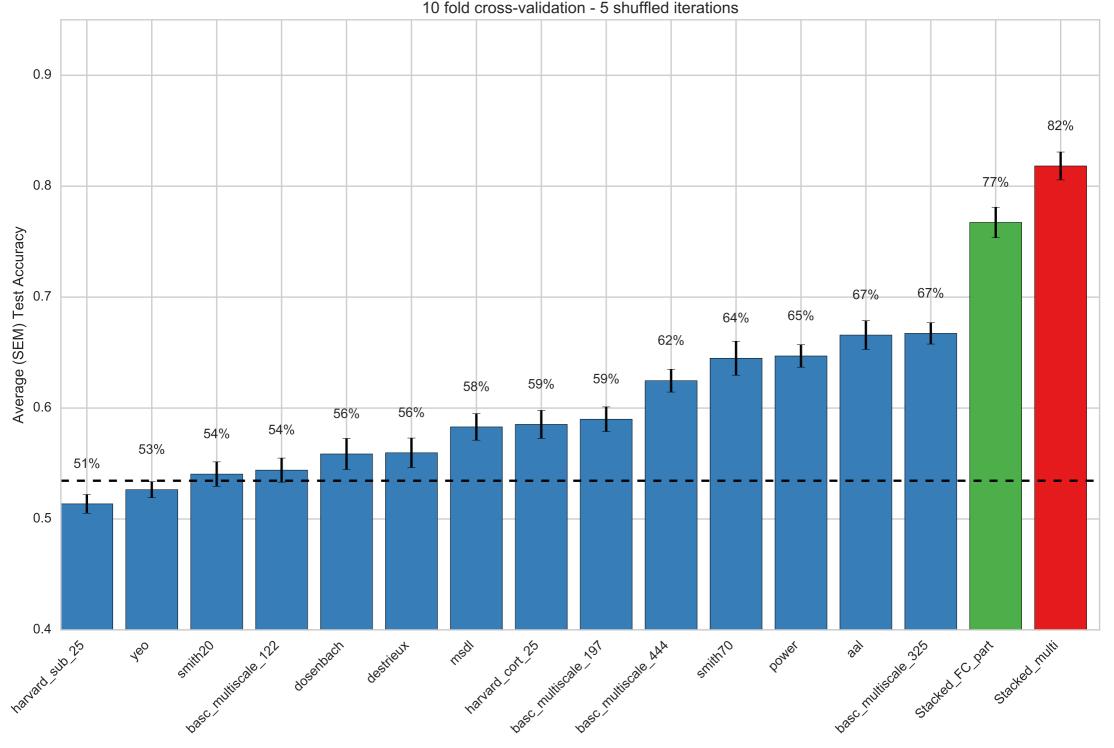
fALFF: Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



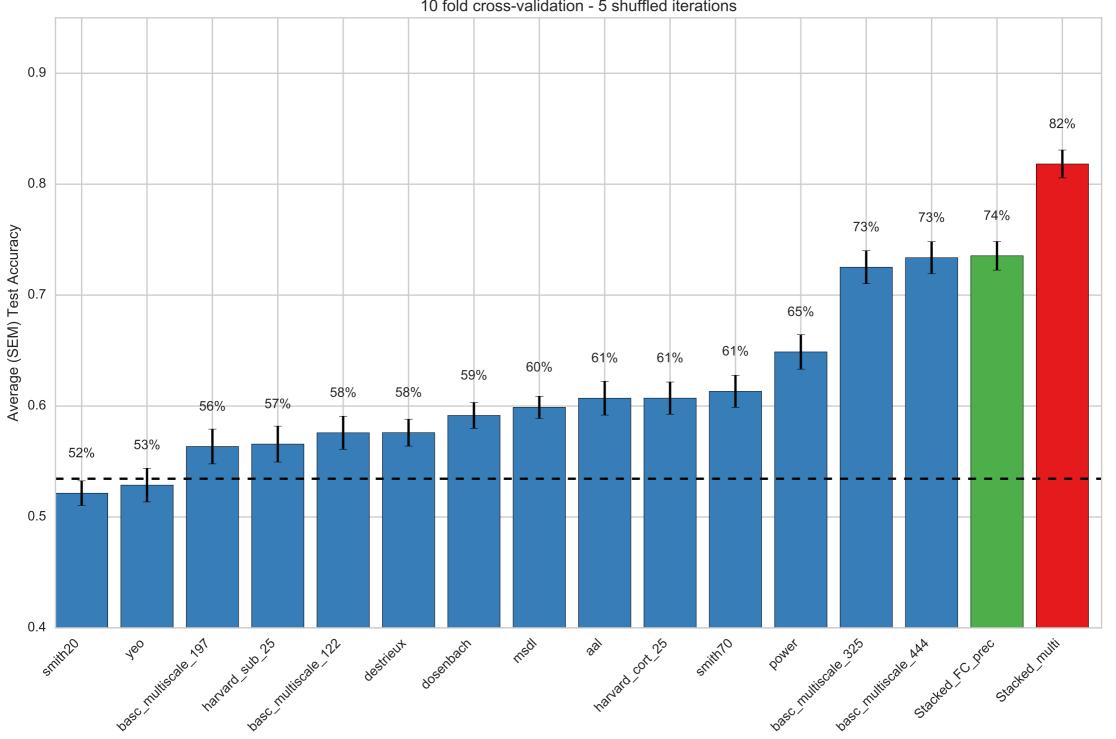
FC_corr: Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



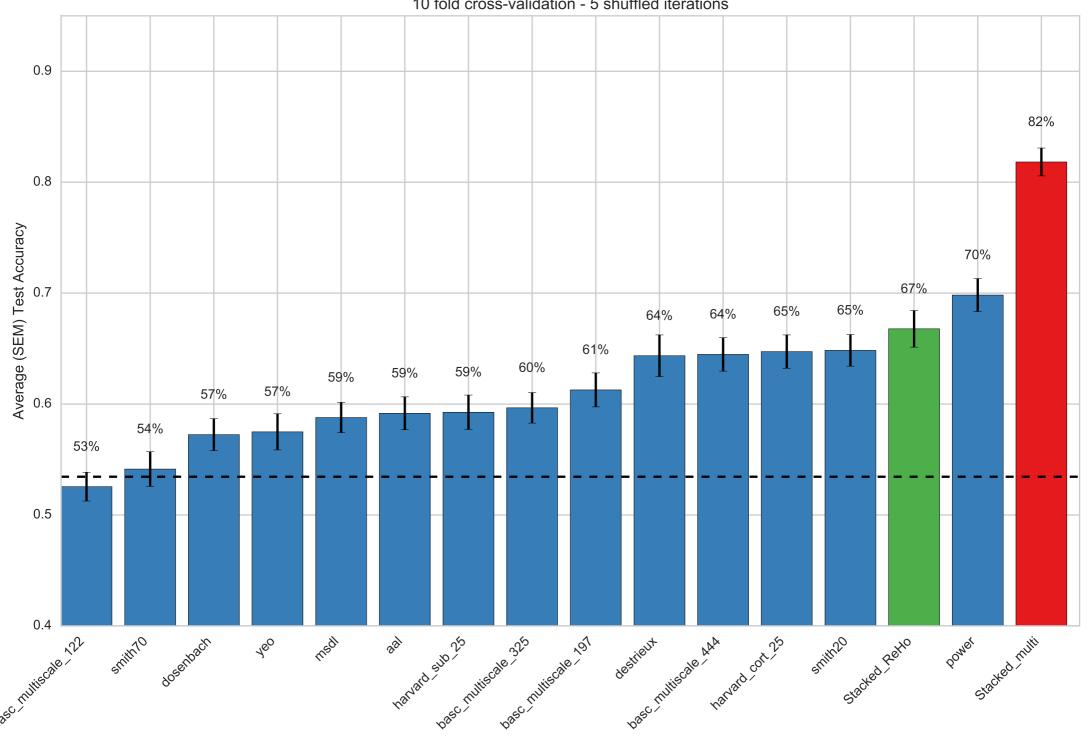
FC_part: Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



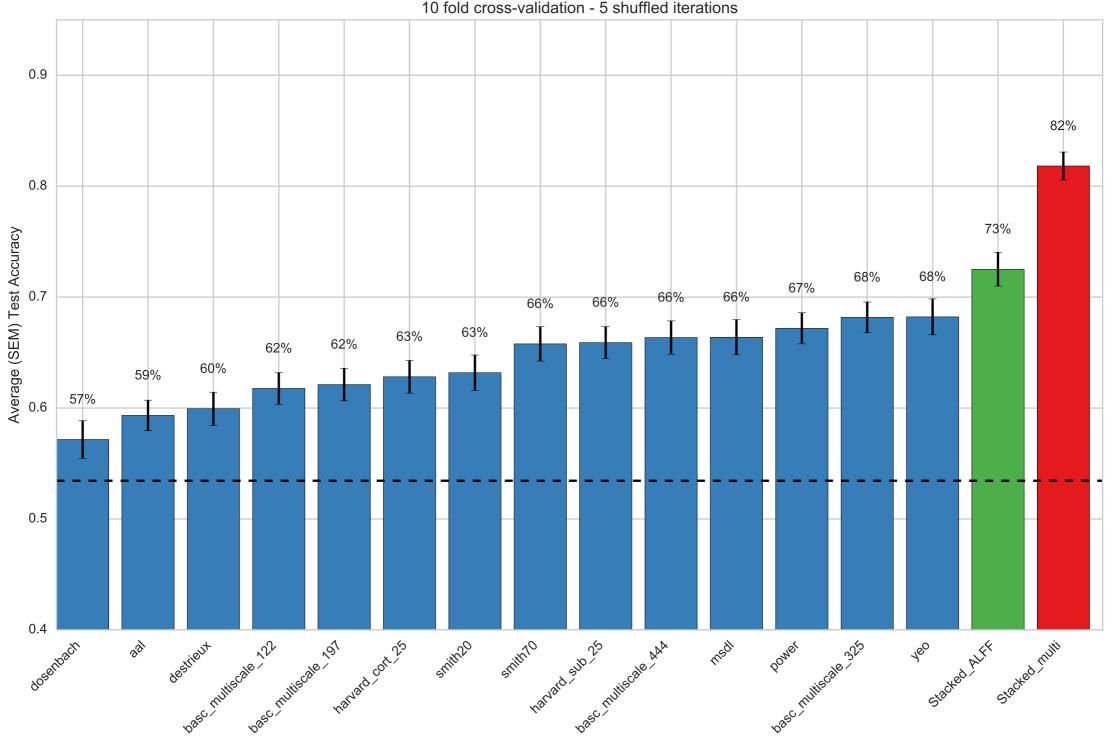
FC_prec : Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

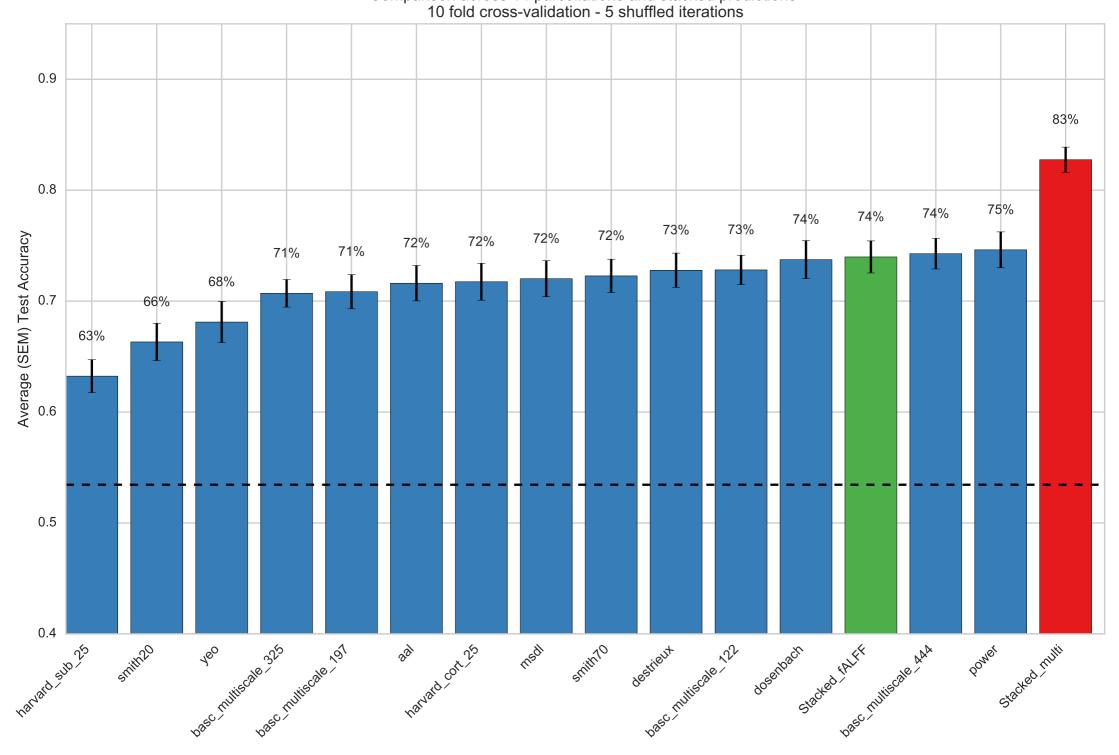


ALFF: Top 0.5% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

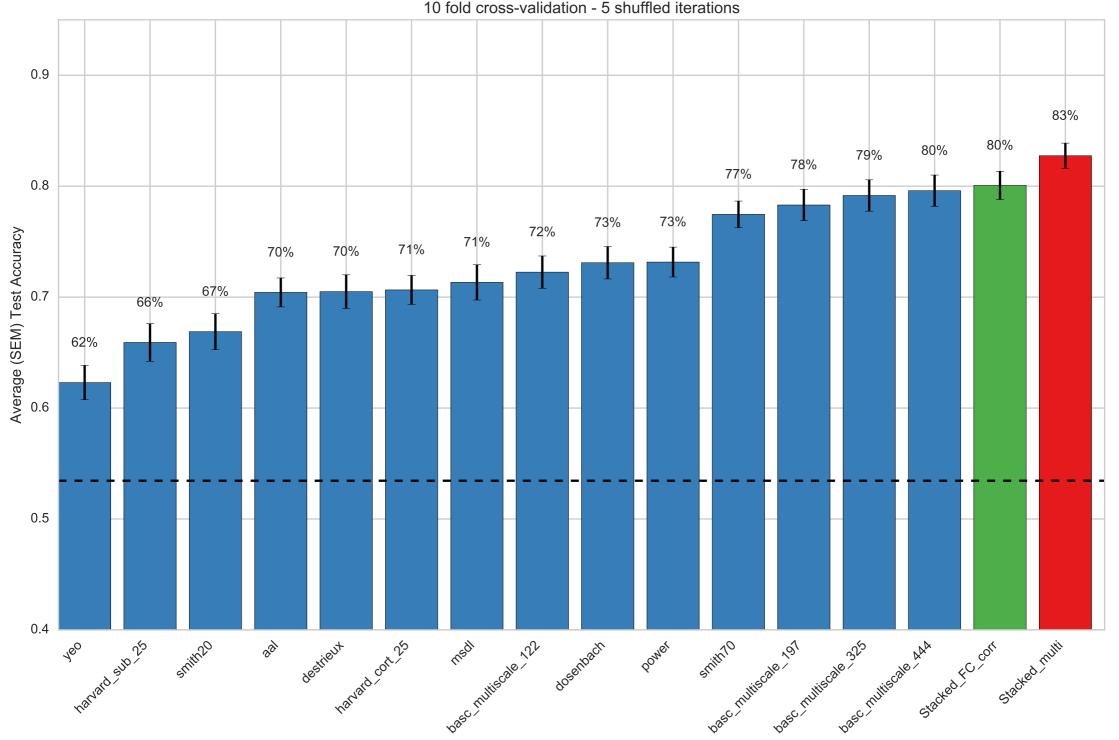




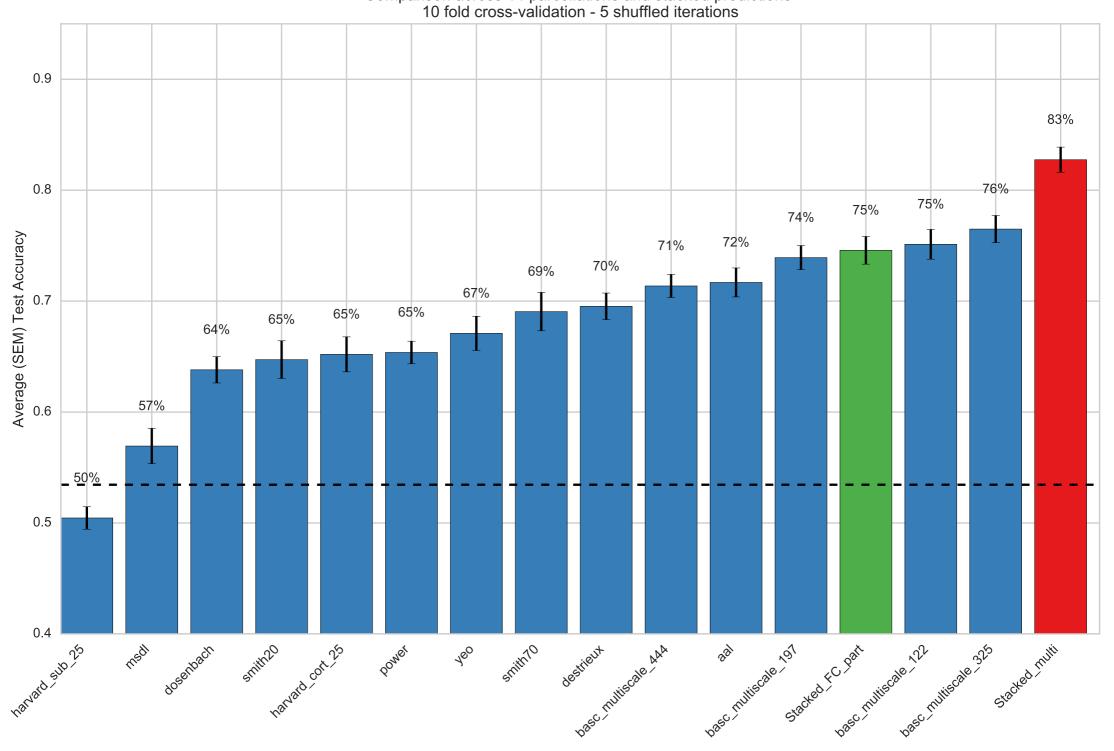
fALFF: Top 30% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



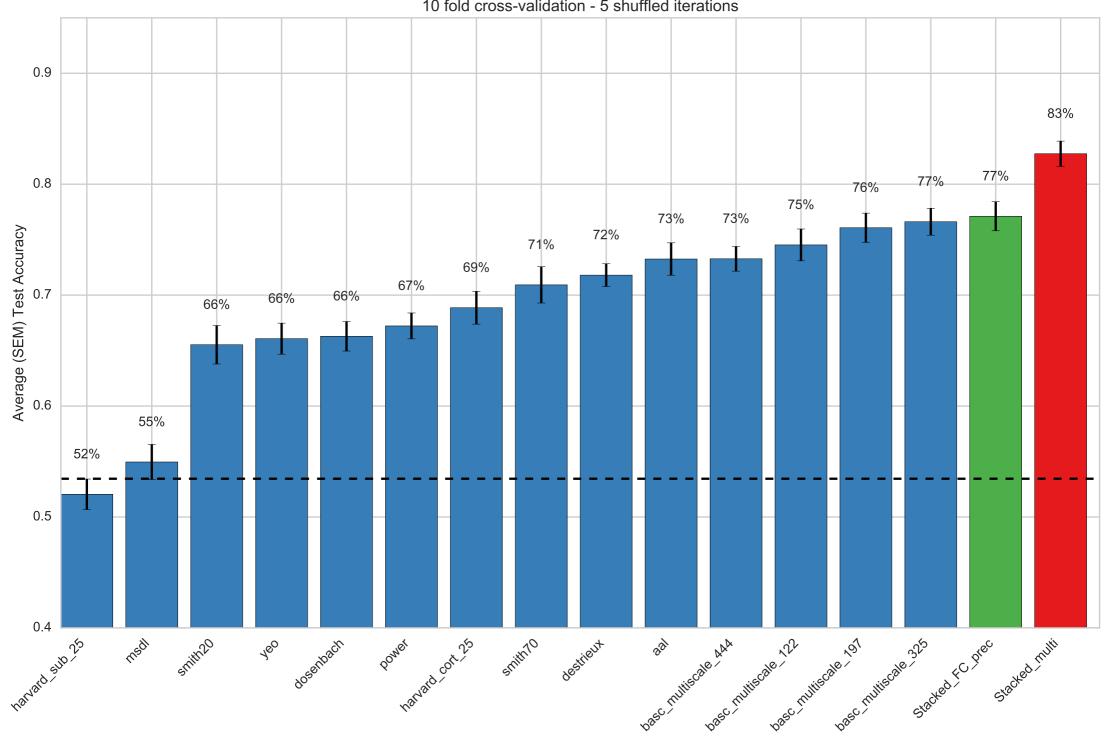
FC_corr: Top 30% Feature Selection
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



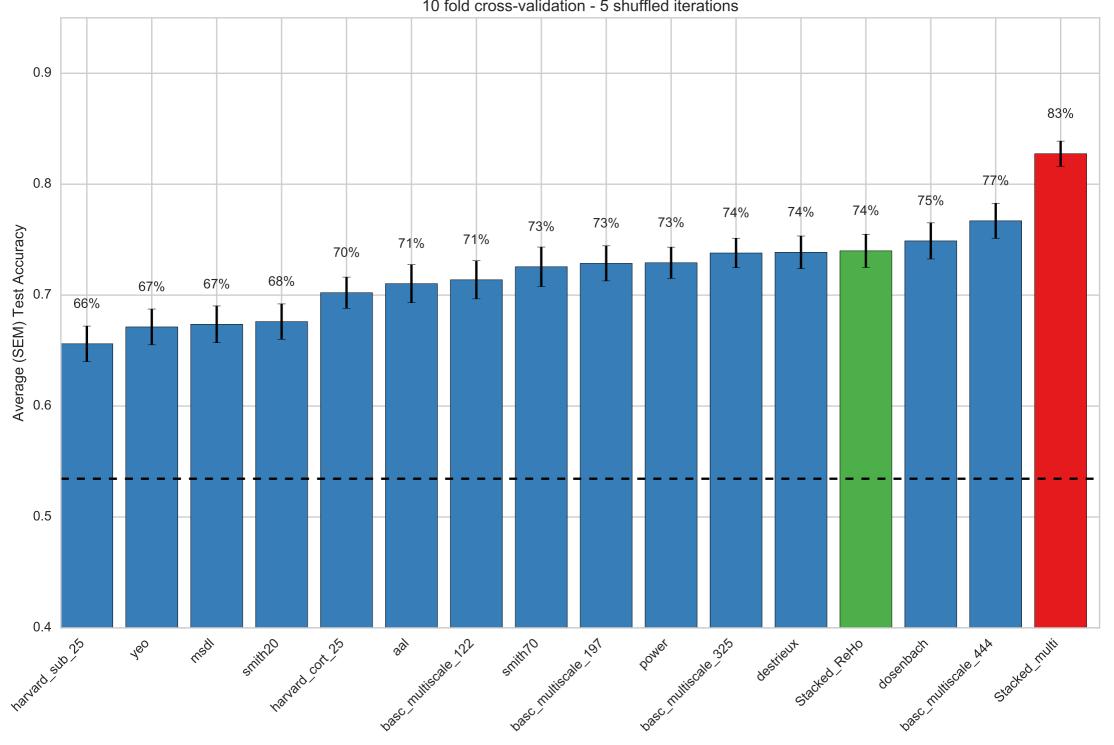
FC_part : Top 30% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



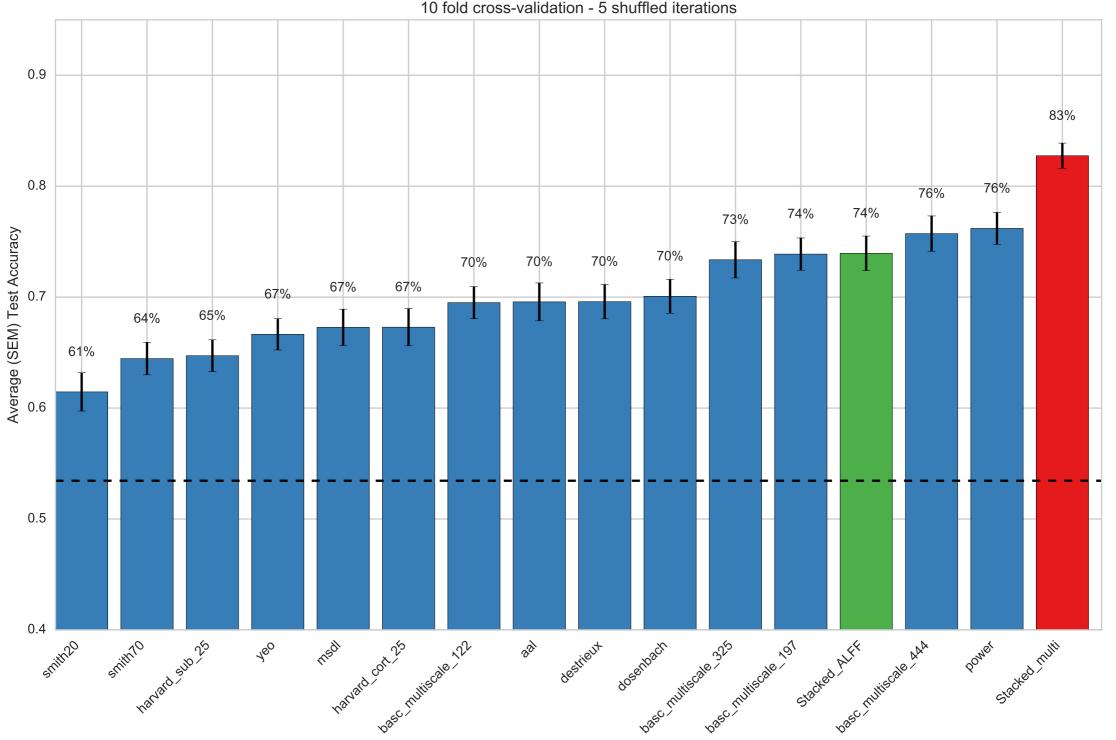
FC_prec : Top 30% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 30% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

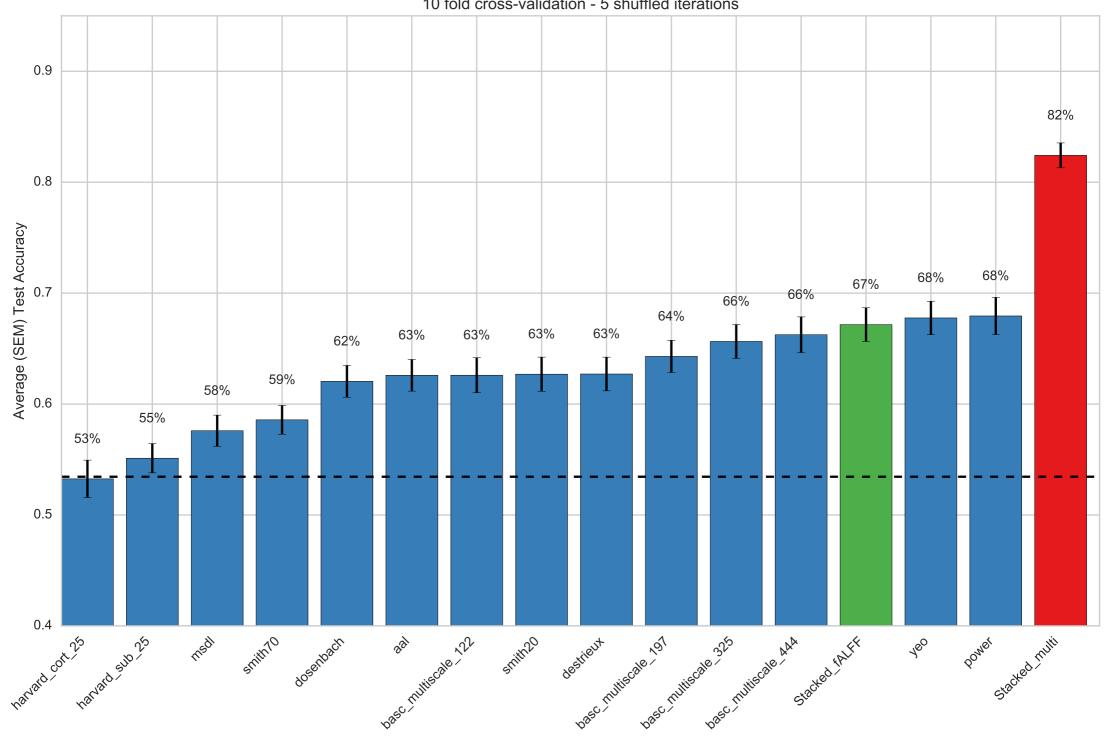


ALFF: Top 30% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

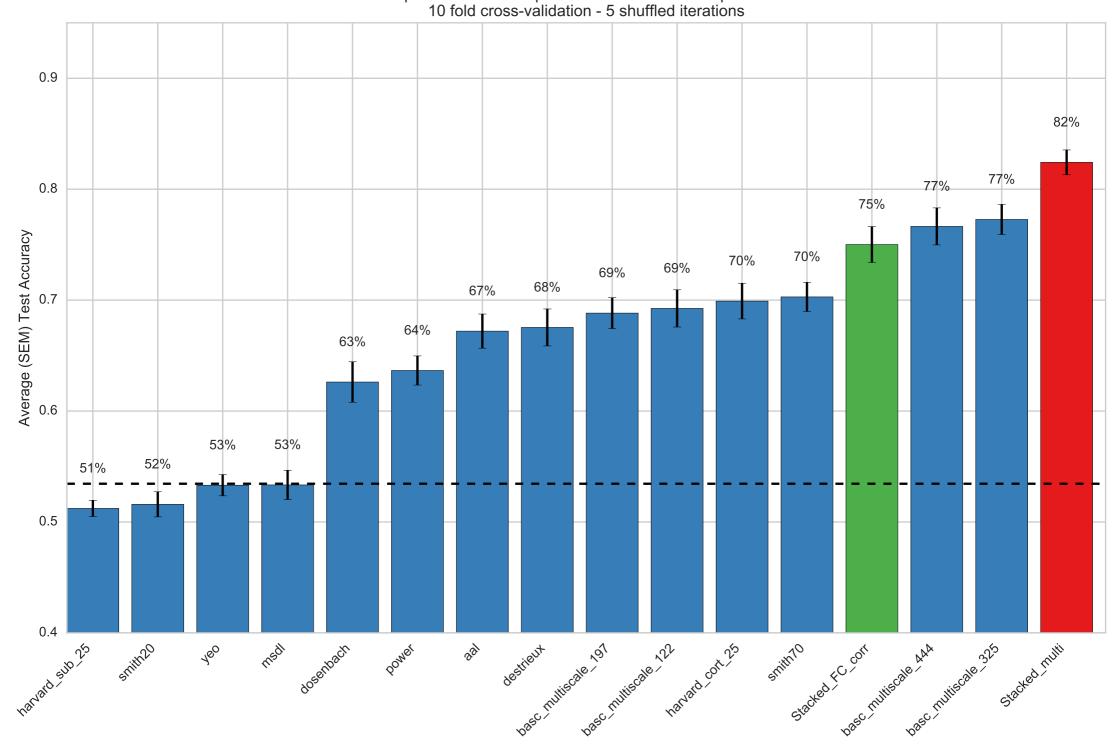




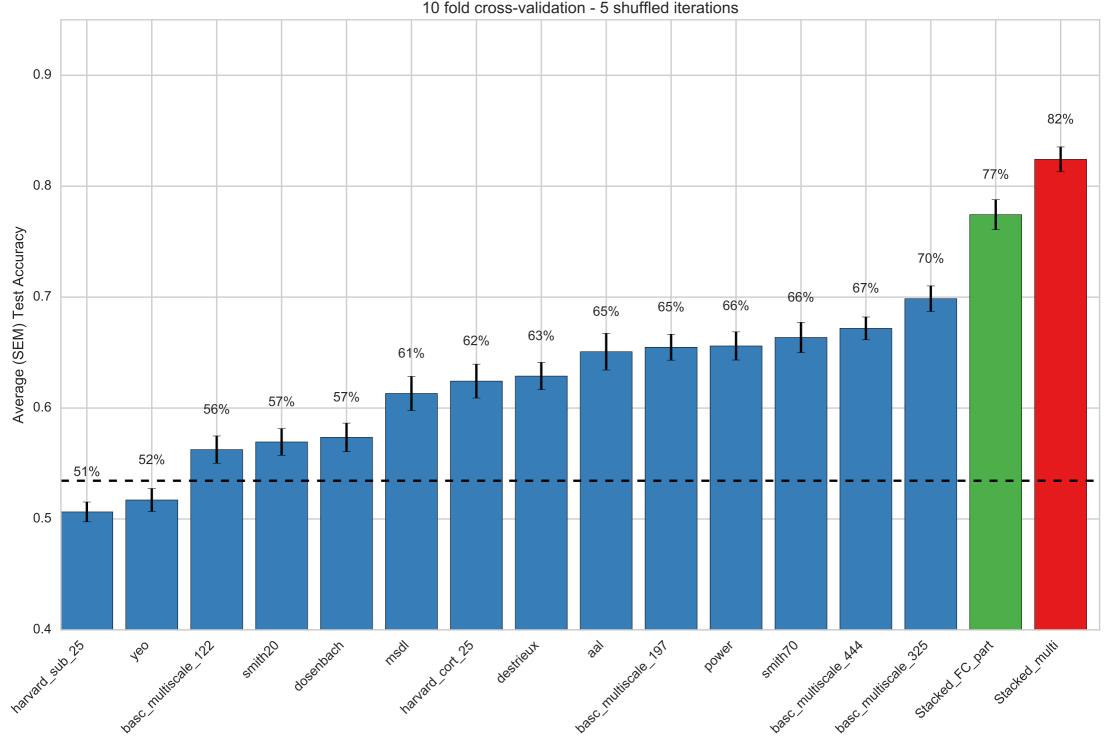
fALFF: Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



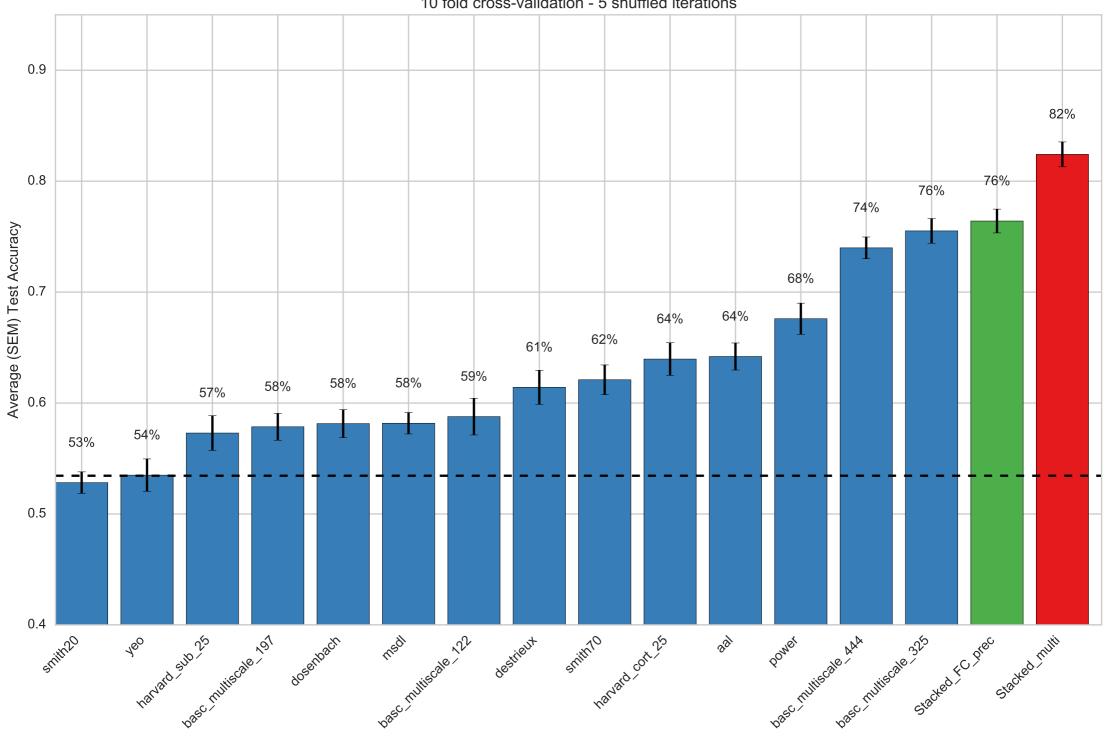
FC_corr : Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



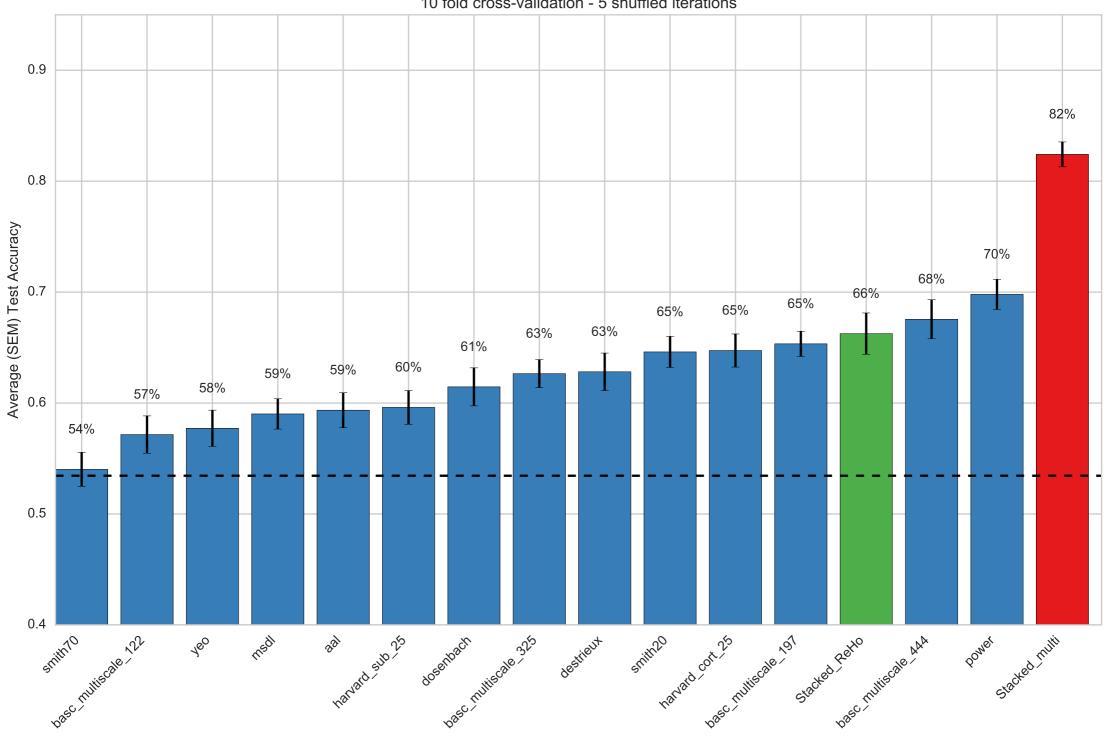
FC_part : Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



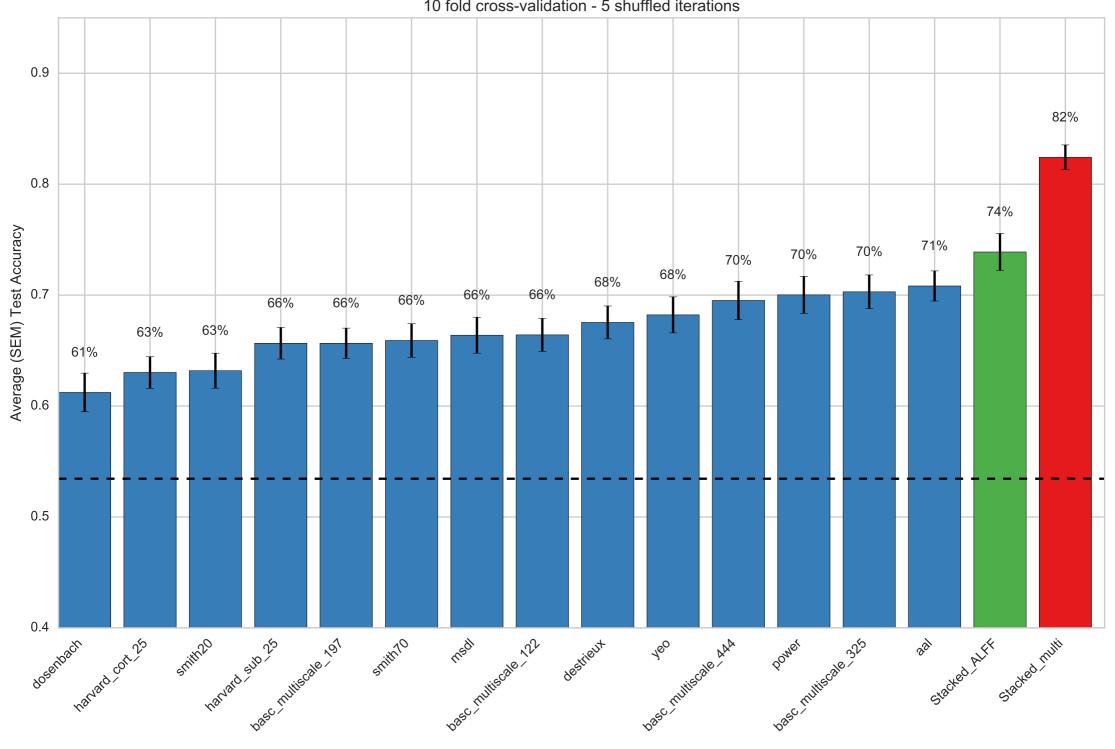
FC_prec : Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

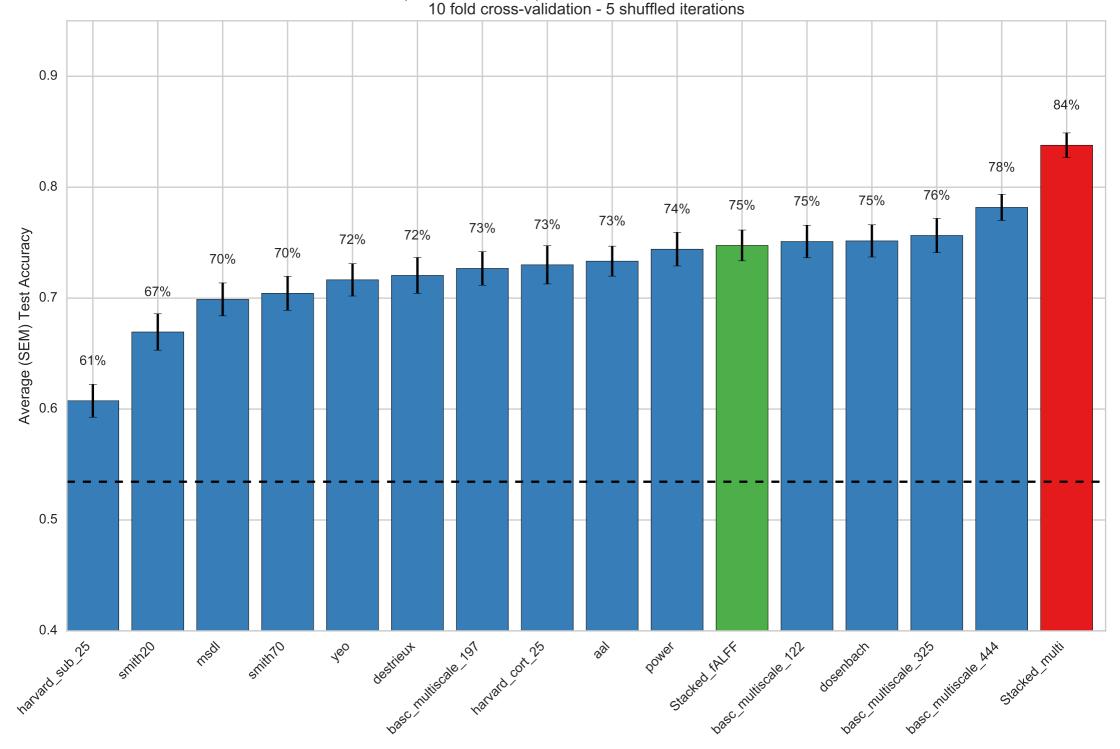


ALFF: Top 1% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

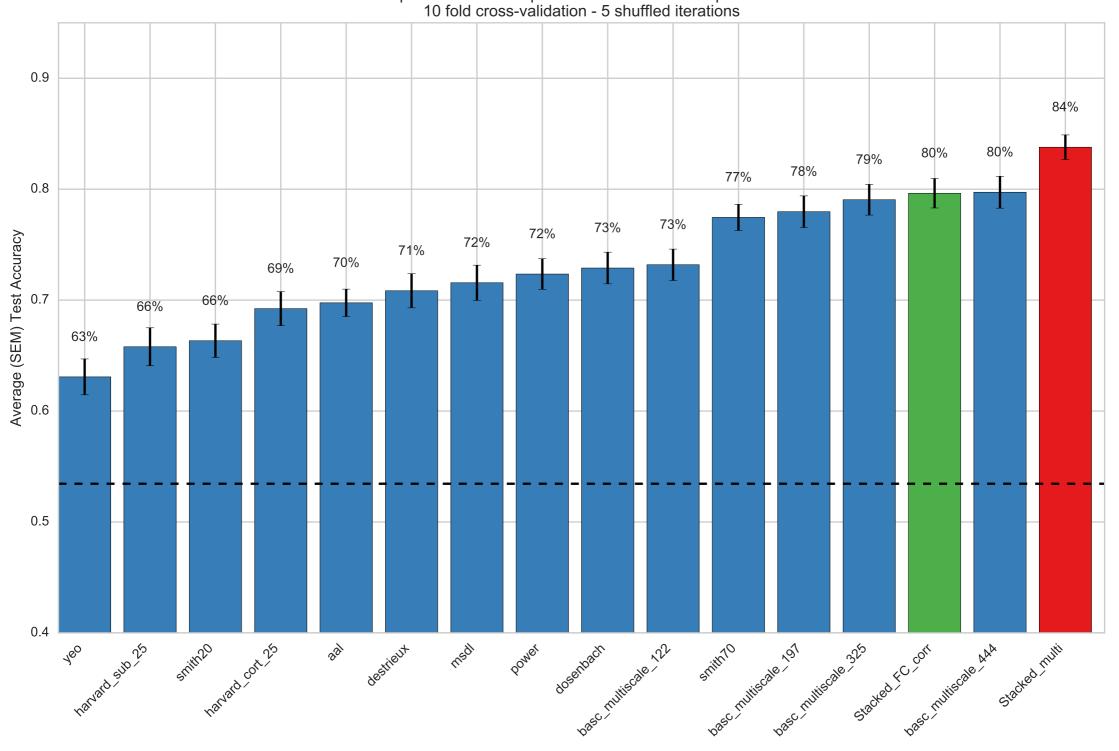




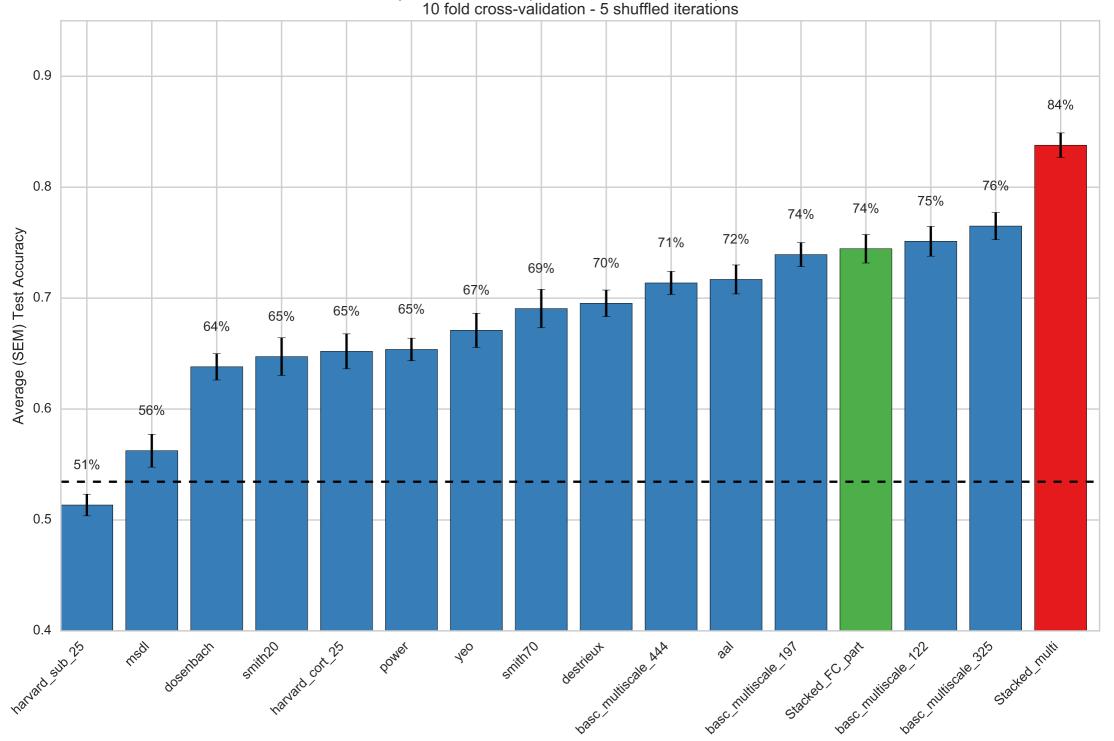
fALFF: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



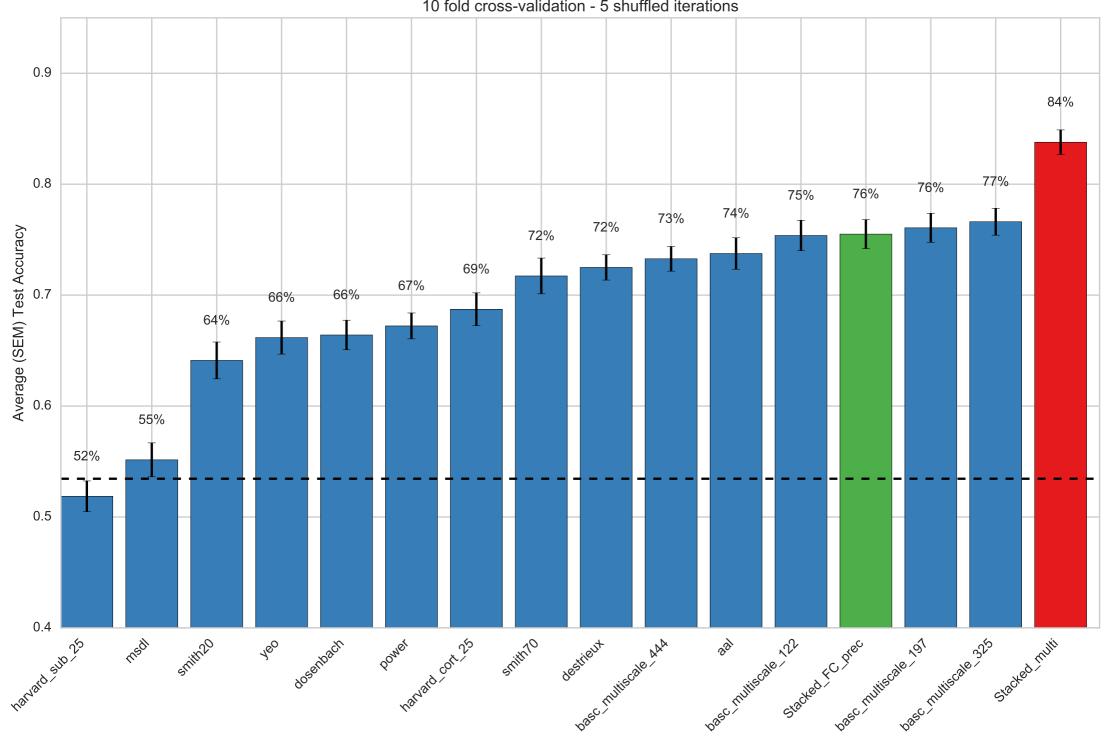
FC_corr: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



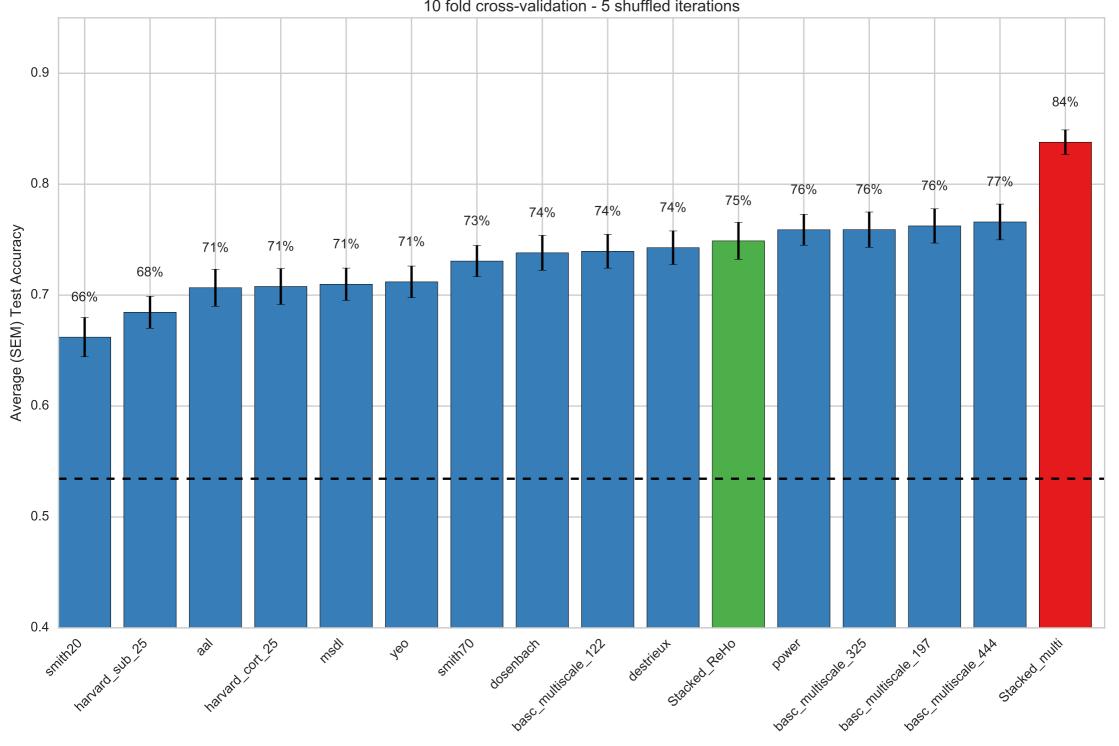
FC_part: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



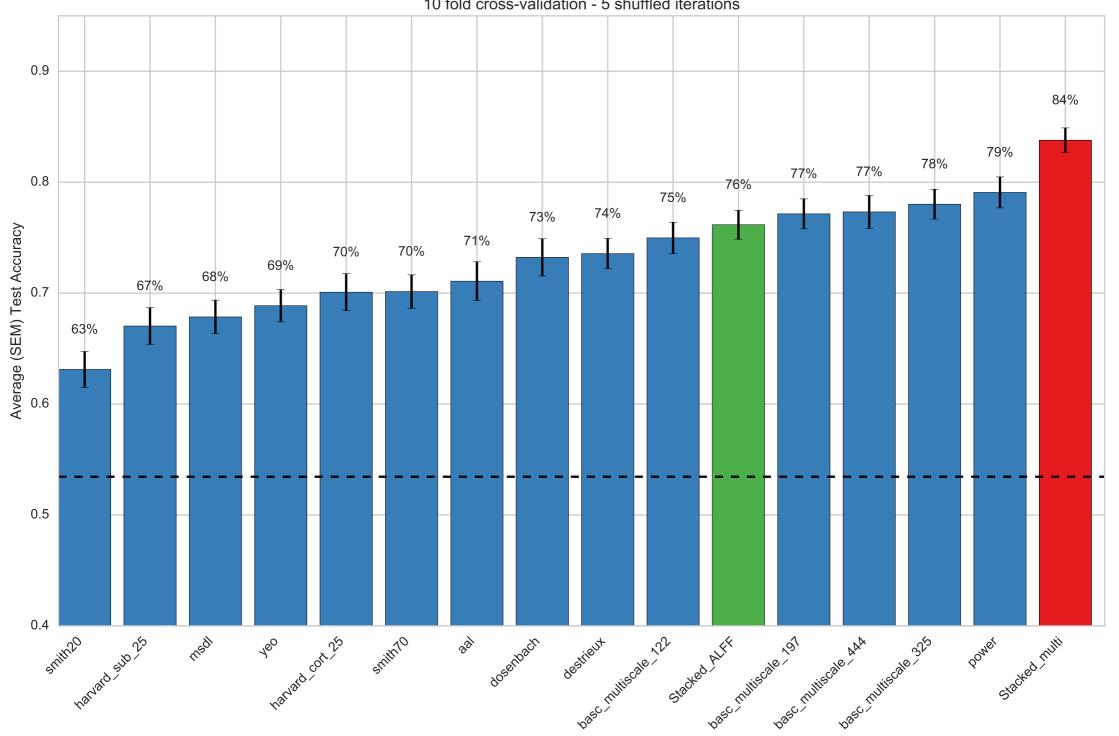
FC_prec: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

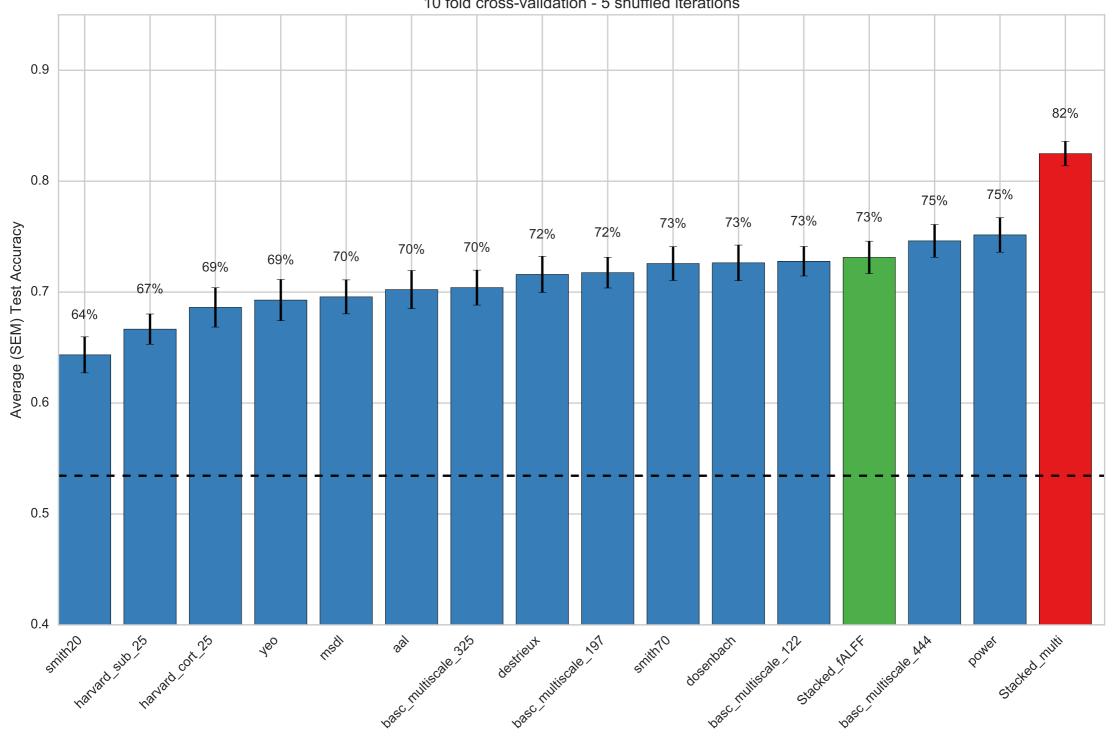


ALFF: Top 30% FC, 100% regional Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

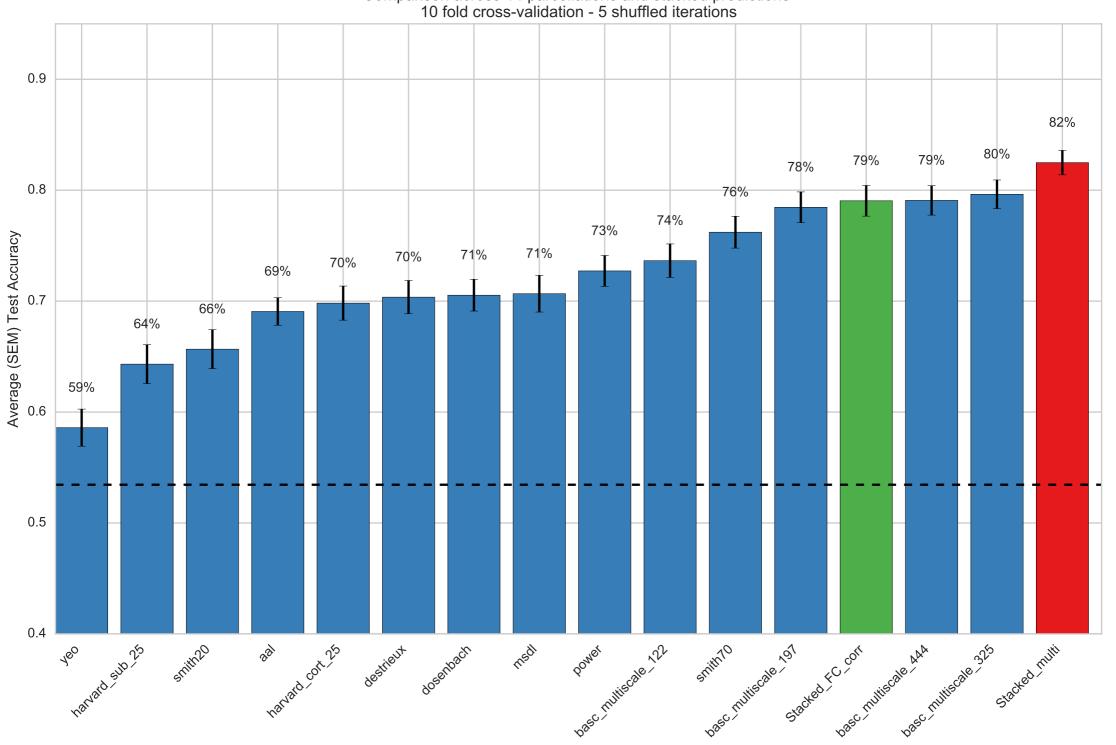




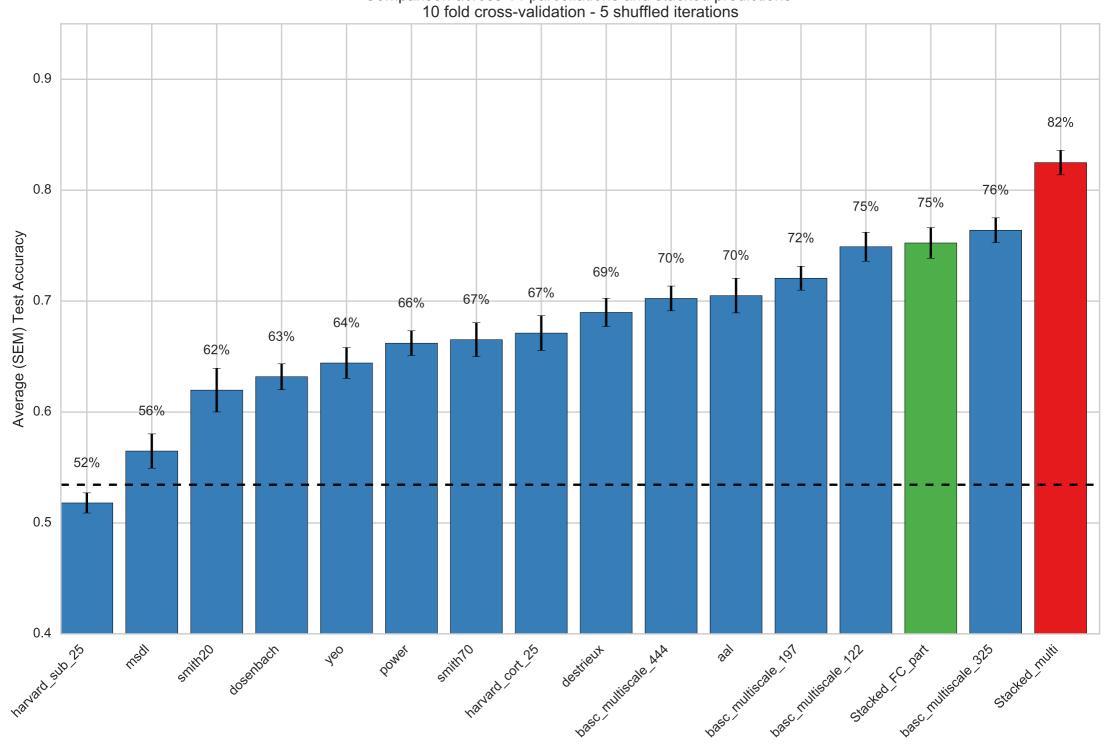
fALFF: Top 20% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



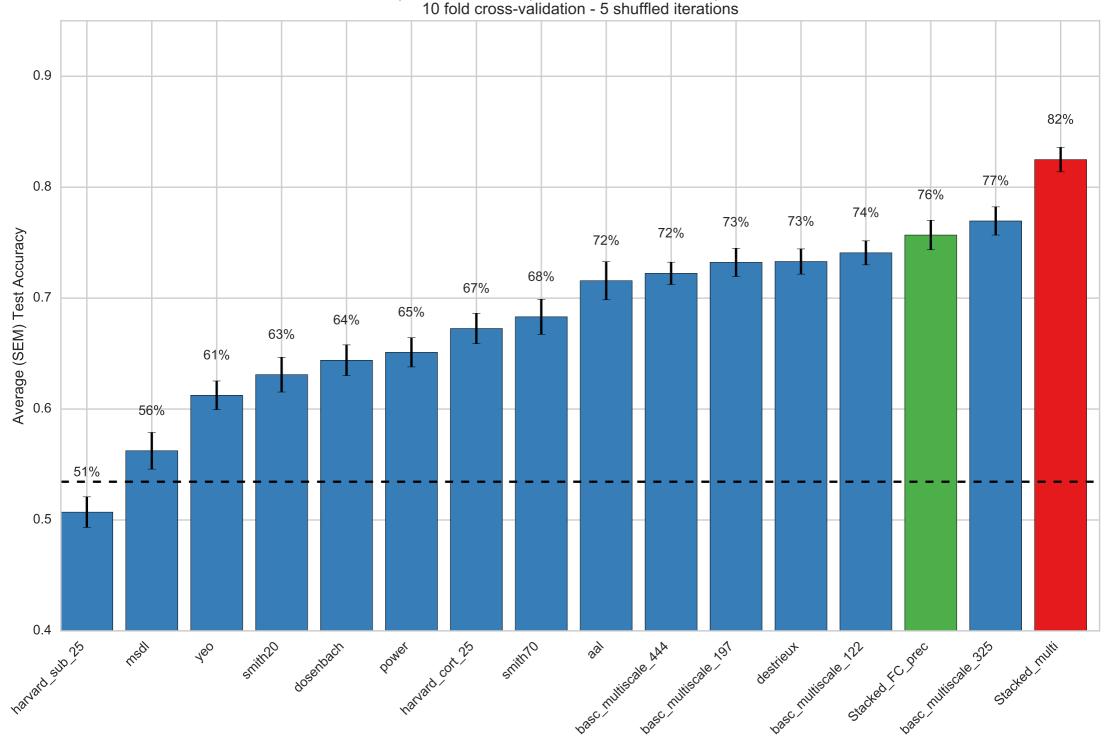
FC_corr: Top 20% Feature Selection
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



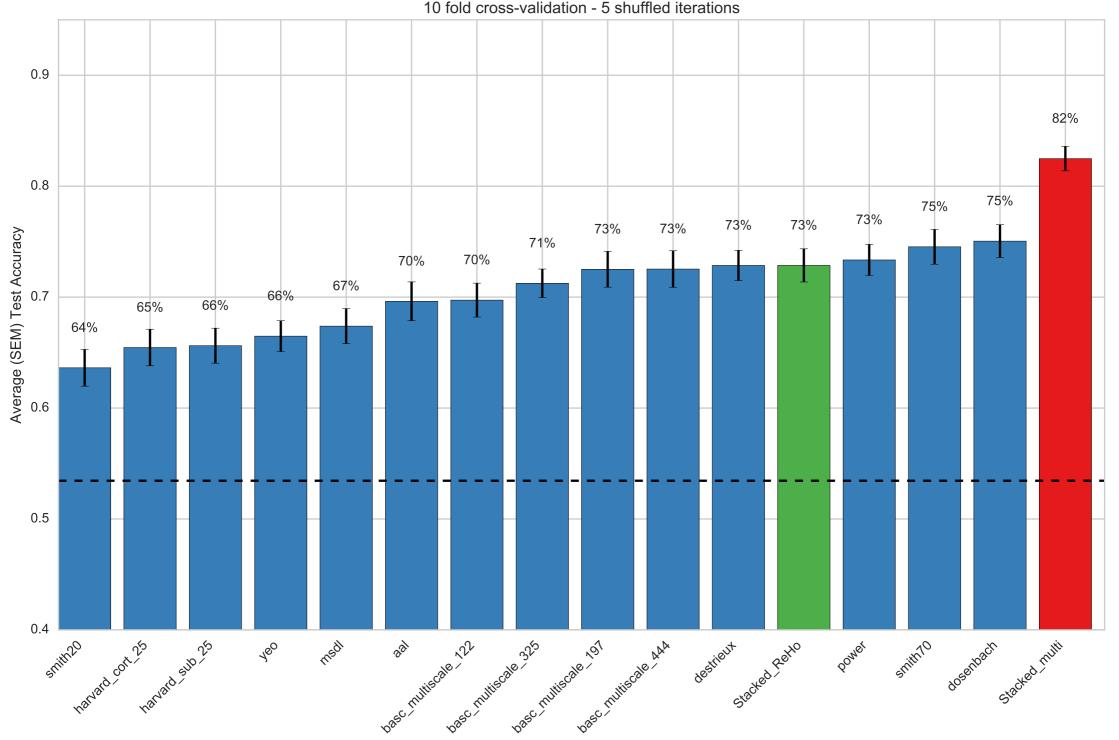
FC_part : Top 20% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



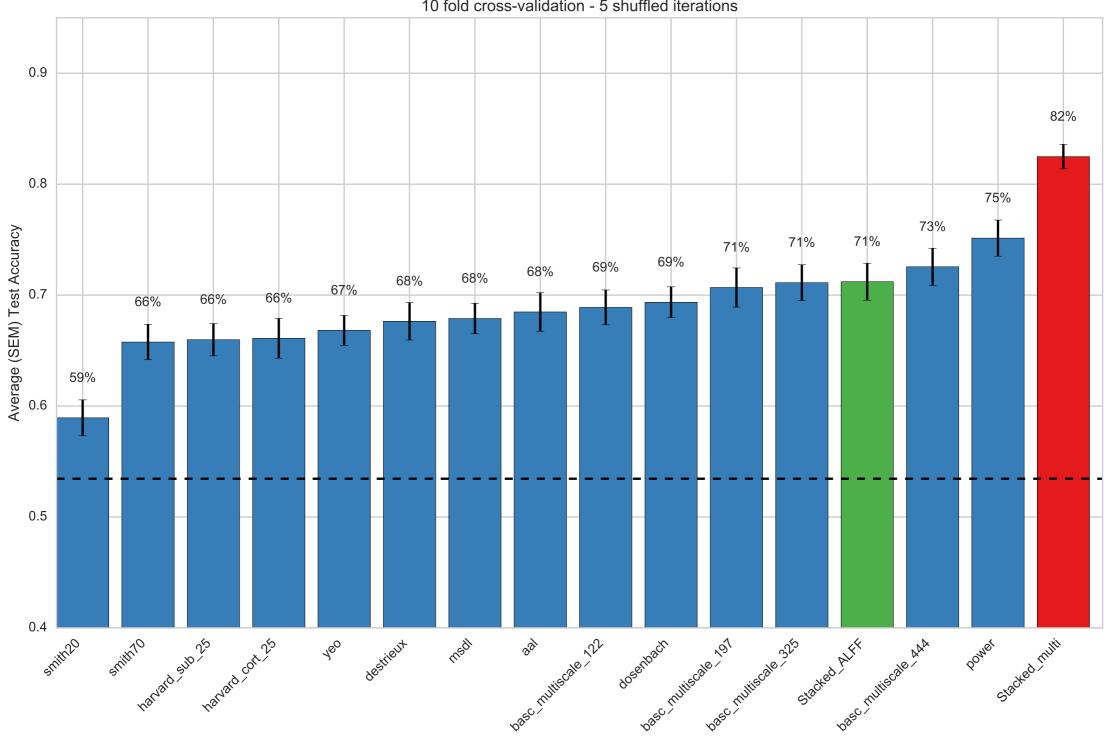
FC_prec : Top 20% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ReHo: Top 20% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

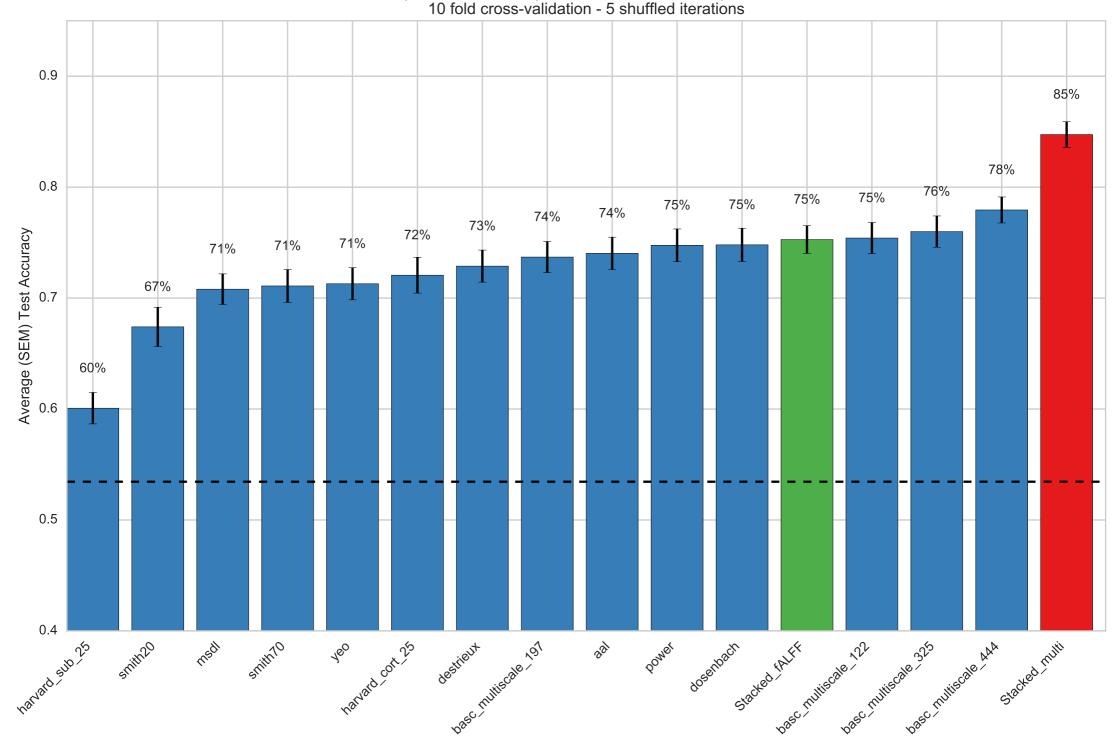


ALFF: Top 20% Feature Selection Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations

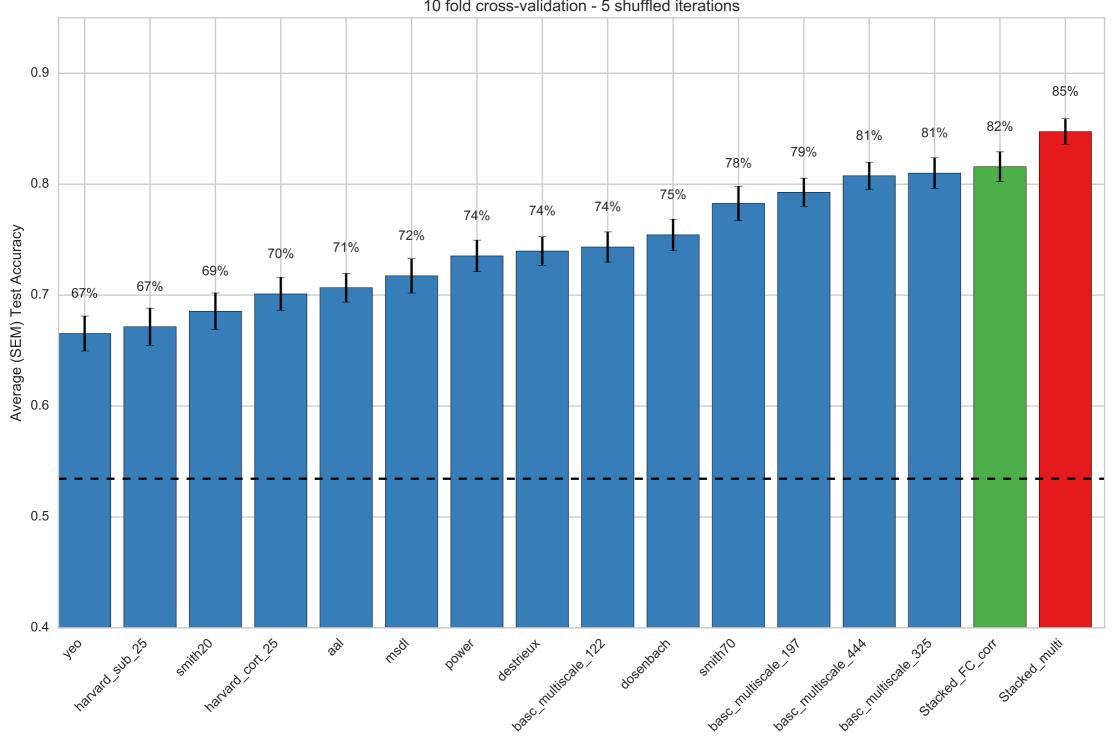




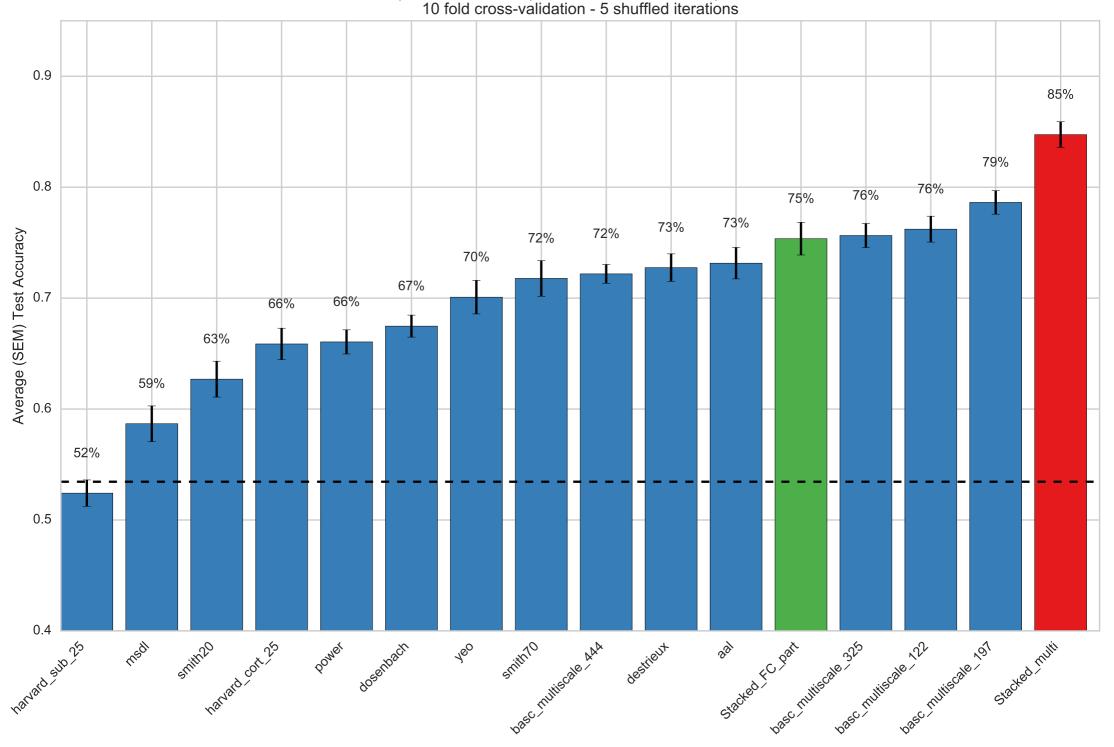
fALFF: 100% Features
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



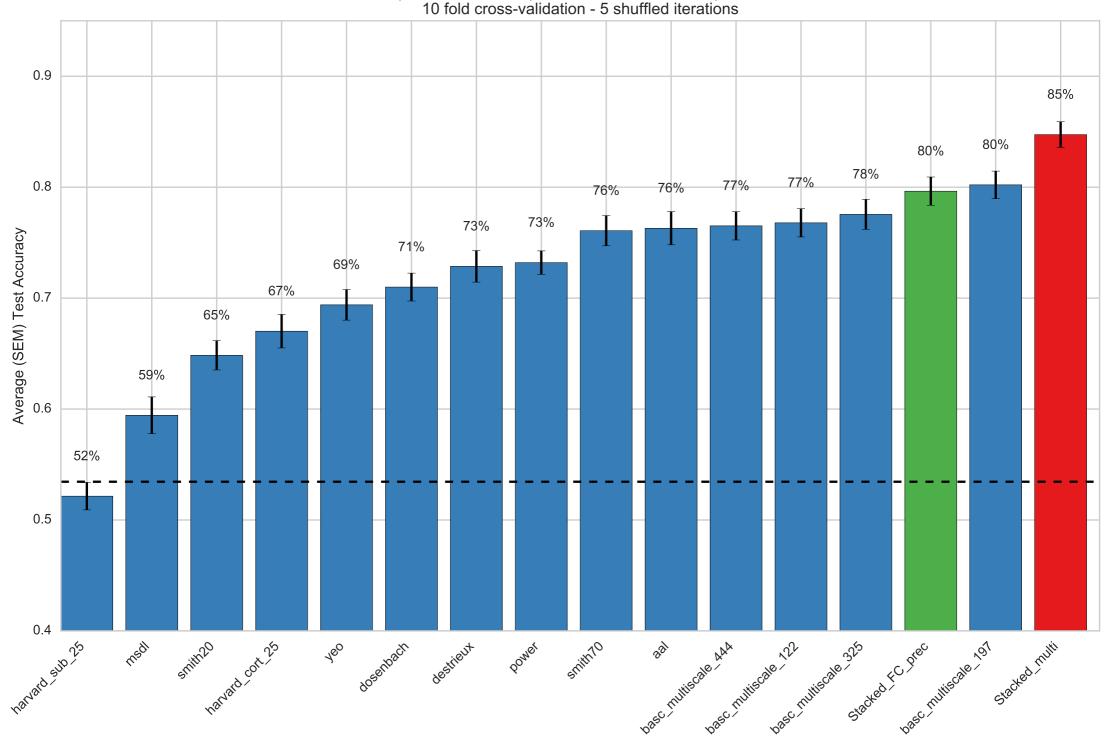
FC_corr : 100% Features
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



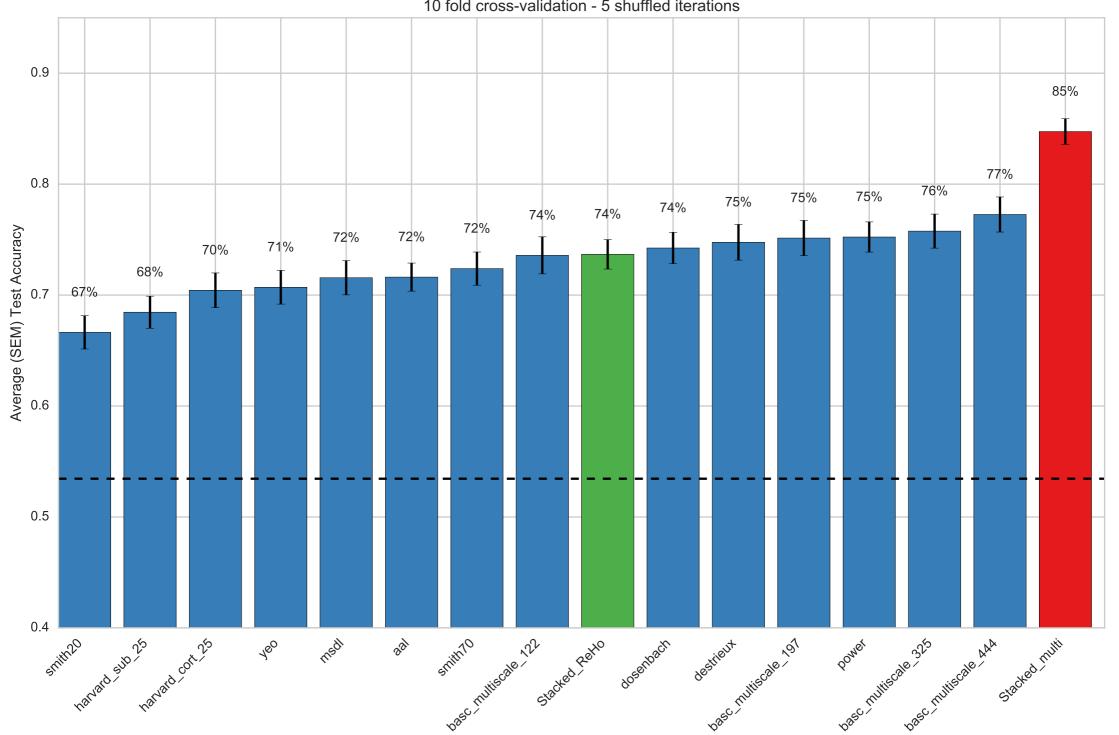
FC_part : 100% Features
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



FC_prec : 100% Features
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations



ReHo: 100% Features Comparison across 14 parcellations and stacked predictions 10 fold cross-validation - 5 shuffled iterations



ALFF: 100% Features
Comparison across 14 parcellations and stacked predictions
10 fold cross-validation - 5 shuffled iterations

