

Predicting genes associated with grey matter density and volume

Project Aim 1: Identify human genes more highly expressed in GM vs. WM

Project Aim 2: Identify human genes that are associated with differences in GM Volume

http://human.brain-map.org/mri_viewers/data

Donor	Age	Sex	Ethnicity	PMI (hours)	Image Files
H0351.1009	57 yrs	M	White or Caucasian	28	T1 T2
H0351.1012	31 yrs	M	White or Caucasian	17	T1 T2
H0351.1016	55 yrs	M	White or Caucasian	18	T1 T2
H0351.2001	24 yrs	M	Black or African American	23	DTI T1 T2
H0351.2002	39 yrs	M	Black or African American	10	DTI
H0351.2003	48 yrs	F	White or Caucasian	24	DTI T1 T2
H372.0006	44 yrs	M	White or Caucasian	24	DTI T1 T2

And corresponding microarray data, for ~28,000 genes (average value across probes) in 363-964 voxels

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Aim 1 Results: Genes correlated with GM vs. WM

GM: positive correlation
2,510 genes at $p < 0.05$ corrected

Top 10:
'HPD'
'NPVF'
'NPTX2'
'SLC8A3'
'DGKB'
'SSTR3'
'FAM153B'
'NEUROD2'
'STX1B'
'EXOC6B

WM: negative correlation
2,810 genes at $p < 0.05$ corrected

Top 10:
'HPX'
'ADM2'
'CKS1B'
'MX1'
'VEGFB'
'A_32_P178241'
'ITPKC'
'BCAS2'
'CXCR5'
'GADD45G

Aim 2 Results: Genes predictive of GM Volume

GM: positive beta weights
432 genes at $p < 0.05$ corrected

Top 10:
A_32_P146826
LOC642929
A_24_P152278
A_32_P77252
NAPRT1
A_24_P109703
A_32_P150269
MUC20
SYCE1
A_32_P42367

Sensitive and specificity checked using a Gold Standard*

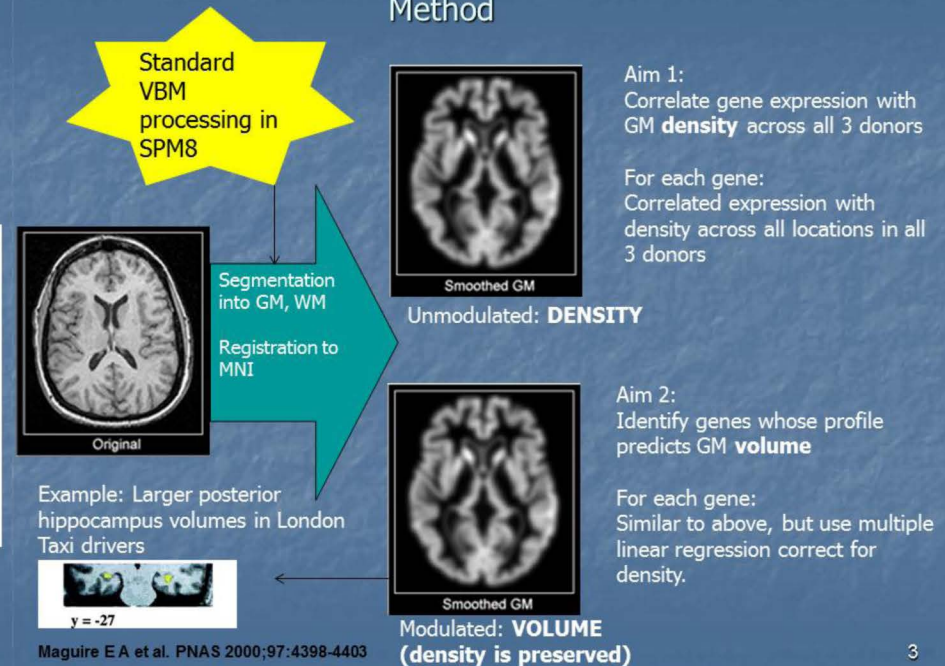
AUC=0.57

AUC=0.55

*Genes encoding CNS cell type-specific markers. Cahoy JD et al.

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Method



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Conclusions and Future Directions

1) **Aim 1: Correlating GM density with gene expression appears to pull out some relevant information regarding cell type specific markers (i.e. GM vs. WM)**

1) **Using original scan coordinates and applying my own estimated transformation could improve results**

2) **Aim 2: Preliminary results obtained but need to be validated**

1) **Using original scan coordinates and applying my own estimated transformation could improve results**

2) **Apply more sensitive multivariate analyses to identify networks of genes**

Spiro Pantazatos
Columbia University

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