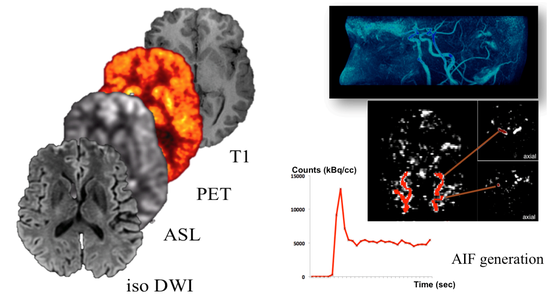
Multivariate hippocampal subfield analysis of PET, DTI and ASL in MCI and AD

Maged Goubran[1,4], Benoit Caldairou[3], Philip DiGiacomo[1], Audrey Fan1, Praveen Gulaka[1], Steven Chao[1], Andrew Quon[1], Andrea Bernasconi[2], Neda Bernasconi[2], Greg Zaharchuk[1], Minal Vasanawala[1], Michael Zeineh[1]

1 Richard M. Lucas Centre for imaging, Department of Radiology, Stanford University, CA, USA
2 Neurology, VA Palo Alto Healthcare system and Stanford University, CA, USA
3 Nuclear Medicine, VA Palo Alto Healthcare system and Stanford University, CA, USA
4 LC Campbell Cognitive Neurology Research Unit, Sunnybrook Research Institute, ON, CA

Introduction

- FDG imaging & fused PET-MR have demonstrated hypometabolism within the hippocampus in AD patients [1].
- AD has been shown to selectively affect the hippocampal subfields [2].
- Metabolic characteristics within subfield structures have not been thoroughly explored with PET
- We present an analysis of metabolism, perfusion and diffusion changes in the subfields, using simultaneous PET-MR and a robust feature sampling approach that minimizes partial volume effects.



Method & Results

Cohort & Image Acquisition:
- 13 subjects with memory complaints were stratified based on their clinical dementia rating (CDR).
- Patients underwent a 75-min FDG scan on a 3T PET-MR (GE) following a 5 mCi injection of 18F-FDG.

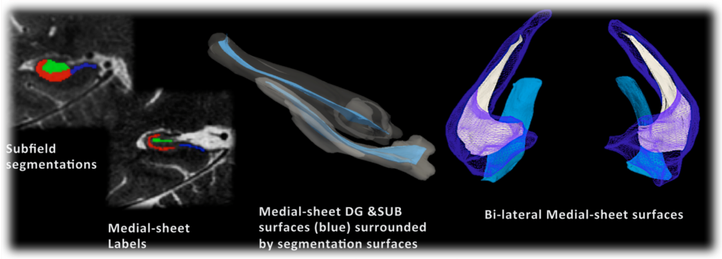
Image Processing:
- All scans were registered to the coronal T2-w images and DTI was corrected for eddy and distortion using *FSL*.
- Cerebral glucose uptake maps (CMRGlc) were computed using a two-compartment model in *PMOD* [3].

Subfield Segmentation & Central Manifold:
- Subfields were segmented automatically using T1-w and T2-w images with *ASHS* [4].
- To minimize partial volume effects, imaging features were sampled along the central manifold of each subfield
- We finally mapped the features (CMRGlu, CBF, FA, MD) to each vertex on the central manifold.

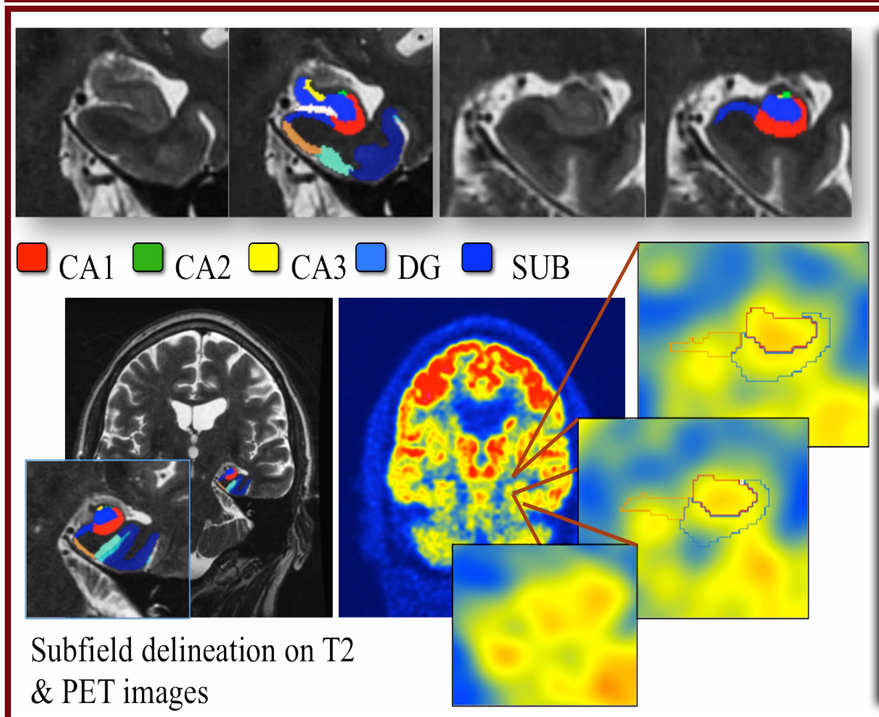
Statistical Analysis
- Statistical analysis between groups was performed in *SurfStat* [6] for subfield thickness, CMRGlu, CBF, FA & MD
- For whole hippocampus analysis, Student's t-test was performed between groups for the same metrics.

Table 1: MR sequences

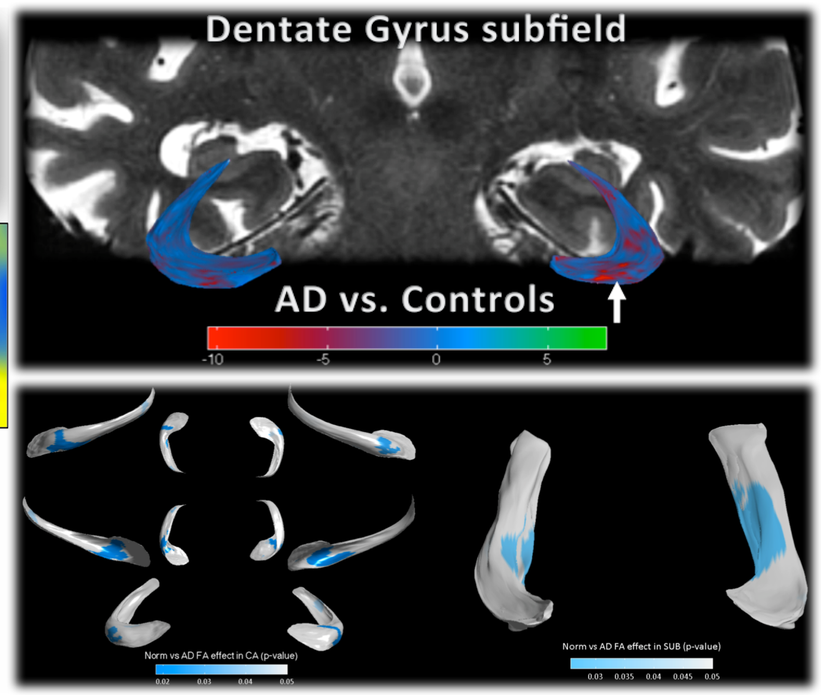
Sequence	Pixel size	Scan Time	Orientation	Function
T1-w IRSPGR	1x1x1.2 mm	5:46	Sagittal	Segmentation
T2-w FSE	0.43x0.43x1.9 mm	3:24	Oblique Coronal	Segmentation
ASL	1.87x1.87x3 mm	5:32	Axial	CBF
DTI (60 dirs.)	1.6 mm isotropic	9:10	Axial	FA/MD
DTI (blip down)	1.6 mm isotropic	0:30	Axial	Distortion correction



Medial sheet generation from subfield segmentations



Overview of ASHS segmentation results on coronal slices of the high-resolution T2 with segmentation overlaid on our CMRGlu maps.

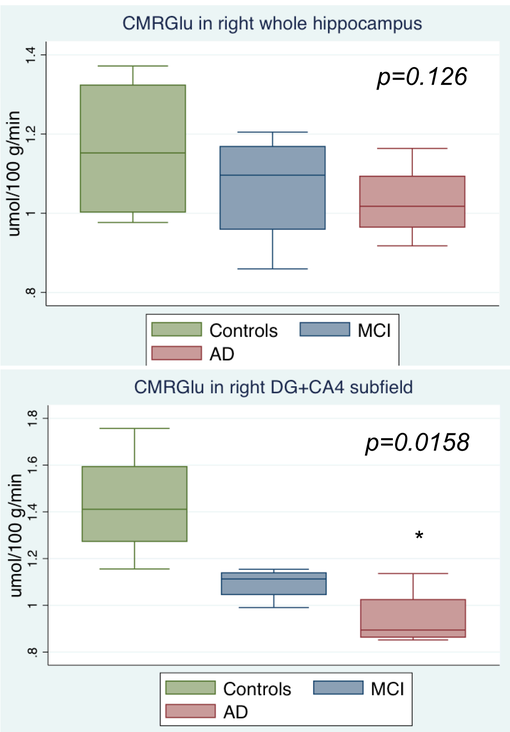


Top: T-statistics of subfield thickness in DG in Controls vs. AD overlaid on medial-sheet surfaces. Bottom: Significant clusters of FA reduction in AD patients (Left: CA, Right: SUB)

Fig.4: Whole-hippocampus CMRGlu showing no sig. difference between groups.

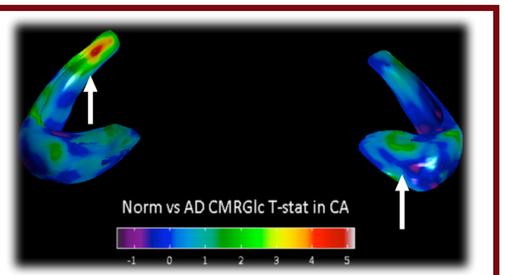
The p-value for the F-tests are at the top, &the asterisk indicates sig. difference between AD and Controls.

In the DG+CA4 subfield showing significant reduction in metabolism across groups.



Discussion

- *Subfield analysis may be more sensitive to pathological changes than global hippocampal assessment*.
- We used a robust surface-based approach by sampling features along the central-manifold.
- This multivariate technique may help disentangle structural & metabolic derangements accompanying dementia.
- Future work will include a larger patient cohort and assessment of resting-state connectivity.



References

[1] Mosconi et al., Neurology 2005;64:1860-1867 [2] West et al., Neurobiol Aging 2004;25:1205-1212
[3] Zanotti-Fregonara et al., J Cereb Blood Flow Metab 2011; 31:1986:1998 [4] Yushkevich et al., Human Brian Mapping 2014; 36:258-287
[5] Kim, Hosung, et al. MICCAI 2014. Springer International Publishing, 2014. 170-178. [6] Worsley, K. J., et al. *Neuroimage* 47 (2009): S102.

maged.goubran@sri.utoronto.ca