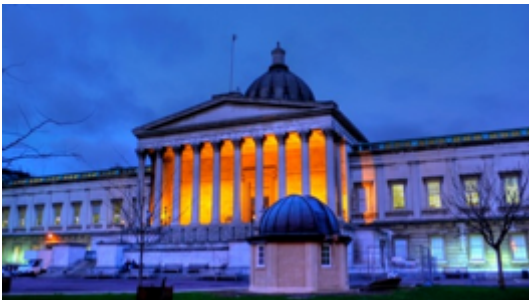


## Images and Genes: From AD to MS



Andre Altmann

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Engineering

Translational Imaging Group (TIG)

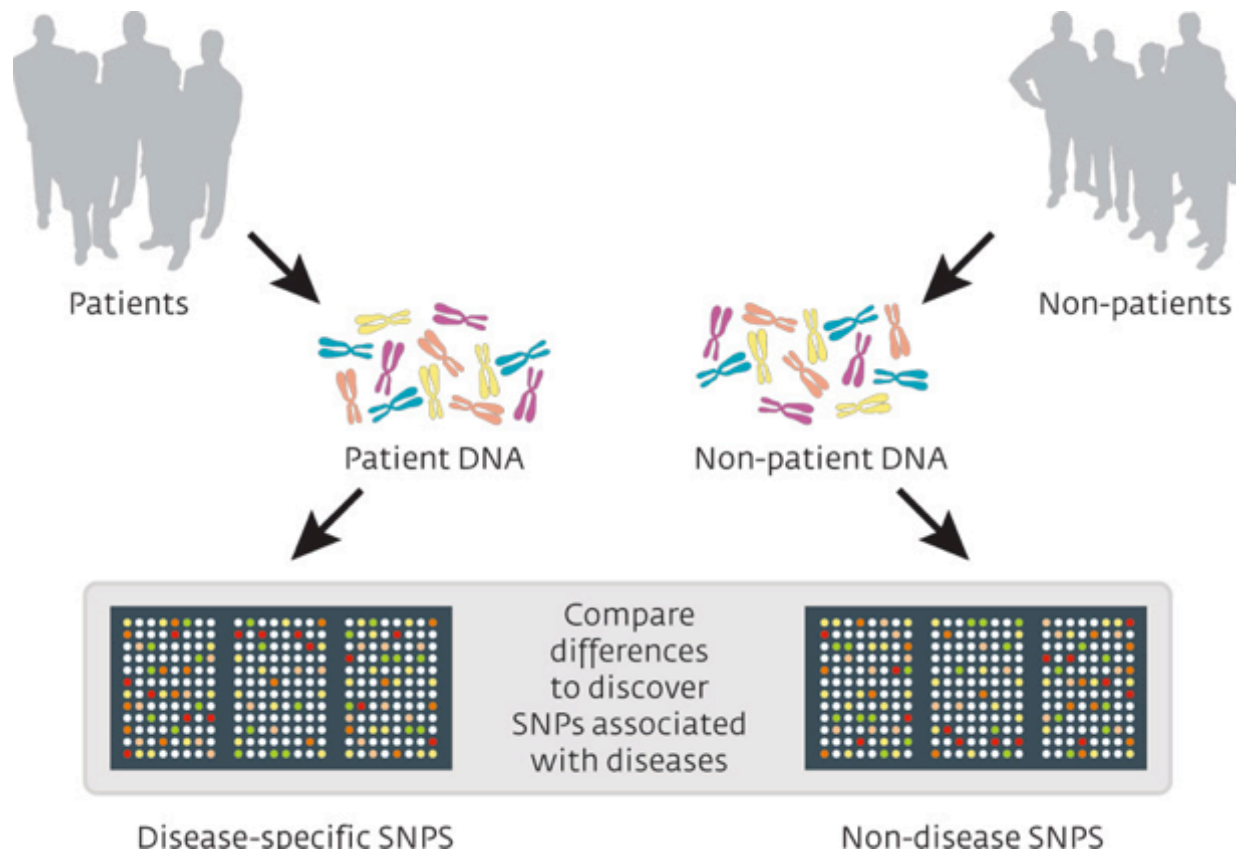
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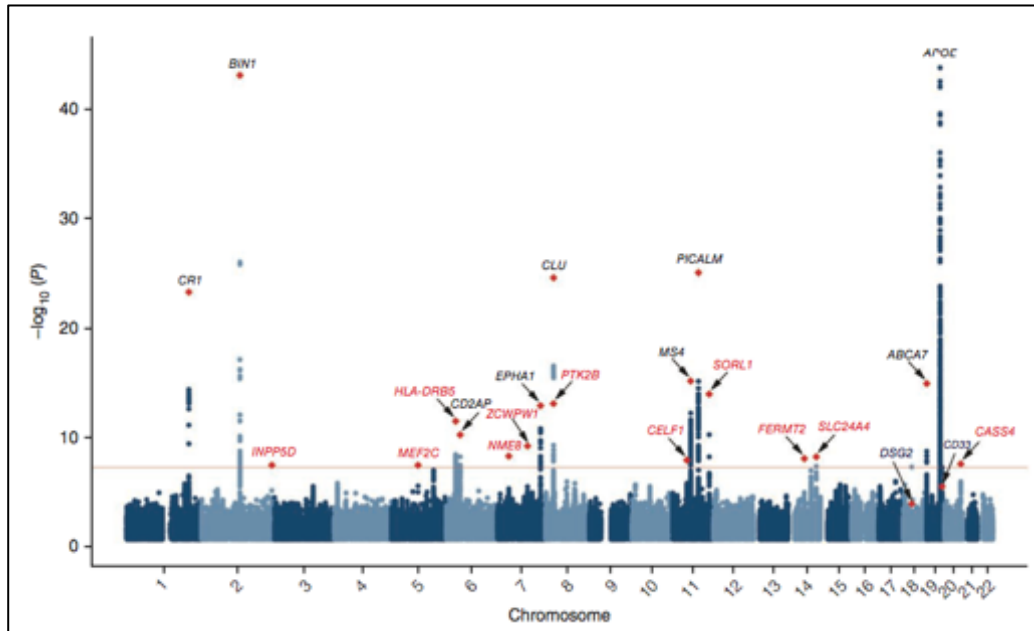
London, January 31<sup>st</sup> 2018

- Single Nucleotide Polymorphisms (SNPs)
- ~ 1 million genetic markers measured (~0.001%)
- Sample acquisition cheap (£30 per participant)

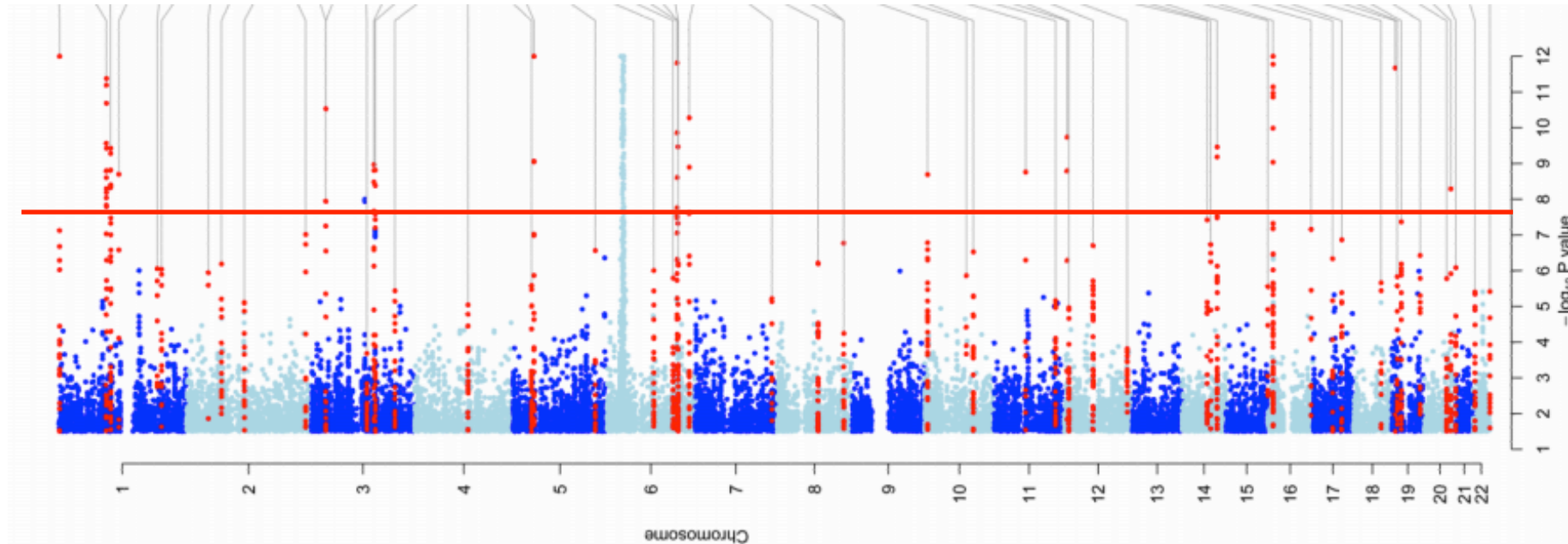




$$= \beta_0 + \beta_1 \times \text{SNP} + \sum_{i=2}^N \beta_i x_i + \epsilon$$

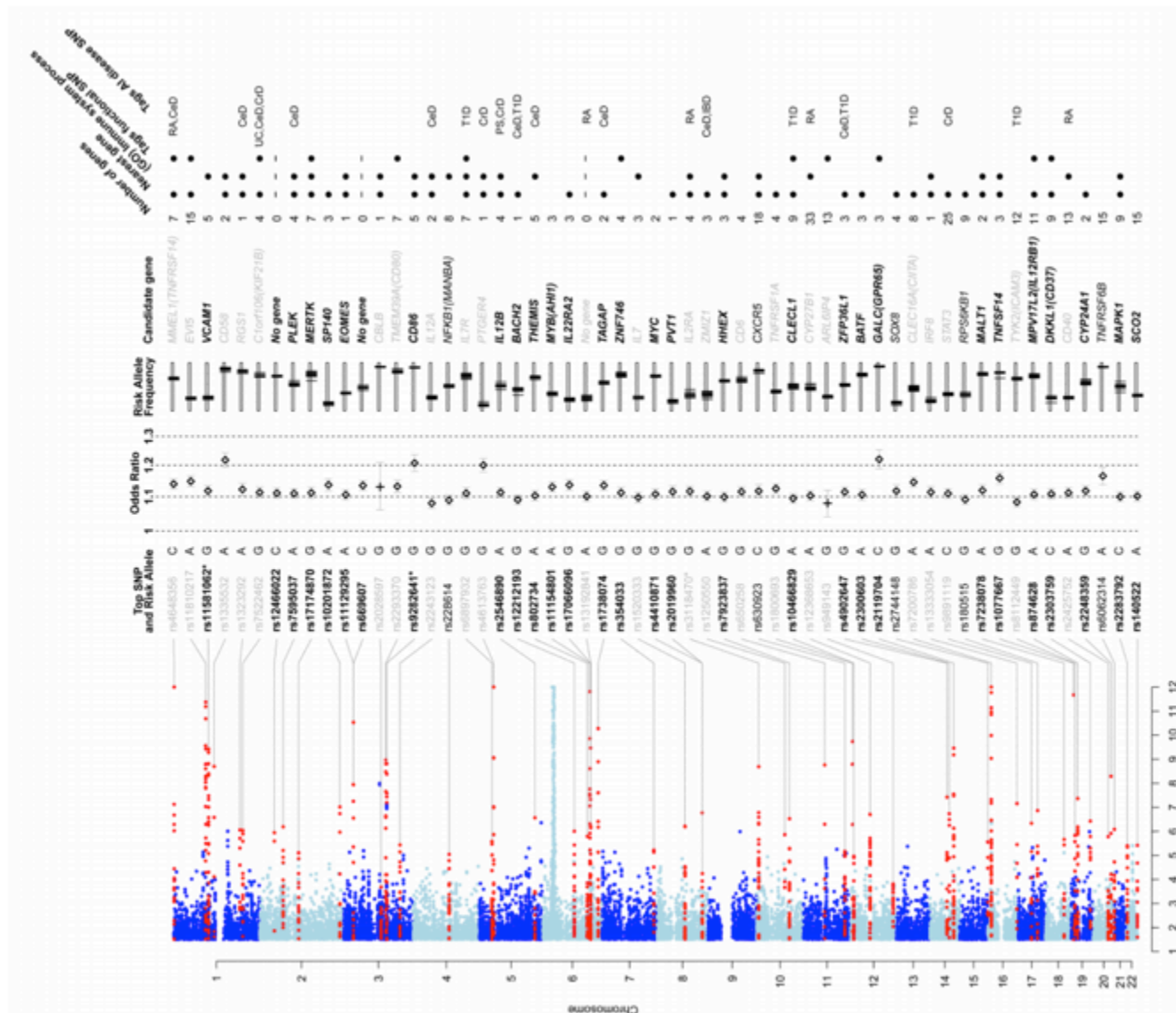


- Mass univariate testing
- $P < 5 \times 10^{-8}$  is 'genome-wide significant'



2011:    ~10,000 cases    doi:10.1038/nature10251  
          ~17,000 controls

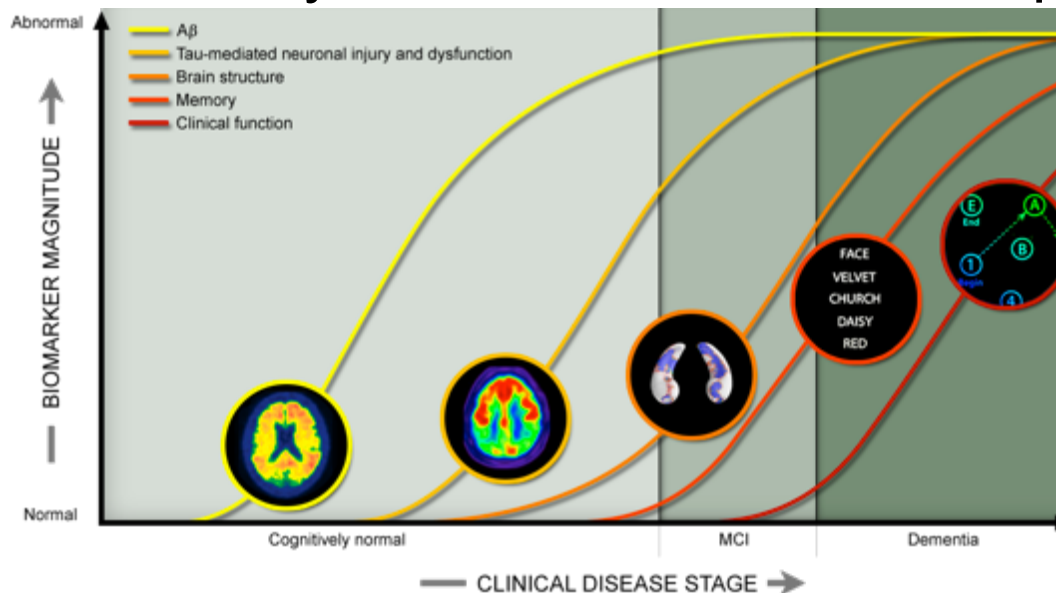
# Genome-wide Association Study (GWAS)



2011: ~10,000 cases      doi:10.1038/nature10251  
 ~17,000 controls

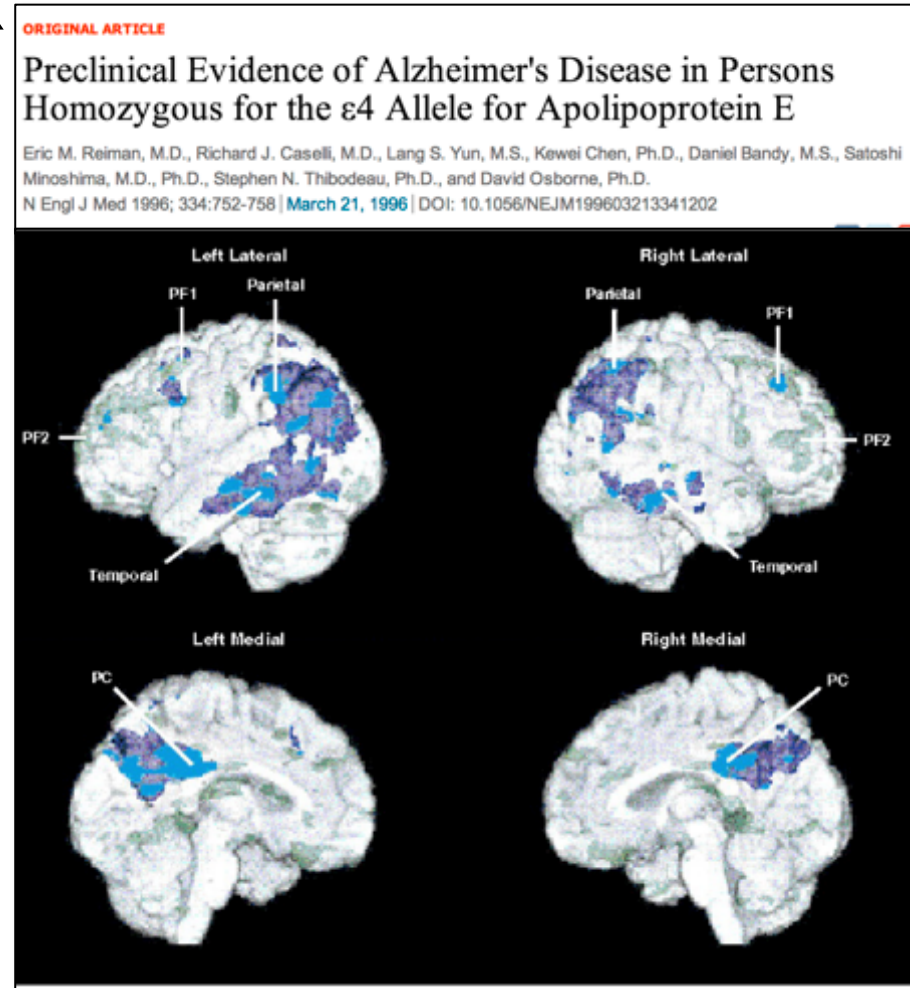


- Imaging genetics uses imaging phenotypes in genetic studies
- Imaging phenotypes are ‘closer’ to the disorder than diagnoses
  - Often diagnoses are ‘mixed bags’
  - Allows us to study how the disorder develops





- APOE-e4 is a strong risk factor for AD
- Reiman et *al.* (1996) studied glucose metabolism
- APOE-e4 homozygotes showed reduced metabolism in typical AD regions





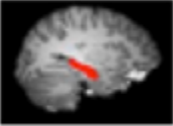
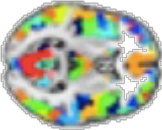
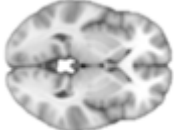
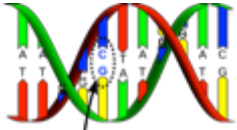


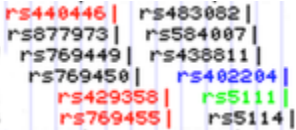
## Imaging Multiple

Stefan Dirk Roosendaal,

2015

**Table 1**  
Relations between MS susceptibility genes and brain MR imaging

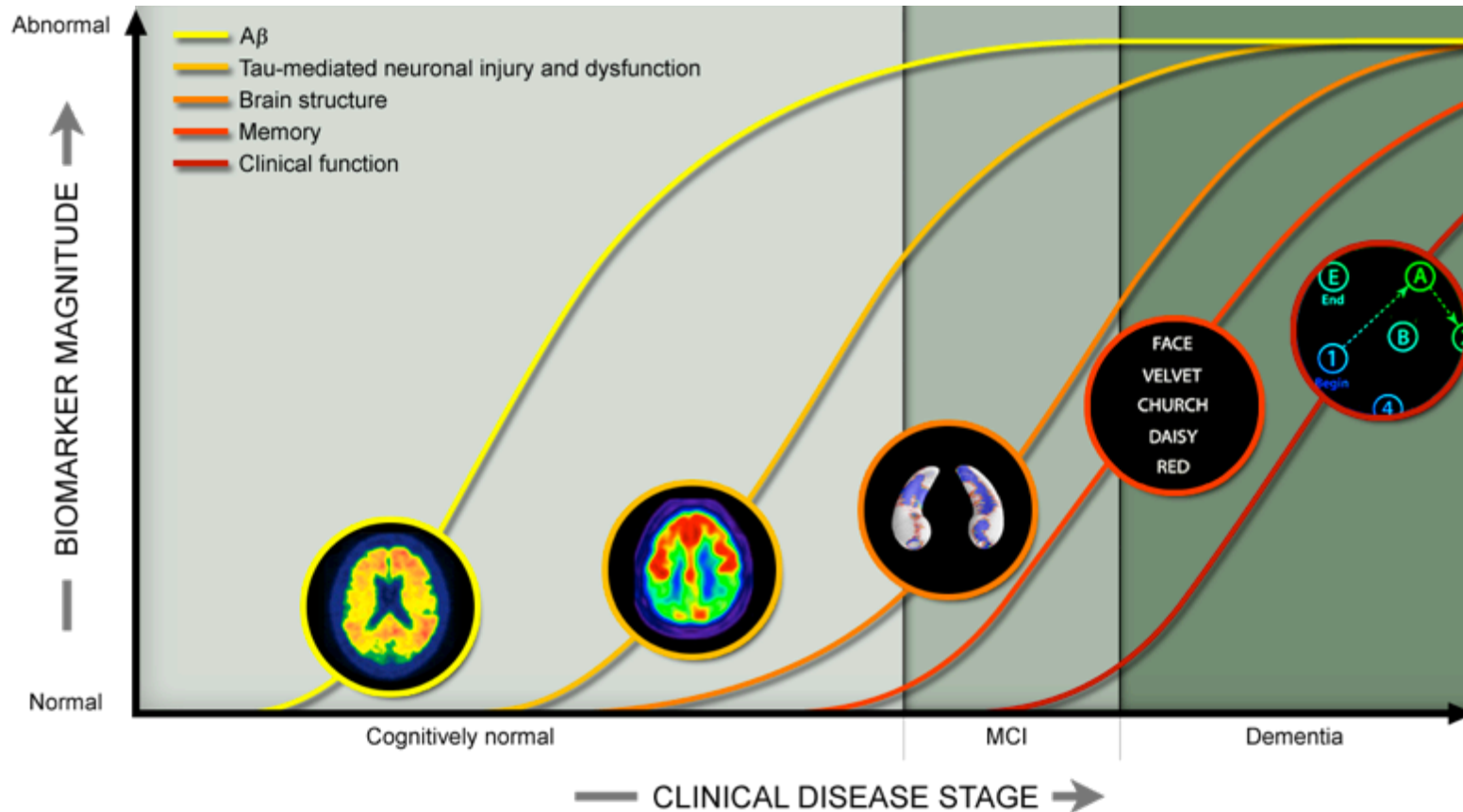
Study, Year	Patients (CIS/RR/SP/PP)	HC	MR Imaging	Most Important Findings
Baranzini et al, <sup>30</sup> 2009	987 (100/659/137/72) <sup>a</sup>	883	T2LL, BV	GWA; T2LL and BV associated with multiple (non-HLA) SNPs, not with HLA-DRB1*1501
Gourraud et al, <sup>38</sup> 2013	484 (76/343/45/20)	—	LPM	GWA; 31 SNPs associated with lesion pattern
Healy et al, <sup>87</sup> 2010	532 (17/351/123/37) <sup>b</sup>	776	T2LL, BV	HLA B44 associated with higher BV and lower T2LL
Hooper-van Veen et al, <sup>36</sup> 2003	492 (-/221/172/99) <sup>c</sup>	228	T1BH, T2LL, BV	No associations interleukin-1 polymorphism with MR imaging
Hooper-van Veen et al, <sup>88</sup> 2006	489 (-/220/175/440) <sup>d</sup>	180	T1BH, T2LL, BV	Change in T1BH associated with CD28, IFNGR2, IL1B-511
Horakova et al, <sup>34</sup> 2011	205 (CIS only)	—	T2LL, T1Gad, BV	HLA-DRB1*1501 associated with higher T1Gad, not with BV
Jensen et al, <sup>89</sup> 2010	1006 (RR and SP <sup>e</sup> )	—	BV (ICR)	No associations 7 susceptibility SNPs with BV
Kalincik et al, <sup>33</sup> 2013	179 (CIS only)	—	T2LL, BV	No associations 16 susceptibility SNPs with T2LL and BV
Karrenbauer et al, <sup>32</sup> 2013	100 (-/79/19/2)	—	T2LL, T1BH, lesion location	No associations HLA-DRB1*15 or *04 with MR imaging
Okuda et al, <sup>24</sup> 2009	505 (88/352/46/14)	—	T2LL, T1Gad, MRS	Higher T2LL and lower NAA in NAWM in HLA-DRB1*1501 + patients
Qiu et al, <sup>70</sup> 2011	252 (-/119/117/16)	—	T2SC	No associations HLA-DRB1 alleles and number/location SC lesions
Sepulcre et al, <sup>37</sup> 2008	50 (15/28/3/4)	—	T2LL, BV, LPM	No association HLA-DR2 status with lesion distribution and BV
Schreiber et al, <sup>28</sup> 2002	71 (21/40/10)	—	T2LL	No associations HLA with T2LL
Sombekke et al, <sup>27</sup> 2009	150 (-/88/32/30)	—	T2LL, T2SC	HLA-DRB1*1501 not associated with T2LL
Sombekke et al, <sup>29</sup> 2011	208 (-/126/42/40)	—	T2LL, LPM	MHC II region SNP associated with lesion distribution
Van der Walt et al, <sup>90</sup> 2011	978 (-/639/339/-) <sup>f</sup>	—	BV (ICR)	No associations HLA-DRB1 alleles with BV
Zivadinov et al, <sup>25,91</sup> 2003; 2009	100 (-/71/16/13)	122	T2LL, T1BH, BV	B7 associated with higher T2LL and T1BH; DRB1*12 with higher T1BH and lower BV
Zivadinov et al, <sup>26</sup> 2007	41 (-/27/7/7)	—	T2LL, T1BH, BV	Multiple HLA alleles associated with MR imaging (eg, HLA-DRB1*1501 associated with lower BV and higher T1BH)

	Candidate ROI 	Many ROIs 	Voxelwise 
Candidate SNP 			[Filippini et al. 2009] 29,812 voxels 1 SNP
Candidate Gene 	[Joyner et al. 2011] 4 ROIs, 11 SNPs		
Genome-wide Gene 			[Hilbar et al. 2011] 31,622 voxels 18,044 Genes
Genome-wide SNP 	[Stein et al. 2012] 1 ROI, 1.1 mio SNPs		[Stein et al. 2010] 31,622 voxels 448,293 SNPs
	[Potkin et al. 2009] 1 ROI, 317,503 SNPs		



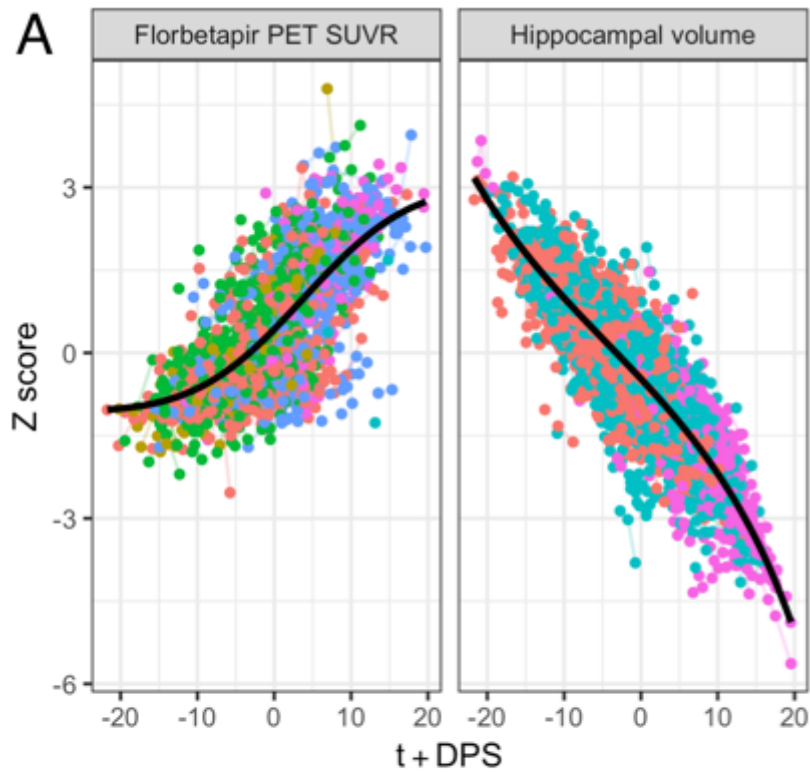
Marzia Scelsi

- One (imaging) biomarker may be noisy
- Considering multiple markers may improve robustness



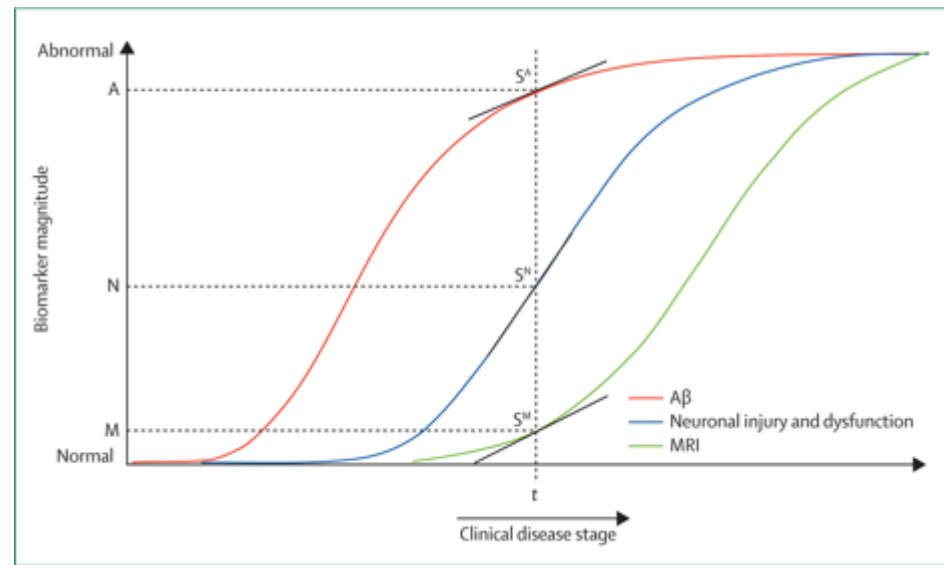
## Disease progression modelling

😊 agreement with theoretical models



Diagnosis

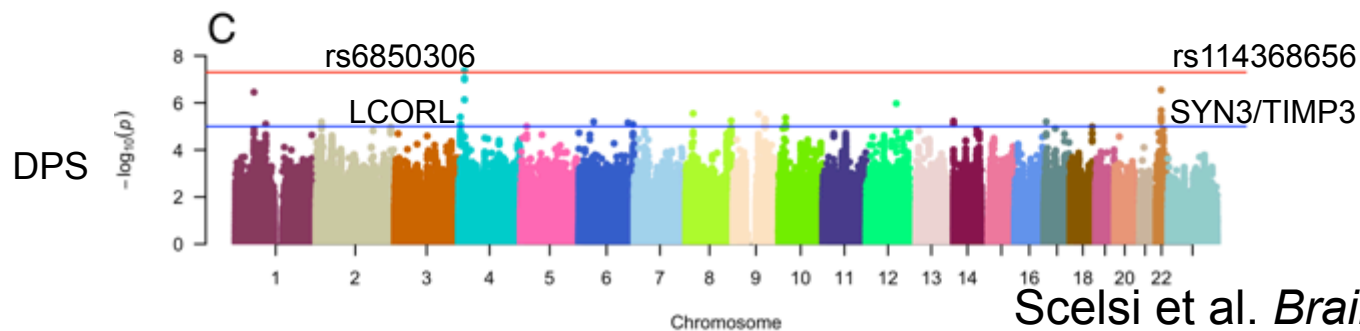
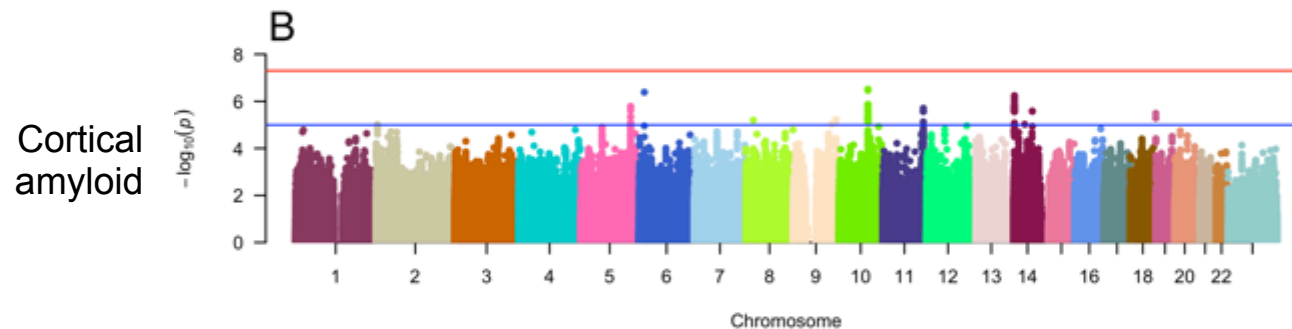
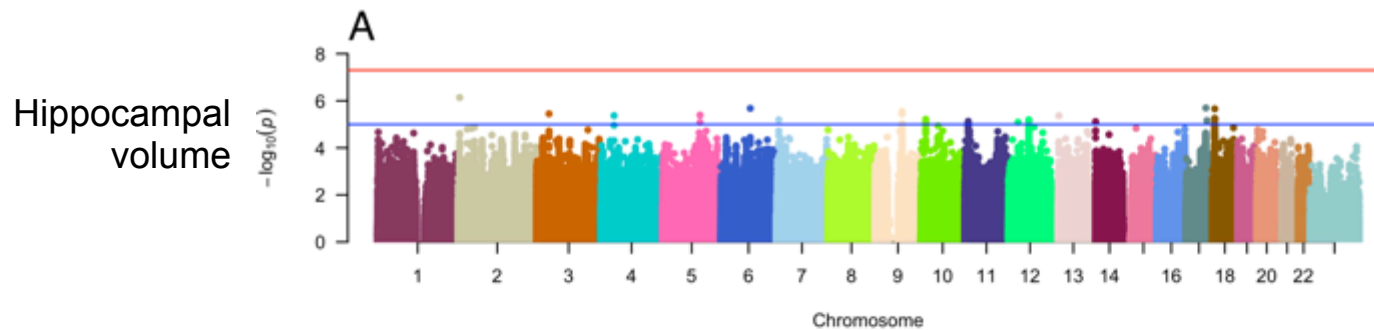
- Normal   ● EMCI   ● LMCI
- SMC   ● MCI   ● AD



Jack et al., Lancet Neur., 2010

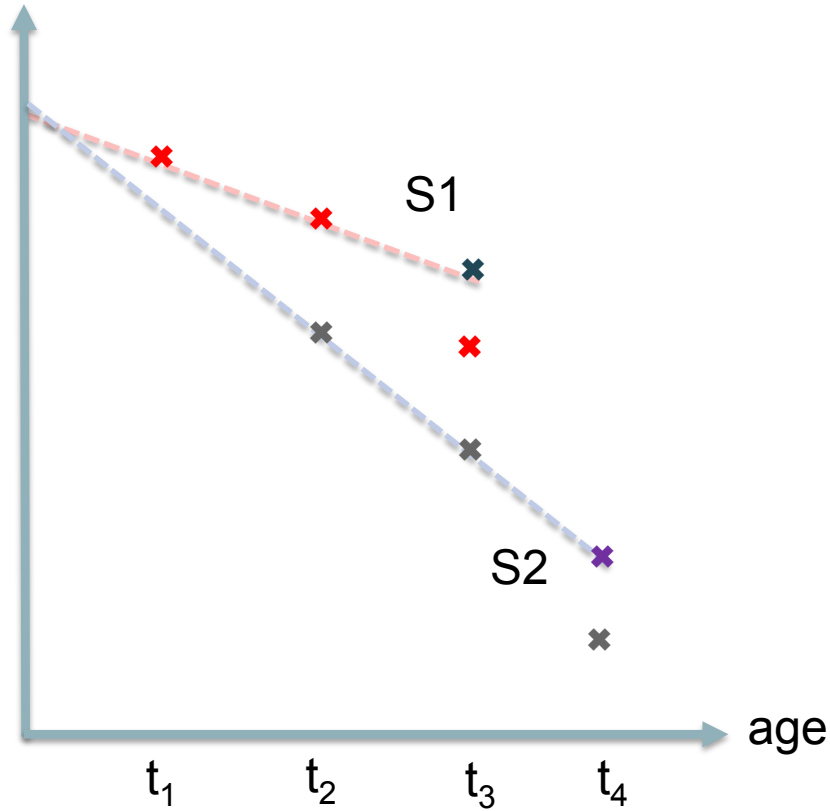
Scelsi et al. *Brain* (in revision)

## Genome-wide association tests



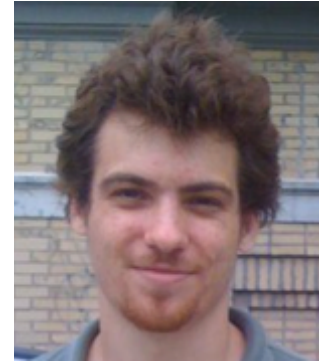
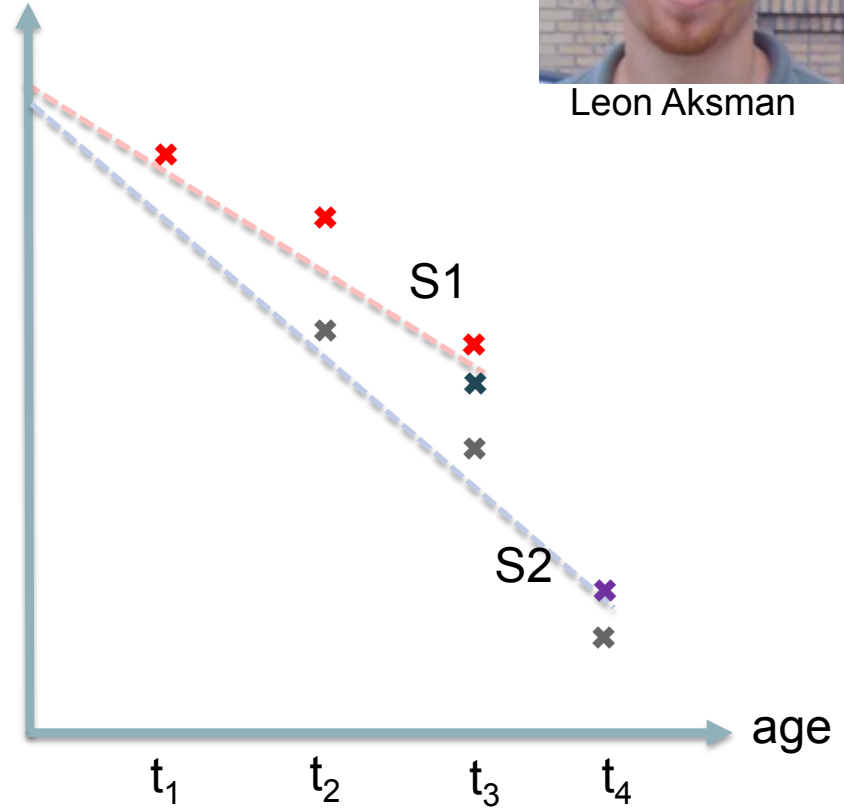
## Independent

hippo volume



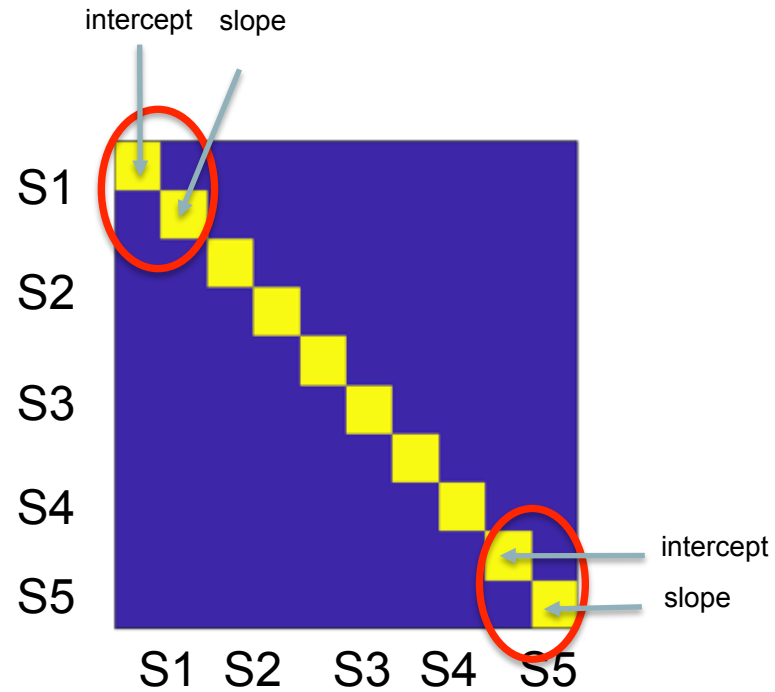
## Coupled

hippo volume



Leon Aksman

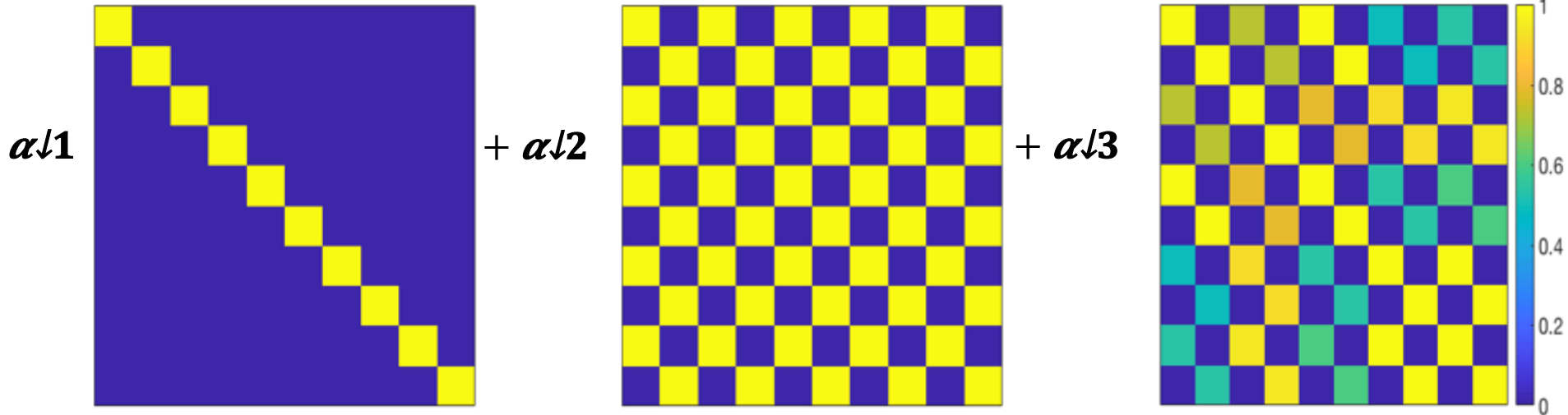




Fully independent

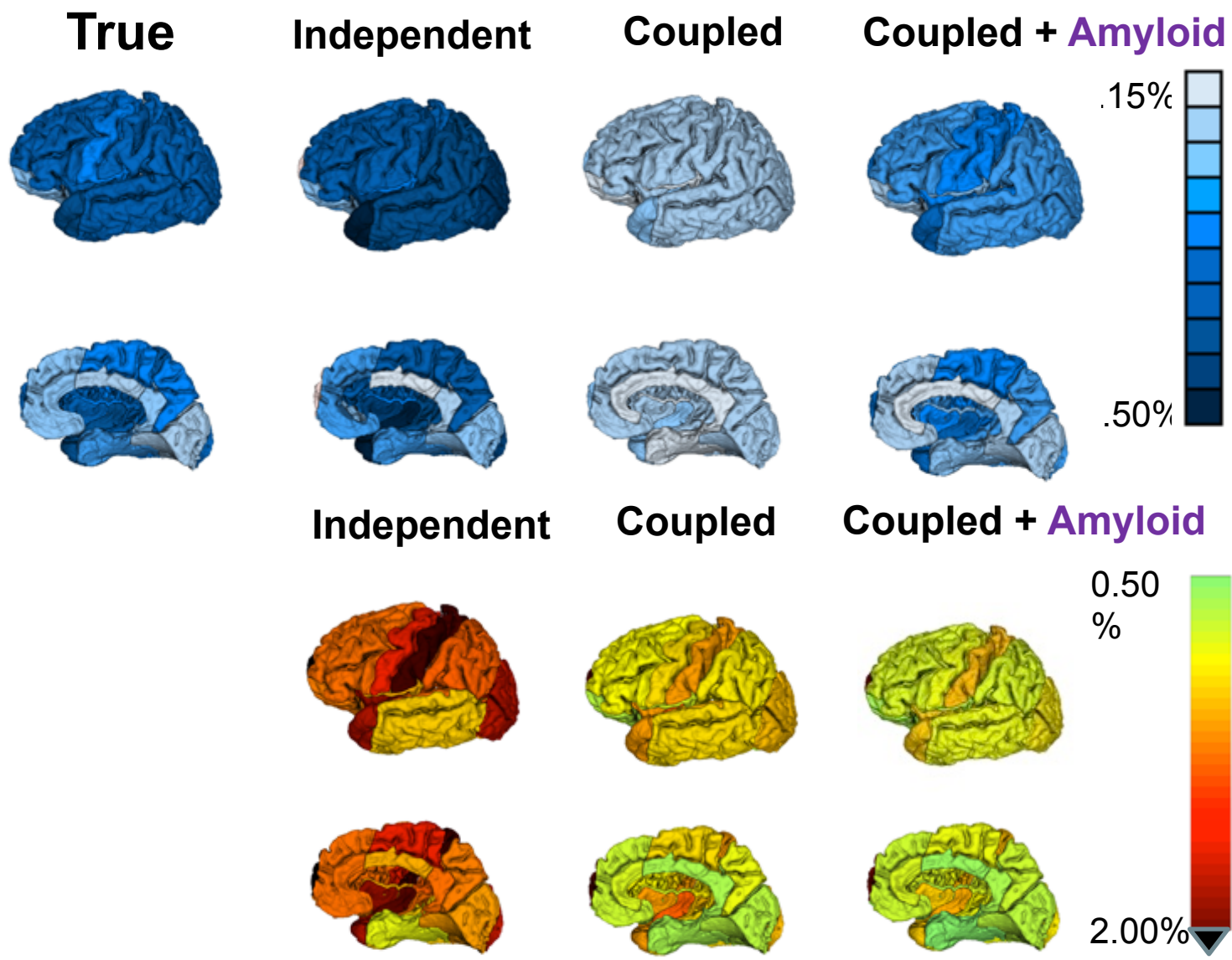
Fully coupled

Biomarker coupled



$\alpha$ 's are learned from data (Bayesian machine learning)

- Smaller prediction errors with coupled
- Further improvement by coupling subjects' trajectories based on amyloid load (PET SUVR)



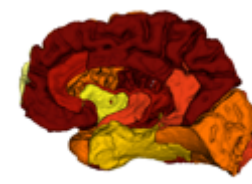
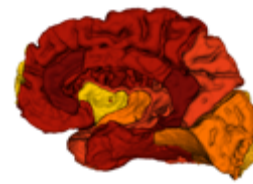
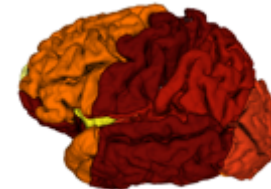
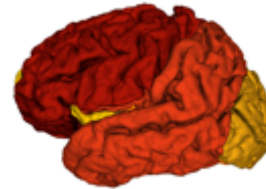
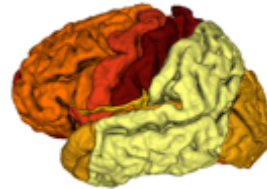
## Intercept Group Differences

- We can look at group differences in trajectories (intercepts, slopes) across subjects

Independent

Coupled

Coupled + Amyloid



$p < 10^{-10}$



- Coupled models: less significant intercept differences, more significant slope differences

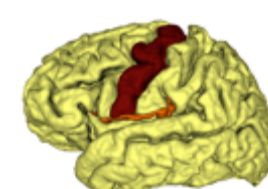
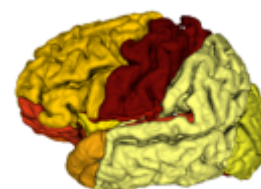
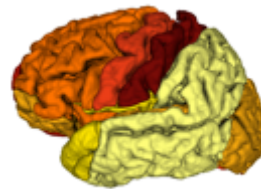
## Slope Group Differences

- These are more plausible models: neurodegeneration initiates from a similar level in developed adults

Independent

Coupled

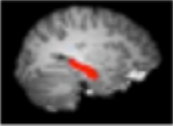
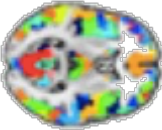
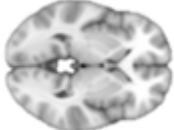
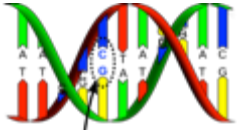


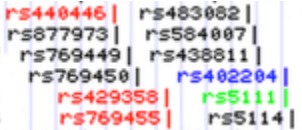
Coupled + Amyloid



$p < 10^{-1}$



- Currently exploring other kernels
  - APOE-e4 kernel
  - Polygenic kernel
  
- In MS?
  - Longitudinal (imaging) biomarker
  - Genetic information from genotyping

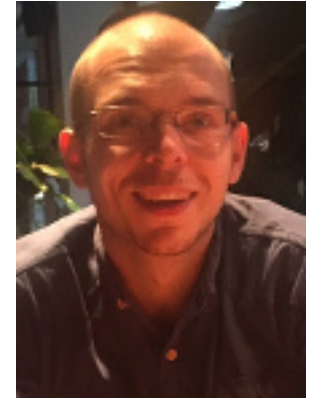
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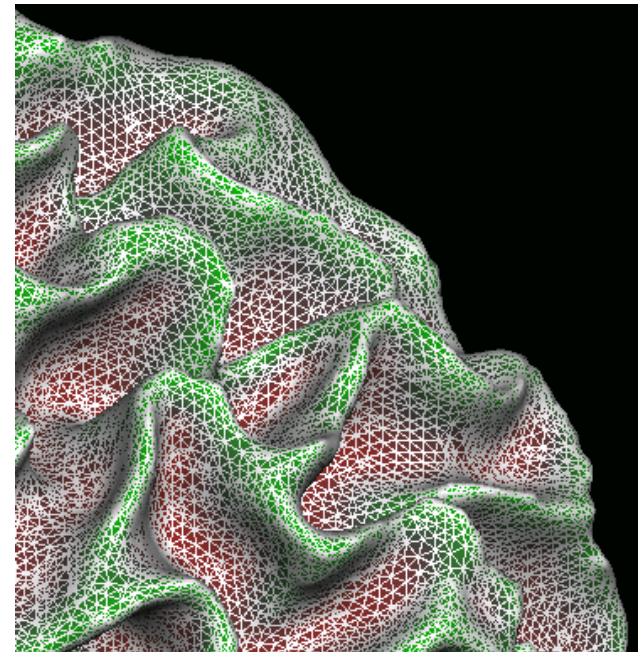
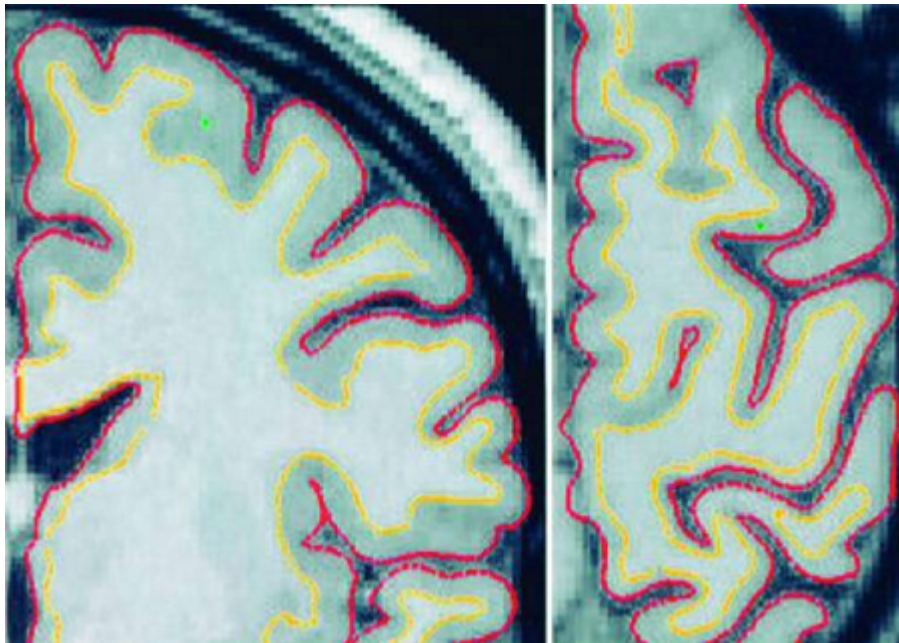


## Genetics of cortical thickness in AD

- Loss of gray matter in AD
- Cortical thickness derived from structural T1 weighted MRI scans



Marco Lorenzi





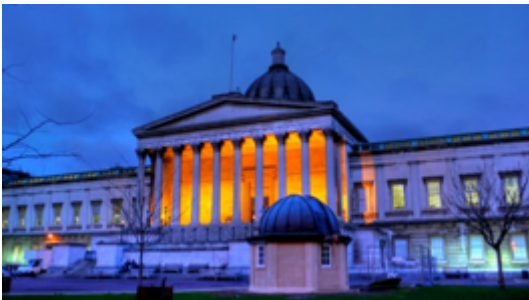


# Acknowledgements



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London, January 31<sup>st</sup> 2018