Transfer Learning from typical Alzheimer's disease to rare dementias using **Disease Knowledge Transfer**

Razvan Marinescu



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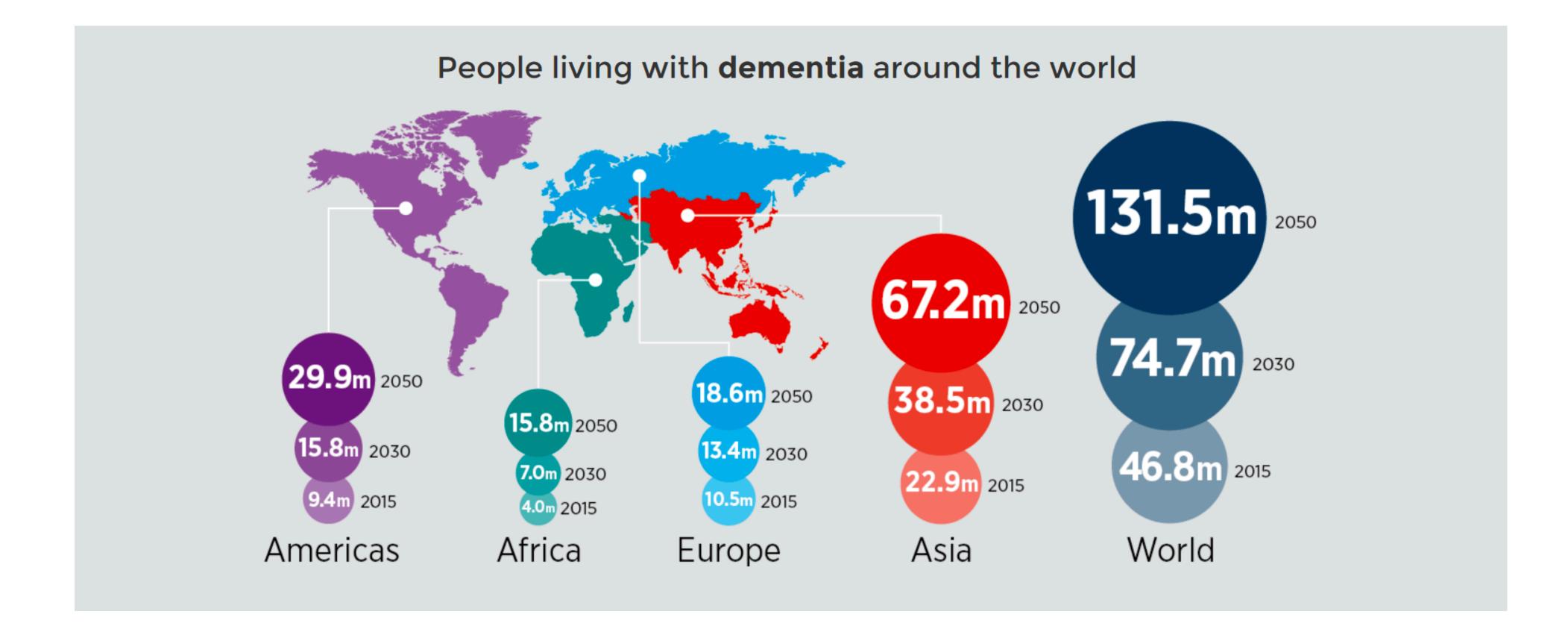


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Alzheimer's disease is a devastating disease



●

Currently no treatment available that can stop, or at least slow down, cognitive decline

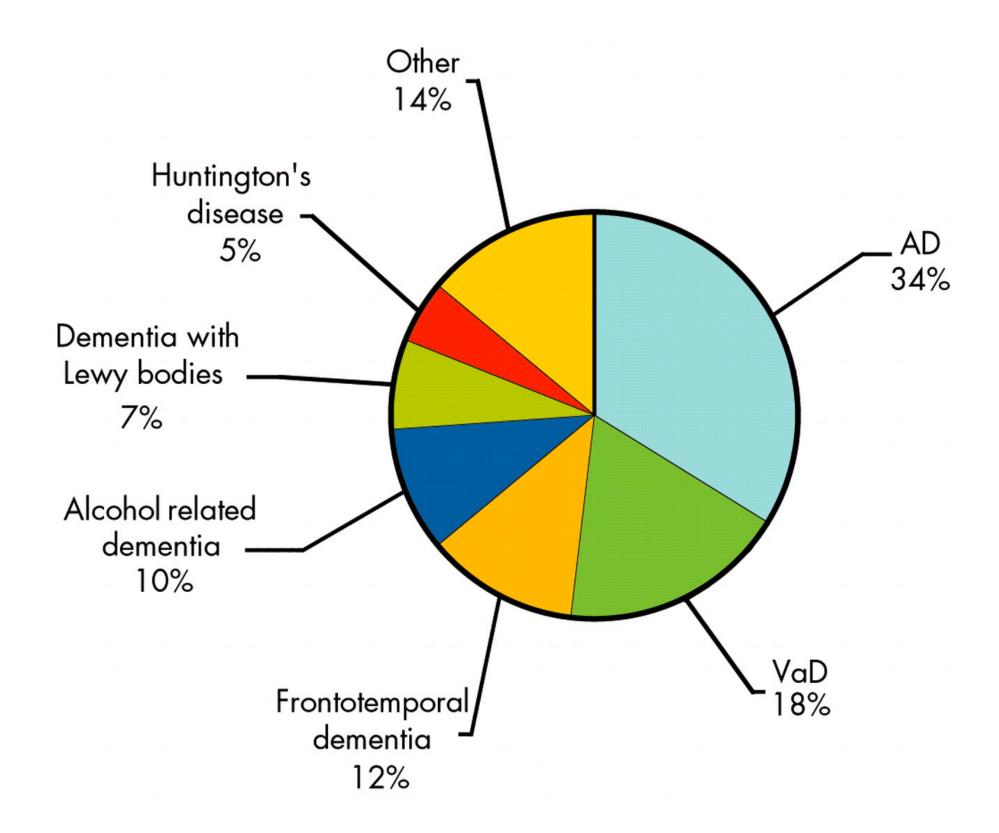
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Neurodegenerative diseases other than Alzheimer's also affect many worldwide

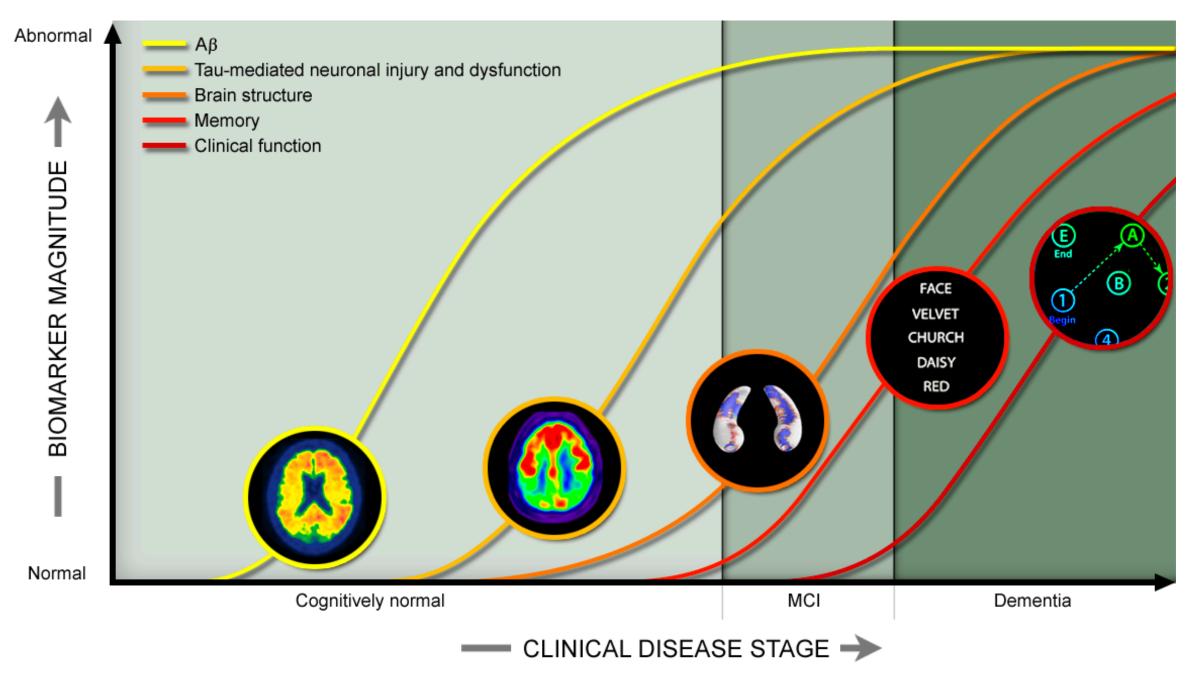
Posterior Cortical Atrophy > 1 million

- Frontotemporal dementia > 6 million
 - All tauopathies ...
- Dementia with Lewy bodies > 1.6 million
- Vascular dementia > 8 million
- Creutzfeld-Jacobs disease > 7000/year
- Parkinson's disease
- Huntington's disease



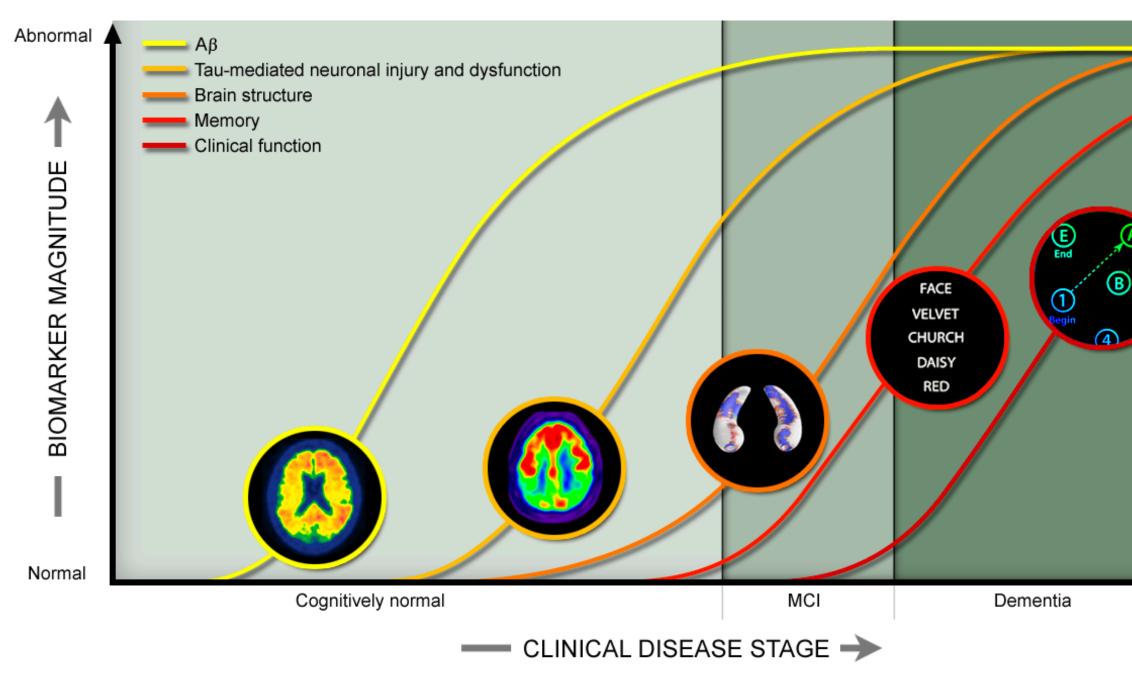






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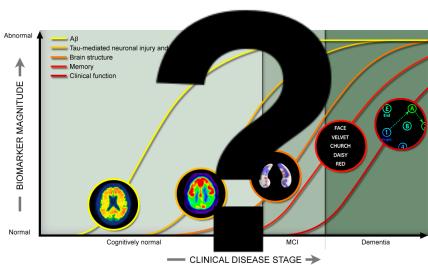




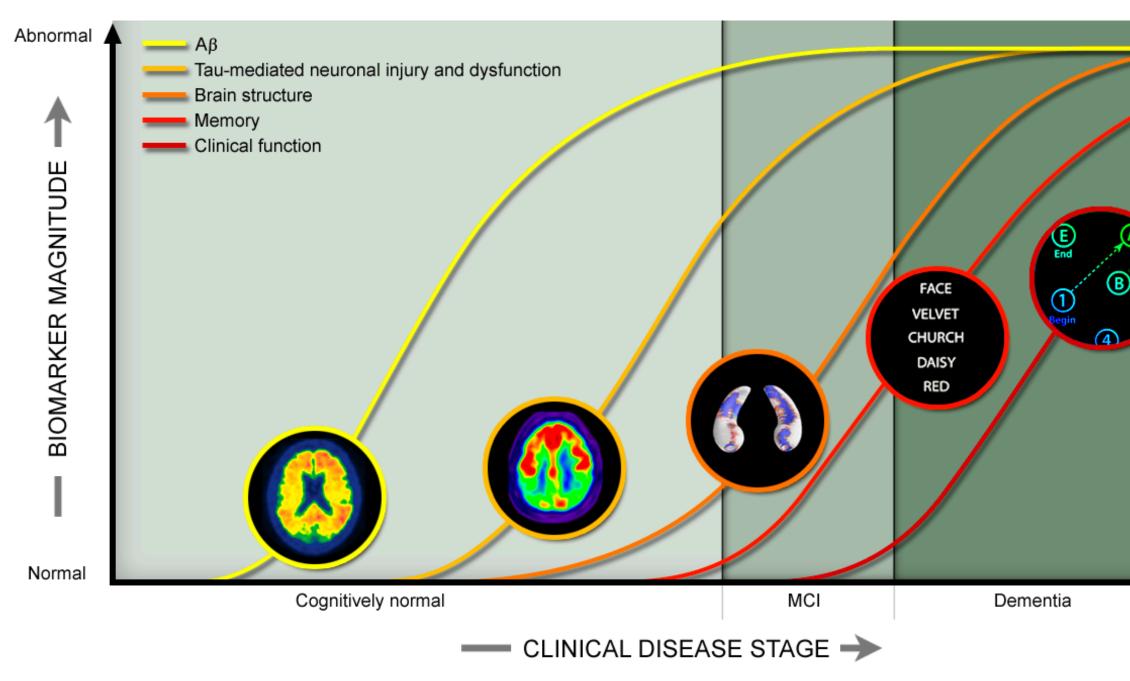
Progression of less common neurodegenerative diseases is not known

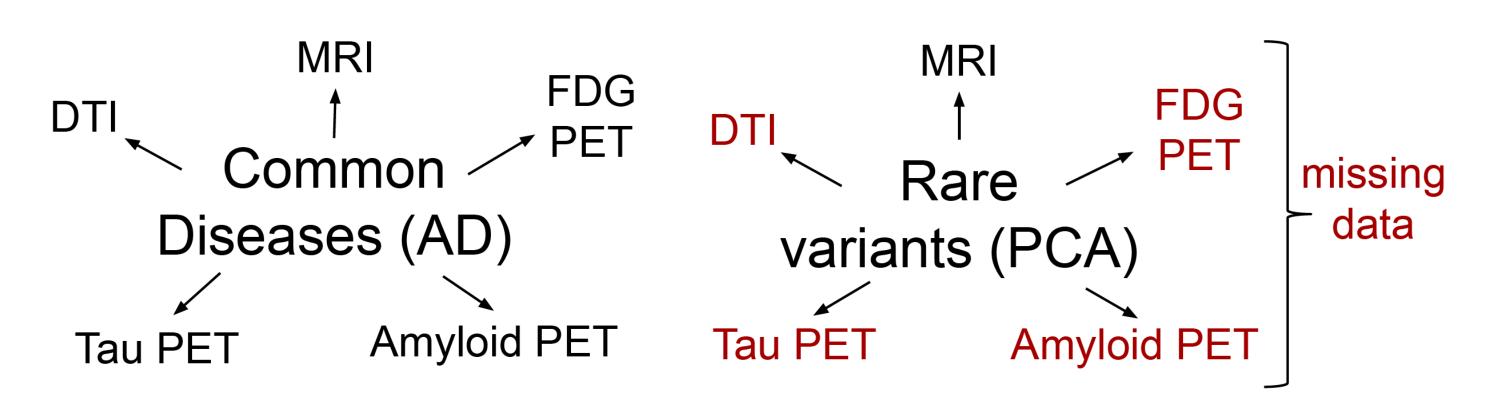
Lack of datasets that are:

- Large \bullet
- Longitudinal \bullet
- Multimodal \bullet





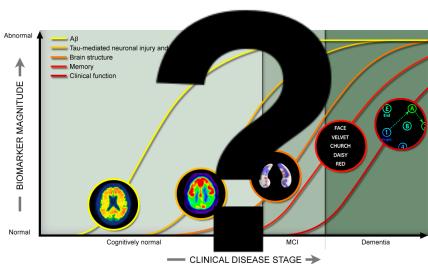




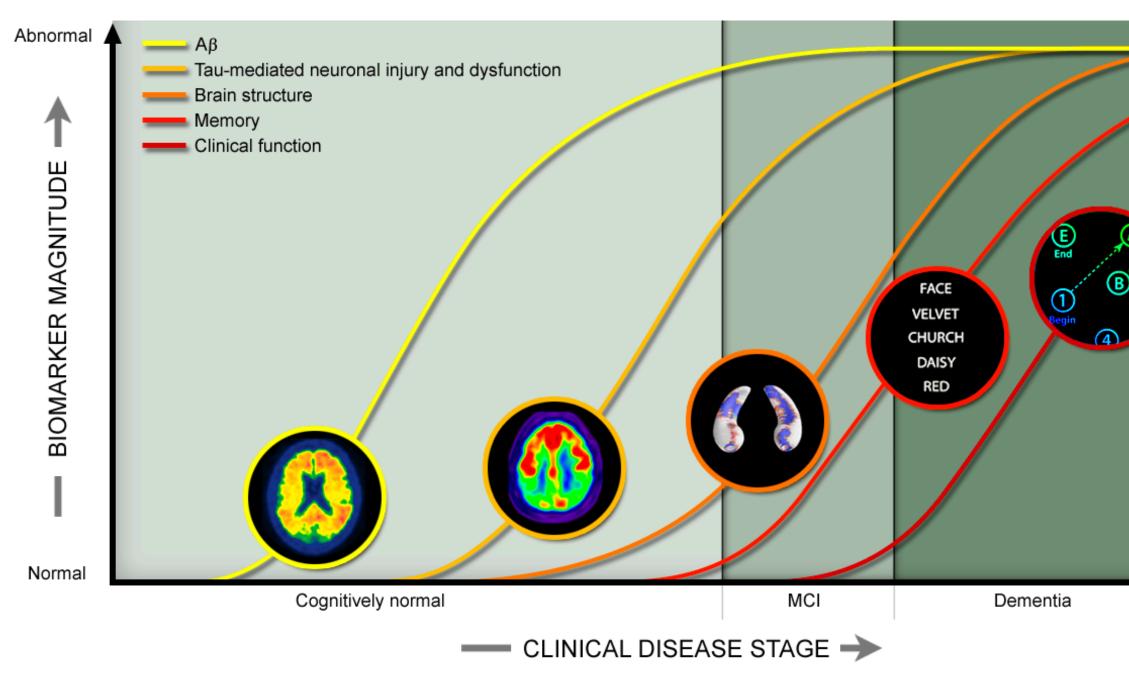
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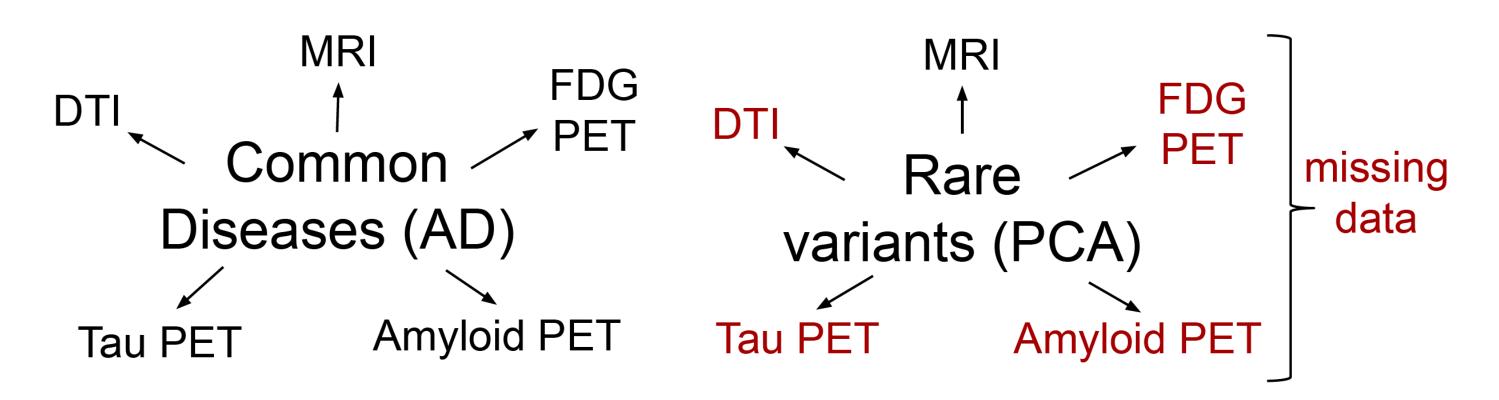
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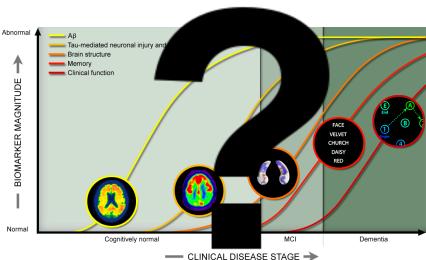




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Transfer learning provides a key solution towards characterizing rare diseases



Previous literature on Transfer Learning for neurodegenerative diseases

- Hon and Khan 2017, Nanni et. al. 2020 transfer from computer vision datasets to medical datasets
- Cheng, Zhang and Shen 2012, Wachinger and Reuter, 2017, Guerrero et. al. 2014, Hofer et. al. 2017 - transfer learning across Alzheimer's disease diagnoses (e.g. CN vs $MCI \rightarrow MCI vs AD)$
- Methods are supervised on clinical diagnosis, which is **unreliable without post-mortem** neuropathology
- No work tried to use transfer learning to improve predictions on rarer neurodegenerative diseases

Reference	Topic	Task	Domain	Transfer type
Brain				
Zhang and Shen (2012)	MCI conversion prediction	different	same	feature, multi-task
Guerrero et al. (20 14)	AD classification	same	different	instance, align
Wachinger and Reuter (2016)	AD classification	same	different	instance, weight
Hofer et al. (2017)	AD classification	same	different	instance, align
Hon and Khan (2017)	AD classification	different	different	feature, pretraining

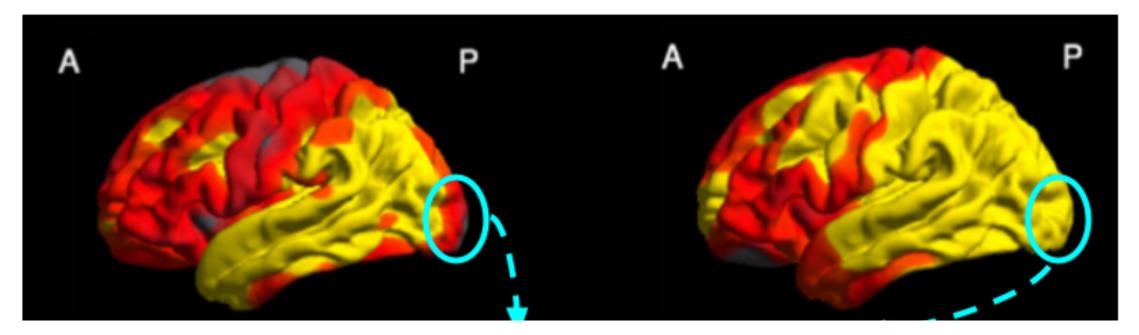
Survey of transfer learning in Alzheimer's research (Cheplygina et. al., 2019)



 Two diseases such as typical AD and Posterior Cortical Atrophy (PCA) affect the brain at different spatial locations

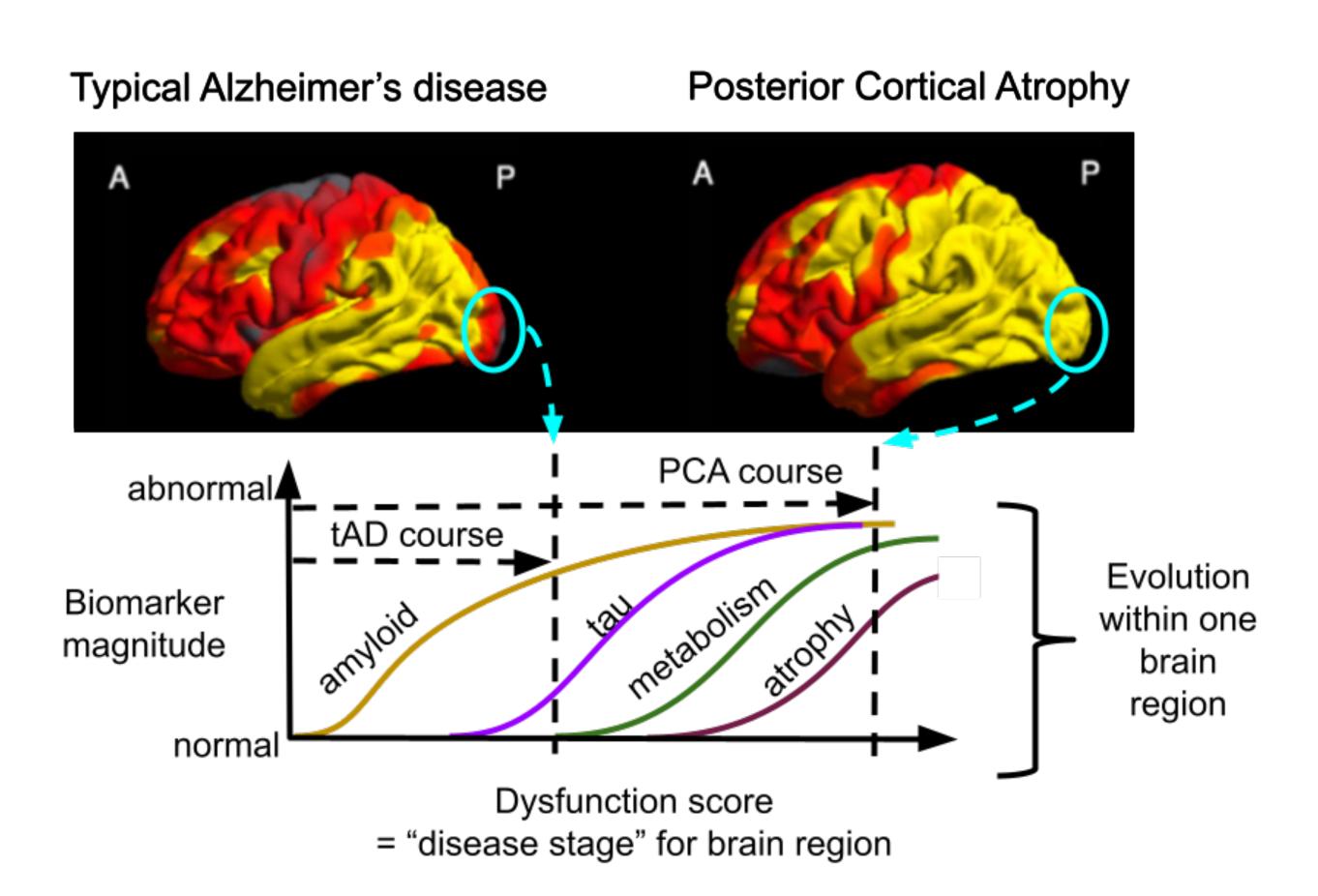
Typical Alzheimer's disease

Posterior Cortical Atrophy





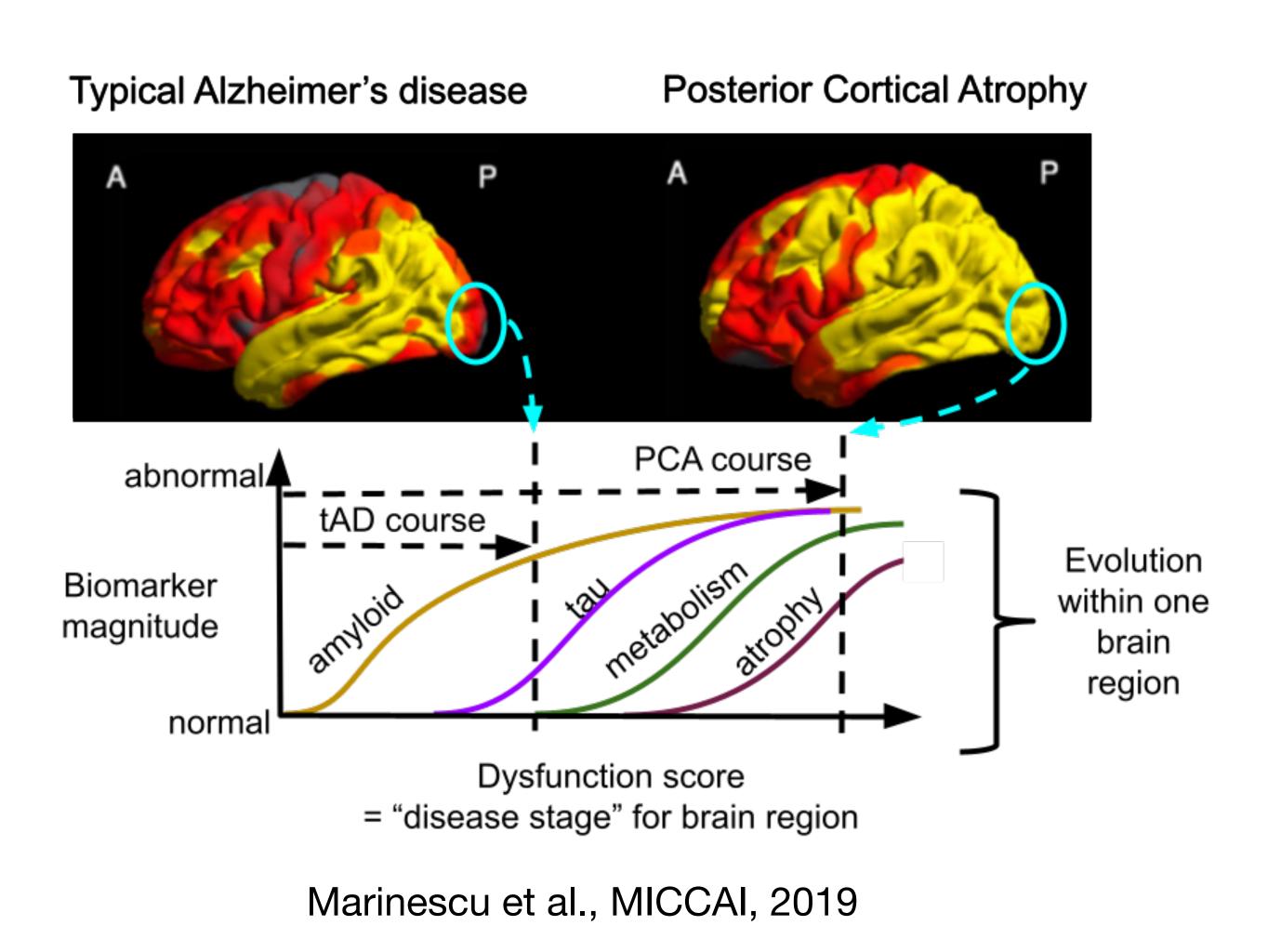
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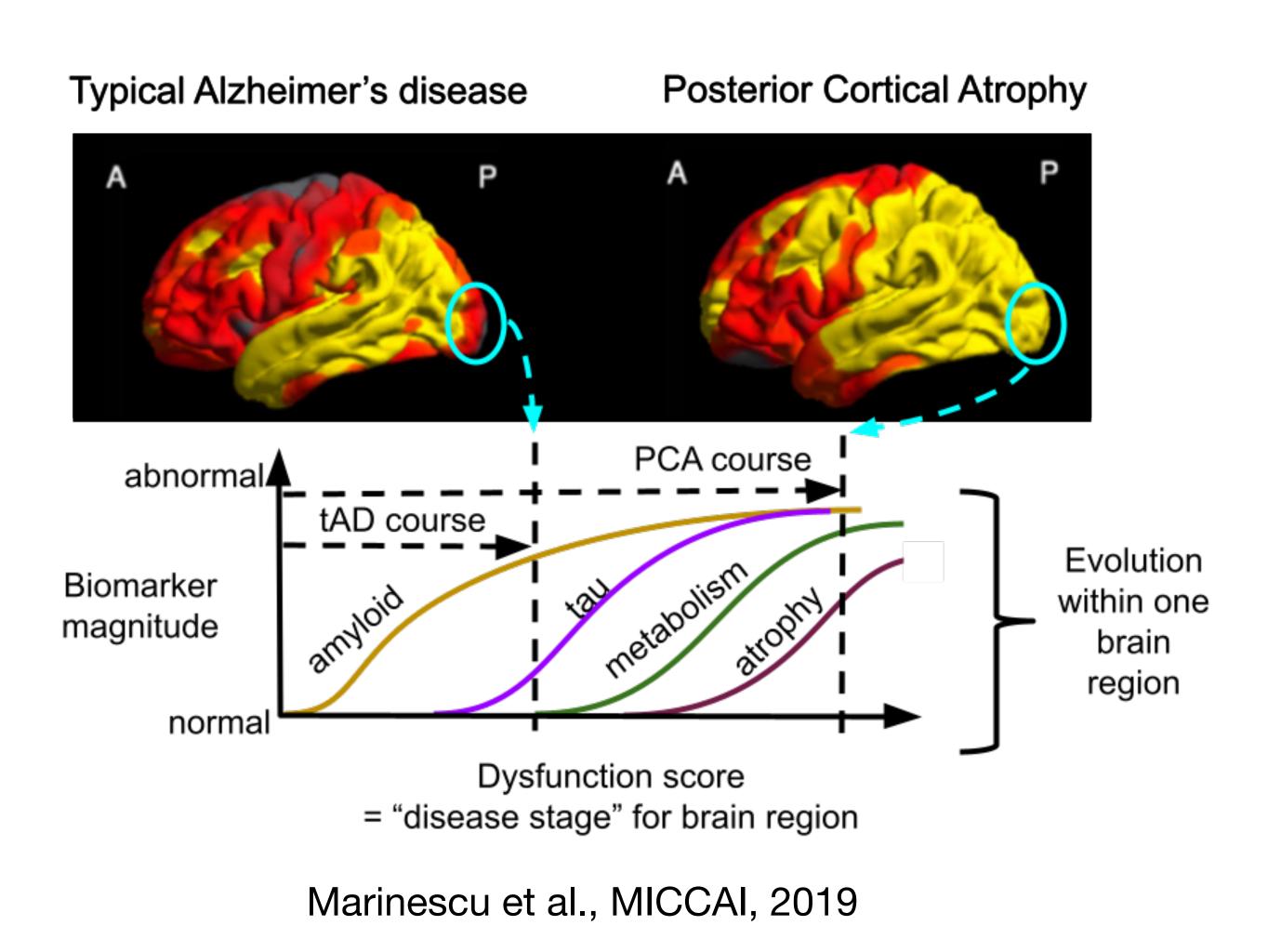
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- Difference between typical AD vs PCA is *the* extent of pathology along the trajectory







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- Current understanding: PCA, as a different syndrome, is modeled separately from tAD

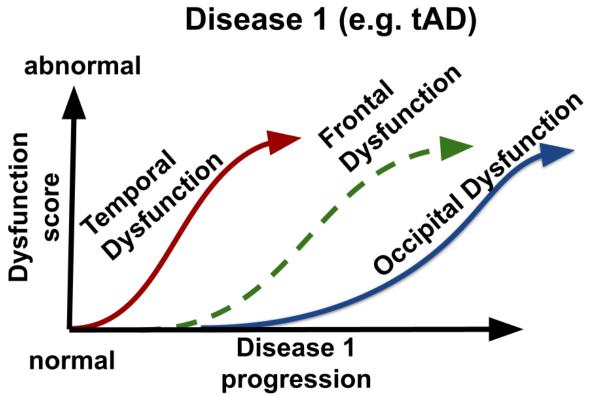








- Model disease as progression of composite \bullet dysfunction scores for each brain region:
 - Typical AD: temporal first
 - PCA: occipital first

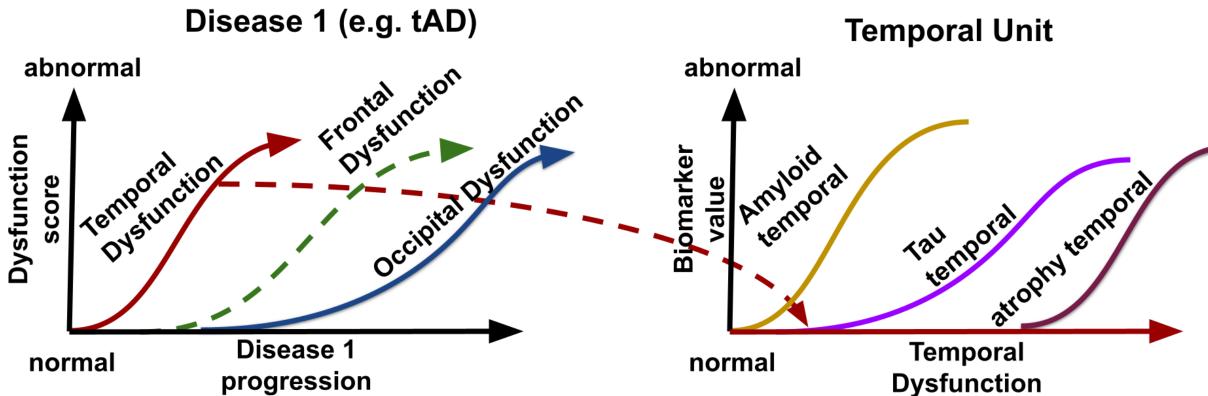


Marinescu et al., MICCAI, 2019

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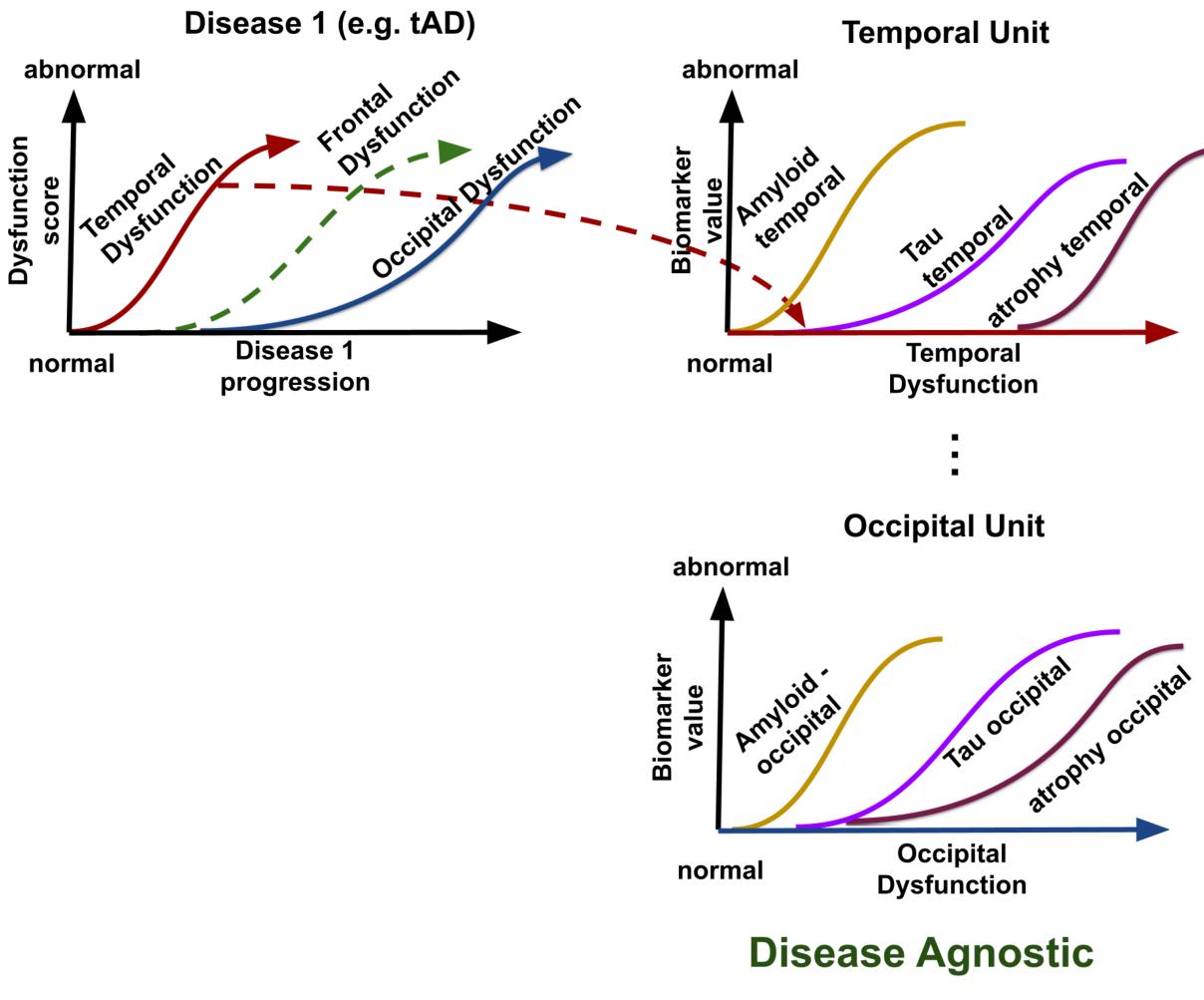
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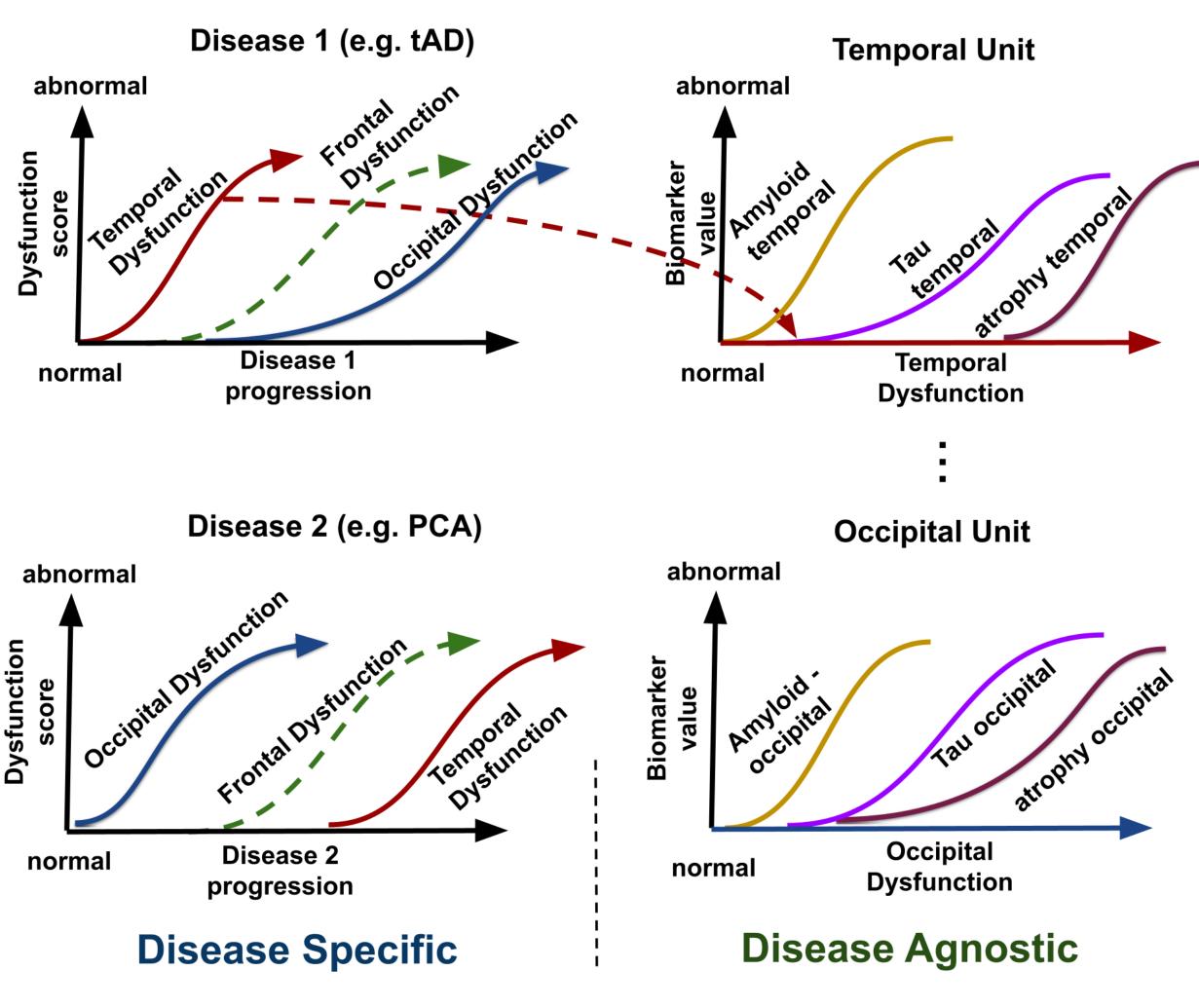
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 - Typical AD: temporal first
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- Model dysfunction scores as "aggregate pathology" from multiple modalities (e.g. amyloid + tau + atrophy)
- Extend dysfunction modeling to all brain regions
- A new disease, e.g. Posterior Cortical Atrophy (PCA) will have **different dysfunction** progression across the brain (disease specific), but **similar** progression within individual regions (disease agnostic)

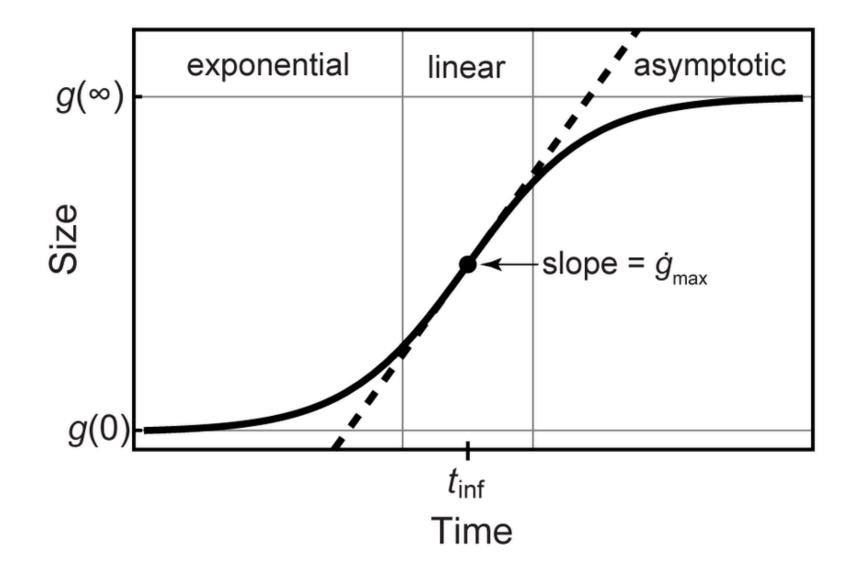


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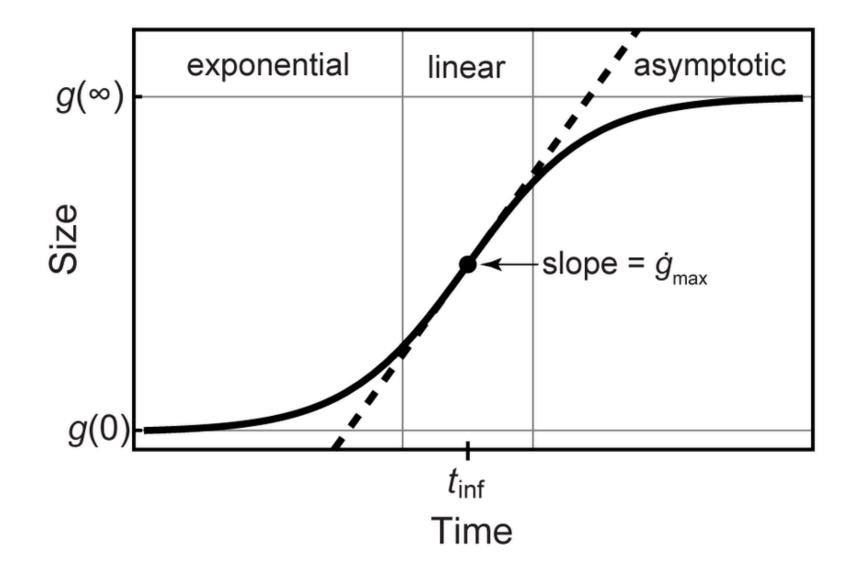
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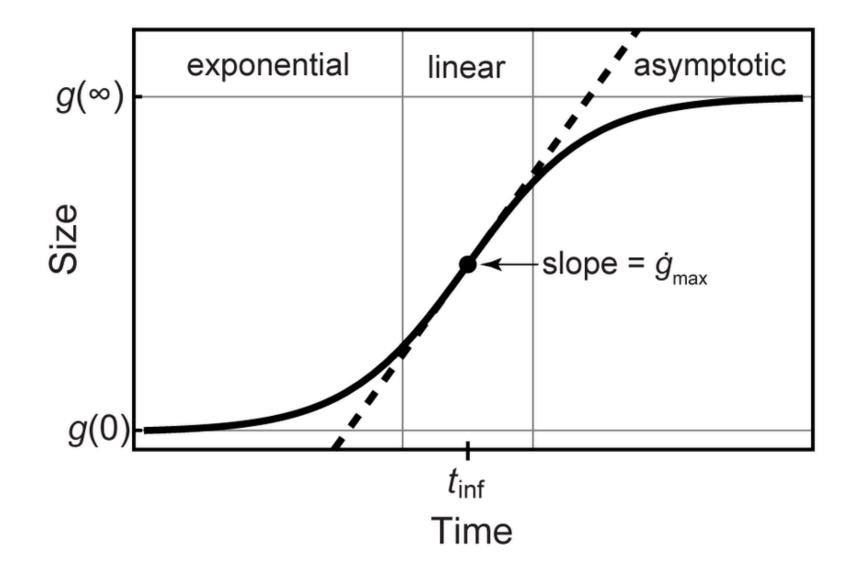
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 $\beta_i + m_{ij}$

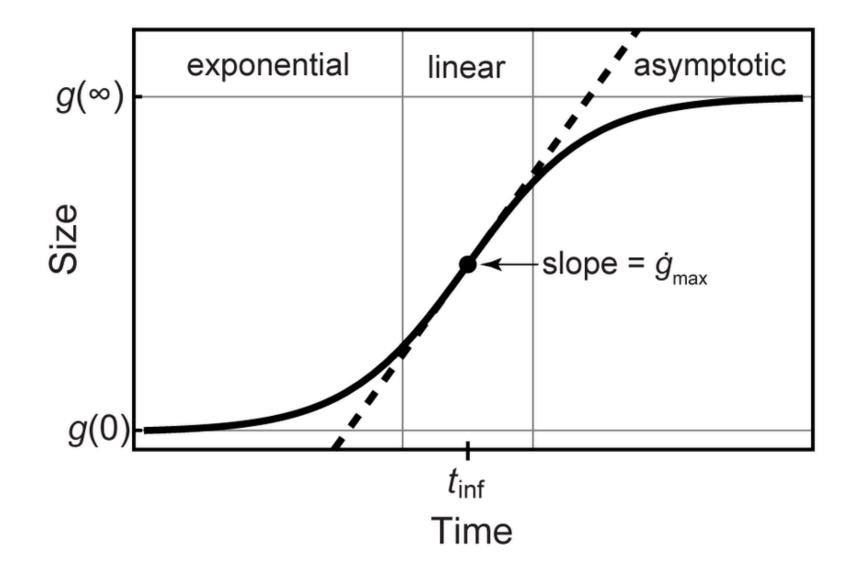




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Estimate dysfunction score of a particular \bullet brain ROI:



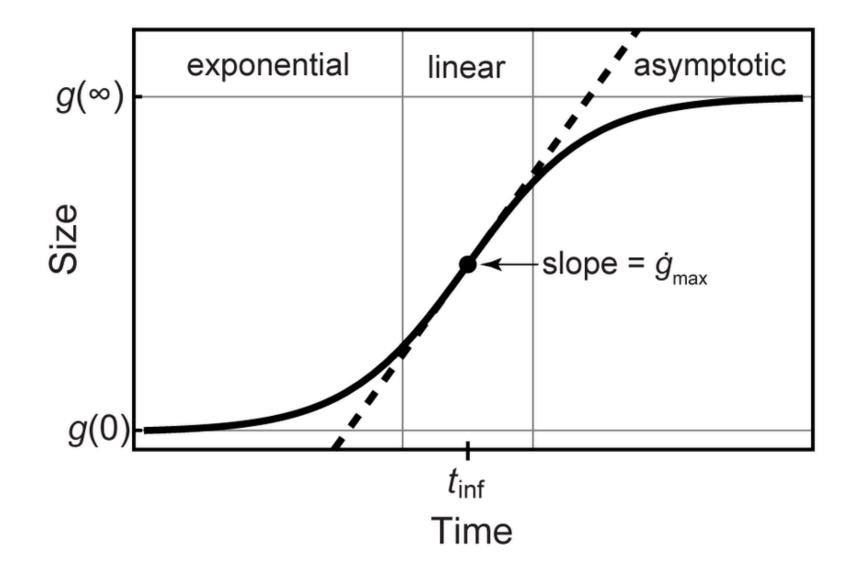


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 $f(\beta_i + m_{ij}; \lambda_{d_i}^{\psi(k)})$





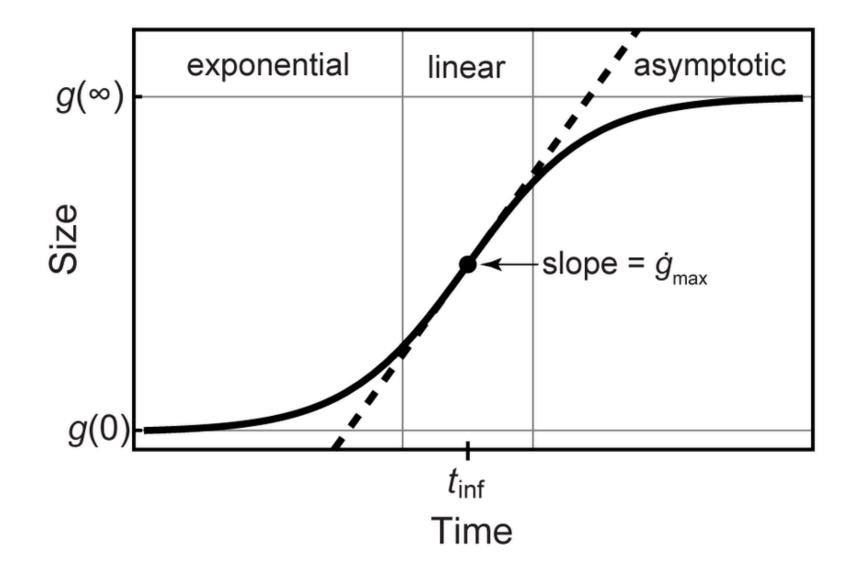
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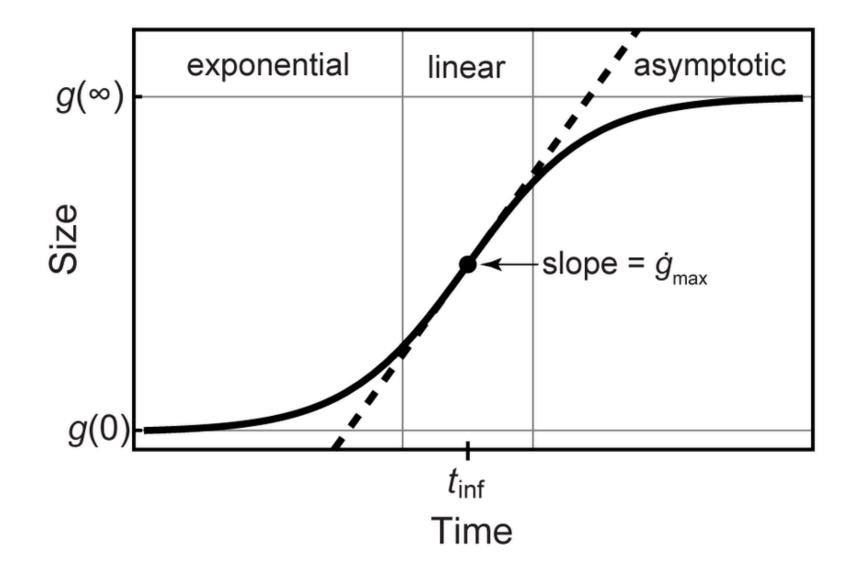
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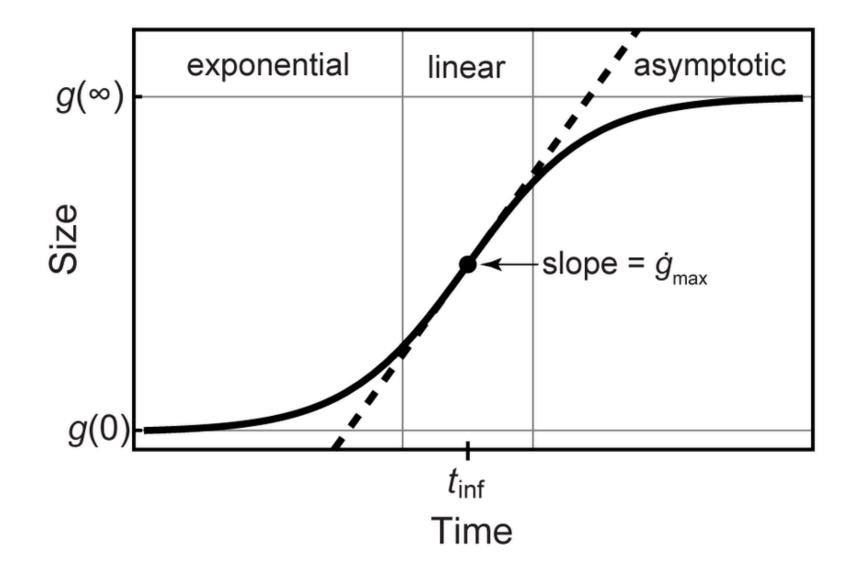
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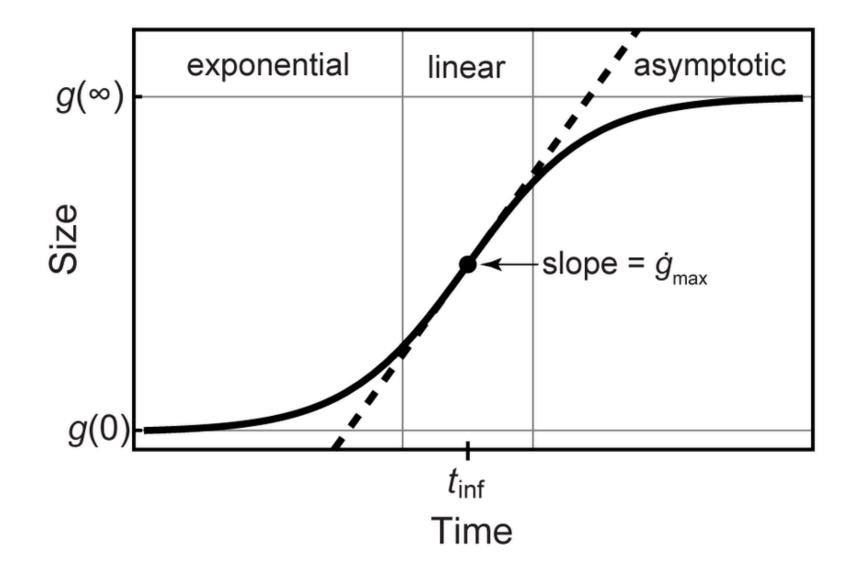
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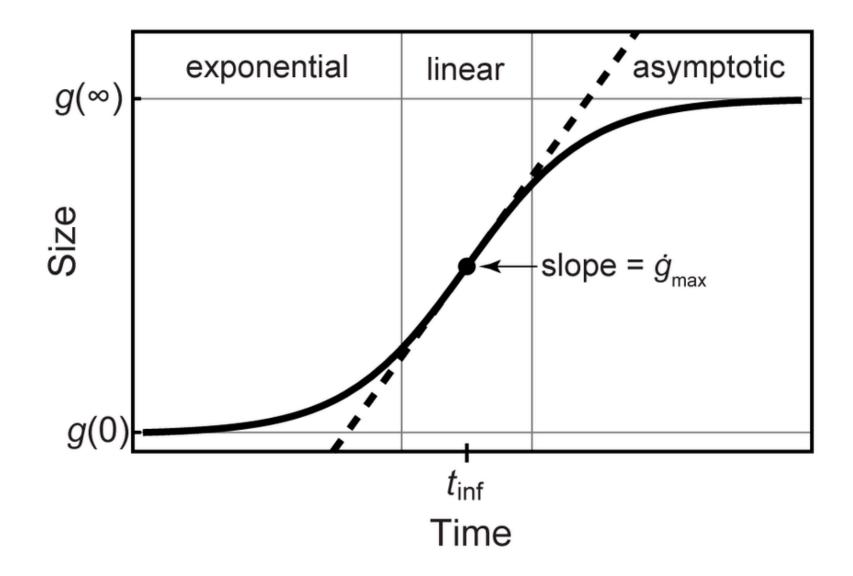
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• Functions f and g are parameterized using sigmoidal curves



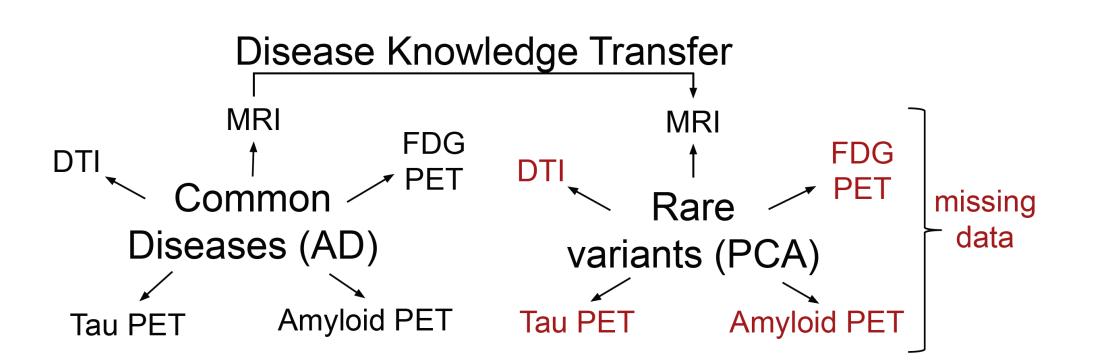


Outline of Results

- Results on simulated data
- Results on patient data from ADNI and the Dementia Research Center UK
- Quantitative evaluation



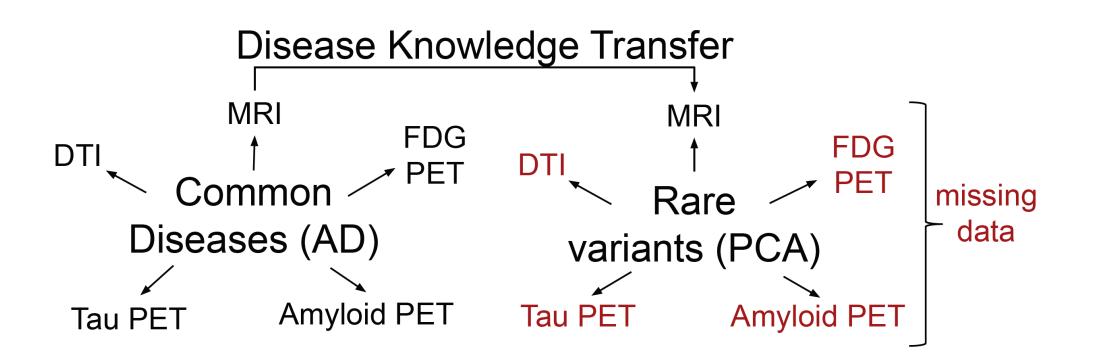
- Simulated 100 subjects with two diseases: synAD & synPCA
- To simulate lack of multimodal data in synPCA, we discarded 4/6 biomarkers



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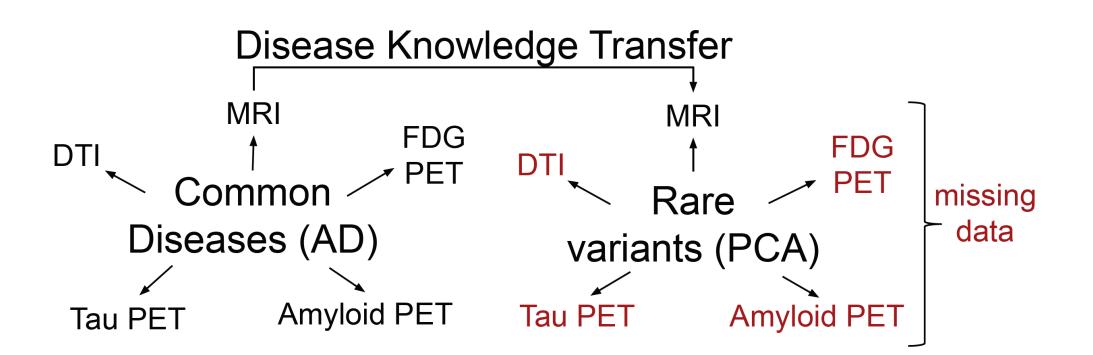
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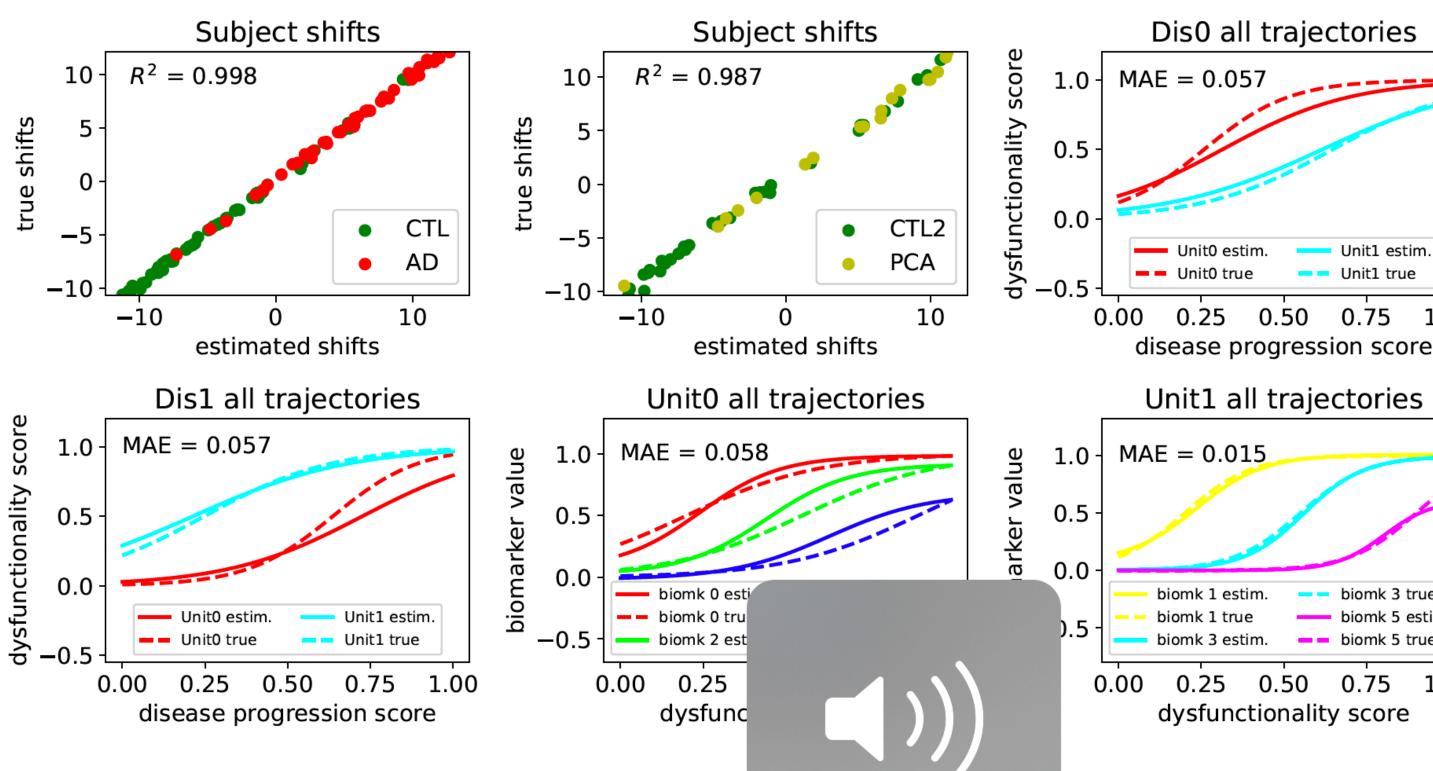
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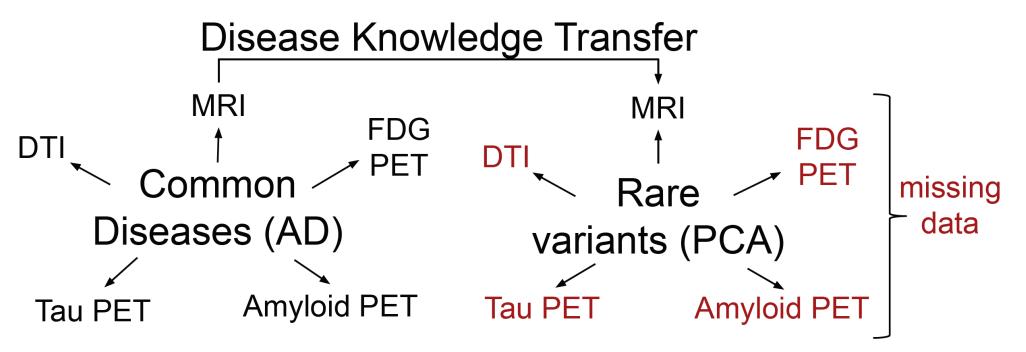


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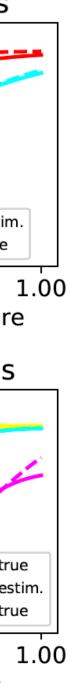




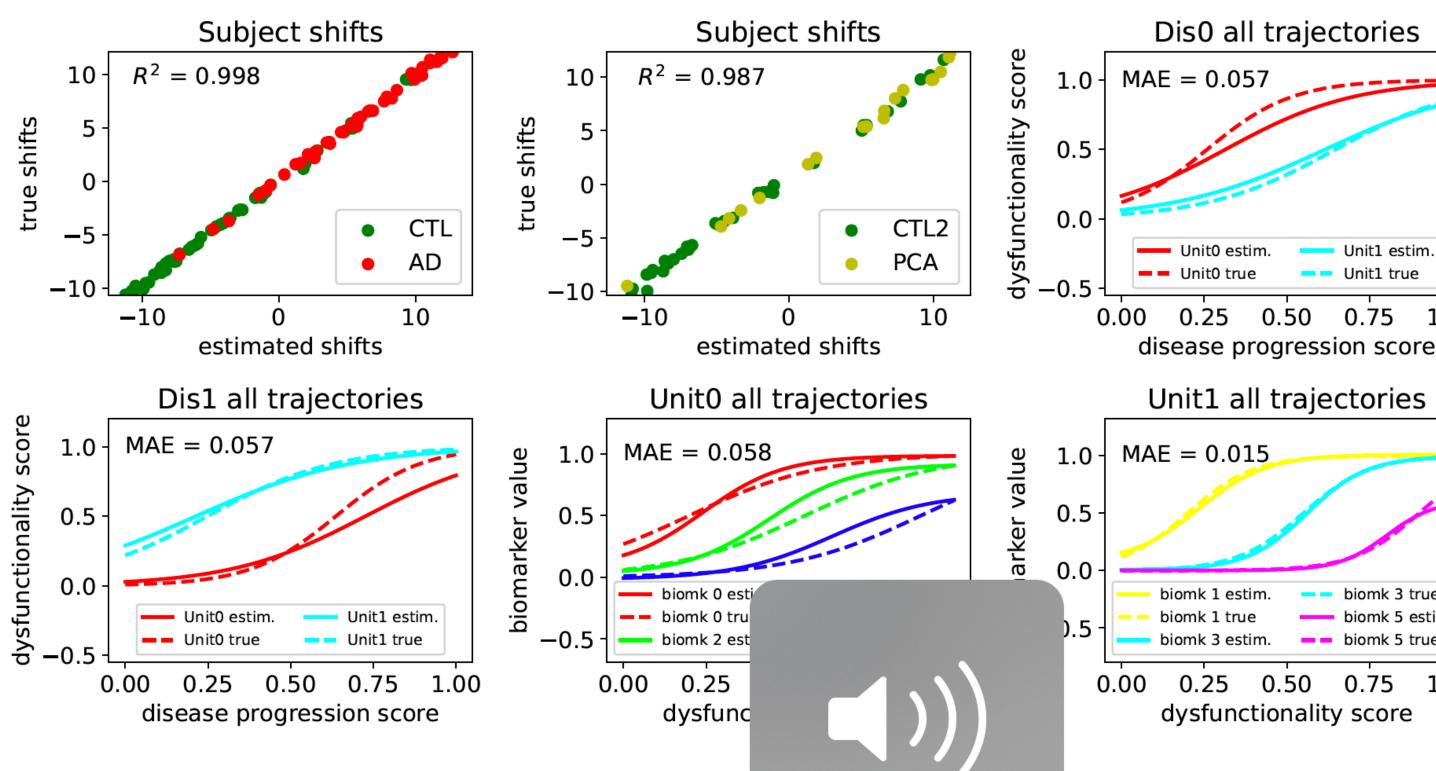
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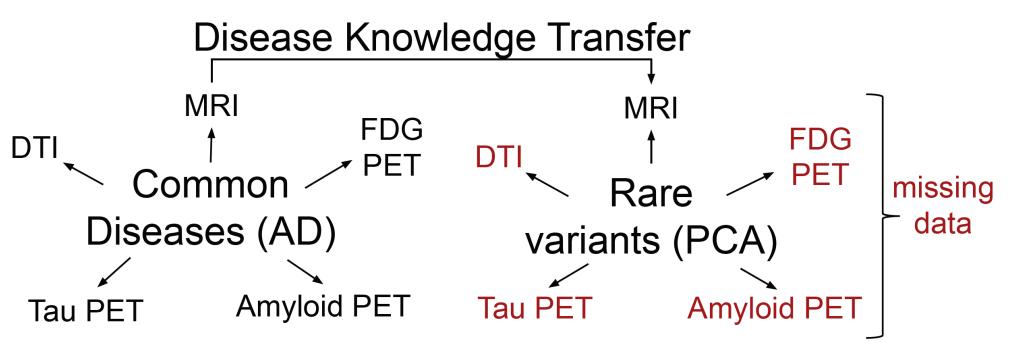
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- Simulated 100 subjects with two diseases: synAD & synPCA
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- DKT was able to:
 - Reliably fit the data
 - Infer the missing biomarkers in synPCA

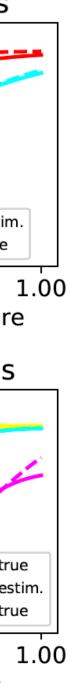


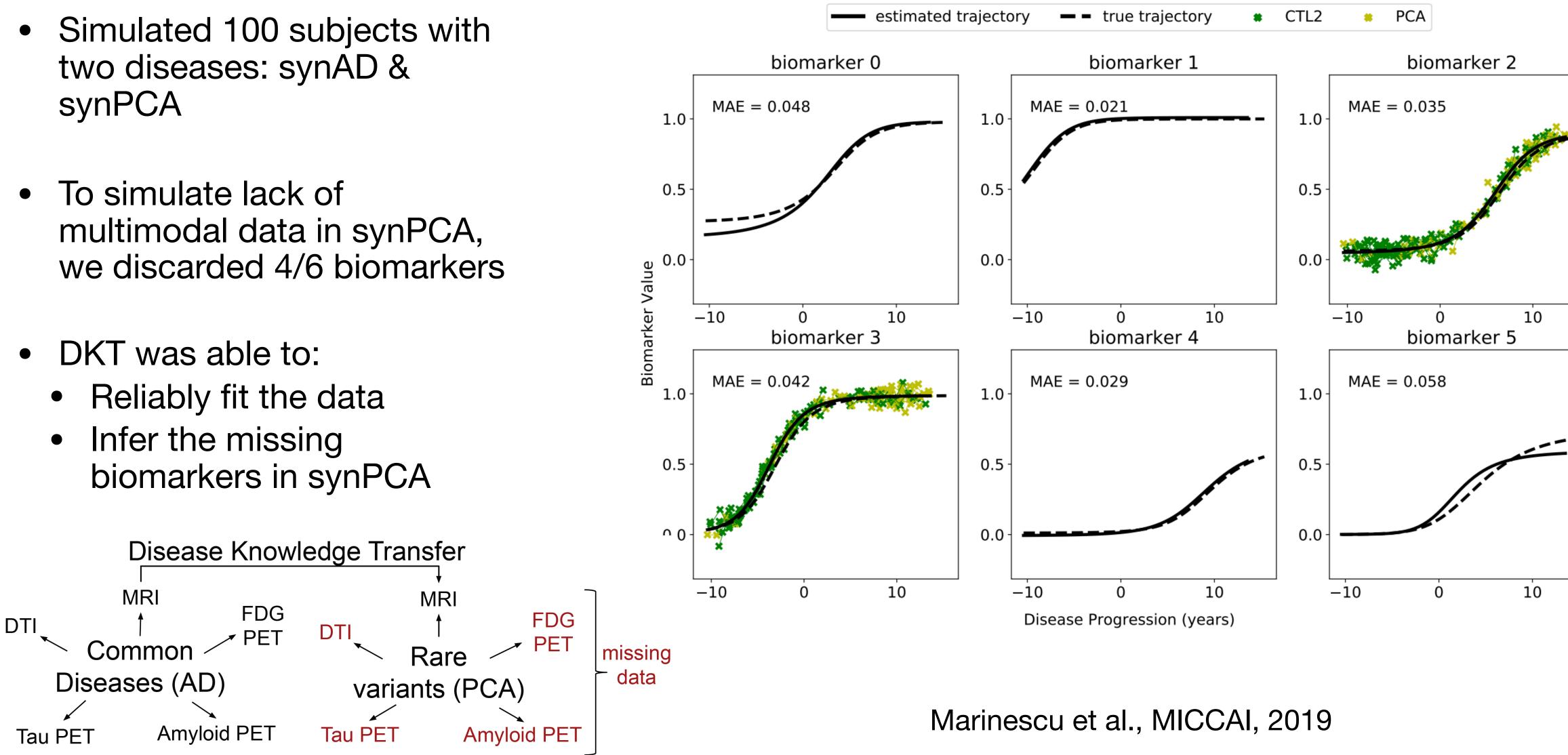


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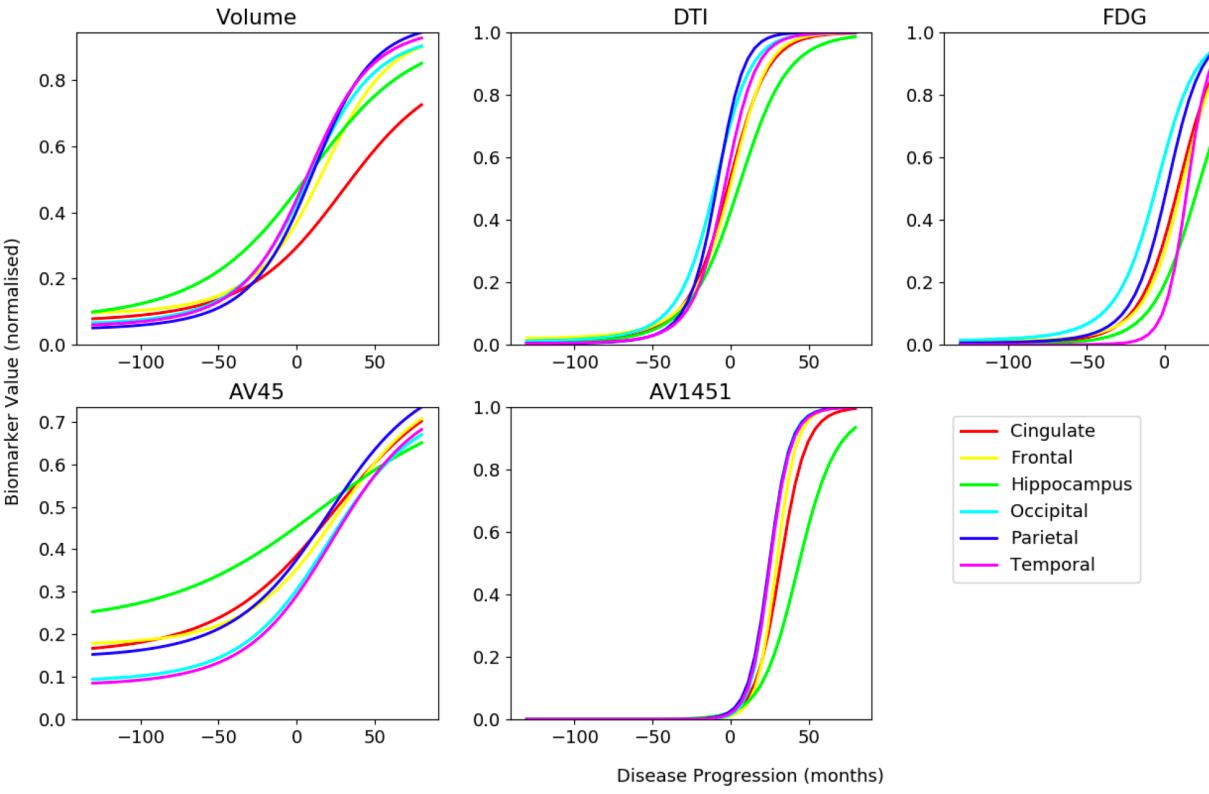






On real data, DKT can estimate *multimodal* trajectories of **Posterior Cortical Atrophy only using structural MRI**

- Ran on 76 PCA subjects from the Dementia Research Center UK
- Given structural MRI, DKT was able to infer lacksquaremissing DTI, FDG, Tau PET and Amyloid PET in PCA, in lack of such data.
 - We subsequently validate the DTI trajectories
- The first such longitudinal trajectories of ulletmultimodal biomarkers in Posterior Cortical Atrophy



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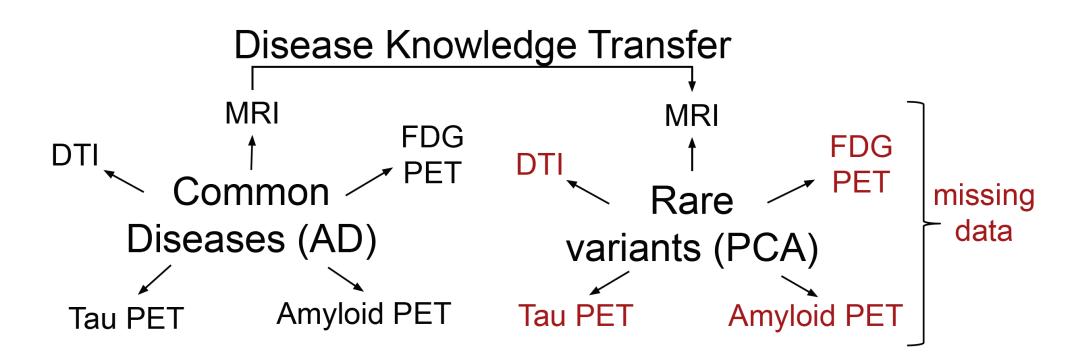


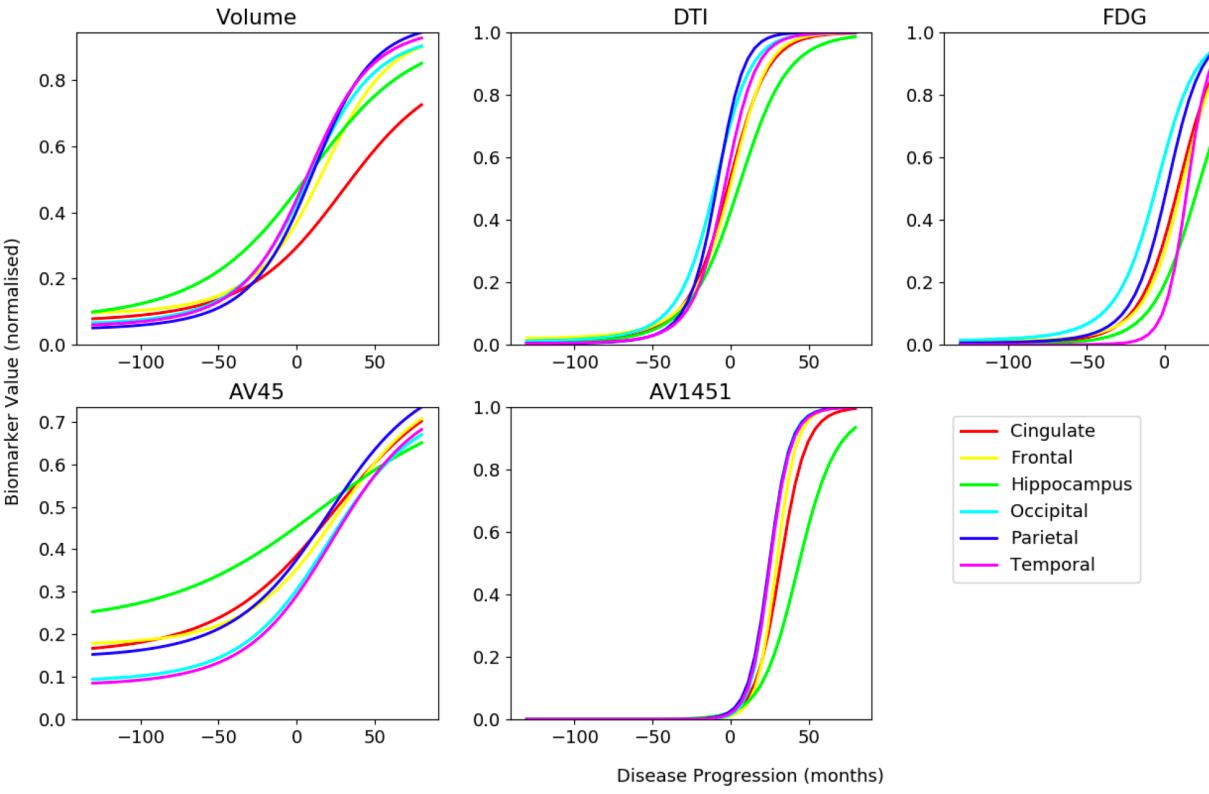


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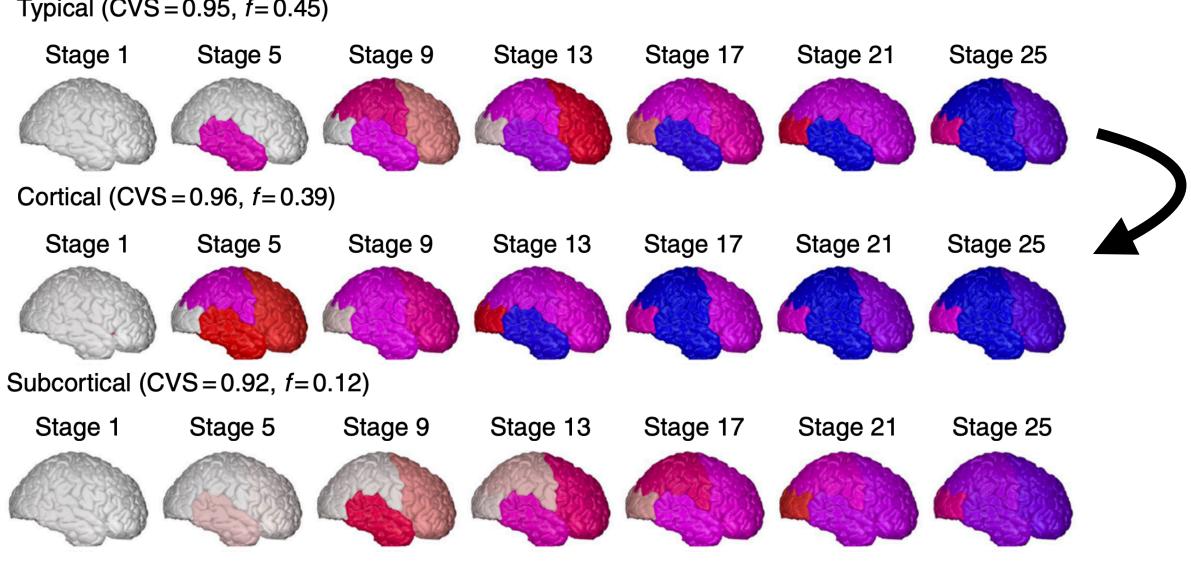
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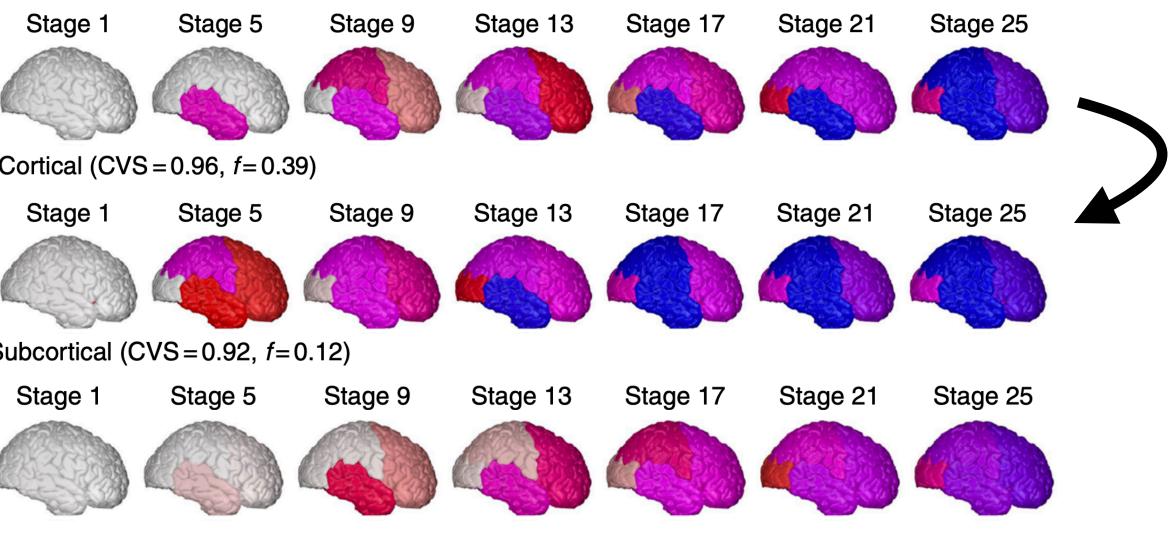


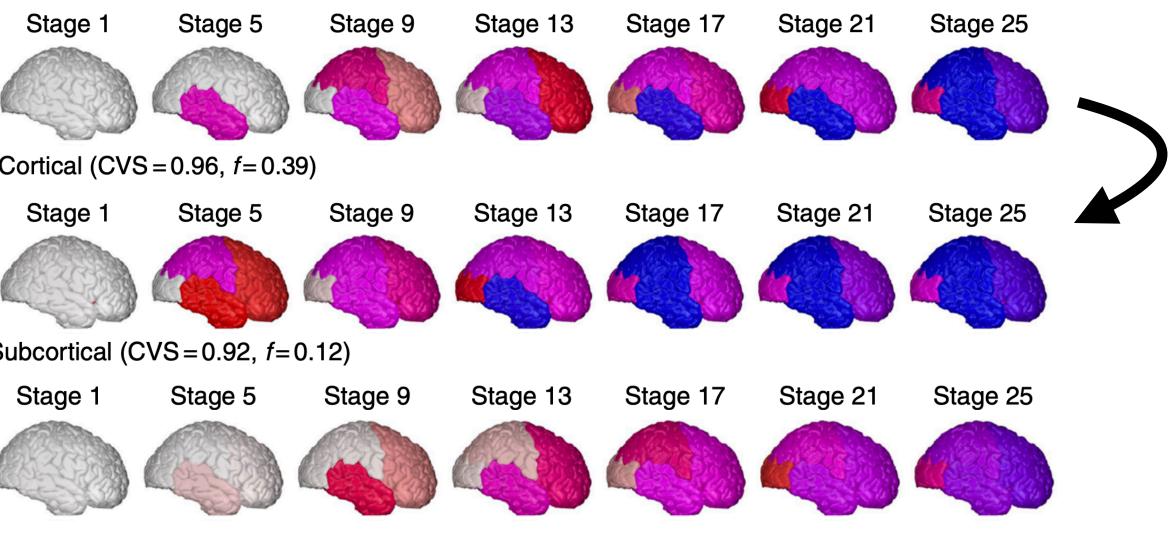


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Split ADNI into three different subgroups with different disease progressions (using SuStaln)







 \mathbf{Mo}

DKTLatent Multiv Spli Line

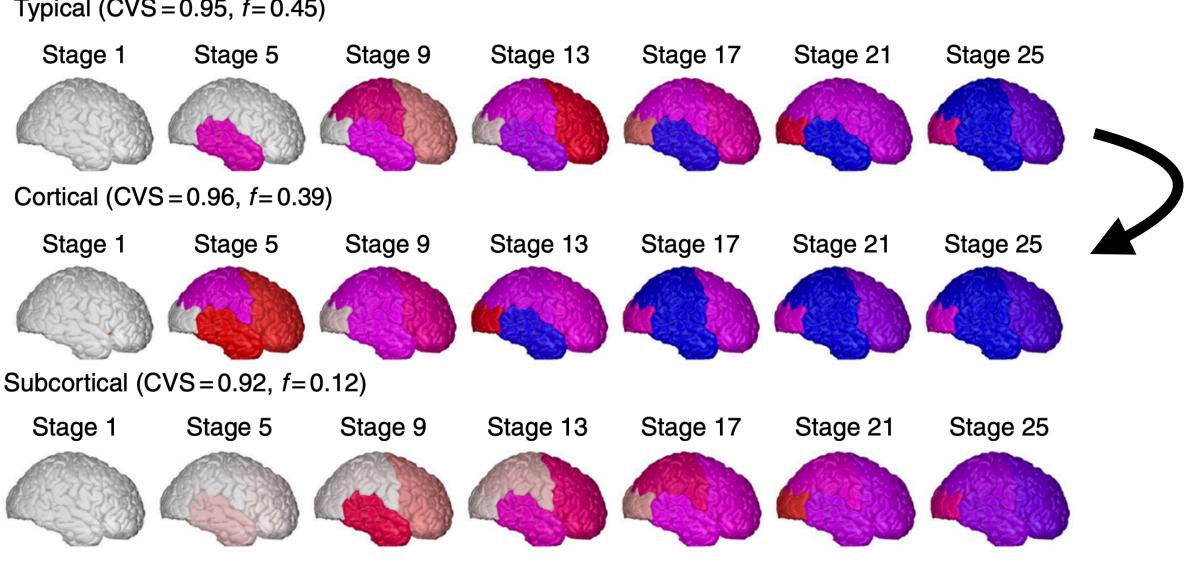
Typical (CVS = 0.95, f = 0.45)

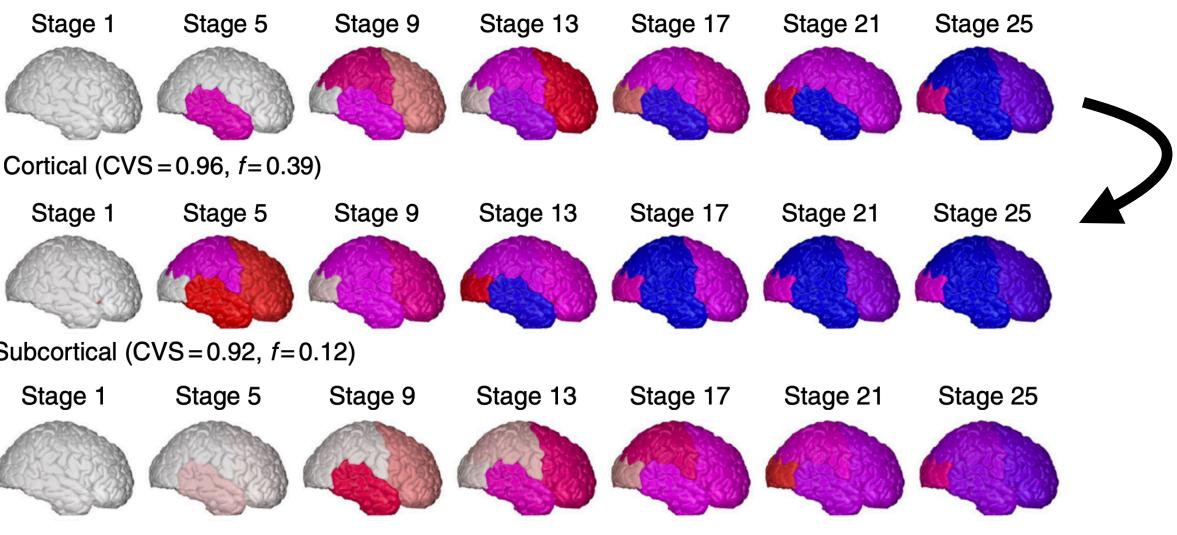
odel	Cingulate	Frontal	Hippocam.	Occipital	Parietal	Temporal
	$\mathbf{T}\mathbf{A}$	DPOLE: Hip	pocampal su	bgroup to C	ortical subgr	oup
(ours)	0.56 ± 0.23	$\textbf{0.35}\pm\textbf{0.17}$	$\textbf{0.58}\pm\textbf{0.14}$	-0.10 \pm 0.29	$\textbf{0.71}\pm\textbf{0.11}$	$\textbf{0.34}\pm\textbf{0.26}$
t stage	0.44 ± 0.25	0.34 ± 0.21	$0.34 \pm 0.24^{*}$	$\textbf{-0.07}\pm\textbf{0.22}$	0.64 ± 0.16	$0.08 \pm 0.24^{*}$
variate	$\textbf{0.60}\pm\textbf{0.18}$	$0.11 \pm 0.22^*$	$0.12 \pm 0.29^*$	-0.22 \pm 0.22	$-0.44 \pm 0.14^{*}$	$-0.32 \pm 0.29^{*}$
oline	$-0.24 \pm 0.25^{*}$	6 -0.06 \pm 0.27*	0.58 ± 0.17	-0.16 ± 0.27	$0.23 \pm 0.25^{*}$	$0.10 \pm 0.25^{*}$
near	$-0.24 \pm 0.25^{*}$	$0.20 \pm 0.25^{*}$	0.58 ± 0.17	-0.16 ± 0.27	$0.23 \pm 0.25^{*}$	$0.13 \pm 0.23^{*}$

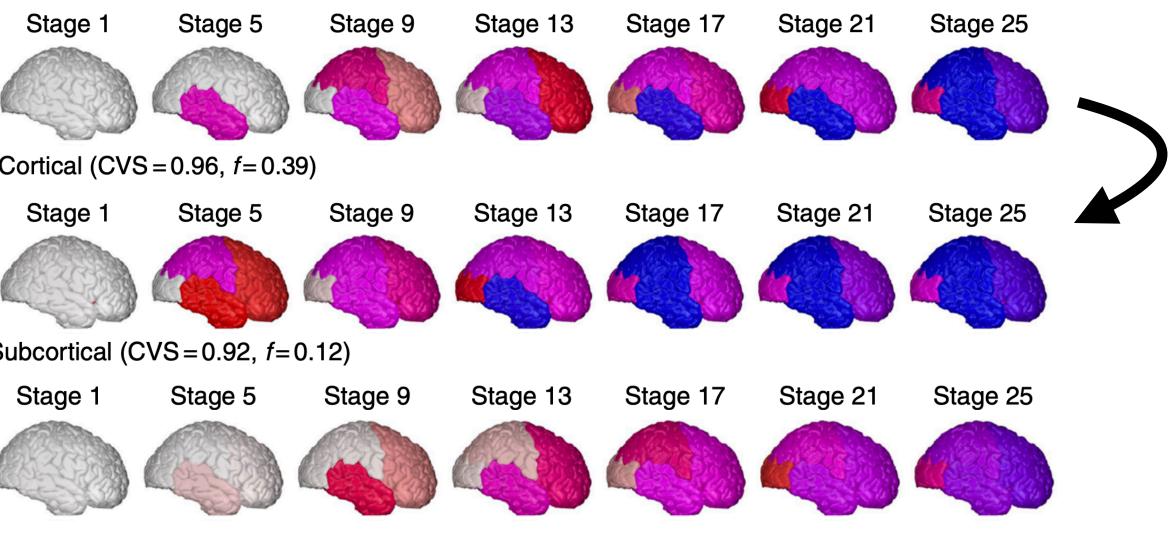
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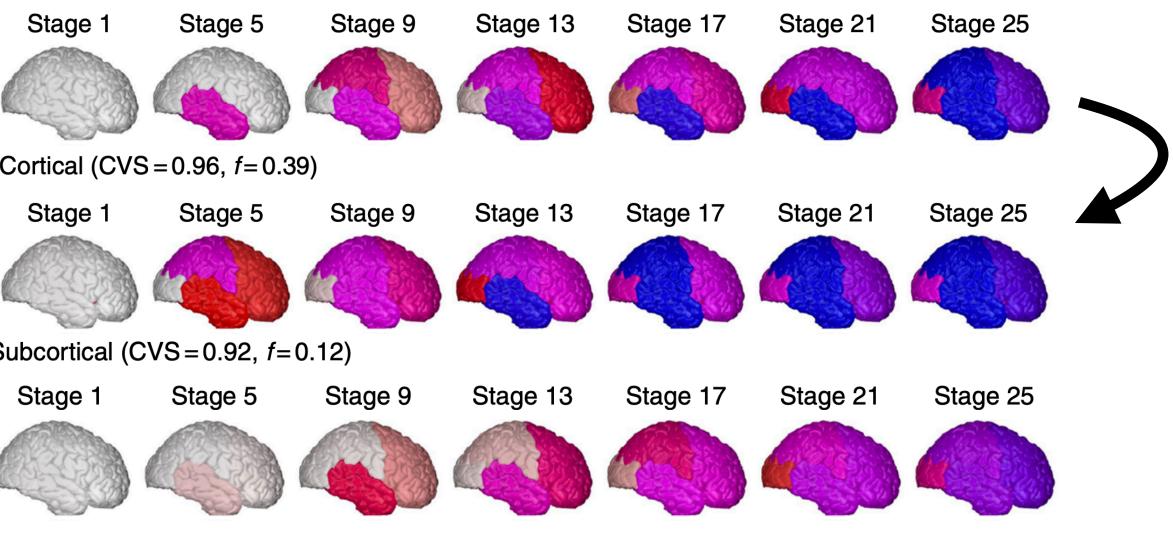


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- Transferred information from Cortical to Hippocampal subgroups









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DKT Latent Multiv Spli Line

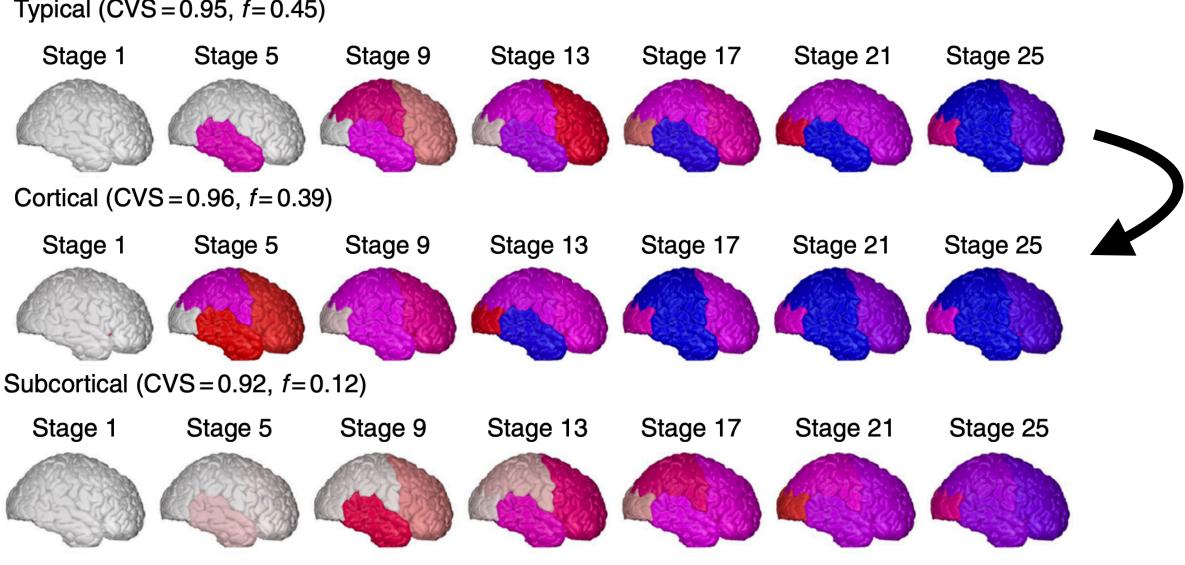
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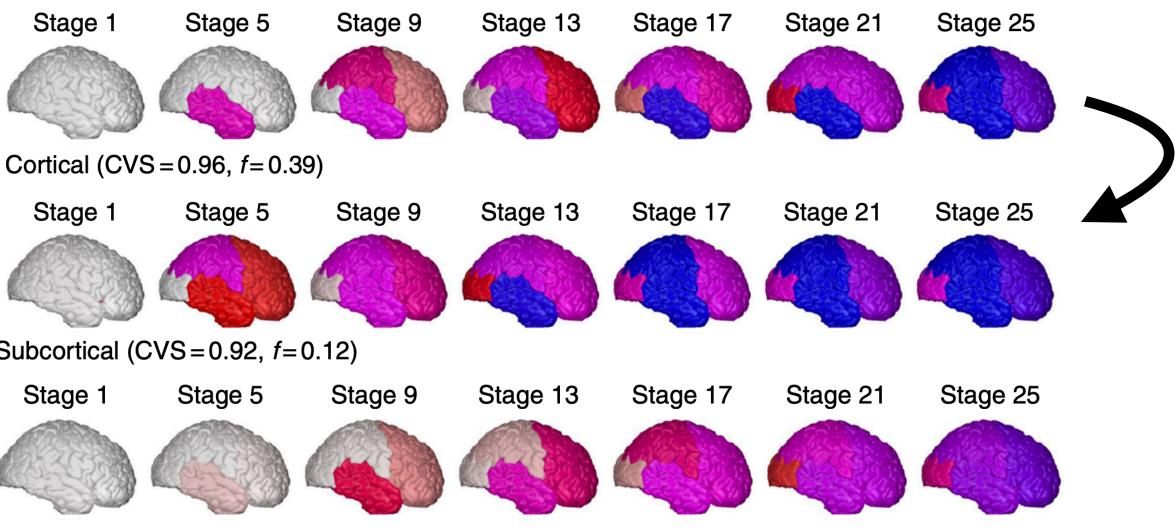
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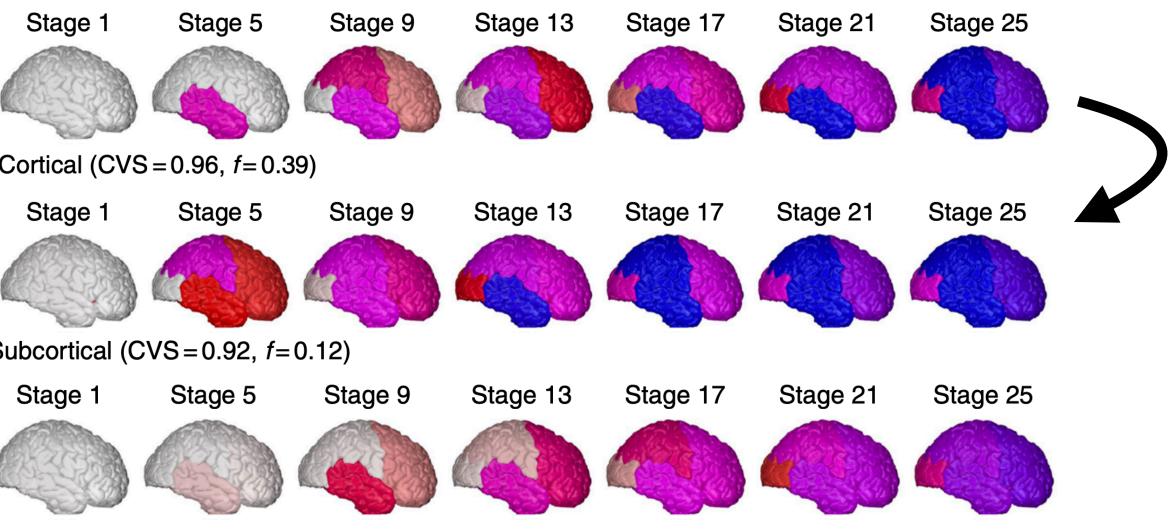
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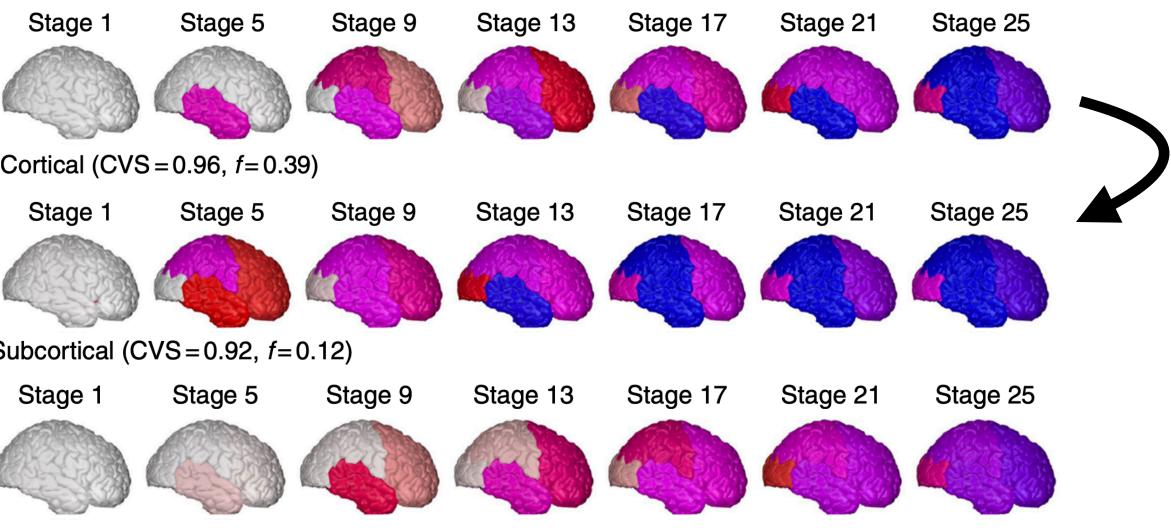


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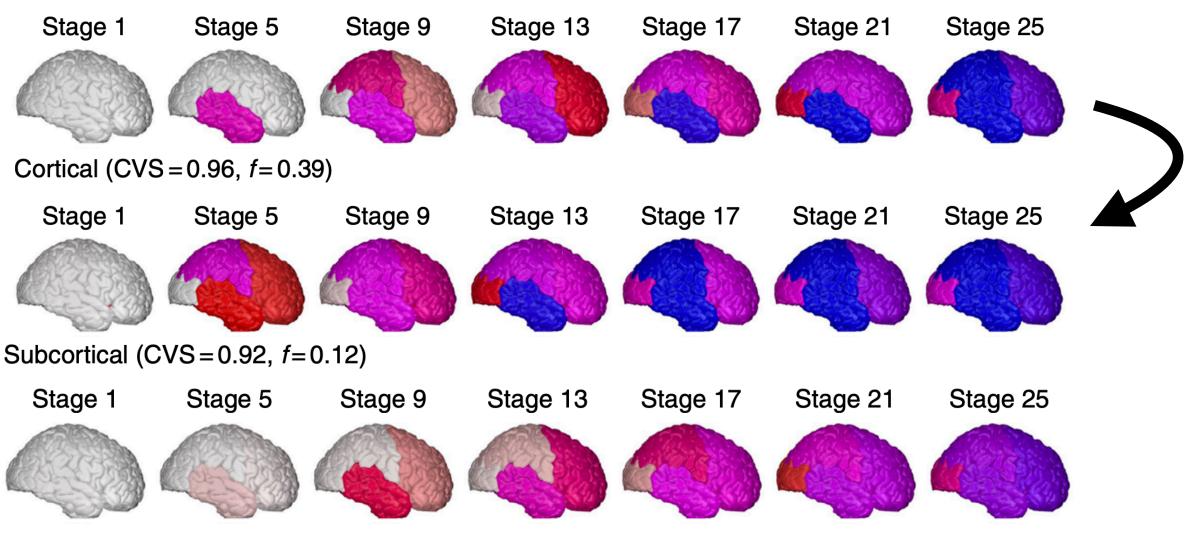
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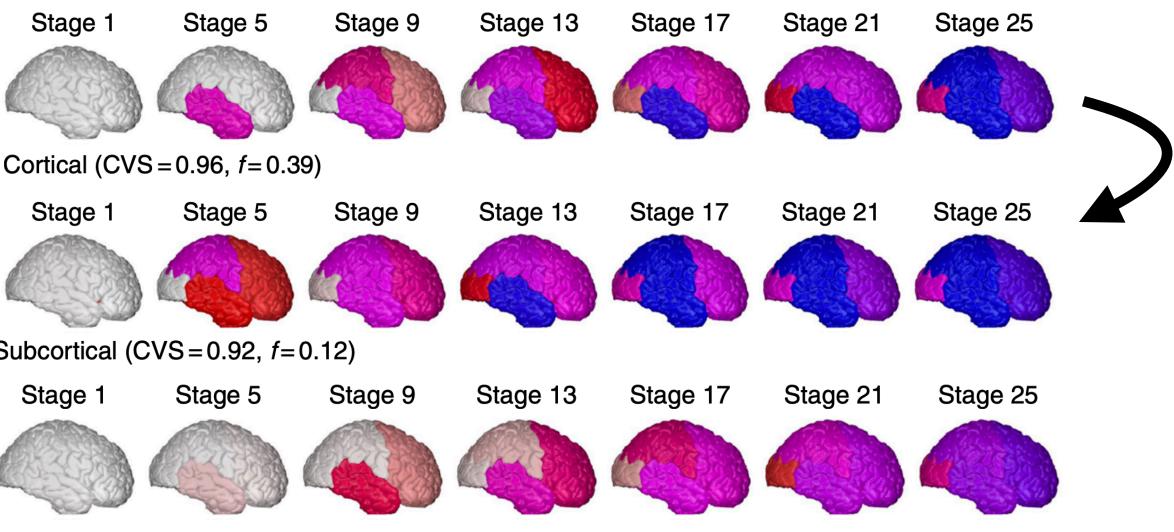
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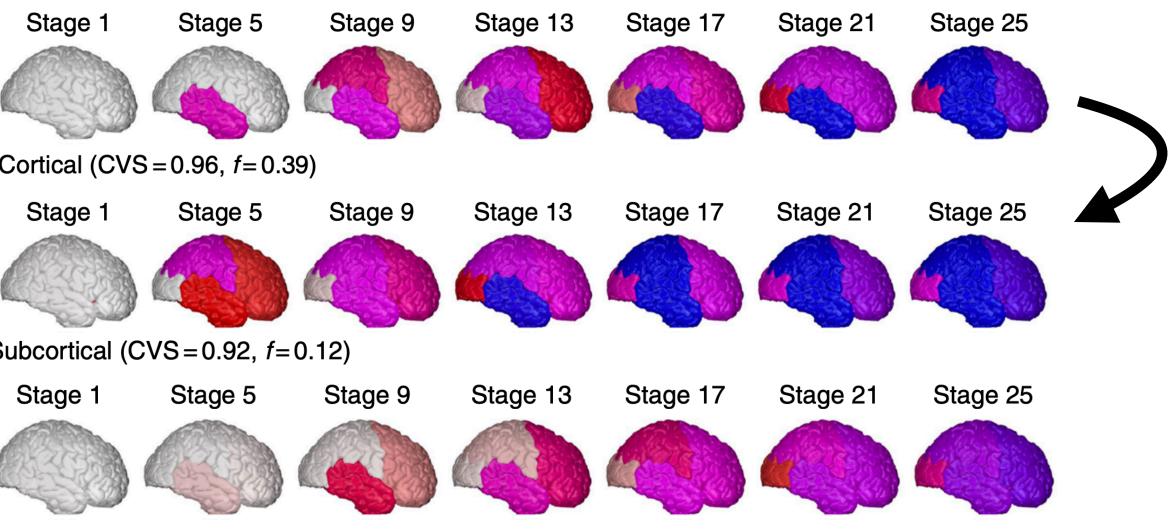
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		typical Alzh	eimer's to P	osterior Cort	ical Atrophy			
(ours)	0.77 ± 0.11	0.39 ± 0.26	0.75 ± 0.09	0.60 ± 0.14	$\textbf{0.55}\pm\textbf{0.24}$	0.35 ± 0.22		
t stage	$\textbf{0.80} \pm \textbf{0.09}$	$\textbf{0.53} \pm \textbf{0.17}$	$\textbf{0.80}\pm\textbf{0.12}$	0.56 ± 0.18	0.50 ± 0.21	0.32 ± 0.24		
variate	0.73 ± 0.09	0.45 ± 0.22	0.71 ± 0.08	-0.28 \pm 0.21*	0.53 ± 0.22	$0.25\pm0.23^{*}$		
line	$0.52 \pm 0.20^{*}$	$-0.03 \pm 0.35^{*}$	$0.66 \pm 0.11^*$	$0.09 \pm 0.25^{*}$	0.53 ± 0.20	$0.30 \pm 0.21^{*}$		
near	$0.52 \pm 0.20^{*}$	0.34 ± 0.27	$0.66 \pm 0.11^*$	$\textbf{0.64}\pm\textbf{0.17}$	0.54 ± 0.22	$0.30 \pm 0.21^{*}$		

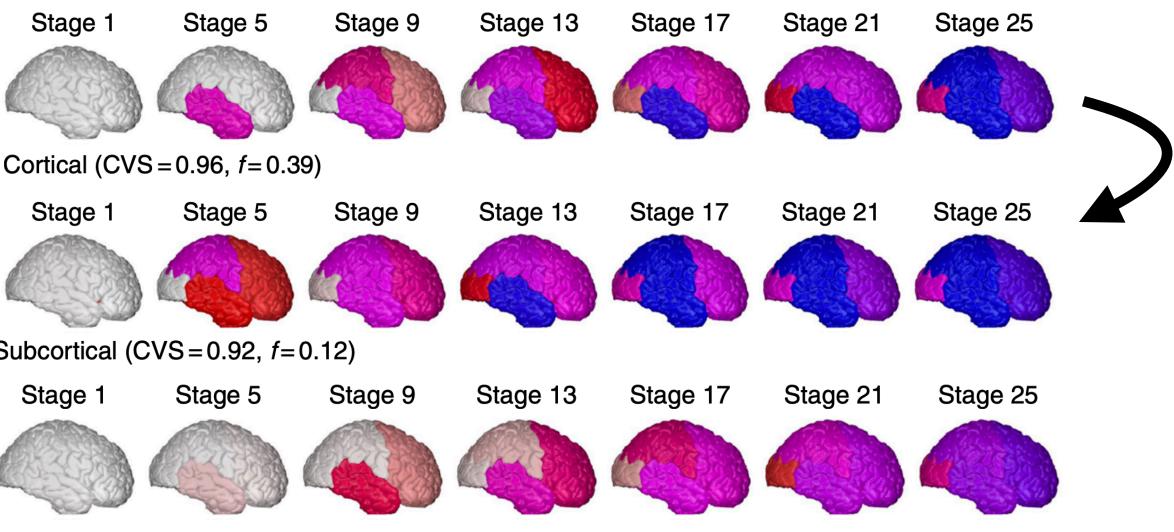


- Split ADNI into three different subgroups with different disease progressions (using SuStaln)
- Transferred information from \bullet Cortical to Hippocampal subgroups
- From typical AD to Posterior **Cortical Atrophy**









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DKT Latent Multiva Spli Line

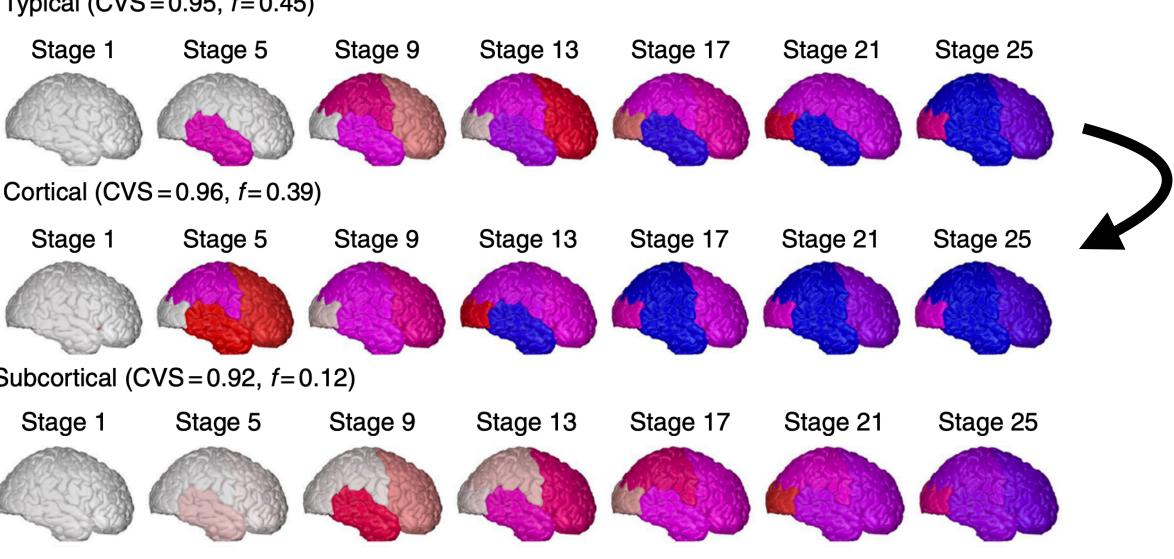
DKTLatent Multiva Spl Line

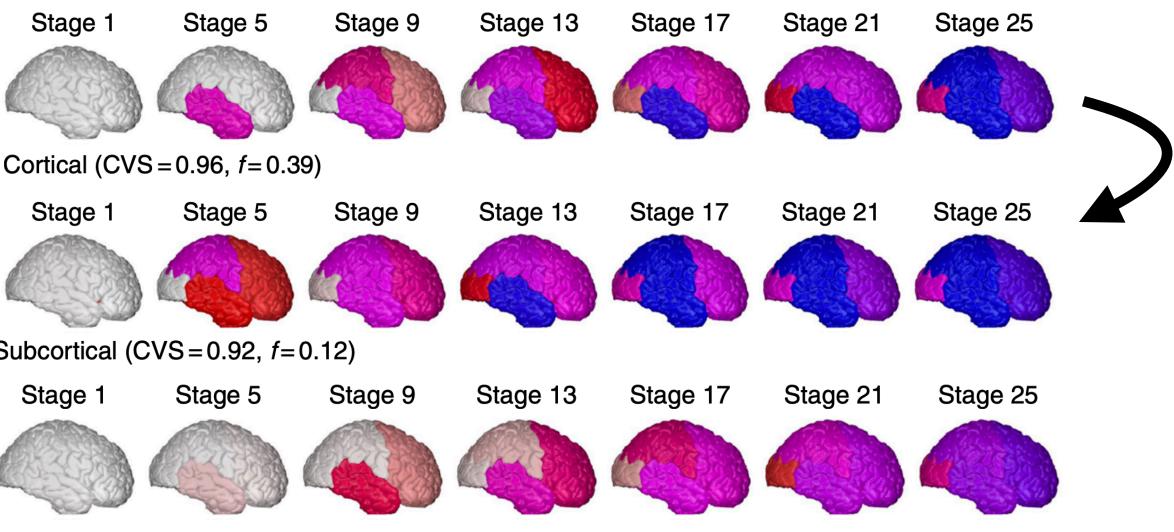
Typical (CVS = 0.95, f = 0.45)

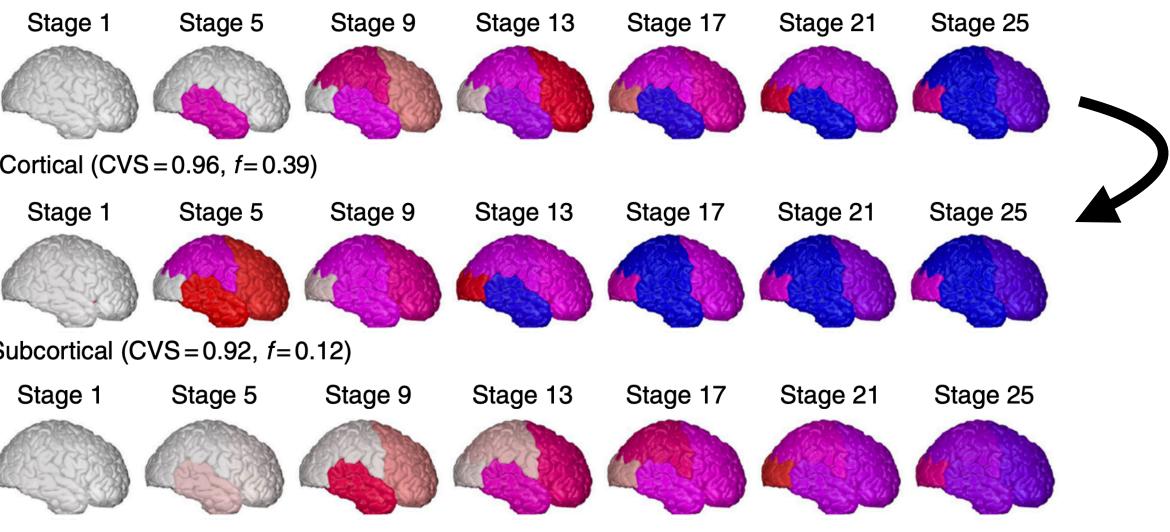
odel	Cingulate	Frontal	Hippocam.	Occipital	Parietal	Temporal		
	TADPOLE: Hippocampal subgroup to Cortical subgroup							
(ours)	0.56 ± 0.23	$\textbf{0.35}\pm\textbf{0.17}$	$\textbf{0.58}\pm\textbf{0.14}$	-0.10 \pm 0.29	$\textbf{0.71}\pm\textbf{0.11}$	$\textbf{0.34} \pm \textbf{0.26}$		
t stage	0.44 ± 0.25	0.34 ± 0.21	$0.34 \pm 0.24^{*}$	$\textbf{-0.07}\pm\textbf{0.22}$	0.64 ± 0.16	$0.08 \pm 0.24^{*}$		
variate	$\textbf{0.60} \pm \textbf{0.18}$	$0.11 \pm 0.22^*$	$0.12 \pm 0.29^*$	-0.22 \pm 0.22	$-0.44 \pm 0.14^{*}$	$-0.32 \pm 0.29^{*}$		
line	$-0.24 \pm 0.25^{*}$	$-0.06 \pm 0.27^*$	0.58 ± 0.17	-0.16 \pm 0.27	$0.23 \pm 0.25^{*}$	$0.10 \pm 0.25^{*}$		
near	$-0.24 \pm 0.25^{*}$	$0.20 \pm 0.25^{*}$	0.58 ± 0.17	-0.16 ± 0.27	$0.23 \pm 0.25^{*}$	$0.13 \pm 0.23^{*}$		
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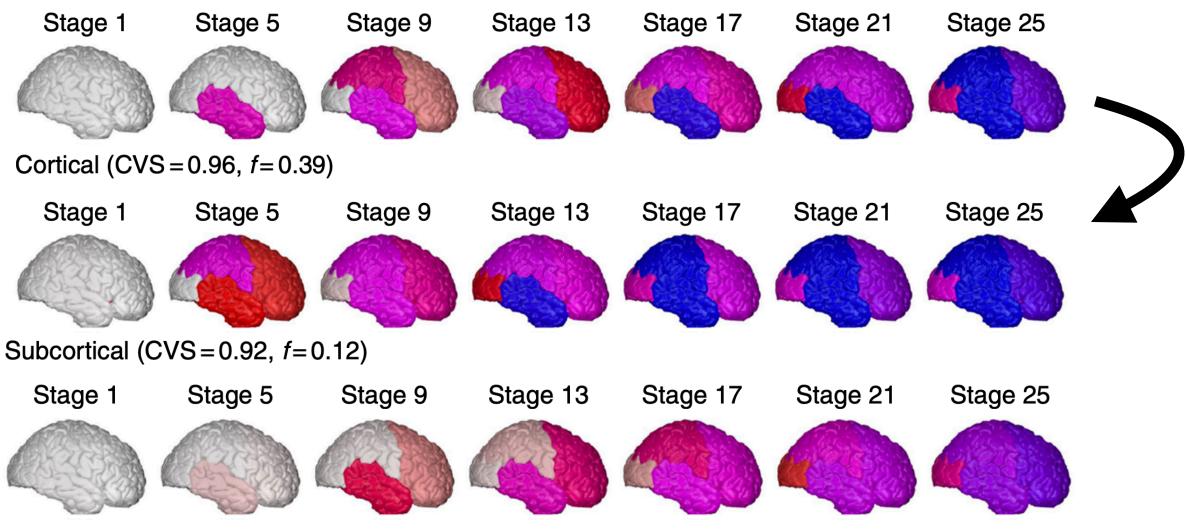


- Split ADNI into three different subgroups with different disease progressions (using SuStaln)
- Transferred information from \bullet Cortical to Hippocampal subgroups
- From typical AD to Posterior Cortical Atrophy
- Validated on 20 left-out diffusion scans on PCA









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DKT Latent Multiva Spli Line

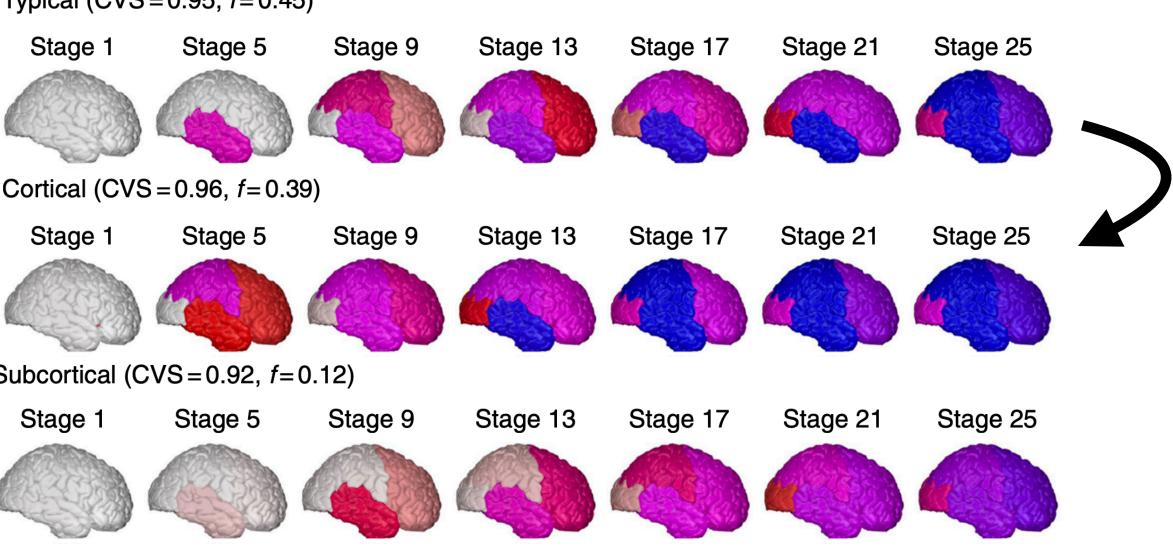
DKTLatent Multiva Spl Line

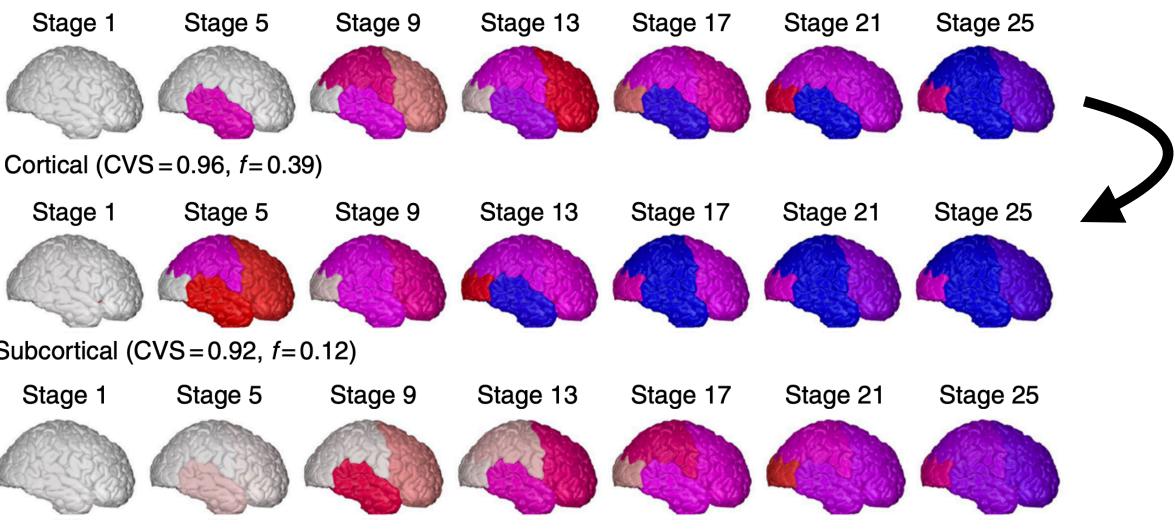
Typical (CVS = 0.95, f = 0.45)

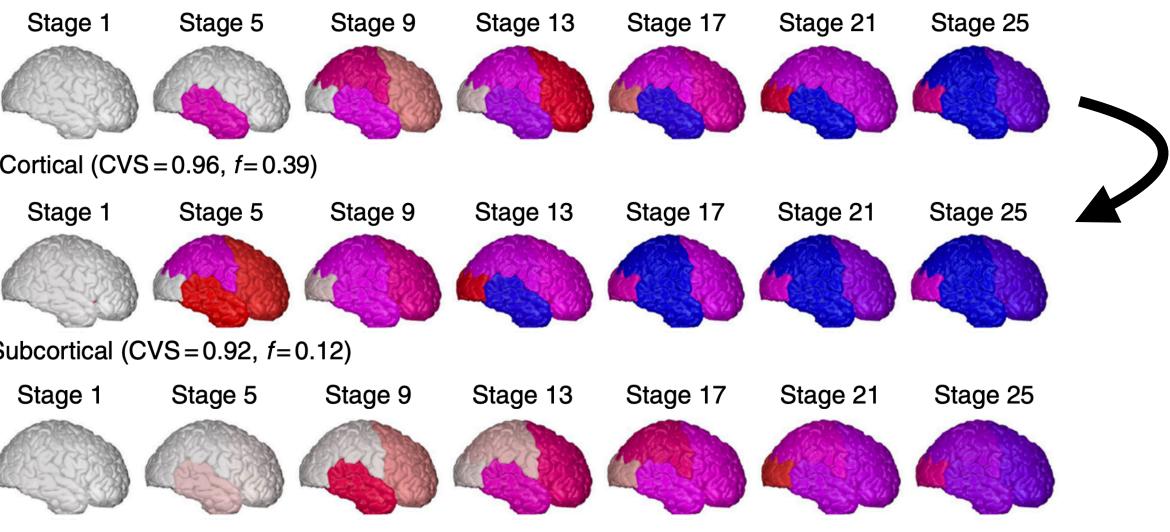
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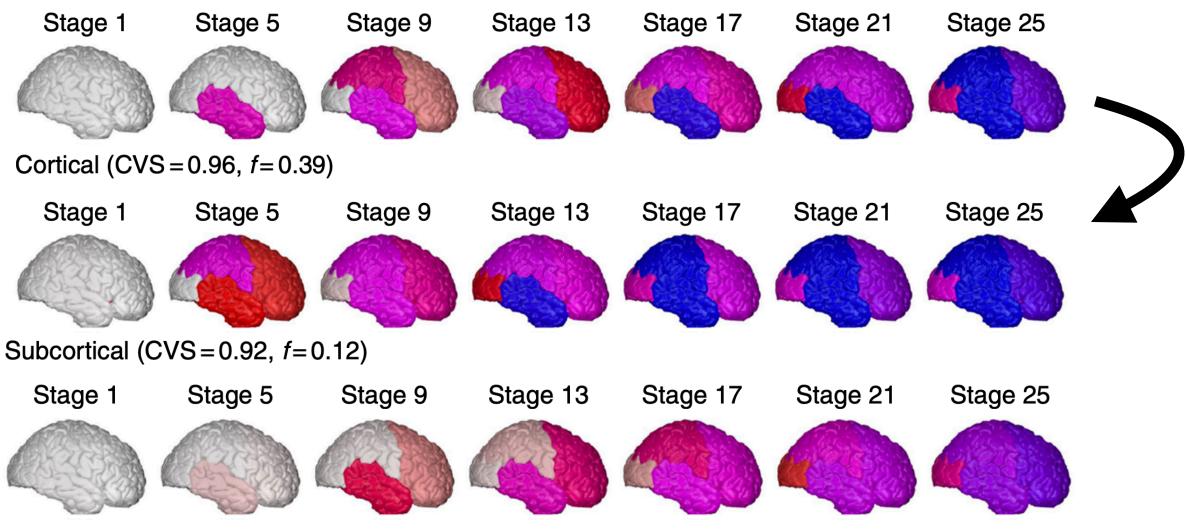


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- From typical AD to Posterior Cortical Atrophy
- Validated on 20 left-out diffusion scans on PCA
 - Fractional anisotropy maps









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DKTLatent Multiva Spl Line

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Summary and future work

- Proposed a model to perform transfer learning across different neurodegenerative diseases
- Transfer learning is done through sharing the underpinning disease mechanisms
- Model evaluated and validated in simulations as well as real data (ADNI & Dementia Research Center UK) on the largest PCA cohort to date
- Future work: transfer learning using deep-learning approaches, by synthesizing PET/DTI/CT scans for rarer neurodegenerative diseases where such data is very limited
- Such synthesis will enable characterizing their progression, which can help identify novel drug targets, stratify cohorts for clinical trials and identify suitable endpoints.



