

Bayesian Multi-modality Disease-progression Models of *Frontotemporal* Dementia

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and Adam Staffaroni, Adam Boxer, Howie Rosen, Brad Boeve (ALLFTD)

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Overview

- Intro: Frontotemporal dementia
- Disease progression modeling

Frontotemporal Dementia (FTD)



- FTD early-onset fatal neurodegenerative disease
- Estimated ~10% of all Dementia cases (rare cf AD)
- Affects people younger than AD (40s and 50s)

FTD Syndromes



- Syndromes related to brain location, e.g.,
 - Behavioral Variant FTD (bvFTD)
 - Language variants (Primary Progressive Aphasia [PPA], sv and NFv)
 - Motor presentations (ALS, PSP, CBS)

Frontotemporal Dementia (FTD)

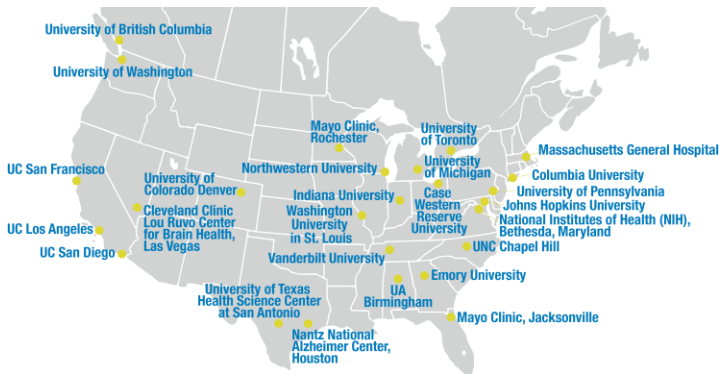


- Familial vs. Sporadic FTD
 - 30% cases Familial – autosomal dominant and high penetrance
 - 3 main genes -- GRN: progranulin, MAPT, C9
 - Presentation proportions vary by genetic variants
 - Critical for early-stage clinical trials, BUT high heterogeneity of age of onset causes difficulties

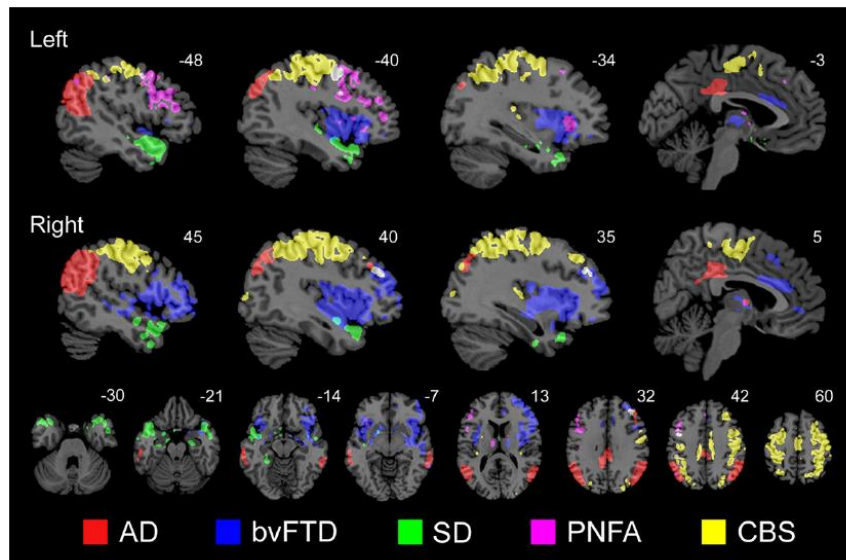


ALLFTD

ARTFL LEFFTDS Longitudinal
Frontotemporal Lobar Degeneration

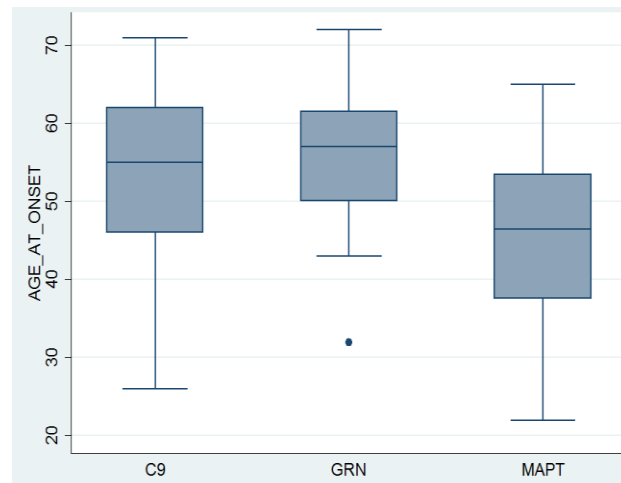


- allftd.org
- Longitudinal multi-center study across USA/Canada
- Cognitive tests, imaging, blood work etc.
- Patient age ~ 40 -- 70



Challenges to conducting f-FTD trials

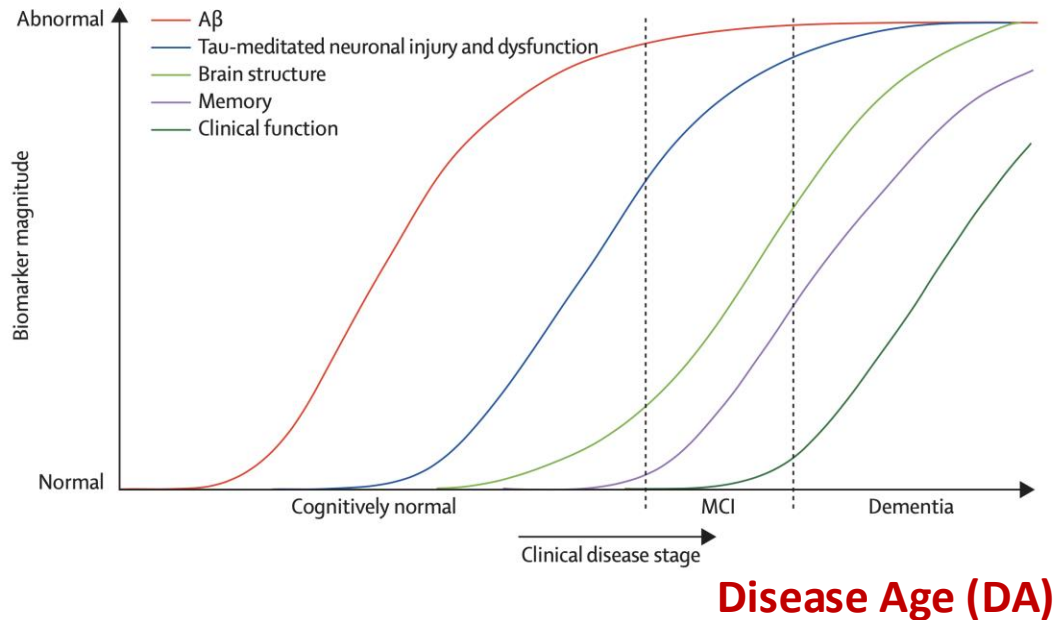
- Best treat f-FTD early (presymptomatic) stages
- Need biomarker/clinical changes f-FTD
 - Age disease onset highly variable
 - Within mutation and within family
 - No good predictors of age of onset
 - Disease course highly variable
 - Each symptom's onset difficult to predict
 - Enrollment criteria?
 - Same endpoints at each disease stage?
- Heterogeneity
- Enter disease progression models (DPMs)?



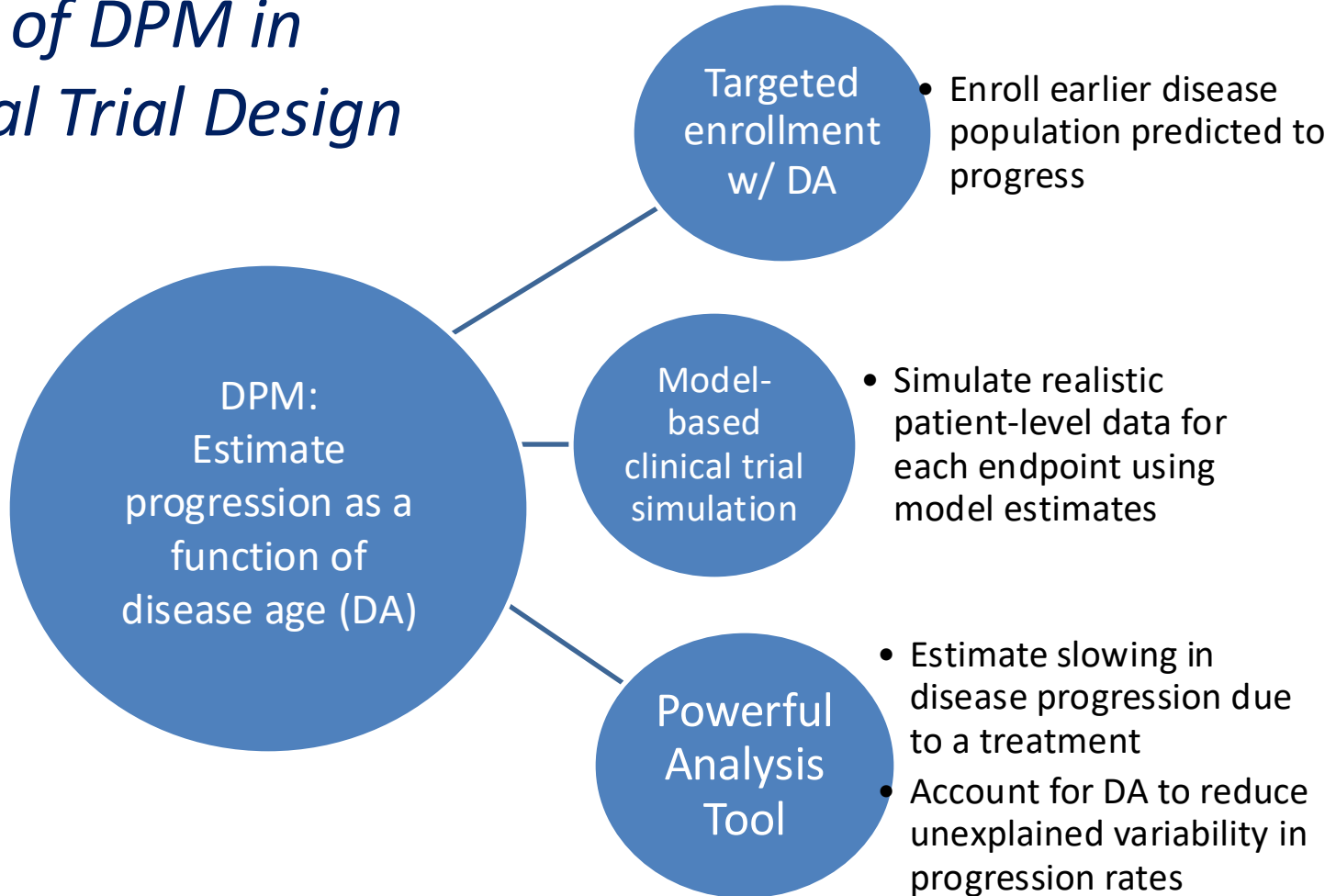
Age at onset,
ARTFL/LEFFTDS f-FTLD
(n= 95)

Disease progression models (DPMs)

- Model progression of disease -- multiple markers
- E.g., the “Cliff Jack model” for AD

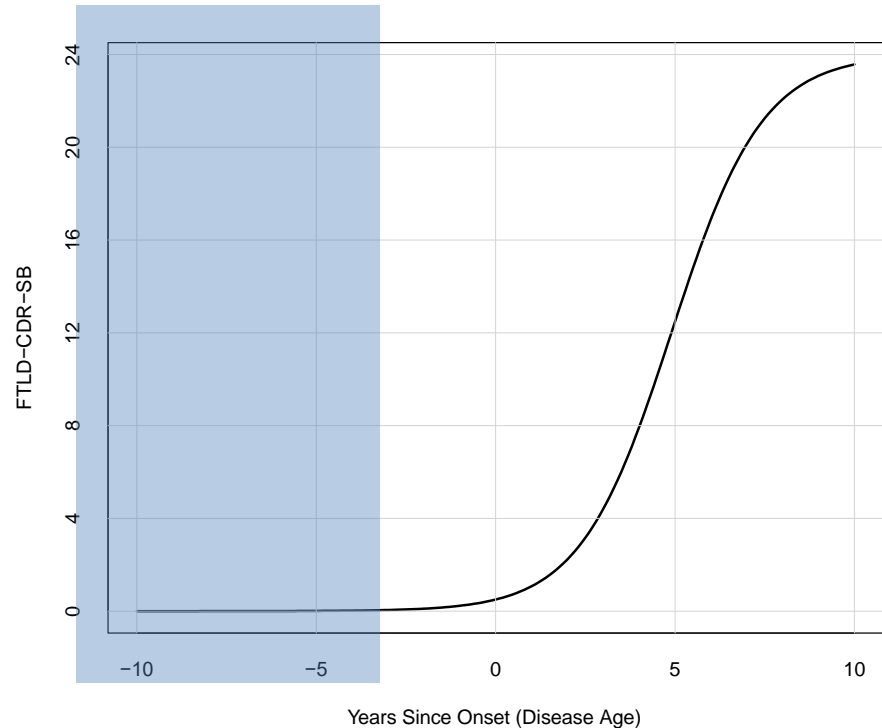


Uses of DPM in In Clinical Trial Design



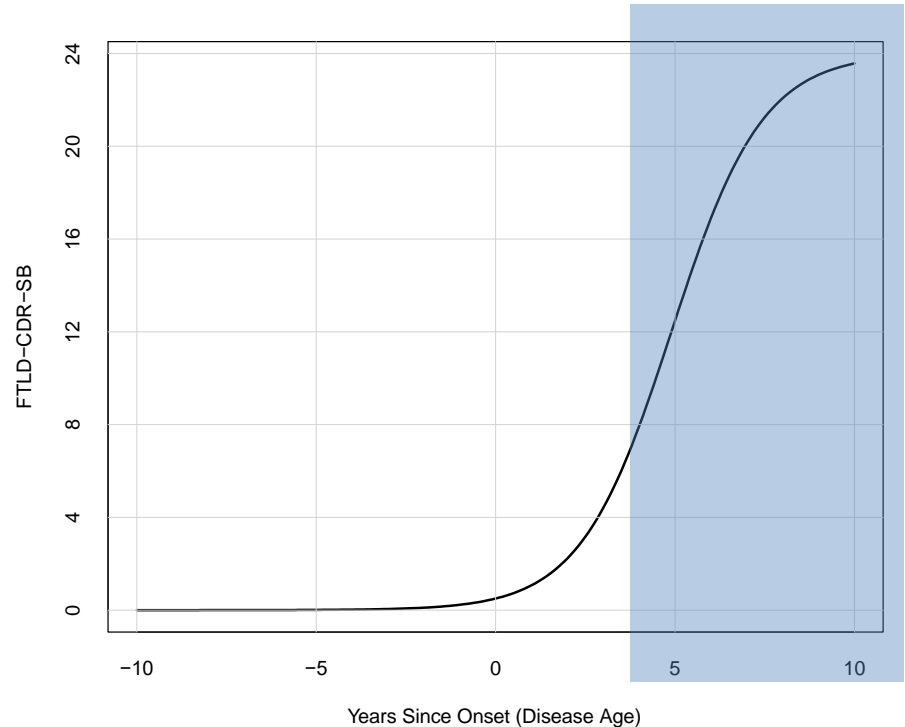
DA based Enrollment in fFTLD

- **Use predicted DA for optimal clinical trial enrollment**
 - Enroll too early – No power



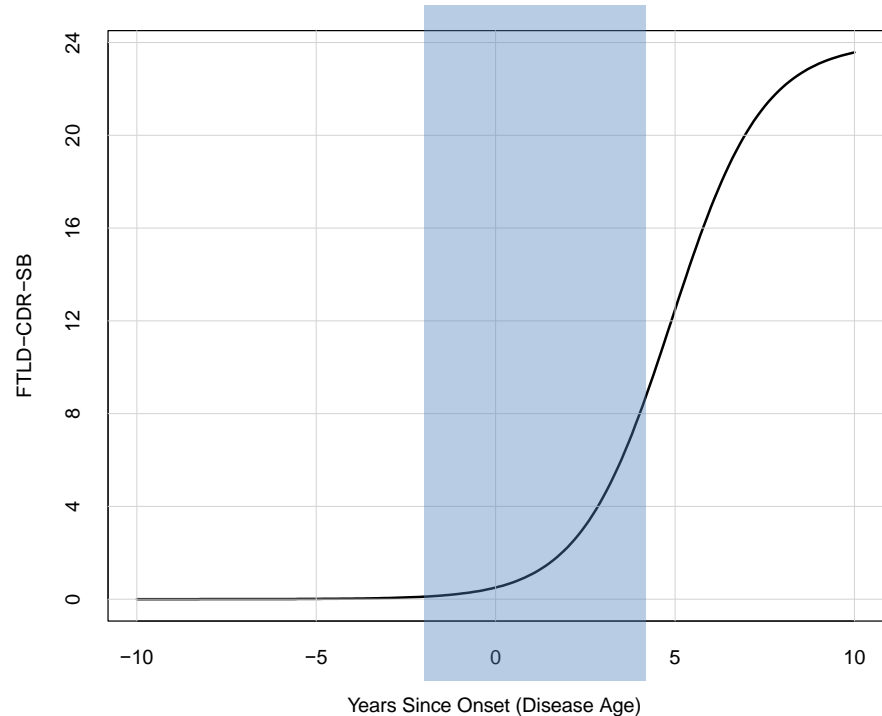
DA based Enrollment in fFTLD

- **Use predicted DA for optimal clinical trial enrollment**
 - Enroll too early – No power
 - Enroll too late – Treatment may not be effective



DA based Enrollment in *f*FTLD

- Use predicted DA for optimal clinical trial enrollment
 - Enroll too early – No power
 - Enroll too late – Treatment may not be effective
 - Enroll an earlier patient population that will likely progress *and* benefit



Familial-FTD DPM

- Joint model clinical endpoints/biomarkers over time
 - CDR[®] + NACC FTLD SB
 - Neuropsych
 - NfL
 - Volumetric ROIs (Frontal and temporal lobes etc.)
- Predictors
 - “disease age” (DA) = *chronological age – “age at onset”*
 - Genetic group

Characteristic	All Carriers	<i>C9orf72</i> +	<i>GRN</i> +	<i>MAPT</i> +	Non-Carriers
Sample Size	1,018	486	322	210	505
Visits (total number)	2.4	2.2	2.4	2.8	2.5
Total number of observations	2,417	1,060	763	594	1290

FTD DPM

i : subject
 j : visit
 k : biomarker
 m : mutation

$$Y_{i,j,k} = (\delta_{0,k} + \delta_{0,k,i}) + \frac{\delta_{1,k} - \delta_{0,k}}{1 + \exp(\theta_{k,m_i} + \beta_{k,m_i} D_{i,j})} + \varepsilon_{i,j,k}$$

Subject-specific random effect
 Normal with SD conditional on $\delta_{0,k}$

Worst value for endpoint
 Normal prior

$N(0, \sigma_k^2)$

Endpoint value at normal
 Normal prior with mean at clinician elicited prior value

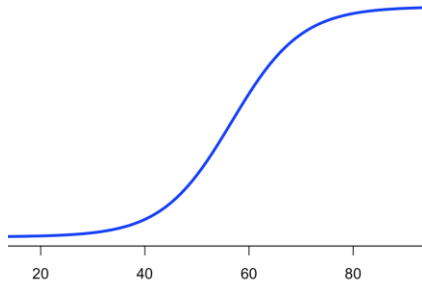
Decay rate
 specific to endpoint/
 mutation type.

Disease age
 $D_{i,j} = X_{i,j} - \alpha_i$

Decay location
 Anchor DPM so DA ($D_{i,j}$) = 0
 \Rightarrow CDR[®]+NACC FTLD-SB = .5
 for each biomarker/mutation

Age at visit

Age at onset



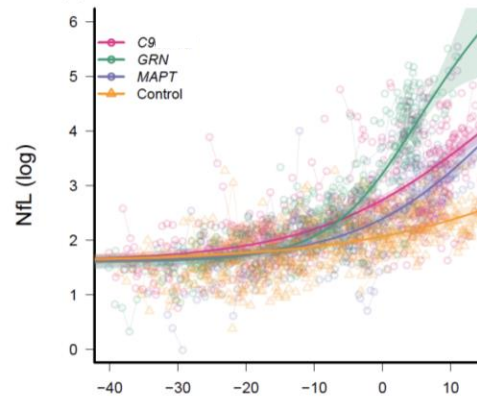
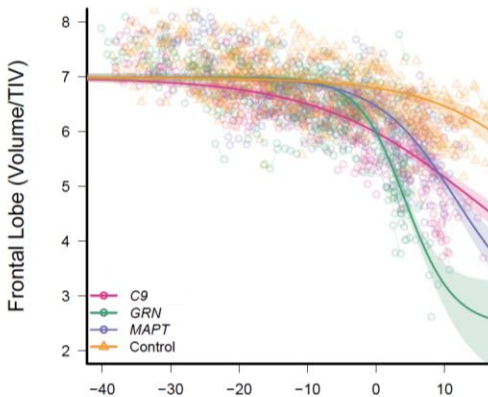
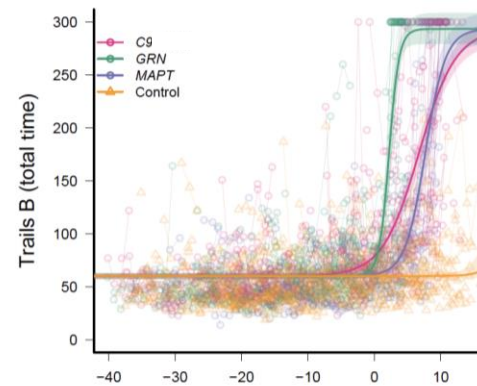
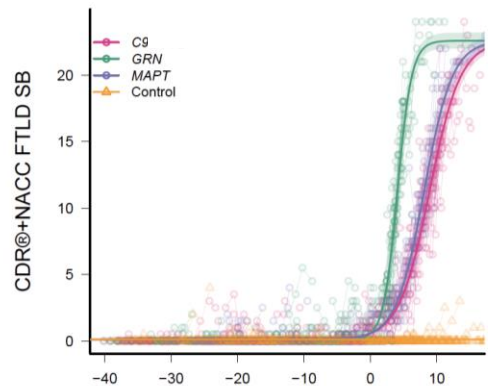
FTD DPM prior

Prior model for “age at onset”:

- If onset observed, model as Normal with mean = clinician estimated value; SD = 4 years
- If not observed, model as Normal with mean for mutation type (i.e., C9, GRN, MAPT); SD = 10 years
- Noncarrier family controls
 - Disease Age based on mean age of their family’s mutation

Temporal order of clinical and biomarker changes in familial frontotemporal dementia

Adam M. Staffaroni^{1,2,3,4,5}, Melanie Quintana^{1,2}, Barbara Wendelberger^{1,2}, Hilary W. Heuer¹, Lucy L. Russell^{1,2}, Yann Cobigo^{1,2}, Amy Wolf¹, Sheng-Yang Matt Goh¹, Leonard Petrucelli¹, Tania F. Gendron^{1,2}, Carolin Heller^{1,2}, Annie L. Clark¹, Jack Carson Taylor^{1,2}, Amy Wise¹, Elise Ong¹, Leah Forsberg¹, Danielle Brushaber¹, Julio C. Rojas¹, Lauren VandeVrede^{1,2}, Peter Ljubenkov¹, Joel Kramer¹, Kathlin B. Casaleto¹, Brian Appleby¹, Yvette Bordenes¹, Hugo Botha^{1,2}, Bradford C. Dickerson¹, Kimiko Domoto-Bally^{1,2}, Julie A. Fields¹, Tatiana Foroud^{1,2}, Ralitza Gavrilova¹, Daniel Geschwind^{1,2,3,4,5}, Nupur Ghoshal^{1,2}, Jill Goldman^{1,2}, Jonathon Graff-Radford¹, Neill Graff-Radford¹, Murray Grossman¹, Matthew G. H. Hall¹, Ging-Yuek Hsiung^{1,2}, Edward D. Huey¹, David Irwin¹, David T. Jones^{1,2}, Kojal Kantarci¹, Daniel Kaufer¹, David Knopman^{1,2}, Walter Kremen¹, Argentina Lario Lopez¹, Maria I. Lapid^{1,2}, Irene Litvan^{1,2}, Diane Lucente¹, Ian R. Mackenzie¹, Mario F. Mendez^{1,2}, Carly Mester¹, Bruce L. Miller¹, Chiadi U. Onyike^{1,2}, Rosa Rademakers^{1,2,3,4,5}, Vijay K. Ramanan^{1,2}, Eliana Maria Ramon¹, Meghana Rao¹, Katya Rascovsky¹, Katherine P. Rankin¹, Erik D. Robertson^{1,2}, Rodolfo Savica¹, M. Carmela Tartaglia^{1,2}, Sandra Weintraub^{1,2}, Bonnie Wong¹, David M. Cash^{1,2}, Arabella Bouzigues^{1,2}, Imogen J. Swift¹, Georgia Peakman¹, Martina Bocchetta^{1,2}, Emily G. Todd¹, Rhian S. Convery¹, James B. Rowe^{1,2}, Barbara Borroni¹, Daniela Galimberti^{1,2,3}, Pietro Tiraboschi¹, Mario Masellis¹, Elizabeth Finger¹, John C. van Swieten¹, Harro Seelaar^{1,2}, Lize C. Jiskoot^{1,2}, Sandro Sorbi^{1,2,3}, Chris R. Butler^{1,2,3}, Caroline Graff^{1,2,3}, Alexander Garhand^{1,2,3,4}, Tobias Langheirich^{1,2,3}, Robert Laforce^{1,2}, Raquel Sanchez-Valle^{1,2}, Alexandre de Mendonça¹, Fermín Moreno^{1,2,3}, Matthias Synofzik^{1,2,3}, Rik Vandenberghe^{1,2,3,4,5}, Simon Ducharme^{1,2,3}, Isabelle Le Ber^{1,2,3,4}, Johannes Levin^{1,2,3,4,5}, Adrian Daneş^{1,2,3}, Markus Otto¹, Florence Pasquier^{1,2,3,4,5}, Isabel Santana^{1,2,3}, John Kornak¹, Bradley F. Boeve^{1,2}, Howard J. Rosen¹, Jonathan D. Rohrer¹, Adam L. Boxer^{1,2,3} and Frontotemporal Dementia Prevention Initiative (FPI) investigators*



Estimated Years Since Onset

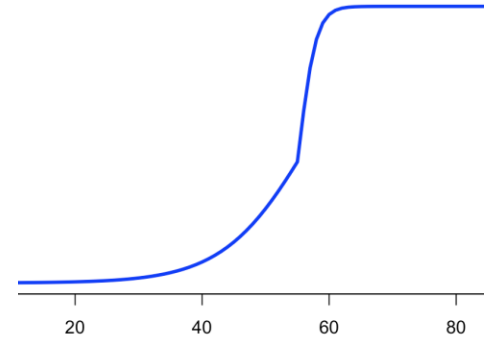
Updated FTD DPM

i : subject

j : visit

k : biomarker

m : mutation



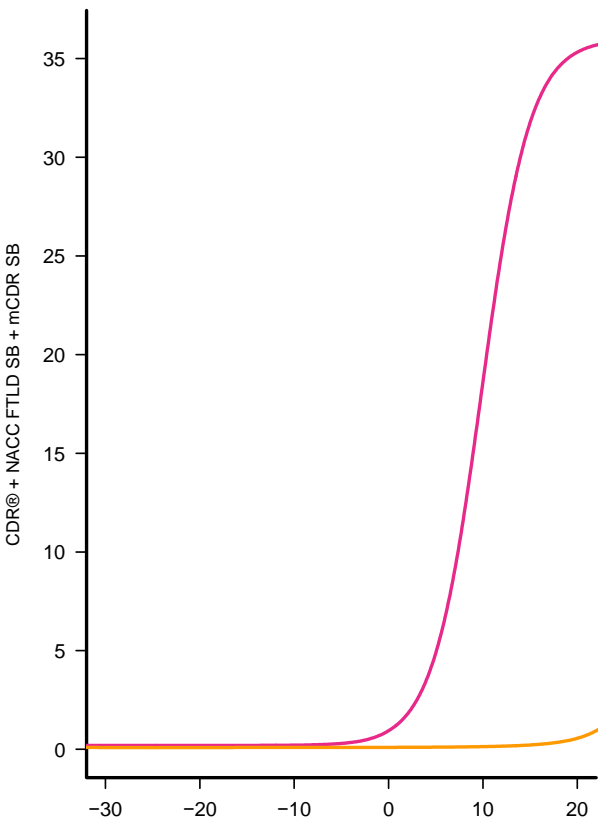
$$Y_{i,j,k} = (\delta_{0,k,m_i} + \delta_{0,k,i}) + \frac{\delta_{1,k} - \delta_{0,k,m_i}}{1 + \exp(\theta_{k,m_i} + \gamma_i \beta_{k,m_i} [\min(\Delta_{k,m_i}, D_{i,j}) + \delta_{k,m_i} \max(0, D_{i,j} - \Delta_{k,m_i})])} + \varepsilon_{i,j,k}$$

Subject-specific
multiplicative adjustment
to rate of progression

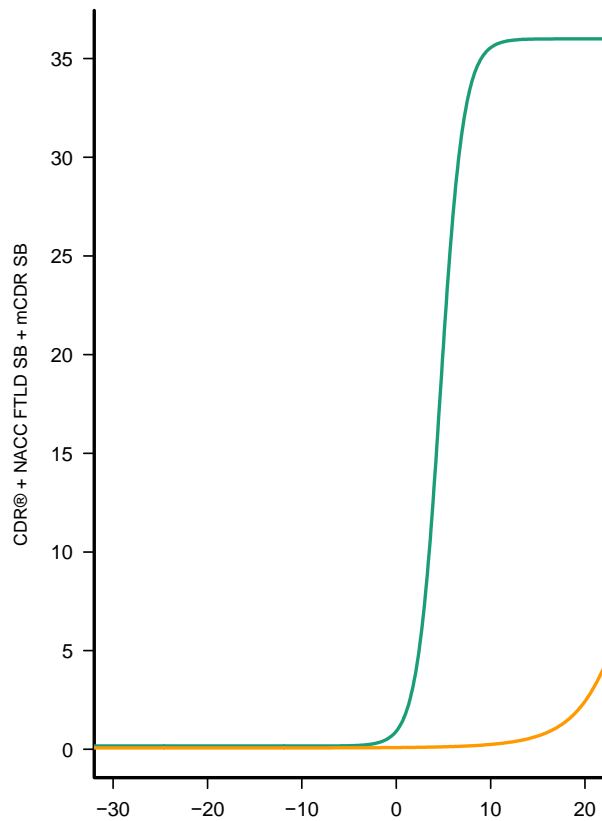
Endpoint and mutation-
specific change-point

Endpoint and mutation-
specific multiplicative change
in rate of progression after
the change point

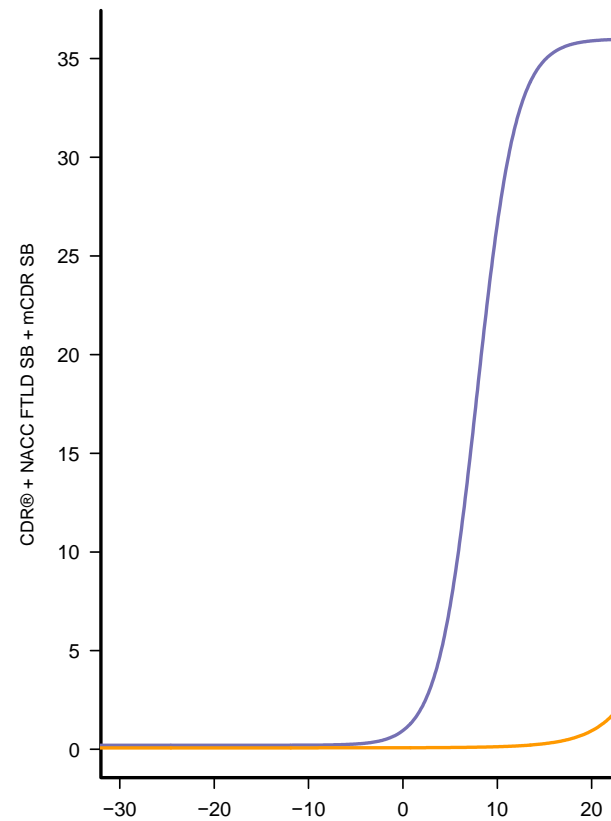
C9orf72



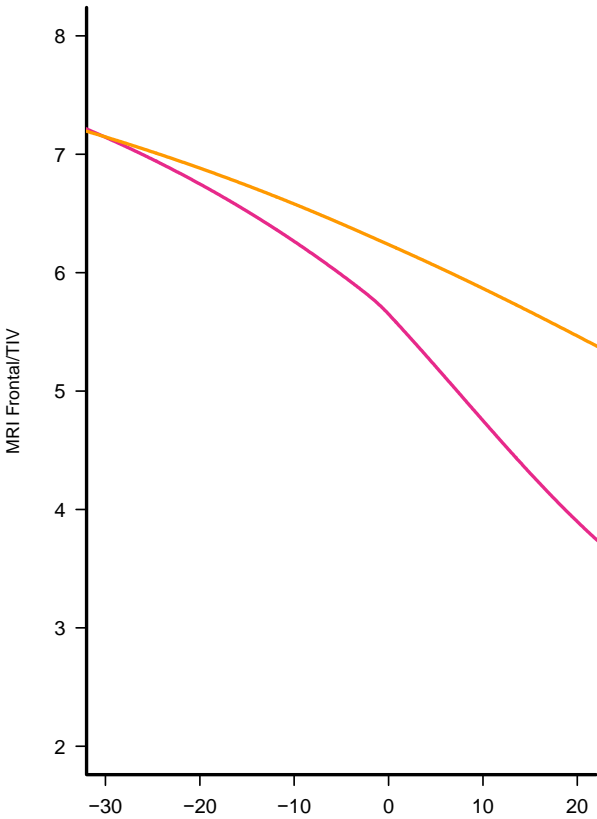
GRN



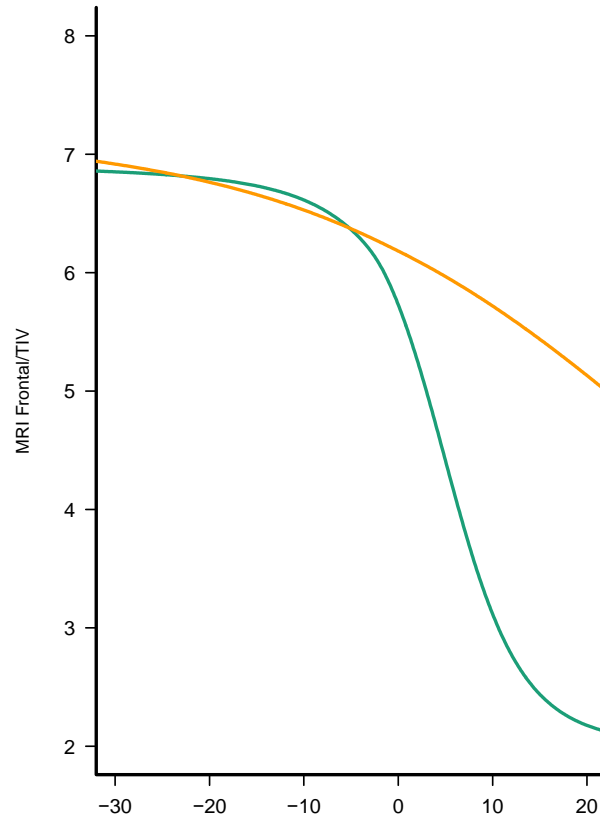
MAPT



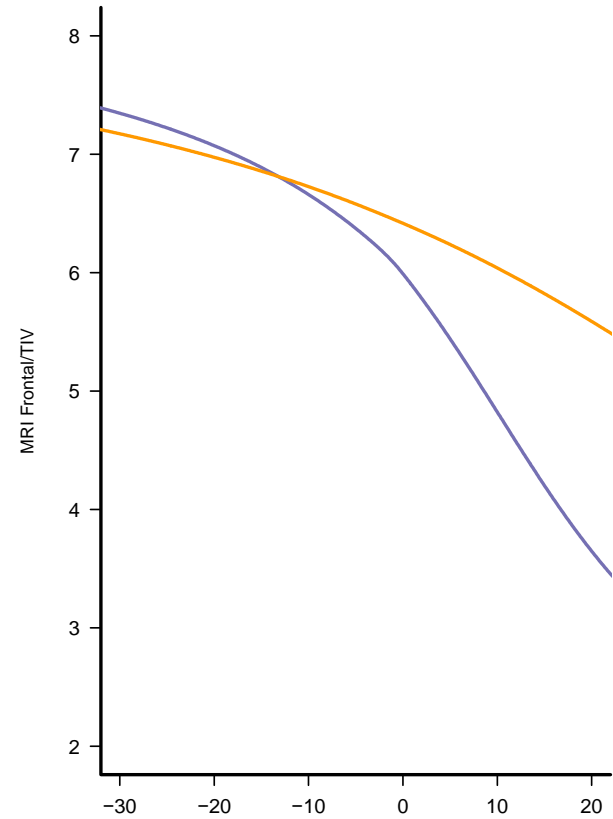
C9orf72



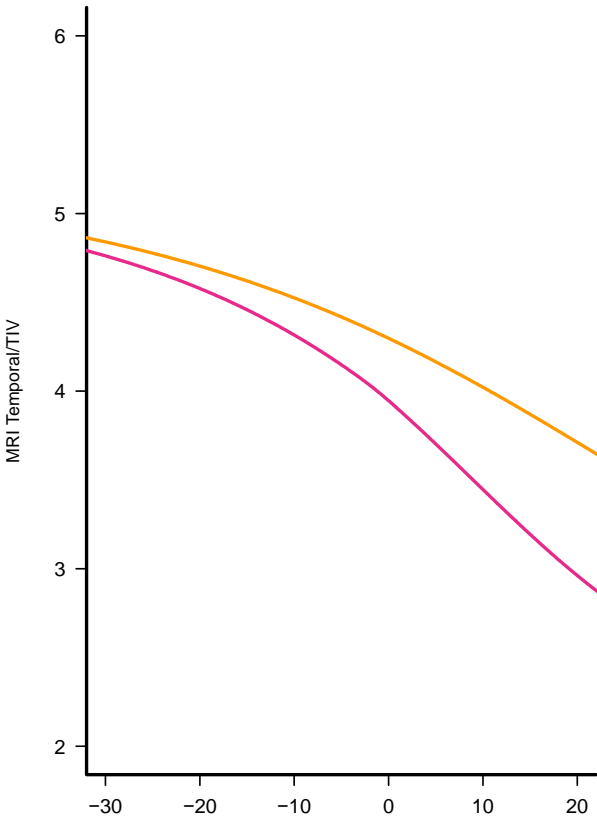
GRN



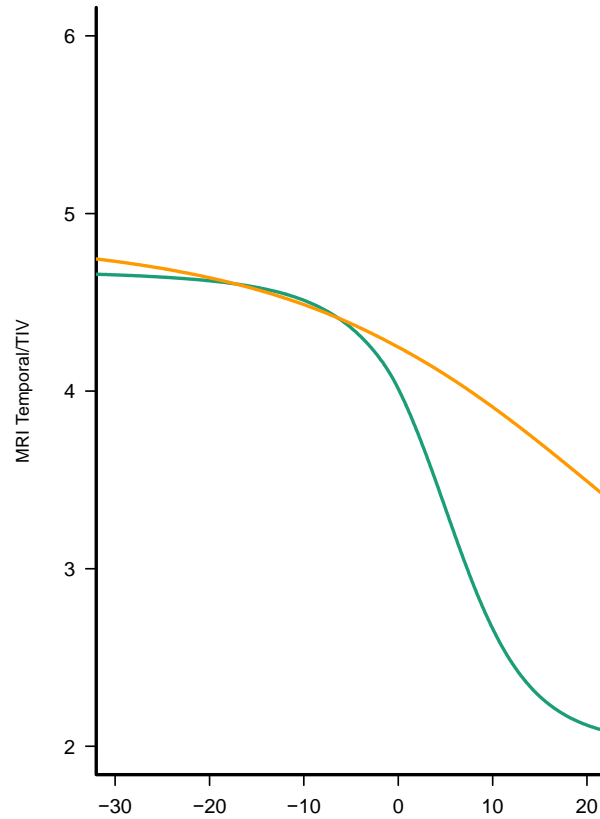
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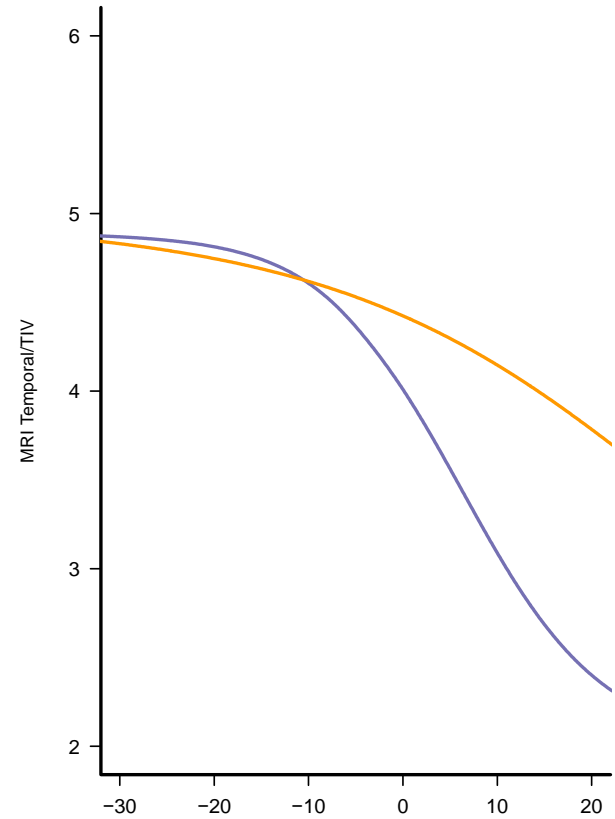
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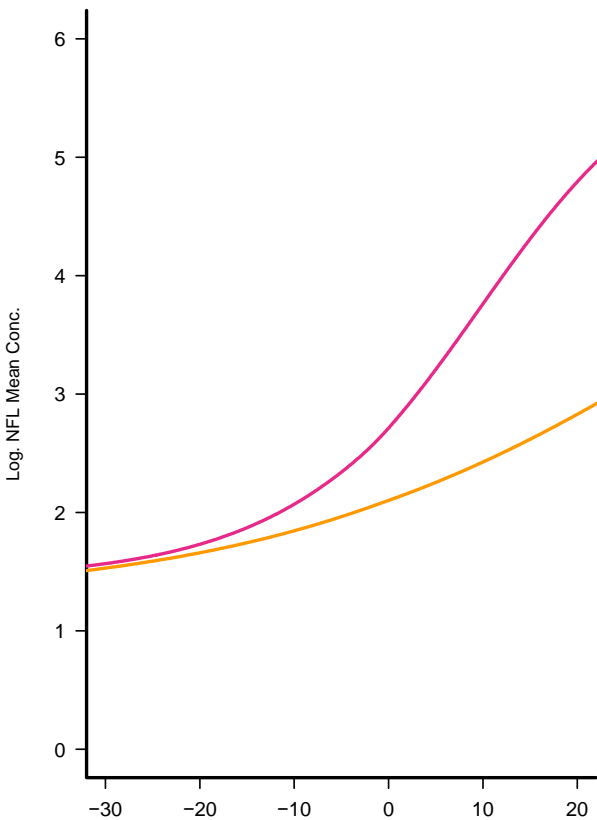
GRN



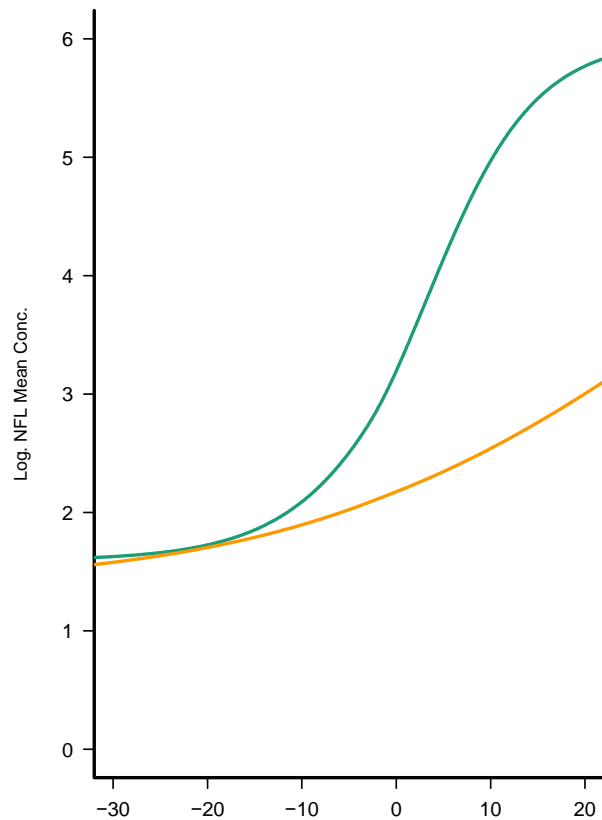
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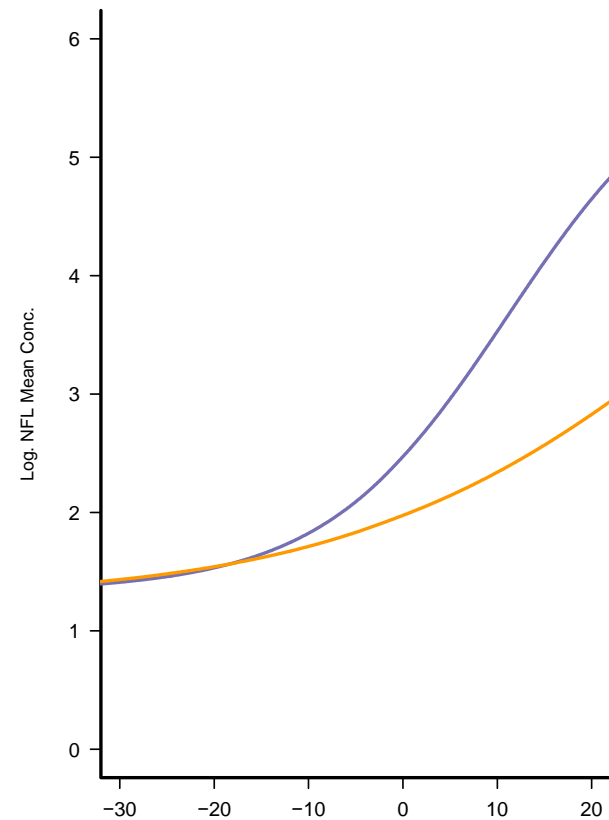
C9orf72



GRN

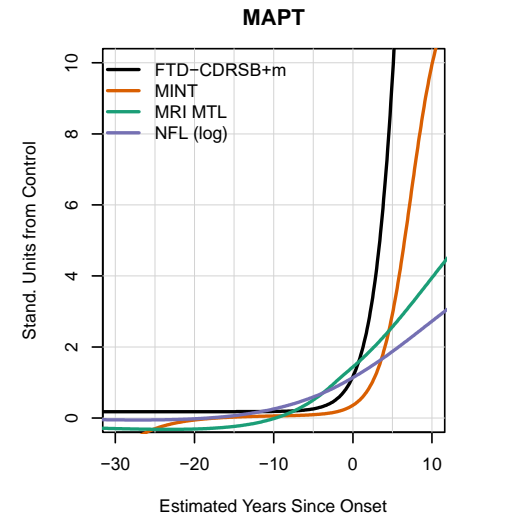
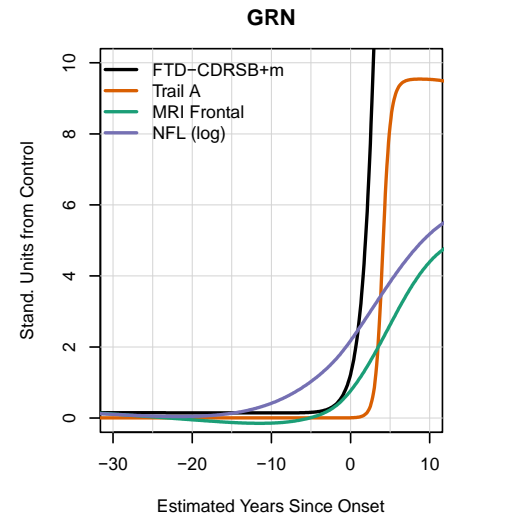
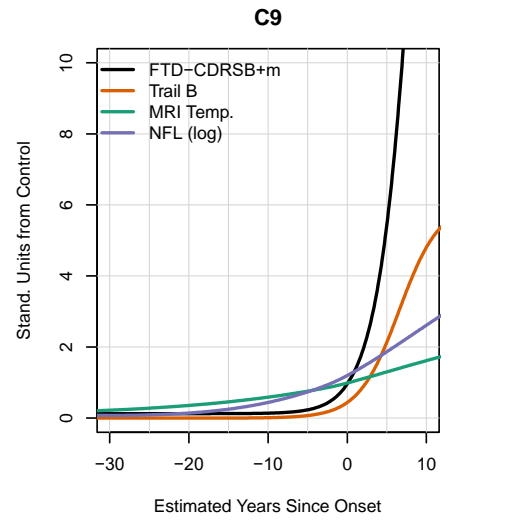
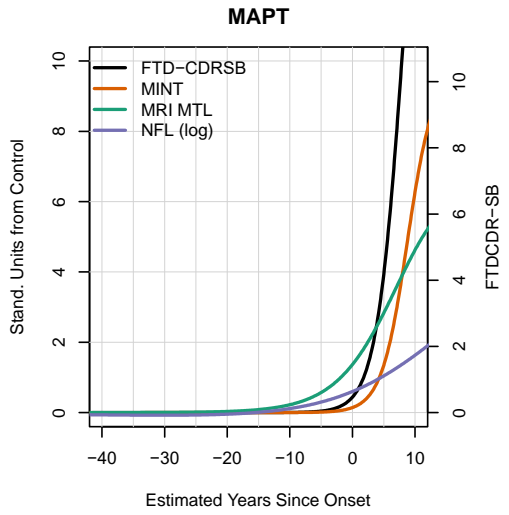
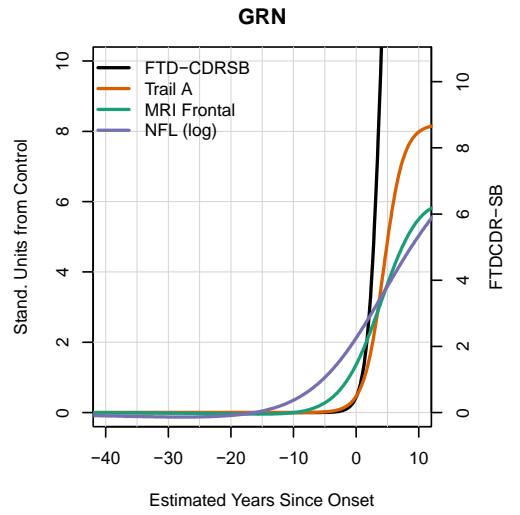
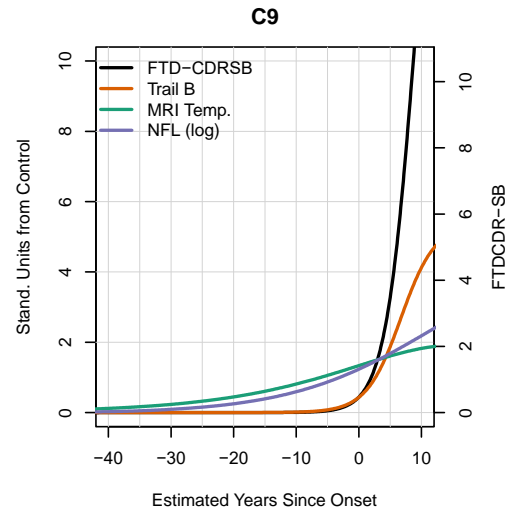


MAPT



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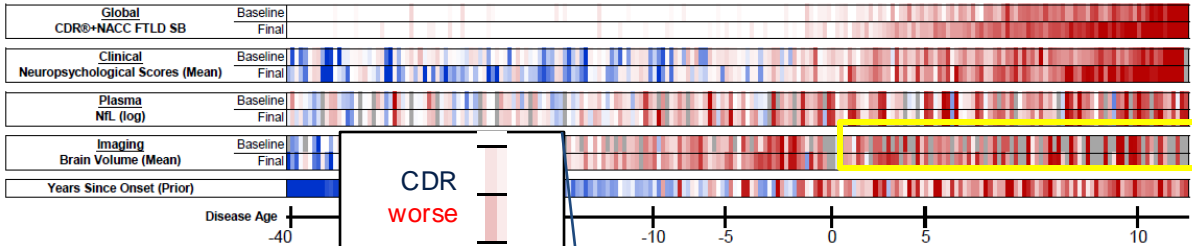
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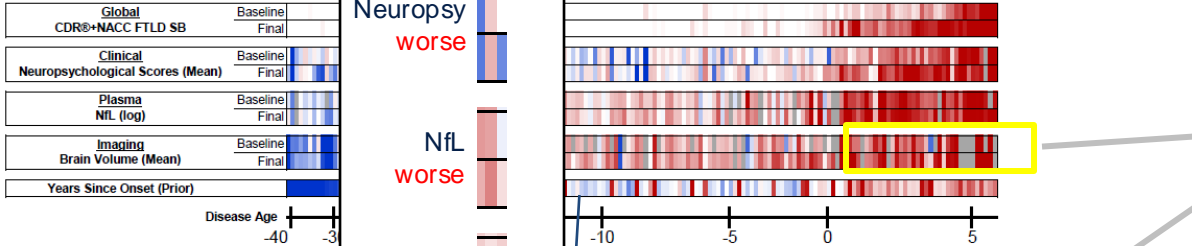
Current Results:
Change point + Model separately per mutation

Clinical validation

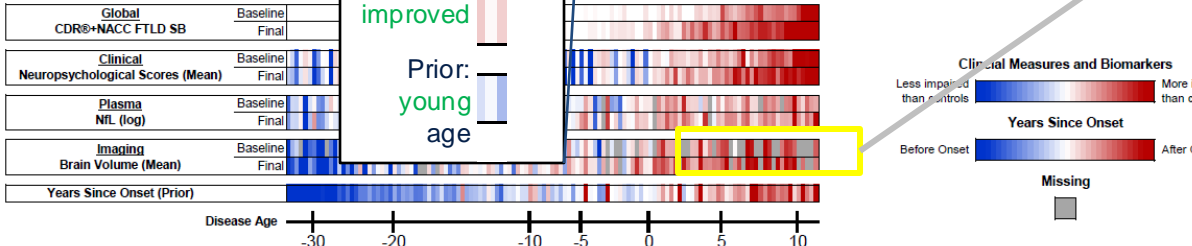
C9orf72



GRN



MAPT



CDR
worse

Neuropsych
worse

NfL
worse

MRI
improved

Prior:
young age

More missing MRI data in advanced disease



Comments

- Are we asking too much of data?
- Within vs. between-subject trajectories?
- Validating predictions?
- Improved determination and/or definition of onset?

Investigators

Brad Boeve	Jon Graff-Radford	Alex Pantelyat
Adam Boxer	Ian Grant	Belen Pascual
Howard Rosen	Murray Grossman	Hank Paulson
Liana Apostolova	Matt Hall	Peter Pressman
Brian Appleby	Robin Hsiung	Vijay Ramanan
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