

# Estimate the time-to-conversion for Alzheimer's Disease using neuroimaging-genomics multi-modal deep survival analysis

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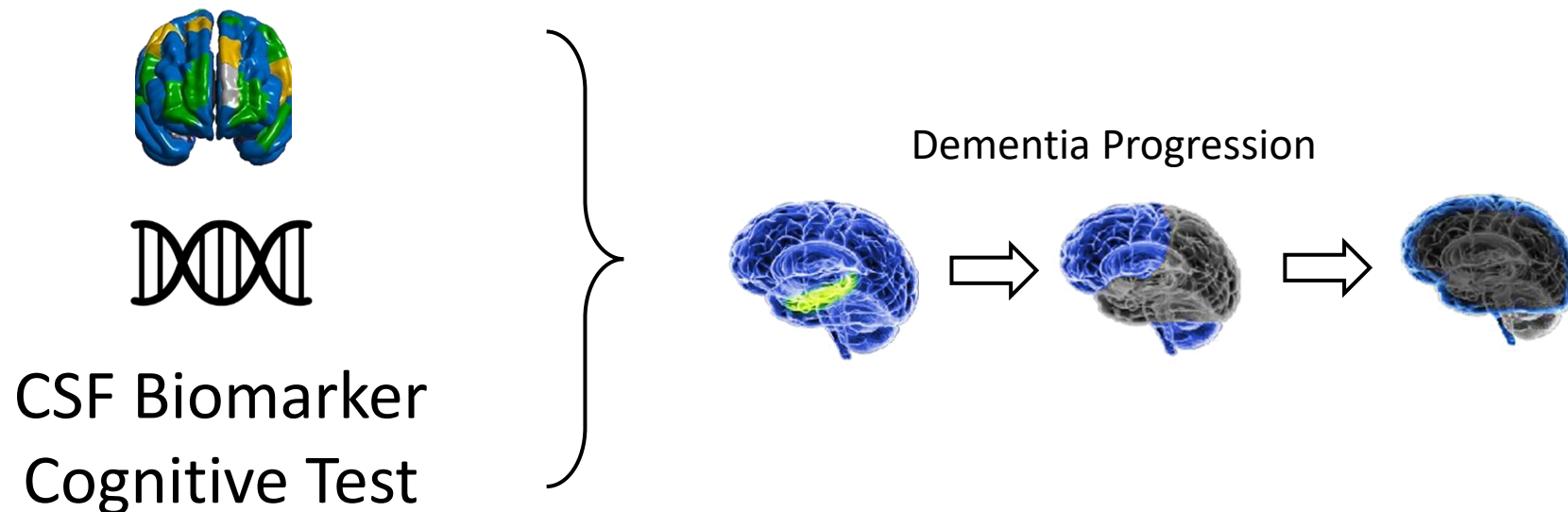
**Wake Forest University**  
**School of Medicine**

# Outlines

- Background / Aims
  - Predict time-to-conversion for dementia
  - Study the influence of different data modality on dementia conversion
- Study Design
  - Outcome measurement
  - Cohort Stratification
  - Independent variables
- Data processing / Feature extraction
  - Multi-type feature selection
  - Feature importance analysis – Permutation test
- Experimental setup
  - Deep Survival Model design
  - Evaluation
- Results
- Conclusion

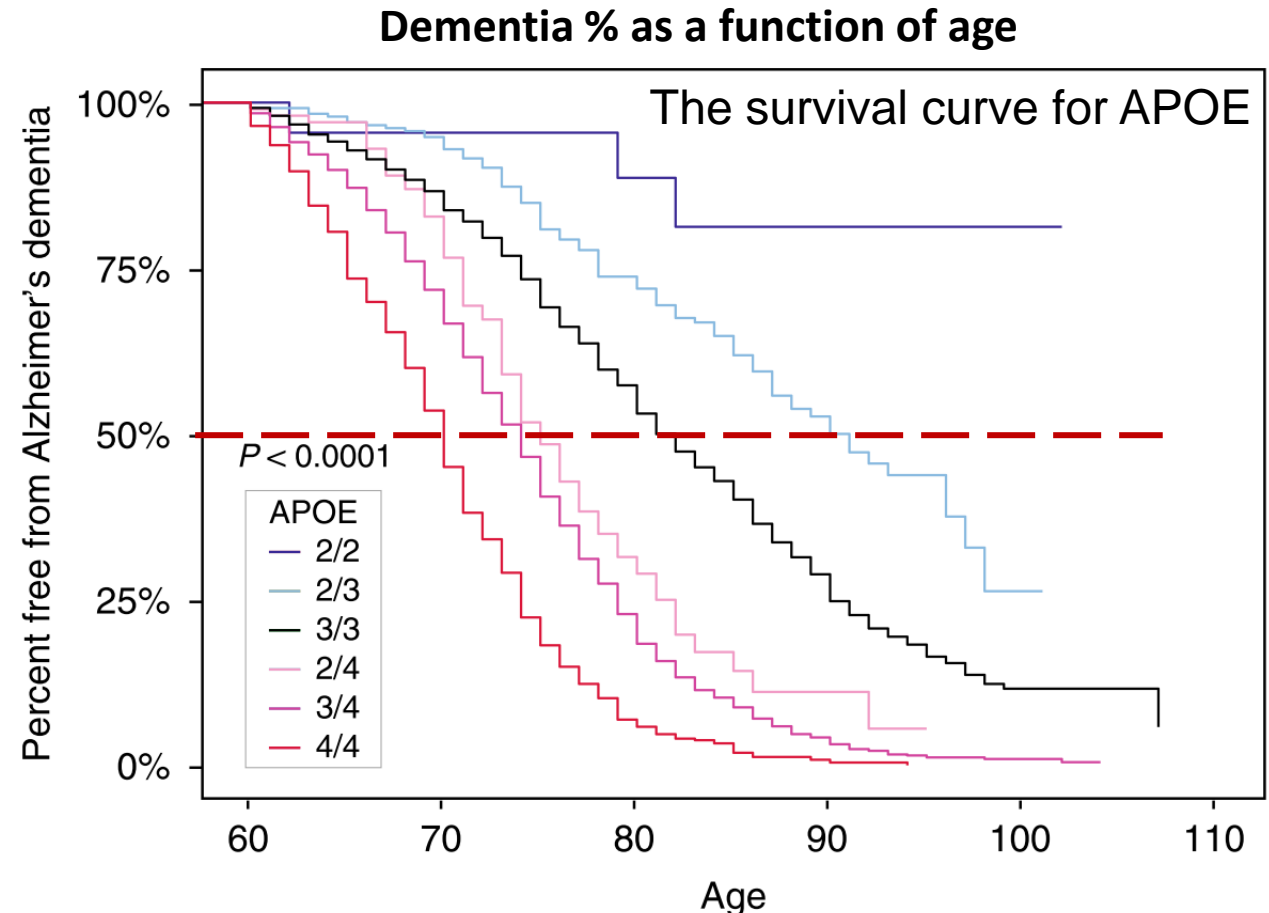
# Study Aims

- Predict time-to-conversion for Dementia of Alzheimer's Type (DAT)
  - Using multi-modal predictor, including:  
MRI, Genetics, Cerebrospinal Fluid (CSF) biomarker, Cognitive tests
- Study the influence of each data modality on disease prediction



## Predicting time-to-conversion - Survival analysis

- *Probability of dementia risk*
  - as a function of time
- Example:
  - APOE allele dementia risk



Reiman et al. 2020 Nature Communication

## Survival analysis - Sensoring

### Survival Analysis:

- Analysis of the time an individual will experience an event of interest

### Event of Interest

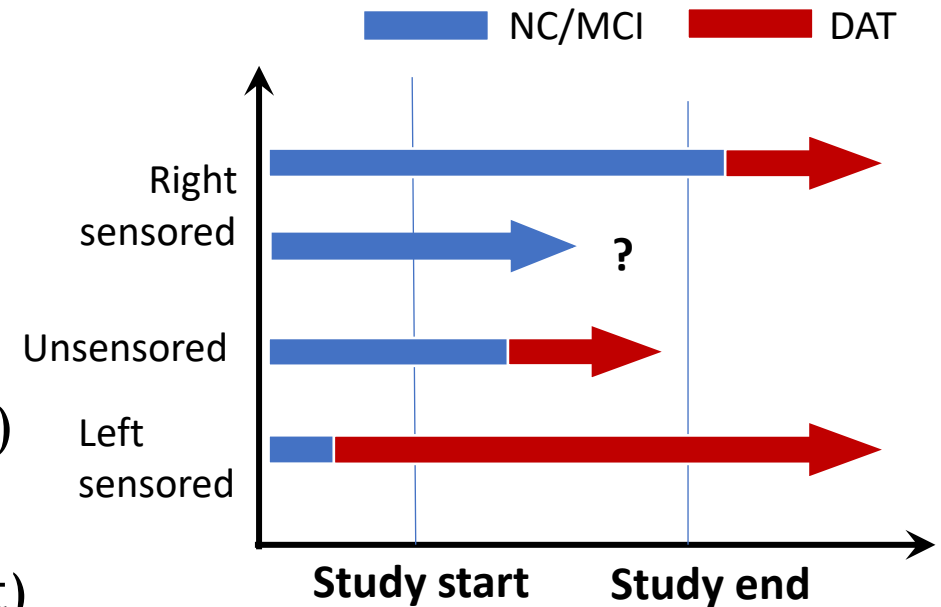
- Dementia onset (DAT diagnosis confirmation)

### Left sensor

- Event happens before the first clinical visit (baseline)

### Right Sensor

- Event happens after last clinical visit (final timepoint)



# Study Design – Outcome Measurements

## Predicting time-to-conversion - Survival analysis

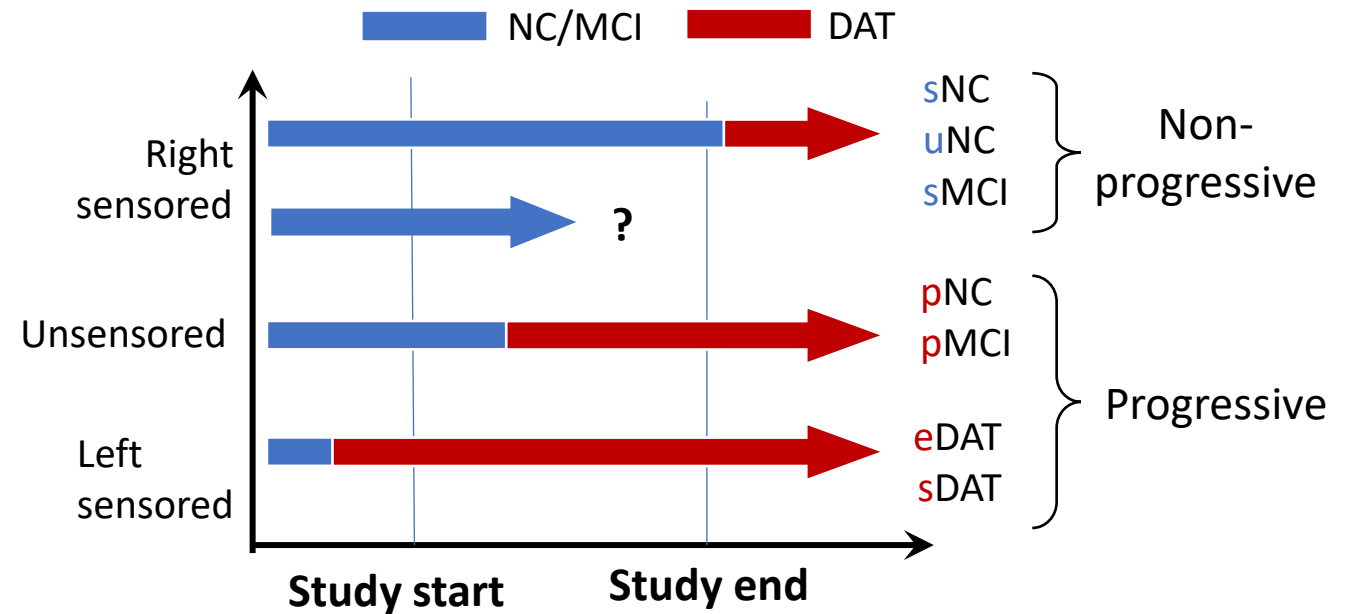
### Ground truth labels

#### 1. Event indicator:

- 0 = Non-progressive (right censored)
- 1 = Progressive

#### 2. Duration:

- **Non-progressive:** Duration between the first and last visit
- **Progressive:** Duration between first visit and DAT diagnosis confirmation



# Data - Study Participants

- Training/evaluation cohort: ADNI-1

Subject grouping

	Group name	Clinical progression	n
<b>Non- progressive</b>	sNC: stable NC	NC → NC	109
	uNC: unstable NC	NC → MCI	22
	sMCI: stable MCI	MCI → MCI	101
<b>Progressive</b>	pNC: progressive NC	NC → MCI → DAT	14
	pMCI: progressive MCI	MCI → DAT	155

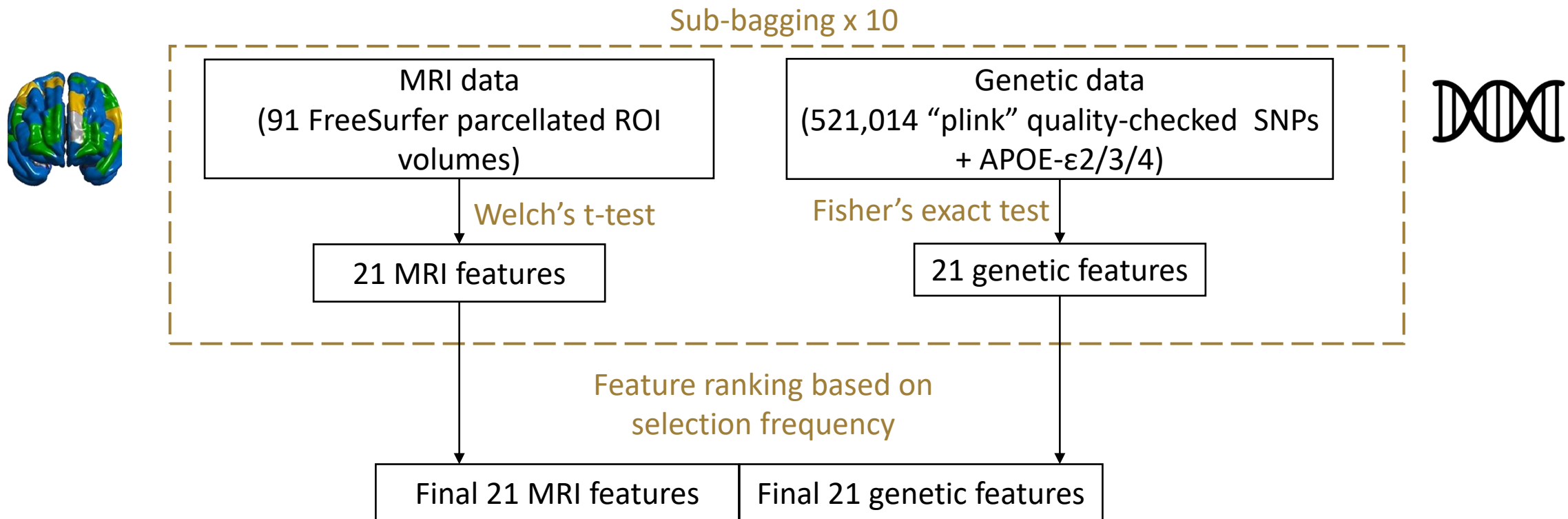
Stratified Train/Valid/Test split

Groups	Training set	Validation set	Testing set	Total
sNC	70	17	22	109
uNC	14	4	4	22
pNC	9	2	3	14
sMCI	65	16	20	101
pMCI	99	25	31	155
Total	257	64	80	401

Only baseline data were used for training

# Data – Input Features

## Neuroimage & Genomic Feature Selection (Within Training Data)





# Data – Input Features

## Data modalities

- **MRI:** 21 ROI volume (Z-standardized) (21 features)
- **Genetic:** 18 SNPs + 3 APOE alleles (21 features)
- **DTC:** 21 features
  - Demographic (4 features)
  - Cognitive Tests (11 features)
  - CSF (7 features)
- **Only baseline data was used for training**

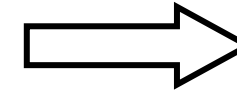
MRI features	Genetic features	DTC features / #missing data
Amygdala - Left	APOE-ε2	AB40 (CSF) / 41
Amygdala - Right	APOE-ε3	AB42 (CSF) / 40
Entorhinal - Left	APOE-ε4	AB (CSF) / 176
Entorhinal - Right	rs524410	ptau (CSF) / 176
Fusiform - Left	rs746947	ptau/AB (CSF) / 176
Fusiform - Right	rs1010616	Tau (CSF) / 176
Hippocampus - Left	rs1864036	tau/AB (CSF) / 176
Hippocampus - Right	rs2085925	Age (DEM) / 0
Inferior-parietal - Left	rs2405940	Sex (DEM) / 0
Inferior-parietal - Right	rs2883782	Education (DEM) / 0
Inferior-temporal - Left	rs4953672	Marital status (DEM) / 0
Inferior-temporal - Right	rs5918417	ADAS11 (TST) / 0
Inferior-lateral-ventricle - Left	rs5918419	ADAS13 (TST) / 1
Inferior-lateral-ventricle - Right	rs6116375	CDRSB (TST) / 0
Middle-temporal - Left	rs6773506	FAQ (TST) / 2
Middle-temporal - Right	rs7627954	LDELTOTAL (TST) / 0
Parahippocampal - Left	rs10465385	MMSE (TST) / 0
Parahippocampal - Right	rs10510985	RAVLT-forgetting (TST) / 1
Precuneus - Left	rs10924809	RAVLT-immediate (TST) / 1
Precuneus - Right	rs12522102	RAVLT-learning (TST) / 1
Supramarginal - Left	rs17197559	RAVLT-%forgetting (TST) / 2

# Method - Deep Survival Model

## Cox regression model

- Hazard function:  $h(t|x) = h_0(t) \exp[g(x)]$

$$g(x) = \beta^T x$$

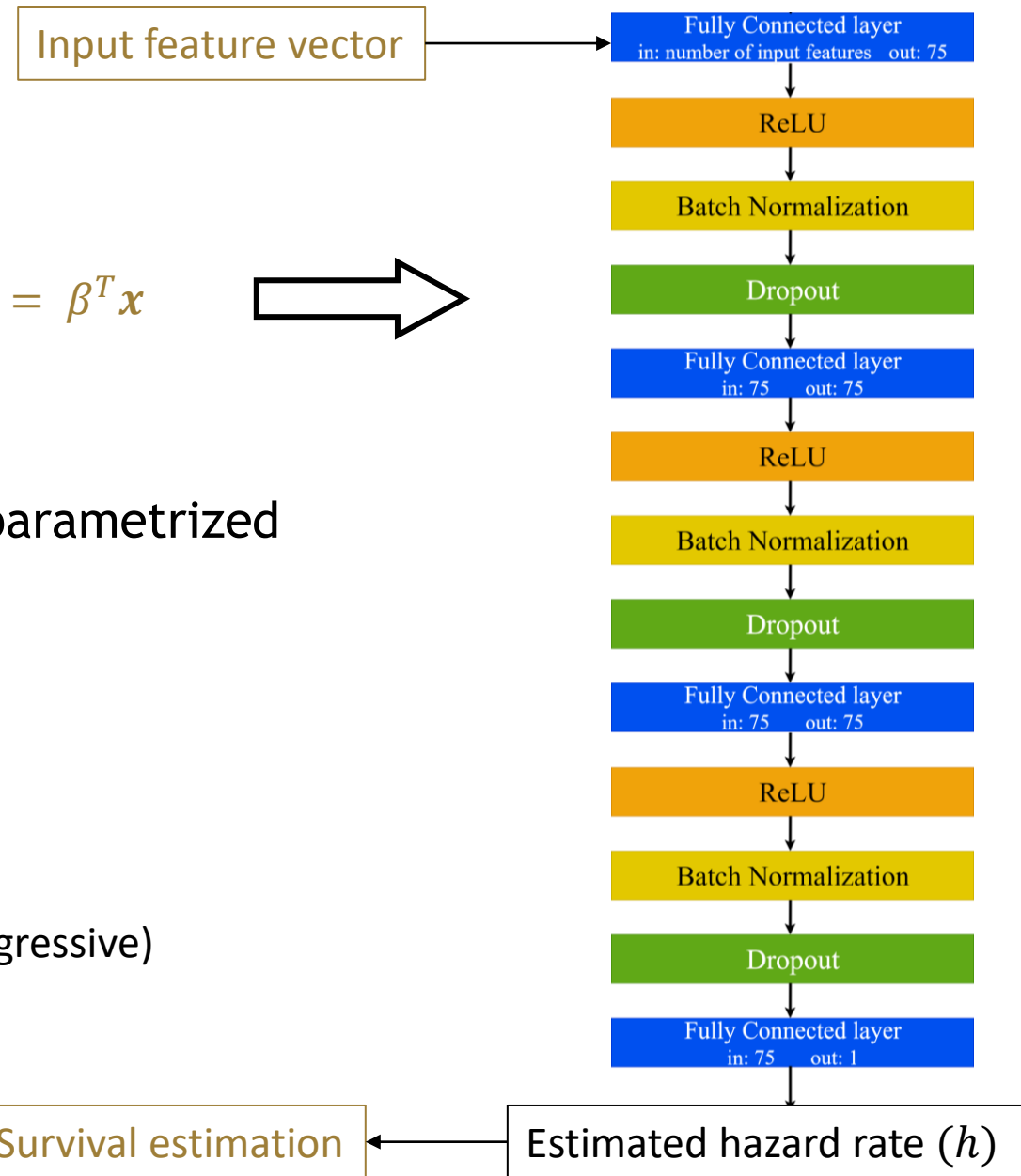


## Deep Survival Model

- a non-linear version of the Cox model where  $g(x)$  parametrized by a neural network (Multi-Layer-Perceptron)

## Loss function

- $loss = \sum_i D_i \log(\sum_{j \in R_i} \exp[g(x_j) - g(x_i)])$ 
  - $D_i$ : event indicator for subject  $i$  (1=progressive, 0=non-progressive)
  - $R_i$ : set of all individuals at risk



## 6 Feature sets combination

1. Genetic data (GEN; 21 features)
  2. MRI data (MRI; 21 features)
  3. Demographic + Cognitive Test + CSF (DTC; 21 features)
- 
4. MRI and genetic data (GEN+MRI; 42 features)
  5. Genetic and DTC data (GEN+DTC; 42 features)
  6. MRI and DTC data (MRI+DTC; 42 features)
  7. All features (GEN+MRI+ DTC; 63 features)

# Evaluation Metrics 1

## Integrated Brier Score (IBS)

- The average squared **distances** between the observed ( $y_i$ ) and predicted survival probability ( $\hat{p}_i$ )

$$\bullet BS = \frac{1}{N} \sum_i (y_i - \hat{p}_i)^2$$

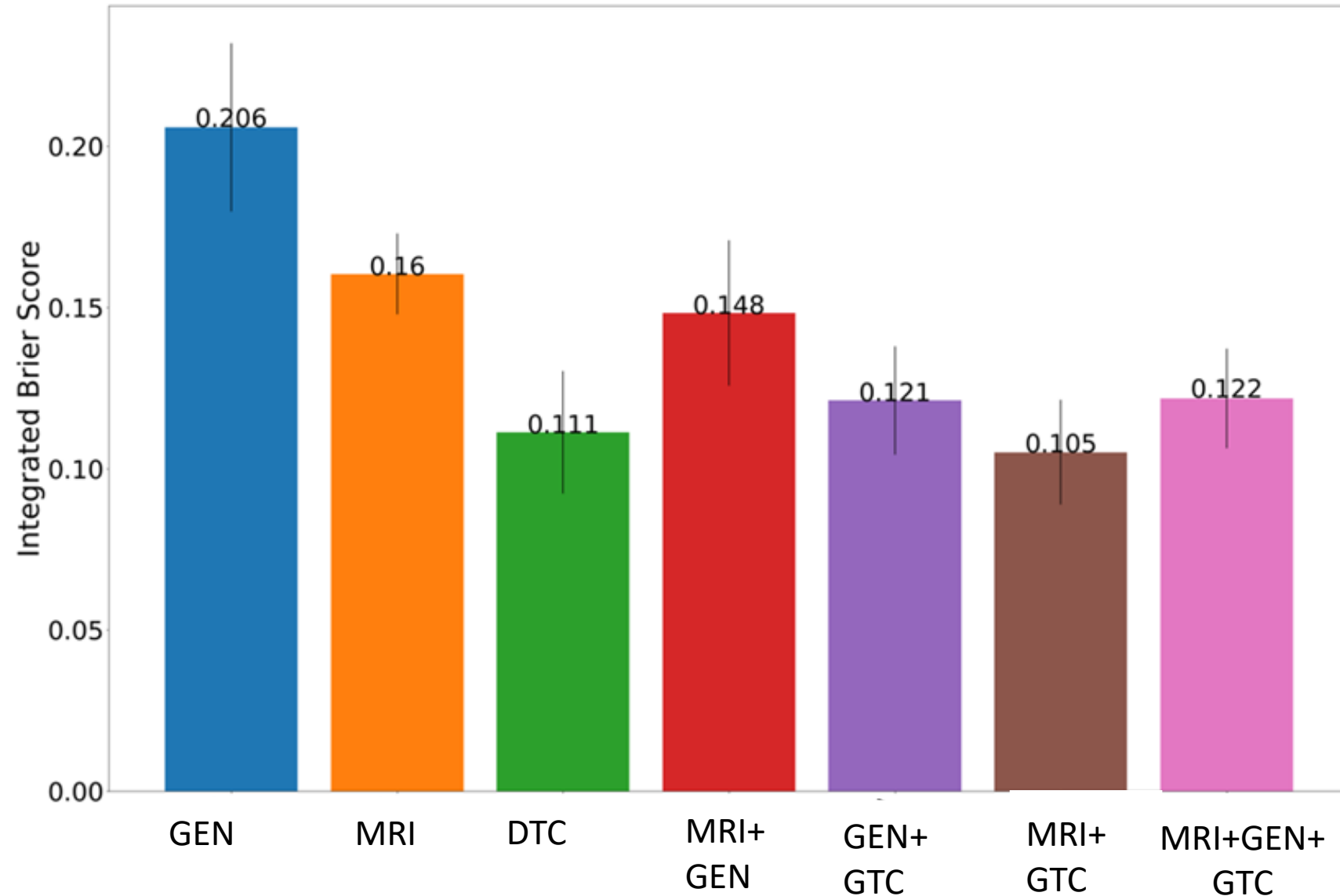
- **0 < IBS < 1** (the smaller the better)

# Evaluation Metrics 1 Results

IBS (the smaller the better)

## Same conclusion:

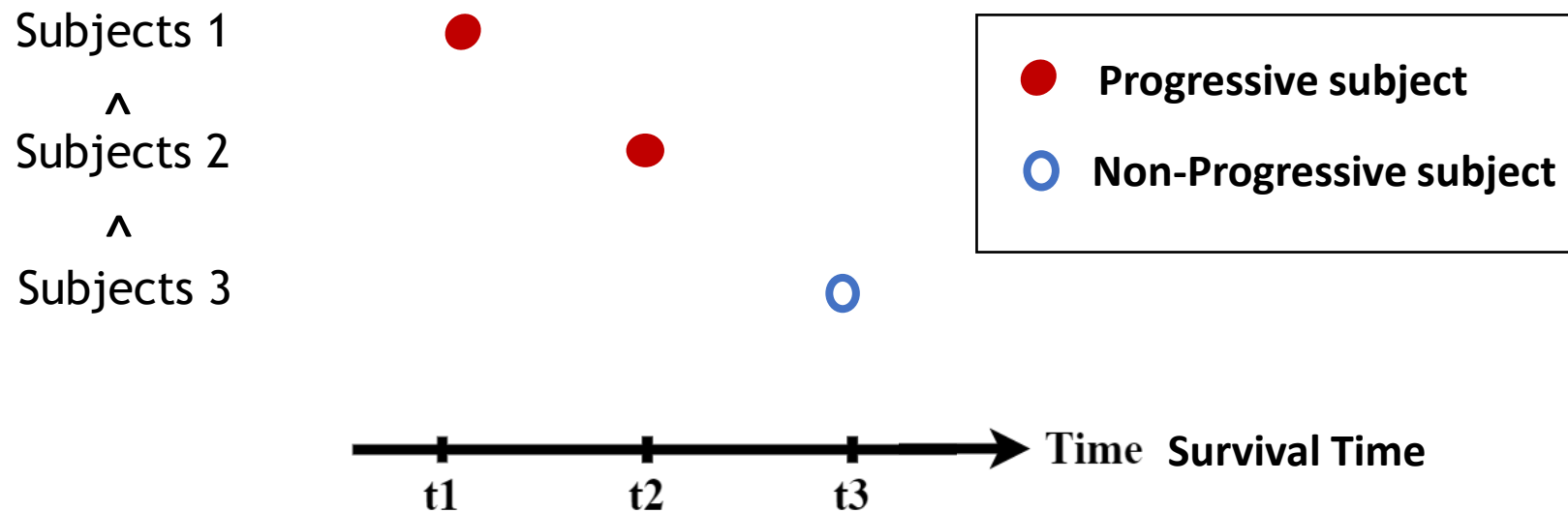
- Combining **MRI** and **GEN** (**MRI+GEN**) improves the performance
- **DTC** works best amongst single modalities
- **MRI + GTC** improved GTC (not statistical significant)



# Evaluation Metrics 2

## Time-dependent Concordance Index ( $C^{td}$ -index)

- Compares the order of predicted survival times with true survival times for a random pair of subjects

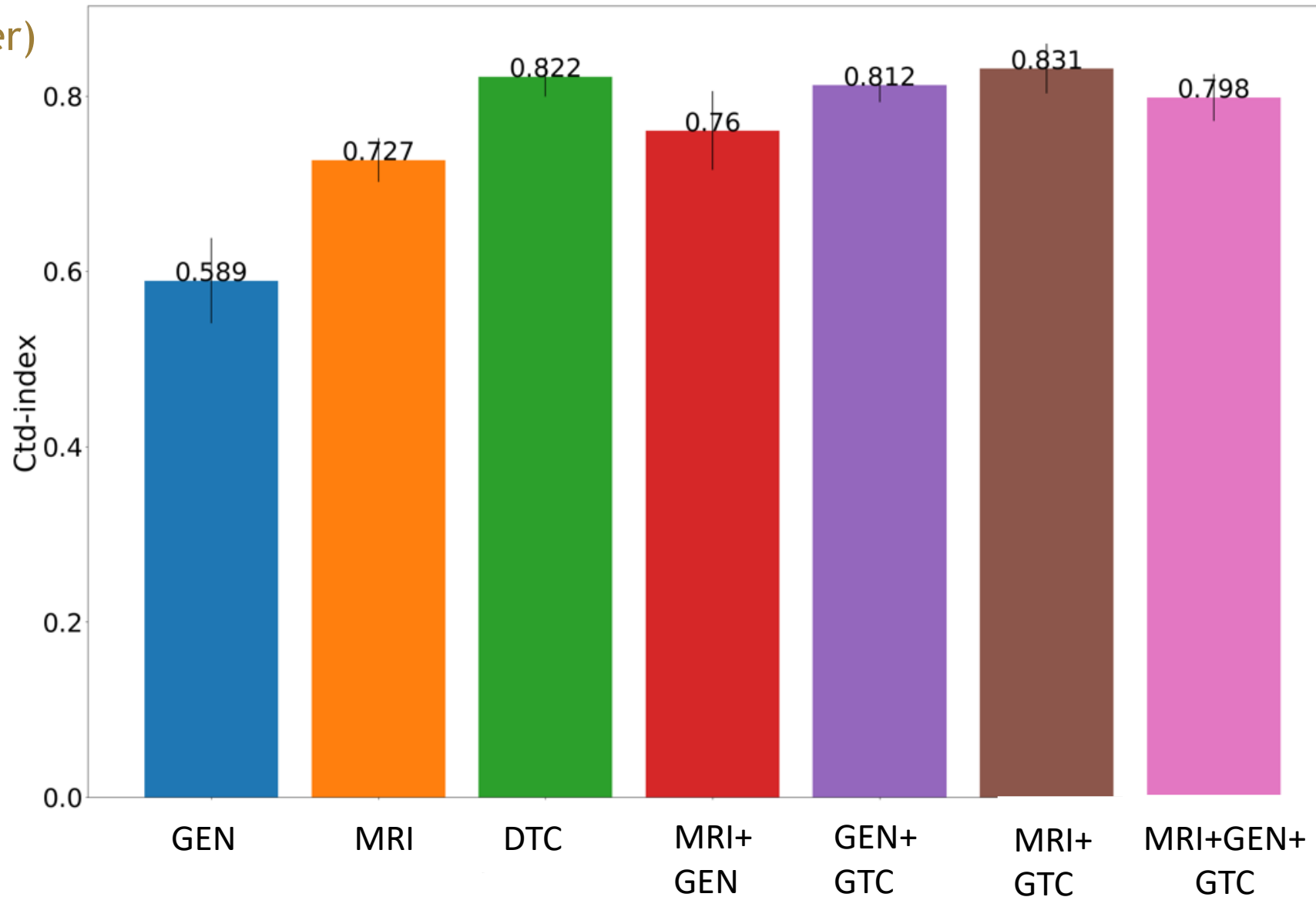


- $0 < C^{td}\text{-index} < 1$  (the bigger the better)

# Evaluation Metrics 1 Results

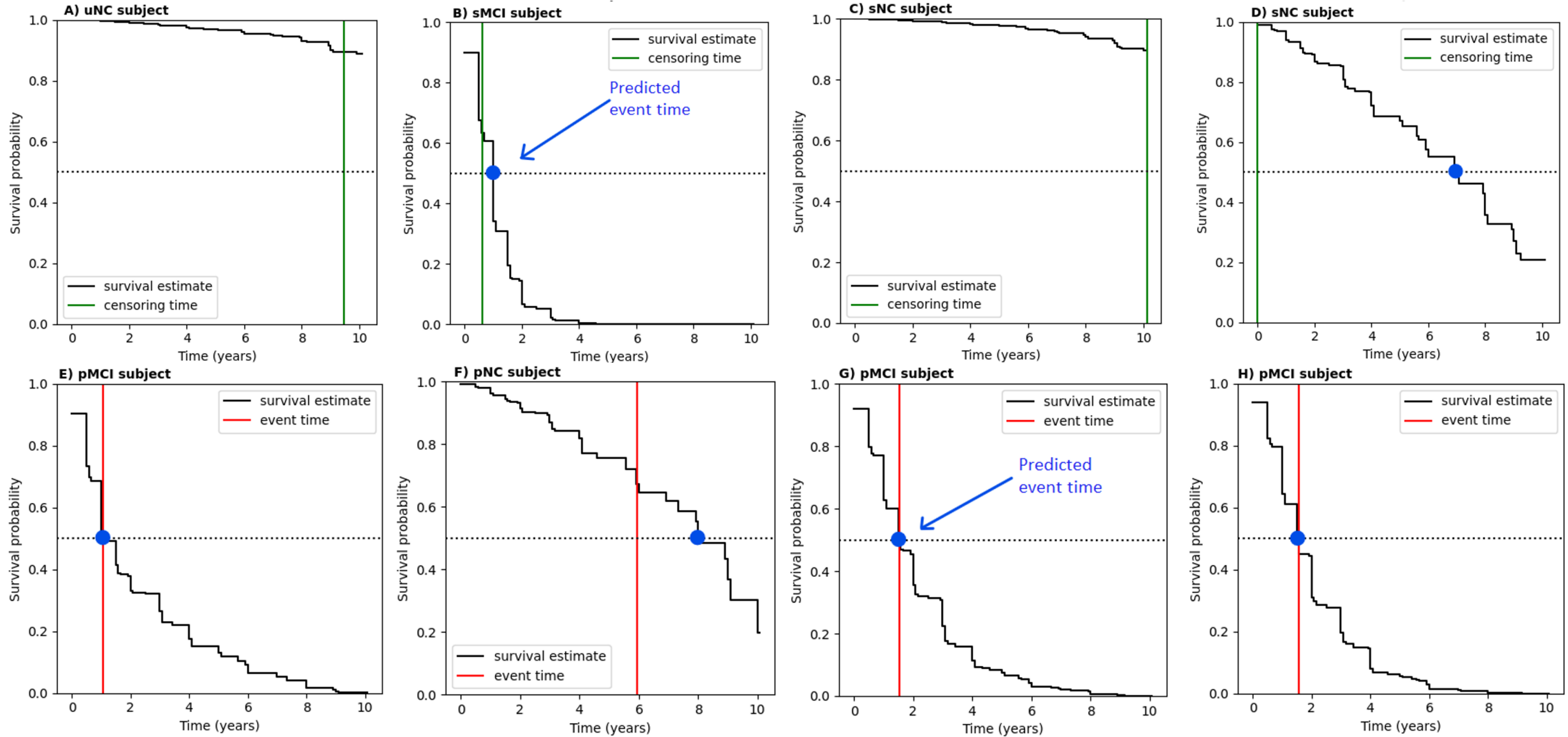
**C<sup>td</sup>-index** (the bigger the better)

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# Results

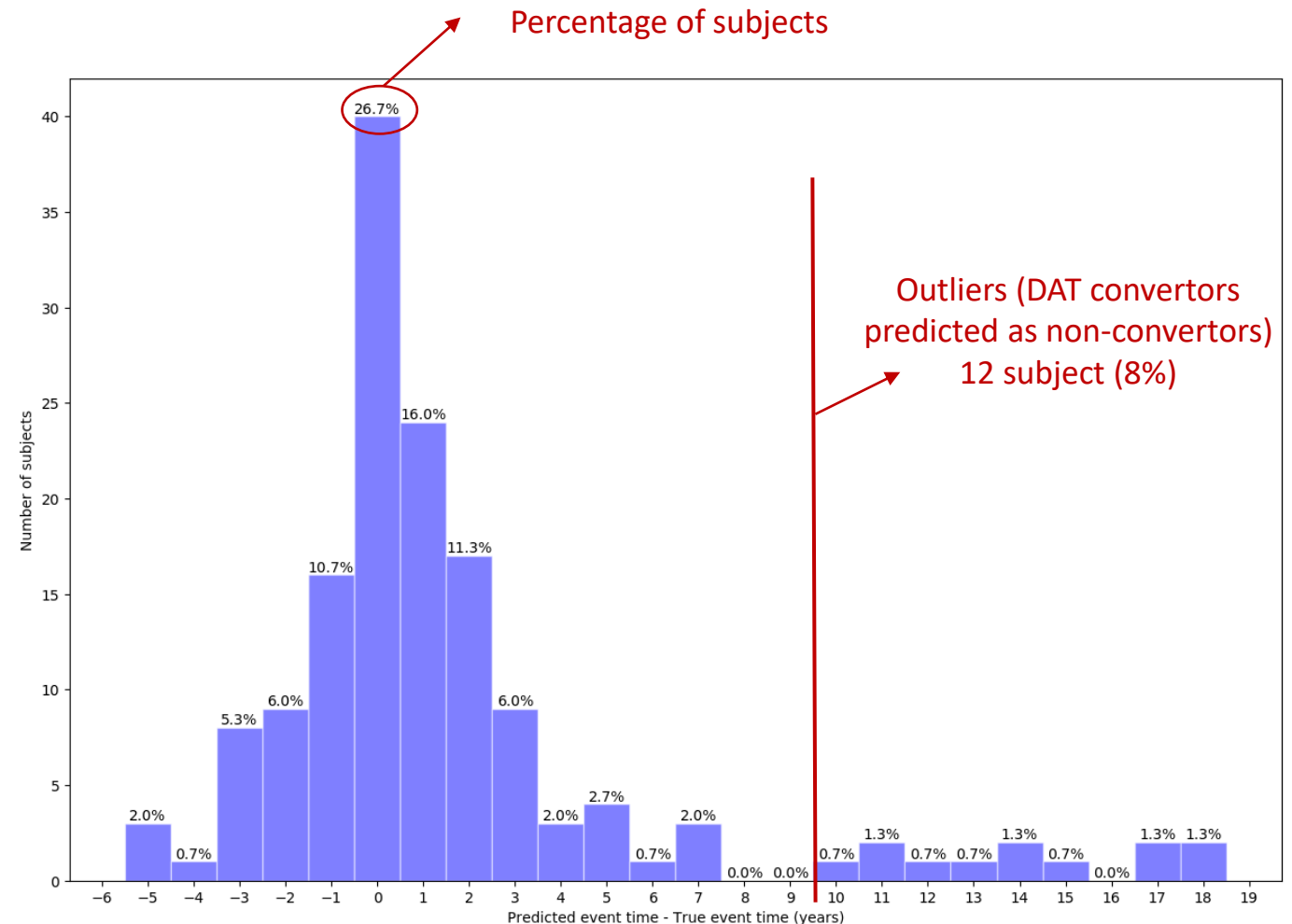
## Predicted vs. true time-to-conversion difference





## Predicted vs. true time-to-conversion difference

- **Predicted time:** the time a subject's survival probability reaches 50%
  - If this doesn't happen:  
Predicted time = 20 years after initial visit
- More than half of the subjects (80/150 or **53.4%**) had a time difference of less than 1.5 years
- The predicted event time was earlier than the actual event time for 37 subjects (**24.7%**)



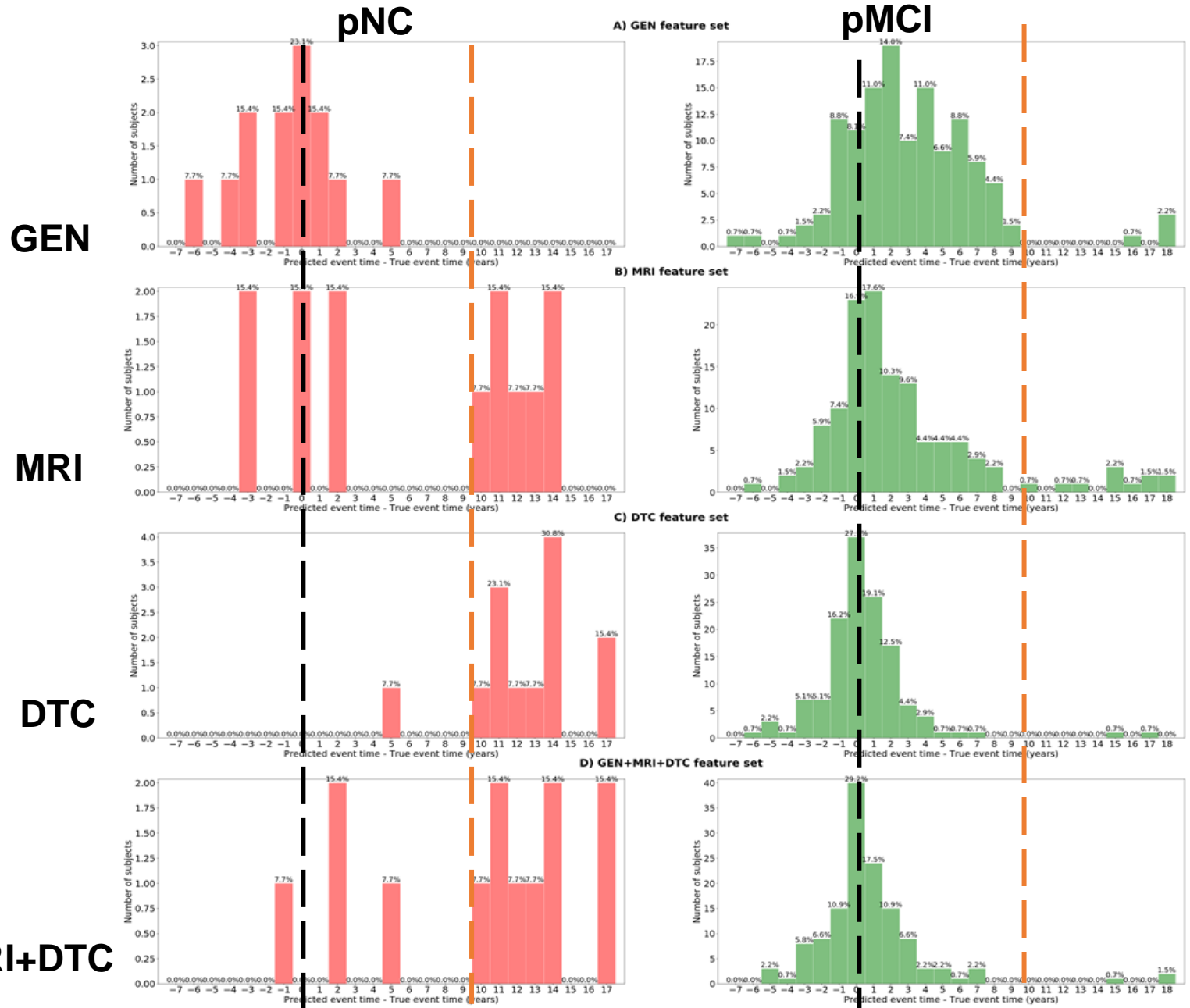
Histogram of the differences between the predicted and true event times for progressive subjects (150 subjects) using the GEN+MRI+DTC feature set

# Results

## Feature type comparison

- Dementia onset time prediction
- DTC
  - Demographic
  - Cognitive test
  - Cerebral Spinal Fluid Biomarker

GEN+MRI+DTC



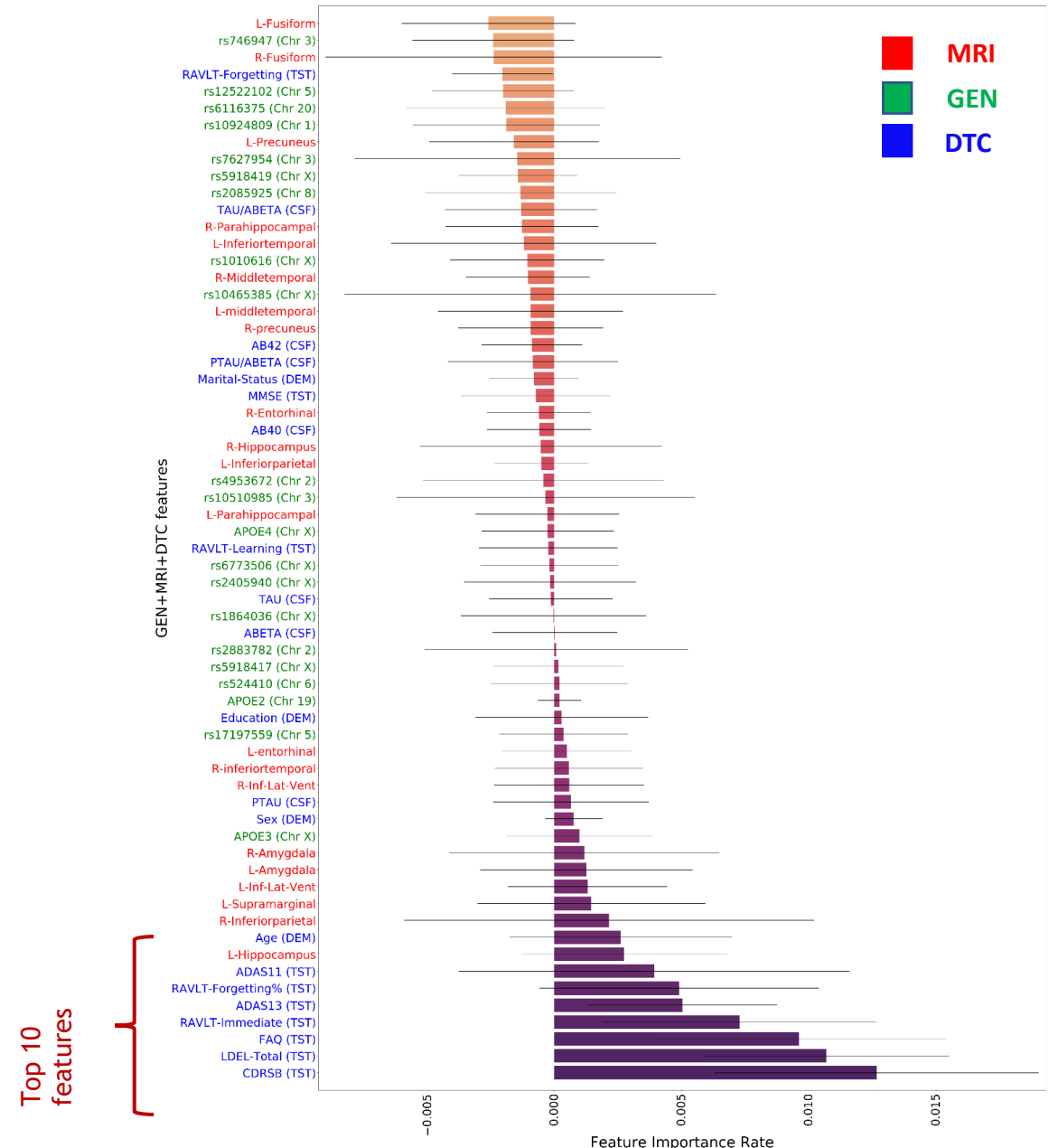
## Feature Importance Analysis

- Explain and compare the contributions of each feature toward the time-to-conversion prediction
- Determine feature contributions through the permutation importance analysis
- Random shuffling of each feature

# Results

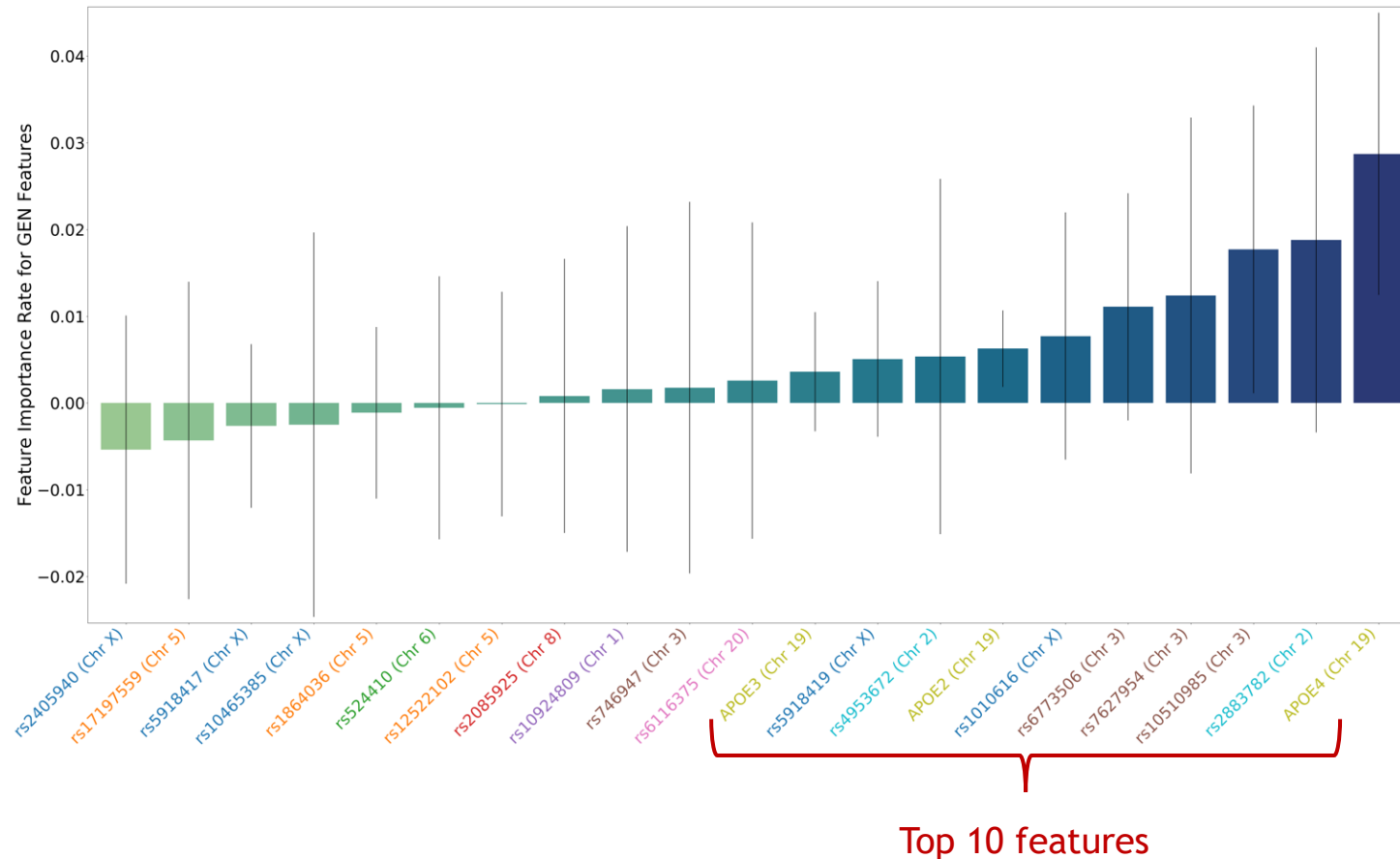
## Feature importance: ALL

- 27/36 features had a positive effect on performance
  - 6 GEN
  - 9 MRI
  - 12 DTC
- 8 of the top 10 features were from DTC including 7 TST features and 1 DEM
- The most important feature was CDRSB (Clinical Dementia Rating Scale)



# Results

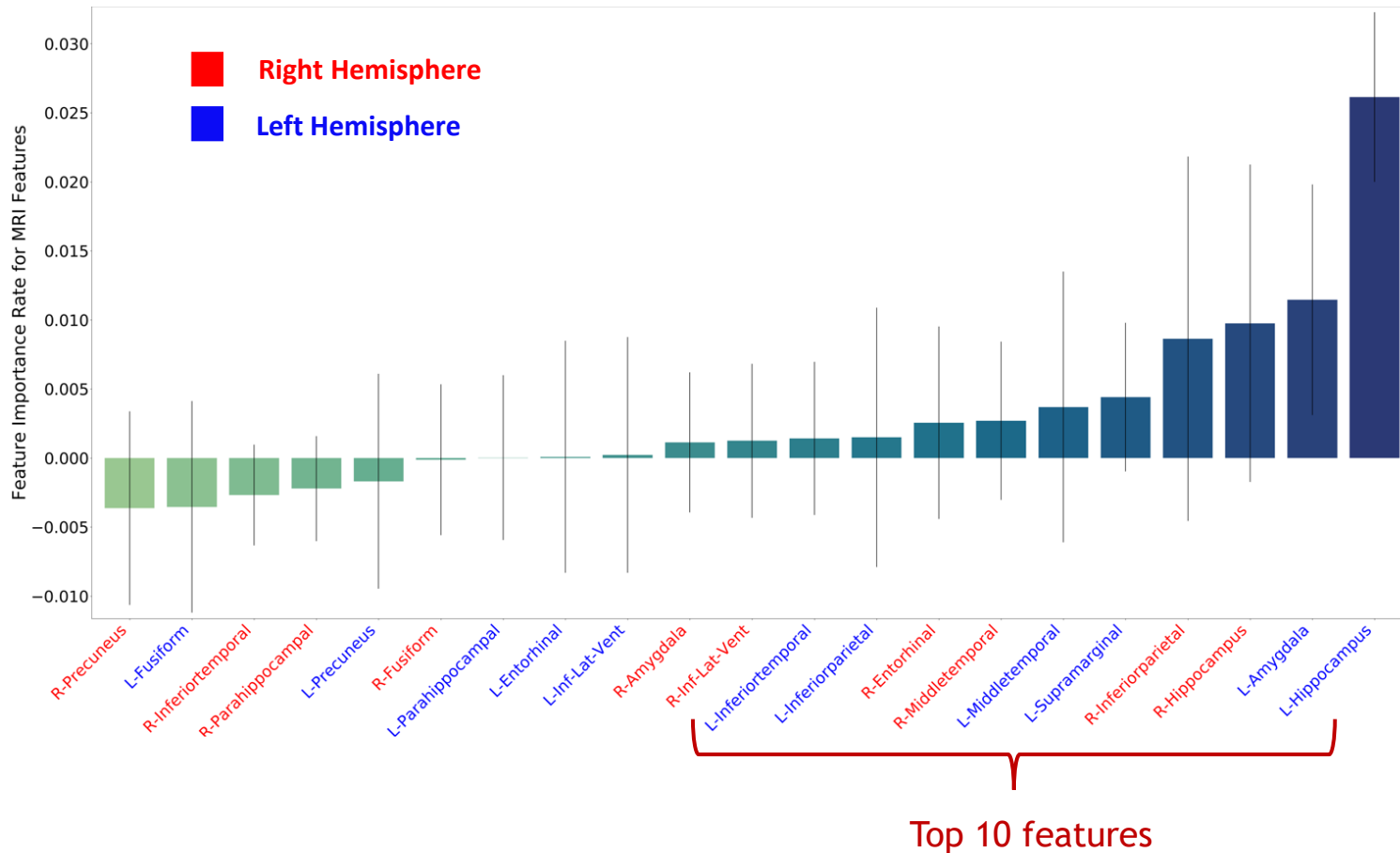
## Feature importance: GEN



- **14/21 features** had a positive effect on performance
- The most important feature was **APOE- $\epsilon$ 4**
- Top 10 most important features were from **chromosomes 2, 3, 19, and X**

# Results

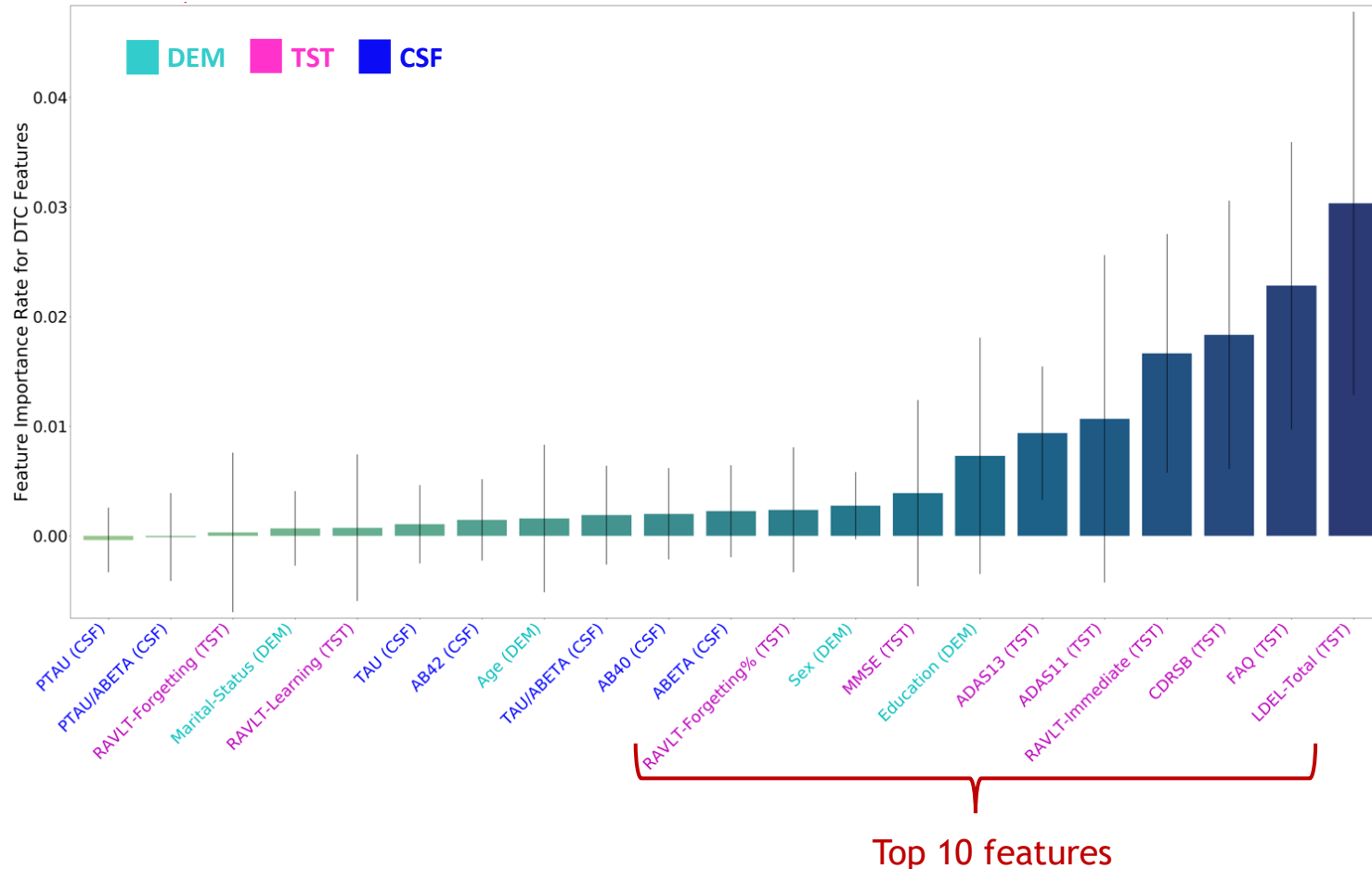
## Feature importance: MRI



- 15/21 features had a positive effect on performance
- The most important feature was **L-Hippocampus**
- Other important features include: **L-Amygdala, R-Hippocampus, and R-inferiorparietal**

# Results

## Feature importance: DTC



- 19/21 features had a positive effect on performance
- 8 of the top 10 features were from **cognitive tests (TST)** and the other 2 were **demographic (DEM)** features
- The most important feature was Delayed recall variable from the Logical memory test (**LDEL-Total**)

# Conclusions

- Modality comparison for Alzheimer's disease time-to-conversion prediction estimation for subjects at different stages of the disease
  - Genomic factor is better at the prodromal stage (pNC)
  - Neuroimage + CSF is better at early disease stage (pMCI)
- Novel AD-related genomic factors are discovered Explainable AI to explore feature importance



# Acknowledgement



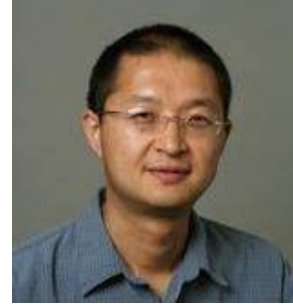
Prof. Suzanne Craft



Prof. Metin Gurcan



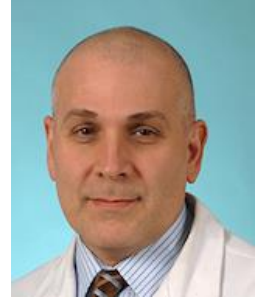
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Prof. Jiguo Cao



Prof. James E. Galvin



Dr. Samuel Lockhart



Dr. Da Ma



Dr. Sieun Lee



Dr. Karteek Popuri



Ms. Ghazal Mirab



Dr. Cedric Beaulac



Dr. Hyunwoo Lee



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Thank you!

Q&A