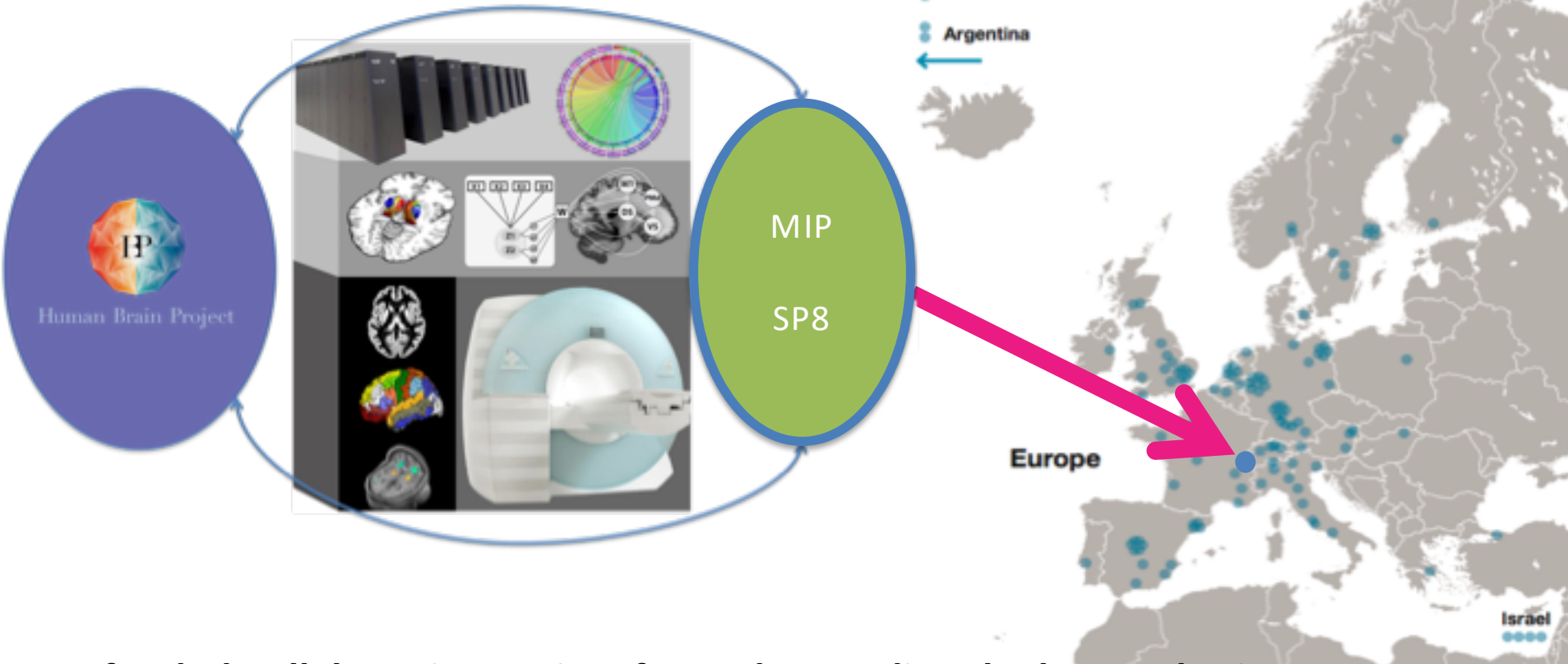




HUMAN BRAIN PROJECT

MEDICAL INFORMATICS PLATFORM



EU funded Collaborative project for understanding the human brain

25 Countries

400 Researchers

2013

10 Years

Richard FRACKOWIAK



THE MEDICAL COMPONENT OF THE HBP



Alzheimer's disease: **20 per cent** beyond the age of 80; dependent within 3-5 years of onset.



Depression: the second most common condition in the world (WHO): **6 per cent** of the population in the Western world.



Cerebral vascular accidents: first cause of adult motor disability. **75 per cent** suffer residual disability.



Parkinson's disease: second cause of motor disability. Affects **0.2 per cent** of the population.



Multiple sclerosis: mainly young people with dependency in **30 per cent**.

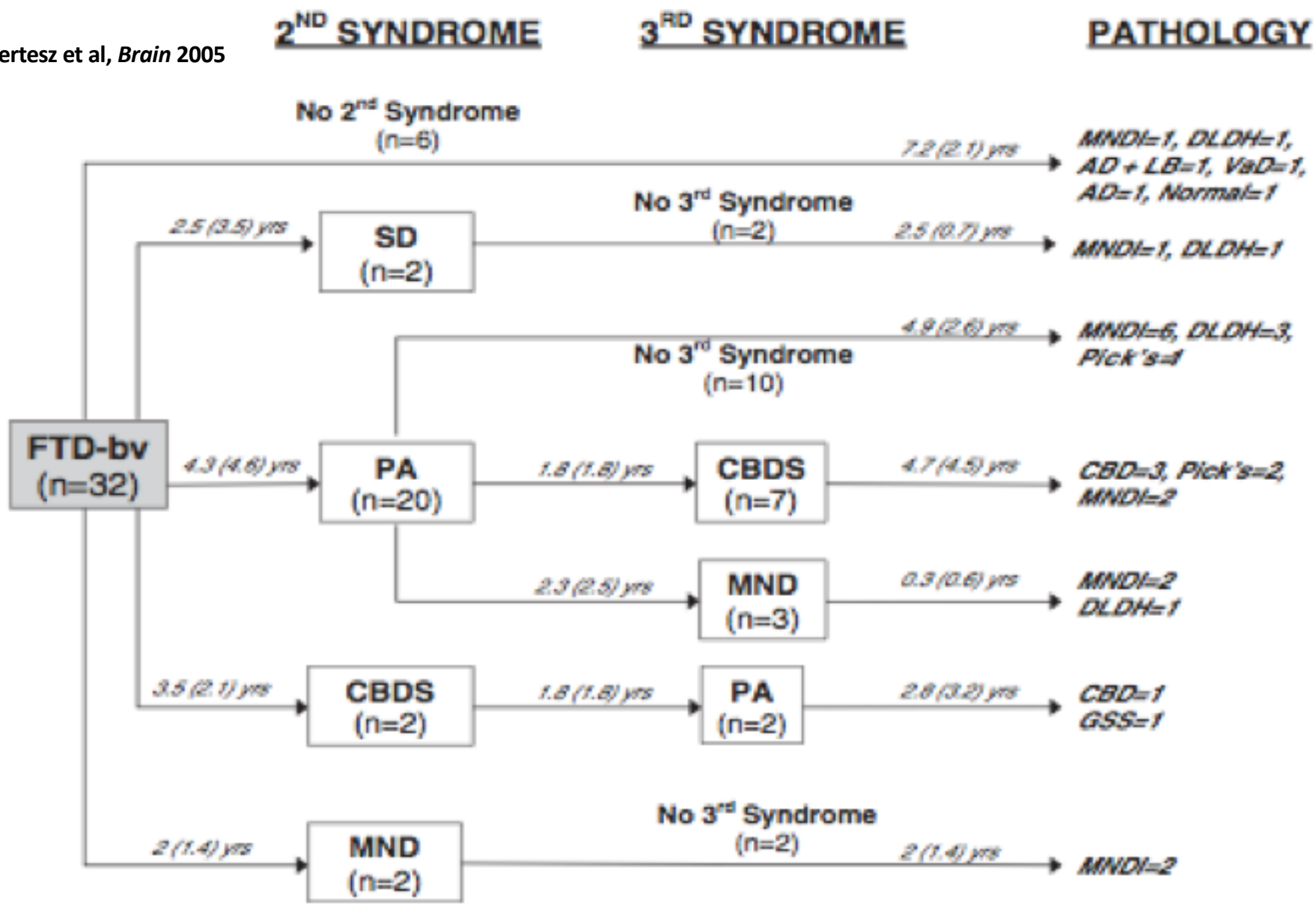


Epilepsy: 50 million people globally of which almost **50 per cent** are aged < 10 years. Social and familial repercussions are **lifelong**.



HAVE WE REACHED A DEAD END CLINICALLY?

Kertesz et al, *Brain* 2005

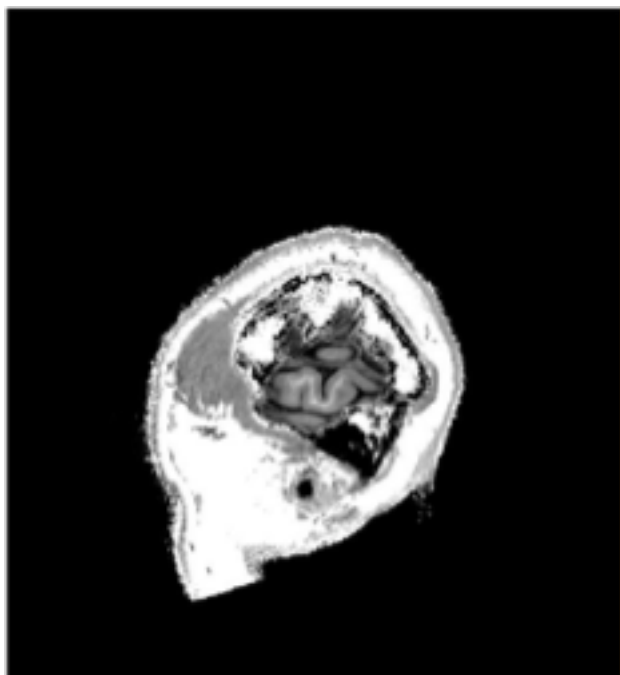
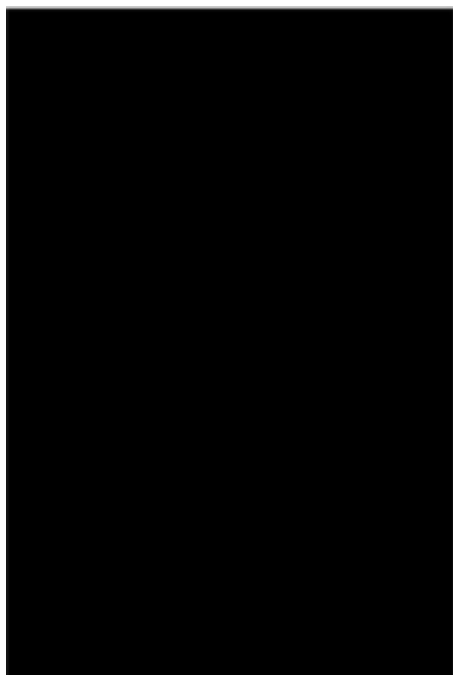
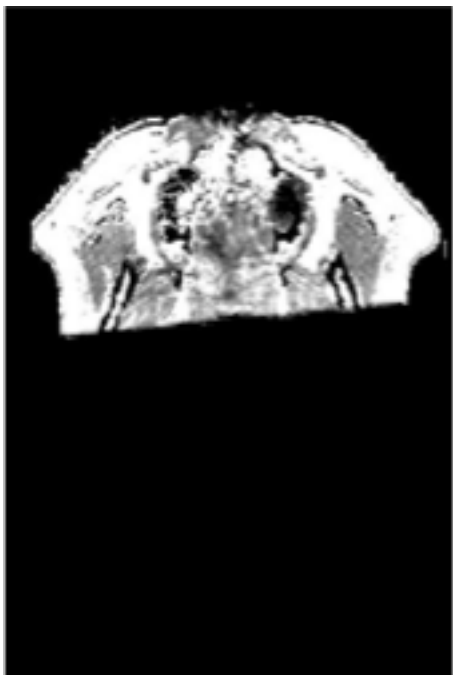
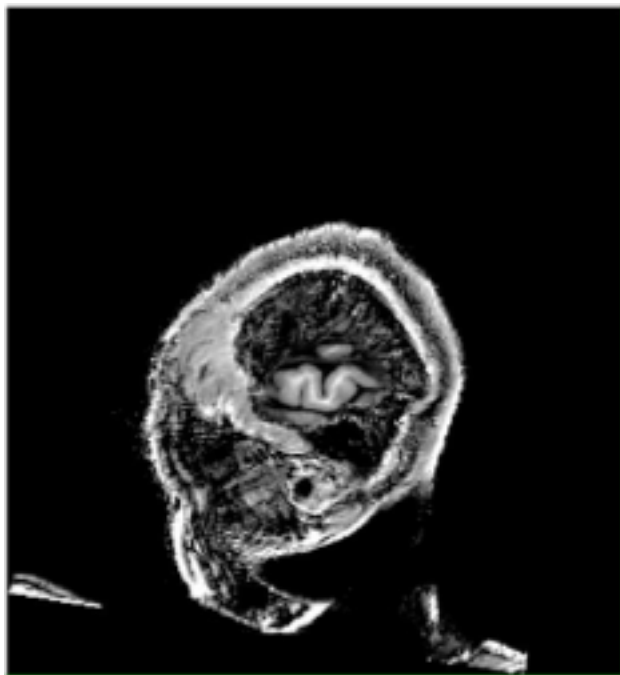
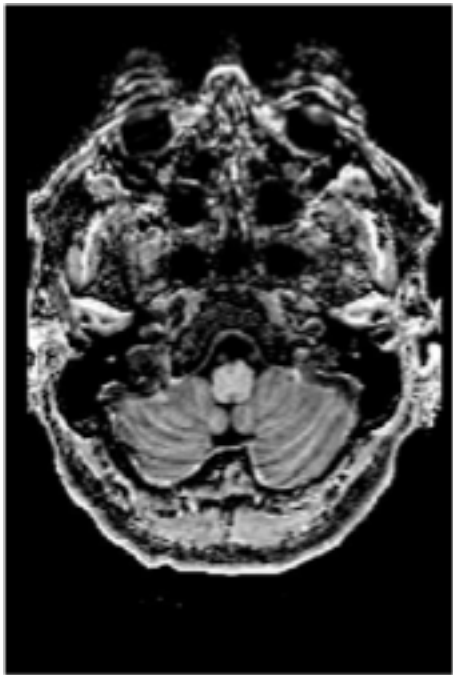




HYPOTHESIS 1

**Phenomenology alone
is insufficiently discriminative
for diagnosis and prognosis**

**Genotyping does not
replace descriptive medicine**





HYPOTHESIS 2

PATTERNS OF PIXEL ABNORMALITIES

ARE OF DIAGNOSTIC

and/or

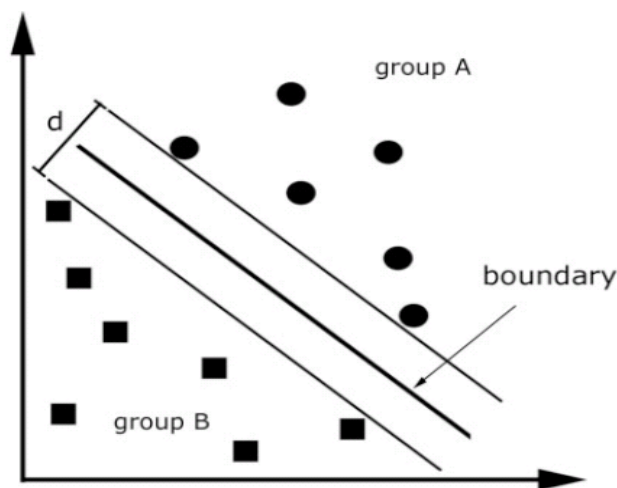
PROGNOSTIC SIGNIFICANCE



INFORMATICS CLASSIFY PATTERNS

	CORRECT	SENSITIVITY	SPECIFICITY
AD & CONTROLS CLINICAL	81%	61%	93%
AD 1 & CONTROLS PATHOLOGY	95%	95%	95%
AD 2 & CONTROLS PATHOLOGY	93%	100%	86%
AD 1 & CONTROLS vs AD 2 PATHOLOGY	96%	100%	93%

**BINARY CLASSIFICATION BY
SUPPORT VECTOR MACHINE**





INFORMATICS REFINE DIAGNOSIS

	CLINICAL AD	CLINICAL NC	ADNI DATABASE
PATHOL AD+	15	3	18
PATHOL AD-	5	17	22
	20	20	

SVM ANALYSIS

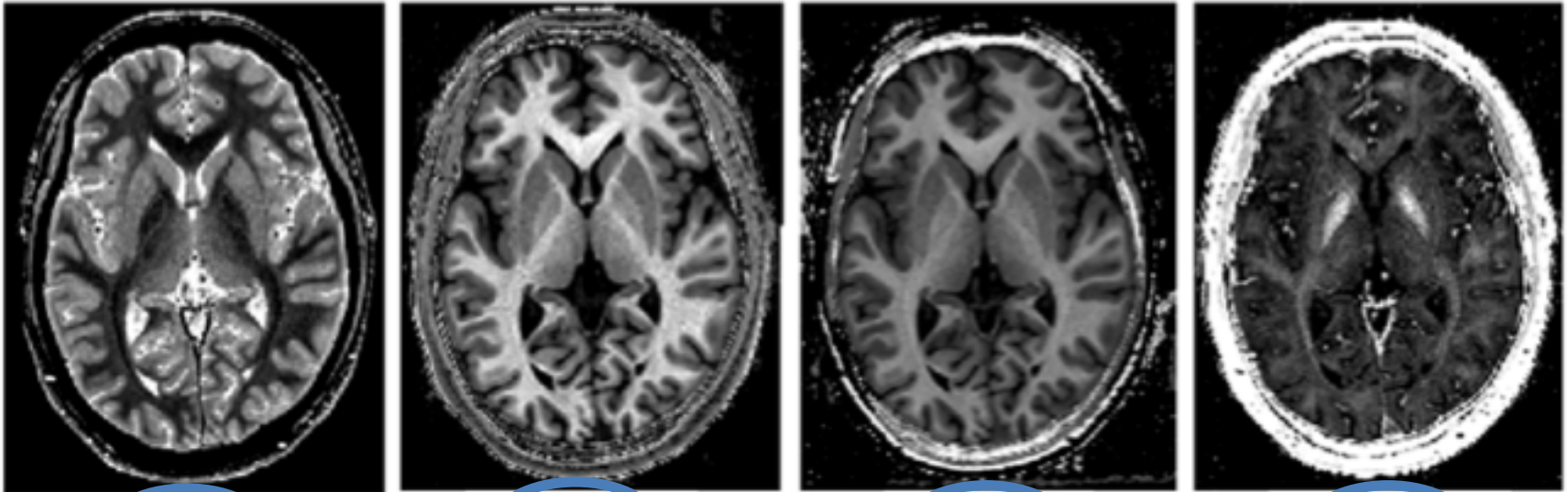


QUANTITATIVE MULTI-PARAMETER MAPPING BASED ON BIOPHYSICAL MODELS

Lorio et al., 2016 *HBMapp*

Lutti et al., 2012 *PLOS One*

Draganski et al., 2011 *NeuroImage*



PD map

MT map

R1 map

R2* map

Proton density
Water content

Magnetization
transfer
saturation
Myelin content

Longitudinal
relaxation rate
***Myelin content &
water compart-
mentalisation***

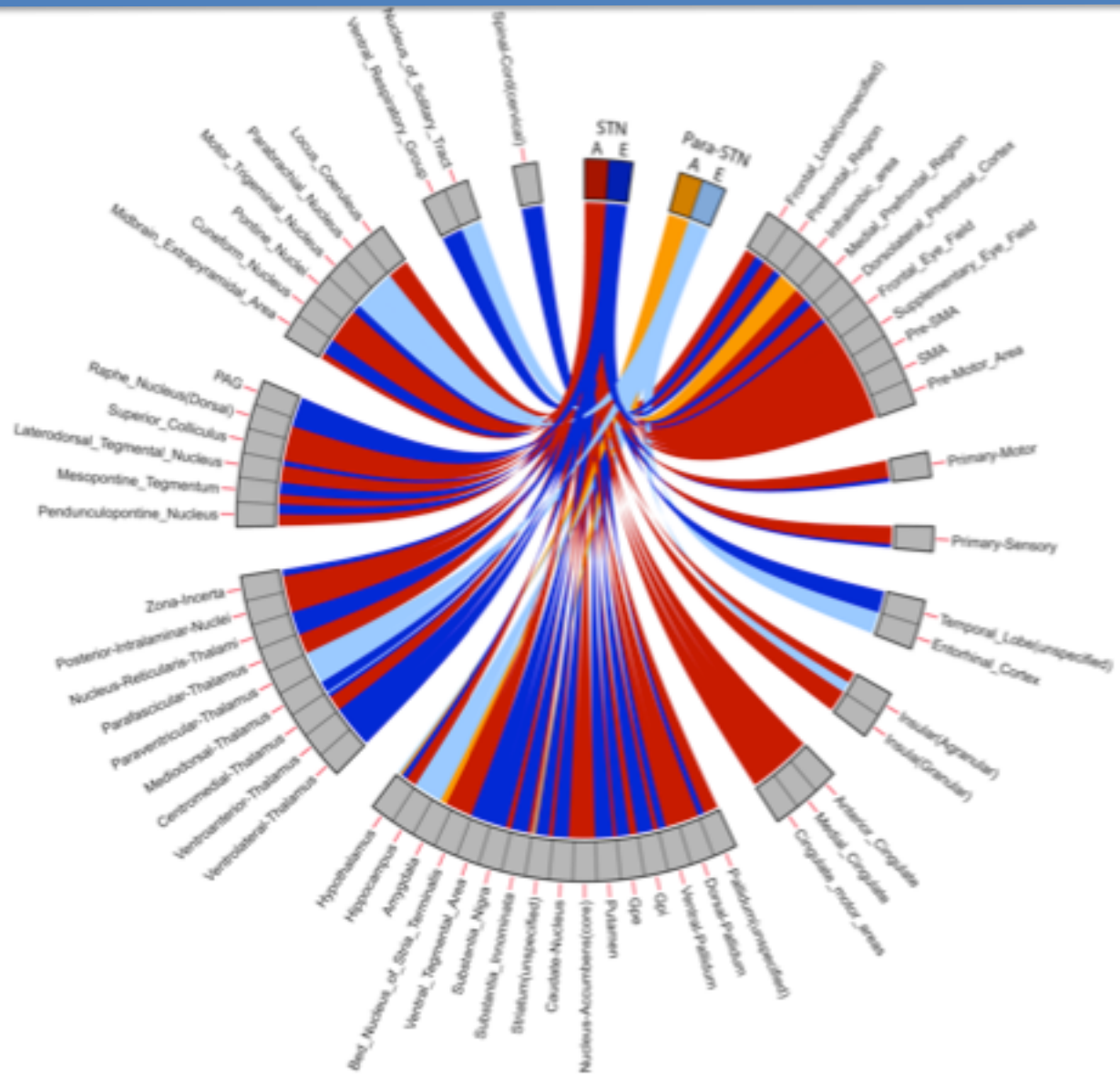
Effective
transverse
relaxation rate
Iron content



INFORMATICS INTEGRATE DATA

A review of the entire tract-tracing literature of the STN between 1947-2011 reveals connectivity between a broad array of cortical, sub-cortical and brainstem structures.

BLUE = EFFERENT
RED = AFFERENT





FUNCTIONAL CONNECTIONS

	LEFT LATERAL VIEW ← Anterior : Posterior →	SUPERIOR VIEW ↓ Anterior : Posterior ↑	ANTERIOR VIEW ↓ Inferior : Superior ↑
Thalamus			
Caudate Nucleus			
Putamen			
Globus Pallidus external segment			
Globus Pallidus internal segment			
Hippocampus			
Amygdala			

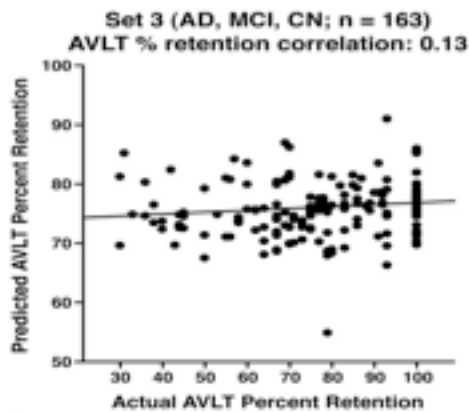
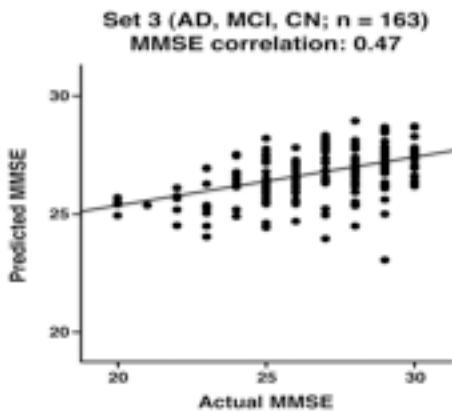
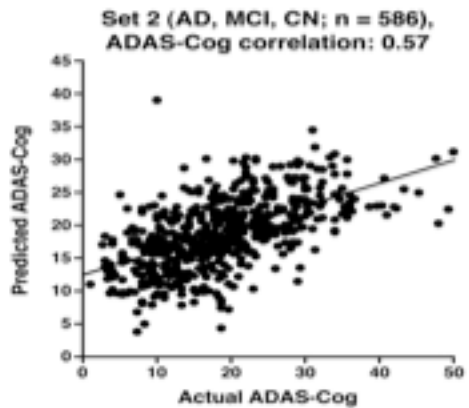
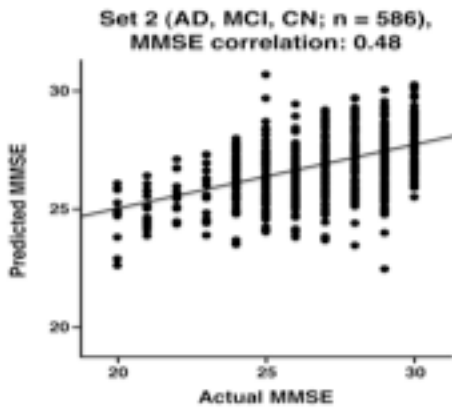
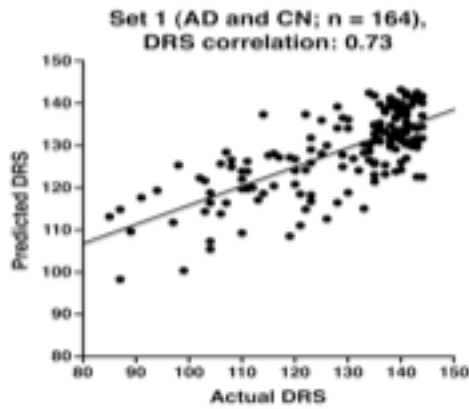
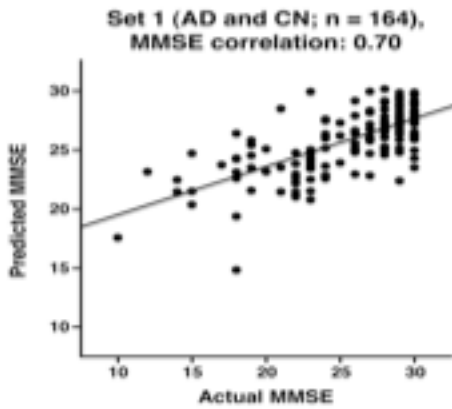
The posterior aspect of the STN projects to structures consistent with a motor structure:

- Posterior putamen
- Posterior GPe
- Mid caudate nucleus
- Ventro-lateral thalamic nuclei
- Posterior Insula
- Posterior hippocampus

The anterior aspect of the STN projects to structures consistent with a limbic structure:

- Baso-lateral amygdala
- Postero-medial GPi
- Inferio-mid putamen
- Mid-GPe
- Ventral-anterior and ventral-lateral thalamus
- Anterior Insula
- Anterior hippocampus

The middle “associative” STN projects to regions encompassing both the motor and limbic projections



**PREDICTING CLINICAL SCORE
COMPARING TO ASSESS RESERVE**



CONFRONTING PARADIGMS

CARTESIAN MODEL (TOP DOWN)

Mentally generated hypothesis
Mathematically expressed in a model
Confrontation with “relevant” data
Parameterisation and optimisation of model
Correlations (non-causal)

SIMULATION MODEL (BOTTOM UP)

Multimodal and multivariate data
Exhaustive mining to demonstrate coherent models
Exploration of these mathematical models as generated hypotheses
Investigation of hypotheses – clinical, mechanistic, prognostic, therapeutic
Knowledge (& causes)



FUNDAMENTAL ISSUE

CLINICAL AND NEUROSCIENCE DATA MUST BE INTEGRATED

SIMULATION is an analytical methodology & depends on high performance computing

SIMULATION is always bottom up – it is a reconstruction from real data

It generates complexity from simpler elements

It results in a PREDICTIVE MODEL that CONSTRAINS next level organisation

SIMULATION can start from any level but always bottom-up and data led

But data are useless unless they help reconstruction from one level to the next.

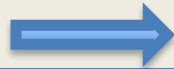
**WE NEED GOOD PREDICTIVE SIMULATION MODELLING TO REDEFINE
& REFINE NEURO-DIAGNOSES IN FUTURE DIAGNOSTIC MANUALS**



BIG DATA & INFORMATICS

RUBBISH IN  RUBBISH OUT

Signal additive
Noise suppressed
Avoids myth of perfect controls – whither RCTs?



GENERATES HYPOTHESES

How big data can help: Bradford Hill (1965)

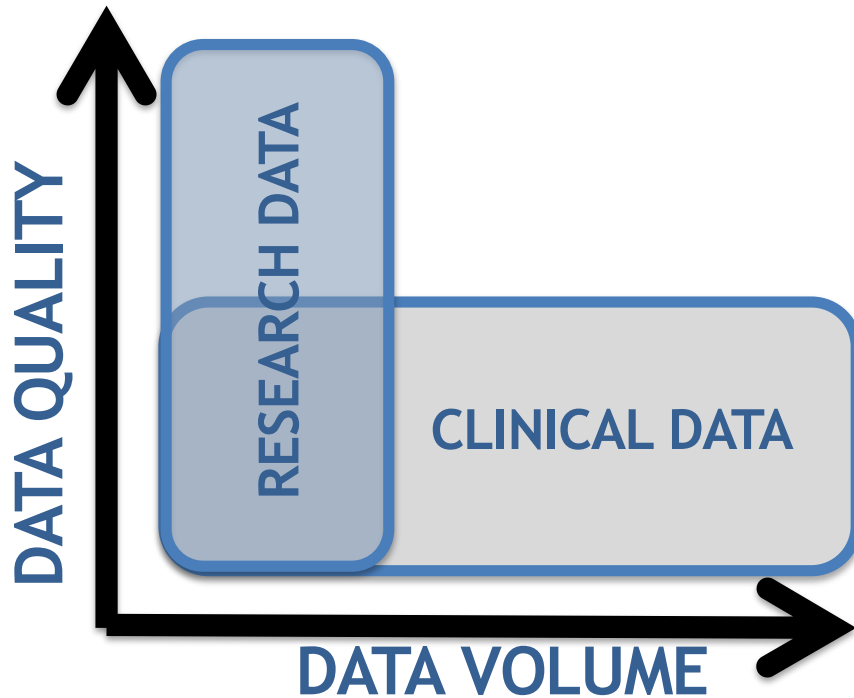
Biologically plausible
Explores multiple (all) models
Multi-scale & dimensional patterns
Additive over time
Built in reproducibility



PREDICTIVE & CAUSAL



DATA SOURCES AND CHALLENGES



HOSPITAL DATABASES

- NOT COMPLETE
- NOT STRUCTURED
- NOT STANDARDISED
- NOT CLEAN
- PROTECTED FOR PRIVACY
- PROTECTED AGAINST CORRUPTION

RESEARCH DATABASES

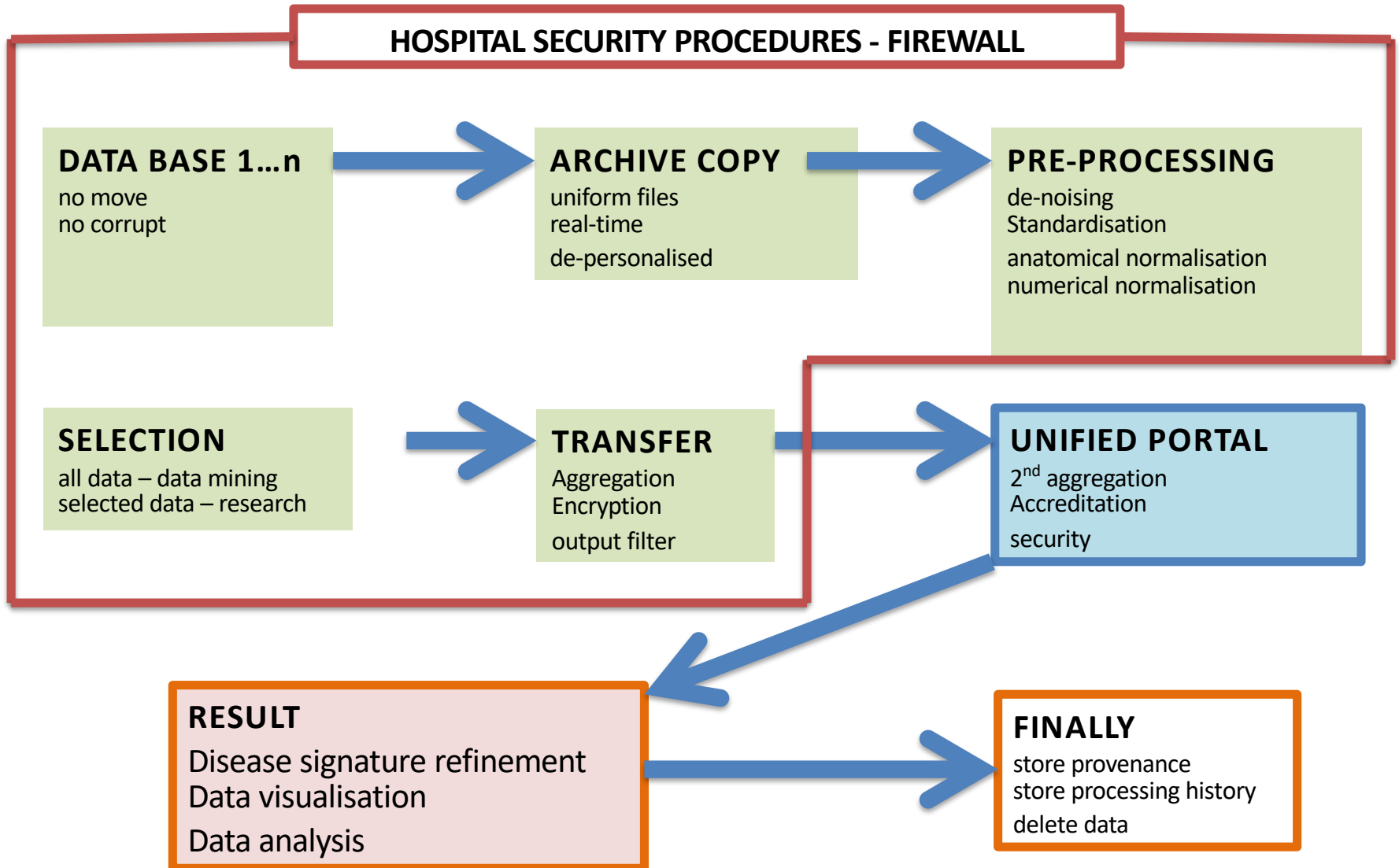
- PROTECTED CULTURALLY

PHARMACEUTICAL DATABASES

- PROTECTED COMMERCIALY

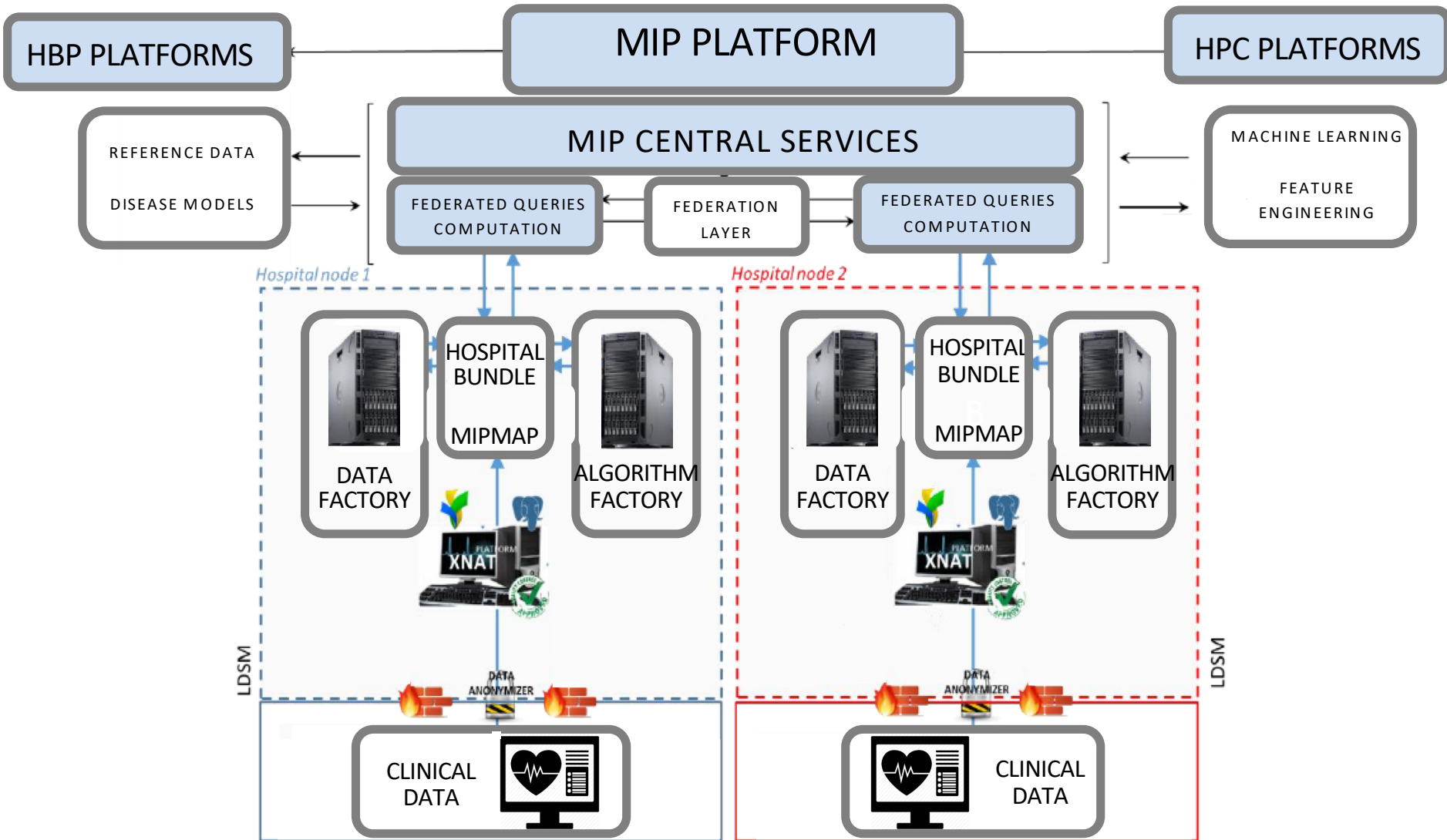


MEDICAL INFORMATICS PLATFORM FEDERATING DATA





MEDICAL INFORMATICS PLATFORM





ETHICAL CHALLENGES

PRIVACY

- DE-PERSONALISATION
- ANONYMISATION

CONSENT

- BROAD CONSENT
- RETROSPECTIVE - PROSPECTIVE

MANAGEMENT OF ETHICS

- LOCAL ETHICS COMMITTEES
- VALUE AND CREDIBILITY OF SCIENCE



SUBJECTS & METHODS

We used 912 AD subjects – **ADNI DATABASE**

For a subsample of 508 we knew gender and age

For a subsample of 184 we knew the MMSE score

We used 5566 normal individuals – **THREE CITIES EPIDEMIOLOGICAL STUDY, FRANCE**

For a subsample of 2096 we knew gender and age

For a subsample of 2091 we knew the MMSE score

For learning we used half the dataset to create the classifier

The learning set = 3239 individuals (465 AD, 2774 controls)

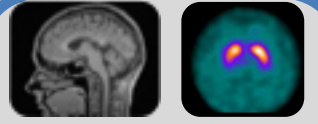
The other half was used to validate the classifier

The testing set = 3239 individuals (447 AD, 2792 controls)

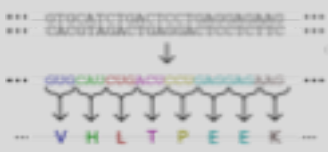


DATA EXTRACTION

DATA



Time	ED	ICU	2nd	HLBD	NIC		
06/24/05 07:44	3	43%	0	0%	16	10%	4
06/24/05 08:50	3	90%	1	3%	13	12%	4
06/24/05 09:12	4	19%	1	12%	7	4%	4
06/24/05 12:30	4	26%	0	0%	4	21%	3
06/24/05 07:42	3	10%	0	0%	4	21%	4
06/24/05 12:24	4	24%	1	12%	4	22%	3
06/24/05 09:31	5	24%	2	16%	4	21%	4
06/24/05 13:07	3	43%	1	3%	4	21%	3
06/24/05 12:16	3	48%	1	33%	4	22%	3
06/24/05 12:27	4	19%	1	33%	4	21%	3
06/24/05 12:46	4	19%	3	27%	4	21%	7
06/24/05 11:02	3	48%	1	33%	4	21%	3
06/24/05 12:41	1	15%	1	16%	4	22%	4
06/24/05 11:50	5	26%	1	33%	4	22%	4
06/24/05 11:37	5	26%	1	33%	4	22%	4
06/24/05 08:02	3	45%	1	2%	4	22%	4
06/24/05 12:20	3	16%	1	21%	0	100%	4
06/24/05 07:21	3	16%	1	21%	0	100%	4



SCALE

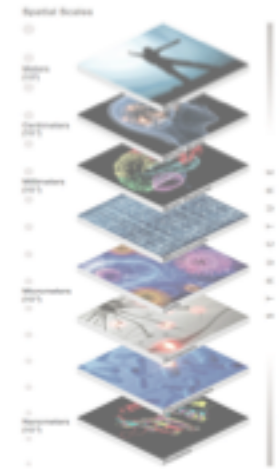
TIME

SPACE

PATHOLOGY

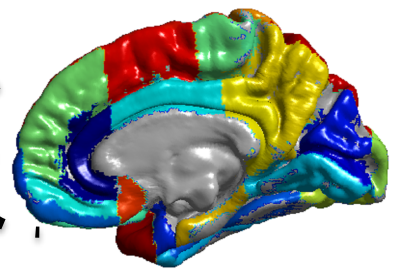
DEMOGRAPHICS

- Genetic
- Molecular
- Cellular
- Circuits
- Systems



- Cross-sectional
- Longitudinal

Brain anatomy



- Pathology confirmed diagnosis
- Risk factors

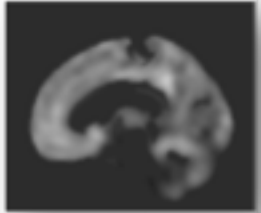
Age, gender ...

VARIABLES

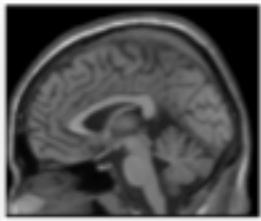


DATA INTEGRATION

BRAIN IMAGING

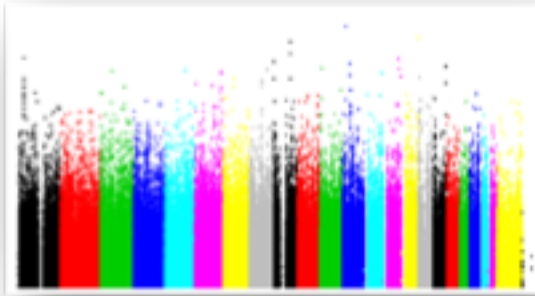


PET



MRI

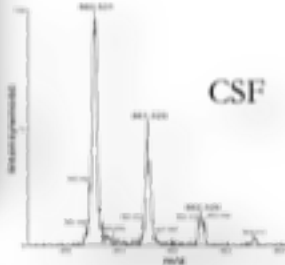
CLINICAL SCALES & MEASUREMENTS



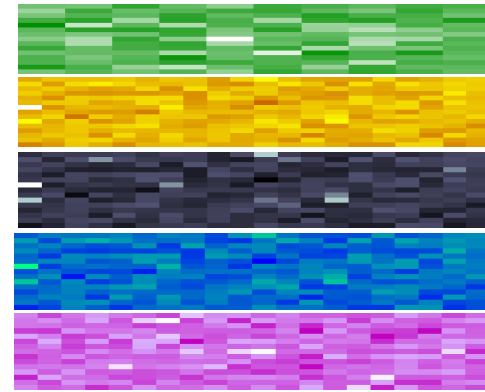
Organising
Tabulating



Processing...



CSF



MRI data

PET data

Gene data

CSF data

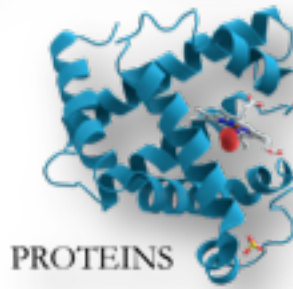
Protein data

*** GTGCATCTGACTCCTGAGGAGAAG ***
*** CACGTAGACTGAGGACTCCTCTTC ***



*** GUGCAUCUGACUCCUGAGGAGAAG ***
↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓
... V H L T P E E K ...

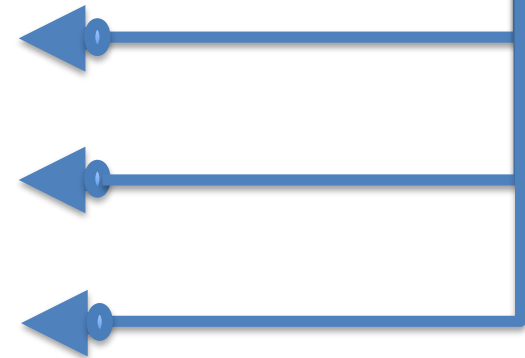
GENES



PROTEINS

912 Alzheimer's patients
5566 Healthy controls

- Phenotype-led Semi-supervised clustering
- Biologically led classification
- High dimensional feature learning

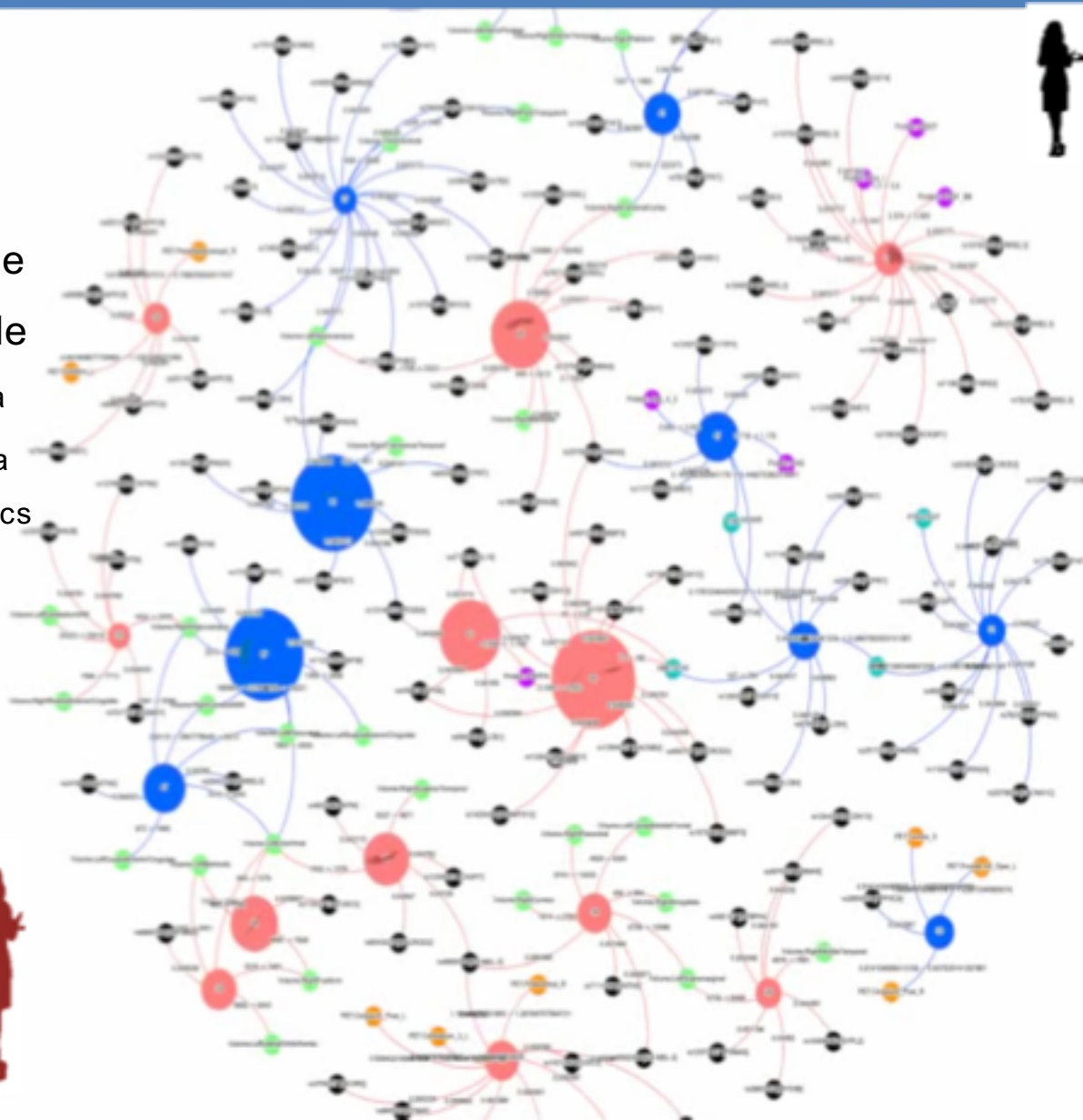




LINKING CLINICS TO BIOLOGY



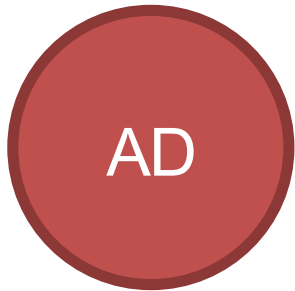
- AD Rule
- NC Rule
- MRI Data
- PET Data
- Proteomics
- CSF
- Genetics





USING ANATOMY TO CONSTRAIN DIAGNOSIS

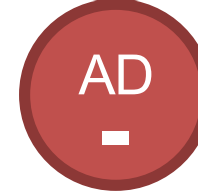
CLINICAL (SYNDROMIC) CLASSIFICATION



INTEGRATING PATHOLOGY INTO DIAGNOSIS



Symptoms +
Pathology +



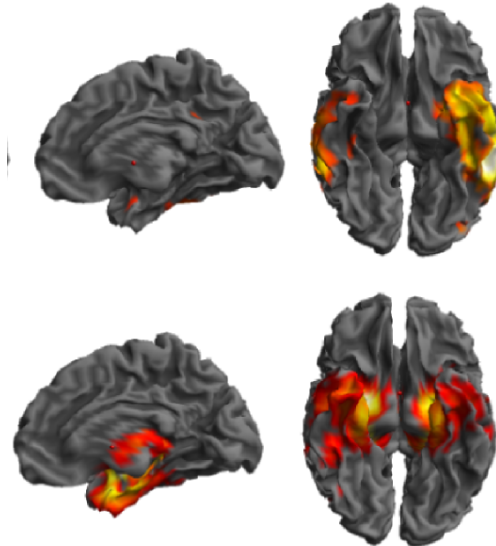
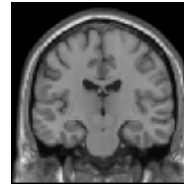
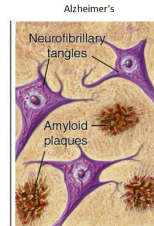
Symptoms +
Pathology -



Symptoms -
Pathology +



Symptoms -
Pathology -

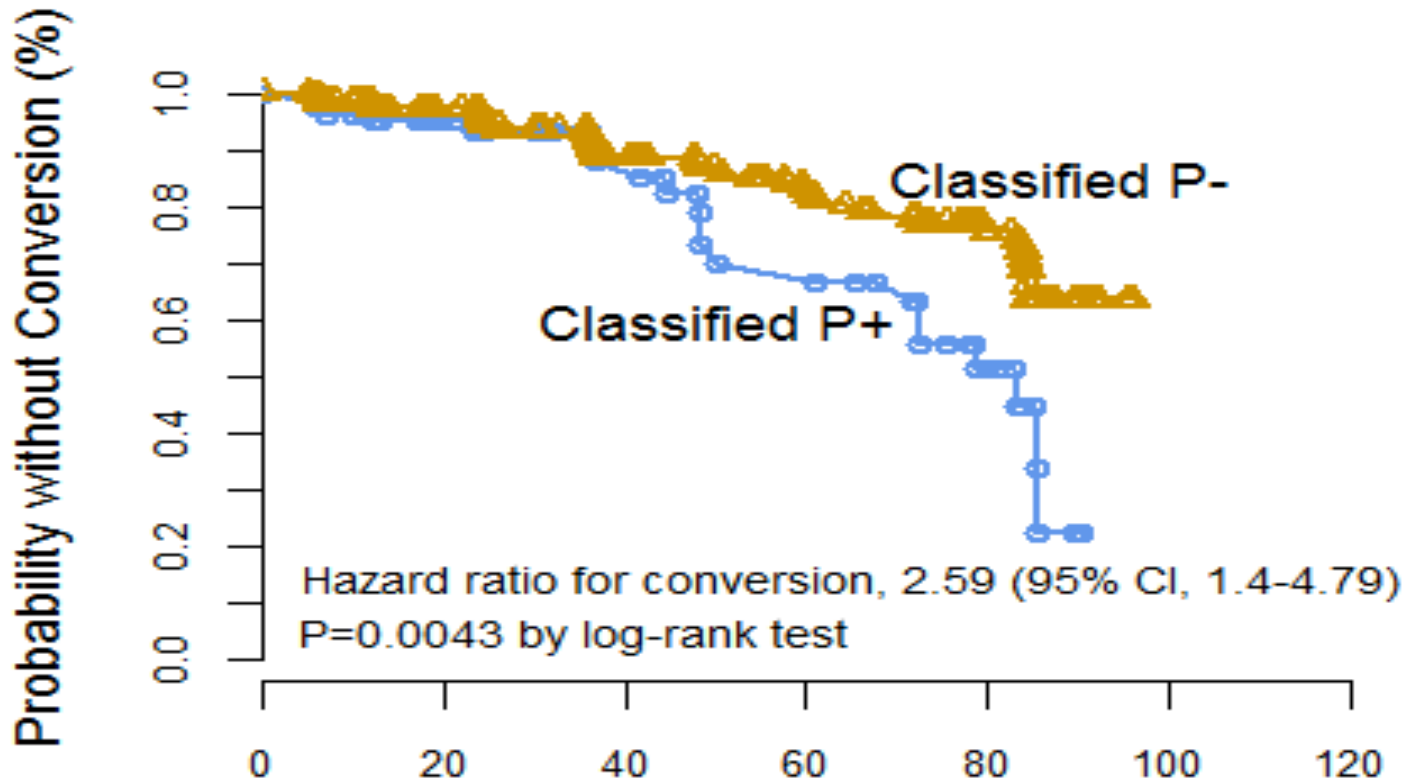


Brain atrophy pattern characteristic of pathological disease provides constraints on diagnosis



PREDICTING OUTCOME MORE ACCURATELY

NC subjects with two patterns of brain atrophy



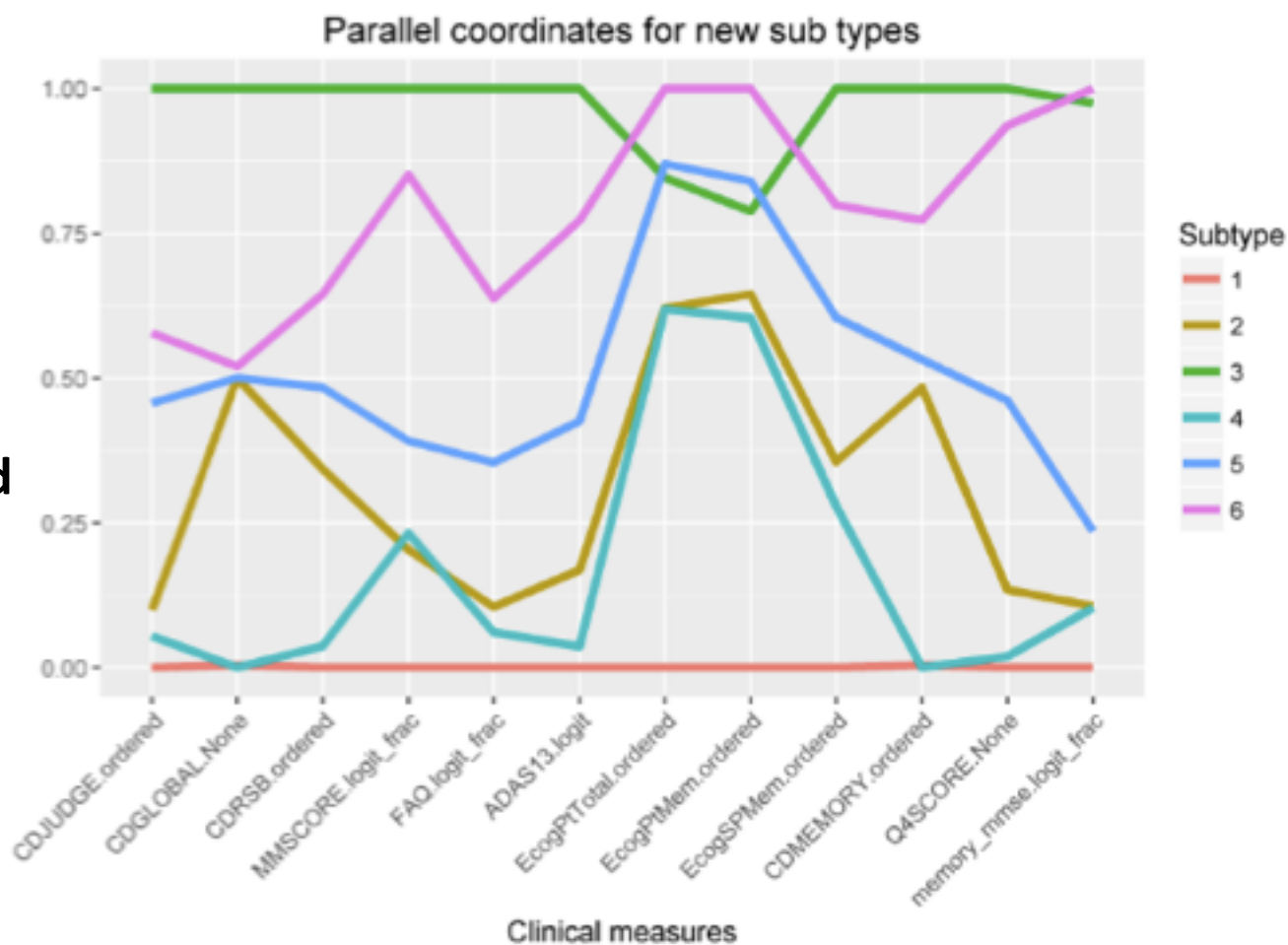
ALL COGNITIVELY NORMAL ON RECRUITMENT AT BASELINE = 0



SUPERVISED SEARCH FOR AD SUBTYPES IN ADNI DATA

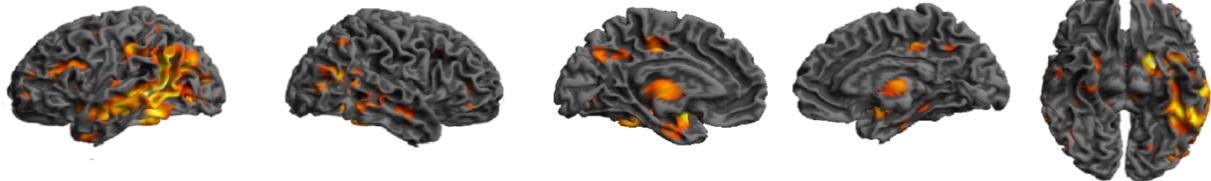
Six subtypes identified

1. Typical AD
2. Atypical AD
3. Hippocampus spared
4. Amnestic MCI
5. Depression suspected
6. Cognitively Normal

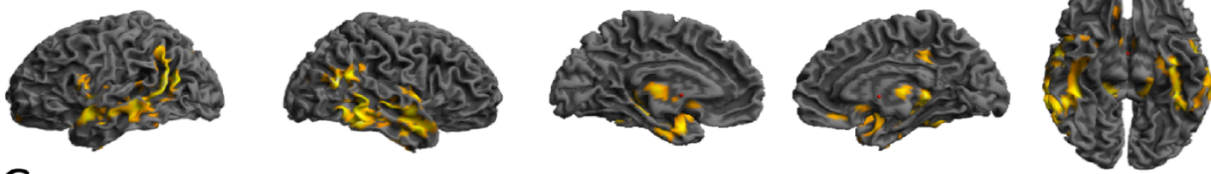




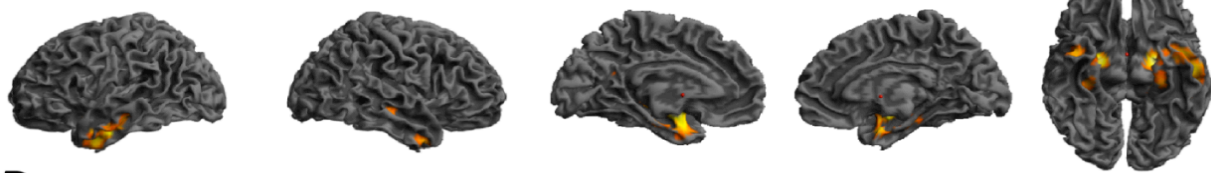
A PPG AD < PPG CN



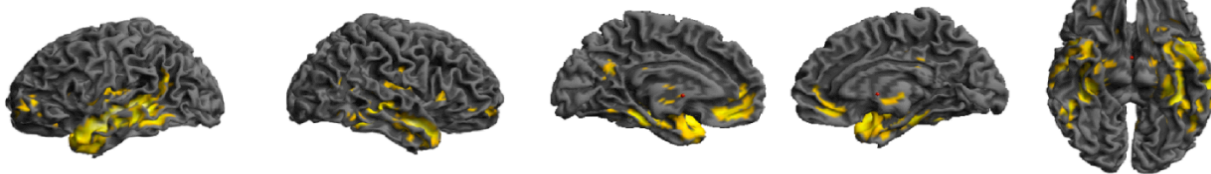
B ADNI (baseline) CN_P+ < CN_P-



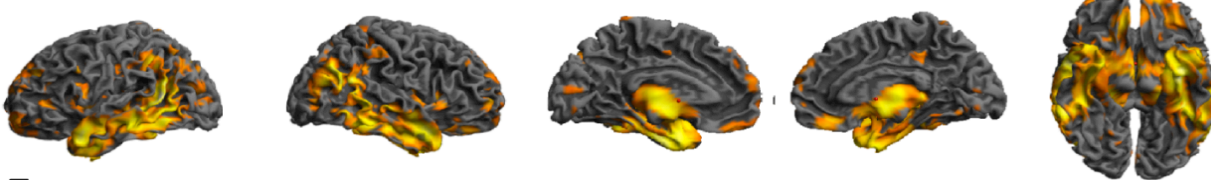
C ADNI (baseline) AD_P+ < CN_P+



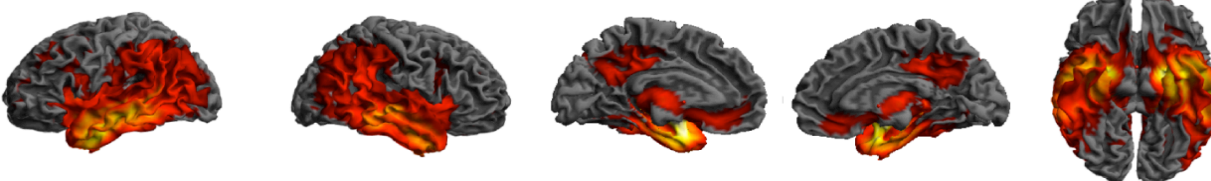
D 3C (Dijon) CN_P+ < CN_P-



E ADNI (longitudinal) CN_P+ < CN_P-



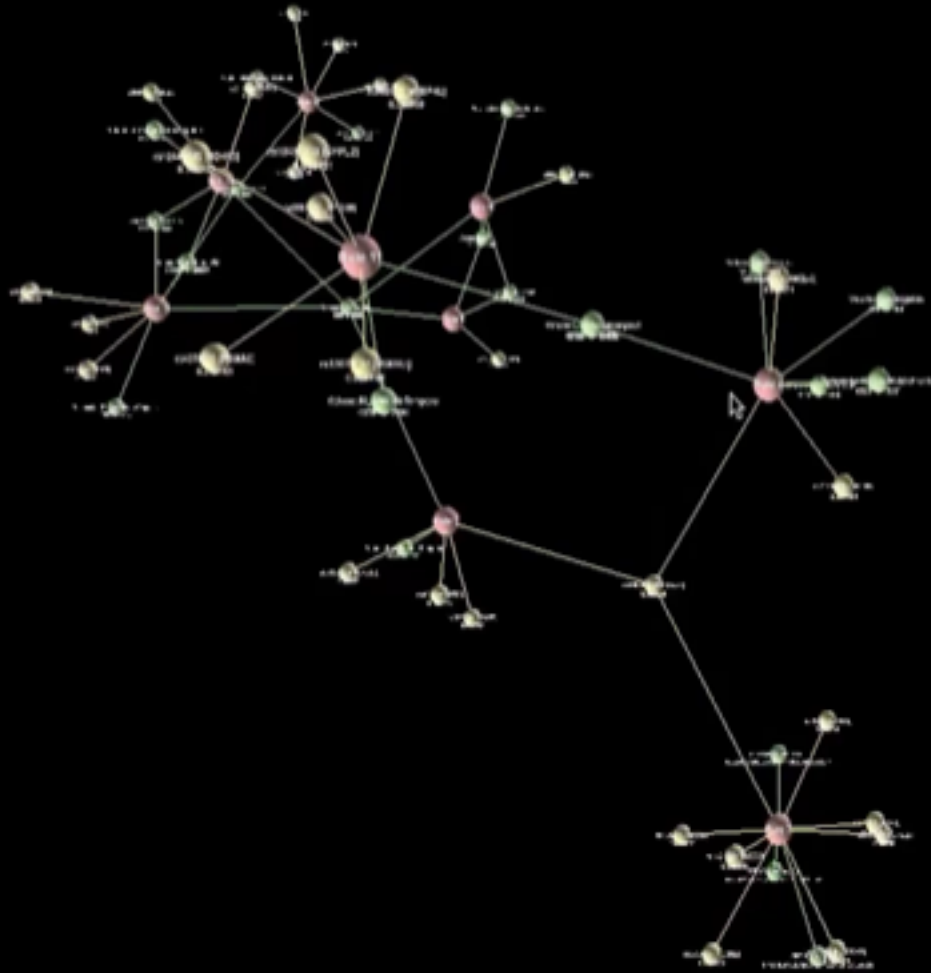
F ADNI (baseline) AD_P+ < CN_P-



DISSECTING CLINICAL GROUPS



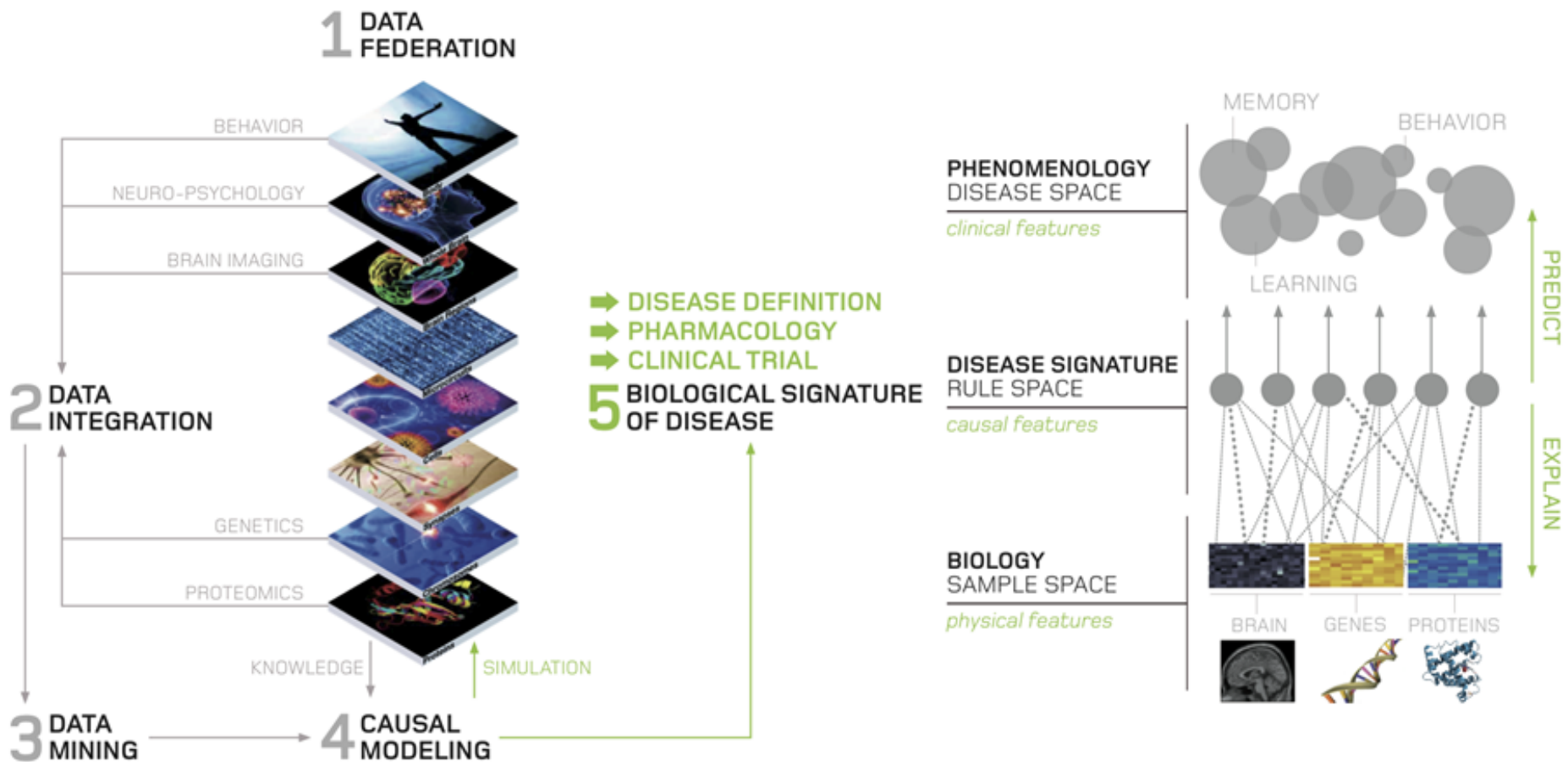
A UNIVERSE OF PERSONALISED DIAGNOSES





MULTI-SCALE DISEASE SIGNATURES

The MIP provides methods to **analyse federated data** from hospitals, research centres and biobanks and aim to **federate the different communities** of users from these different locations.



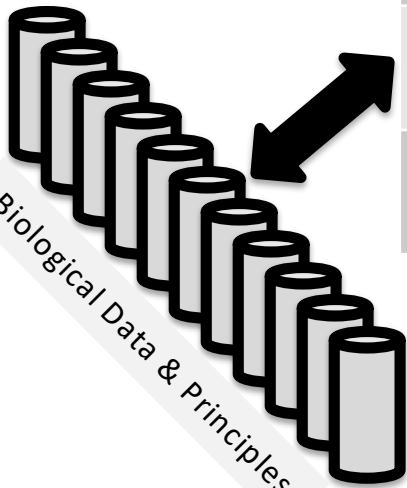
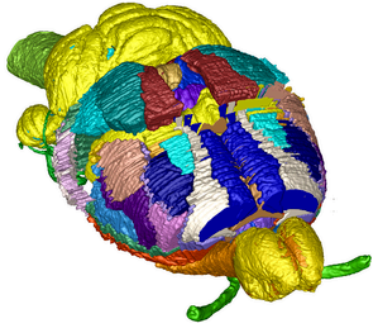


REVERSE ENGINEERING – TO VALIDATE

Brain Atlases
Data source

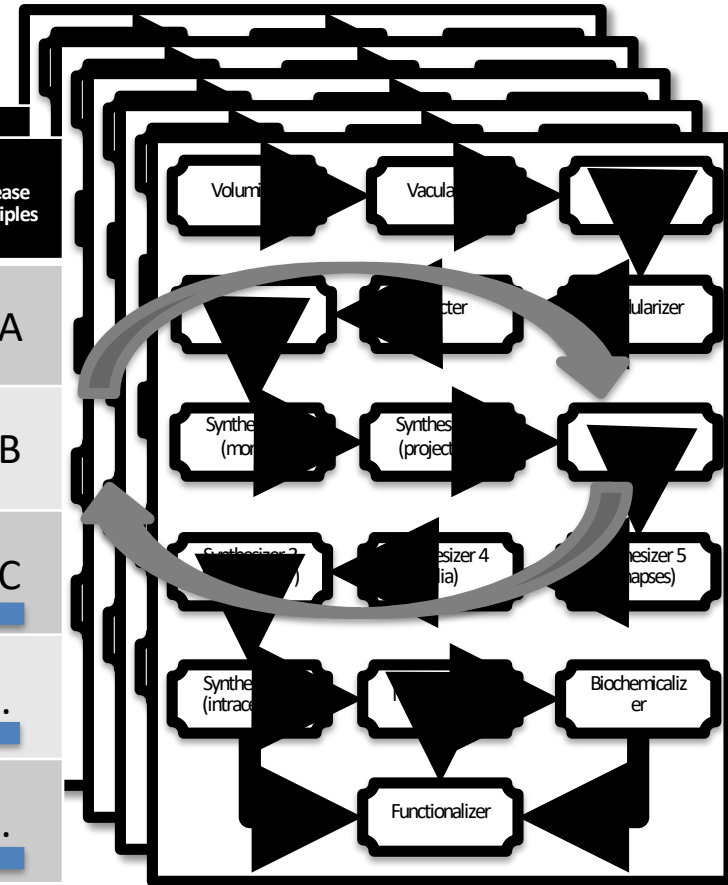
Biological Parameter Constraints & Biological Principles
Configurations

Multi-constraint Algorithms
Brain Reconstruction Workflows



		Data	Principles	Disease Data	Disease Principles
S	Bouton density	A	AA	A	AA
S	Synapse density	B	BB	B	BB
S	Syns/connect	C		C	CC
C	P Connect				...
C	Synaptic Response				...

NORMAL



DISEASE

**DATA INTEGRATION
AND
CAUSAL ANALYSIS**

DISEASE SIGNATURES

**THEN
MEDICAL PHENOMENOLOGY
GENETIC & –OMIC CHARACTERISATION
DYSFUNCTIONAL SYSTEM IDENTIFICATION
(POLY)PHARMACOLOGY**



ICONOCLASTIC CHALLENGES

A PIXEL is an INFORMATION ANCHOR with COORDINATES in STANDARD BRAIN ANATOMICAL SPACE THAT LINKS TO INFORMATION ABOUT IT IN THE LITERATURE

PATTERNS OF PIXEL ABNORMALITIES ARE OF DIAGNOSTIC and/or PROGNOSTIC SIGNIFICANCE

PATTERNS ARE THOUGHT TO BE MECHANISTICALLY SPECIFIC and SO MORE RELEVANT to THERAPEUTICS – TO BE PROVEN

THE FUTURE IS IN DATA-LED HYPOTHESIS GENERATION FOLLOWED by CLINICAL, BIOLOGICAL AND GENETIC CHARACTERISATION – DISEASE SIGNATURES

SUCH CHARACTERISATION SHOULD GENERATE THERAPEUTIC STRATEGIES AND TARGETS IN A MORE PRINCIPLED MANNER THAN AT PRESENT – TO BE PROVEN

RCTs MAY HAVE MORE FOCUSED USES – BIG DATA ANALYSES TO REPLACE DOUBLE BLIND CONTROLS BY REMOVING NOISE - MASSIVE DATA SETS DO NOT NEED TO BE COMPLETE, CLEAN OR UNIFORM – TO BE VALIDATED



THE ROLE OF DISRUPTIVE SCIENCE IN HBP-MIP

1. Move to a “**no database**” federated data analysis infrastructure

- ✓ Security, privacy, research, ethics considerations
- ✓ Advances in “virtualisation” “streaming” and “peer-to-peer” technologies
- ✓ Use of products of EC funded research (eg Exareme)
- ✓ Open source and cross-disciplinary specification
- ✓ Unlocking hospital databases for research

2. Breaking **conservative** medical IT culture





- ✓ Recruitments of university hospitals
- ✓ Recruitment of structured research databases
- ✓ Playing to “data sharing” revolution (NIH, EC, Wellcome initiatives)

3. Introduction of “**disease signatures**” concept

- ✓ Cultural change from pure symptomatic & syndromic disease definitions
- ✓ Preliminary classifications



HBP MEDICAL INFORMATICS PLATFORM

-  Clinical neuroscientist
-  Computer scientist
-  Statistician neuroscientist
-  Ethics



Bogdan Draganski

Ferath Kherif

Richard Frackowiak

Mira Marcus Kalish

Saso Dzezowski

Boudewijn Lelieveldt

Anastasia Ailamaki

Vasilis Vassalios

Yannis Ioannidis

Frank Schneider

Andrew Pocklington

John Ashburner

Alexis Brice

Kathinka Evers

Jean-Francois Dartigues

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