

AETIONOMY - Data, Disease Modeling and Reasoning

Martin Hofmann-Apitius

Academic Co-Coordinator of
AETIONOMY

PRISME Forum Spring 2017
Meeting

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Mission

To increase knowledge of the causes of Alzheimer's and Parkinson's Disease by generating a mechanism-based taxonomy; to validate the taxonomy in a prospective clinical study that demonstrates its suitability for identifying patient subgroups (based on discrete disease mechanisms); to support future drug development and lay the foundation for improved identification and treatment of patient subgroups currently classified as having AD or PD.



A Non-Trivial Challenge:
Development of a
“mechanism-based
taxonomy for
neurodegenerative
diseases”



In 2011, Kola and Bell published a remarkable paper in Nature Reviews Drug Discovery. With their **“Call to reform the taxonomy of human disease”** they proposed a new, **mechanism-based classification of human disease.**

A call to reform the taxonomy of human disease

Ismail Kola and John Bell

A coordinated effort to incorporate advances in the understanding of the molecular and genomic variations in common diseases, such as hypertension, into their diagnosis and treatment could transform drug development and medicine.

Many common human diseases are still diagnosed as if they were homogenous entities, using criteria that have hardly changed for more than a century. For example, a person with a systolic blood pressure of 140 mm Hg or greater and a diastolic blood pressure of 90 mm Hg or greater is diagnosed with hypertension, irrespective of the heterogeneous underlying molecular mechanisms in different individuals. Furthermore, the treatment approach for diseases that are diagnosed in this way is generic, with empiricism as its cornerstone. Continuing

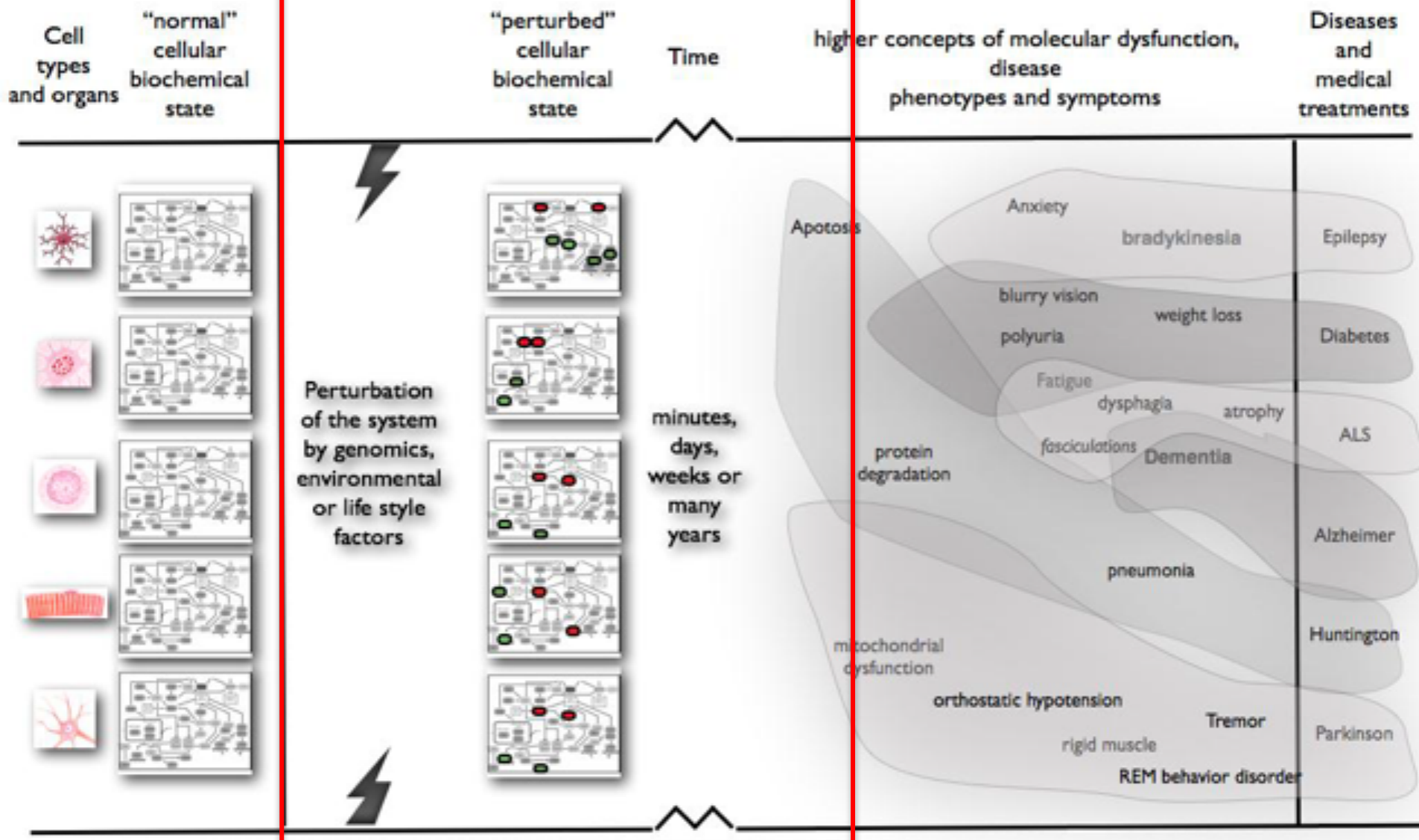
based on the presence of a shared mutation and/or a deregulated pathway, rather than on tumour location, has not yet been initiated to our knowledge, but is an approach that regulatory agencies may be comfortable with in the future.

The lack of recognition of disease heterogeneity in clinical development and medical practice has a number of well-known consequences. First, it will probably reduce the likelihood of success of clinical trials, perhaps more so for targeted therapies that have been pursued in

Kola, I., & Bell, J. (2011). A call to reform the taxonomy of human disease. *Nature Reviews Drug Discovery*, 10(9), 641-642.

"healthy"

"diseased"



Biological Ontologies

missing links

Medical Ontologies



Data and Knowledge in
Neurodegenerative
Disease Research:
incomplete, scattered,
mono-modal



Data resources



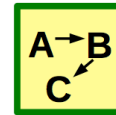
Ontologies



Imaging indices



PPI networks



Pathways



**BEL&SBML
models**



Gene Expression

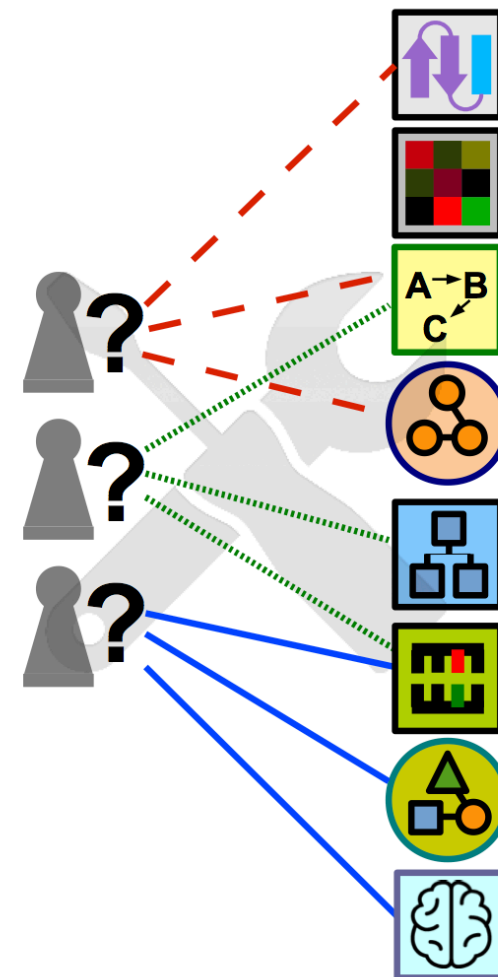
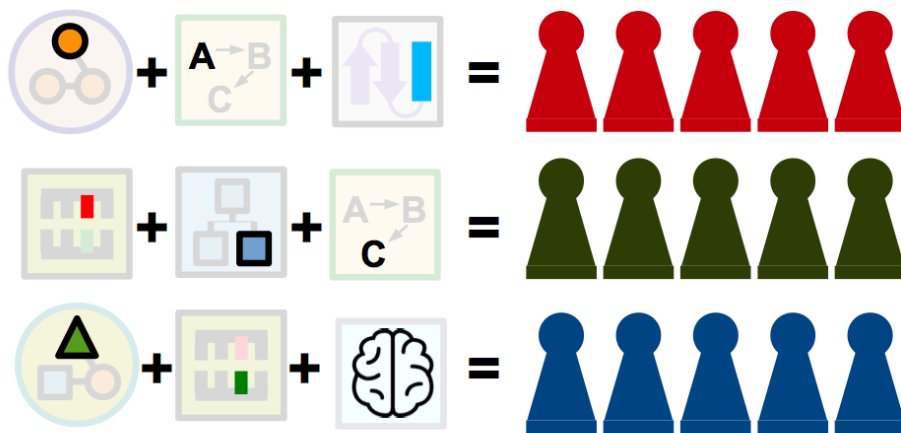


SNP



**Protein domains
& families**

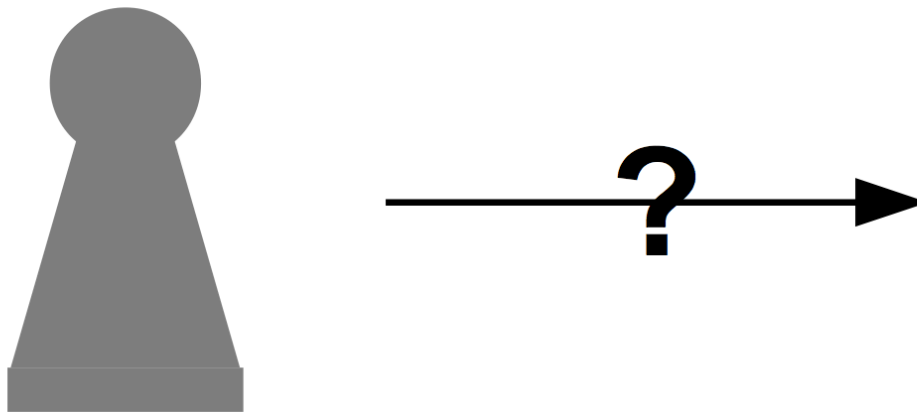
Additional: UniProt, PubMed, OMIM, Reactome, HGNC, ENSEMBL, ChEMBL, ...



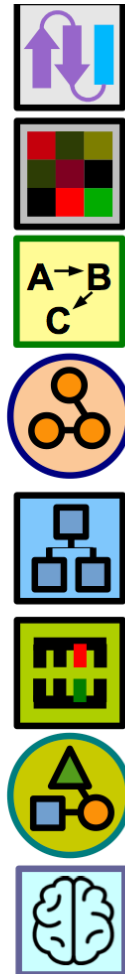


classifying system / patient cohort covering all tests?

correlations between different parameters?



We therefore need to integrate heterogeneous data and knowledge and glue them together in *models*



Excursion:

Making Data Findable,
Accessible, Interoperable,
and Re-Usable:
FAIR data principles





Making Data and Knowledge FAIR

FAIR data principles:

- **F**indable
- **A**ccessible
- **I**nteroperable
- **R**e-usable

This is about (clinical) data and their role in translational biomedicine

This is also about the way we do science:

Iqbal, S. A., Wallach, J. D., Khoury, M. J., Schully, S. D., & Ioannidis, J. P. (2016). *Reproducible research practices and transparency across the biomedical literature*. *PLoS Biol*, 14(1), e1002333.



Making Data and Knowledge FAIR

To be Findable:

F1. (meta)data are assigned a globally unique and eternally persistent identifier.

F2. data are described with rich metadata.

F3. (meta)data are registered or indexed in a searchable resource.

F4. metadata specify the data identifier.



Making Data and Knowledge FAIR

To be Accessible:

A1 (meta)data are retrievable by their identifier using a standardized communications protocol.

A1.1 the protocol is open, free, and universally implementable.

A1.2 the protocol allows for an authentication and authorization procedure, where necessary.

A2 metadata are accessible, even when the data are no longer available.



Making Data and Knowledge FAIR

To be Interoperable:

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles.
- I3. (meta)data include qualified references to other (meta)data.



Making Data and Knowledge FAIR

To be Re-usable:

R1. meta(data) have a plurality of accurate and relevant attributes.

R1.1. (meta)data are released with a clear and accessible data usage license.

R1.2. (meta)data are associated with their provenance.

R1.3. (meta)data meet domain-relevant community standards.



Step 1: Building Resources



Taking care of interoperability of data and knowledge: Shared Semantics



Ashutosh
Malhotra



Erfan
Younesi



ADO: Alzheimer Disease Ontology

ADO: A disease ontology representing the domain knowledge specific to Alzheimer's disease

Ashutosh Malhotra^{a,b}, Erfan Younesi^{a,b}, Michaela Gündel^a, Bernd Müller^a, Michael T. Heneka^c,
Martin Hofmann-Apitius^{a,b,*}

^aDepartment of Bioinformatics, Fraunhofer Institute for Algorithms and Scientific Computing, Sankt Augustin, Germany

^bRheinische Friedrich-Wilhelms-Universität Bonn, Bonn-Aachen International Center for IT, Bonn, Germany

^cDepartment of Neurology, Clinical Neurosciences Unit, University of Bonn, Bonn, Germany

Abstract

Background: Biomedical ontologies offer the capability to structure and represent domain-specific knowledge semantically. Disease-specific ontologies can facilitate knowledge exchange across multiple disciplines, and ontology-driven mining approaches can generate great value for modeling disease mechanisms. However, in the case of neurodegenerative diseases such as Alzheimer's disease, there is a lack of formal representation of the relevant knowledge domain.

Methods: Alzheimer's disease ontology (ADO) is constructed in accordance to the ontology building life cycle. The Protégé OWL editor was used as a tool for building ADO in Ontology Web Language format.

Results: ADO was developed with the purpose of containing information relevant to four main biological views—preclinical, clinical, etiological, and molecular/cellular mechanisms—and was

Malhotra, A., Younesi, E., Gündel, M., Müller, B., Heneka, M. T., & Hofmann-Apitius, M. (2014).
ADO: A disease ontology representing the domain knowledge specific to Alzheimer's disease.
Alzheimer's & dementia, 10(2), 238-246.



PDON: Parkinson Disease Ontology integrating Mechanisms

Class hierarchy

Class hierarchy (inferred)

Class hierarchy: 'PARK6 mutation parkinsonism'

- 'Neurobehavioral biomarker of Parkinson disease'
- 'Neuroimaging biomarker of Parkinson disease'
- 'Neuroprotective biomarker of Parkinson disease'
- 'OMICS biomarkers of Parkinson disease'
- 'Pathological biomarker of Parkinson disease'
- 'Physiological biomarker of Parkinson disease'
- 'agnostic criteria for Parkinson disease'
- 'differential diagnosis of Parkinson disease'
- 'evaluation of Parkinson's disease'
- 'etiology of Parkinson disease'
- 'genetic etiology of Parkinson disease'
- 'dopamine deficiency'
- 'hereditary form of PD'
- 'Monogenic form of Parkinson disease'
- 'Autosomal dominant form of parkinsonism'
 - 'PARK1 mutation parkinsonism'
 - 'PARK10 mutation parkinsonism'
 - 'PARK11 mutation parkinsonism'
 - 'PARK2 mutation parkinsonism'
 - 'PARK3 mutation parkinsonism'
 - 'PARK4 mutation parkinsonism'
 - 'PARK5 mutation parkinsonism'
 - 'PARK6 mutation parkinsonism'
 - 'PARK7 mutation parkinsonism'
 - 'PARK8 mutation parkinsonism'
- 'Autosomal recessive form of parkinsonism'
- 'mitochondrial DNA mutation'
- 'mitochondrial complex I deficiency'
- 'general glutathione deficiency'
- 'sporadic parkinson disease'
- 'aging etiology'
- 'epidemiological history'
- 'genetic cause of parkinsonism'
- 'iatrogenic cause of parkinsonism'
- 'factors for Parkinson disease'

Annotations

Usage

Annotations: 'PARK6 mutation parkinsonism'

results of this study and the previously reported subclinical nigrostriatal dysfunction in carriers of heterozygous PINK1 mutations suggest the possibility that these heterozygous mutations are a significant risk factor in the development of later onset PD."

p(HGNC:PINK1, sub(G,309,D)) -> path(MESHD:"Parkinson Disease")

#####

SET Citation={"PubMed","Rinsho Shinkeigaku. 2005 Nov;45(11):899-901.", "16447757"}

SET Evidence = "The deposition of alpha-synuclein (aS), a product of pathogenic gene for dominantly inherited familial Parkinson's disease (PD; park1), as fibrillary aggregates like Lewy bodies (LB), is a hallmark lesion of a set of neurodegenerative disorders termed synucleinopathies, including sporadic PD and dementia with Lewy bodies (DLB). We found that aS is the major component of LBs and further identified a specific phosphorylation of Ser129 of insoluble aS by mass spectrometric analysis. The roles of DJ-1 and PINK-1, products of pathogenic genes for autosomal recessive forms of early-onset parkinsonism, have subsequently been examined. Overexpression of DJ-1 conferred cultured cells resistance to oxidative stress, suggesting an antioxidant function of DJ-1. We also confirmed the anti-PTEN function of DJ-1 that may promote cell survival, showing decreased phosphorylation of Akt through upregulation of PTEN activity upon siRNA knockdown for DJ-1. PINK-1, that had been identified as a gene upregulated by PTEN overexpression, turned out to be a protein kinase localized in mitochondria. Collectively, information derived from studies on pathogenic genes for familial PD will open up the way toward the clarification of the pathogenesis of PD, underscoring the roles of protein aggregation, proteolysis, oxidative stress and protein phosphorylation in PD."

#N
p(HGNC:PARK7) -| bp(GO:"response to oxidative stress")
p(HGNC:PARK7) -> bp(GO:"cytokine activity")

#D
p(HGNC:PARK7) -- path(MESHD:"Parkinson Disease")

UNSET STATEMENT_GROUP

Reference

Jankovic, J. J. T. E., & Tolosa. (2007). Parkinson's disease and movement disorders. E. Tolosa (Ed.). Lippincott Williams & Wilkins.

synonyms

PINK1

Younesi, E., Malhotra, A., Gündel, M., Scordis, P., Page, M., Müller, B., ... & Hofmann-Apitius, M. (2015).

PDON: Parkinson's disease ontology for representation and modeling of the Parkinson's disease knowledge domain. *Theoretical Biology and Medical Modelling*, 12(1), 1.



Shared semantics for Neurodegeneration Research

Synonym: "Substantia nigra pars compacta, dopaminergic cell"

reference: "http://neurolex.org/wiki/Category:Substantia_nigra_pars_compacta_dopaminergic_cell"

is Defined By: "Nigral dopaminergic cell is a neuron found in the midbrain of vertebrates. These neurons comprise most of the substantia nigra and mainly regulate motor and sensorimotor functions within the brain."

Description:

Soma Location: Substantia nigra pars compacta
Spine density on dendrites: Aspinous Dendrite Quality

Axon Specific Properties:
Axon projection laterality: Ipsilateral
Location of axon arborization: Nigrostriatal
Cellular synaptic target: Nigrostriatal medium spiny neuron
Neurotransmitter: Dopamine

Description: Substantia nigra pars compacta, dopaminergic cell

Equivalent classes:

Superclasses:

Inferred anonymous superclasses:

- has_part some Substantia nigra pars compacta
- has_part some Substantia nigra pars reticulata
- has_part some CA3, alveus
- has_part some Piriform cortex layer 1
- has_part some Neocortex layer 4
- has_part some Chemoarchitectural part
- has_part some CA1, alveus
- has_part some CA3, stratum lucidum
- has_part some Hindbrain
- has_part some Piriform cortex layer 2
- has_part some Aggregate regional part of brain
- has_part some Regional part of forebrain
- has_part some Molecular layer of dorsal cochlear nucleus
- has_part some Trigeminal nucleus
- has_part some Regional part of midbrain
- has_part some Composite part spanning multiple base regional parts of brain
- has_part some Regional part of hindbrain

Human Physiology Simulation Ontology (HUPSON)

(Gündel et al., 2013)

Brain Region and Cell- Type Terminology (BRCT)

(unpublished)

Clinical Trial Ontology (NDD-CTO)

(unpublished)

Alzheimer Disease Ontology (ADO)

(Malhotra et al., 2013)

Parkinson Disease Ontology (PDON)

(Younesi et al., 2015)

Multiple Sclerosis Ontology (MSO)

(Malhotra et al., 2015)

Biomarker Terminology

(Younesi et al., 2012)

Hypothesis Finder

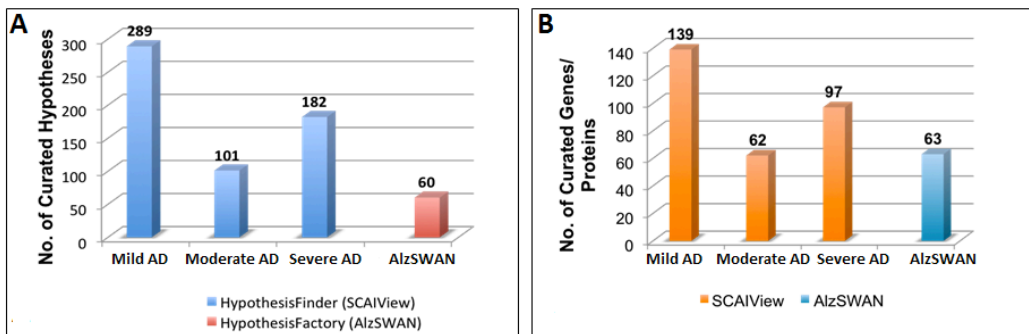
(Malhotra et al., 2013)

Pathway Terminology System

(Iyappan et al., 2016)

PTSD Terminology

(Kodamullil et al., in preparation)





Usage of Ontologies / Terminologies in Text Mining Services

**NDD-CTO
terminology
markup**

8. Long-term efficacy and safety of donepezil in the treatment of Alzheimer's disease: final analysis of a US multicentre open-label study.

PubMed PubMedCentral 10793322 **Authors:** Rogers, S L; Doody, R S; Pratt, R D; Ieni, J R **Date:** 2000-05 **Journal:** European neuropsychopharmacology : the journal of the European College of Neuropsychopharmacology **SciMago:** **Affiliation:** Eisai Co. Ltd., 6-10 Koishikawa 4 chrome, Bunkyo-ku, Tokyo, Japan.
☐ Statistics

This multicentre, open-label study evaluated the long-term efficacy and safety of donepezil in the treatment of patients with mild to moderately severe Alzheimer's disease (AD). The 133 patients who entered the study had previously completed a 14-week randomized, double-blind, placebo-controlled study with donepezil. In this open-label study, patients were treated initially with 3 mg per day donepezil, which could be increased to 5, 7 and 10 mg per day in a step-wise fashion. Patients attended the clinic for assessments at 3-week intervals for the first 12 weeks, then subsequently at 12-week intervals for up to 240 weeks (254 cumulative weeks). Efficacy was assessed using the Alzheimer's Disease Assessment Scale-cognitive subscale (ADAS-cog) and the Clinical Dementia Rating-Sum of the Boxes scale (CDR-SB), and data were compared with those predicted for historical untreated AD patients. During the first 6-9 months of the study, mean ADAS-cog and CDR-SB scores showed evidence of clinical improvement from baseline. After this time scores gradually deteriorated. Overall the decline was less than that estimated if this cohort of patients had not been treated. The most common adverse events were related to the nervous and digestive systems, and were generally mild and transient, resolving without the need for dose modifications. There was no evidence of hepatotoxicity. In conclusion, these data demonstrate that donepezil is a well-tolerated, realistic symptomatic treatment for AD over a period of up to 4.9 years. An interim report of the first 98 weeks of the study has been published previously.

MeSH: Aged; Aged, 80 and over;
Aged; Neuropsychological Tests;

Title and Me

1. Altered expression of zinc transporters-4 and -6 in mild cognitive impairment, early and late Alzheimer's disease brain.

PubMed 16580781 **Authors:** Smith, J L; Xiong, S; Markesbery, W R; Lovell, M A **Date:** 2006-07- **Journal:** Neuroscience **Affiliation:** Department of Chemistry, University of Kentucky, Lexington, KY 40536, USA.

☐ Statistics ☐ Select ID with comment:

Accumulating evidence suggests that a disruption of zinc (Zn) homeostasis may play a role in the pathogenesis of Alzheimer's disease. Although several Zn transporter proteins responsible for the regulation of Zn balance are present in the brain, there has been little study of these proteins in Alzheimer's disease. To determine if alterations of Zn transporter proteins exist, levels of Zn transporter-4, which functions to remove Zn from the cytoplasm to endosomal/lysosomal compartments, and Zn transporter-6, which allocates cytoplasmic Zn to the trans-Golgi network, were measured in the hippocampus/parahippocampal gyrus, superior and middle temporal gyrus, and cerebellum of subjects with mild cognitive impairment, early Alzheimer's disease, late stage Alzheimer's disease, and age-matched controls using Western blot analysis and protein specific antibodies. Our results show that Zn transporter-4 and Zn transporter-6 are significantly ($P < 0.05$) increased in hippocampus/parahippocampal gyrus of early Alzheimer's disease and Alzheimer's disease subjects. Zn transporter-6 is also increased ($P < 0.1$) in the superior and middle temporal gyrus of Alzheimer's disease brain.

**BRCO + ADO
terminology
markup**



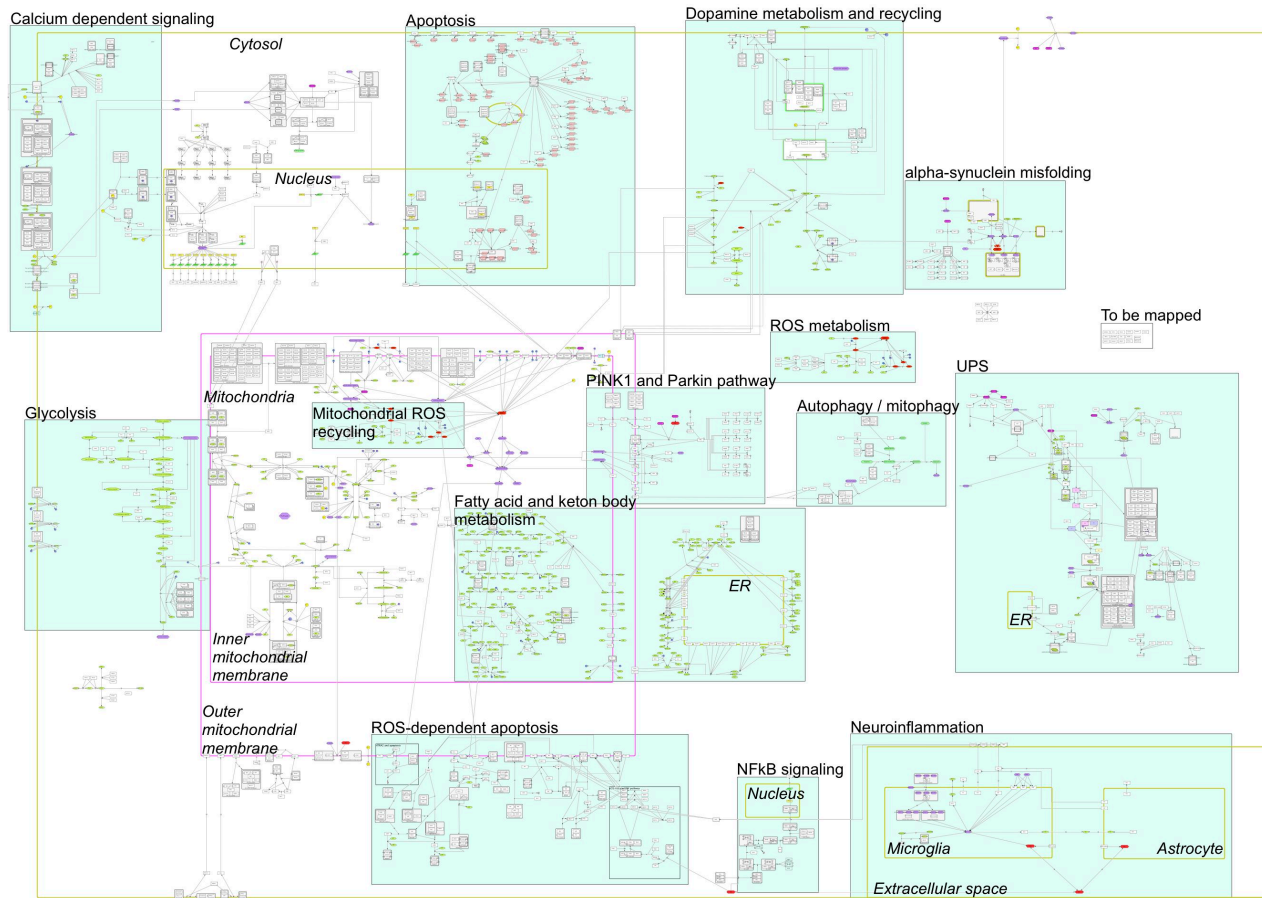


Alpha Tom
Kodamullil



Stephan
Gebel

Generating Models of Disease: A Plurality of Modeling Approaches



“PD map”
SBML model
representing
essential processes
and pathways in
Parkinson’s Disease
(generated by
partner LCSB)

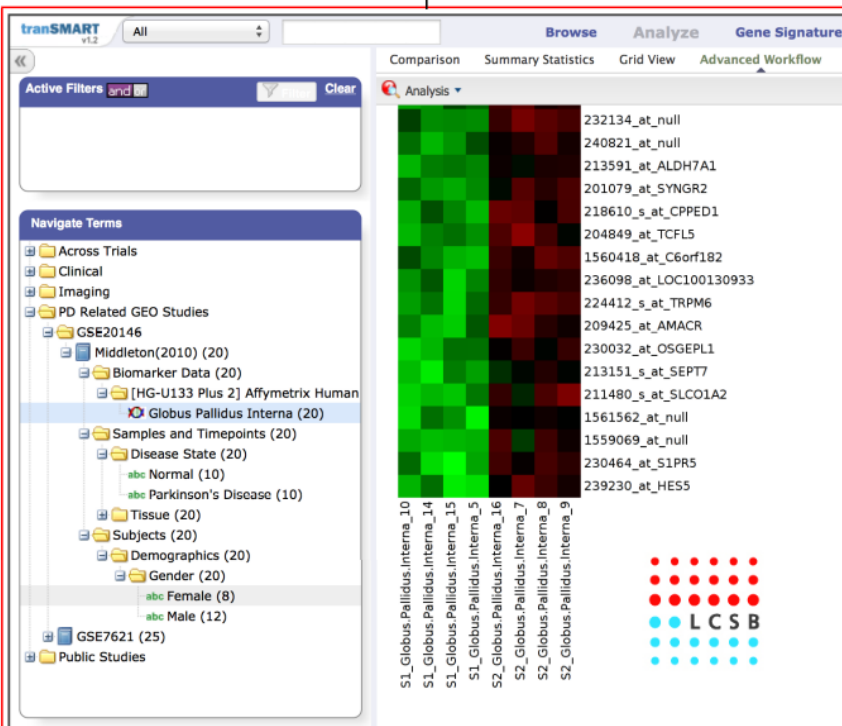
http://pdmap.uni.lu/pd_map/

Fujita, Kazuhiro A., et al. "Integrating pathways of Parkinson's disease in a molecular interaction map." *Molecular neurobiology* 49.1 (2014): 88-102.



Overlay Marker Selection Results to PD Map

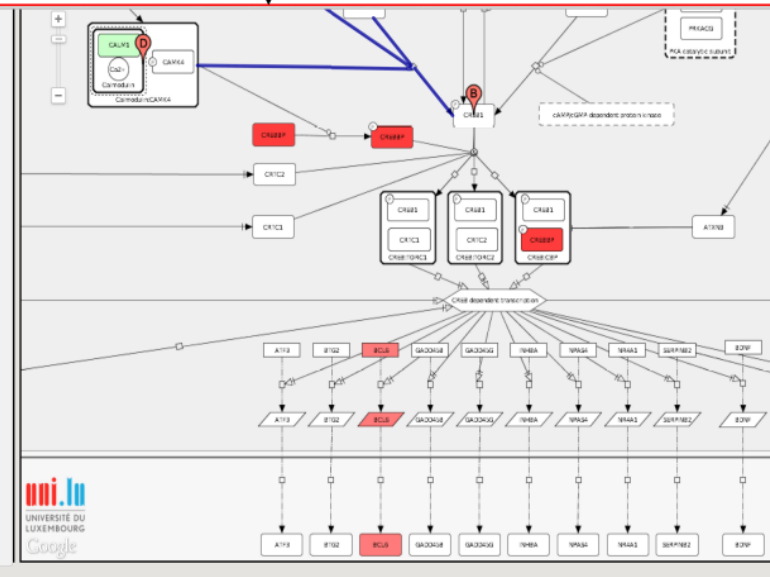
Marker selection from
GSE20146



Name	View
Normal	
PD Substantia Nigra FDR=0.01	
PD Substantia Nigra FDR=0.05	
Aging	
Pathways and compartments	

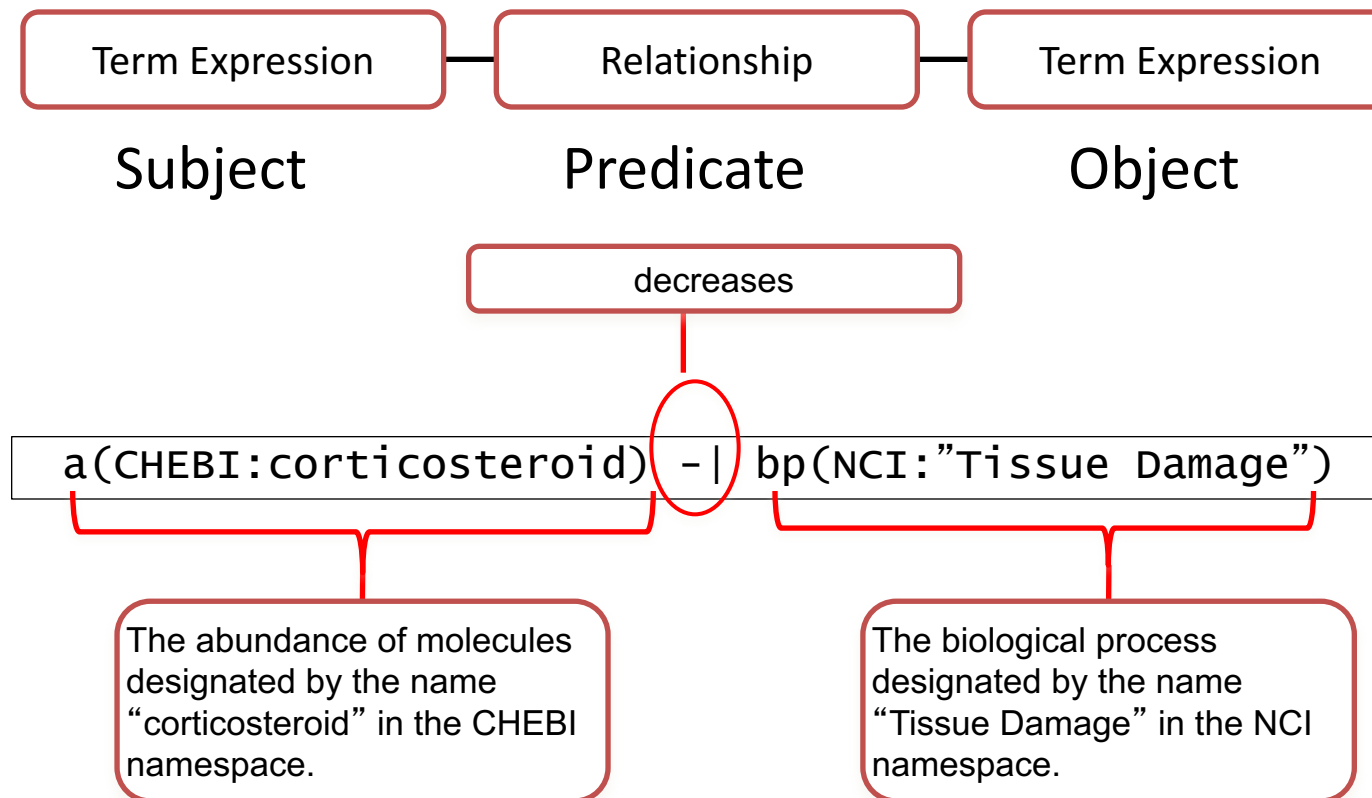
Custom layouts:

Name	Status	View	Edit
307870E19UCUUEJ8	OK		
02360C20FD66CD50	OK		
4D1AFF4C6773986B	OK		
30C020DD0285241B	OK		
2FE009B719F340D6	OK		
8BD85A3DF679C36A	OK		
1433791591	OK		
1433791762	OK		
1433791885	OK		
1433792016	OK		
1433792237	OK		
1433792296	OK		
1433792328	OK		





Capturing Knowledge on Causes and Effects: OpenBEL





OpenBEL: Capturing of Knowledge and “encoding” of data

Phosphorylation of **glycogen synthase kinase 3beta** at **Threonine, 668** **increases** the **degradation** of **Amyloid precursor protein**.

p (HGNC:**GSK3B**, **pmod** (P,T,668)) -> **deg** (**p** (HGNC:**APP**))

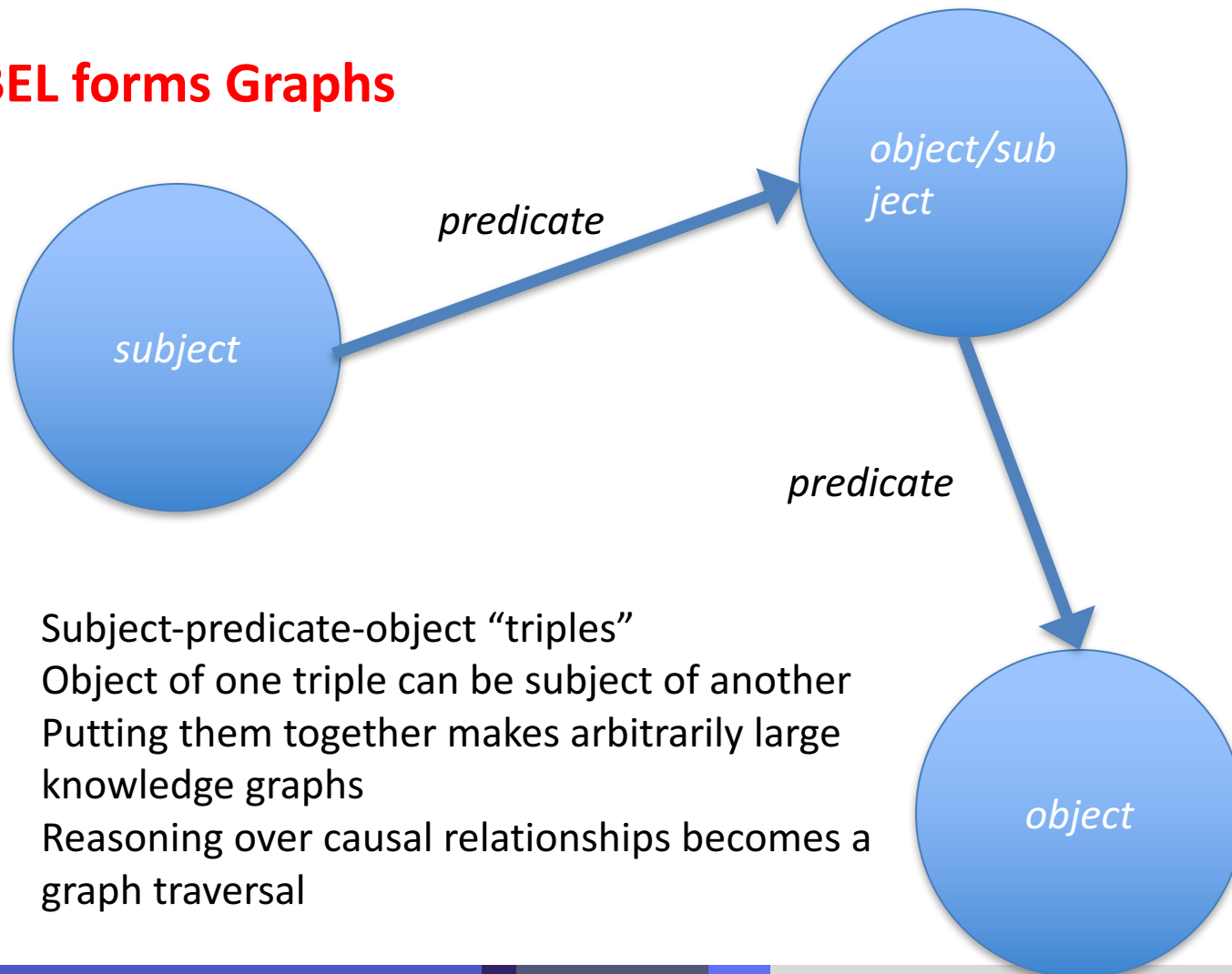
BEL Functions

Namespace Identifiers

Entity Definitions



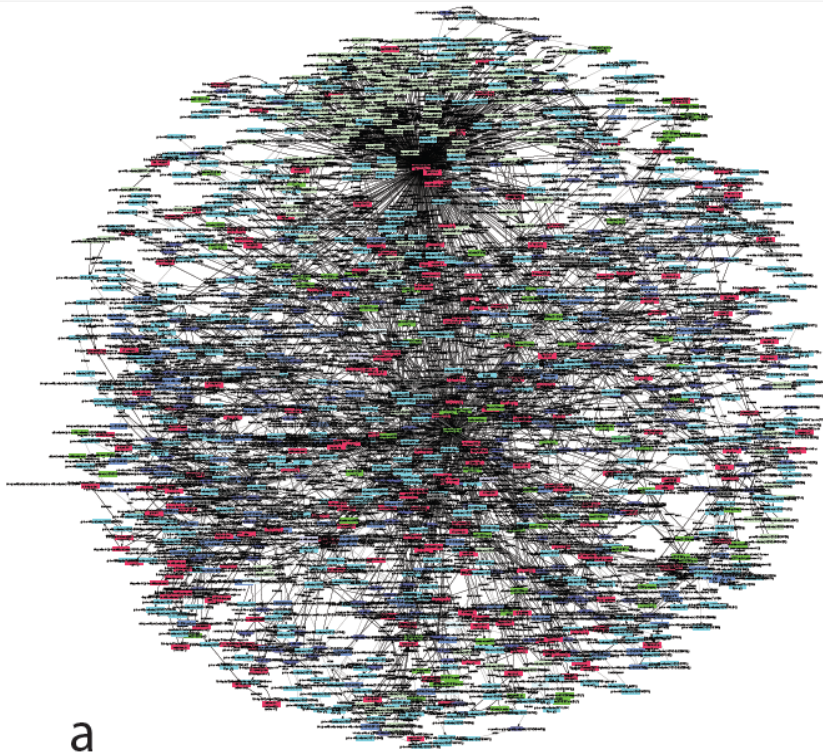
BEL forms Graphs



- Subject-predicate-object “triples”
- Object of one triple can be subject of another
- Putting them together makes arbitrarily large knowledge graphs
- Reasoning over causal relationships becomes a graph traversal

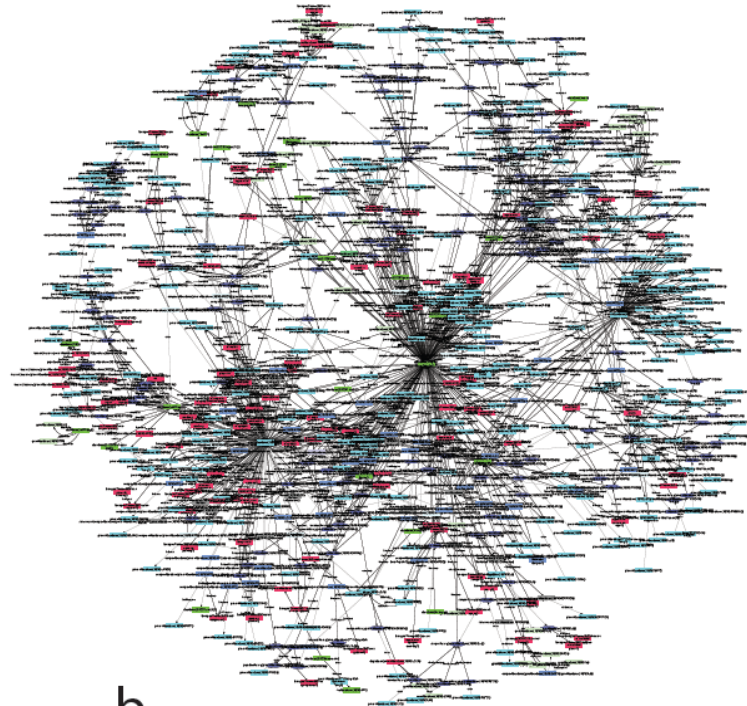


Model-driven Integration of Data- and Knowledge in AD



a

diseased



b

normal

Kodamullil, A. T., Younesi, E., Naz, M., Bagewadi, S., & Hofmann-Apitius, M. (2015). **Computable cause-and-effect models of healthy and Alzheimer's disease states and their mechanistic differential analysis.** *Alzheimer's & Dementia*, 11(11), 1329-1339.



The AETIONOMY Knowledge Base



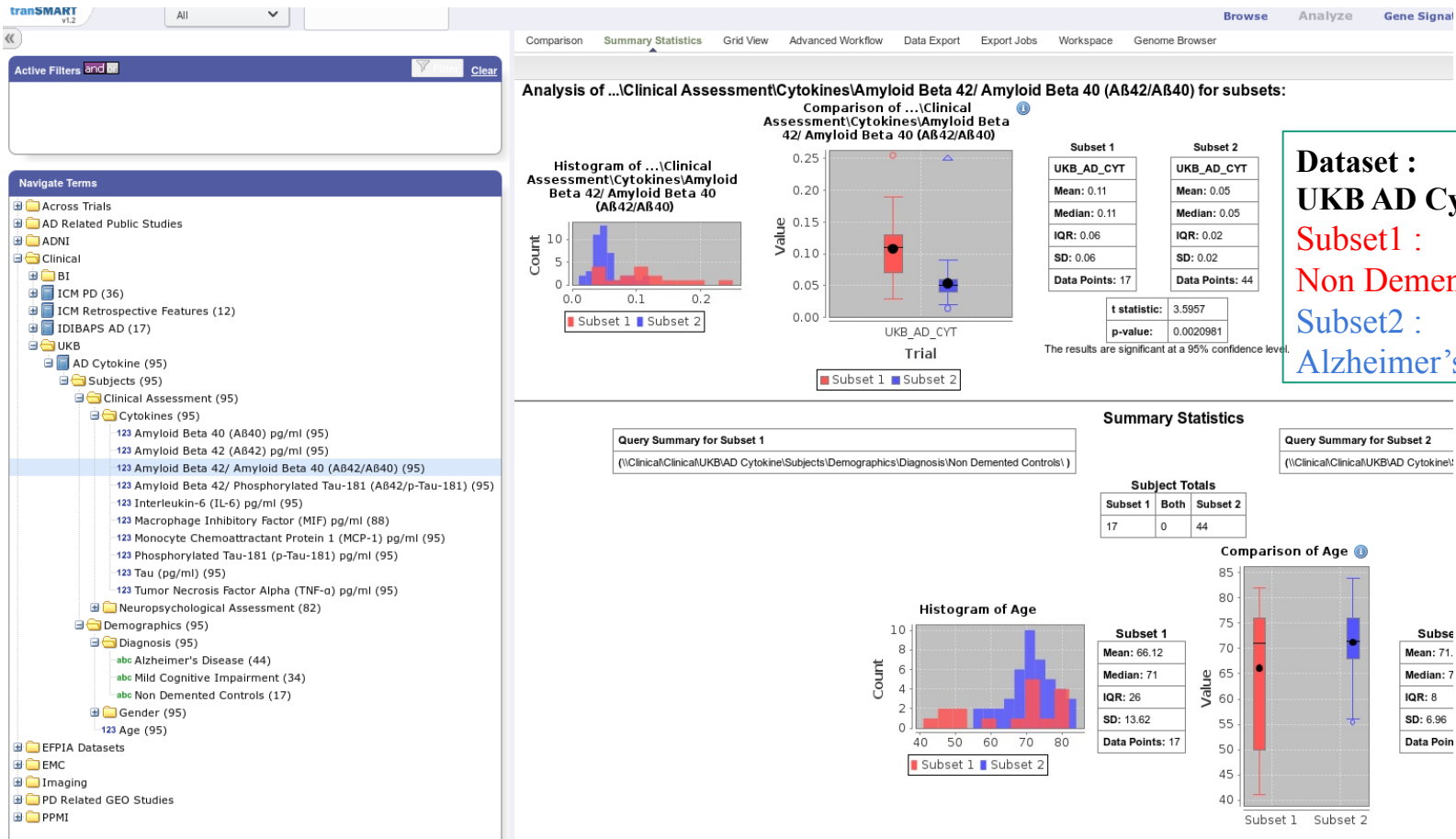
Christian Ebeling



Aishwarya Alex

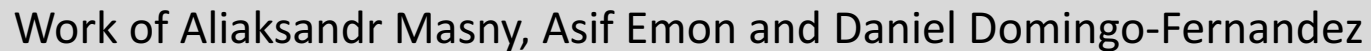


tranSMART : Summary Statistics for Selected Cohorts





<http://aetionomy.scai.fhg.de>







Step 2: Making Use of the Resources



Identification of Candidate Mechanisms: The Mining Strategies



Anandhi Iyappan



Shweta Bagewadi



Alpha Kodamullil



Erfan Younesi



Reverse Causal Reasoning (RCR; Catlett et al., 2013)

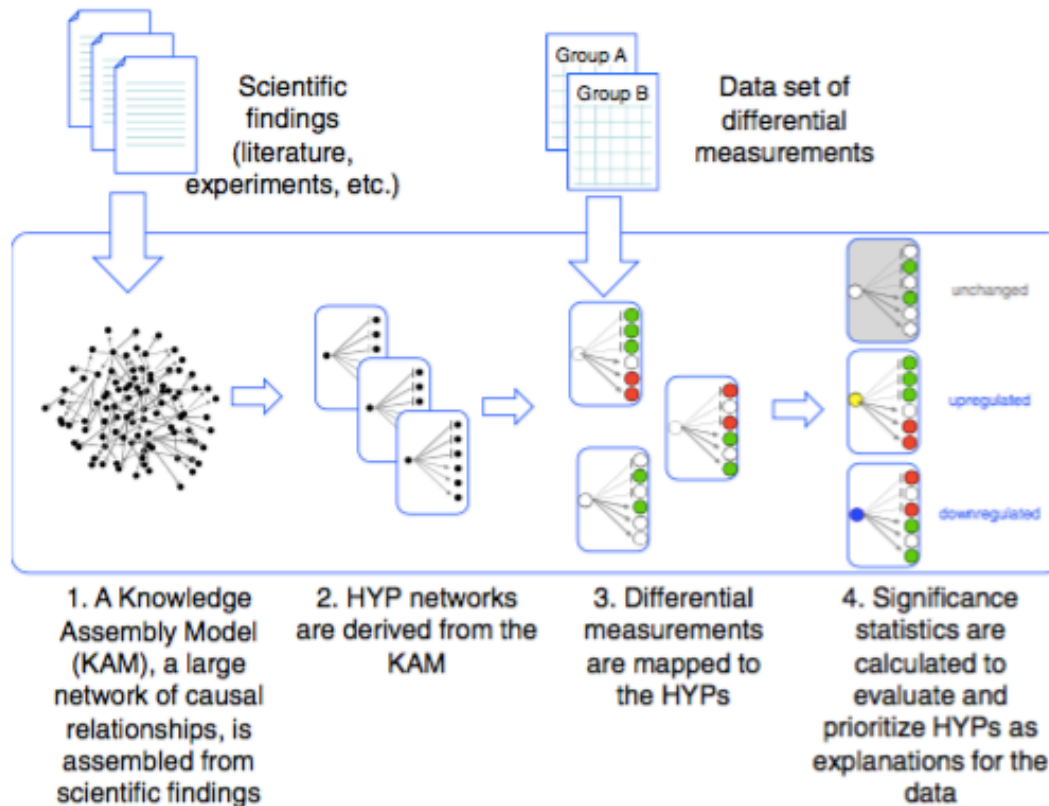
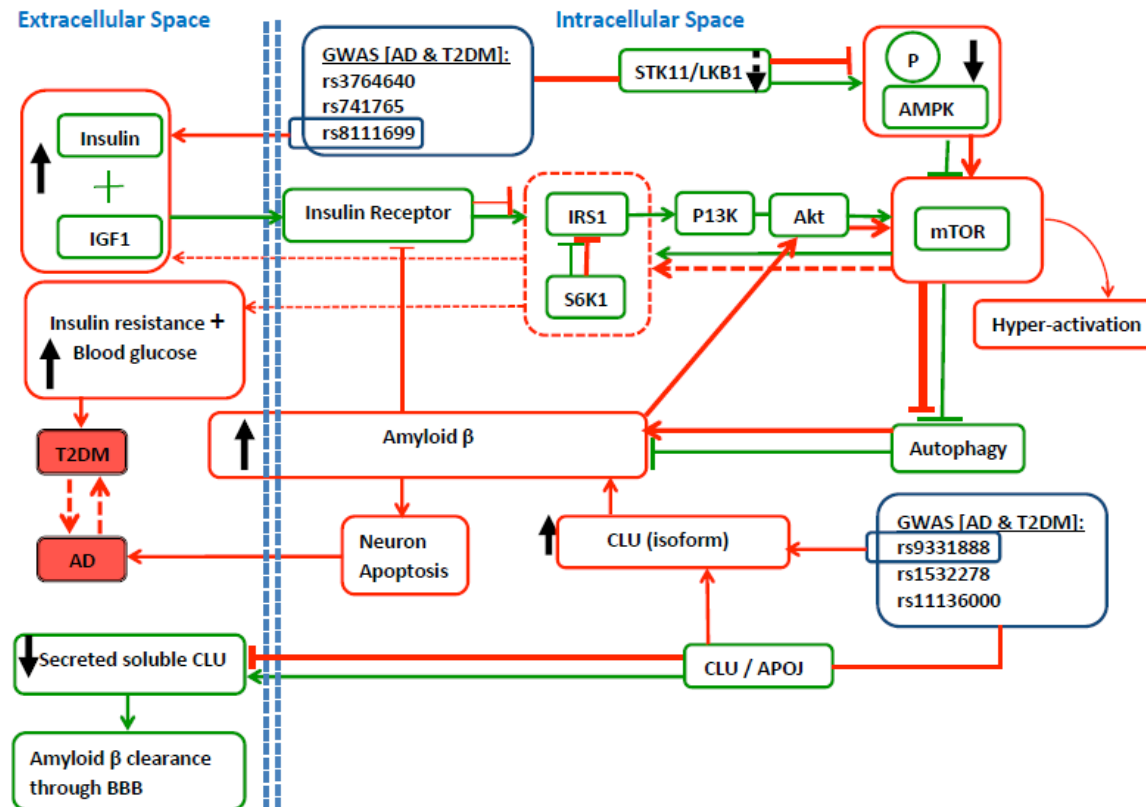


Figure 1 Overview of whistle. Whistle evaluates molecular mechanisms as potential explanations for gene expression data by mapping measurements and differentially expressed genes to a directed network of prior scientific knowledge.



A Mechanistic Link between AD and T2DM



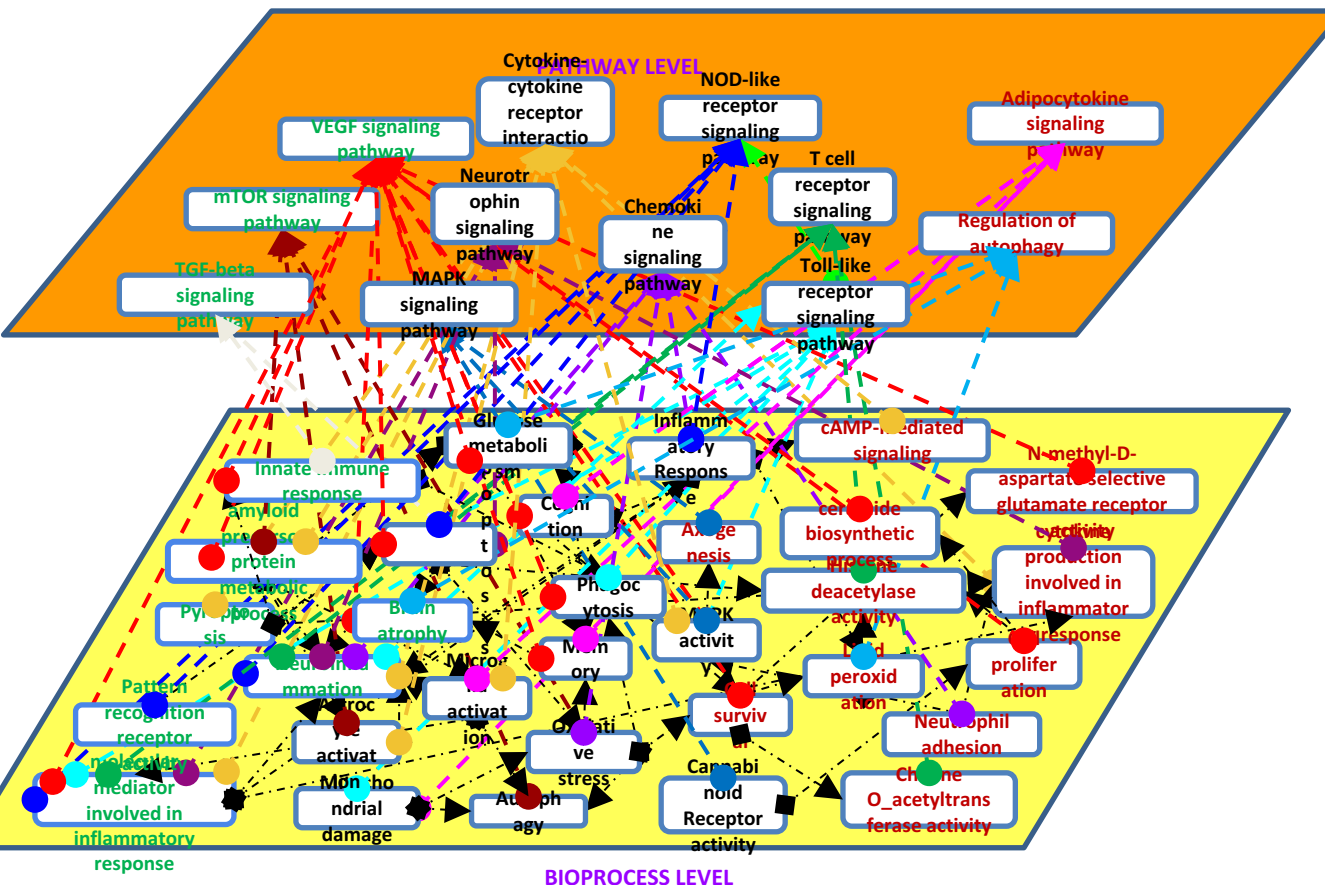
Mining of co-morbidity information results in the second mechanism-hypothesis generated in AETIONOMY: a possible link between insulin receptor pathway, mTOR-induced autophagy and APP peptide clearance

Supportive evidence from SNPs that are shared by AD and T2DM



Comparative Modeling of Neuroinflammation in Mice and Men

Kodamullil, A. T., et al., submitted



Separate modeling of causes-and-effects in neuroinflammation in mice and men reveals insight into the functional repertoire and the functional equivalence of rodent models. Our findings put a question mark behind the extensive usage of mouse models for neuroinflammation studies.



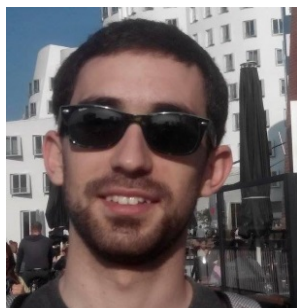
NeuroMMSigDB – a server for mechanism- enrichment



Christian
Ebeling



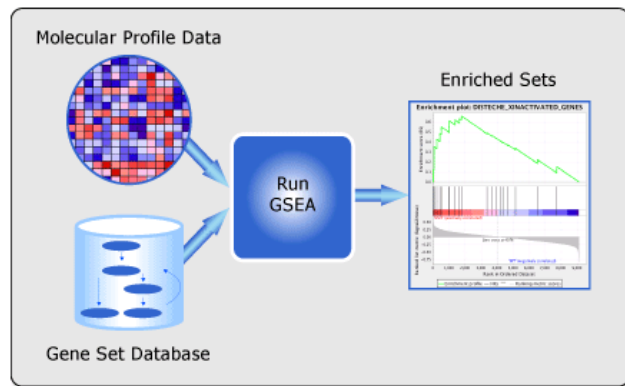
Alpha T. Kodamullil



Daniel
Domingo-Fernandez



An Adaptation of GSEA / MSigDB: Mechanism Enrichment Server



Gene Identifiers

APP
NOTCH1
NOTCH2
PSEN1
PSEN2

Compute Overlaps

☐ H: hallmark gene sets

☐ C1: positional gene sets

☐ C2: curated gene sets

☐ CGP: chemical and genetic perturbations

☐ CP: Canonical pathways

☐ CP-BIOCARTA: BioCarta gene sets

☒ CP-KEGG: KEGG gene sets

☐ CP-REACTOME: Reactome gene sets

☐ C3: motif gene sets

☐ MIR: microRNA targets

☐ TTF: transcription factor targets

☐ C4: computational gene sets

☐ CGN: cancer gene neighborhoods

☐ CM: cancer modules

☐ C5: GO gene sets

☐ BP: GO biological process

☐ CC: GO cellular component

☐ MF: GO molecular function

☐ C6: oncogenic signatures

☐ C7: immunologic signatures

show top 10 gene sets

with FDR q-value below 0.05

Compendia expression profiles

☒ Human tissue compendium (Novartis)

☐ Global Cancer Map (Broad Institute)

☐ NCI-60 cell lines (National Cancer Institute)

display expression profile

Gene families

show gene families

We have adapted the strategy underlying **GSEA / MSigDB**

(developed by the Broad Institute
<http://www.broadinstitute.org/gsea/msigdb/index.jsp>)

for the area of dementia research.

Compute Overlaps for Selected Genes

Collections	# Overlaps Shown	# Gene Sets in Collections	# Genes in Comparison (n)	# Genes in Universe (N)
CP-KEGG	3	186	5	45956

Click the gene set name to see the gene set page. Click the number of genes [in brackets] to download the list of genes.

Color bar shading from light green to black, where lighter colors indicate more significant FDR q-values (< 0.05) and black indicates less significant FDR q-values (>= 0.05).

Save to: Excel | GenomeSpace

Gene Set Name [# Genes (K)]	Description	# Genes in Overlap (k)	k/K	p-value	FDR q-value
KEGG_NOTCH_SIGNALING_PATHWAY [47]	Notch signaling pathway	4		4.8 e-12	8.92 e-10
KEGG_ALZHEIMERS_DISEASE [169]	Alzheimer's disease	3		4.86 e-7	4.52 e-5
KEGG_DORSO_VENTRAL_AXIS_FORMATION [25]	Dorso-ventral axis formation	2		2.84 e-6	1.76 e-4



NeuroMMSig DB Server is different from GSEA / MSigDB

Molecular Profiles are highly specific for Neurodegenerative Diseases: the “profiles” or “signatures” in NeuroMMSigDB are graph models representing pathophysiology context

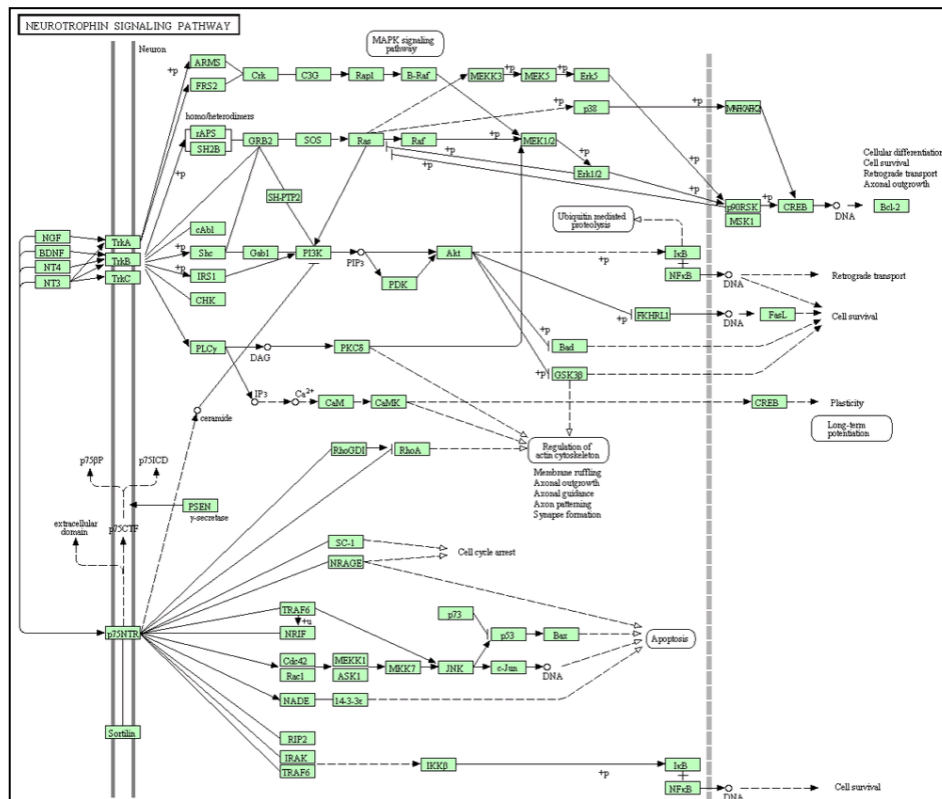
NeuroMMSigDB entries are Multimodal: Multiple entity types constitute knowledge based mechanistic models. They contain genes, proteins, chemicals, ions, drugs, SNPs, epigenetics, imaging features, cognitive tests, clinical data, etc.

Mechanisms are not pathways: canonical pathways (KEGG, REACTOME etc) are usually not disease specific. Pathways representing “how stuff works” in a general way, pathways are **not disease mechanisms**. Dysregulation of pathways may be a disease mechanism.
Examples:

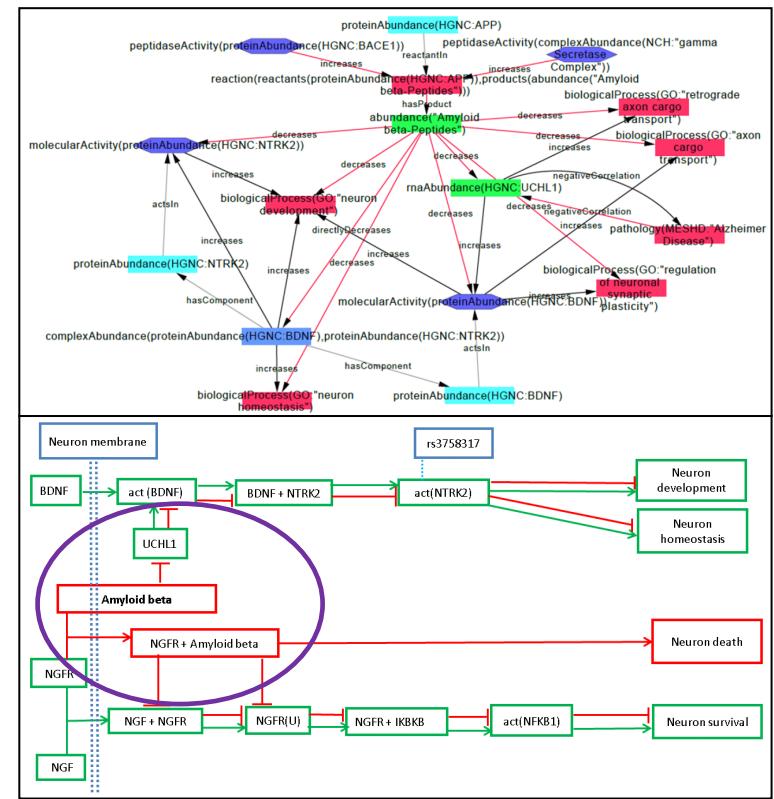
- According to KEGG, there are only 10 pathways under NervousSystem
- Not all genes and relationships described in one canonical pathway **may or may not be involving as same as** in a disease specific mechanism or **some genes are irrelevant** to disease context.



Canonical Pathways are NOT Disease Mechanisms



Canonical Pathway



Cause and effects of an entity from BEL mechanistic model



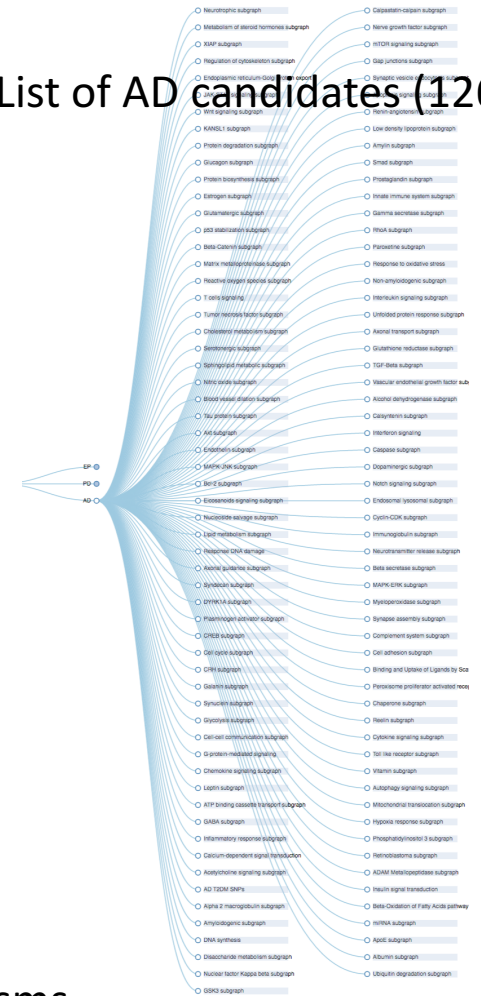
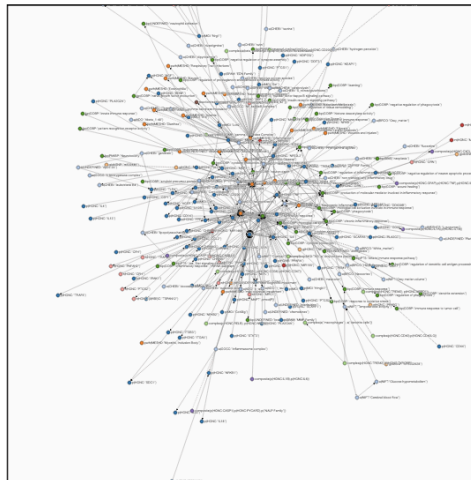
NeuroMMSigDB – the mechanism-inventory

CHI3L1 (YKL-40) subgraph

List of PD candidates (76)

List of AD candidates (126)

Inflammatory response subgraph



Domingo-Fernandez et al., submitted

Subgraph example and tree representations of candidate mechanisms



Current Design of the NeuroMMSigDB Mechanism Inventory

Root Pathways	Sons of Root Pathways	BEL Sub-Networks	BRCO Terms associated from BEL models	Genetic Variants from literature	Genes associated with SNPs	PMIDs for Genetic variants	Imaging Features	Brain Region	PMIDs for imaging	Genes from GE data
Innate immune system pathway	Cytokines pathway		astrocytes, microglia, neuron	rs1800587, rs1800896 (protective),	IL1-A, IL10	24103372, 23838435	neuronal damage, axonal degeneration, Serotonin	striatum, hippocampus,	15465624, 17189680, 25069615,	IL13, TNFRSF25, ACVR1, TNFRSF21, TNFRSF11B, GH1, BMPR1B, IL17RA, CCL22, CXCL2, KIT, FLT1, LIFR, AMHR2, IFNL2, TNFSF8, CTF1 IL1B, CLCF1, CX3CR1, NGFR,, EPOR, CCL3L3, LEP, IFNAR1, IFNGR1, PDGFRB
	Tumor necrosis factor pathway		astrocytes, hippocampus, brain, neuron	rs1799724	TNF-a	21509504	hippocampal volume, neuronal damage,	hippocampus, cortex, amygdala	24938671, 22666474, 19320056, 15626822	-



Use Case Scenarios for Mechanism-Enrichment: Genes

INPUT	OUTPUT	
List of differential expressed genes	Enriched Mechanisms from disease specific model	
<ul style="list-style-type: none"> ✓ APP ✓ PSEN ✓ NOTCH1 ✓ NOTCH2 	<p>Amyloid beta signaling</p> <p>Notch signaling</p>	



Use Case Scenarios for Mechanism-Enrichment: Genetics

INPUT	OUTPUT		
List of SNPs from a disease subgroup	Associated genes	Enriched Mechanisms	
rs12769316, rs1056890, rs11160707, rs1799724	NFKB2, TNF	Nuclear factor kappa signaling, Tumour Necrosis Factor signaling	



Ranking of Candidate Mechanisms

1. Map gene expression values (different stages of the disease) to BEL networks

2. Devise a scoring function
 - Apply Network Perturbation Amplitude (NPA) algorithm (*see the work of Florian Martin, Julia Hoeng, and Manuel Peitsch on that method*)
 - Calculate score for dysfunctional mechanism(s) for different stages
 - $$\text{Score} = \frac{1}{N} \sum_{i=1}^N S_i \cdot \beta_i$$

where
 β is \log_2 fold change
 S is the sign (+1 for increase, -1 for decrease)
 N is the no. of downstream nodes
 - Rank mechanisms based on the score



Ranking of Candidate Mechanisms part II

Represent clinical data in Bayesian dependency graphs

Devise a scoring function

Systematically test subgraphs in the conditional dependency graph for their concordance with BEL-encoded cause-and-effect graphs

Score each individual triple match

Score each individual directionality match

Flag concordance / discordance areas

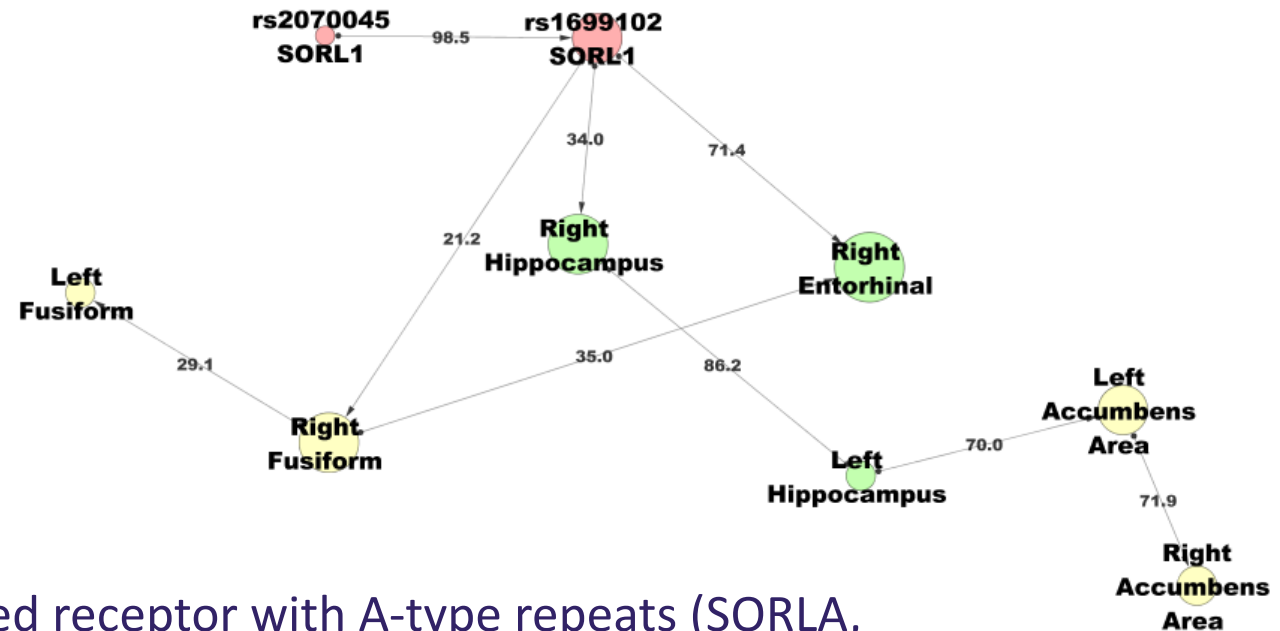


Conditional Dependency Graph representing Patient Level data: Bayesian Network learned from ADNI

Work of Shashank Khanna (Fraunhofer)
Supported by Prof. Holger Fröhlich (UCB)

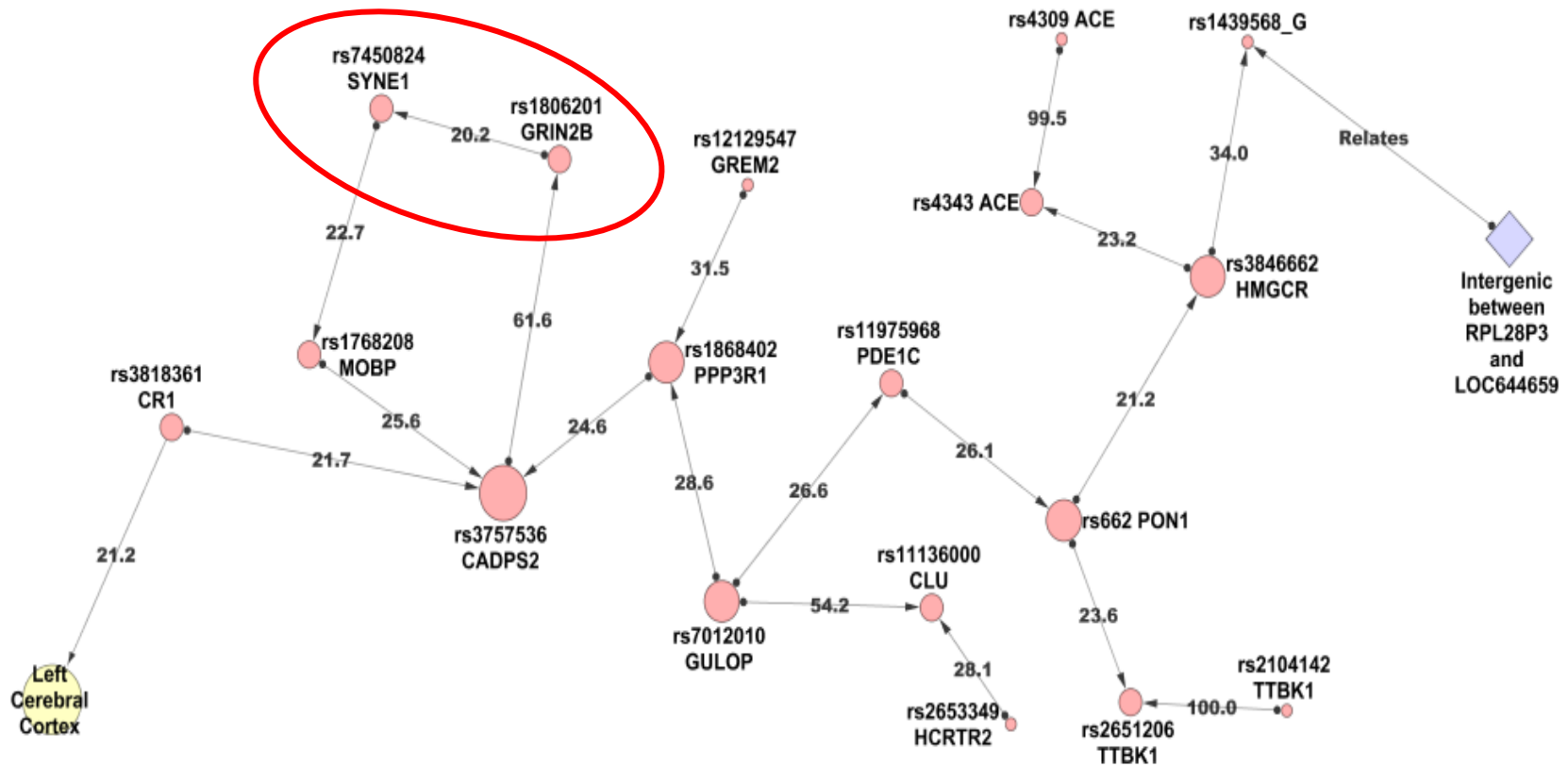


Bayesian Network links SNPs to Brain Regions



Sorting protein-related receptor with A-type repeats (SORLA, also known as LR11) is a type 1 membrane protein highly expressed in neurons of the cortex, hippocampus, and cerebellum.^{1,2}

Genetic data and protein levels revealed that two SNPs in SORL1, **rs2070045** and **rs1699102**, are associated with reduced SORLA expression levels in the brain

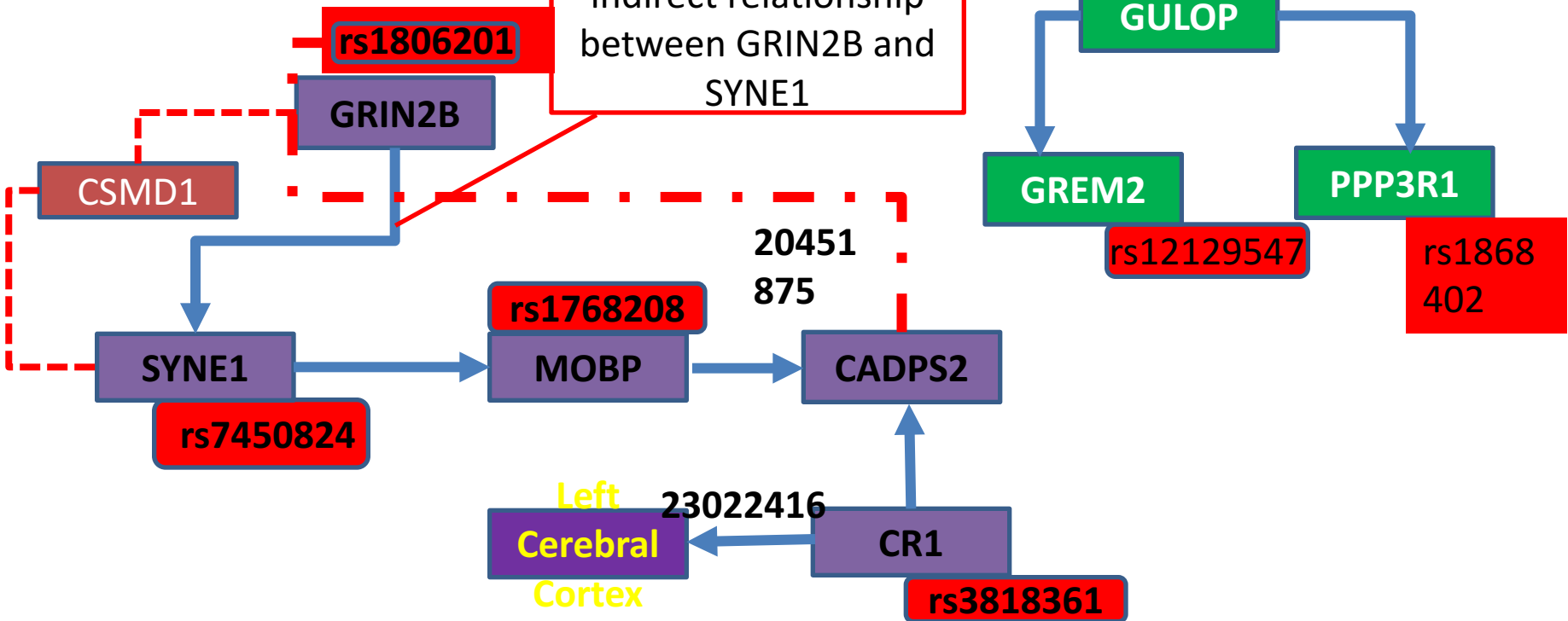


A link between GRIN2B and SYNE1 is shown by the BN.



“Learning” indirect relationships from data

Bayesian network was able to learn the indirect relationship between GRIN2B and SYNE1



From literature we get to know that GRIN2B is connected to CSMD1; CSMD1 is regulating the expression of gene SYNE1 btw: This would be represented in a BEL model. Since we did not have any SNP related to CSMD1 in our data, therefore this link was generated by the BN but the indirect link between GRIN2B and SYNE1 was created.



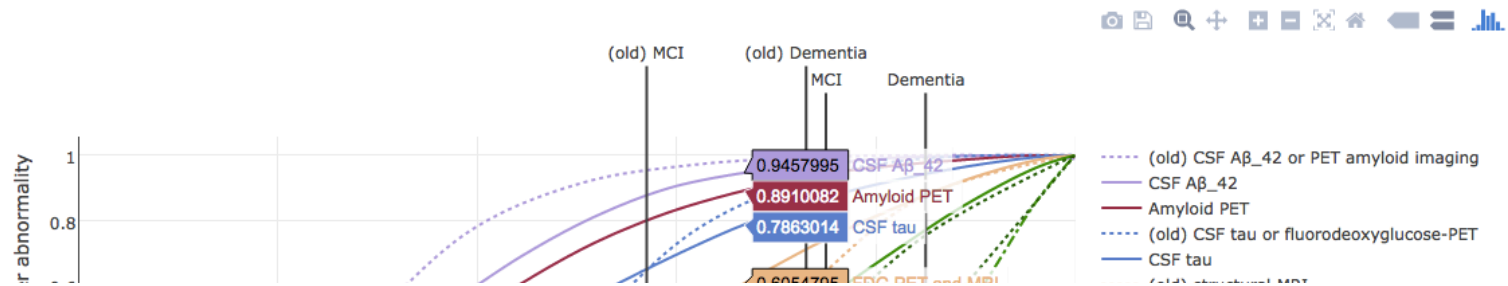
Temporal and Spatial Representation of Simulated Patients: Virtual Dementia Cohort

Marc Jacobs
Sven Hodapp
Meemansa Sood

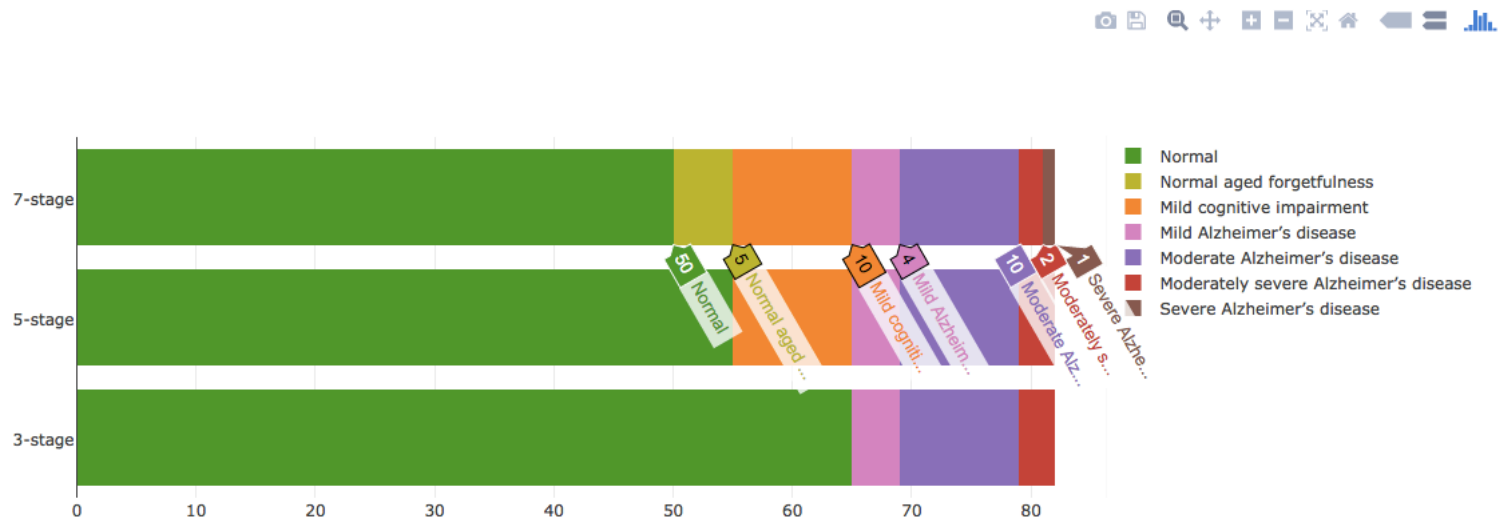
for the EPAD
consortium

EPAD Longitudinal Study Viewer

Hypothetical longitudinal standard model for Alzheimer's disease



Clinical stages of Alzheimer's disease



Referen

1. Jac
2. Jac
3. Wir
4. Hyr

<http://epad.scai.fraunhofer.de/app/alzheimer-model>

Extraction from Tables

Amyloid β deposition, neurodegeneration, and cognitive decline in sporadic Alzheimer's disease: a prospective cohort study

	Healthy controls (n=145)	Mild cognitive impairment (n=36)	p value*	Alzheimer's disease (n=19)	p value*
Age, years	71.3 (7.1)	74.6 (6.5)	0.012	69.8 (9.4)	0.49
Male sex	74 (51%)	20 (56%)	0.71	10 (53%)	1.00
MMSE	28.9 (1.1)	27.3 (2.1)	<0.0001	22.0 (2.9)	<0.0001
CDR-SOB	0.06 (0.3)	1.03 (0.7)	<0.0001	3.84 (1.1)	<0.0001
Positive for APOE ϵ 4	58 (40%)	20 (58%)	0.037	12 (63%)	0.047
Years of education	13.6 (3.7)	13.0 (3.8)	0.36	12.6 (3.8)	0.28
Episodic memory composite score	-0.23 (0.88)	-2.10 (0.91)	<0.0001	-3.21 (0.6)	<0.0001
Non-memory composite score	-0.15 (0.65)	-0.77 (0.80)	<0.0001	-2.46 (1.19)	<0.0001
Grey matter volume (cm ³)†	349 (15)	339 (16)	0.0012	326 (23)	0.0008
Hippocampal volume (cm ³)†	4.18 (0.30)	3.76 (0.60)	0.005	3.92 (0.37)	0.014
Amyloid β burden (SUVR)	1.38 (0.39)	1.94 (0.64)	<0.0001	2.27 (0.43)	<0.0001
High ¹¹ C-PiB retention	38 (26)%	24 (67%)	<0.0001	18 (95%)	<0.0001

Data are mean (SD) or number (%) unless otherwise stated. MMSE=mini-mental state examination. CDR-SOB=clinical dementia rating scale sum of boxes. APOE=apolipoprotein E. SUVR=standard uptake value ratio. ¹¹C-PiB=Carbon-11-labelled Pittsburgh compound B. *Compared with healthy controls. †Grey matter and hippocampal volumes normalised to intracranial volume.

Table 1: Characteristics of the study cohort

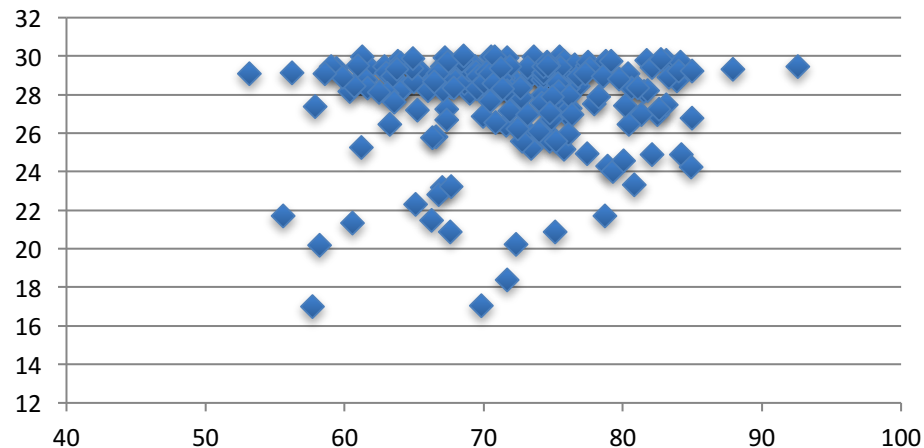


Generation of a Virtual Cohort

Male		Positive for		Years of		Episodic	Non-	Grey	Hippoca	Amyloid	High	DX
Age	sex	MMSE	CDR-SOB	APOE ε4	education	memory composite score	memory composite score	matter volume (cm3)†	mpal volume (cm3)†	β burden (SUVR)	11C-PiB retention n	
1	75 M	26	0,009	1	9	0,532	-0,275	354,847	3,947	1,315	1	NL
2	72 M	29	-0,031	1	16	-0,111	-1,934	348,312	3,803	1,585	1	NL
3	82 M	27	0,246	1	8	-1,020	0,364	335,034	4,225	1,706	1	NL
4	64 M	30	-0,221	1	9	0,403	-0,212	351,737	4,381	1,112	1	NL
5	59 M	29	-0,825	1	9	-0,480	-0,517	355,043	4,123	1,888	1	NL
6	74 M	28	-0,104	1	20	-0,176	0,056	318,458	4,247	1,577	1	NL
7	64 M	28	-0,027	1	12	1,750	-0,506	358				
8	65 M	27	-0,239	1	12	0,207	-0,794	346				
9	74 M	29	-0,109	1	19	0,570	0,684	375				
10	73 M	29	0,171	1	14	0,431	-0,352	358				
11	82 M	30	0,373	1	13	0,985	-0,159	337				
12	67 M	29	0,600	1	14	0,167	0,855	345				
13	74 M	29	0,356	1	13	-0,520	-0,049	324				
14	70 M	27	0,043	1	17	-0,830	-0,645	335				
15	62 M	29	-0,039	1	5	1,828	-1,137	344				
16	75 M	29	-0,386	1	18	1,376	0,292	356				
17	72 M	30	0,194	1	18	0,394	-0,387	346				
18	61 M	30	0,183	1	11	-0,769	0,622	357				
19	69 M	29	0,087	1	12	-0,346	0,611	320				
20	67 M	30	0,332	1	11	-0,373	-0,603	384				
21	71 M	28	0,093	1	17	-0,650	-0,134	354				
22	75 M	30	0,419	1	19	1,035	0,440	347				
23	68 M	28	0,092	1	14	-1,389	-1,551	377				
24	69 M	29	0,033	1	13	-0,013	0,522	354				
25	71 M	30	-0,097	1	13	1,732	-0,092	344				

Sampling of distributions taken from the literature

MMSE vs Age



Task: Correlating Biomarkers to Disease Stages

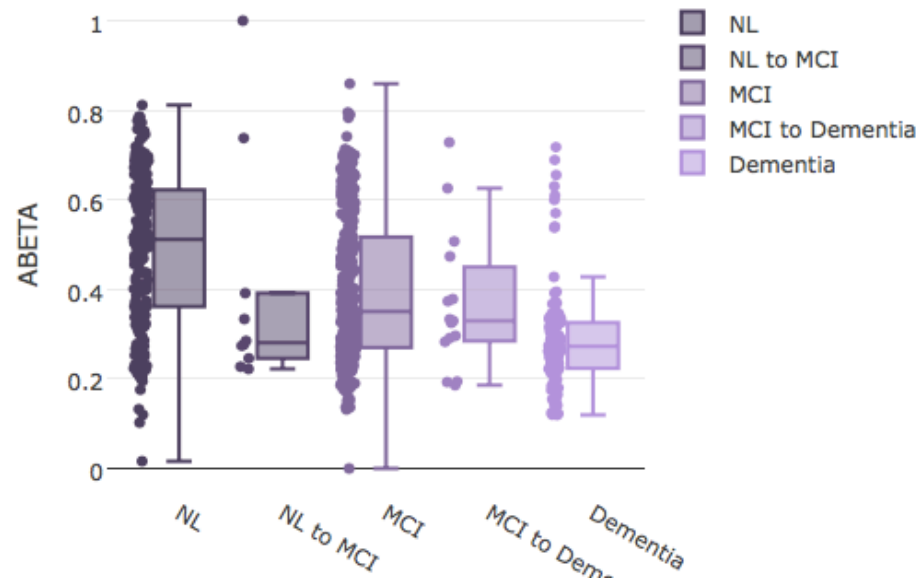
ADNI data

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Meemansa, Sven, Marc. *Fraunhofer SCAI: ADNI Plot Experiment 1* 2016 n/a.

[https://api.scaiview.com/\\$\\$:header/adni.experiment1](https://api.scaiview.com/$$:header/adni.experiment1)

Distributions
taken from
patient data





The Virtual Dementia Cohort

As never seen before:

- Here should have been the Virtual Dementia Cohort video -



The People and the Institutions behind the Project



AETIONOMY Partners

