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Item response models for analysing assessments in rare diseases

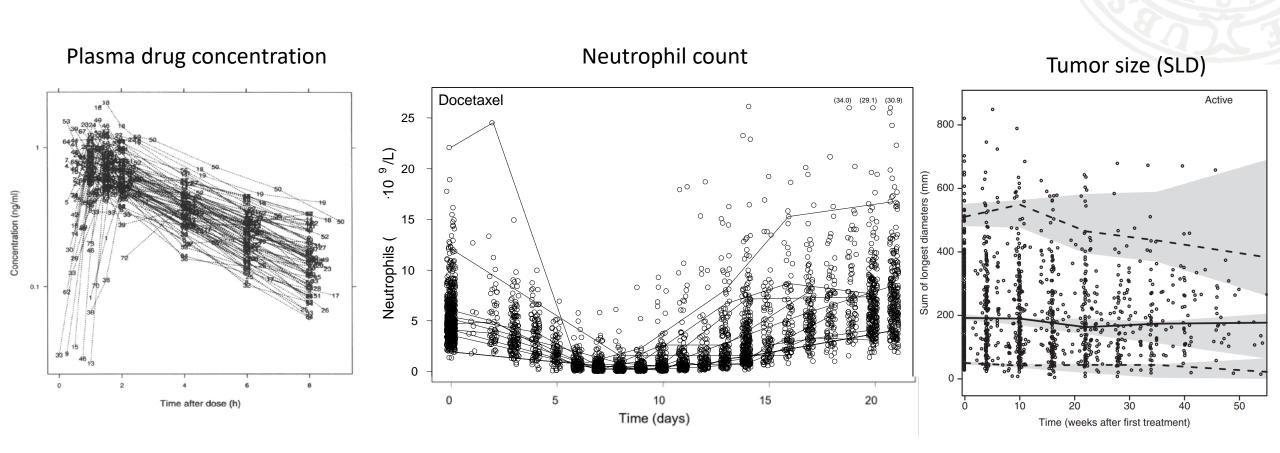
Mats O Karlsson

Department of Pharmacy Uppsala University Uppsala, Sweden

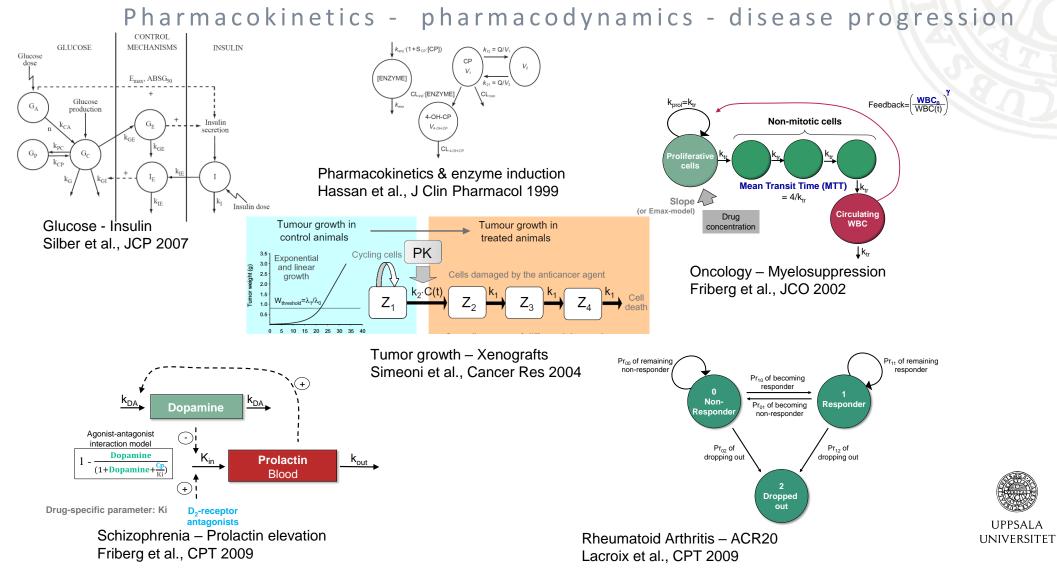


Pharmacometrics

Pharmacokinetics - pharmacodynamics - disease progression



Pharmacometrics



Drug development and model building Learning and confirming

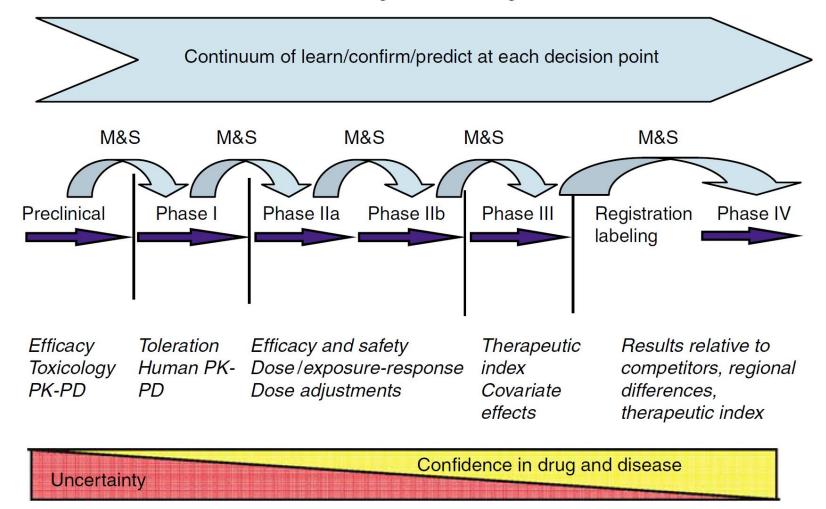
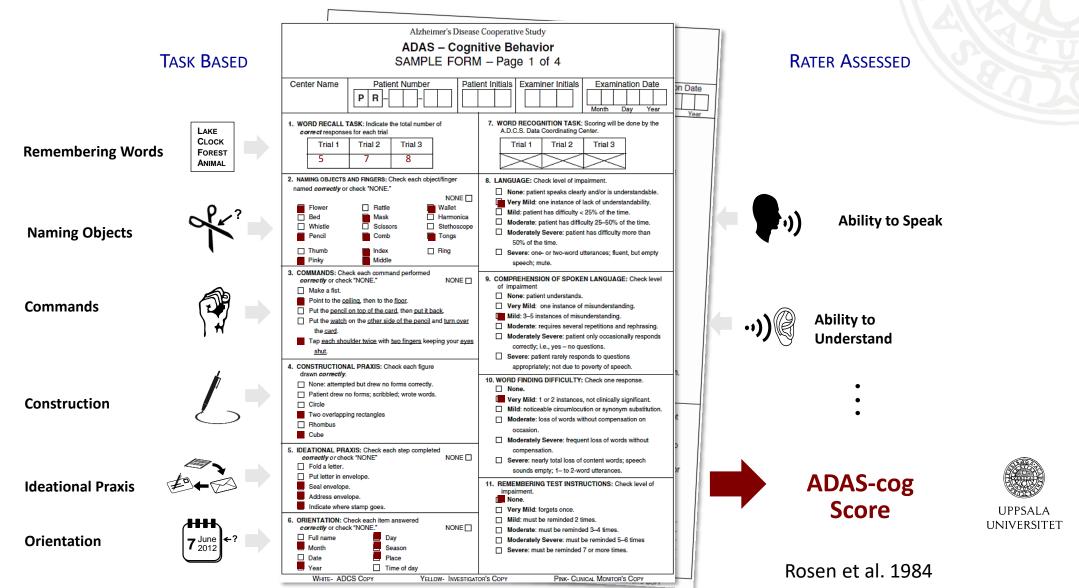


Figure 1 Modeling and simulation (M&S) are performed before each decision point to quantitatively assess risk in moving forward. The drug and disease model is continuously updated to include new information acquired during drug development.

Lalonde et al. Clin Pharmacol Ther 82:21-32 (2007)

ADAS-cog test for Alzheimer's Disease patients



Types of Clinical Outcome Assessments

Patient-reported outcome (PRO) measures

Reports come directly from the patient

Clinician-reported outcome (ClinRO) measures

Reports come from a trained health-care professional using clinical judgment

Performance outcome (PerfO) measures

A measurement based on standardized task(s) actively undertaken by a patient according to a set of instructions

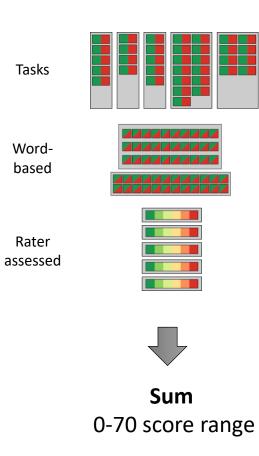
Observer-reported outcome (ObsRO) measures

Reports come from someone other than the patient or a health professional (e.g., a parent or caregiver) who has opportunity to observe the patient in everyday life



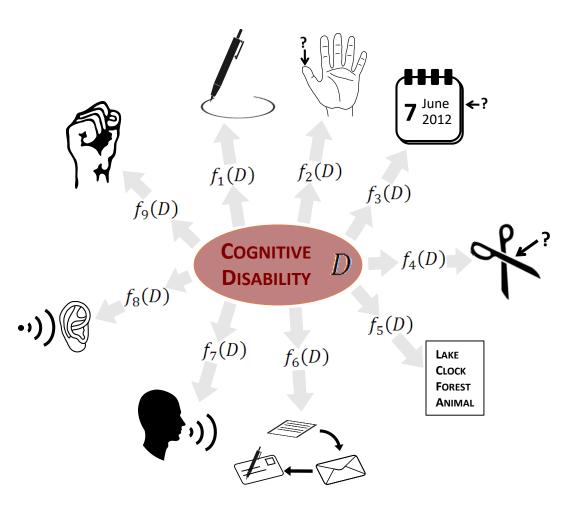
ADAS-Cog in Alzheimer's Disease

Alzheimer's Disease Assessment Scale - Cognition





Responses assumed dependent on an underlying Cognitive Disability

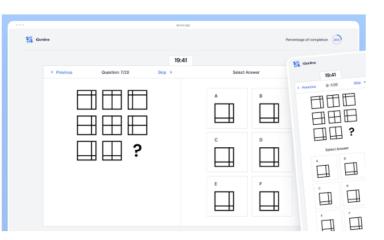




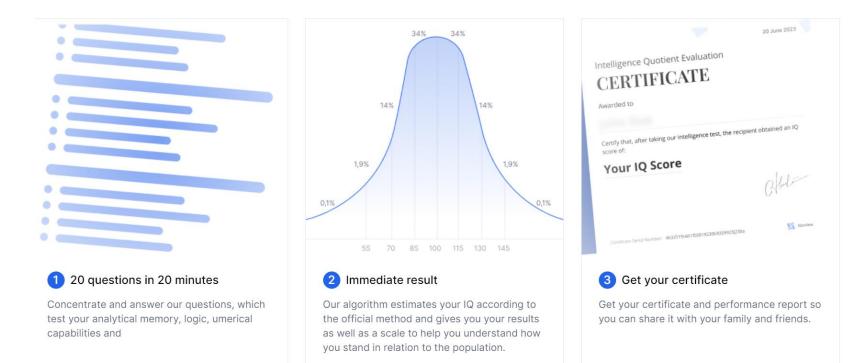
Official IQ Test

The average IQ score in Europe is 100. Are you ready to test your brain?

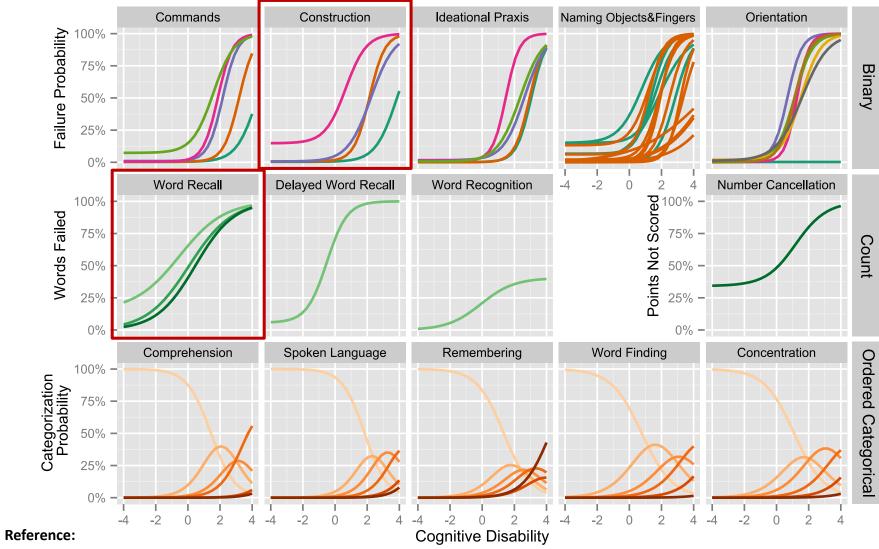
ightarrow Test My IQ Now!



How does it work?



Item Characteristic Curves ADAS-Cog





Ueckert et al. Pharm Res 31(2014)



IRT Analysis of the SARA in ARCAs

Item Response Theory

Item-based analysis

Scale for the Assessment and Rating of Ataxia

Clinical Outcome Assessment (COA)

Autosomal Recessive Cerebellar Ataxias

Rare Neurodegenerative Disease (RND)



Autosomal Recessive Cerebellar Ataxias (ARCAs) a heterogenous group of rare and ultra-rare neurodegenerative diseases



Progressive disease

 Loss of coordination & ambulation Affects the cerebellum and associated tracts

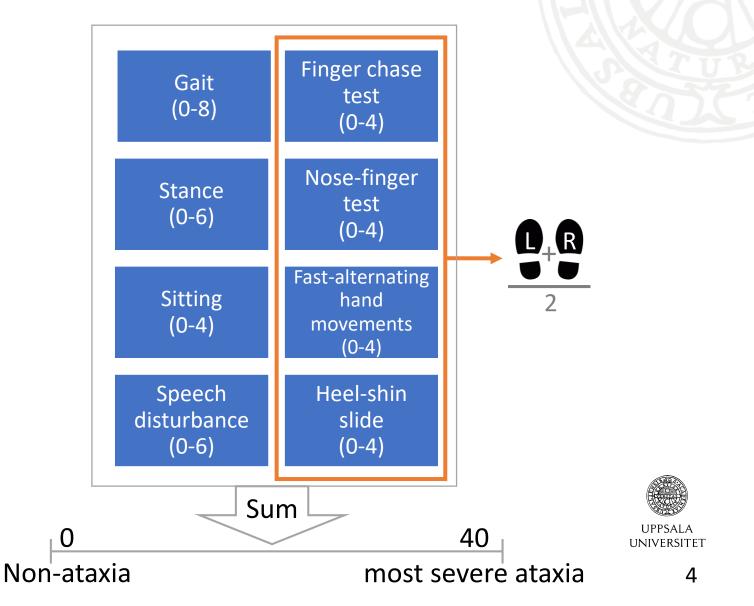


Genetically defined >200 disease types



How to measure the ataxia severity? Scale for the Assessment and Rating of Ataxia (SARA)

- The most widely used outcome measure for ataxias
- Developed in 2004
- Clinician reported outcome (ClinRO)



SARA as a primary outcome measure in treatment trials?

Problem

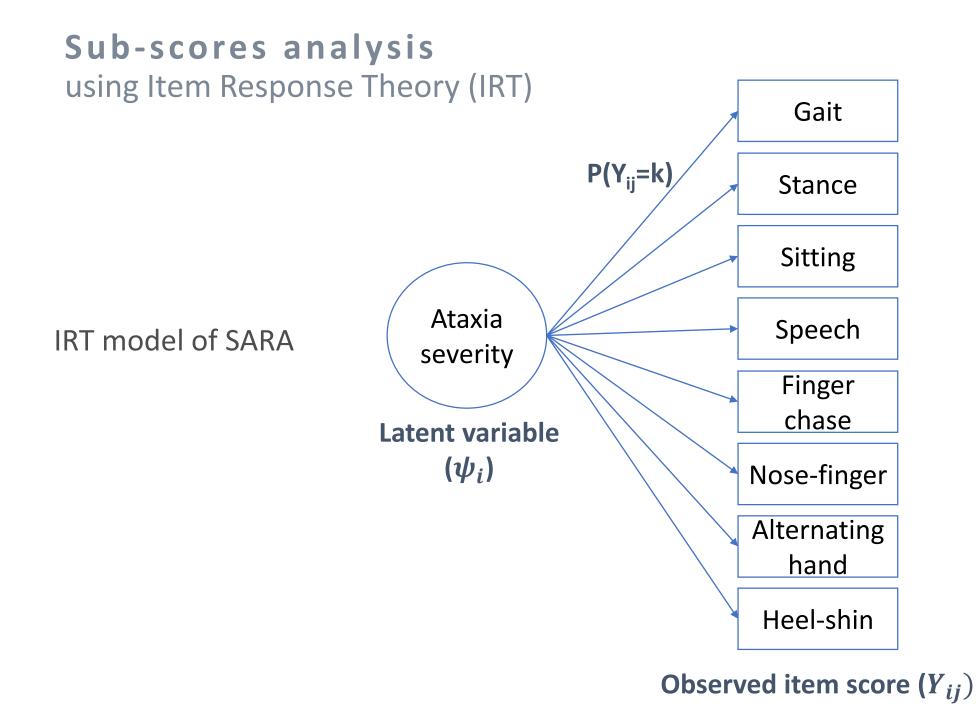
- Concerns about SARA metric properties from regulatory agencies and recent studies
 - Modifications to optimize the SARA
- Scarce data evidence and validation
- Analysis based on SARA total score

Aim

Evaluate the **metric properties and performance** of the SARA using **Item Response Theory (IRT)**











Sub-scores analysis using Item Response Theory (IRT)

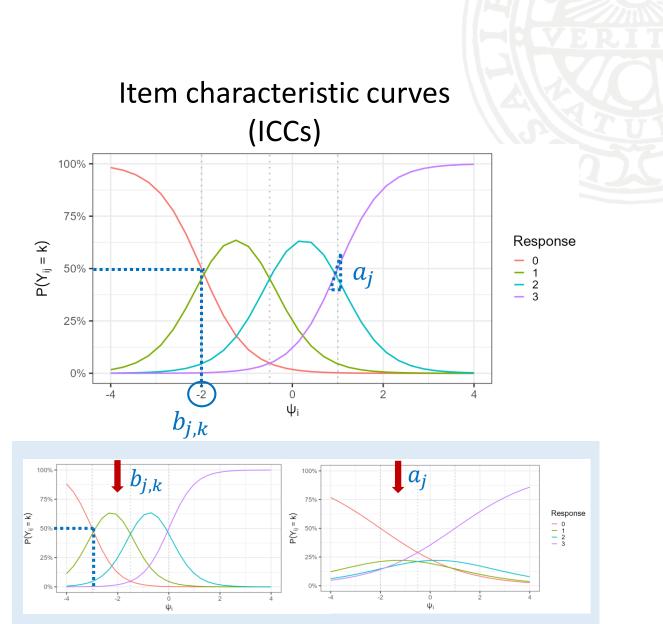
2-parameters logit functions

 $P(Y_{ij} \ge k) = \frac{e^{(a_j(\psi_i - b_{j,k}))}}{1 + e^{(a_j(\psi_i - b_{j,k}))}}$ $P(Y_{ij} = k) = P(Y_{ij} \ge k) - P(Y_{ij} \ge k + 1)$ $Y_{ij}: \text{ observed item score for individual } i \text{ and item } j$ k: item response score

Scale characteristics

-)@_-

- *a_j*: Item discrimination
- *b_{j,k}*: Item difficulty
- Subjects characteristics
 - ψ_i : Latent variable





Dataset Autosomal Recessive Cerebellar Ataxias Registry

- 990 patients
- 1932 visits
- 69% of patients have genetically defined diagnosis
- 115 ARCA genetic subpopulations
- SARA sub-scores data





The questions we want to answer in this IRT analysis

Do all SARA items share one common underlying latent variable?

What are the characteristics (and performance) of each SARA item?

Is one IRT model applicable to all ARCA genetic subpopulations?





The questions we want to answer in this IRT analysis, and how

Do all SARA items share one common underlying latent variable? (*i.e.*, unidimensional)

Methods

- Data correlations
- Residuals correlations

What are the characteristics (and performance) of each SARA item?

- ltem parameters
- Item characteristics curves
- Fisher information

Is one IRT model applicable to all ARCA genetic subpopulations?

 Model fit for each subpopulation



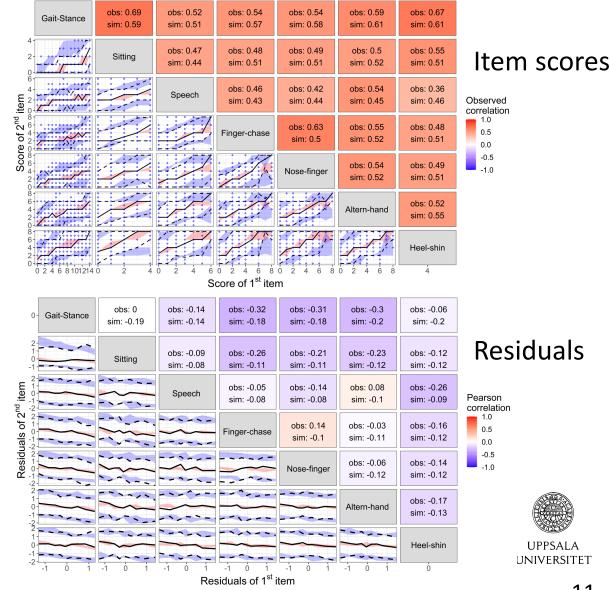
Item-pairs correlations to evaluate SARA dimensionality

Upper matrix

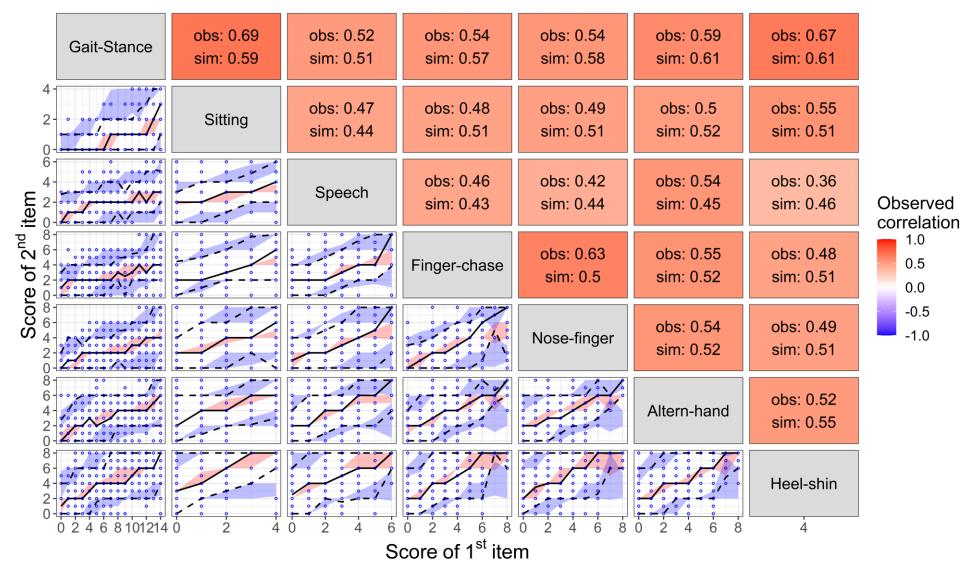
- 1. Data correlations \rightarrow before modelling
- 2. Residual correlations \rightarrow after modelling
- 3. Average correlations for 100 simulations

Lower matrix

- 4. Visual (VPC) diagnostic
 - The 5th, 50th, and 95th percentiles (lines)
 - 95% confidence intervals of the corresponding percentiles (shaded areas)

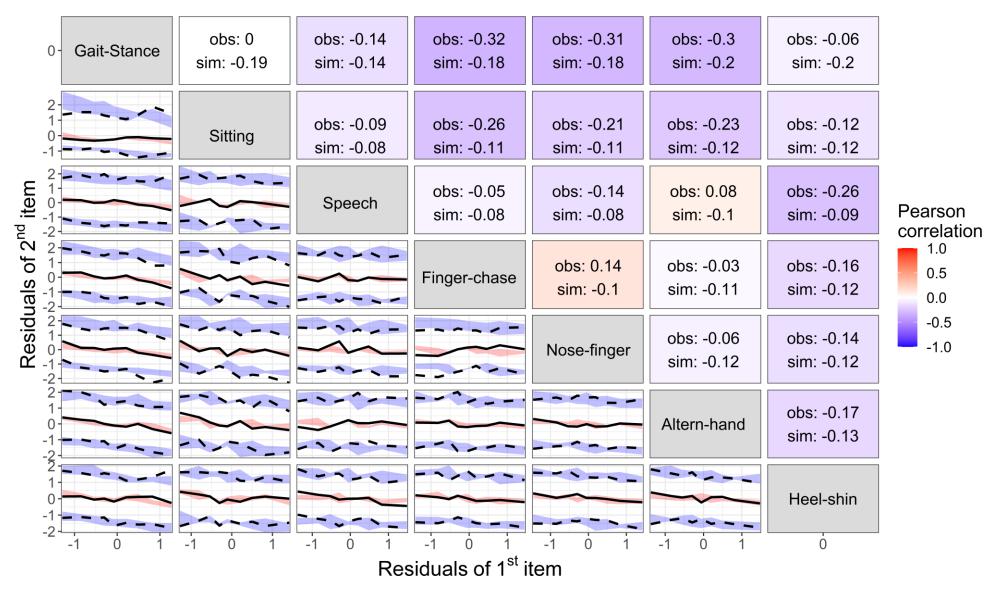


High (and similar) levels of correlations indicate unidimensionality
 Data correlation patterns of simulated datasets mimic the original dataset





Low negative residual correlations indicate a good fit of the unidimensional model
 Correlation patterns were mimicked in the simulations



Results

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The questions we want to answer in this IRT analysis, and how

Methods

- Data correlations

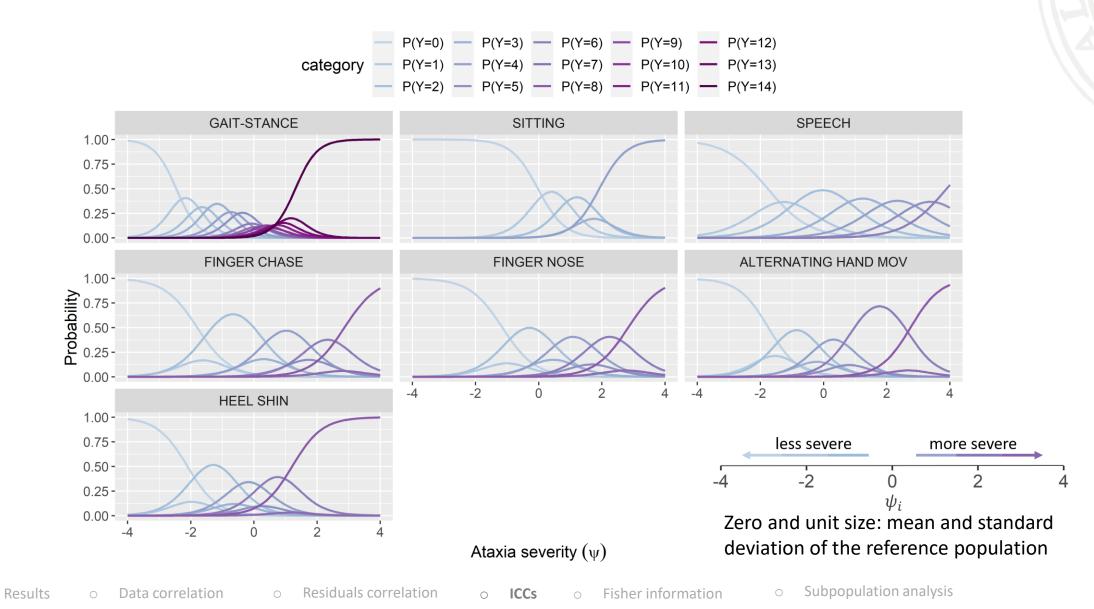
What are the characteristics (and performance) of each SARA item? Item parameters ٠ ٠

- Item characteristics curves
- **Fisher information**

Model fit for each

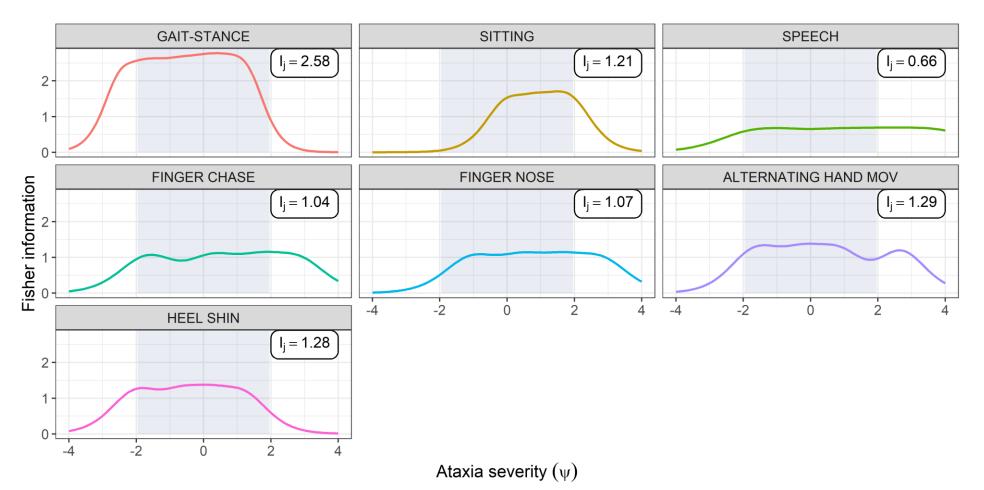


ICCs with separated curves and high discrimination parameters indicate properly designed response categories of SARA



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All SARA items are informative with varying importance at different disease severity levels



Shaded areas: the ataxia severity interval for 95% of the studied population I_i: total item information in the population



The questions we want to answer in this IRT analysis, and how

Do all SARA items share one common underlying latent variable?

Methods

- Data correlations
- Residuals correlations

What are the characteristics (and performance) of each SARA item?

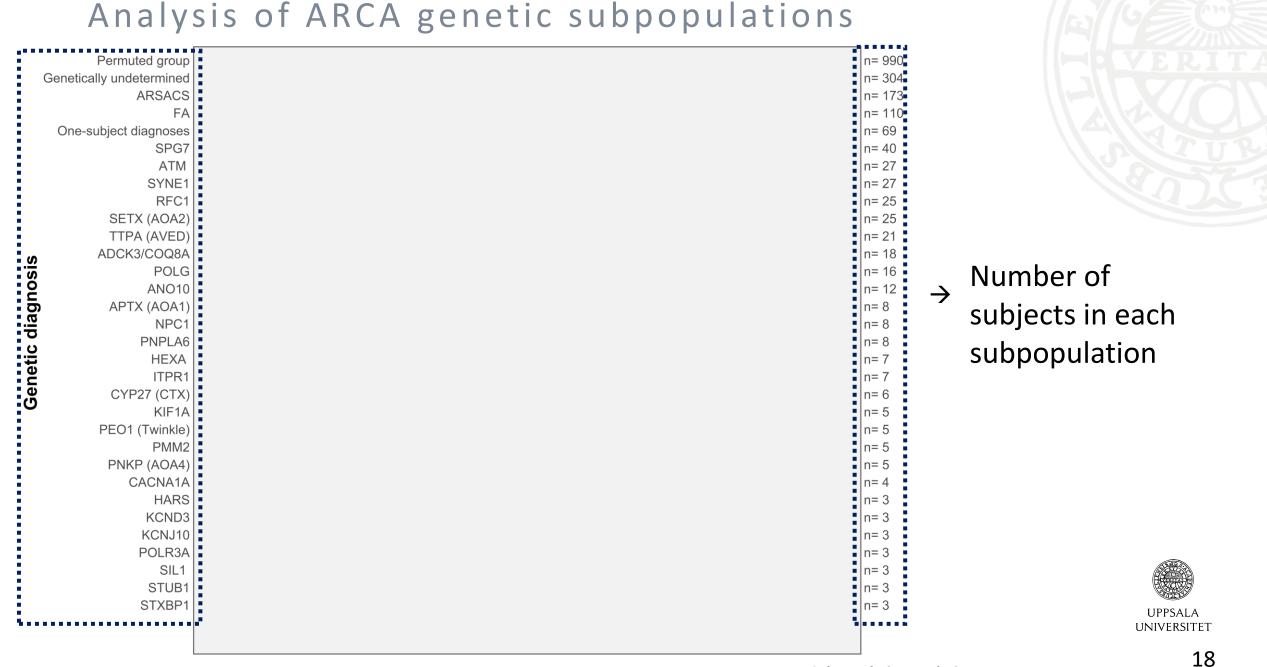
- Item parameters
- Item characteristics curves
- Fisher information

Is one IRT model applicable to all ARCA genetic subpopulations?

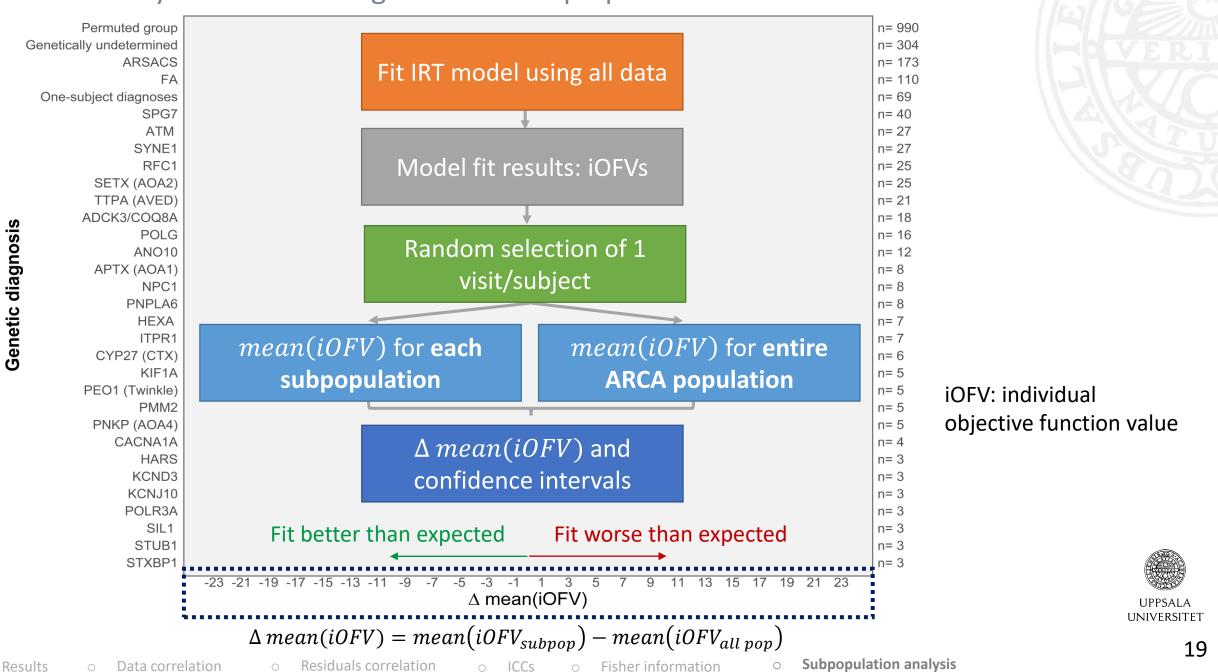
 Model fit for each subpopulation

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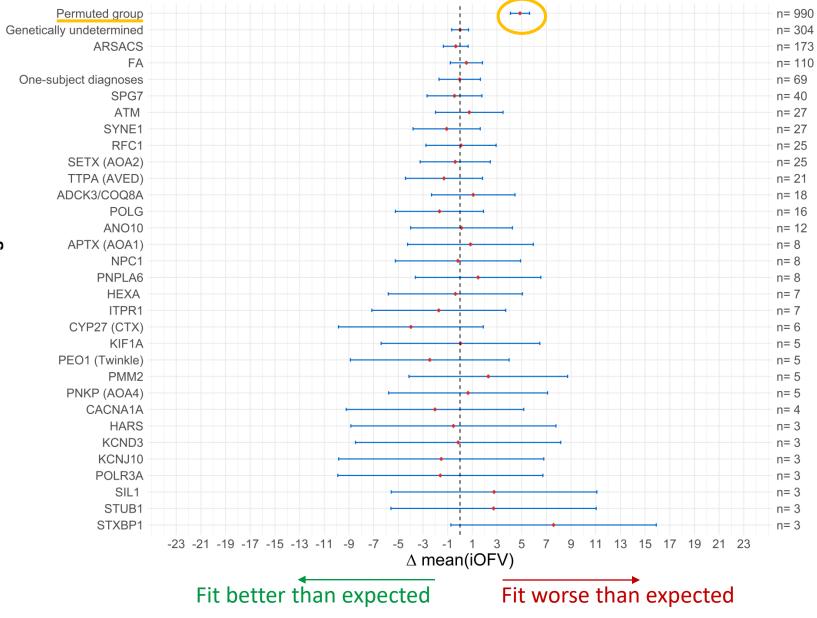




Analysis of ARCA genetic subpopulations



Absence of evidence for differences between ARCA subpopulations



Permuted group: <u>a hypothetical</u> subpopulation created by permuting the subscores of each item across individuals.

- Red points: difference in means of iOFVs
- Error bars: 95% confidence intervals (based on pooled two-sampled t-test assuming equal variances)
- n: number of subjects in each group



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Conclusions SARA Score

Unidimensional- one single latent variable captures data

SARA is well-performing with high discrimination values

All items are informative with varying importance at different disease severity levels

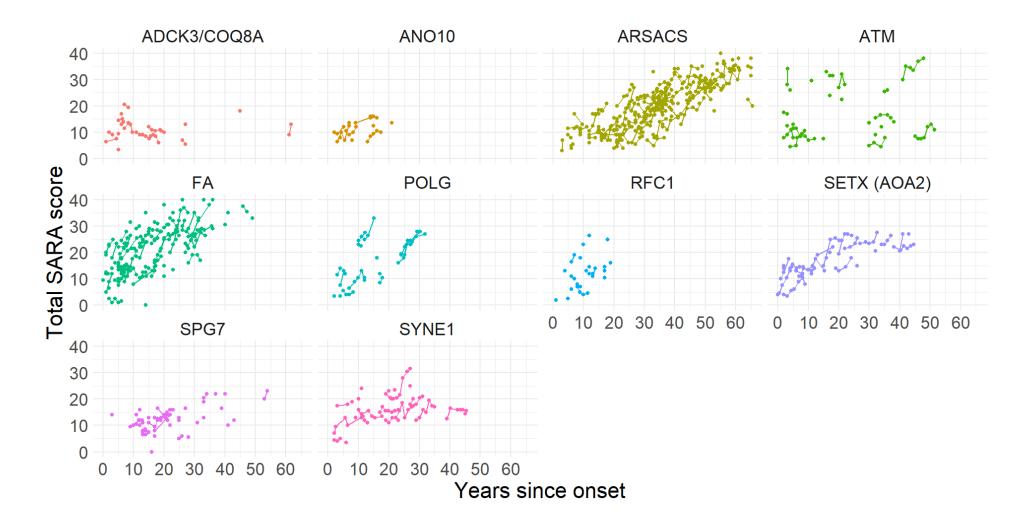
IRT model is applicable across genetic subtypes with no evident item patterns differences





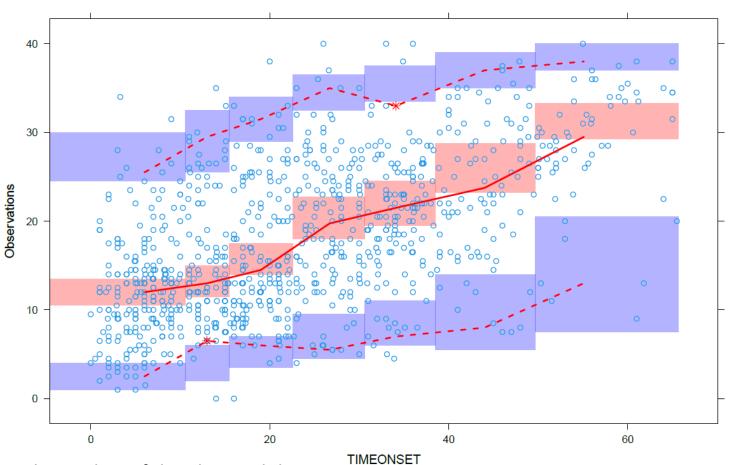


Disease progression in the 10 ARCA subpopulations





Visual Predictive Check illustrate IRT model goodness of fit to total score data

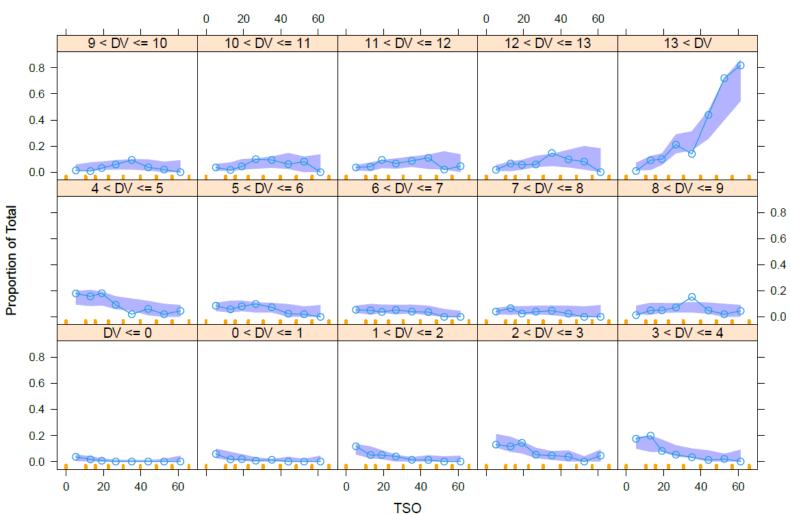


- Solid line: the median of the observed data
- Dashed lines: 2.5th and 97.5th percentiles (dashed lines) of the observed data
- Shaded areas: 95% confidence intervals for the corresponding percentiles of the simulated data
- Note: total scores were calculated as the sum of the individual items score



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VPC stratified on each item

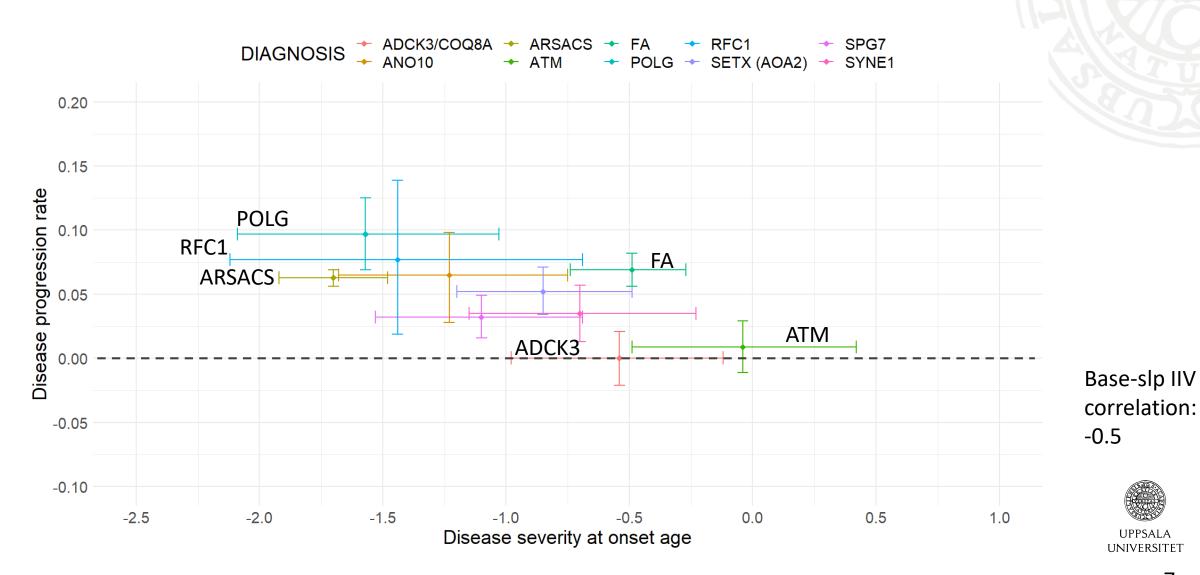


ITEM == 1



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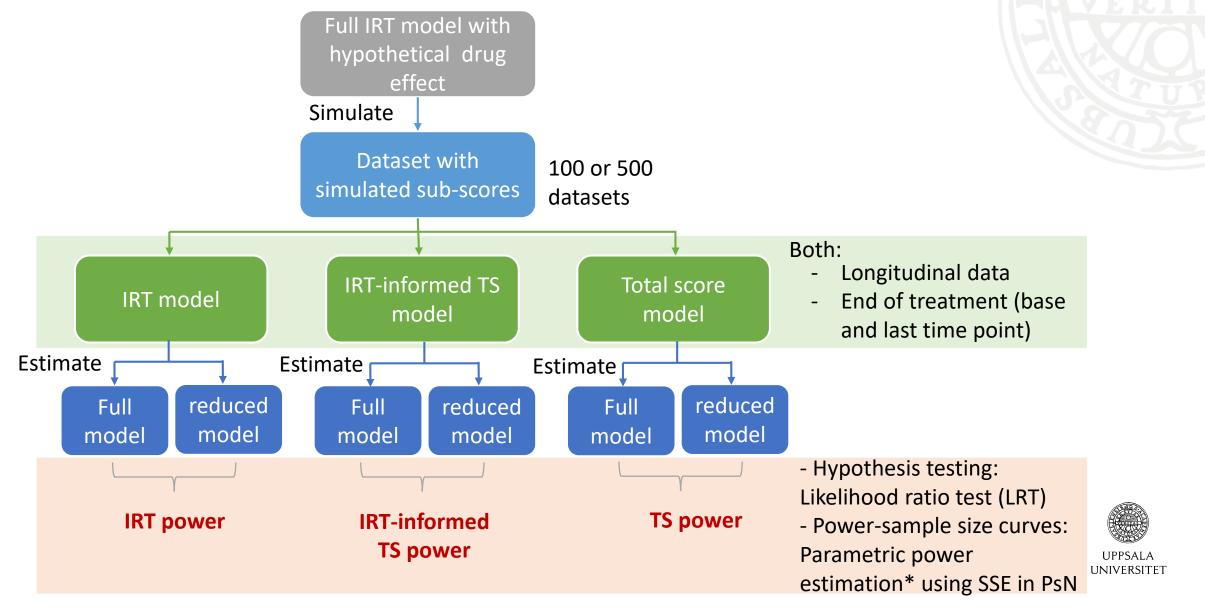
Model parameter estimates and confidence intervals*



* Computed using sampling importance resampling (SIR) procedure

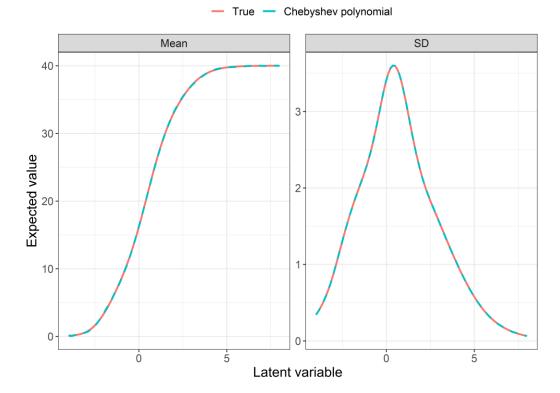
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Clinical trial simulations and power/sample size calculations



IRT-informed link function for SARA scores

Total score



 $egin{aligned} \Psi_{ij} &= hig(arOmega, \eta_i, t_{ij}, X_i ig) \ Y_{ij} &= pn_1ig(\Psi_{ij} ig) + arepsilon_{ij} \cdot pn_2ig(\Psi_{ij} ig) \ \eta_i &\sim Nig(0, \omega^2 ig) \ arepsilon_{ij} &\sim N(0, 1) \end{aligned}$

- **h()** function is the disease progression function on the latent variable
- ψ : latent variable
- Y: total score
- Pn: polynomial functions describing the theoretical expectations of mean and variance. (derived from the base IRT model)



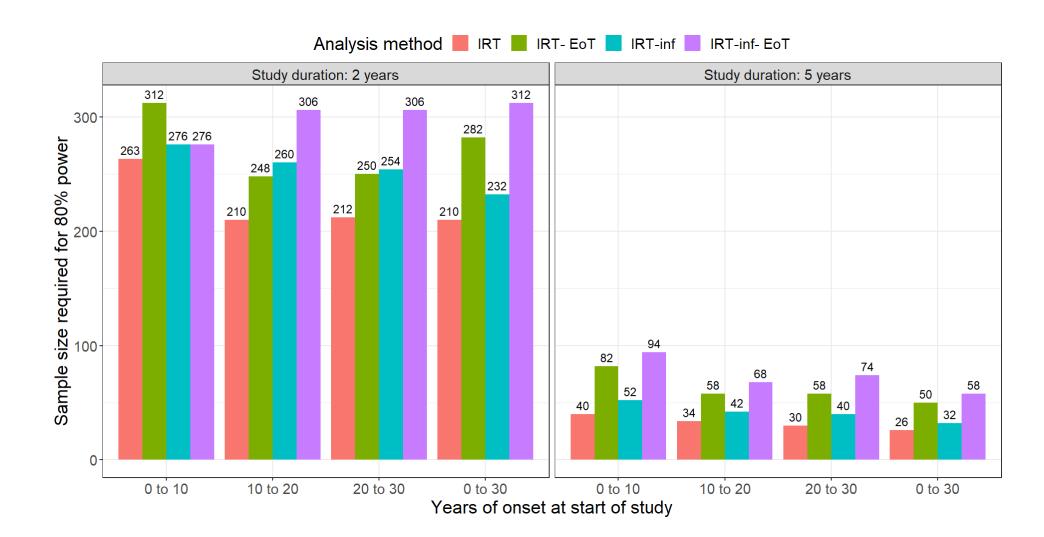
ARSACS- sample size for 80% power 5-year study with disease-modifying treatment Visits every 6 month

	Analysis	Sample size (treatment+control, 1:1) for 80% power				
Drug effect		Early pop. 0-10 yr	Intermed. pop. 10-20 yr	Late pop. 20-30 yr	Heterogenous pop. 0-30 yr after onset	
	Tot score	200	130	130	100	
	IRT	134	122	118	94	
50% inhibition	IRT-inf	178	160	150	114	
	IRT EOT	258	222	222	174	
	IRT-inf EoT	302	264	284	222	
100% inhibition	Tot score	56	40	32	30	
	IRT	40	34	30	26	
	IRT-inf	52	42	40	32	
	IRT EoT	82	58	58	50	
	IRT-inf EoT	94	68	74	58	



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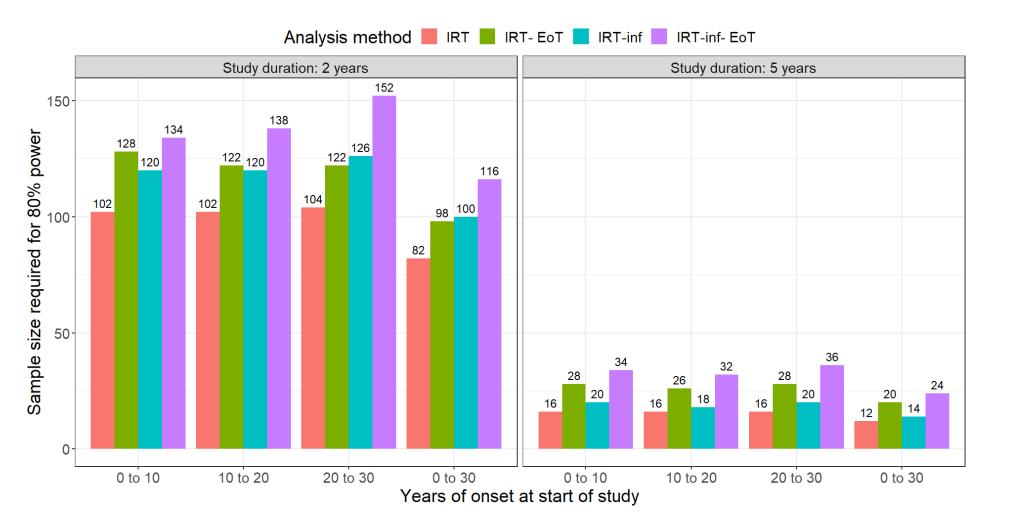
100% inhibition *ARSACS*- Comparison of sample sizes across different: Study durations & Analysis methods





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100% inhibition *POLG*- Comparison of sample sizes across different: Study durations & Analysis methods





Progressive Supranuclear Palsy (PSP)

- Neurodegenerative
 - –Unknown cause
- Symptoms include:
 - -Problems with walking, balance and eye movements
 - -Cognitive impairment
 - -Speech impairment
 - -Difficulty swallowing

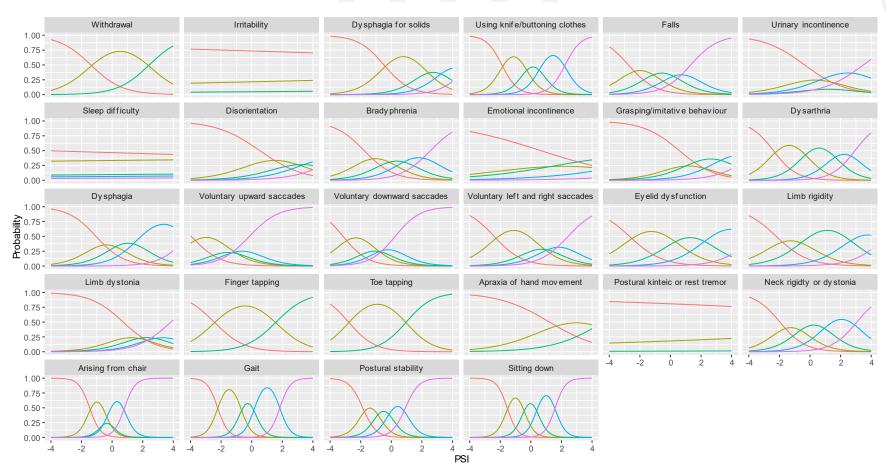


Data description PSPRS Progressive Supranuclear Palsy Rating Scale

Study	#patients	Mean #visits	Mean study duration (yr)	Mean disease duration (yr)	#arms	Mean age (yr)	Study type
Abbvie	377	4.3	1	3.2	3	69	interv
Biogen	161	2.8	1	1.5	1	69	interv
Prospera	44	4.1	1	3.3	2	67	interv
Tauros	138	5.7	1.2	3.4	2	68	interv
Describe PSP	127	2.4	2.8	1.1	1	70	observ
ProPSP	132	2.6	1.6	4.3	1	69	observ

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Item Characteristic Curves for PSPRS -Progressive Supranuclear Palsy Rating Scale

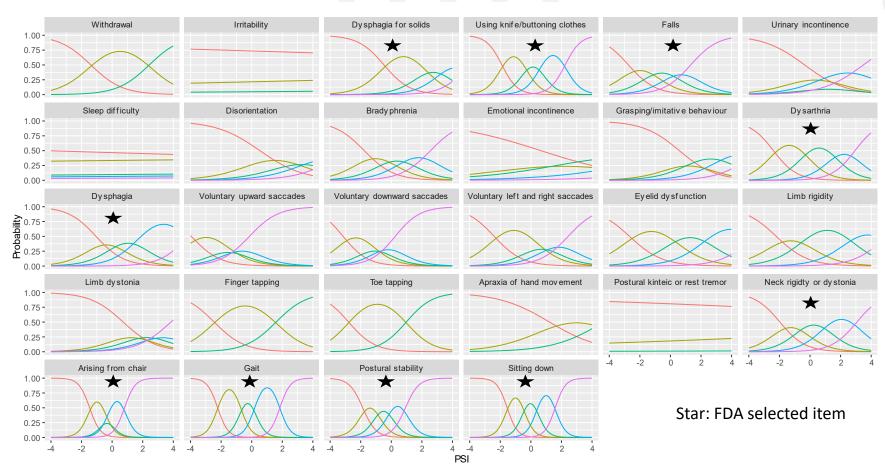


- P(Y=0) - P(Y=1) - P(Y=2) - P(Y=3) - P(Y=4)



Item Characteristic Curves for PSPRS -Progressive Supranuclear Palsy Rating Scale

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- P(Y=0) - P(Y=1) - P(Y=2) - P(Y=3) - P(Y=4)

PSP Ranking Scale items ranked by information content

 \bigstar : FDA selected item

		Information	Discrimination	Number of
	ITEM	content	parameter	categories
★ 🗌	28	2.16	2.97	5
★ 🗌	25	1.99	2.86	5
★	26	1.91	2.93	5
★	27	1.4	2.29	5
★ 🗌	4	1.05	1.98	5
★ 🗌	12	0.48	1.32	5
	24	0.43	1.21	5
★ 🗌	15	0.41	1.24	5
★ 🗌	5	0.39	1.14	5
★ 🔽	13	0.35	1.1	5
★ 🗌	3	0.34	1.19	5
	16	0.34	1.08	5
	9	0.33	1.03	5
	14	0.29	1.07	5
	21	0.28	1.17	3
	18	0.26	0.96	5
	17	0.24	0.93	5
	20	0.21	1.01	3
	1	0.21	0.97	3
	19	0.19	0.93	5
	11	0.17	0.85	5
	6	0.16	0.75	5
	8	0.12	0.71	5
	22	0.08	0.6	3
	10	0.02	0.33	5
	23	0.001	0.07	3
	2	0.001	0.04	3
	7	0.001	0.03	5





Sample size calculation - PSP

- Parallel group study, 1:1 randomization placebo:active treatment
- 1 year study, 5 visits/patient, no dropout
- Treatment effect: 50% progression inhibition
- Disease progression rate as estimated from interventional studies
- 80% power

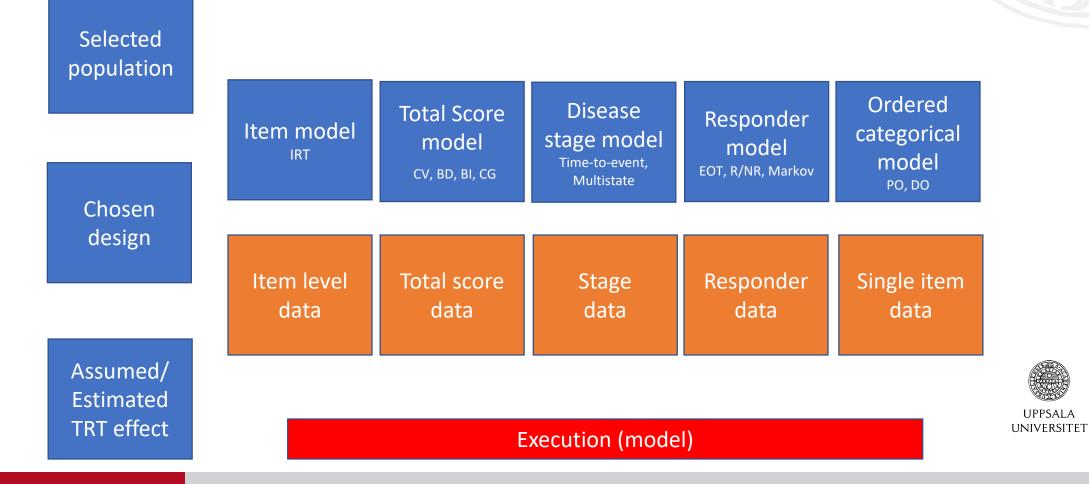
Total number of subjects					
	scale	PSPRS	FDA	FDA rescore	
model		FJFNJ	FDA	FDATESCOLE	
IRT model (item level data)		36	36	40	
IRT-informed model (total score data)		50	48	50	
Linear mixed effects model (total score data)		62		84	



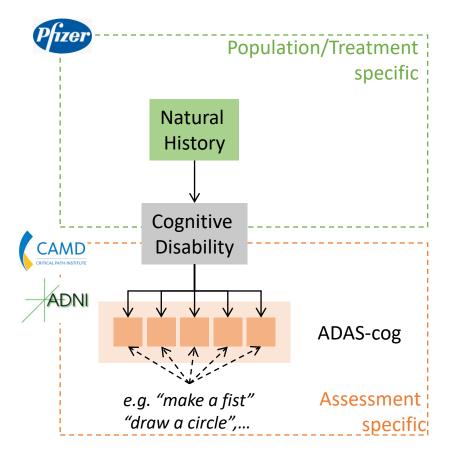
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Understand relation between endpoints

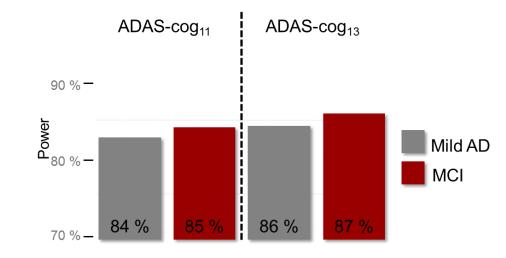
An IRT model can inform trial choices of population, instrument, design and analysis



Separately determined ICCs Example: Alzheimer's Disease



- Utilize data from public or in-house clinical trial databases
- Study influence of patient population & assessment variant independent from another

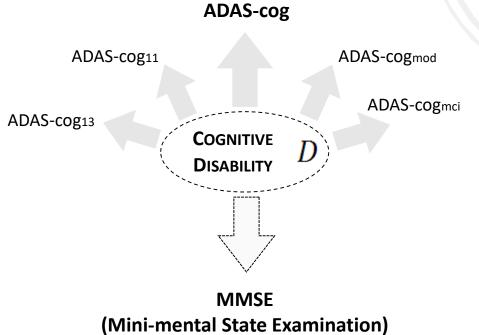


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Reference: Ueckert et al. Pharm Res 31(2014)

Item information

Component	Information	% Total
1 Delayed Word Recall	4.79	33.6
2 Word Recall	3.81	26.7
3 Orientation	0/ 1.64	11.5
4 Word Recogniti	0 1.40	9.8
5 Naming O&F	0.82	5.7
6 Number Cancellation	0.37	2.6
7 Construction	0.29	2.0
8 Word Finding	0.20	1.4
9 Ideational Praxis	0.18	1.3
10 Concentration	0.18	1.2
11 Remembering	0.16	1.1
12Comprehension	0.16	1.1
13 Commands	0.15	1.1
14 Spoken Language	0.10	0.7



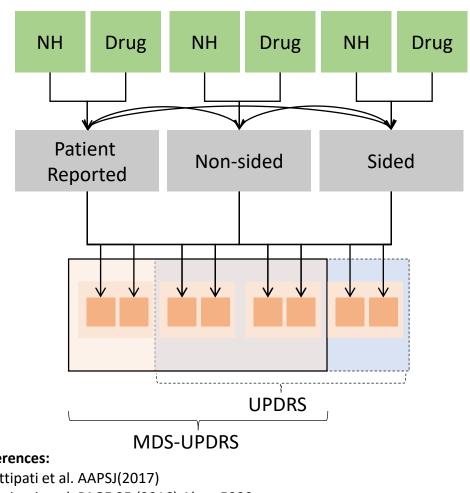
Reduced tests options:

Screening tests

- Trial conduct with limited tests
- Trial conduct with individualized dynamic testing



Example: Parkinson's Disease



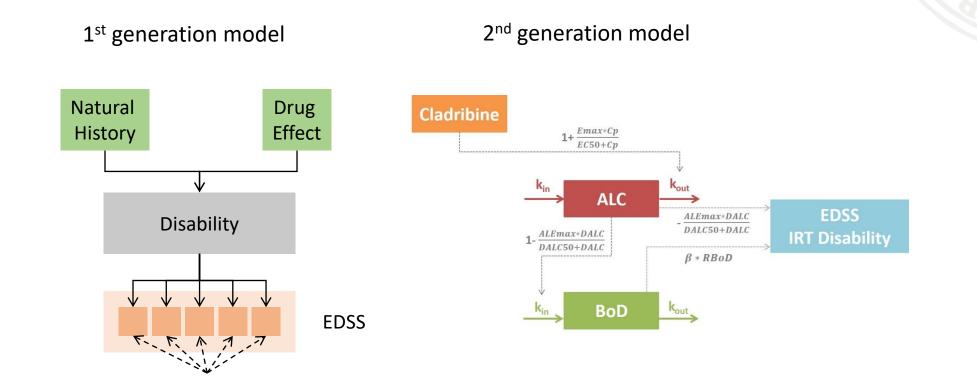
- Model links established (UPDRS) and + novel endpoint (MDS-UPDRS)
 - + Leverage historic data
 - Comparison with older + compounds
 - + Joint framework for complete disease severity range
- + Also done in AD for MMSE (often used for screening & diagnosis) & ADAS-cog (regulatory accepted endpoint)
 - + Utilize all collected data
 - + Leverage clinical routine data
 - + Predict clinical endpoint from screening



References:

Gottipati et al. AAPSJ(2017) Gottipati et al. PAGE 25 (2016) Abstr 5990 Jönsson et al PAGE (2017) Abstr 7236

Biomarker – endpoint models Multiple Sclerosis



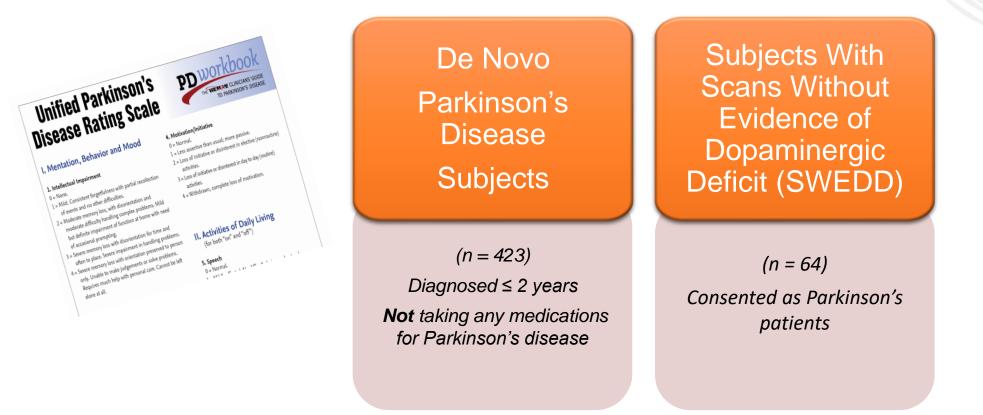
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References:

Novakovic A et al., AAPSJ 19(1): 172-179 (2017) Novakovic A et al., J Clin Pharmacol 58(10): 1284-94 (2018)

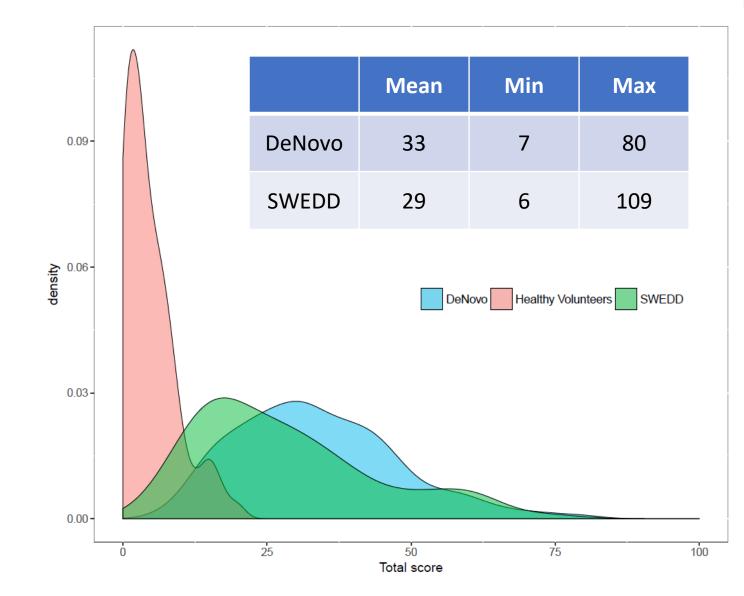
IRT model based subpopulation identification

• Parkinson Progression Markers Initiative (PPMI) Database:





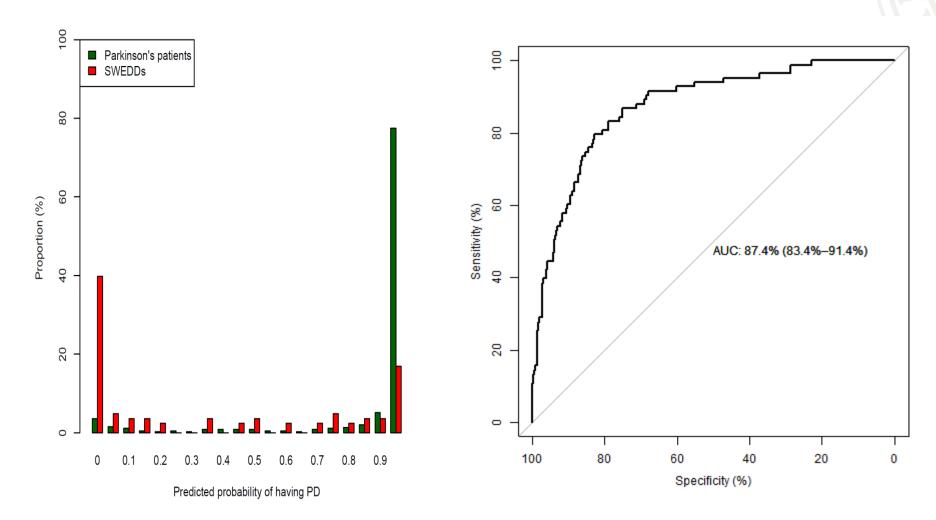
MDS-UPDRS total score





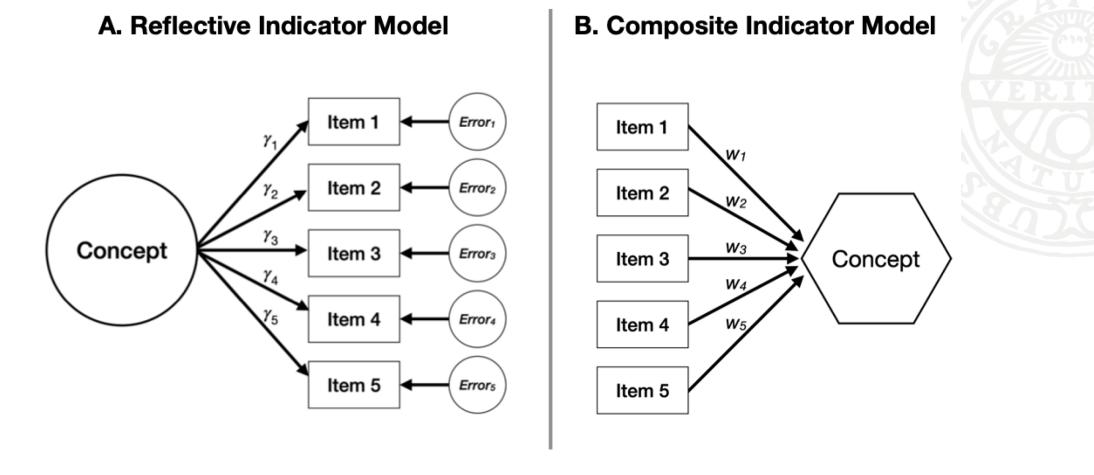


Item Response Model-based patient classification



Differentiation and prognosis of healthy subjects, SWEDDs and Parkinson's patients using a multi-dimensional item response theory model. S.C. van Dijkman, S. Ueckert, E.L. Plan, M.O. Karlsson. Journal of the Neurological Sciences, Volume 381, Supplement, 15 October 2017, Pages 97-98 <u>https://doi.org/10.1016/j.jns.2017.08.317</u>





Note: In panel A, the concept within a circle is conceptualized as a latent variable; the smaller circles represent measurement error that contributes to the responses of each item; γ denotes the causal effect of the concept on the item response. In panel B, the concept within a hexagon is conceptualized as a composite variable; *w* indicates the weight (may or may not be equally weighted) used for the item response in computing the calculated composite score that represents the concept.

Patient-Focused Drug Development: Selecting, Developing, or Modifying Fit-for-Purpose Clinical Outcome Assessments, FDA Draft guidance, June 2022



Systemic Lupus Erythematosus Disease Activity Index 2000 (SLEDAI-2K) 🛱

New onset sensory or motor neuropathy nvolving cranial nerves	No 0	Yes +8
upus headache Severe, persistent headache (may be migrainous out must be nonresponsive to narcotic analgesia)	No 0	Yes +8
Proteinuria >0.5 g/24 hours	No 0	Yes +4
Pyuria >5 WBC/high-power field; exclude infection	No 0	Yes +4
Low complement CH50, C3, or C4 decreased below lower limit of normal for lab	No O	Yes +2
High DNA binding Increased above normal range for lab	No 0	Yes +2
WBC <3 x 10 ⁹ /L Exclude drug causes	No O	Yes +1

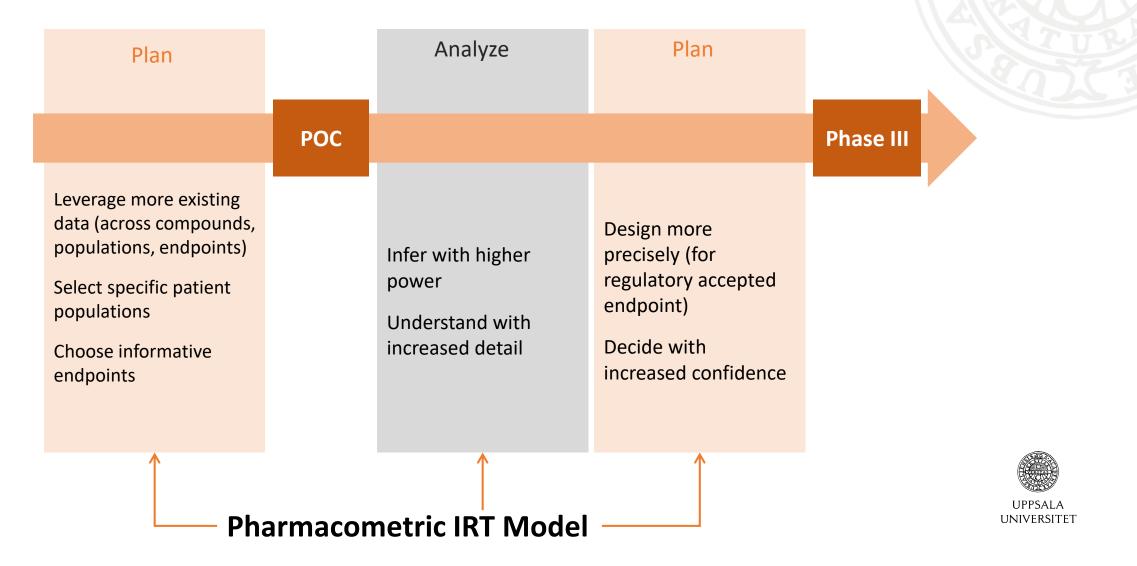
VERITA VERITA

O points

Authors recommend a cutoff of 3 or 4 to define active disease and the need to increase therapy (see Evidence for details)



Potential of IRT modeling in clinical drug development



Potential of IRT modeling in clinical drug development

	Enroll & run	Interim analysis	Final analysis	SETUR SEDECT
Phase III				
	Inclusion criteria component	Futility analysis	E-R analysis Benefit-risk _i	
	Dynamic selection of tasks during trial	Adaptive design (drop arm, revision of sample size)	Disease-modifying effect Biomarker validation	
	Pharmad	UPPSALA UNIVERSITET		

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- Andrew Hooker
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- Franz König
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- Mohamed Gewily

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