

nature  
neuroscience

# Building better biomarkers: brain models in translational neuroimaging

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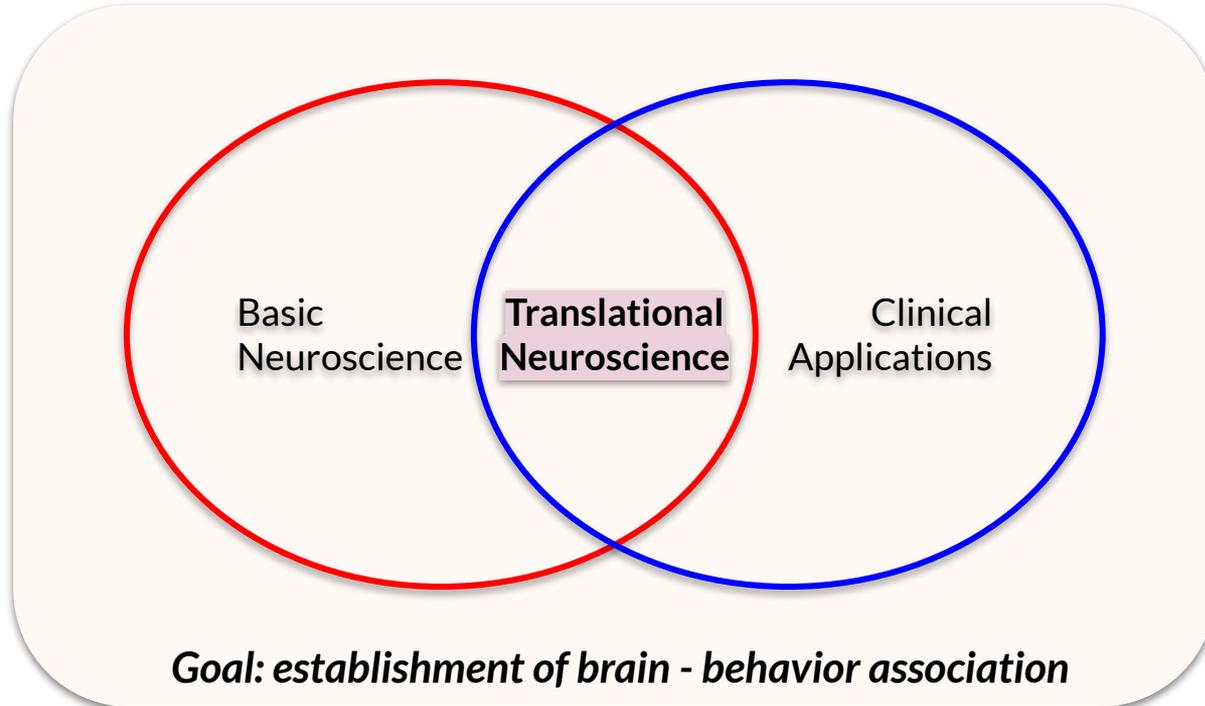
2020.06.01

Computational Clinical Science Lab

**Jihyun Hur**

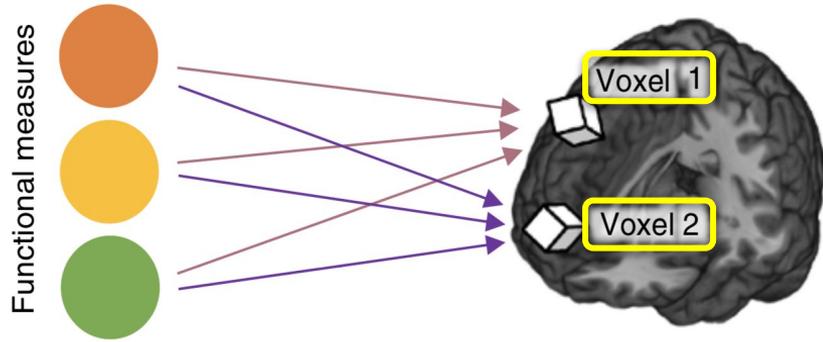


# *Translational Neuroscience*



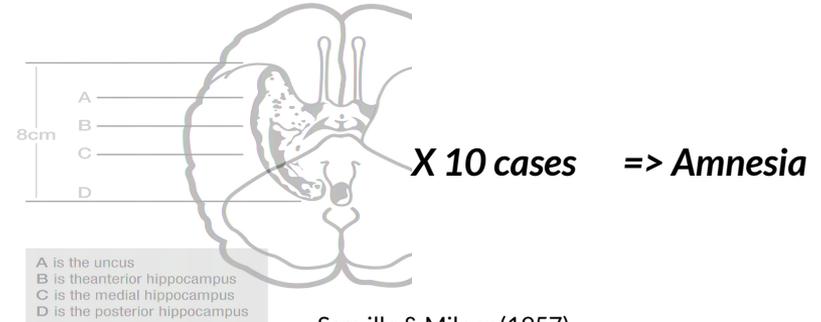
# Early: Traditional Brain Mapping

## Traditional Brain Mapping



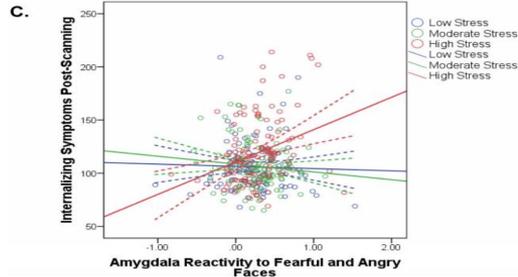
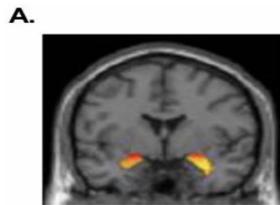
Woo et al. (2017)

## Foundation I: Lesion Studies



Scoville & Milner (1957)

## Traditional Study Example :

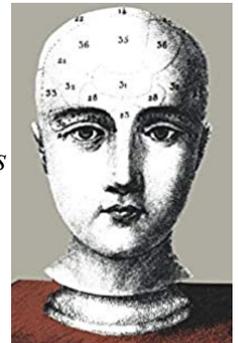


Swartz et al. (2015)

## Foundation II: Theory of Modularity

*“Faculty Psychology ... the mental causation of behavior typically involves the simultaneous activity of a variety of distinct psychological mechanisms”*

Fodor (1983)



# Problems of Traditional Brain Mapping

1. Central problem: the main goal of traditional brain mapping!

(= to understand localized brain function)

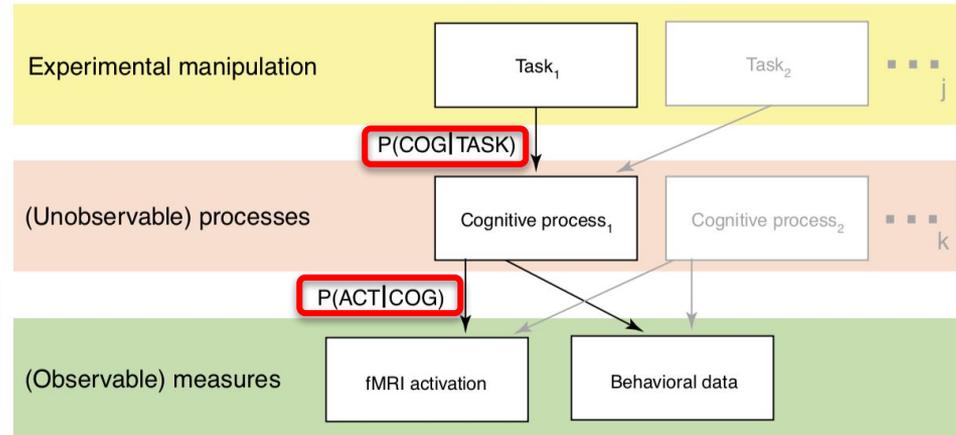
2. A voxel = ~5.5 million neurons

3. Reverse Inference

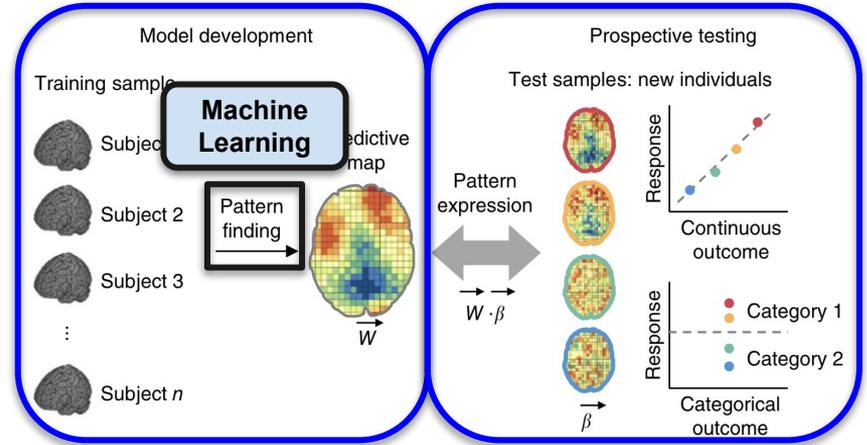
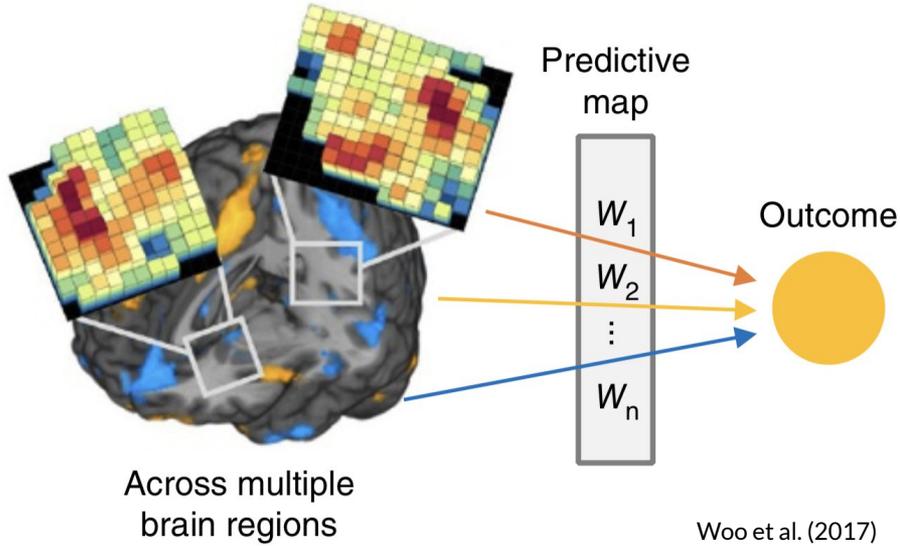
$P(\text{COG}|\text{ACT}) \neq P(\text{ACT}|\text{COG})$

$$P(\text{COG}_X|\text{ACT}_Z)$$

$$= \frac{P(\text{ACT}_Z|\text{COG}_X)P(\text{COG}_X)}{P(\text{ACT}_Z|\text{COG}_X)P(\text{COG}_X) + P(\text{ACT}_Z|\sim\text{COG}_X)P(\sim\text{COG}_X)}$$



# Now: Predictive Modeling

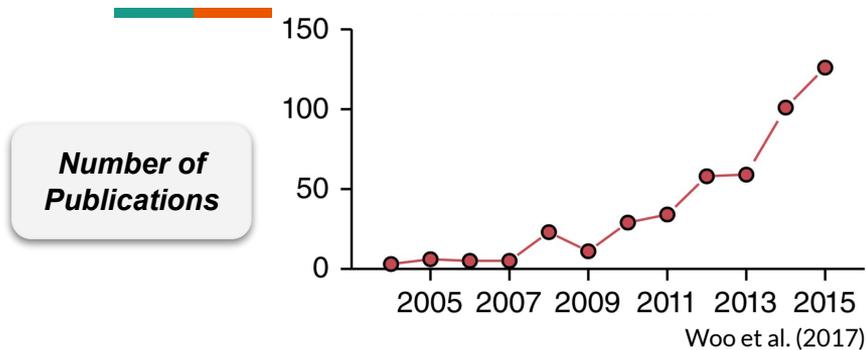


## Benefits:

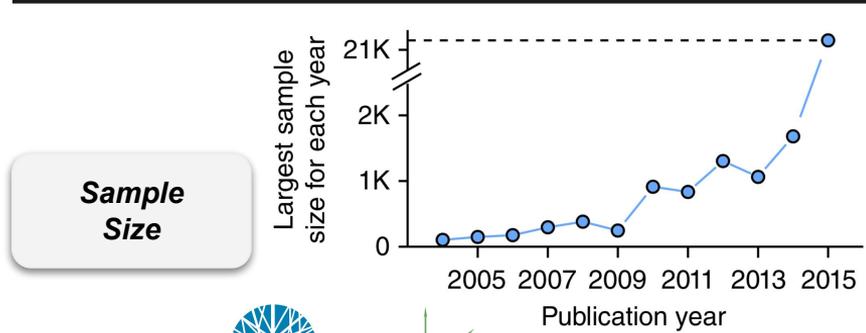
- *Direction of Inference*
- *Integrate brain regions and make a single best guess*
- *Cross-validation*
- *Information from multiple spatial scales*

*Assumption: "many features of neurologic and psychiatric disorders are encoded in distributed neural systems"*

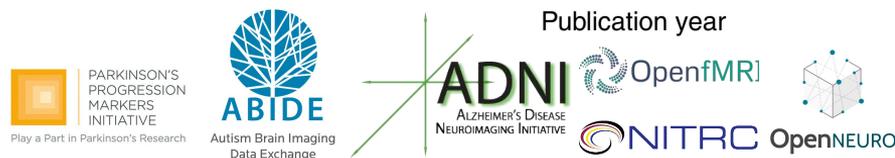
# Current State of Clinical Predictive Modeling



- Research Topics**
- Past:**
- Alzheimer's disease (AD)
- Now:**
- Parkinson's disease
  - Pain disorders
  - Psychosis
  - Depression ...



- Research Goals**
1. Patients vs. Health
  2. Difficult classification



# 1) Risk Assessment, Conversion Prediction and Early Detection

**Goals**

- : who is *at risk*?
- : who will *convert into a disease state*?
- : who is *at the early stage of a disease*?

*SPARE-AD* ↑,  
*More AD-like*

Model I: Spatial Pattern of Abnormality for Recognition of Early AD (SPARE-AD)

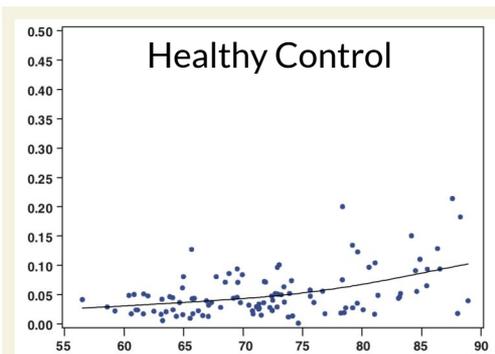


Figure 4 Rate of SPARE-AD change as a function of average age during follow-up period, for the 109 CN individuals.

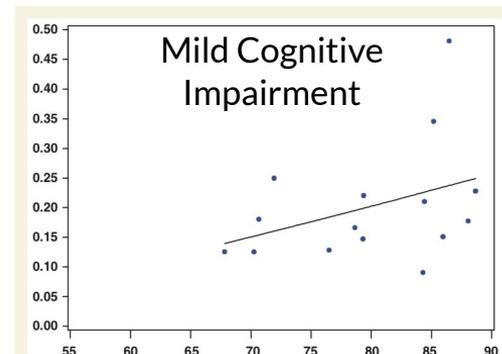
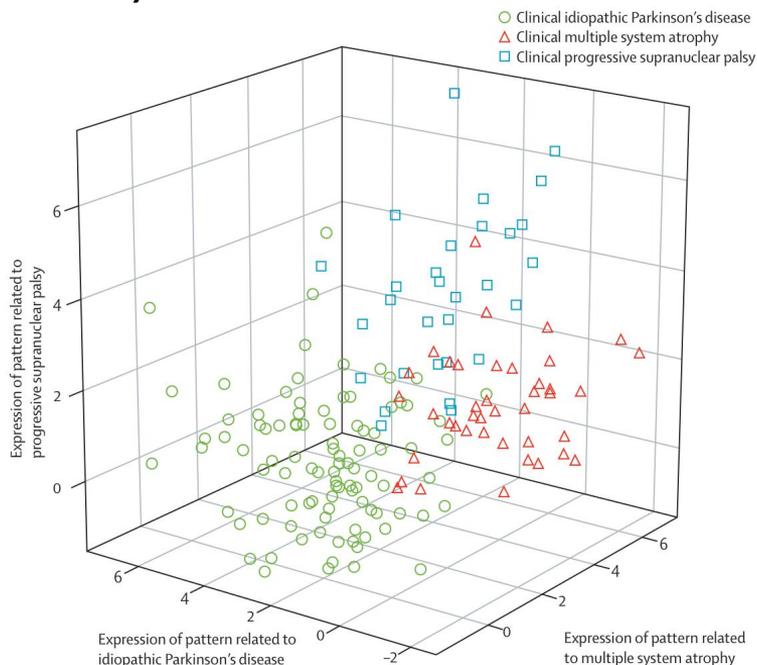


Figure 5 SPARE-AD annual change rates plotted against age for all MCI individuals.

## 2) Differential Diagnosis<sup>1</sup> & Subtyping<sup>2</sup>

### Study I: Parkinson's disease<sup>1</sup>



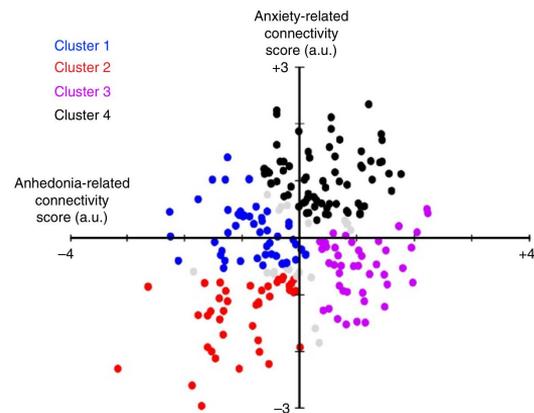
3D plot of FDG-PET pattern expression

| All patients                          |              |
|---------------------------------------|--------------|
| <b>Idiopathic Parkinson's disease</b> |              |
| Sensitivity                           | 84% (81/96)  |
| Specificity                           | 97% (69/71)  |
| Positive predictive value             | 98% (81/83)  |
| Negative predictive value             | 82% (69/84)  |
| <b>Atypical parkinsonian syndrome</b> |              |
| Sensitivity                           | 82% (58/71)  |
| Specificity                           | 98% (94/96)  |
| Positive predictive value             | 97% (58/60)  |
| Negative predictive value             | 88% (94/107) |
| <b>Multiple system atrophy</b>        |              |
| Sensitivity                           | 85% (29/34)  |
| Specificity                           | 96% (25/26)  |
| Positive predictive value             | 97% (29/30)  |
| Negative predictive value             | 83% (25/30)  |
| <b>Progressive supranuclear palsy</b> |              |
| Sensitivity                           | 88% (21/24)  |
| Specificity                           | 94% (34/36)  |
| Positive predictive value             | 91% (21/23)  |
| Negative predictive value             | 92% (34/37)  |

Data are % (calculation).

Tang et al. (2010)

### Study II: Depression<sup>2</sup>



Drysdale et al. (2017)

### 3) Predicting Treatment Outcome

**Goal** To customize treatment based on brain measures (= precision medicine)

#### Research

- Mostly focused on *depression and anxiety disorders*
- Mostly predicted *cognitive behavioral therapy (CBT) response*

#### Study I: Social Anxiety Disorders with CBT

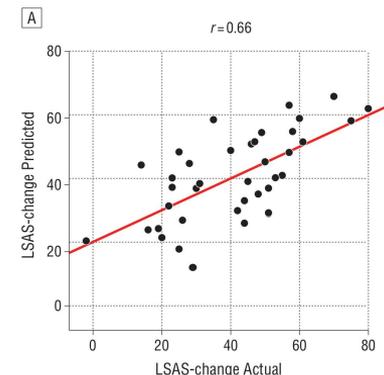
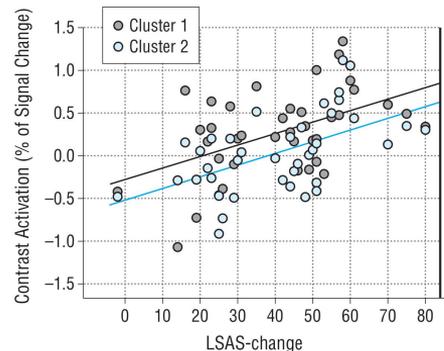
Functional MRI



Angry face

Neutral face

LSAS: Liebowitz Social Anxiety Scale



Doehrmann et al. (2013)

## *Four Characteristics of Desirable Model*



- 1 Diagnostic Value
- 2 Neuroscientific Validity
- 3 Deployability and Scalability
- 4 Generalizability

# Diagnostic Value

|                 |          | True class                        |                                   | Measures  |
|-----------------|----------|-----------------------------------|-----------------------------------|---|
|                 |          | Positive                          | Negative                          |   |
| Predicted class | Positive | True positive<br><i>TP</i>        | False positive<br><i>FP</i>       | Positive predictive value (PPV)<br>$\frac{TP}{TP+FP}$ |
|                 | Negative | False negative<br><i>FN</i>       | True negative<br><i>TN</i>        | Negative predictive value (NPV)<br>$\frac{TN}{FN+TN}$ |
| Measures        |          | Sensitivity<br>$\frac{TP}{TP+FN}$ | Specificity<br>$\frac{TN}{FP+TN}$ | Accuracy<br>$\frac{TP+TN}{TP+FP+FN+TN}$               |

- Sensitivity** How robustly the measure responds when the outcome is present
- Specificity** Whether the measure responds only in the presence of the target outcome

## C.f. Predictive Value and Base Rate (Prevalence)

**A**

$$\text{PPV} = \frac{\text{SENSITIVITY} \times \text{PREVALENCE}}{\text{PROBABILITY OF POSITIVE BIOMARKER}}$$

$\text{PPV} = \frac{P(\text{Chronic pain} | \text{Positive Biomarker})}{P(\text{Chronic pain} | \text{Positive Biomarker})}$

**B**

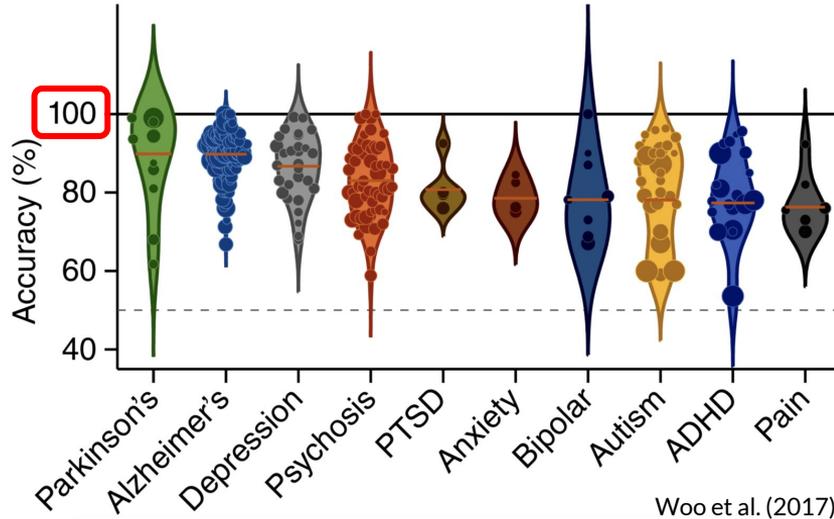
$$\text{NPV} = \frac{\text{SPECIFICITY} \times (1 - \text{PREVALENCE})}{\text{PROBABILITY OF NEGATIVE BIOMARKER}}$$

$\text{NPV} = \frac{P(\text{No pain} | \text{Negative Biomarker})}{P(\text{No pain} | \text{Negative Biomarker})}$

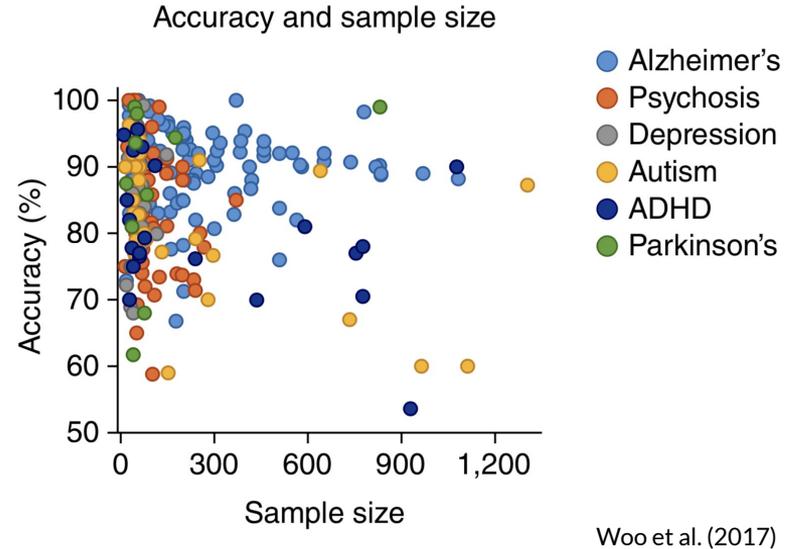
Robinson et al. (2016)

# Diagnostic Value - Accuracy Issues

## 1. Biases in Accuracy



## 2. Variability in Accuracy based on Sample Size



# Why Accuracy Bias, and How to Reduce it

Accuracy is inflated because of:

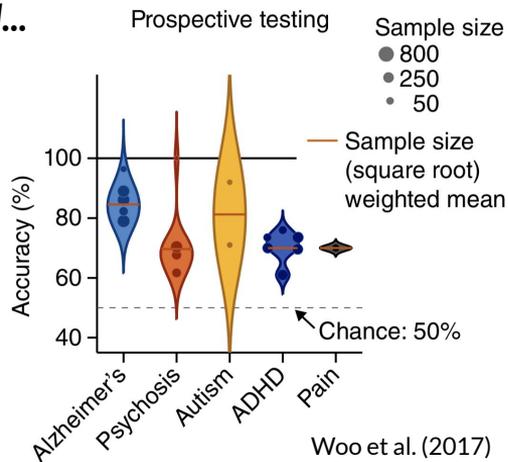
1. Dependence of test datasets
2. Overfitting

Solutions:

- Testing on an independent sample
- Testing only one model

Currently in the field...

**Only ~9%!**



→ **Reserve hold-out test data!**

# Neuroscientific Validity

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## Plausibility

- fMRI signal in the ventricles?  
→ implausible

## Interpretability

- Machine Learning algorithms  
→ too many features  
→ LASSO / ridge-regularization

## Systematic Approach

1. Summarize and visualize the model in **human-readable way**
2. **Evaluate the neuroscientific plausibility** of the predictive weights
3. Examine **confounding factors**

# *Deployability and Scalability, Generalizability*

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- **Deployability and Scalability:**

- *Easily applicable to new individuals and shareable across labs*
- *Standardized data formats and software (= named models like SPARE-AD)*

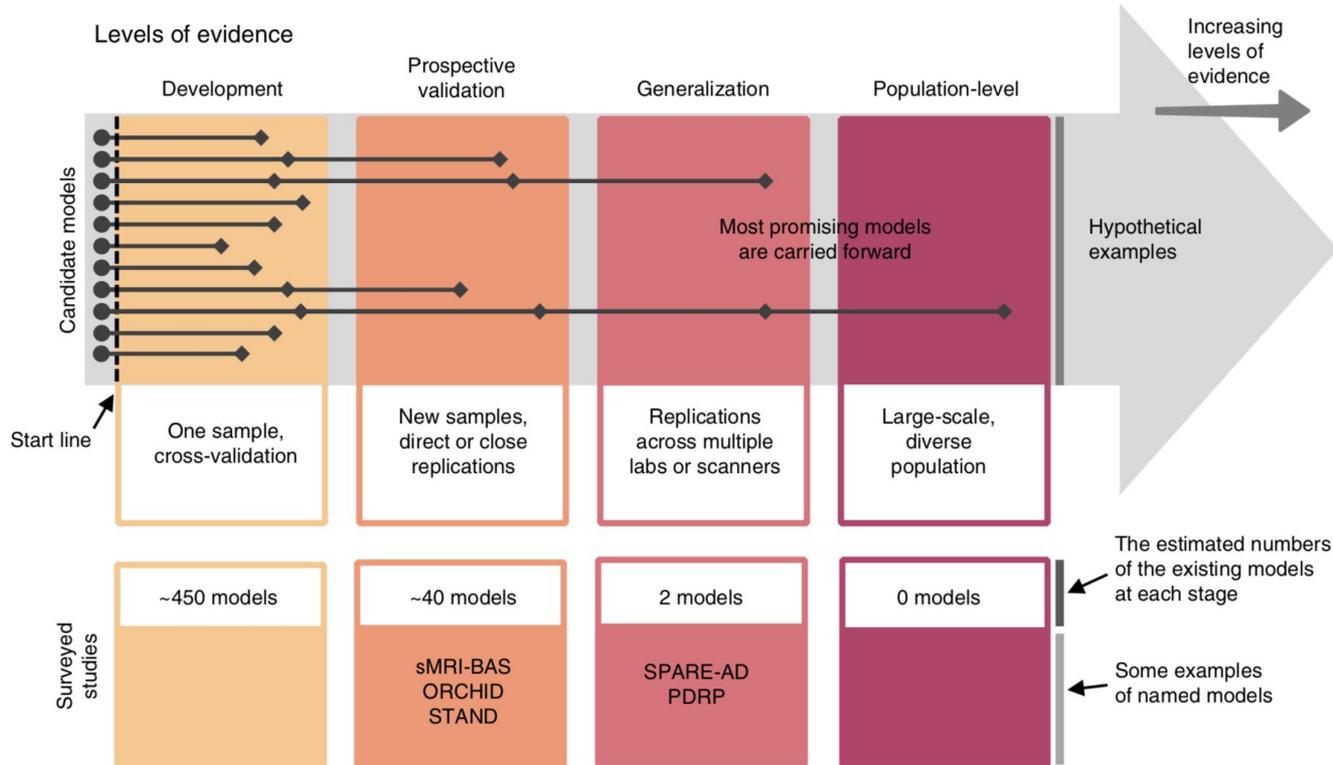
- **Generalizability:**

- *To new individuals*
- *Across labs, scanners, and minor variants in testing conditions*
- *Similar results to other outcomes with the same construct (e.g. mathability)*

*Ecologically valid datasets* : *have samples that are representative of the broader population*

*Big data approaches* : *test specificity over multiple alternatives (open-process)*

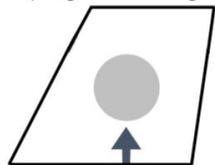
# Shareable Research Products



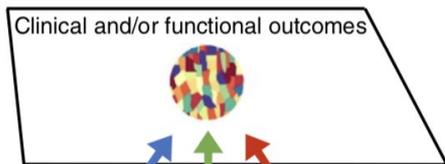
# Process-based predictive models

**a** Direct prediction approach

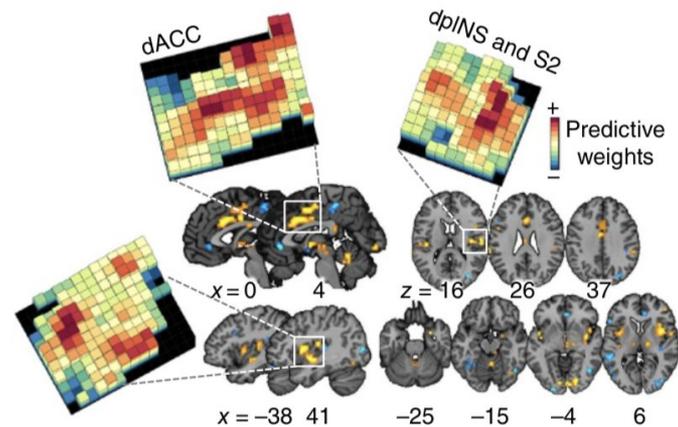
Clinical outcomes  
(diagnostic categories)



**b** Component process approach

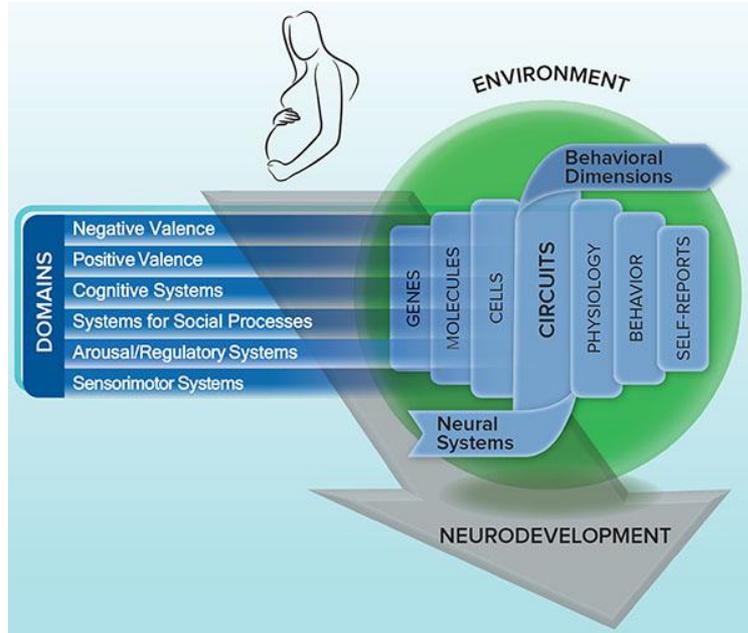


**c** An example: Neurologic Pain Signature



# Process-based predictive models

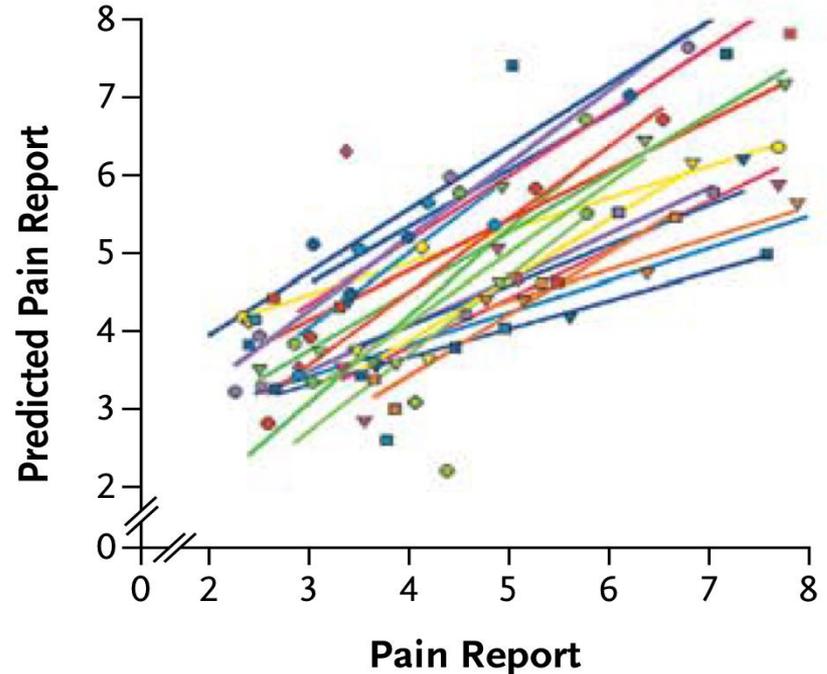
## Research Domain Criteria (RDoC)



<https://www.nimh.nih.gov/research/research-funded-by-nimh/rdoc/constructs/rdoc-matrix.shtml>

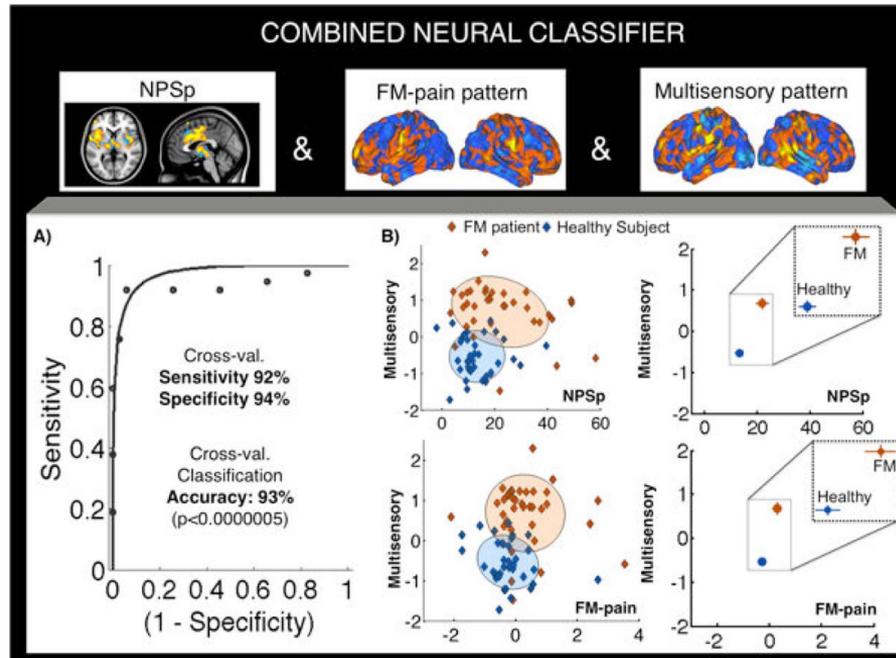
## Study I: Neurologic Pain Signature

### B Cross-Validated Prediction of Pain



# Process-based predictive models

## Study II: Clinical Pain Components



## Conclusion: Summary

### Box 2 Recommendations for future efforts

#### Model development:

- Increase focus on classification and prediction problems that cannot be easily achieved with existing clinical measures. Problems include early detection, prognosis, differential diagnosis, patient stratification and predicting treatment response (**Fig. 2c**).
- Increase focus on process-based predictive models and intermediate basic processes that may map more closely onto patterns of brain activity than clinical categories themselves and may reveal patterns of dysfunction and neuropathology across disorders (**Fig. 4b**).
- Homogeneous samples can be used for discovery, but the models should eventually be tested on more ecologically valid (i.e., more heterogeneous) samples.

#### Model validation:

- Plan proper prospective tests with independent test data from the early stages of study design and analysis planning (**Fig. 2e**).
- Test model specificity over multiple alternative conditions (for example, differential diagnoses, multiple cognitive and affective processes).
- Demonstrate models' neuroscientific validity (see “A systematic approach to improving neuroscientific validity”).

#### Cumulative science:

- Treat brain models as sharable research products that can be tested and annotated across different laboratories.
- Name newly developed predictive models to facilitate subsequent model-sharing and prospective testing (**Table 2**).
- Identify promising models and test them in increasingly broad and rigorous ways.

#### Big data approaches:

- Include multiple disease groups and task conditions in large-scale data initiatives. Important problems such as patient stratification and specificity testing can only be achieved with data that cut across multiple conditions and diagnoses.
- Establish quality-control standards and abide by established ones.
- When developing models on multisite data, carefully consider issues of variables that may be unbalanced across study sites (for example, patient/control ratios and measurement variances), and thus create confounds. Where such confounds are unavoidable, consider a strategy of developing models on one sample and then testing generalizability to other samples, rather than pooling data across sites.



“This new way of thinking about neuroimaging results integrates ideas from machine learning, big data, reproducible research and open science to bring translational goals within reach.”

Woo et al. (2017)

***Thank you!***

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