# IMPACT-Yale: Merging theory- and data-driven approaches

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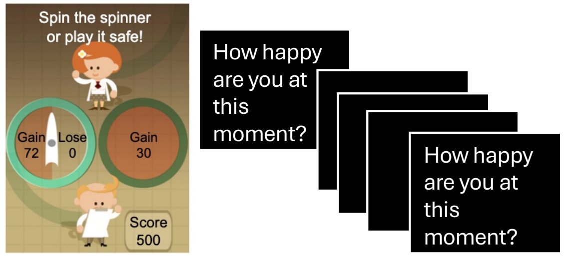
## A. Traditional computational psychiatry approach

Computational level:
Tasks designed to measure specific behaviors / processes




Data from homogenous cohort

Single timepoint assessment

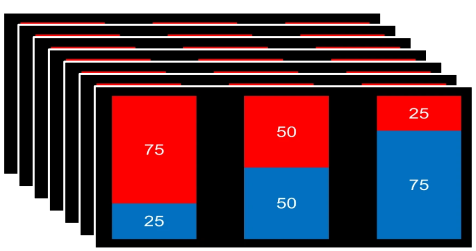
Algorithmic level:
Mathematical modeling of *how* the behavior/process occurs (e.g., how input is transformed into output)

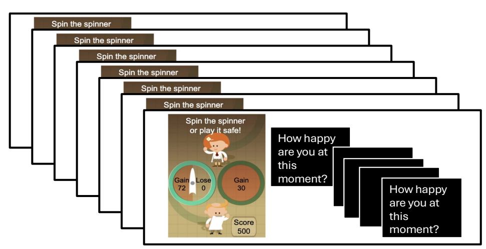
$$Happiness\,(t) \;=\; w_0 + w_1 \sum_{j=1}^{t} \gamma^{t-j} CR_j + w_2 \sum_{j=1}^{t} \gamma^{t-j} EV_j + w_3 \sum_{j=1}^{t} \gamma^{t-j} RPE_j$$

Single task
Single diagnosis
Single timepoint

Implementation level:
How the neural process occurs (e.g., network connections supporting process)

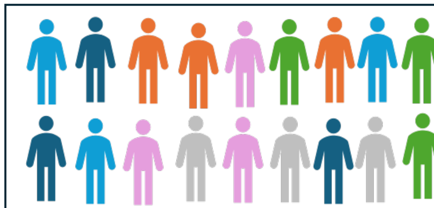
## B. IMPACT-Y's longitudinal computational psychiatry approach




Repeated behavioral testing over two years using multiple tasks

+



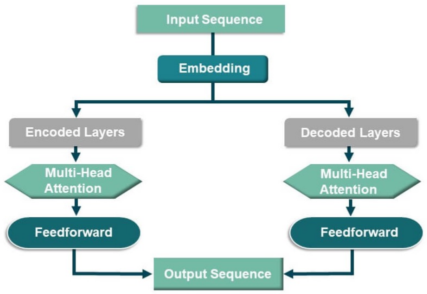
Heterogenous transdiagnostic cohort (N=2400) collected in 3 separate waves of 800 individuals.

Cheng et al., In Press, BP:CNNI

# Data streams

| | |
|---|---|
| ‘Standard’ clinical measures | DIAMOND diagnostic interview, self-report symptoms assessments |
| Electronic health records | Major medical events, social determinant of health |
| NIH Toolbox measures | Basic cognitive tasks, transdiagnostic measure of functioning |
| Spoken narrative data | Responses to standardized prompts for natural language processing (NLP) |
| Behavioral tasks tapping ‘latent’ constructs | Reward-sensitivity, ambiguity tolerance, susceptibility to conditioned hallucinations |

## AIM 1 – Individual predictions of outcomes




Hypothesis 1:

NLP + computational tasks will provide improved prediction of clinical outcomes over 2 years across a range of traditional diagnostic categories.

Transformer modeling

## AIM 2 – Characterization of trajectories

Hypothesis 2:

Identify families of trajectories that cut across traditional diagnoses and which can be used to generate normative models.

Latent growth curve modeling

## AIM 3 – Identification of biotypes

Bayesian clustering

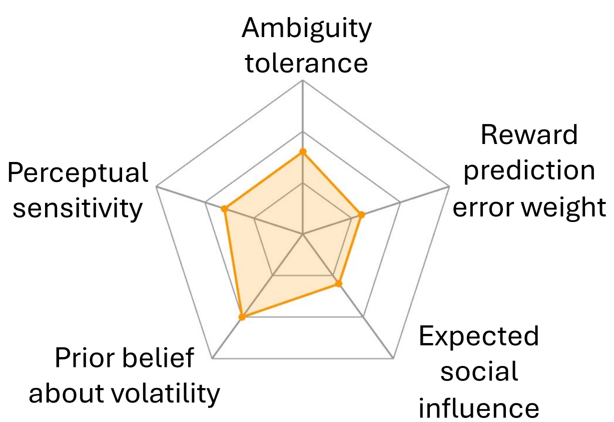
Hypothesis 3:

Person-centered subgrouping of multidimensional baseline data to identify biotypes that share similar clinical outcomes

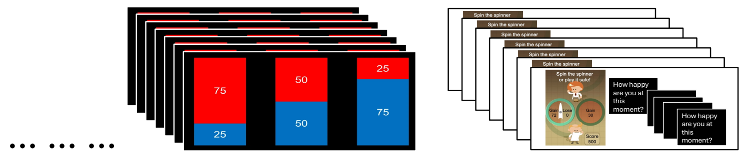
*biotypes*

# Computational ’snapshots’

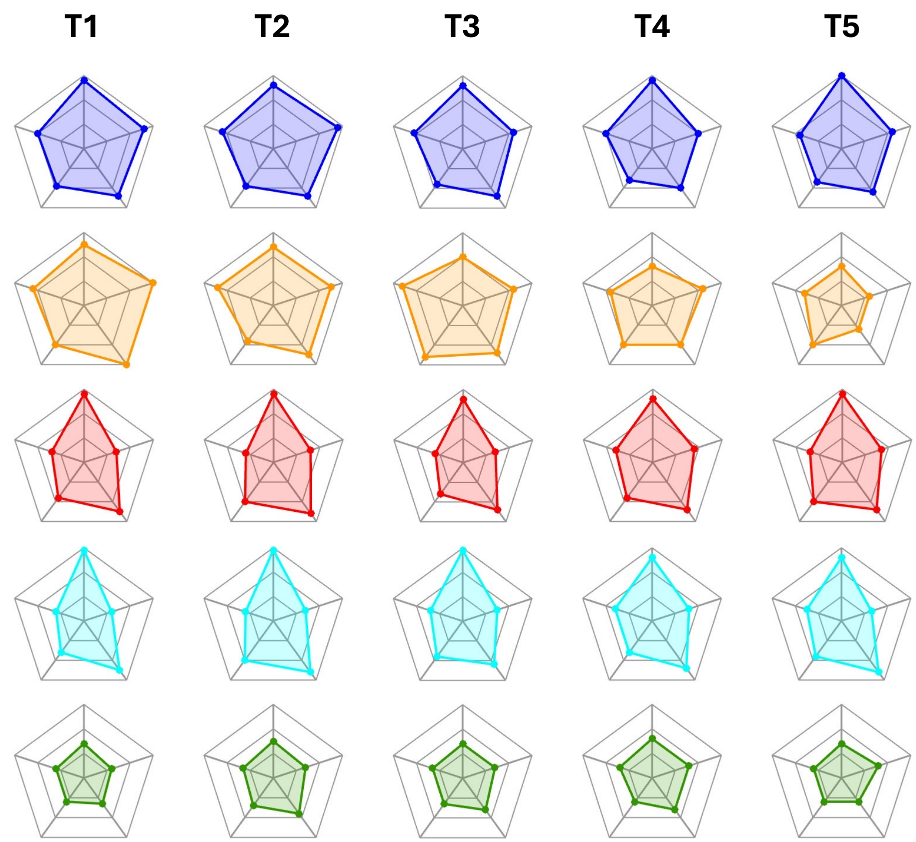
**<u>A. Computational snapshot at one timepoint</u>**




1. Index multiple computational processes for a given individual at a given time

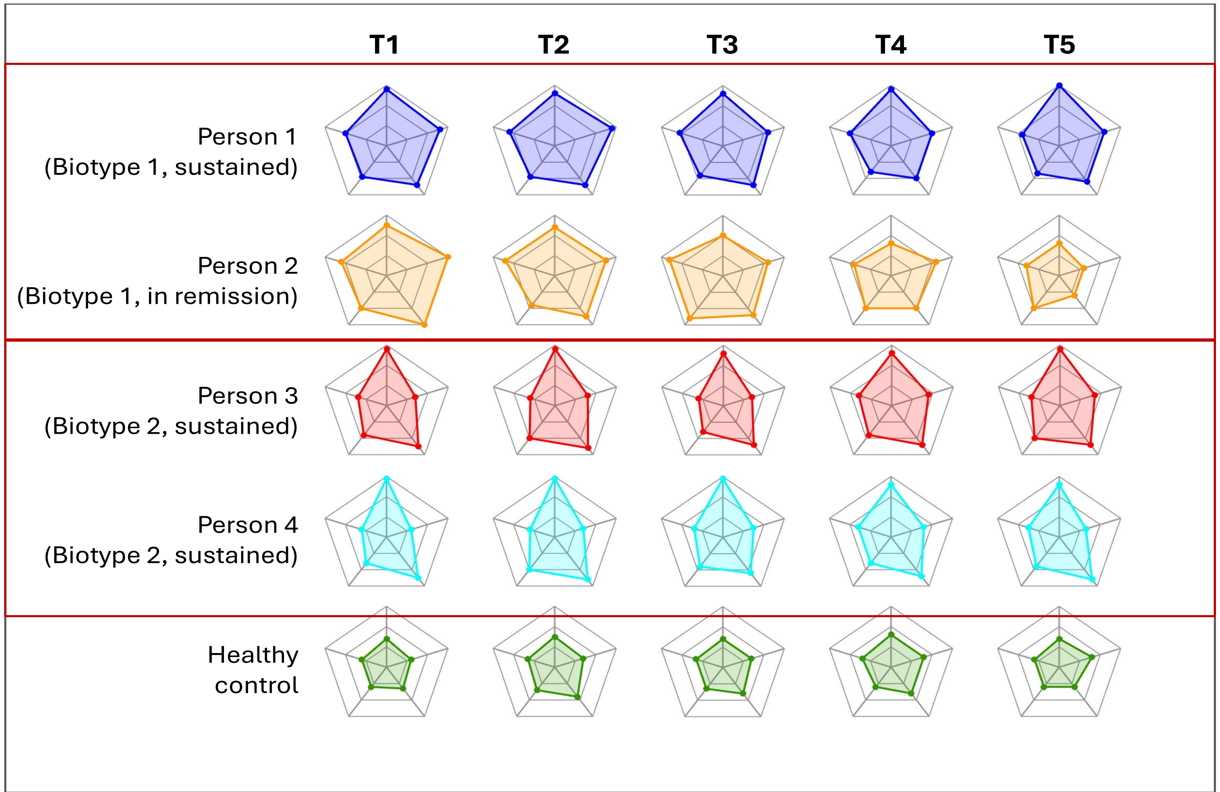



2. Identify data-driven subtypes and trajectories

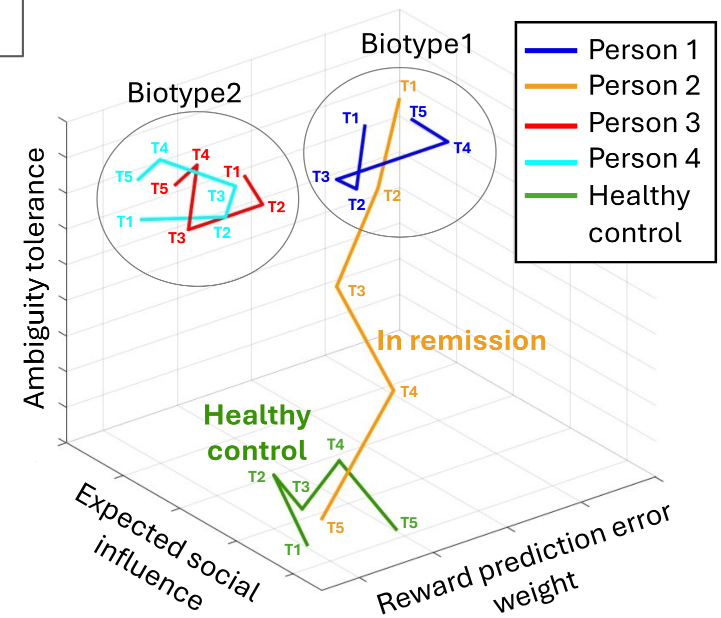



****Compare within and between task parameters across heterogeneous diagnoses****

Cheng et al., In Press, BP:CNNI

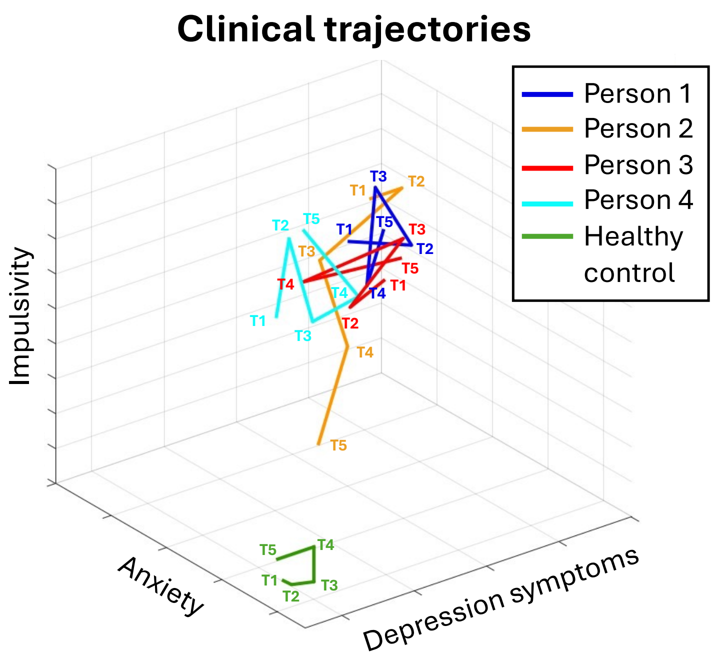



Computational snapshot may wax and wane w/ clinical trajectory….

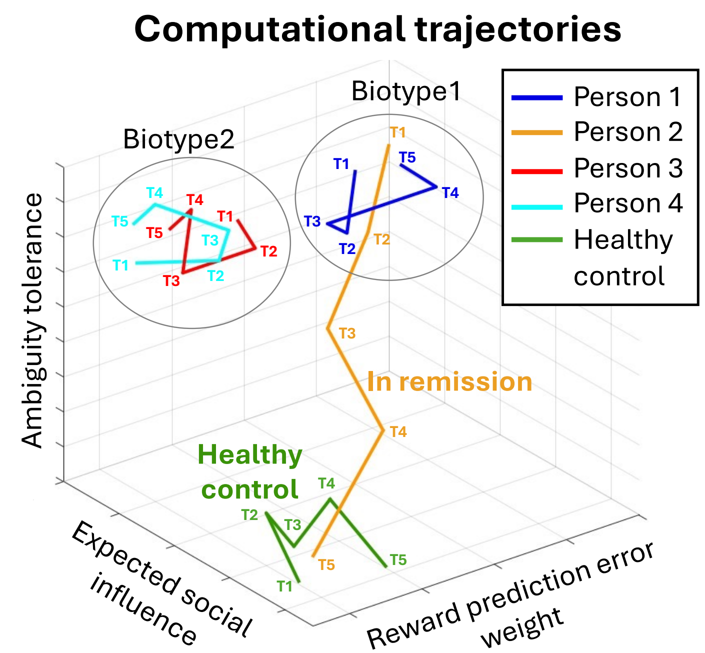



Cheng et al., In
Press, BP:CNNI

# Merging theory- and data-driven




Data-driven models to elucidate complex relationships between clinical and computational trajectories




Cheng et al., In Press, BP:CNNI

# Threading the needle: Practical considerations for merging theory-driven computational psychiatry with data-driven analytics to enhance precision health at scale

Annie Cheng [1], Anna Konova [2], Albert Powers [1 16], Philip Corlett [1 16 17], Ifat Levy [3 13 15 17], Xiaosi Gu [1 12 16], Quentin Huys [4], Helen Pushkarskya [1], Sarah Fineberg [1], Tobias Hauser [5 6 7 8], Danilo Bzdok [9 10], Ilan Harpaz-Rotem [1 13 16 17], Theresa Babuscio [1], Lisa Nichols [1], Yize Zhao [11], Manu Sharma [1], Daniella Meeker [12], Hua Xu [12], Robb B. Rutledge [1 13], Godfrey D. Pearlson [1 15 17 18], Christopher Pittenger [1 13 14 15 16 17], Sarah W. Yip [1 14 16 17]