



Background & Motivation

A Validated Benchmark

An external EEG dataset acquired during the **Wisconsin Card Sorting Test (WCST)** demonstrated robust discrimination across the Alzheimer's disease (AD) spectrum, providing evidence that this protocol captures disease-related neural alterations. These findings motivated **the adoption of the WCST in the PREDICTOM study** as the task protocol for evaluating cognitive control.

Two Linked Hypotheses

Discrimination Today, Risk Prediction Tomorrow

H1 · Cross-Paradigm Generalization

A network-based EEG connectivity framework, originally developed and validated on resting-state data, will generalize in the WCST.



H2 · Translation to Early Risk Stratification

The protocol can be replicated and adapted within the PREDICTOM study to discriminate high-risk vs. low-risk individuals — shifting the target from diagnostic stage to future dementia risk.

Methods

From Diagnostic Discrimination to Risk Stratification

Methodological adaptation - The established network-based framework is adapted to the new protocol by:

- **Preserving** the core network methodology
- **Tailoring** the analysis to protocol-specific neural features (brain regions, frequency bands, etc.)
- **Refocusing** the classification objective from multi-stage diagnosis to binary risk stratification

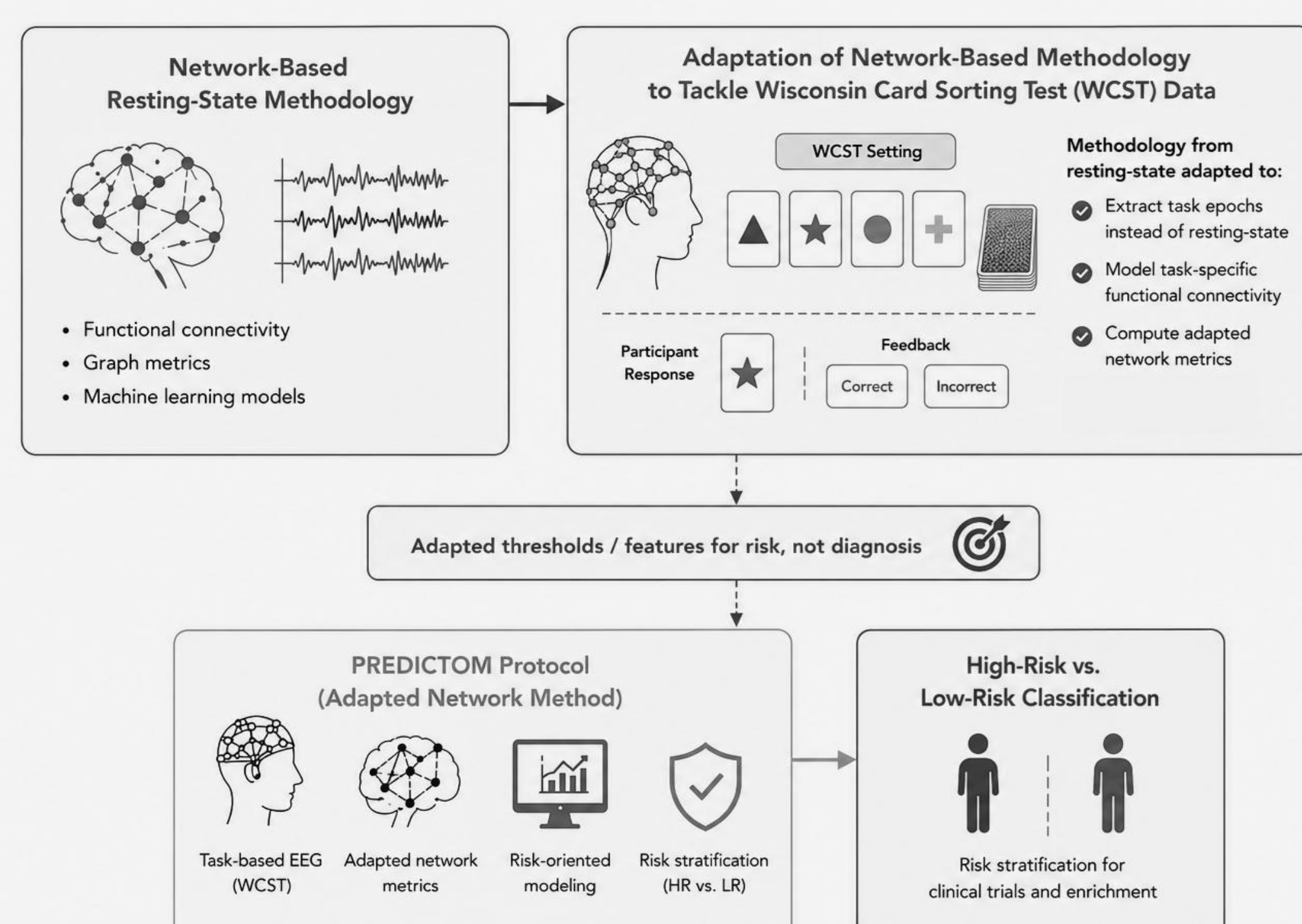
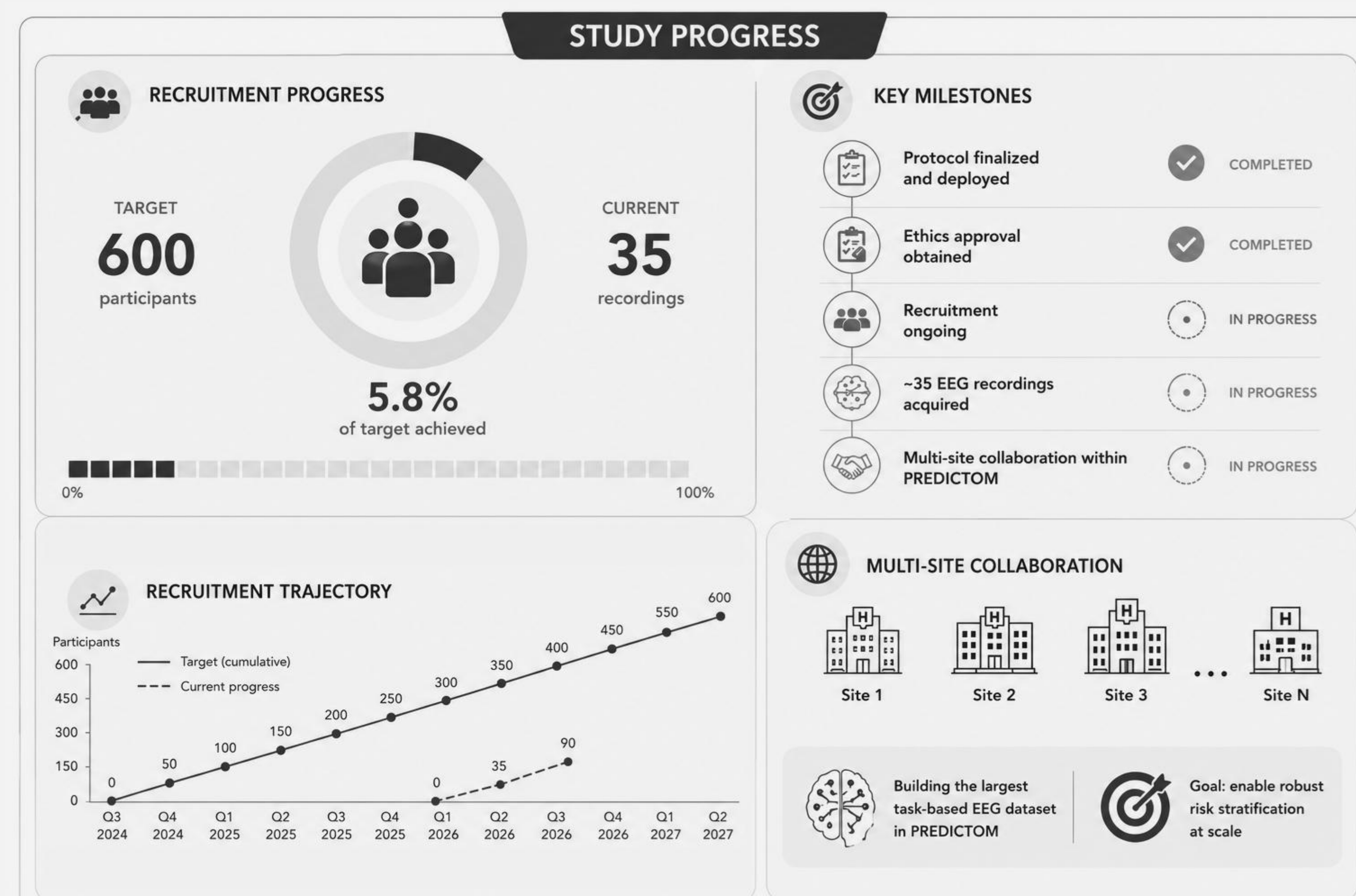


Figure 1. Overall methodological framework and workflow.

Translational Value

A unified network-based biomarker framework that generalizes from resting-state to task-based EEG (WCST) and from AD-spectrum classification to high- vs. low-risk stratification would provide a flexible, scalable tool, bridging clinical staging with early preventive screening for dementia.

PREDICTOM Study Status



Closing the loop

- **H1 — Generalized?** Does the network-based approach perform well in WCST EEG data?
- **H2 — Translated?** Does the same approach, adapted, separate high-risk from low-risk individuals in PREDICTOM?

As recruitment and validation progress, both will be answered establishing whether a single resting-state biomarker pipeline can serve as an early risk predictor.

