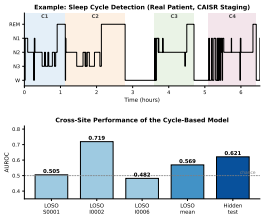
Sleep Architecture Dynamics Enable Cross-Site Cognitive Impairment Prediction

Junseob Kim, Aditya Nagori, Tilendra Choudhary, Md Hassanuzzaman, Rishikesan Kamaleswaran

Duke University
Durham, NC, USA

Machine-learning models applied to polysomnography have demonstrated increasing potential for predicting future cognitive impairment, yet cross-site generalizability remains a critical barrier to clinical deployment. Conventional EEG spectral and heart-rate-variability features encode equipment-specific characteristics rather than disease-relevant physiology, causing models to fail when transferred across hospitals with different hardware or acquisition protocols.

We address this through sleep cycle dynamics, a representation that is inherently invariant to voltage, amplifier gain, and electrode configuration. Grounded in established sleep physiology, normal adult sleep consists of four to five NREM–REM cycles that evolve systematically across the night, with slow-wave (N3) duration decreasing and REM episodes lengthening. In cognitive decline, these progressions are disrupted, producing fewer complete cycles, attenuated stage transitions, and greater within-cycle fragmentation. To capture these disruptions, we detect individual NREM–REM cycles from automated sleep stage annotations, defining each cycle as a contiguous NREM period of at least 15 minutes terminated by a REM episode of at least 5 minutes, with brief wake intrusions tolerated. Each recording is then summarized by 25 cycle-level descriptors: cycle counts (3), cycle durations (6), progressive N3 and REM trends across successive cycles (6), within-cycle stage composition (6), and regularity metrics including duration entropy and inter-cycle compositional similarity (4). These are combined with 32 ratio-normalized summaries capturing broader sleep architecture, respiratory and arousal event rates, stage transitions, and fragmentation, plus five demographic variables, for 62 features in total. All features are z-score normalized per site before classification with a LightGBM model. On leave-one-site-out cross-validation, the model achieved a mean AUROC of 0.569. On the hidden test set from unseen recording sites, the model achieved an AUROC of 0.621, confirming that sleep cycle dynamics constitute a site-invariant representation of disease-relevant physiology.



Representative NREM–REM cycle progression (top) and cross-site AUROC results (bottom).