Phenotypic Characterization of Sleep Apnea using Clusters Derived from Subject-Based SpO_2 Weighted Correlation Networks

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Background

OSA affects >1billion adults globally with cardiovascular, metabolic, and neurocognitive complications

Current limitations: Traditional *k*-means clustering on polysomnography metrics fails to capture complex physiological interdependencies

Critical gap: SpO_2 signals contain unexplored phenotypic information despite being central to apnea-hypopnea scoring

Objective

To develop a novel clustering framework using subject-based SpO_2 weighted correlation networks for identifying clinically distinct OSA phenotypes.

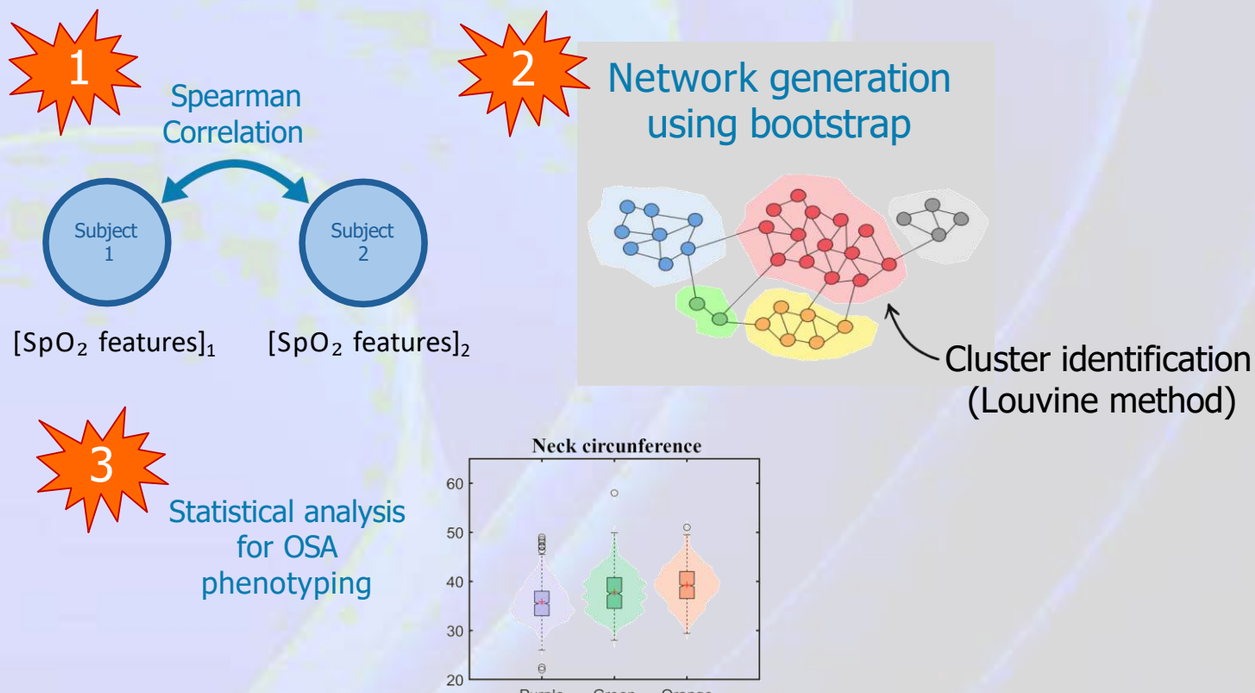
Materials and Methods

Study Population:

2,641 subjects from Sleep Heart Health Study (SHHS)

Novel Approach:

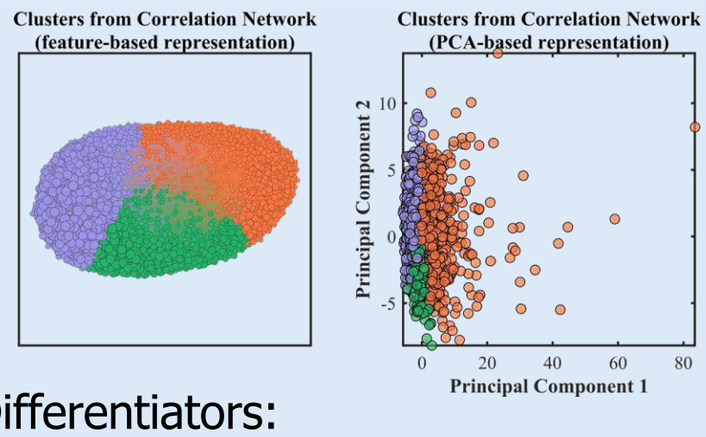
- 43 SpO_2 features from overnight PSG
- Subject-based correlation networks
- Louvine method for cluster identification
- Phenotyping using 73 sociodemographic, clinical, and anthropometric variables



Key Results

Cluster Identification:

- 3 distinct phenotypes automatically identified
  - 1,056 subjects (39.98%)
  - 934 subjects (35.37%)
  - 651 subjects (24.65%)



Superior Performance vs. K-means:

- 35 significantly different variables (correlation networks) vs. 28 variables (*k*-means)
- Enhanced detection of clinically meaningful characteristics

Clinical Differentiators:

- Anthropometric: BMI, neck circumference, height, weight
- Cardiovascular: Systolic/diastolic blood pressure
- Sleep-related: AHI, arousal index, total sleep time, Epworth sleepiness scale

Conclusions

Subject-based SpO_2 correlation networks revealed clinically meaningful subgroups missed by traditional methods. This approach advances personalized medicine by leveraging routine SpO_2 monitoring data for precise phenotype identification.

Acknowledgement

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