

Data Augmentation for Cognitive Biomarker Prediction – Solving the Small Sample Size Problem in Clinical Research

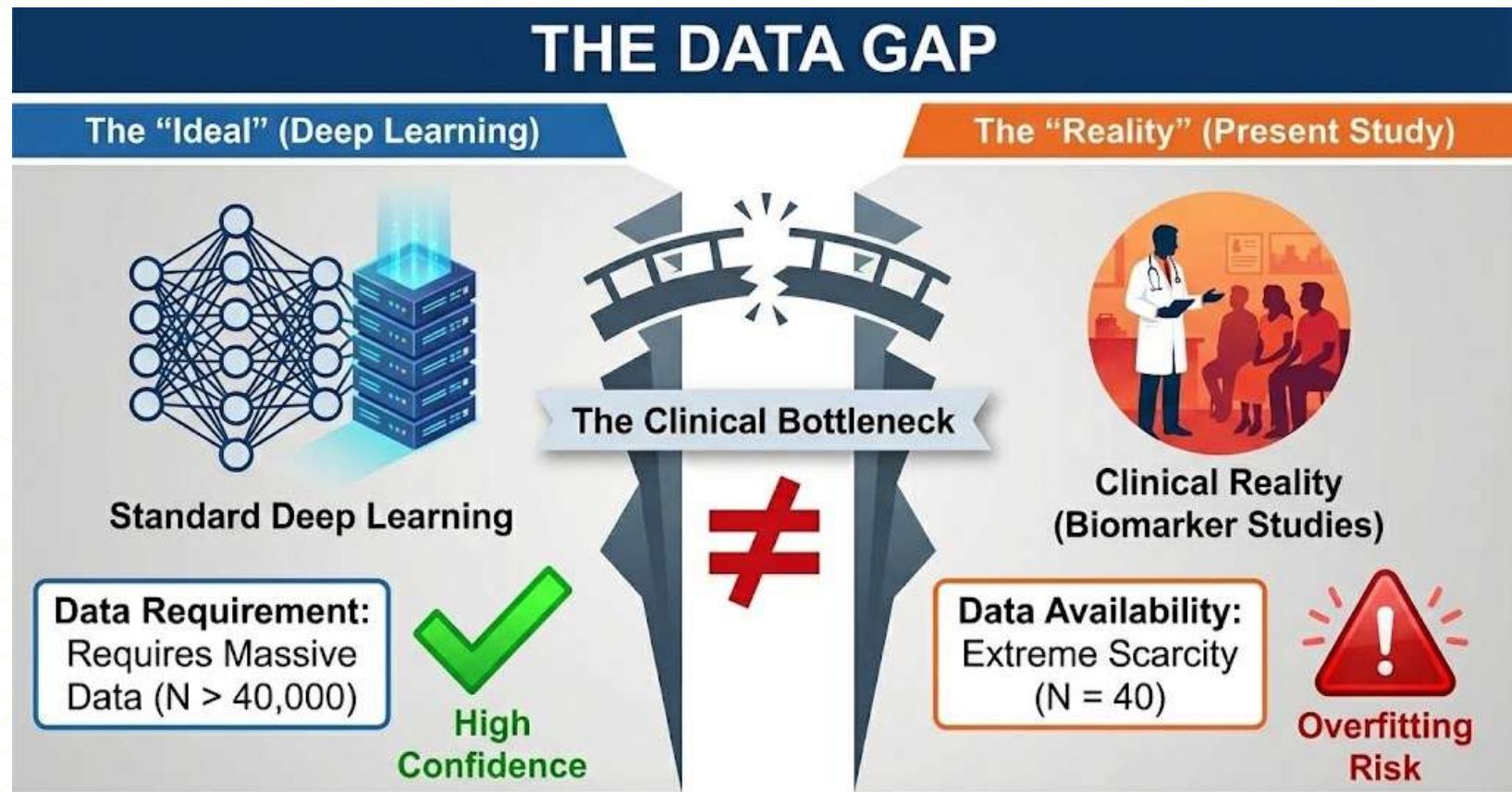
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CMPS 7010 – Research Seminar

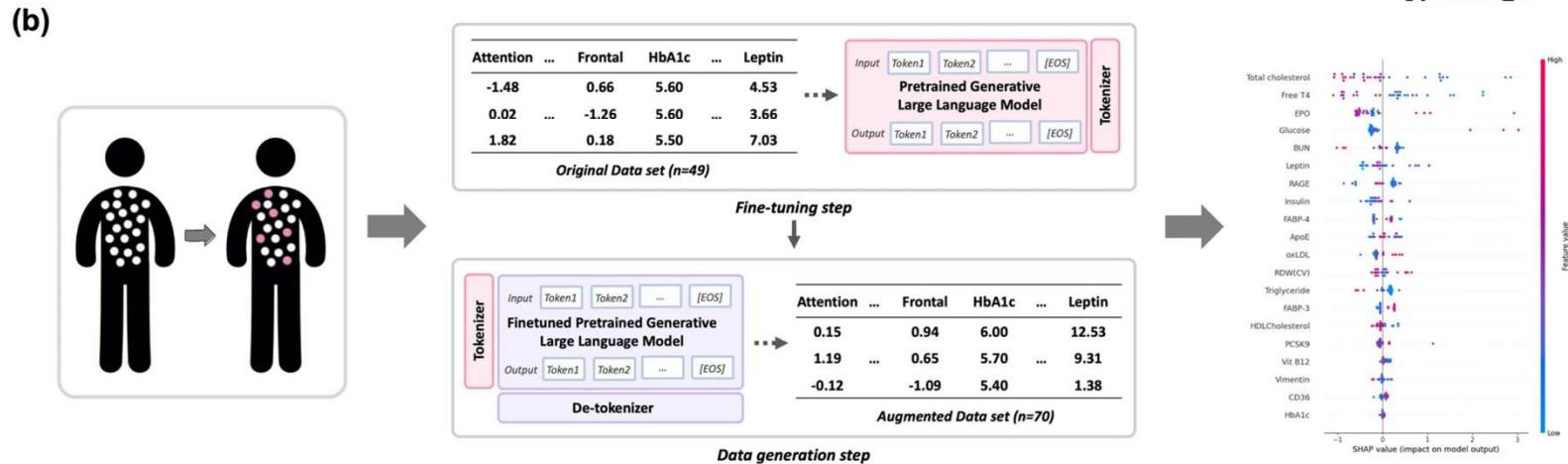
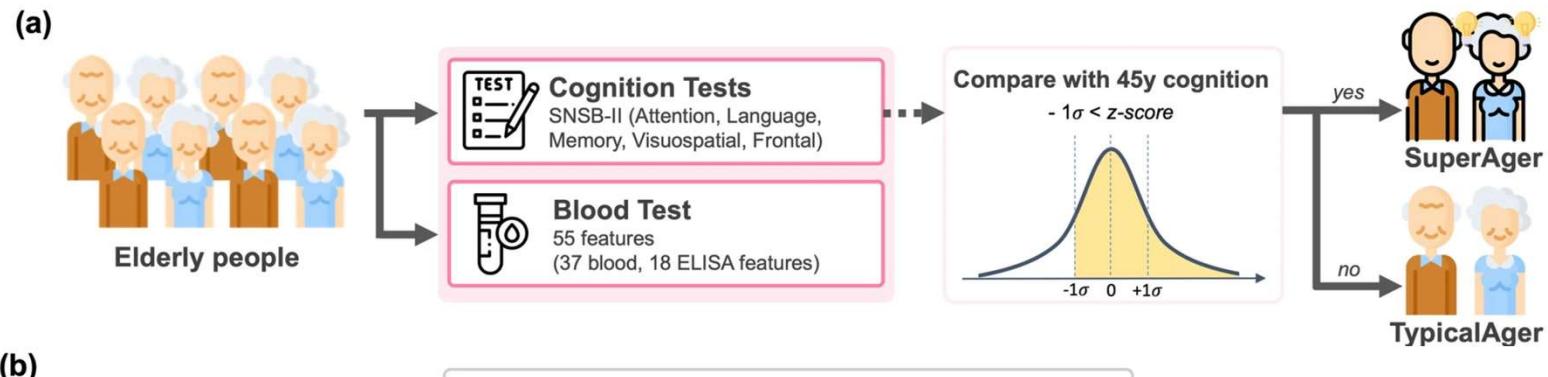
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The Problem: Data Scarcity in Clinical Research



Blood Biomarkers and SuperAger Status



Feature Selection
RFE, BORUTA

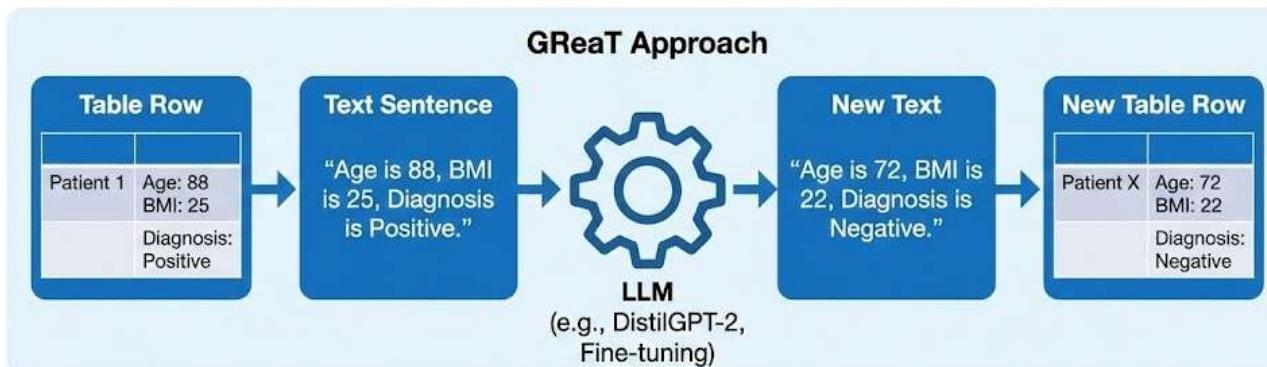
Data Augmentation
Large-Language Model based 'GReaT'

Model Interpretation
Explainable AI based 'SHAP'

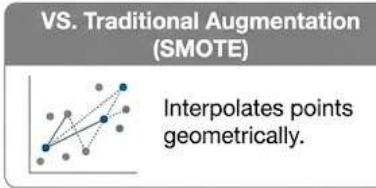


Generating New, Synthetic Patients to Increase Sample Size

The Solution: GReaT (Generative Realistic Tabular Data)

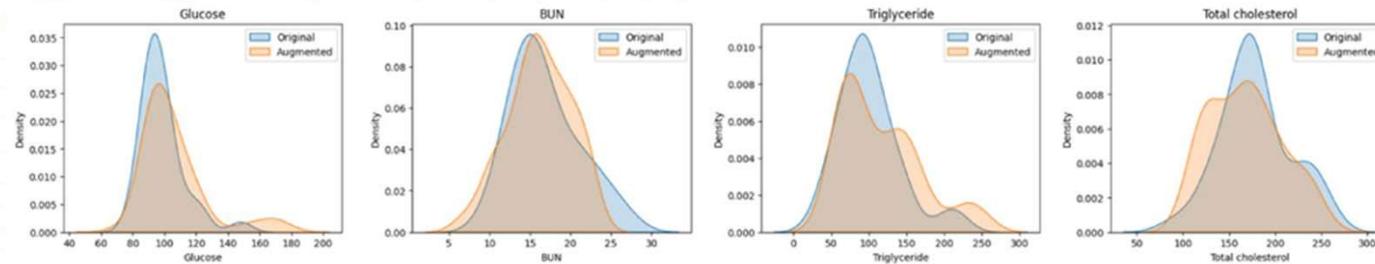


- ✓ GReaT Approach: Treats patient data as language.
- ✓ Captures complex, non-linear dependencies between features (Age, BMI, biomarkers).
- ✓ Allows LLM to “write” new, realistic patient profiles.



Validating the Synthetic Data

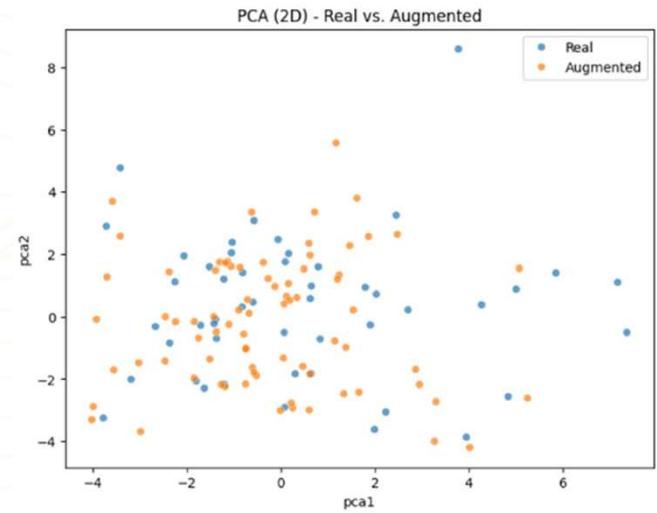
A – Kernel Density Estimation Plots



KDE plots show distribution similarity between real (blue) and augmented (orange) data across SuperAger status and key biomarkers -> substantial overlap indicates augmented data preserves statistical properties of the original data

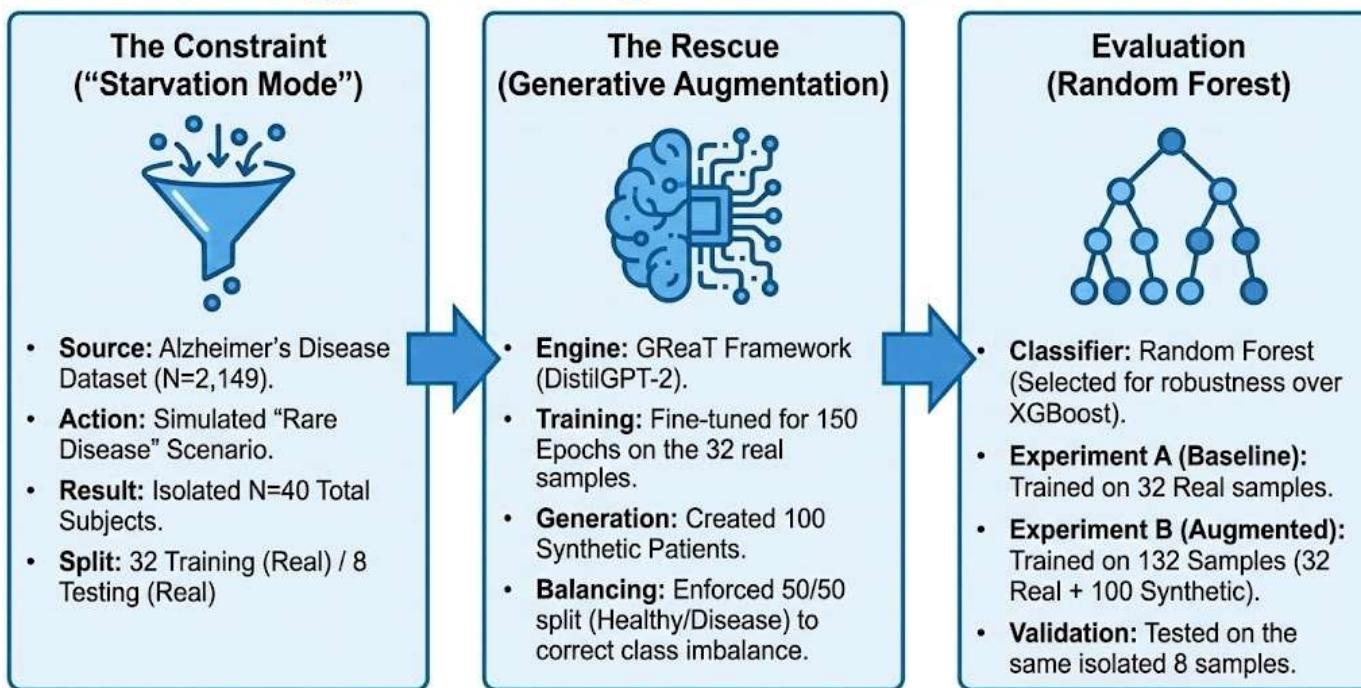
Demonstrates the 2D distribution of real and augmented samples. Similar scatter patterns confirm the augmented data maintains the same variance structure as the original data

B – Principal Component Analysis (PCA)

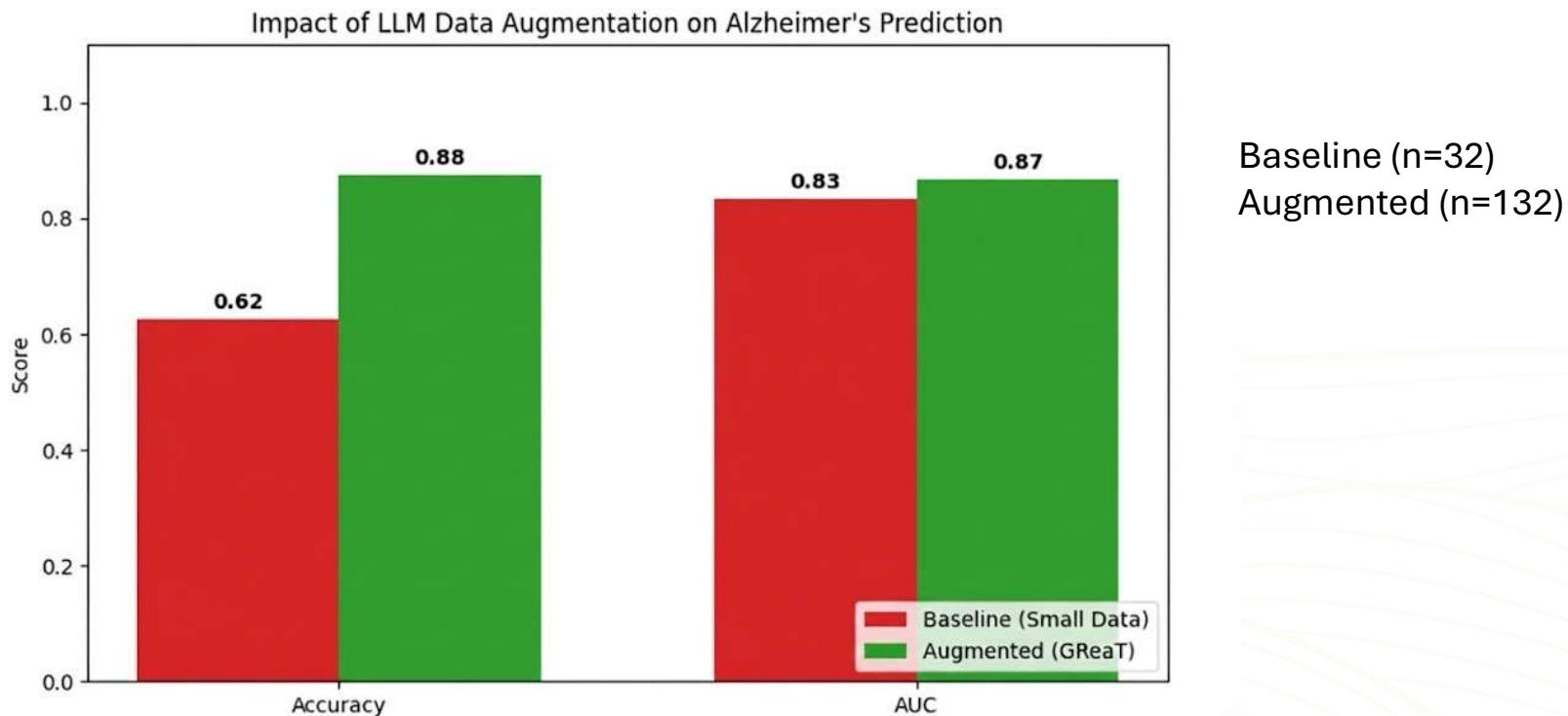


The Present Replication Setup

Methodology: “Starving” the Model & LLM Rescue



Results – Data Augmentation

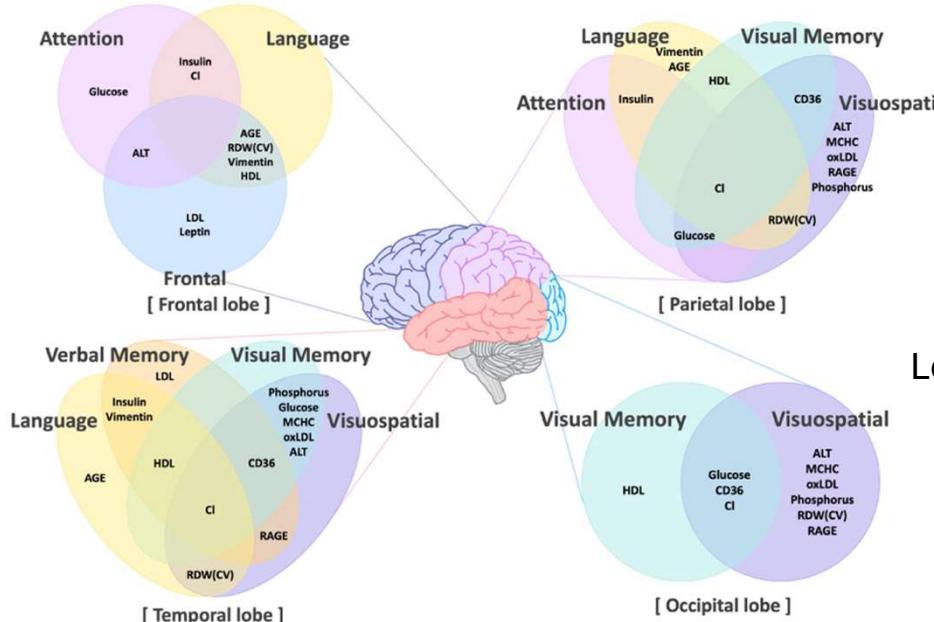


- Generative augmentation stabilizes models in data-scarce scenarios
- **This replicates a key finding from Lee et al. (2025)**



Clinical Significance & Discussion

- Easily accessible, simple and scalable blood biomarkers can be used to identify cognitive status
- Beyond math, such biomarkers may be relevant for certain dimensions of cognitive assessment mapping to specific brain regions



Lee HB et al. *Scientific Reports*, 2025



Limitations

- Small test sample
- “Seed bias” due to training on a small “seed” of only 32 patients
- Possible hallucinations with synthetic data generation using an LLM
- Limitation to tabular data only (no genetics or imaging)



Conclusions & Future Work

- We were able to replicate the ability of synthetic data augmentation using the GReaT LLM model to improve predictive ability of blood biomarkers from an initial small patient sample
- This suggests enormous future potential for clinical studies with small sample size
- Future work: Apply this to multi-omics data such as presented in Zhou et al. (2025) discussed previously





References

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