Temporal Clustering in Alzheimer's Dataset

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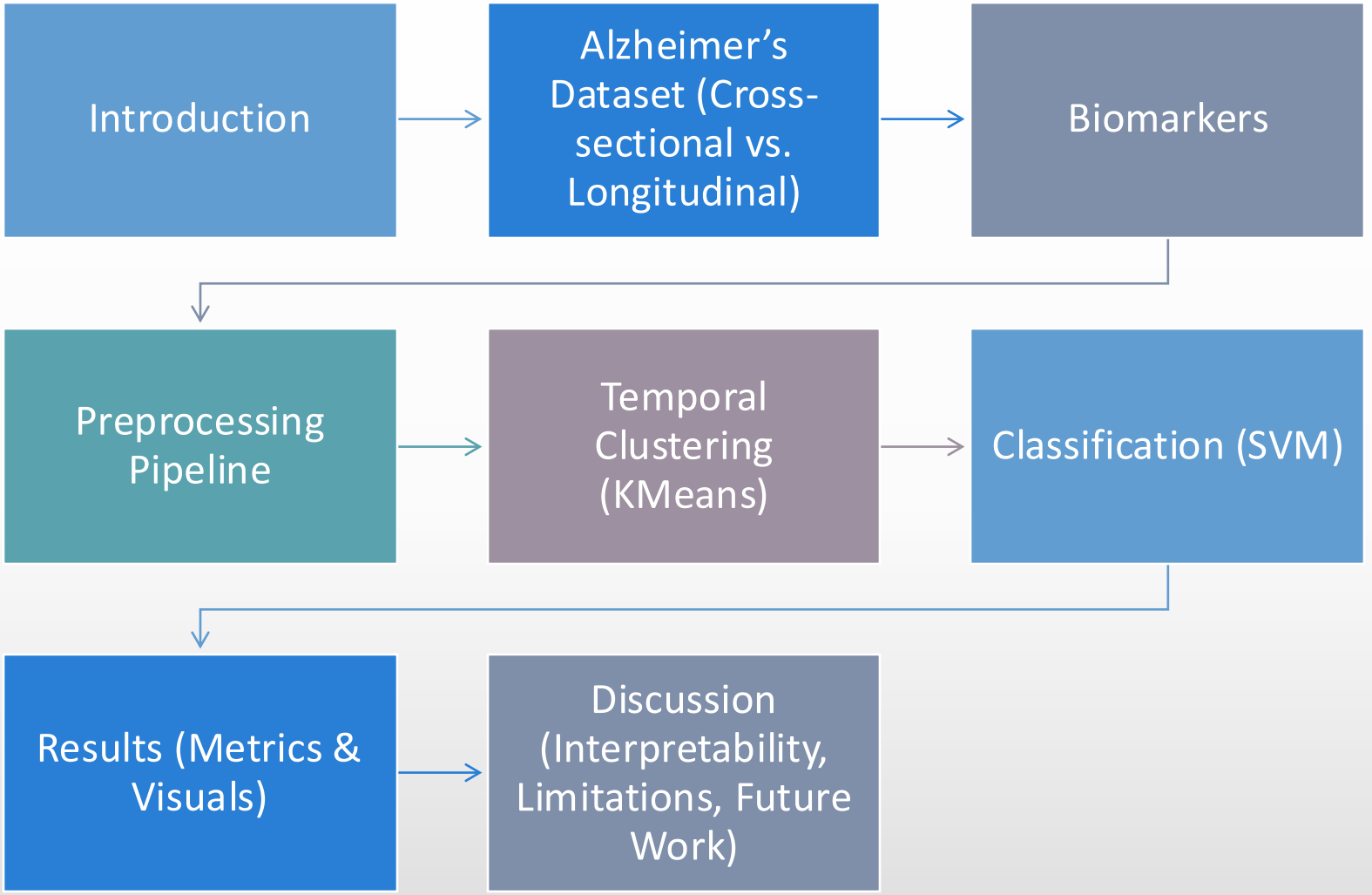
AGENDA


Introduction
Alzheimer's Dataset (Cross-sectional vs. Longitudinal)
Biomarkers
Preprocessing Pipeline
Temporal Clustering (KMeans)
Classification (SVM)
Results (Metrics & Visuals)
Discussion (Interpretability, Limitations, Future Work)

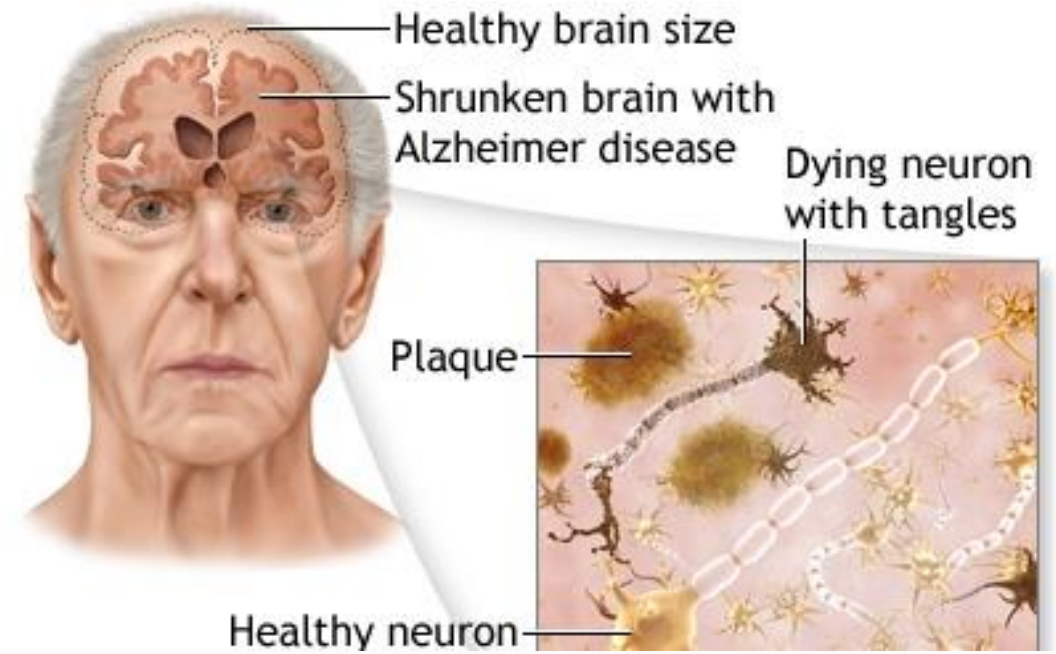
Introduction

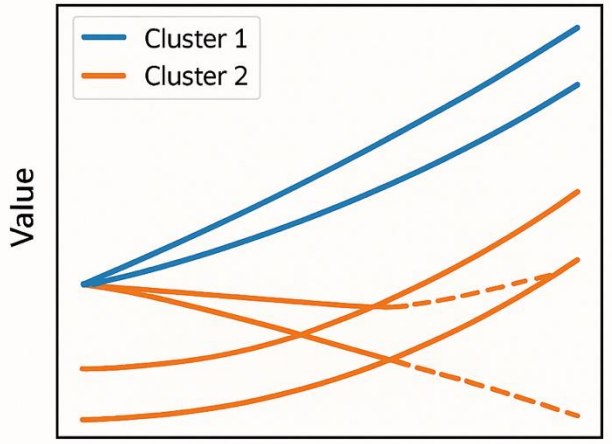
Temporal clustering

- Groups data on patterns **change over time**,
- Considers **trajectories or sequences**.

What is Alzheimer's?

- **Neurodegenerative disorder**
- Leads to **progressive memory loss** and **cognitive decline**
- Most common cause of **dementia** worldwide





INTRODUCTION

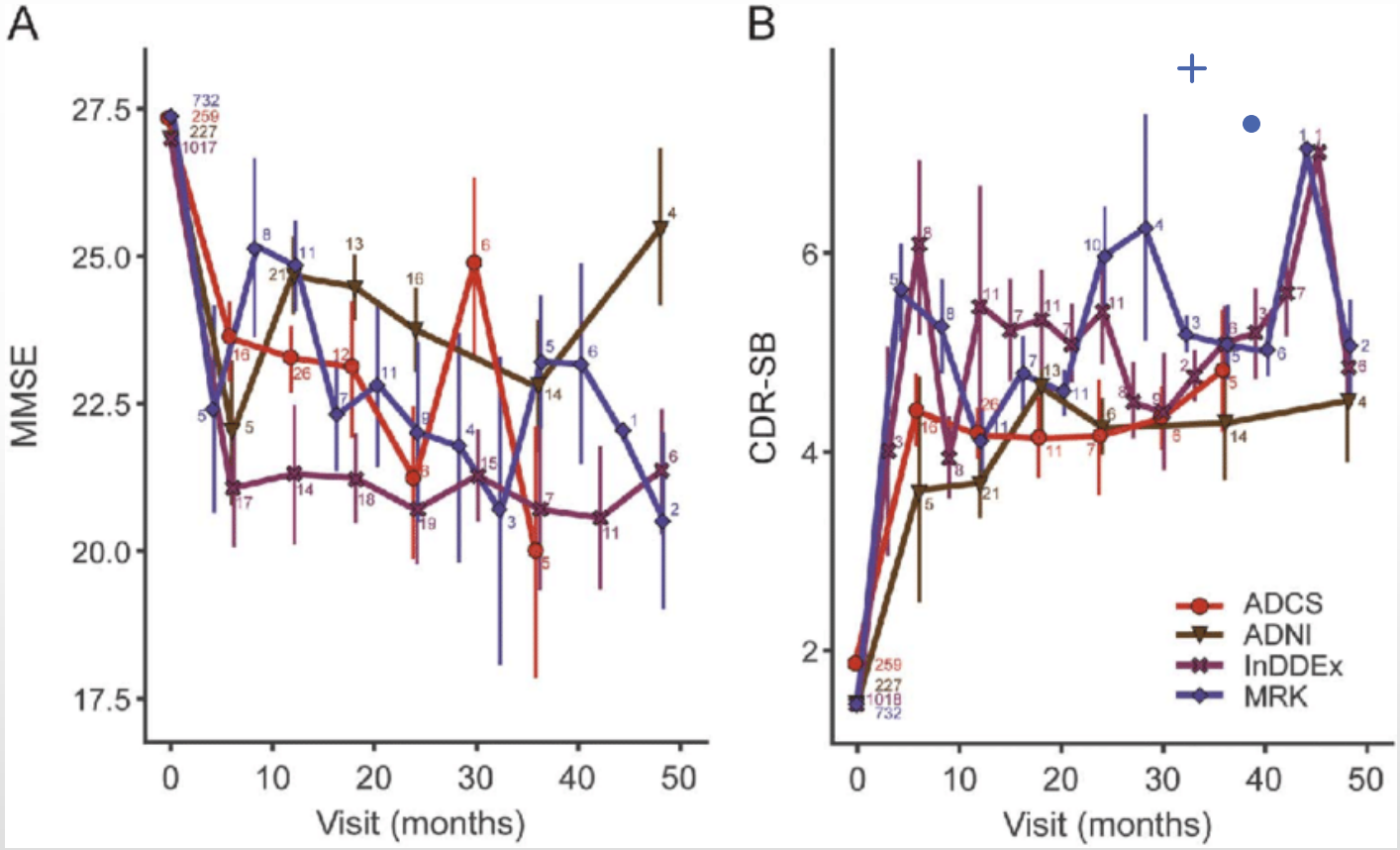
Alzheimer’s → progressive neurodegenerative disease.

Most ML studies: single snapshot (cross-sectional).

Challenge: disease evolves → requires **longitudinal modeling**.

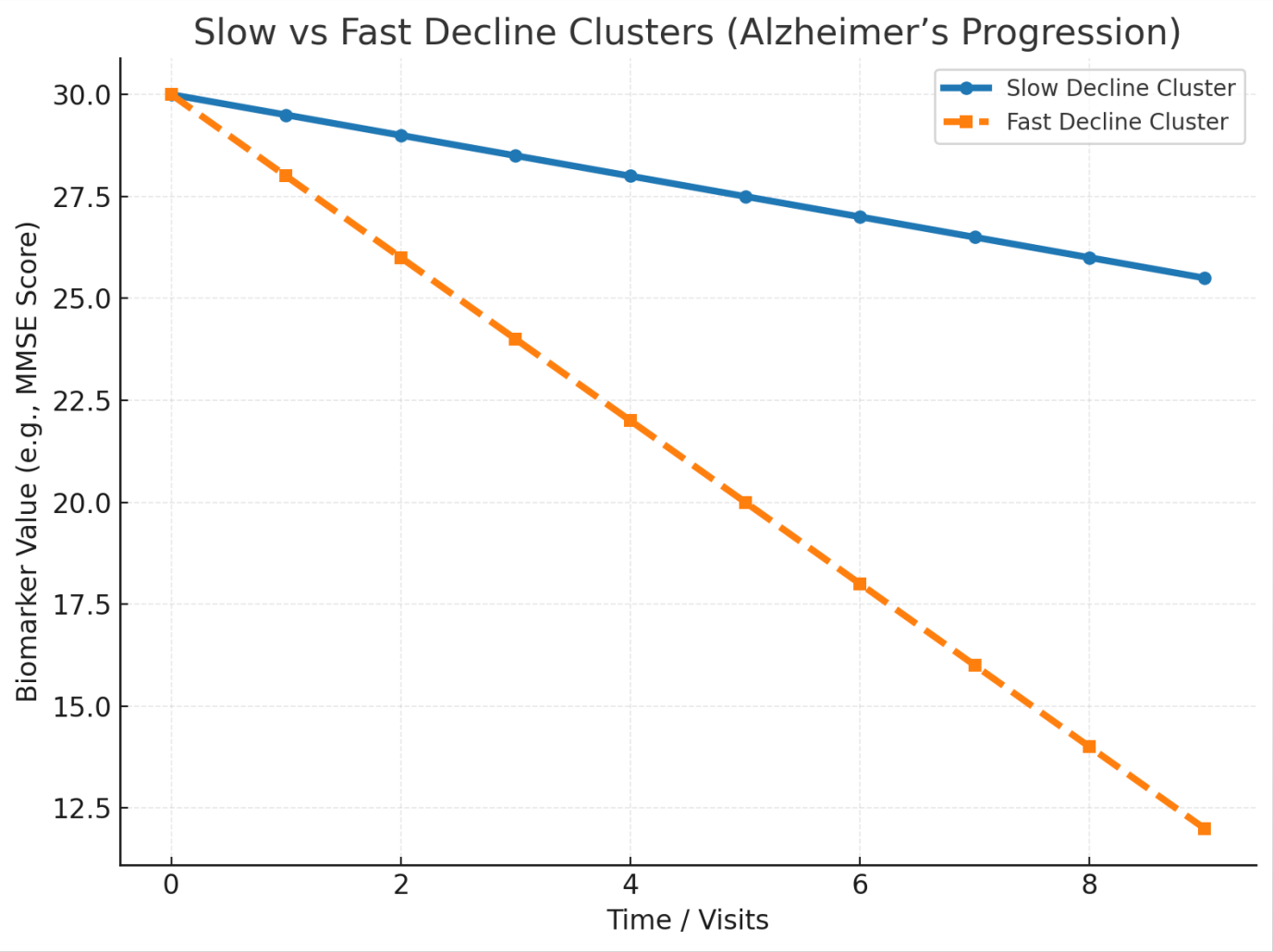
Introduction

- Patient biomarkers evolve across visits
  - **MMSE** (cognitive score)
  - **CDR** (dementia rating)
  - **Brain volume**



Introduction

- Temporal clustering groups patients into:
  - **Slow decline** cluster
  - **Fast decline** cluster



DATASET

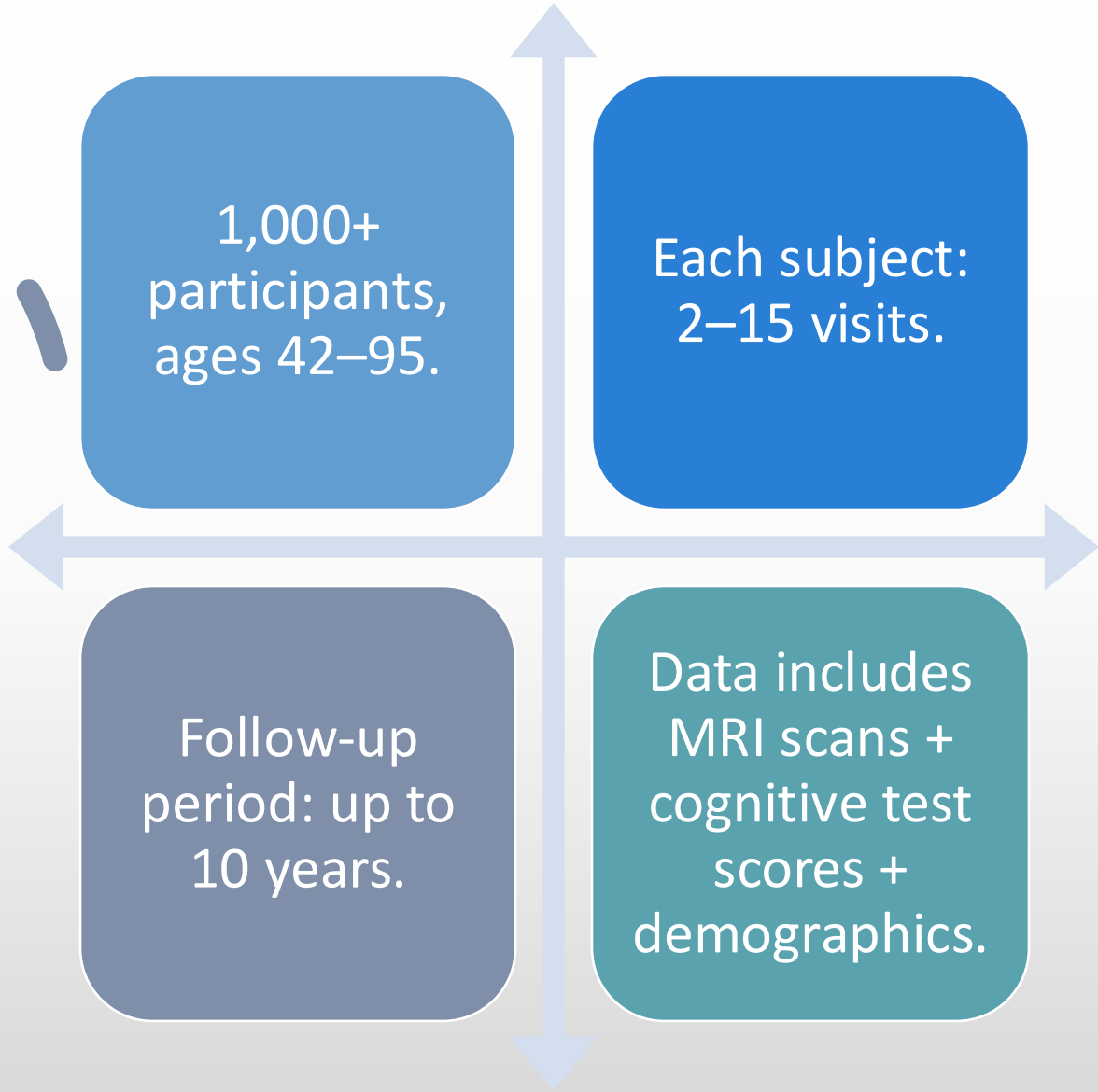
Dataset: Alzheimer's dataset (OASIS-3, via Kaggle).

Cross-sectional: single visit per subject.

Longitudinal: repeated MRI + cognitive assessments across years.

Why longitudinal? → progression tracking.

Dataset Structure



BIOMARKERS

CDR: Clinical Dementia Rating (0 → normal, 0.5+ → dementia).

MMSE: cognitive ability (0–30 scale).

eTIV: estimated intracranial volume (brain size baseline).

nWBV: normalized whole brain volume.

PREPROCESSING PIPELINE

Filter: subjects with ≥6 visits.

Interpolation: fill missing visits → regular timeline.

Normalization: Z-score across biomarkers.

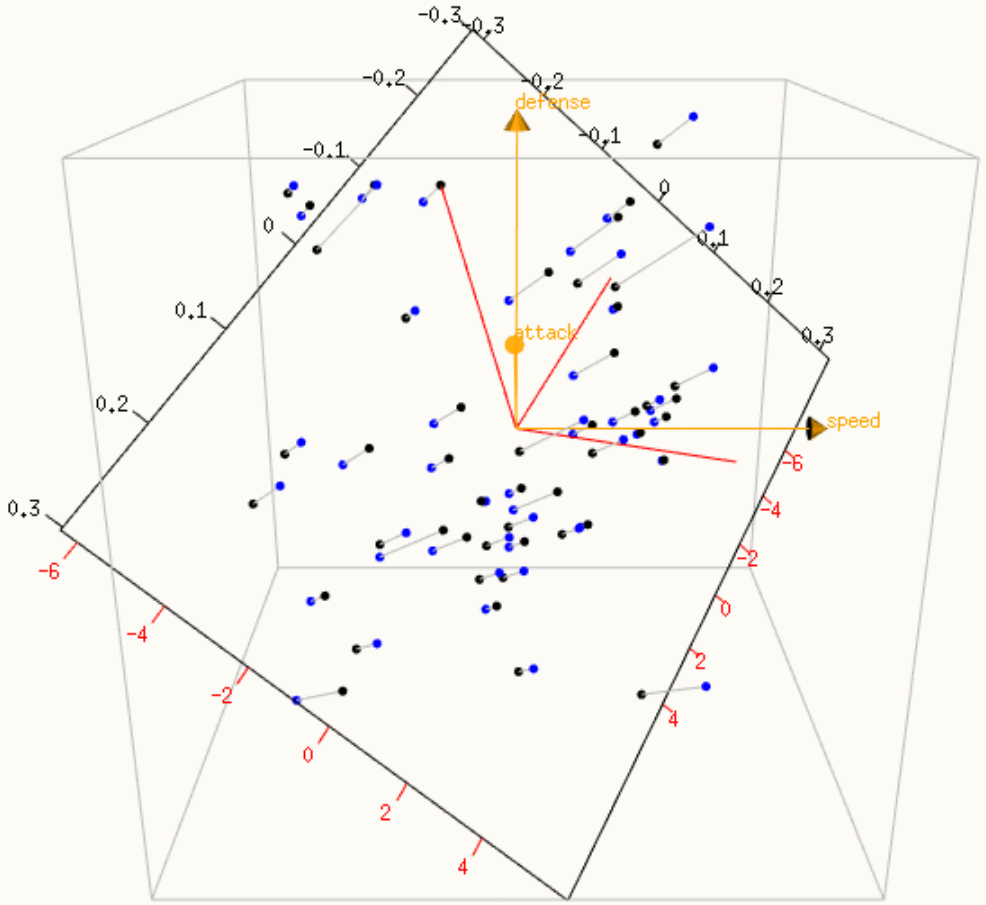
PCA: reduce dimensionality of biomarker time series.

Why PCA?

Alzheimer’s biomarkers correlate.

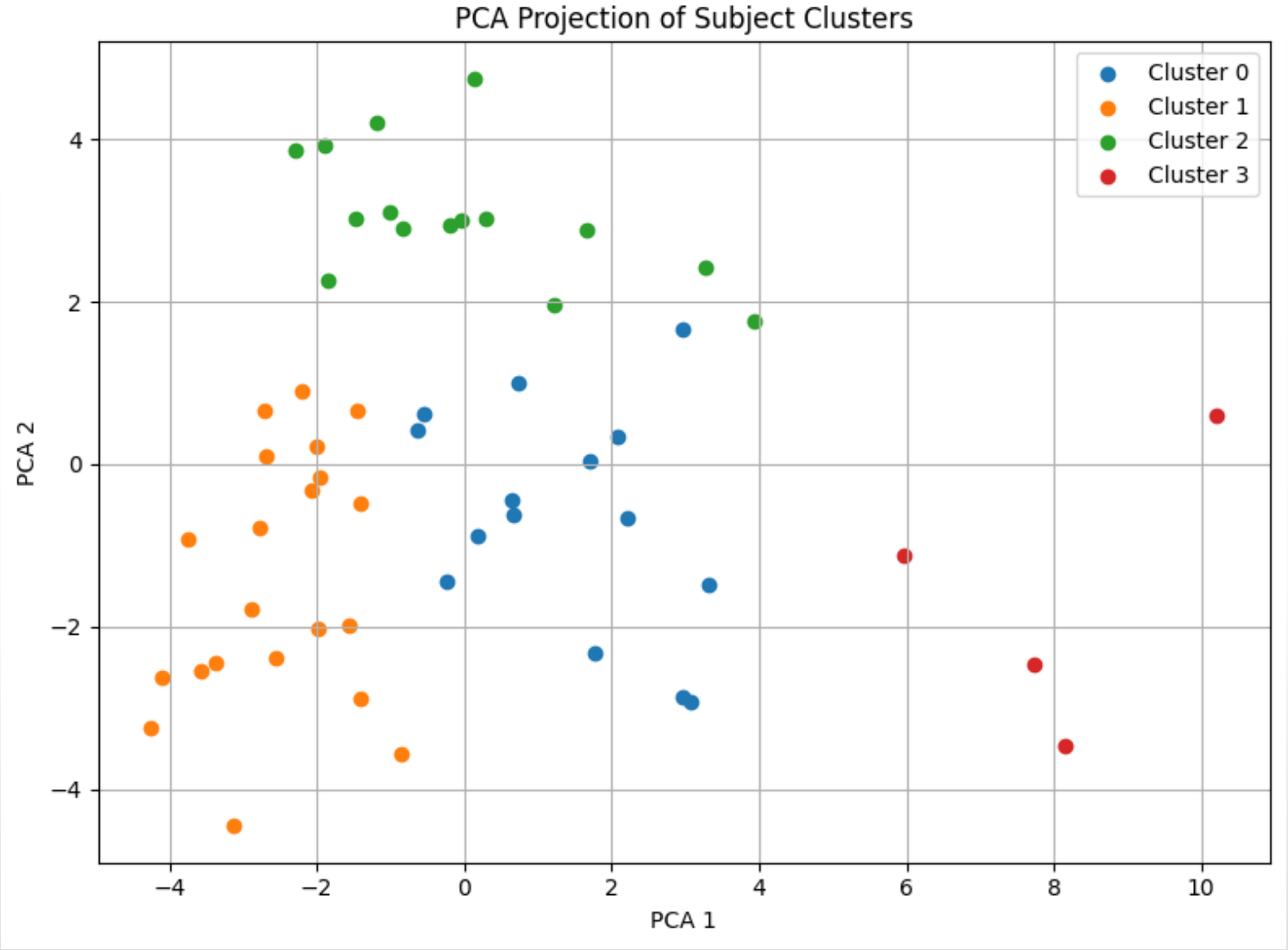
PCA removes redundancy, reduces noise.

Trajectories become more stable + easier to cluster.



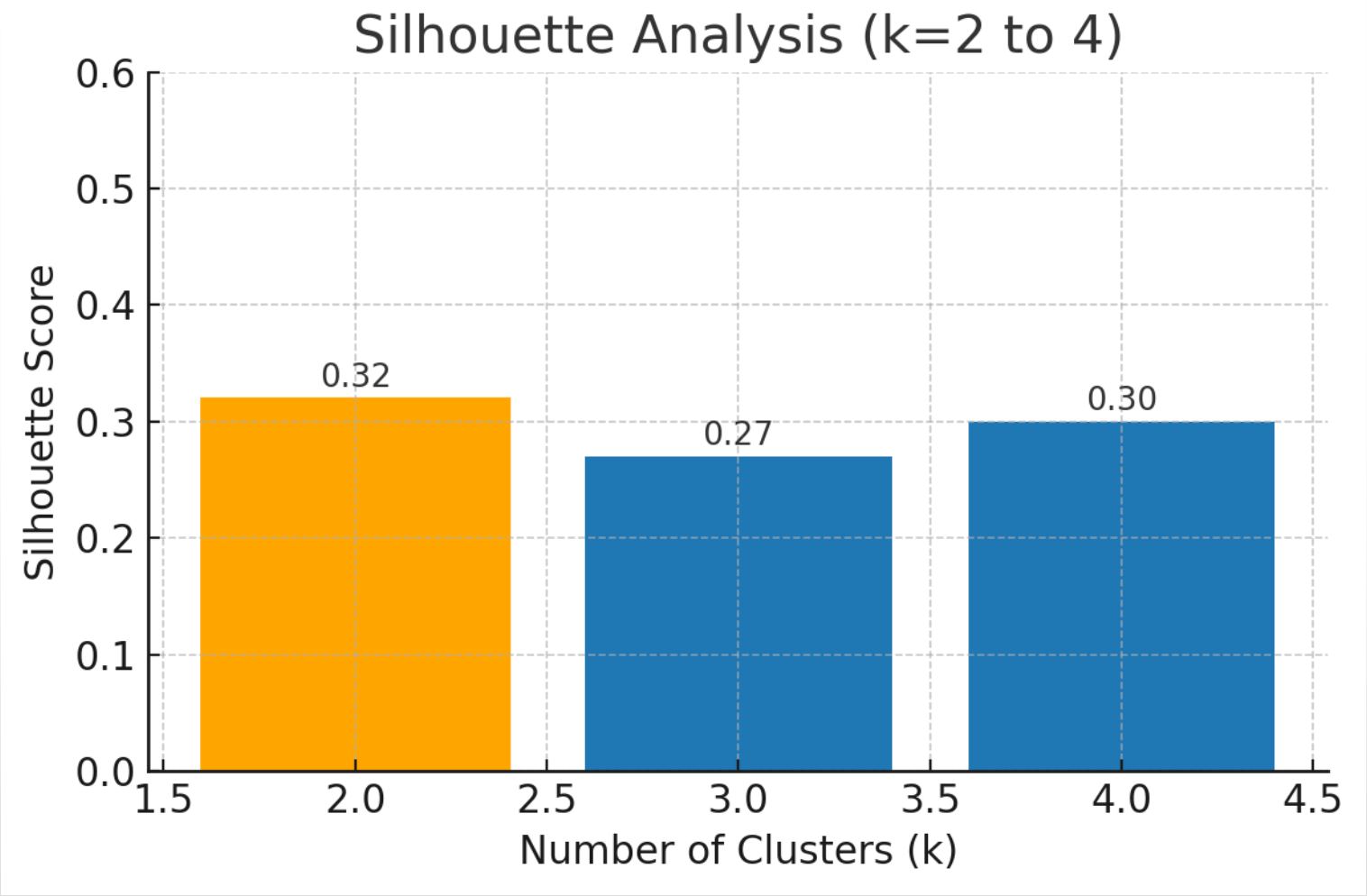
Temporal Clustering

- Algorithm: **KMeans** on PCA-based trajectories.
- Tried on k=2–4 clusters.
- Evaluated using Silhouette Score.



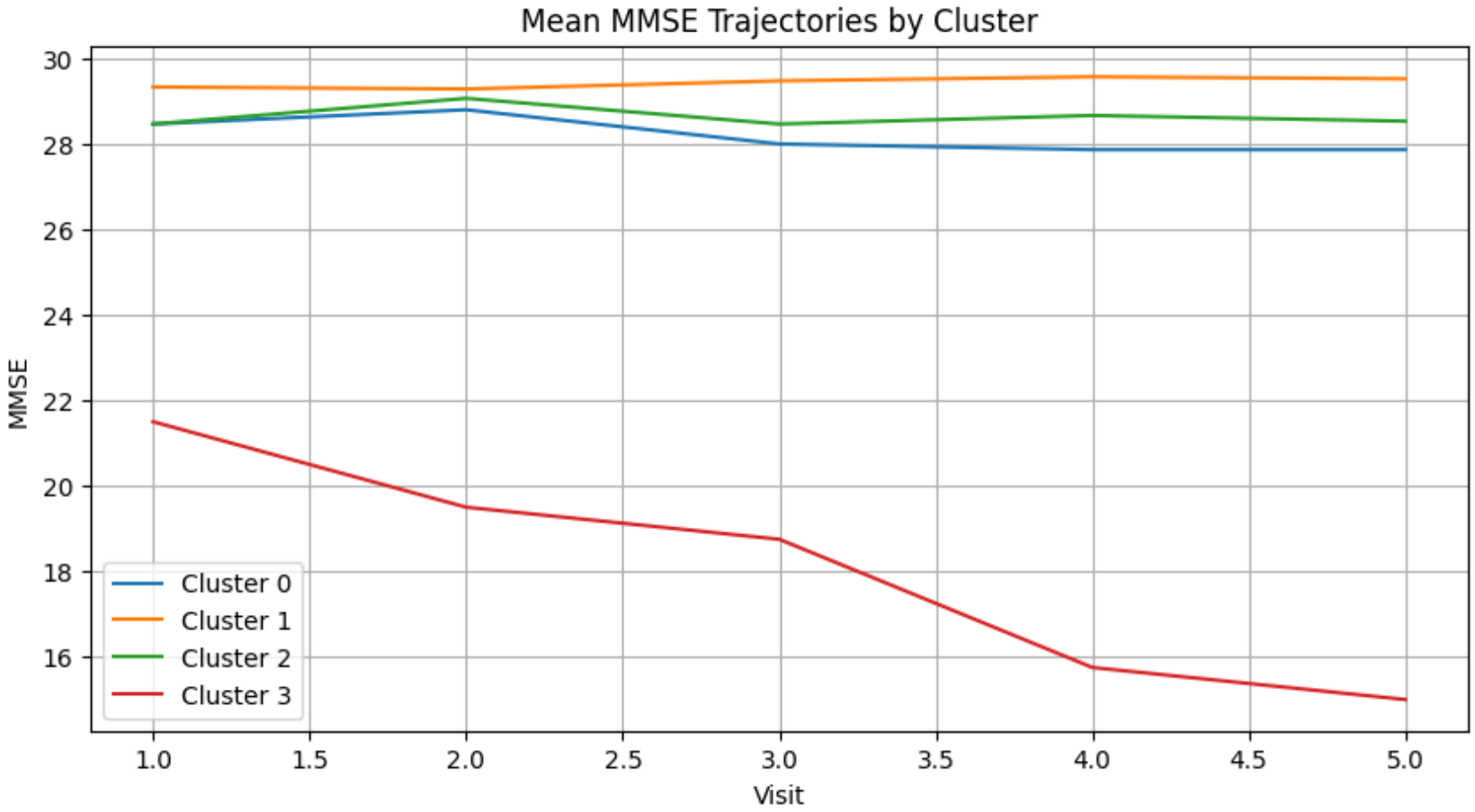
Silhouette Analysis

- **Obtained value: 0.32**
- **Range:** –1 → +1
- **~0.0** → overlapping clusters (poor separation)
- **0.25–0.50** → *reasonable* structure (moderate separation)
- **>0.50** → strong cluster separation



CLUSTERED TRAJECTORIES

- Stable vs. steep decline → clear **slow vs fast clusters**
- Strong **cognitive progression marker**

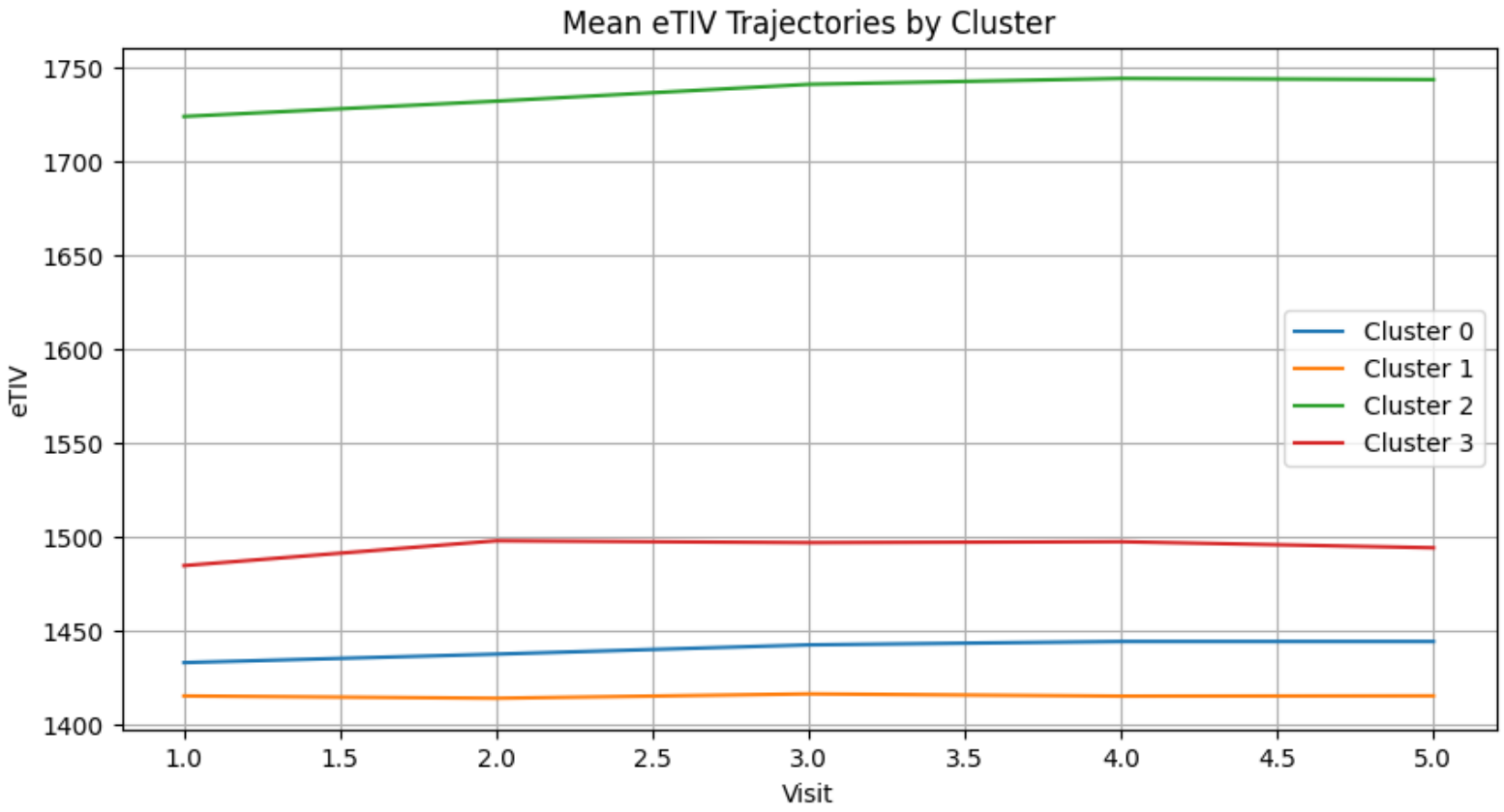


CLUSTERED TRAJECTORIES

- Separates **normal vs dementia** stages
- Less sensitive to **gradual progression**

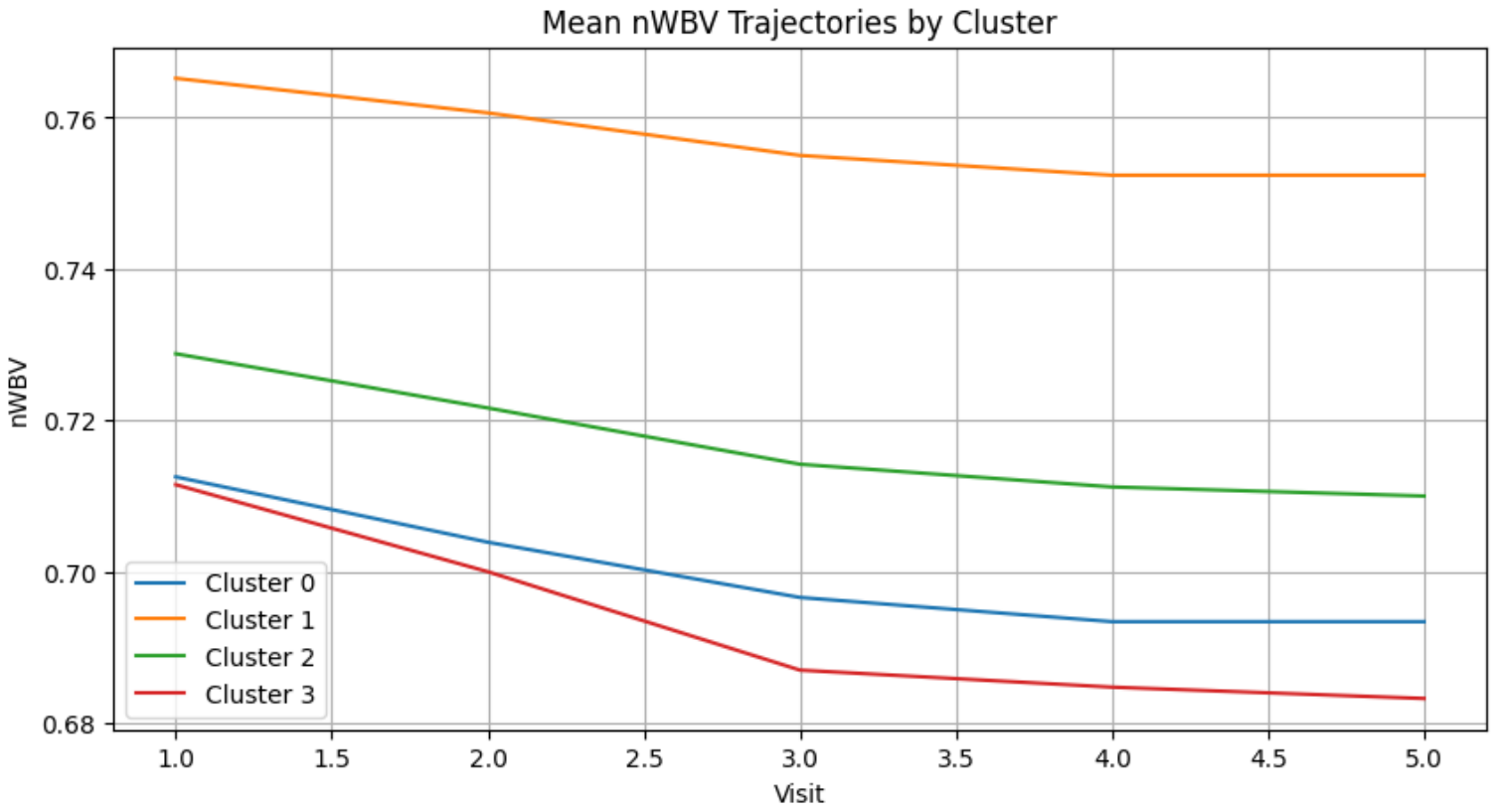
CLUSTERED TRAJECTORIES

- **Stable baseline** across visits
- Useful for **normalization, not progression**



CLUSTERED TRAJECTORIES

- Shows **consistent decline** over visits
- Strong **structural progression marker**



RECOMMENDED MARKERS

MMSE & nWBV → effective for temporal clustering (progression captured).

CDR → reliable for diagnosis/labels, less sensitive for clustering.

eTIV → stable baseline, useful for normalization, not progression.

CLASSIFICATION SETUP

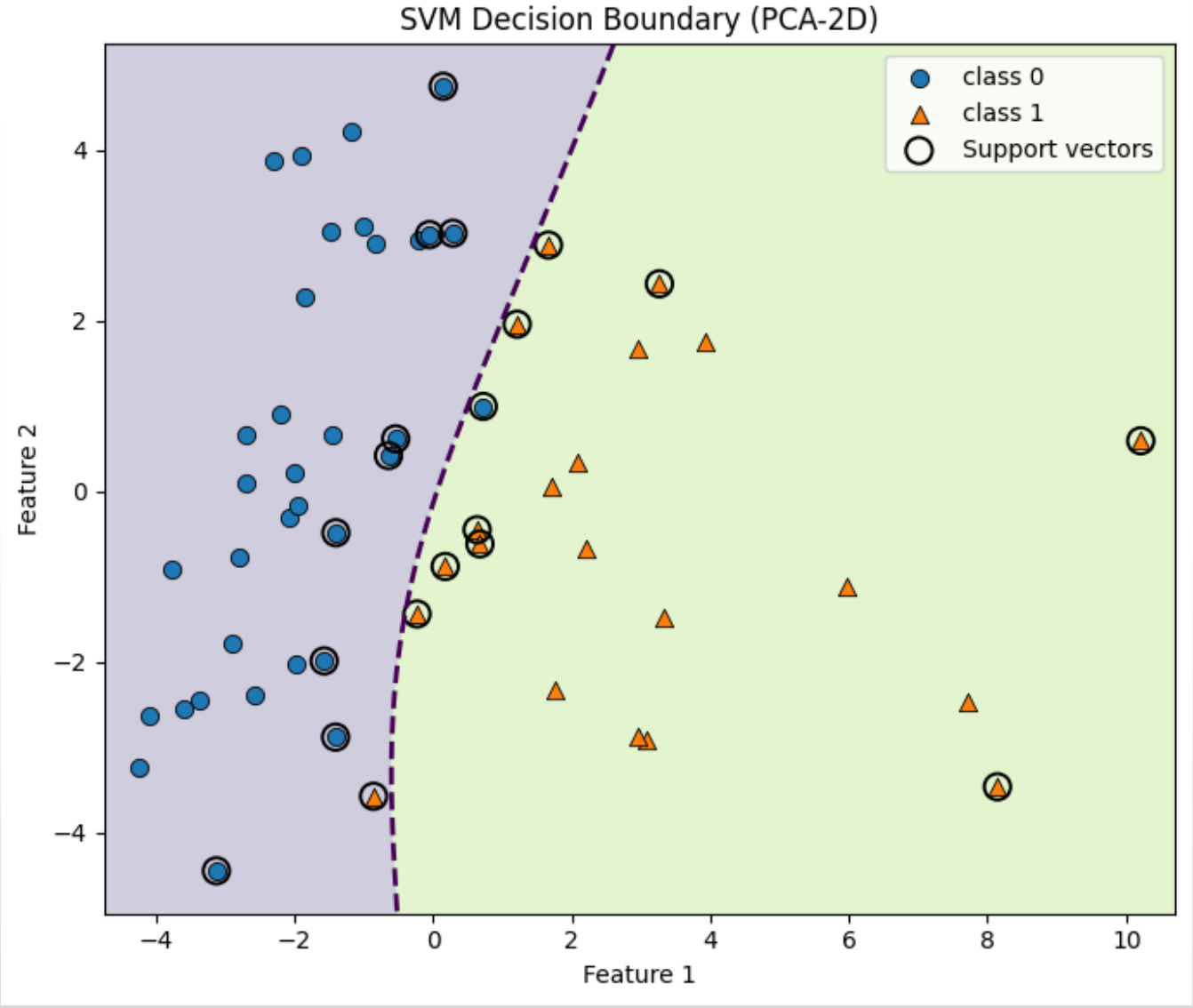
Goal: detect Alzheimer’s vs. non-Alzheimer’s.

Label: Alzheimer’s if CDR ≥0.5.

Model: Support Vector Machine (SVM).

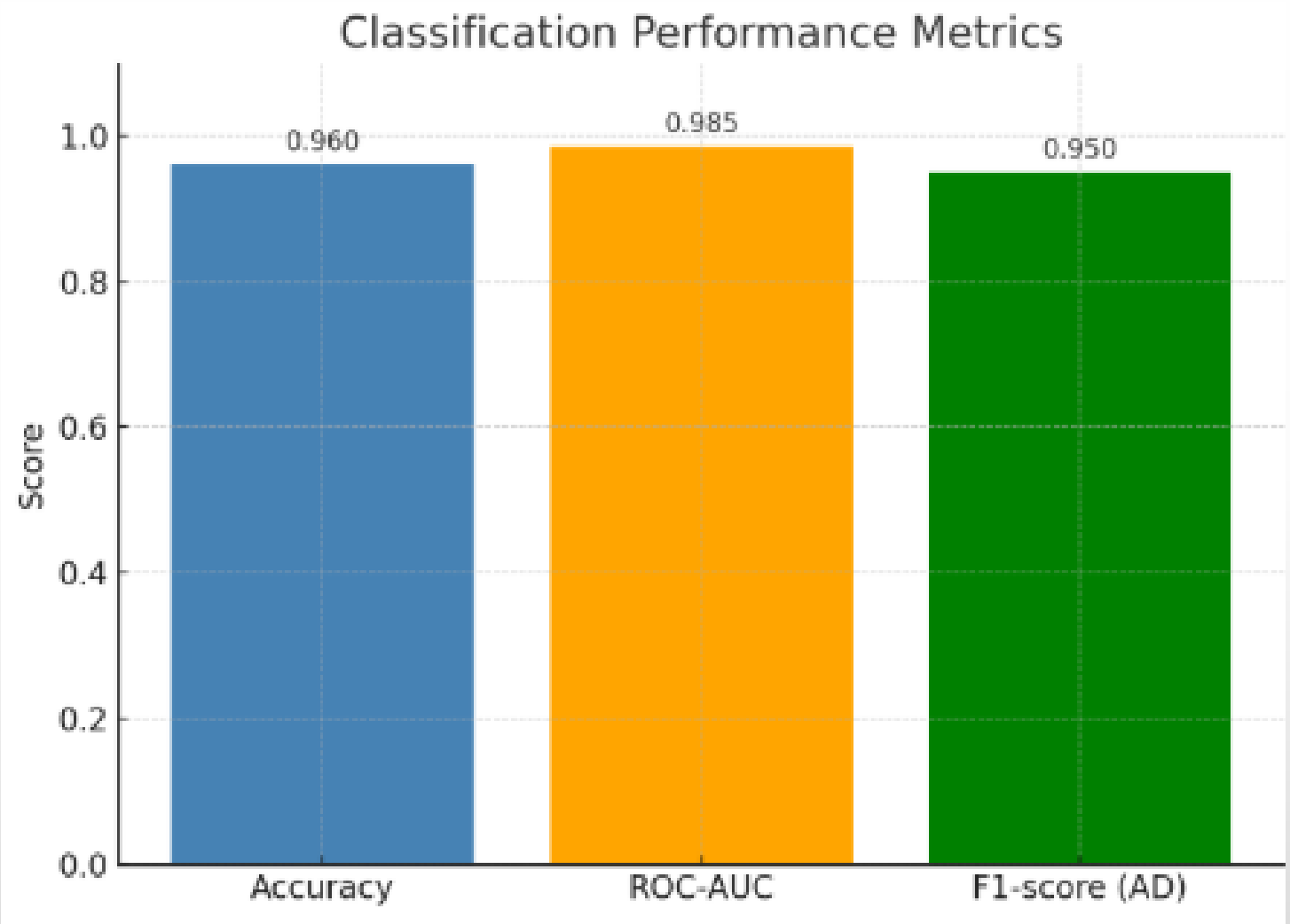
Features: PCA components from biomarker sequences.

SUPPORT VECTOR MACHINE (SVM)



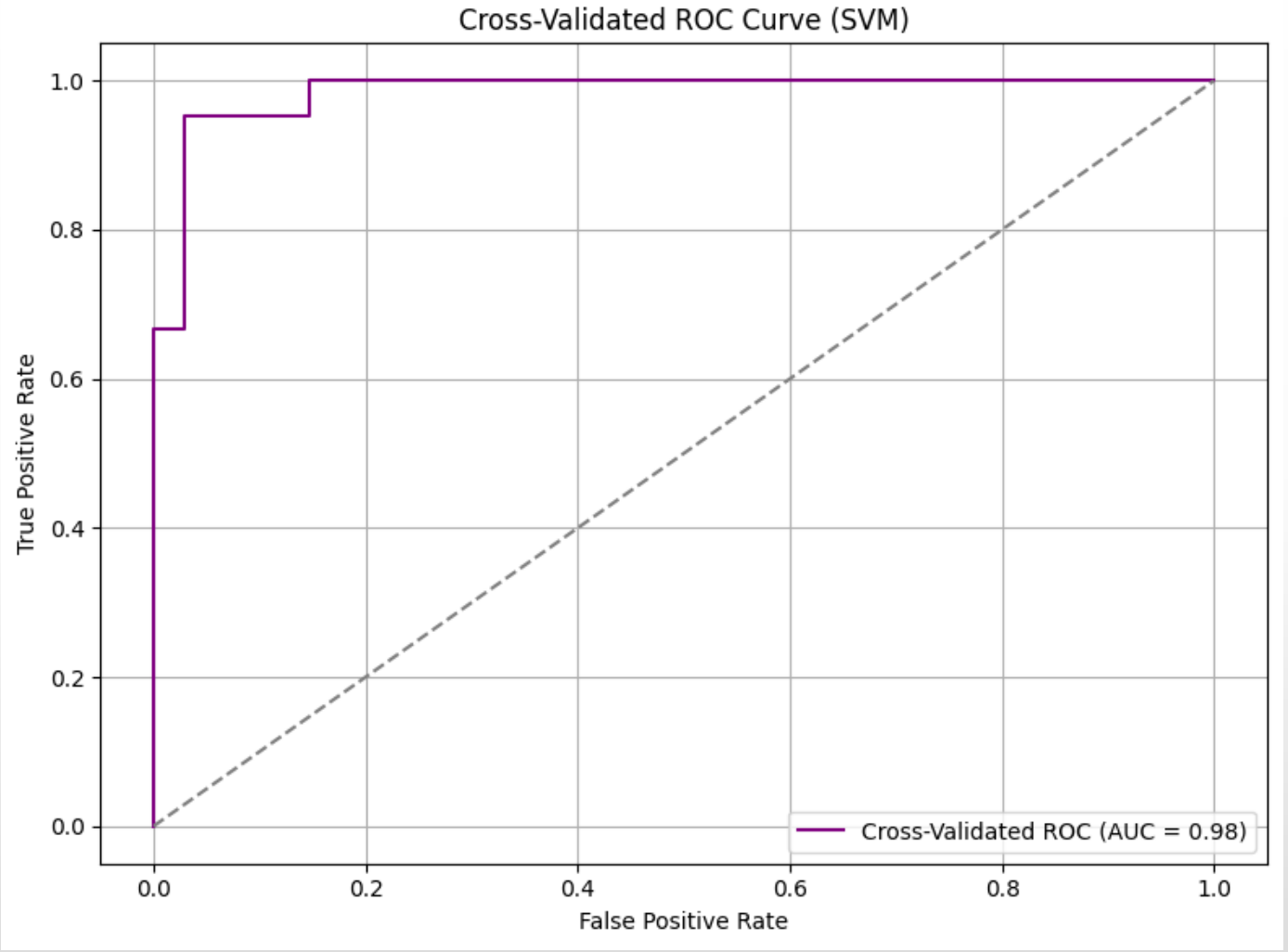
Evaluation Metrics

- Accuracy: **96%**
- ROC-AUC: **0.985**
- F1-score (AD): **0.95**
- Strong predictive performance.



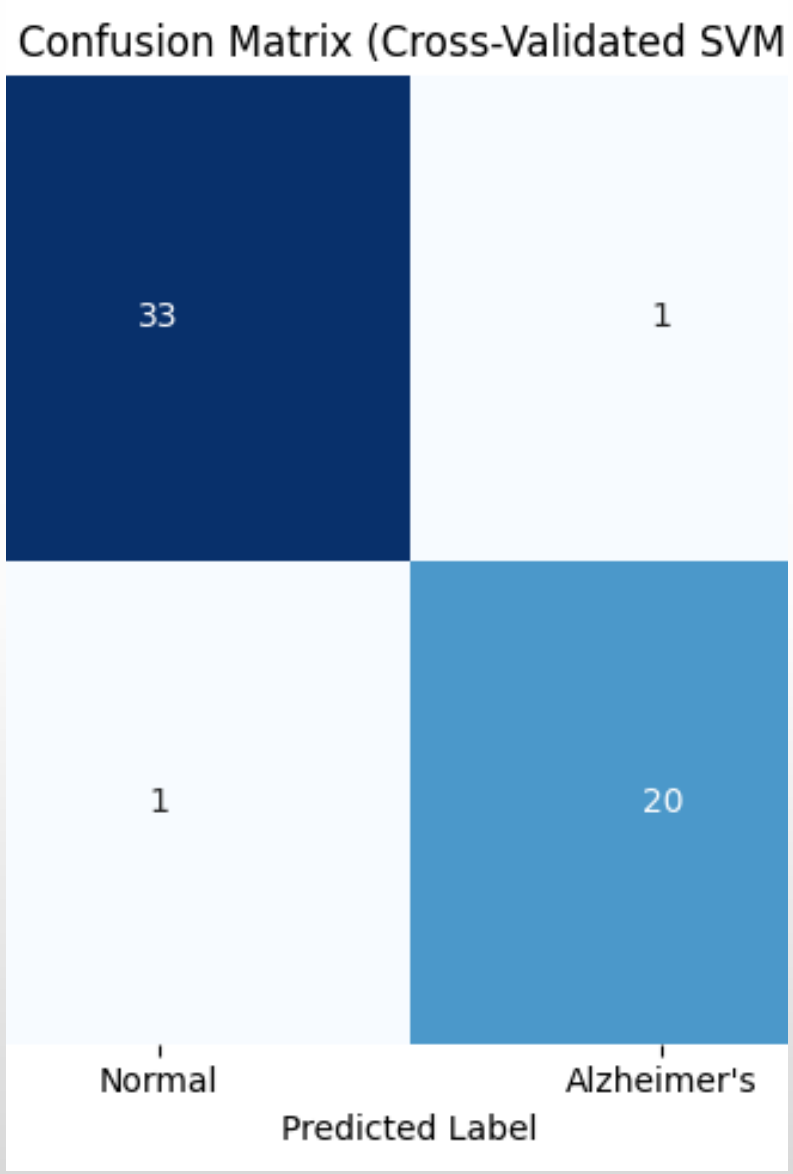
Cross Validation on ROC Curve

- **AUC = 0.98** → excellent classification performance.
- Curve lies close to the **top-left corner**, showing strong separation



Cross-validation

- 5-fold validation for robustness.
- Cross-validated AUC: **0.984**.
- Confirms generalization of model.



INTERPRETABILITY

Two clusters = interpretable subgroups: fast vs. slow progressors.

Supports clinical decision-making.

ML outputs aligned with medical knowledge.

TECHNOLOGY STACK

Python 3.x, Jupyter Notebook

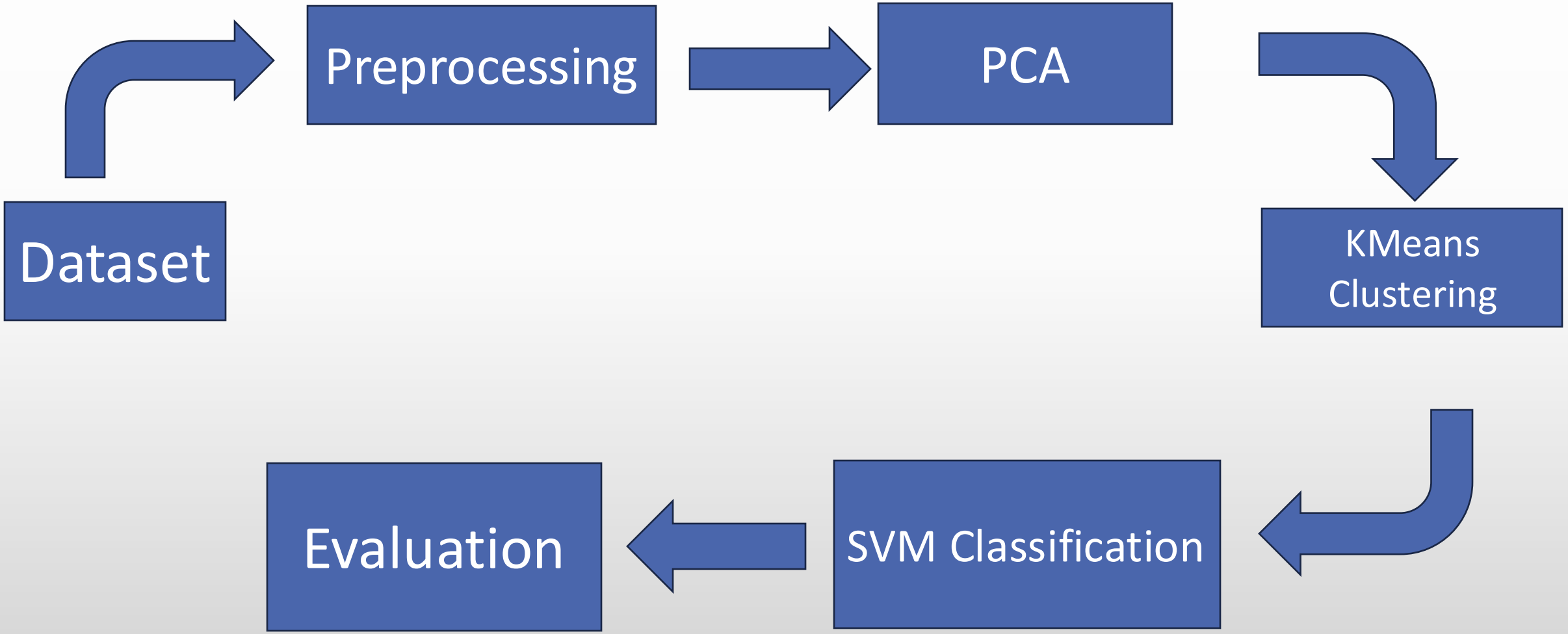
scikit-learn (PCA, KMeans, SVM)

NumPy, Pandas

Matplotlib, Seaborn

GitHub for reproducibility

Pipeline Flow



Why This Work Stands Out

Most studies → **cross-sectional** (single visit, one biomarker)

My work → **longitudinal + multi-biomarker** analysis

Combines **clustering + classification (SVM)**

Validated with **Silhouette, ROC, Confusion Matrix, CV**

LIMITATIONS

- Restricted biomarker set
- Interpolation assumptions
- Class imbalance
- Model simplicity

FUTURE WORK

Extend biomarkers → PET, advanced MRI features.

Apply sequence models → HMM, LSTM, DTW clustering.

External dataset validation.

Explainability → SHAP, LIME.

SUMMERY

MMSE & nWBV best markers for progression.

Clustering distinguishes slow vs. fast decline.

SVM achieves high accuracy (96%, AUC=0.985).

Approach demonstrates temporal clustering is effective for Alzheimer’s biomarker analysis.

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GitHub Repository (Code & Documentation):

Temporal Clustering in Dynamic Medical Datasets – GitHub

THANK YOU

Any Questions!