

# Ph.D. Dissertation Defense

## Novel Deep Learning methods for Early Detection of Neurological Disorders

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# Acknowledgments



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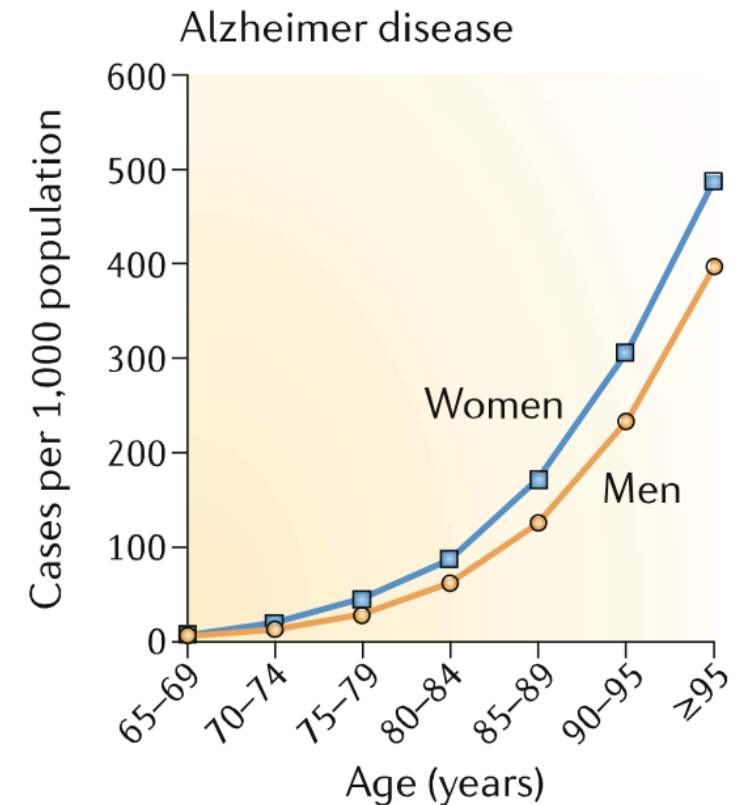
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1. Motivation
2. Phase I: Brain Age prediction
3. Phase II: Medical image compression
4. Phase III: PET Imaging Super-Resolution

1. Motivation
2. Phase I: Brain Age prediction
3. Phase II: Medical image compression
4. Phase III: PET Imaging Super-Resolution

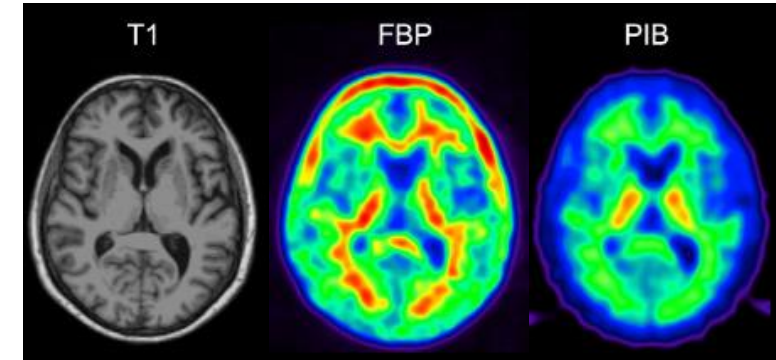
- Age is the biggest known risk factor for most neurodegenerative disorders  
Alzheimer's disease, Parkinson's disease, and others
- Causes irreversible structural damage
- Early detection  
Effective interventions  
Preventing brain damage



Hou, Yujun, et al. "Ageing as a risk factor for neurodegenerative disease." *Nature Reviews Neurology* (2019)

Alzheimer's disease (AD) is a multi-factorial disorder

1. Brain structure damage can be quantified using T1w-MRI



2. AD pathogenesis starts with amyloid-beta ( $A\beta$ ) deposition  
Brain damage  $\leftrightarrow$   $A\beta$  plaques  
PET tracers (FBP, PiB, others) help quantify early AD onset

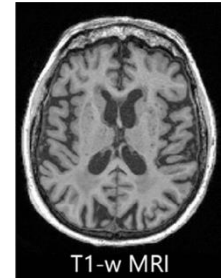
pet = positron emission tomography; FBP = florbetapir; PiB = pittsburgh compound B

# Motivation

## Deep learning based Brain Age prediction

Models lack precision, show age-related systematic bias

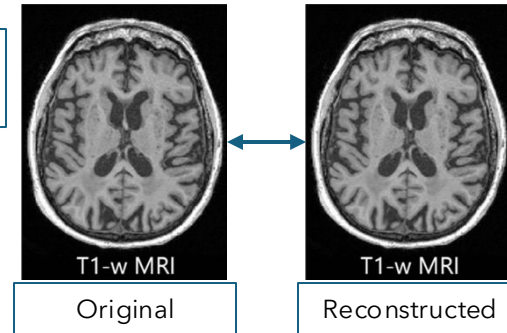
**Phase I**



## Medical Image compression

Codebook collapse, reconstruction fidelity, practical utility

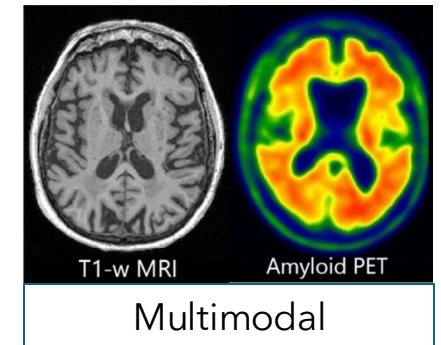
**Phase II**



## PET Imaging Super-Resolution

Quantifying  $A\beta$  deposition

**Phase III**



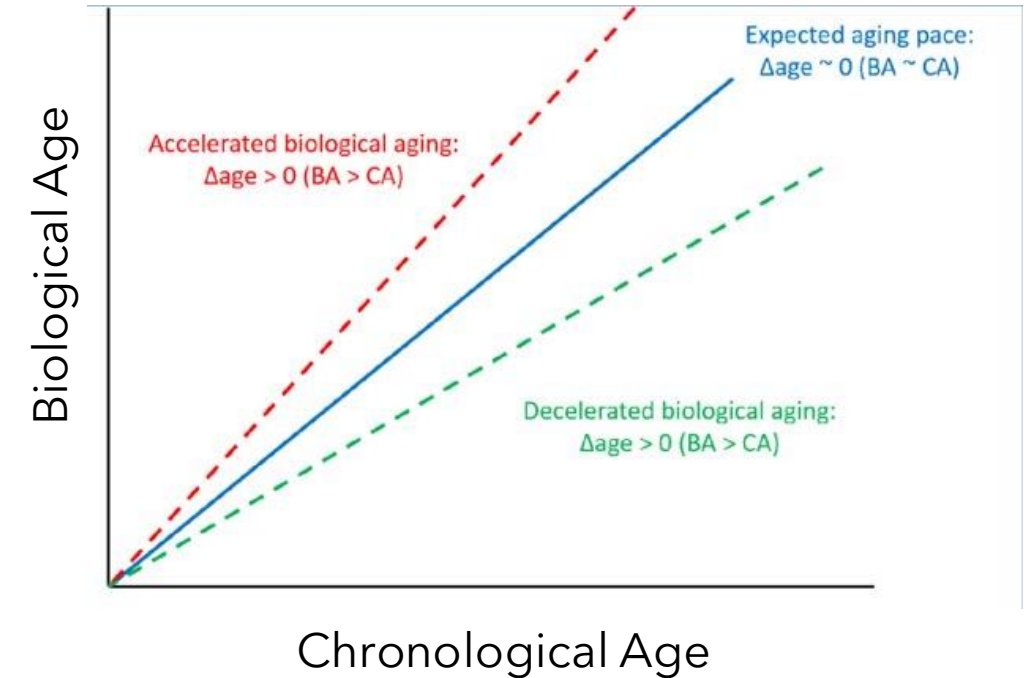
(more details in later slides)



# Phase I: Brain Age prediction

Aging in humans is complex

- Biological aging  $\neq$  chronological aging  
brain can age faster or slower
- Variations in individuals  
due to genetic, environmental, neurological  
predispositions



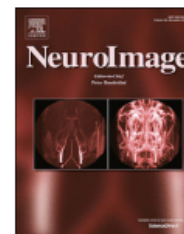


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Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

NeuroImage

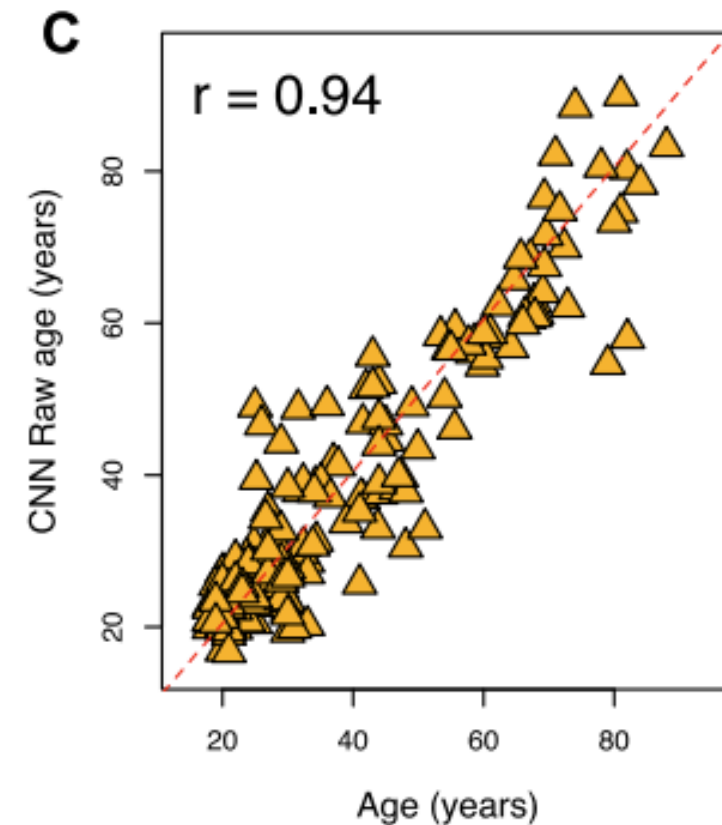
journal homepage: [www.elsevier.com/locate/neuroimage](https://www.elsevier.com/locate/neuroimage)



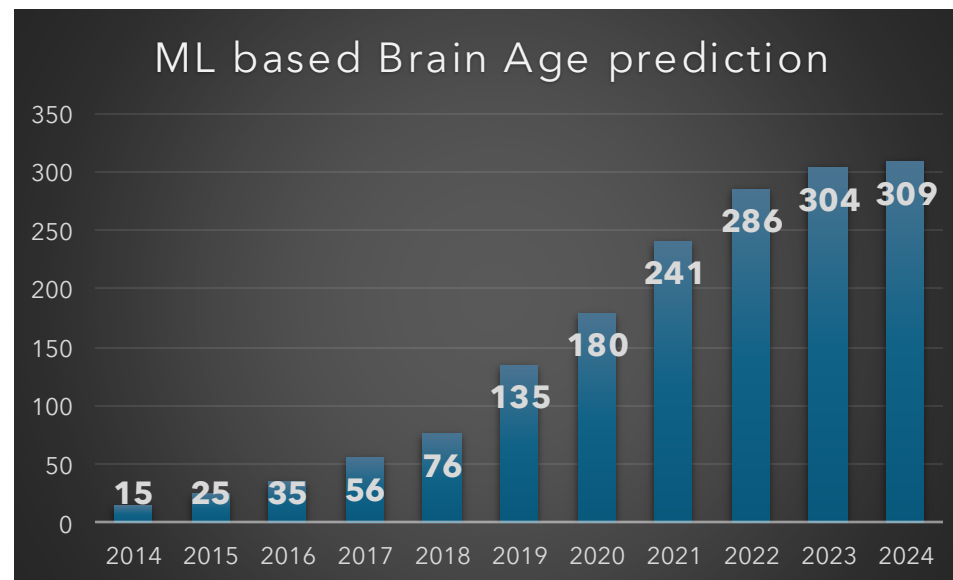
## Predicting brain age with deep learning from raw imaging data results in a reliable and heritable biomarker

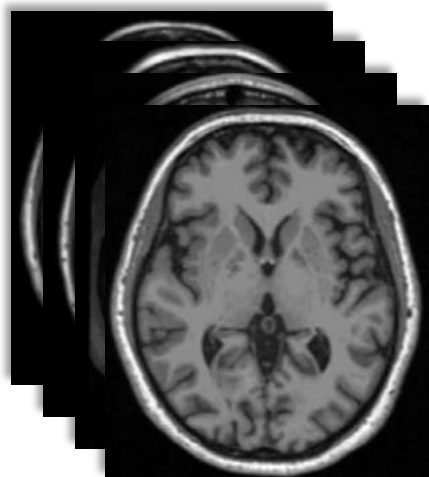


James H. Cole<sup>a</sup>, Rudra P.K. Poudel<sup>b</sup>, Dimosthenis Tsagkrasoulis<sup>c</sup>, Matthan W.A. Caan<sup>d</sup>,  
Claire Steves<sup>e</sup>, Tim D. Spector<sup>e</sup>, Giovanni Montana<sup>b,c,\*</sup>



Number  
of articles





3D MRI scans  
(Healthy subjects)



Chronological  
Age



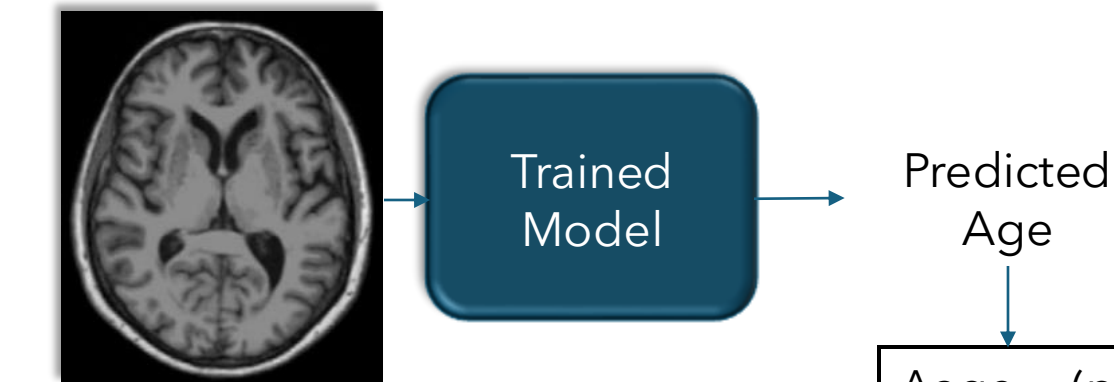
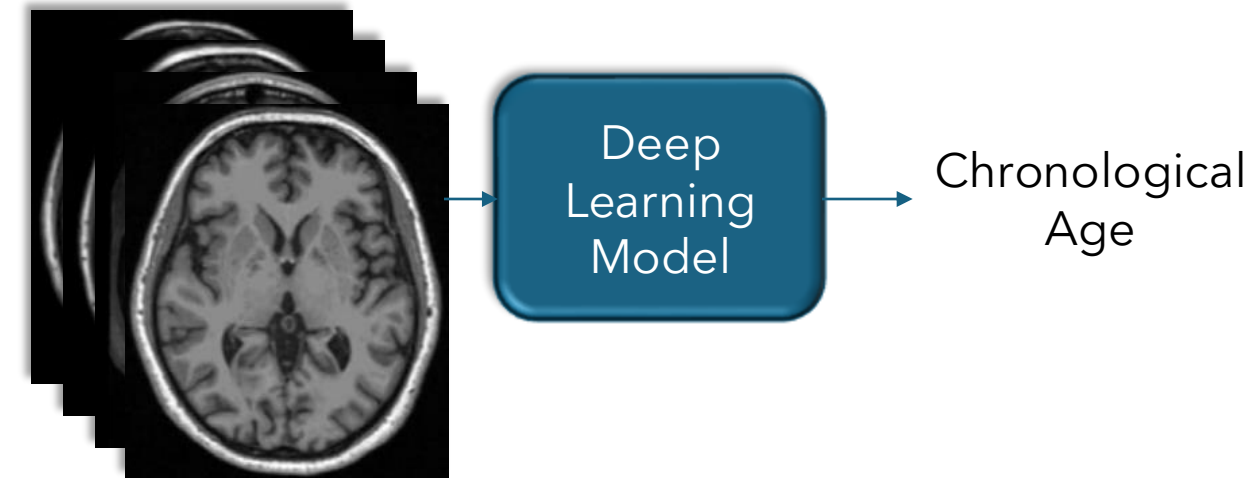
3D MRI scan  
(Healthy/AD subject)



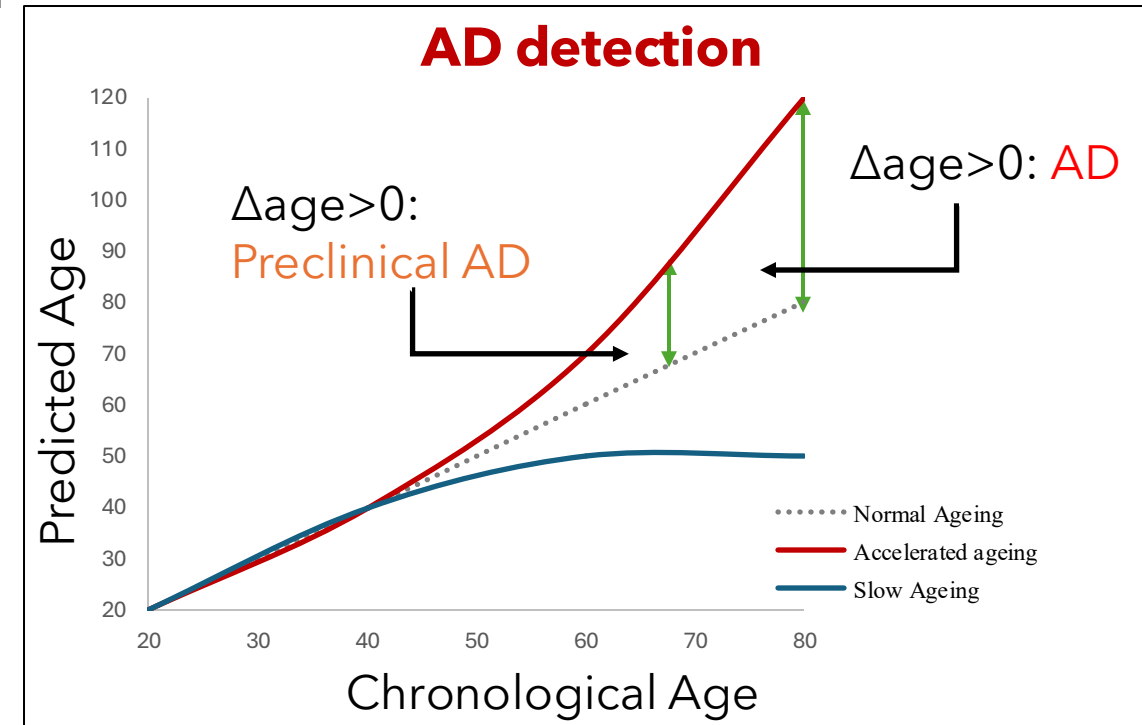
Predicted  
Age

$$\Delta \text{age} = (\text{predicted} - \text{chronological}) \text{ age}$$

## Regression



$$\Delta \text{age} = (\text{predicted} - \text{chronological}) \text{ age}$$



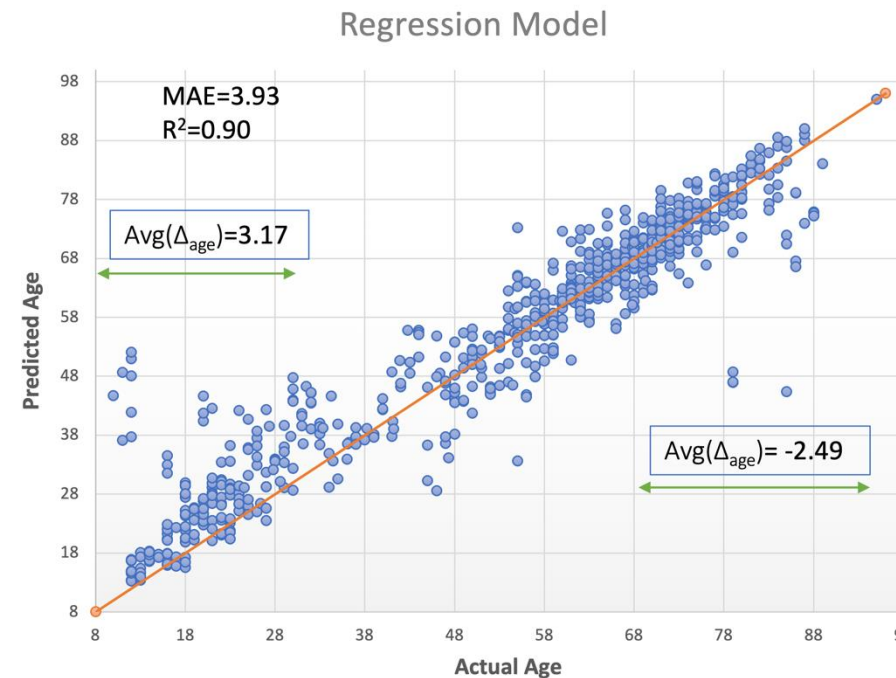
- Lifespan cohort (7,377) 3D MRIs Healthy
  - IXI, ABIDE, ICBM, NACC and OASIS (public)
  - age [8-95]
- Discovery cohort (1,584) 3D MRIs Healthy/MCI/AD
  - ADNI database
  - age [55-98]
- Train: Val: Test = 80: 10: 10  
(stratified on age groups 8-12, 12-16, ...)

| Dataset | Count | Age Range (yrs) | Mean $\pm$ STD  |
|---------|-------|-----------------|-----------------|
| NACC    | 4,132 | 18 - 95         | 67.5 $\pm$ 10.8 |
| OASIS   | 1,432 | 8 - 94          | 27.9 $\pm$ 20.7 |
| ICBM    | 1,101 | 18 - 80         | 37.6 $\pm$ 15.4 |
| IXI     | 536   | 20 - 86         | 48.8 $\pm$ 16.5 |
| ABIDE   | 176   | 18 - 56         | 26.1 $\pm$ 7.0  |
| ADNI    | 1,584 | 55 - 98         | 73.3 $\pm$ 7.3  |

# Existing Gaps

## Models are not accurate!

- Age-related systematic bias  
Young subjects are over-estimated; under-estimation in Old  
Inherent to regression<sup>a</sup>
- Well observed<sup>b</sup>, not due to  
Model selection, imbalance, heterogeneity<sup>b</sup>  
Current approaches → post-hoc correction
- Most Alzheimer's patients are age > 50



ResNet-18 (regression) model trained  
on 6617 HC, tested on 760 HC

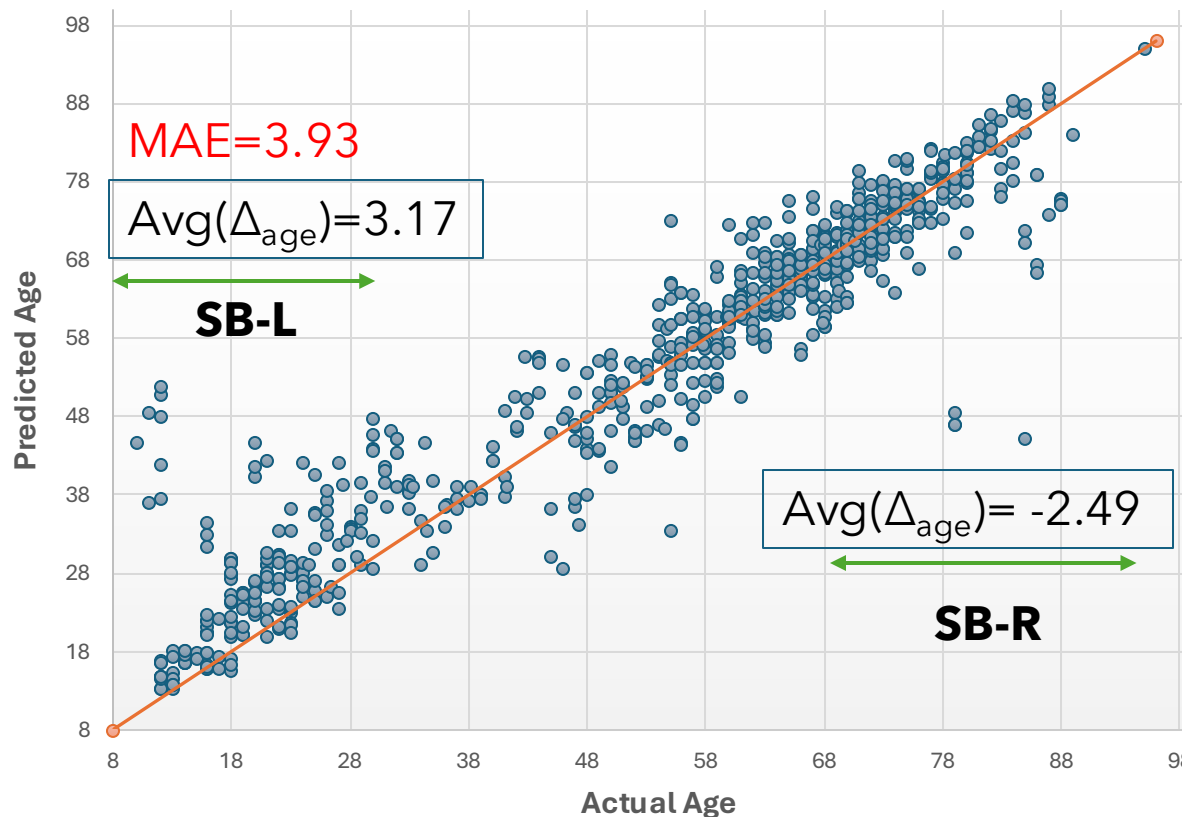
Hypothesis: Age prediction as regression causes regression-to-mean (RTM)  
→ Leading to systematic bias

<sup>a</sup>Gardner, M. J., and J. A. Heady. "Some effects of within-person variability in epidemiological studies." Journal of Chronic Diseases (1973)

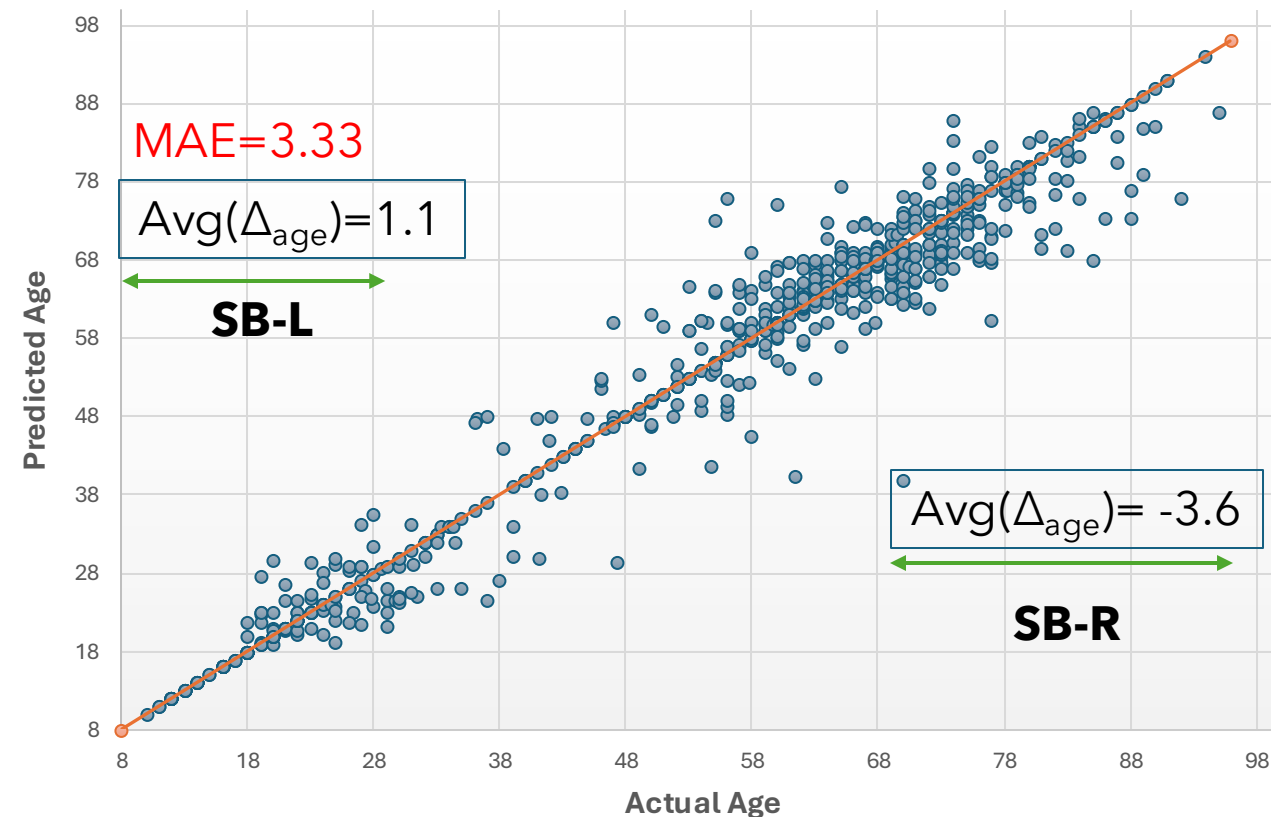
<sup>b</sup>Liang, Hualou et al. "Investigating systematic bias in brain age estimation with application to post-traumatic stress disorders". Human Brain Mapping (2019)

# Regression as Classification

Regression (MSE Loss)

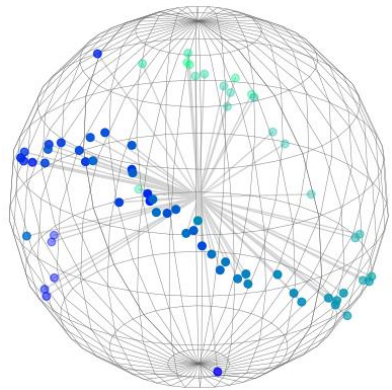


Classification (Cross Entropy Loss)



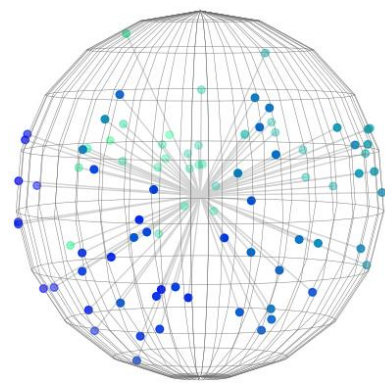
## Measuring Systematic Bias:

One standard deviation from mean: systematic bias-left ( $\mu - \sigma$ ) and right, ( $\mu + \sigma$ ) [SB-L, SB-R]



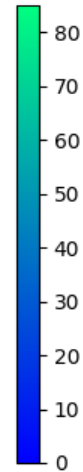
MSE

Ordinality score: 0.99



Cross Entropy

Ordinality score: 0.31



- $C = \{1, 2, \dots, (c-1)\}$  where  $c$  is #classes
- $X = \{x_1, x_2, \dots, x_n\}$  - penultimate layer features
- $F_c = \{f_1, f_2, \dots, f_c\}$  - feature centroids

Manhattan distances between  $f_1$  and other feature centroids

- $D = \{d_{12}, d_{13}, \dots, d_{1c}\}$

Ordinality score = Pearson ( $D, C$ )

Classification beats Regression

Due to ability to learn high entropy discriminative feature representation<sup>a</sup>

But lacks **ordinality**!

Cross entropy treats each class independent from each other

Ex: *Patient of Age 52 misclassified as 51 vs. 14 hampers clinical decision making*

<sup>a</sup>Zhang, Shihao, et al. "Improving Deep Regression with Ordinal Entropy." *ICLR* (2023)



Phase I

# How to preserve Ordinality in Classification?

- While reducing RTM bias
- And improving age prediction

# ORDER loss

**Aim:** Ordinal information from target space (age) into learned feature space ( $\mathbf{z}$ )

To guarantee:

$$z_c > z_{c+1} > z_{c+2} > \dots > z_C$$
$$z_c > z_{c-1} > z_{c-2} > \dots > z_1$$

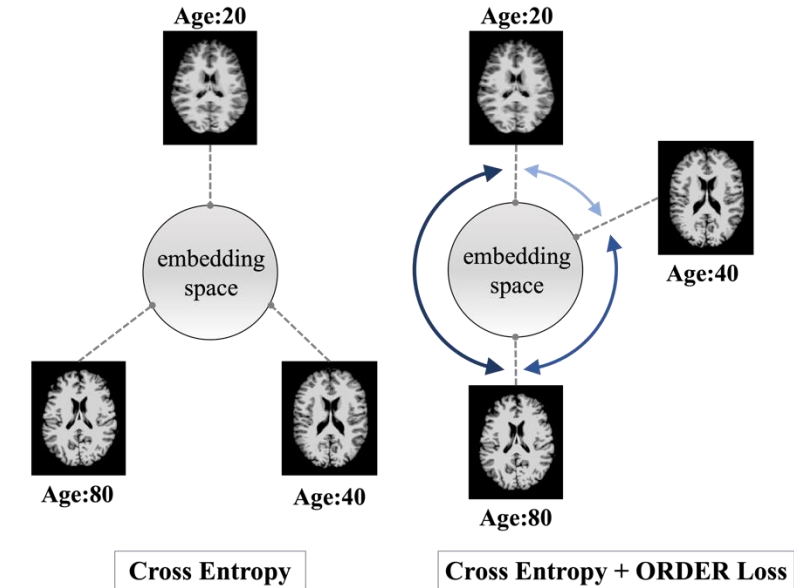
Cross Entropy:

$$L_{CE} = -\frac{1}{N} \sum_{i=1}^N \log \frac{e^{z_i}}{\sum_{j=1}^C e^{z_j}}$$

Regularization:

$$z'_i = W_{y_i}^T x_i + \varphi(x_i)$$

$$\varphi(x_i) = \frac{1}{N-1} \sum_{j=1, j \neq i}^N |i-j| |\bar{x}_i - \bar{x}_j|_{manh}$$



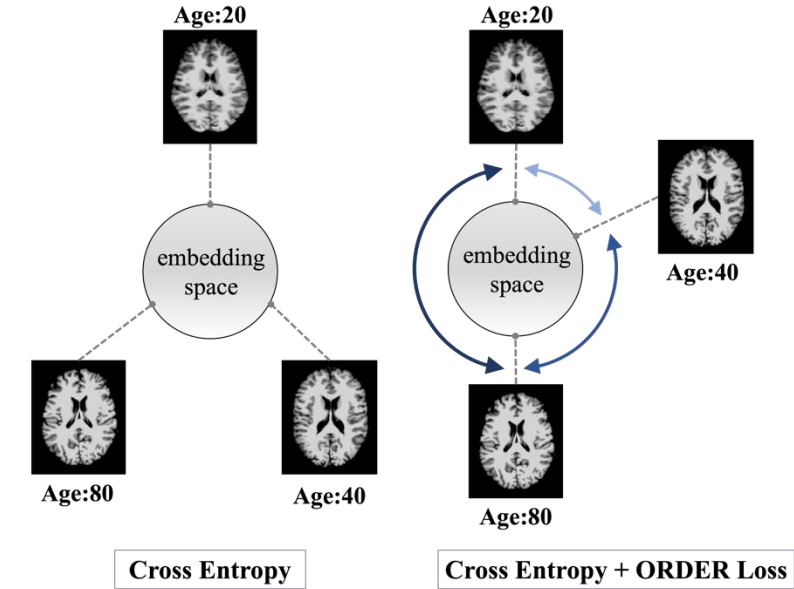
ORDER - ORdinal Distance Encoded Regularization

Manhattan distance (L1 norm) is consistently preferable than the Euclidean distance (L2 norm) for high-dimensional data

Aggarwal, Charu C., et al. "On the surprising behavior of distance metrics in high dimensional space." Database theory-ICDT (2001)

# ORDER loss

$$\begin{aligned}
 L_T &= -\frac{1}{N} \sum_{i=1}^N \log \frac{e^{W_{y_i}^T x_i + \varphi(x_i)}}{\sum_{j=1}^C e^{W_{y_j}^T x_i}} \\
 &= -\frac{1}{N} \left[ \sum_{i=1}^N \log \frac{e^{W_{y_i}^T x_i}}{\sum_{j=1}^C e^{W_{y_j}^T x_i}} + \sum_{i=1}^N \varphi(x_i) \right] \\
 &= -\frac{1}{N} \sum_{i=1}^N \log \frac{e^{W_{y_i}^T x_i}}{\sum_{j=1}^C e^{W_{y_j}^T x_i}} \\
 &\quad - \frac{1}{N(N-1)} \sum_{j=1, i \neq j}^N |i - j| \|\bar{x}_i - \bar{x}_j\|_{manh} \\
 &= L_{CE} + L_{ORDER}
 \end{aligned}$$



Shah, Jay, et al. "Ordinal classification with distance regularization for robust brain age prediction." Proceedings of the IEEE/CVF Winter Conference on Applications of Computer Vision. 2024.

- Baseline loss functions
- 3D ResNet-18
- Stratified oversampling [8-12, 12-16, ...]
- 100 epochs, *AdamW* opt, batch size=4
- $LR=1e-3$ , *weight decay*= $1e-2$

|                | Method (Loss)                     |
|----------------|-----------------------------------|
| Regression     | MSE                               |
|                | MSE + Euclidean norm <sup>a</sup> |
| Classification | CE                                |
|                | CE + mean-variance <sup>b</sup>   |
| Ours           | CE + ORDER                        |

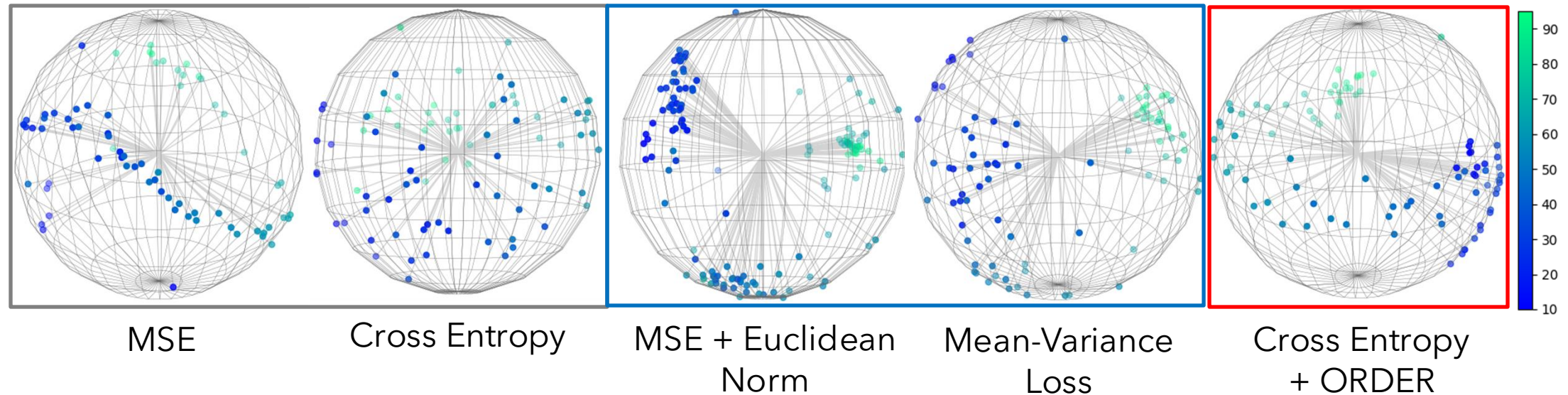
CE=cross entropy  
MSE=mean squared error

<sup>a</sup>Zhang, Shihao, et al. "Improving Deep Regression with Ordinal Entropy." ICLR (2023).

<sup>b</sup>Pan, Hongyu, et al. "Mean-variance loss for deep age estimation from a face." CVPR (2018).

# Results

On Lifespan ([healthy](#)) cohort

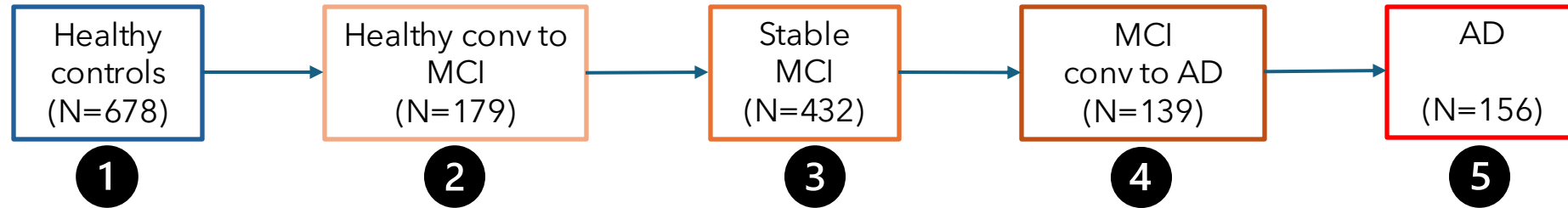


Embedding space analysis (512-dim)

On Lifespan ([healthy](#)) cohort

|                | Method (Loss)        | MAE         | Ordinality  | Systematic Bias |             |
|----------------|----------------------|-------------|-------------|-----------------|-------------|
|                |                      |             |             | SB-L            | SB-R        |
| Regression     | MSE                  | 3.93        | <b>0.99</b> | 3.4             | -4.2        |
|                | MSE + Euclidean norm | 4.57        | 0.95        | 4.8             | -4.1        |
| Classification | CE                   | 3.33        | 0.31        | 1.1             | -3.6        |
|                | CE + mean-variance   | <u>2.65</u> | 0.58        | <u>0.4</u>      | <u>-4.2</u> |
| Ours           | CE + ORDER           | <b>2.56</b> | <u>0.98</u> | <b>0.1</b>      | <b>-2.5</b> |

5 clinical groups with increasing order of severity



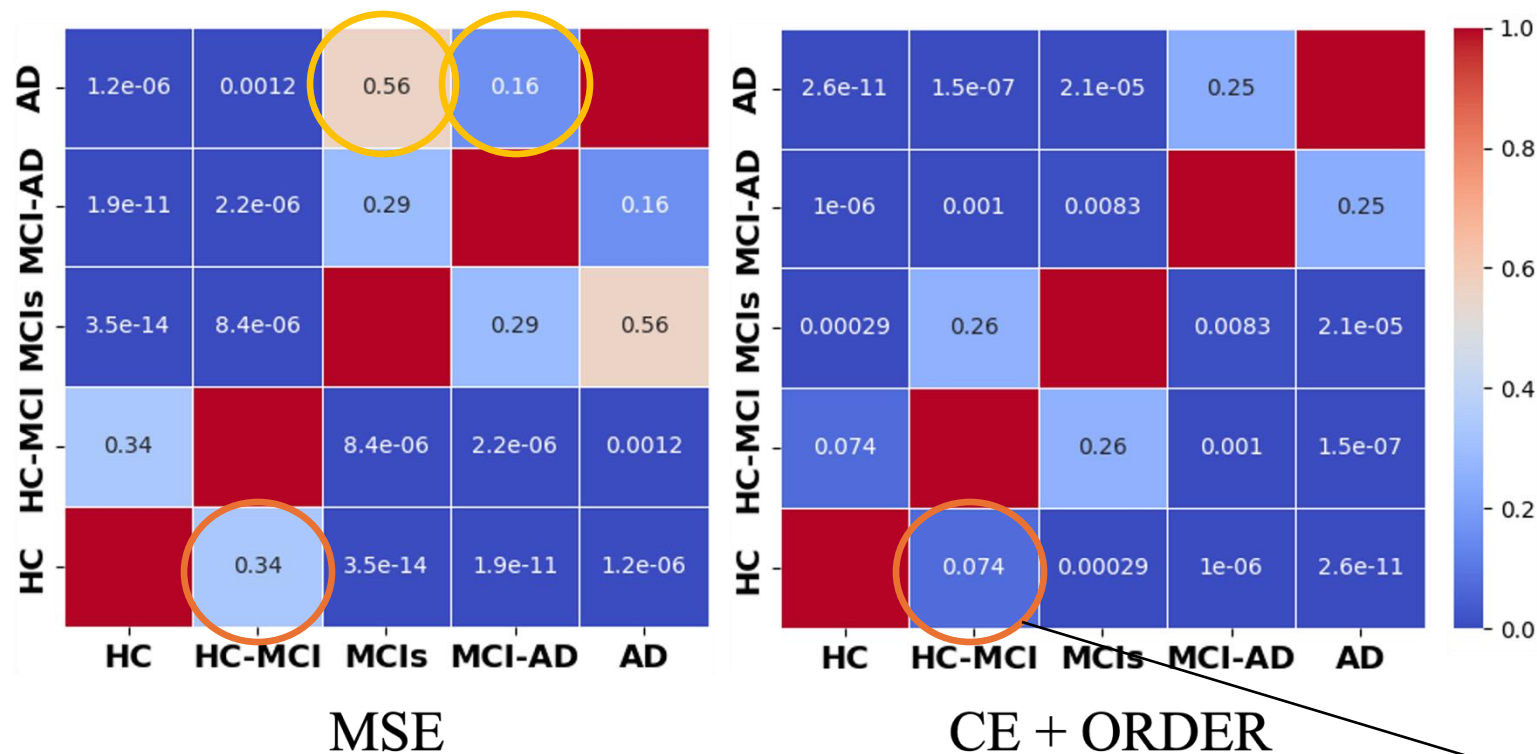
On Discovery (**mixed**) cohort

|      | Method (Loss)        | Healthy<br>(1) | HC conv MCI<br>(2) | MCI-stable<br>(3) | MCI conv AD<br>(4) | AD<br>(5) | Pearson<br>Correlation |
|------|----------------------|----------------|--------------------|-------------------|--------------------|-----------|------------------------|
| Reg  | MSE                  | -1.2           | -0.8               | -0.3              | 0.8                | 1.5       | <b>0.98</b>            |
|      | MSE + Euclidean norm | -2.7           | -1.9               | -1.7              | -0.9               | 0.9       | 0.94                   |
| CLS  | CE                   | -1.9           | -1.5               | -3.4              | -2.3               | -4.1      | -0.75                  |
|      | CE + mean-variance   | -1.6           | -0.3               | -0.5              | 0.8                | 2.8       | 0.94                   |
| Ours | CE + ORDER           | -1.5           | -0.7               | -0.3              | 1.2                | 2.0       | <b>0.98</b>            |

Correlation with  
disease severity

# MSE vs. ORDER

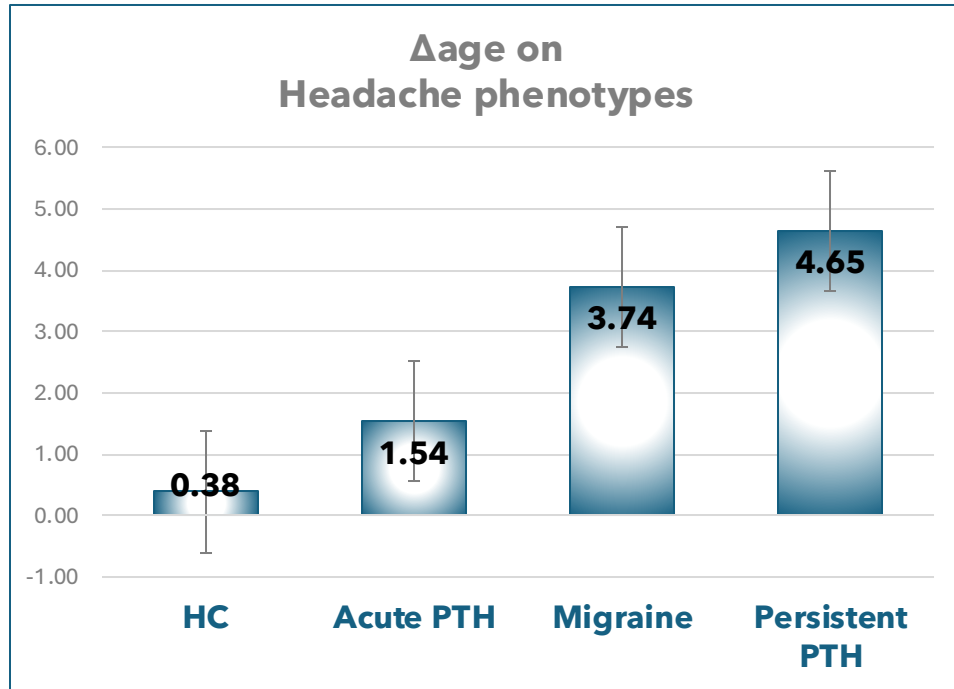
Statistical significances between clinical groups as  
*p*-values on predicted BrainAGE



More accurate for early detection

- MSE - disruptive trend
- CE + ORDER - consistent trend





HC = Healthy Controls

PTH = Post Traumatic Headache

\*in-house data collected from Mayo Clinic, Arizona

## Findings:

- $\Delta$ age(P-PTH) <  $\Delta$ age(A-PTH)  
suggesting more structural decline related to PTH persistence over time
- Headache frequency associated with structural damage  
 $\Delta$ age(P-PTH) >  $\Delta$ age(Mig) >  $\Delta$ age(A-PTH)
- Early detection potential  
structural decline acutely following TBI at risk for developing persistent PTH

Shah, Jay, et al. "Capturing MRI Signatures of Brain Age as a Potential Biomarker to Predict Persistence of Post-traumatic Headache (S20.006)." *Neurology*. Vol. 102. No. 17\_supplement\_1. Hagerstown, MD: Lippincott Williams & Wilkins, 2024.

1. Cross-entropy learn high-entropy (discriminative) feature representation  
To [reduce RTM bias](#) from regression
2. ORDER loss can preserve ordinality in feature space  
To [improve overall prediction](#) accuracy
3. Model achieved MAE=2.56 on Healthy  
Compared to 3.93 (MSE), 35% improvement↑  
Biomarker [reliability](#)
4. Can detect subtle difference in clinical groups  
Crucial for [early detection](#) (Alzheimer's & Headache)

Neural Image Compression

# Locality Constrained Vector Quantization

- Rapid growth of medical imaging in modern medicine

Petabytes (PB) of MRI data generated annually

Radiology data at Stanford grew by ~450 TB per year<sup>a</sup>

**Requires:** Network bandwidth & Storage

- Efficient compression matters

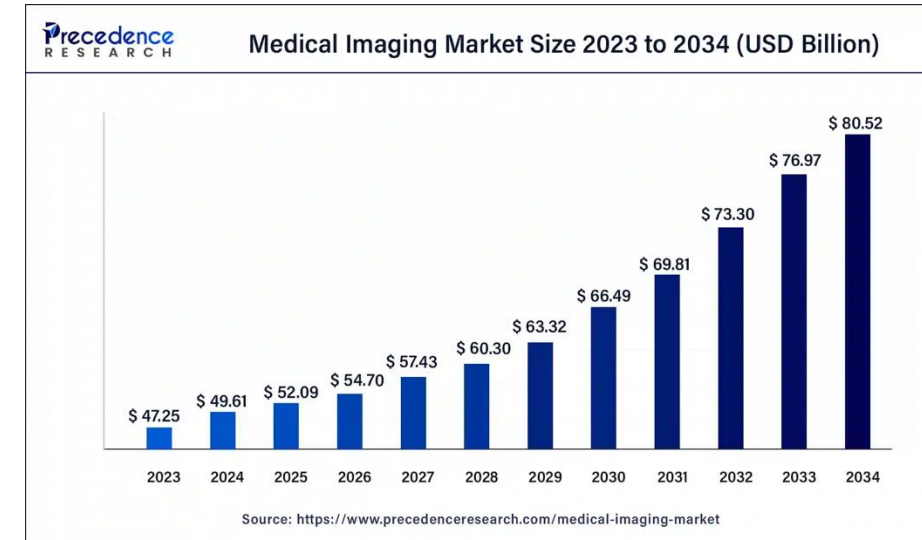
1. Storage burden

FreeSurfer processed image: 16-60 MB

Entire folder: 300-370 MB

2. Impractical for telemedicine<sup>b</sup>

Limited bandwidth (rural or mobile)



<sup>a</sup>Mesterhazy, Joseph et al. "High performance on-demand de-identification of a petabyte-scale medical imaging data lake." arXiv preprint (2020).

<sup>b</sup>Elhadad, Ahmed, et al. "Reduction of NIFTI files storage and compression to facilitate telemedicine services based on quantization hiding of downsampling approach." Scientific Reports (2024)

# Image Compression

## Lossless

- Huffman coding
  - ~3.7:1 on DICOM
  - Cannot exploit spatial correlations<sup>a</sup>
- JPEG-LS
  - 2-3x on MRI<sup>b</sup>
- gzip
  - ~30-40% on NIfTI
  - nontrivial CPU overhead
  - Not ideal for real-time telemedicine

## Lossy

- DCT based JPG
  - Scalar quantization introduces artifacts<sup>c</sup>
  - Loss of anatomical info (edges)
- JPEG2000
  - Limited real utility
  - Info loss at higher rates<sup>d</sup>
- 3D wavelet + DWT-VQ
  - Volumetrics wavelets improve distortion
  - Lacks end-to-end optimization
  - Heavy compute cost<sup>e</sup>

<sup>a</sup>Rahmat, Romi Fadillah et al. "Analysis of DICOM Image Compression Alternative Using Huffman Coding." Journal of healthcare engineering 17 Jun. 2019

<sup>b</sup>[https://dicom.nema.org/medical/dicom/current/output/html/part05/sect\\_8.2.3.html](https://dicom.nema.org/medical/dicom/current/output/html/part05/sect_8.2.3.html)

<sup>c</sup>Luo, Ying et al. "Removing the blocking artifacts of block-based DCT compressed images." IEEE transactions on Image Processing (2003)

<sup>d</sup>Dennison, Don et al.. "Informatics challenges—lossy compression in medical imaging." Journal of Digital Imaging (2014)

<sup>e</sup>Bruylants, Tim et al. "Wavelet based volumetric medical image compression." Signal processing: Image communication (2015)

- Auto-Encoders (AE)

Latent maps via MSE

Blurry reconstructions and no entropy coding control

- Variational AE (VAE)

KL regularization for smoothness

Suffers from blurriness

- Vector-Quantized VAE

Discrete codebooks reduce blur

- VQVAE consists:

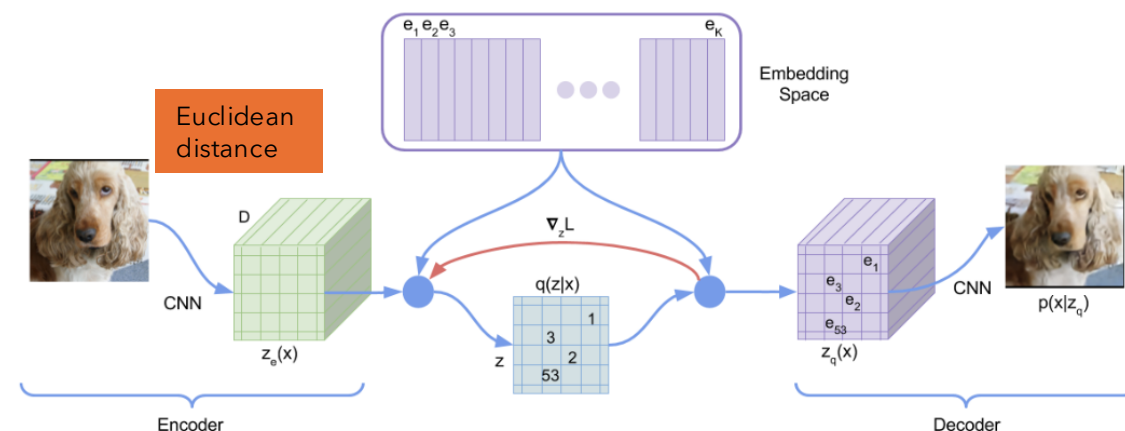
1. Analysis transform:  $y = g_a(x)$
2. Quantization:  $\hat{y} = Q(y)$
3. Entropy coding
4. Synthesis transform:  $\hat{x} = g_s(\hat{y})$

- Traditional methods focus on:

- entropy coding (3),
- ignoring [quantization step](#) (2)  
→ Euclidean Nearest Neighbor

# Revisiting Quantization

- Encoder  $\rightarrow$  continuous latent vector  $e_z$ , quantized to nearest codebook entry  $e^k$  via Euclidean
- Commitment loss term  $\| \text{sg}[z_e] - e^{k*} \|$  encourages encoder outputs close to their assigned embeddings
- Codebook update: minimizing the average Euclidean distance to the batch of assigned encoder outputs, effectively K-means-style centroid updates



Van Den Oord, Aaron, and Oriol Vinyals. "Neural discrete representation learning." *Advances in NeurIPS* (2017).

Observation: Reliance on plain Euclidean distance treats all latent dimensions equally and ignores their covariance<sup>a</sup>

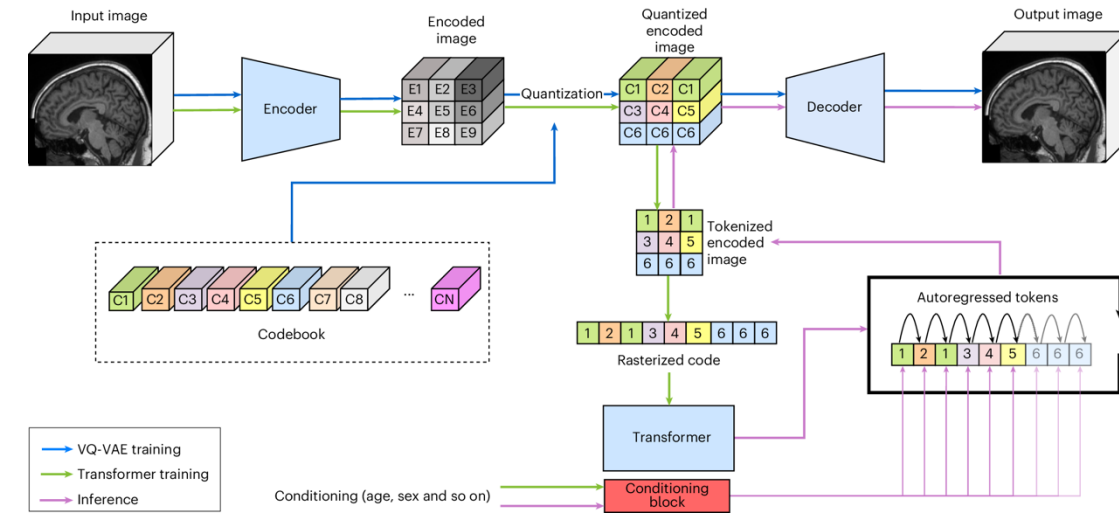
<sup>a</sup>Mimmack, Gillian M., Simon J. Mason, and Jacqueline S. Galpin. "Choice of distance matrices in cluster analysis: Defining regions." *Journal of climate* (2001)

# Brain Imaging Gen (existing work)

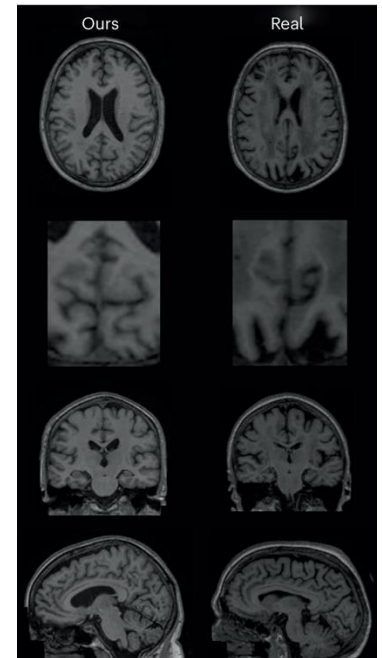
- Generates morphology preserving synthetic MRIs
  - Stage-1: VQVAE to compress
  - Stage-2: Autoregressive transformer for conditional generation (age, sex, etc.)

## Novelties:

- Freq domain sharpness (Anatomy):  
 $MSE(X, \hat{X}) + MSE(FFT(X), FFT(\hat{X}))$
- Perceptual loss (Stability):  
2D AlexNet-based LPIPS
- PatchGAN adversarial term (Realism)  
Discriminator (LSGAN)



| Data | FID    | MS-SSIM         |
|------|--------|-----------------|
| UKBB | 0.0026 | $0.67 \pm 0.05$ |
| ADNI | 0.0075 | $0.69 \pm 0.07$ |



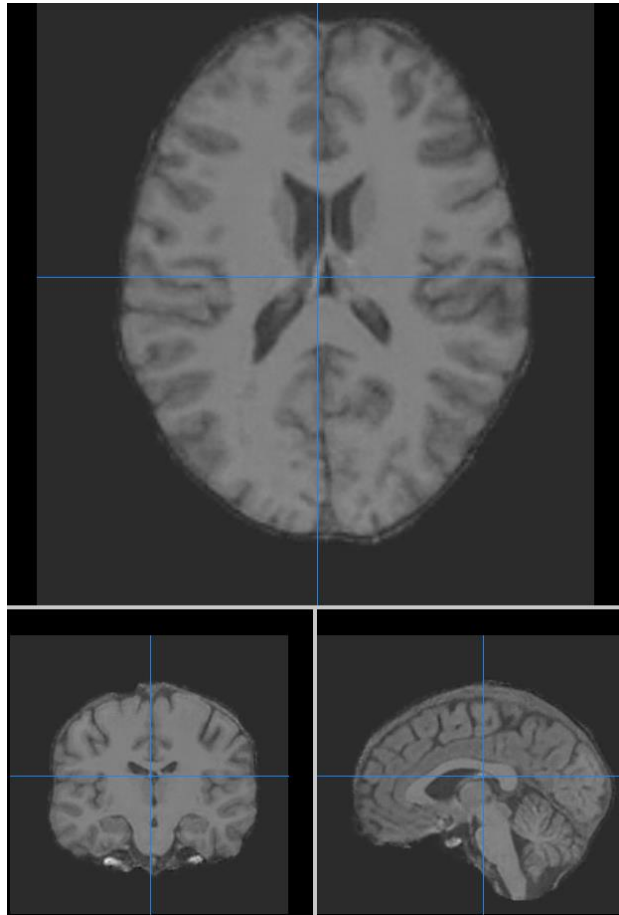
We use this VQVAE as baseline

Tudosiu, Petru-Daniel, et al. "Realistic morphology-preserving generative modelling of the brain." *Nature Machine Intelligence* (2024)

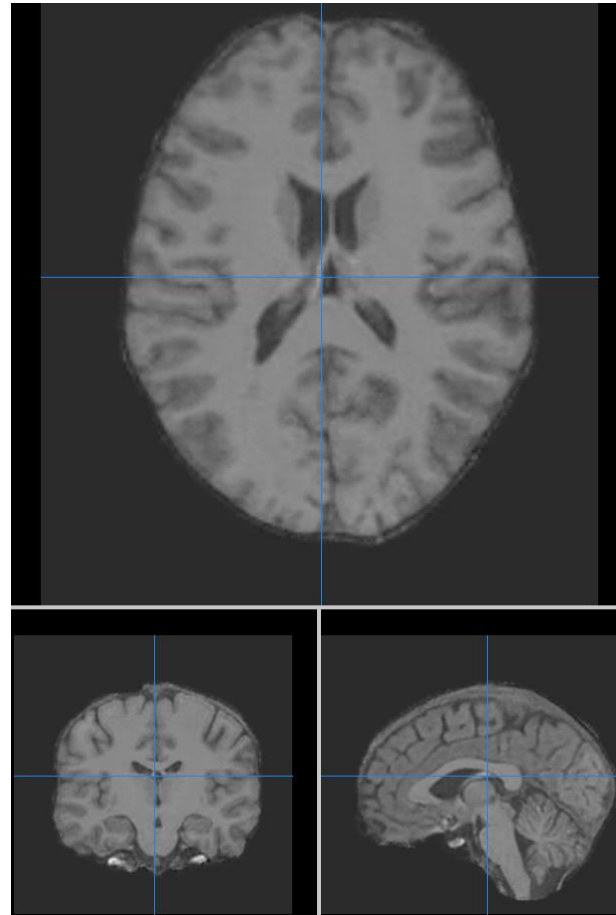


- Lifespan cohort (7,932) 3D MRIs Healthy
  - IXI, ABIDE, ICBM, NACC and OASIS (public)
  - age [18-93]
- Discovery cohort (9,913) 3D MRIs Healthy/MCI/AD
  - ADNI database
  - age [49-98]

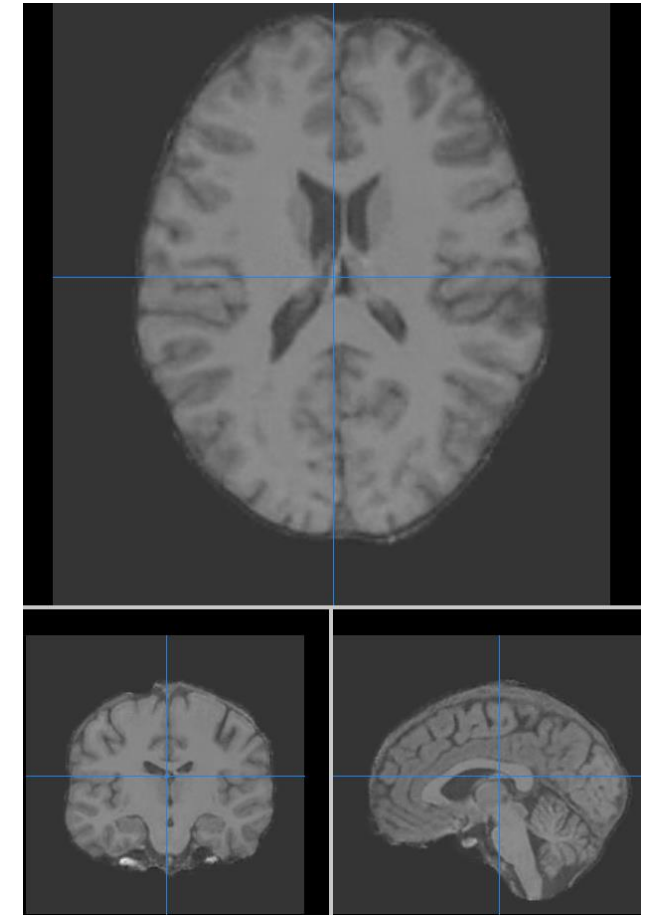
| Dataset | Count | Age Range (yrs) | Mean $\pm$ STD (yrs) |
|---------|-------|-----------------|----------------------|
| NACC    | 4,649 | 18 - 93         | 67.8 $\pm$ 11.1      |
| OASIS   | 1,839 | 18 - 93         | 55.4 $\pm$ 25.1      |
| ICBM    | 814   | 19 - 80         | 41.6 $\pm$ 15.2      |
| IXI     | 529   | 20 - 86         | 48.5 $\pm$ 16.5      |
| ABIDE   | 101   | 18 - 56         | 25.9 $\pm$ 7.6       |
| ADNI    | 9,913 | 49 - 98         | 75.2 $\pm$ 7.5       |



K=1

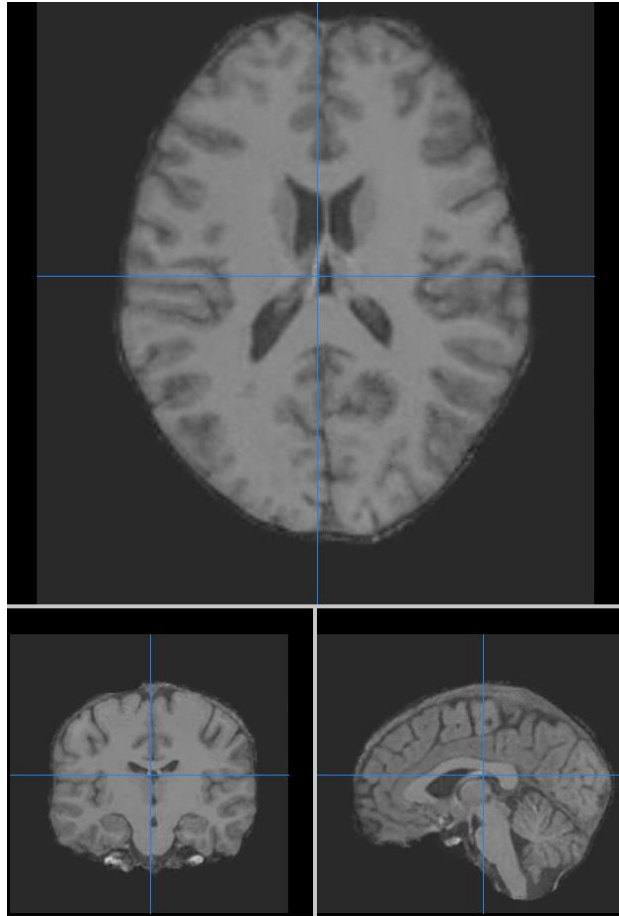


K=2

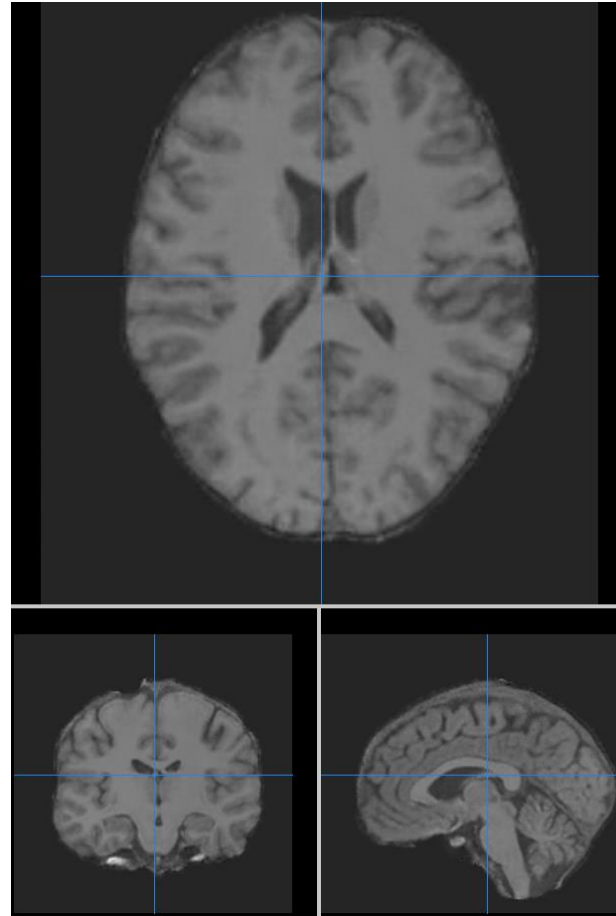


K=3

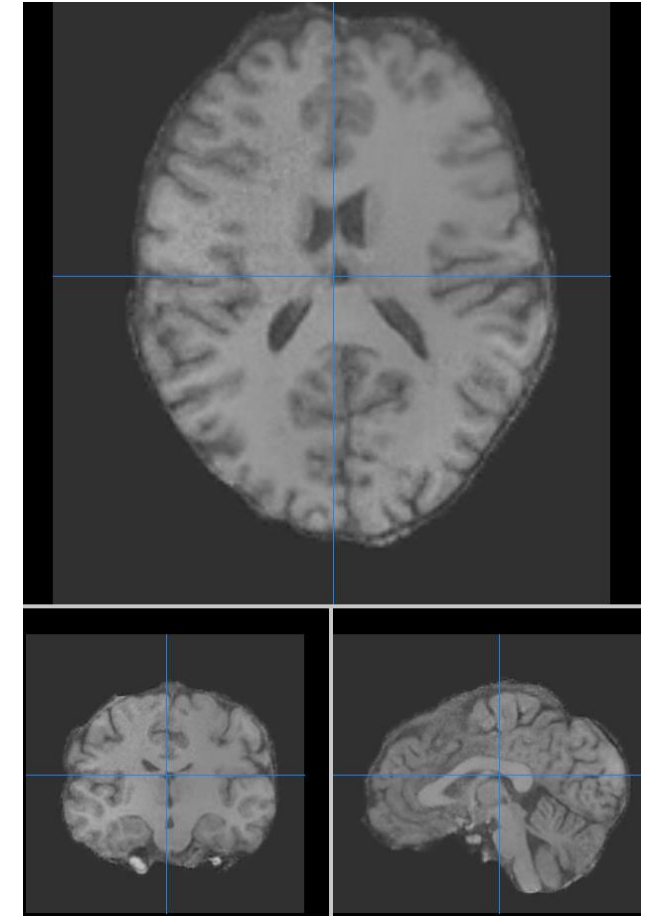
$K \rightarrow$  kth nearest codebook element using Euclidean distance



K=4

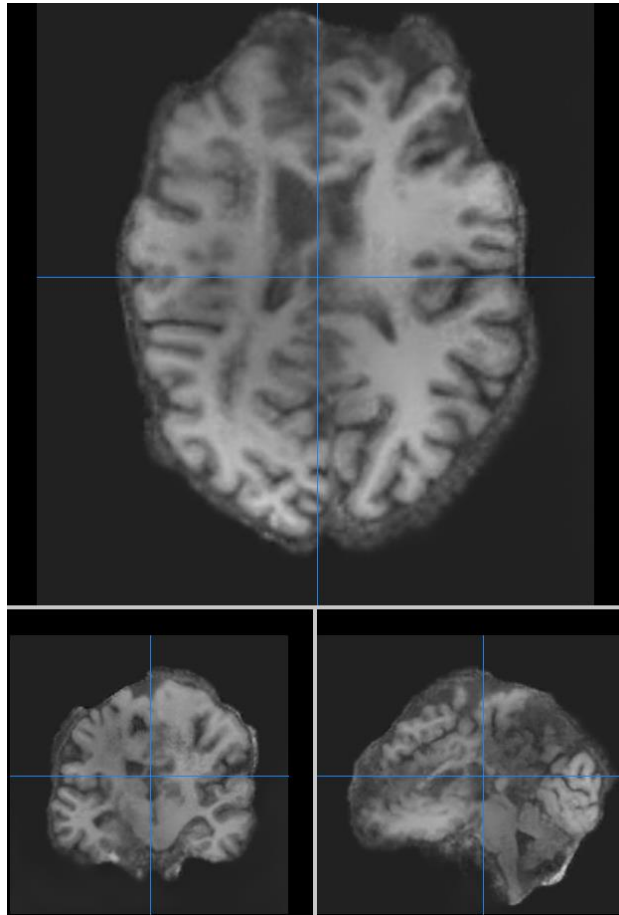


K=5

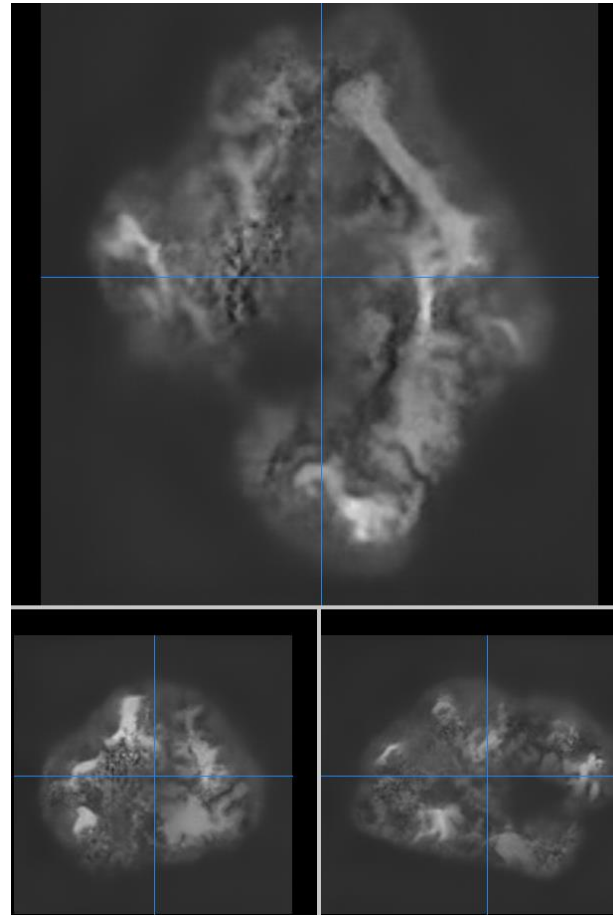


K=15

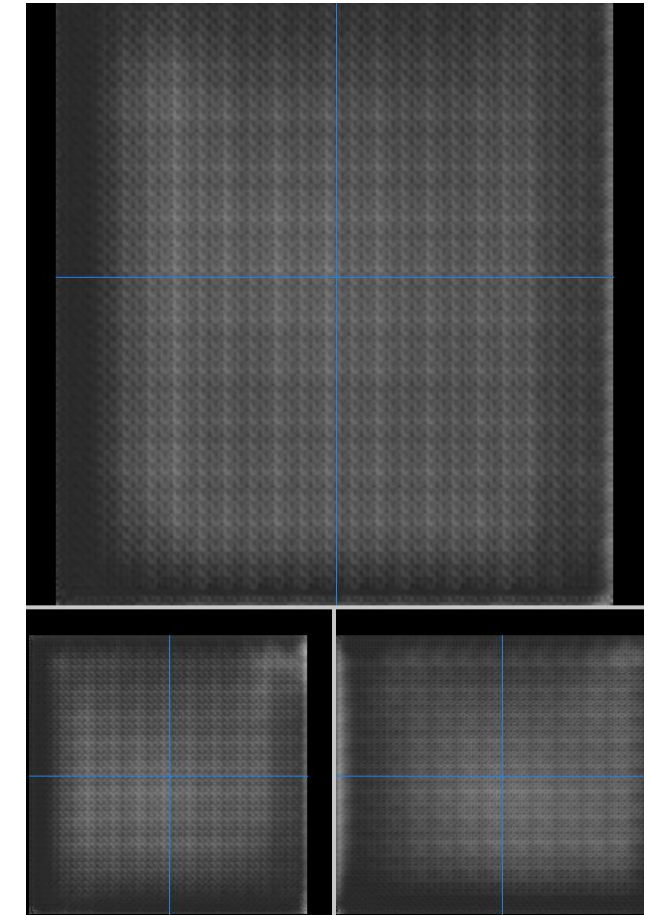
$K \rightarrow$  kth nearest codebook element using Euclidean distance



K=25



K=35



K=45

$K \rightarrow$  kth nearest codebook element using Euclidean distance

# Empirical observations

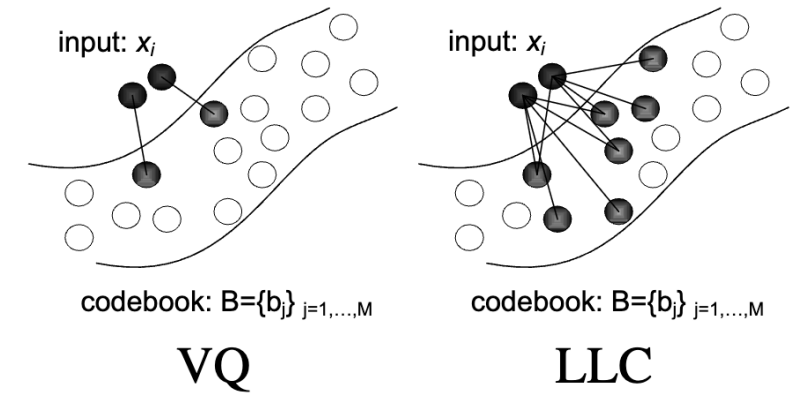
- Codebook neighborhoods encode **coherent semantic** information
- Codebook is **underutilized<sup>a</sup>** (79/2048 ~ 4%)

## 1. Locality constrained Linear coding (Wang et al., 2010) replaces hard VQ in Bag-of-Features

each descriptor  $\rightarrow$  into its local coordinate system (K nearest bases)

- **How to extend LLC to deep neural nets?**

## 2. Improving Codebook Utilization



Wang, Jinjun, et al. "Locality-constrained linear coding for image classification." *IEEE computer society conference on CVPR*, 2010.

| Category                       | Cons                                           | Names                                  |
|--------------------------------|------------------------------------------------|----------------------------------------|
| Regularization & Reset         | Agnostic to the local geometry of latent space | HVQ-VAE, Jukebox                       |
| Soft & Stochastic Quantization | Random/poor selection of codes                 | SQVAE, Affine Reparam, CVQ-VAE, Gumbel |

- **How local-structure/feature-covariance improve codebook usage?**

<sup>a</sup>Huh, Minyoung, et al. "Straightening out the straight-through estimator: Overcoming optimization challenges in vector quantized networks." *ICML*, 2023.

Neural Image Compression

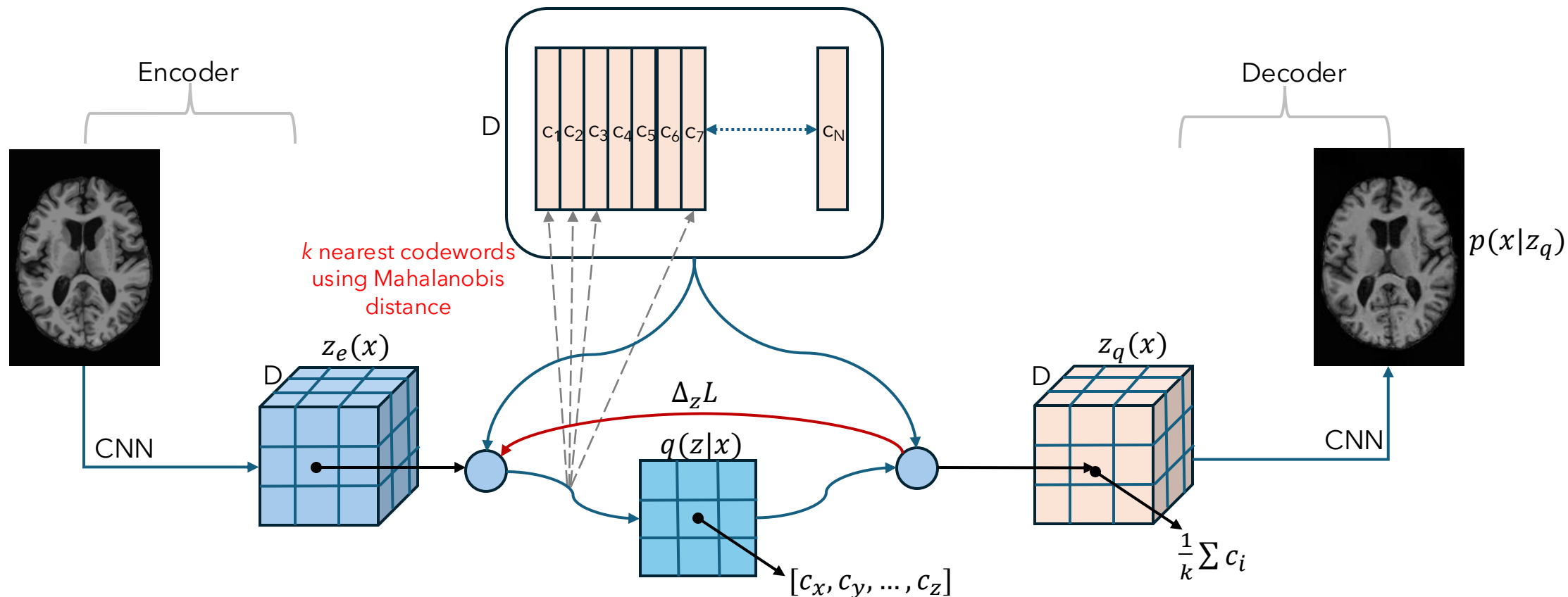
# Locality Constrained Vector Quantization

1. Locality informed soft-quantization
2. Optimal codebook usage

## Locality constrained VQ (LCVQ)

**Problem:** Euclidean nearest-neighbor **ignores latent covariance**

**Goal:** Leverage local latent geometry via *Mahalanobis distance* to improve codebook utilization and reconstruction fidelity



1. Center codebook & calculate covariance
  - How latent dimensions co-vary across embeddings
2. Mahalanobis distance to each  $c_i$ 
  - Prioritizes codewords that lie along high-variance axes
3. Top-K selection & aggregation
  - Instead of a single “hard” nearest neighbor, average the K most “informative” neighbors under the true geometry

**Algorithm 1:** Mahalanobis-based Top- $K$  Quantization for a single input  $x$

**Input:**  $x \in \mathbb{R}^D$ ,  $C \in \mathbb{R}^{N \times D}$  (codebook),  $K$

$\bar{C} = C - \text{mean}(C)$  # Center codebook

$\Sigma = \frac{1}{N-1} \bar{C}^\top \bar{C}$  # Compute covariance

$\Sigma^{-1} = \text{pinv}(\Sigma)$  # Pseudo-inverse for stability

$d_i = \sqrt{(x - C_i)^\top \Sigma^{-1} (x - C_i)} \quad \forall i = 1, \dots, N$  # Mahalanobis distances

$I = \text{argsort}(d)[1 : K]$  # Indices of top- $K$  neighbors

$q = \frac{1}{K} \sum_{i \in I} C_i$  # Average embeddings

**Return**  $q$

**Richer Representations**

**Higher Codebook Utilization**

**Smoother Reconstructions**

→ Leverages **local neighborhoods** in covariance-adjusted space.

→ **Spreads** assignments across more embeddings

→ **Soft aggregation** reduces quantization artifacts, anatomical errors.

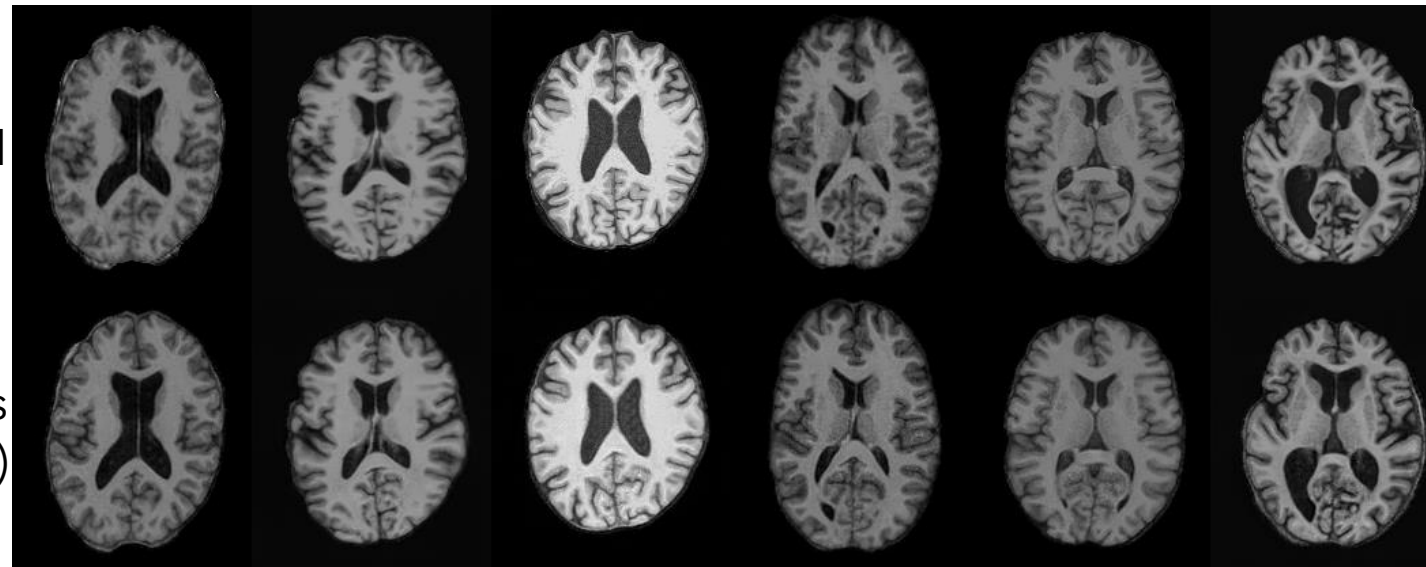


| Methods                              | MSE ( $10^{-3}$ ) ↓ | MS-SSIM ↑     | Perplexity ↑ |
|--------------------------------------|---------------------|---------------|--------------|
| VQ-VAE <sup>a</sup>                  | 2.01                | 0.9421        | 66.5         |
| w/ Affine <sup>b</sup>               | 2.12                | 0.9419        | 63.1         |
| w/ LCVQ (k=15)                       | <b>1.20</b>         | <b>0.9684</b> | <b>368.9</b> |
| w/ Affine <sup>b</sup> + LCVQ (k=15) | 1.52                | 0.9602        | 354.9        |

Perplexity → codebook usage

Given a distribution  $q$  over codebook entries, the perplexity is defined as:

$$\text{codebook perplexity} = \exp \left( - \sum_i q_i \log q_i \right)$$



Original

Predictions  
(LCVQ)

<sup>a</sup>Tudosiu, Petru-Daniel, et al. "Realistic morphology-preserving generative modelling of the brain." *Nature Machine Intelligence* (2024)

<sup>b</sup>Huh, Minyoung, et al. "Straightening out the straight-through estimator: Overcoming optimization challenges in vector quantized networks." *ICML*, 2023.

## Brain Age prediction

On Lifespan (**healthy**)

| Data                              | MAE (years) | Training time       |
|-----------------------------------|-------------|---------------------|
| Raw Imaging<br>(w/o quantization) | 5.10        | ~ 4 days            |
| Quantized Imaging<br>(LCVQ)       | 5.32        | ~ <b>15 minutes</b> |

Raw Imaging → (176, 208, 176)  
Quantized Imaging → (11, 13, 11)  
  
Compression ratio → **4096: 1**

On Discovery (**Unhealthy**)

| Data                              | MAE (years) |      |             |      | Brain Age delta (years) |       |              |       |
|-----------------------------------|-------------|------|-------------|------|-------------------------|-------|--------------|-------|
|                                   | AD ↑        | MCI  | HC ↓        | All  | AD ↑                    | MCI   | HC ↓         | All   |
| Raw Imaging<br>(w/o quantization) | 5.93        | 4.93 | 4.58        | 5.00 | 3.01                    | -0.14 | -2.15        | -0.21 |
| Quantized Imaging<br>(LCVQ)       | <b>6.01</b> | 4.53 | <b>4.29</b> | 4.73 | <b>3.43</b>             | 0.50  | <b>-1.56</b> | 0.36  |

AD=Alzheimer's disease, MCI=mild cognitive impairment, HC=healthy controls

## Ablation studies (k)

- $k=5 \rightarrow$  perplexity  $\uparrow$  (tight neighborhood)
- $k=100 \rightarrow$  MSE  $\uparrow$  SSIM  $\downarrow$  (diffuse neighborhood)

## Adaptive k via $\chi^2$ Thresholding

Squared Mahalanobis distance follows a chi-squared dist with D degrees of freedom<sup>a</sup>:

$$d_M^2(x, c_i) = (x - c_i)^T \Sigma^{-1} (x - c_i) \sim \chi_D^2$$

Thresholding:

$$\tau^2 = \chi_D^2 (1 - \alpha), \mathcal{N}_\tau(x) = \{c_i | d_M^2(x, c_i) \leq \tau^2\}$$

If  $|\mathcal{N}_\tau| = 0$ , revert to top-k

| k in VQVAE + LCVO             | MSE ( $10^{-3}$ ) $\downarrow$ | MS-SSIM $\uparrow$ | Perplexity $\uparrow$ |
|-------------------------------|--------------------------------|--------------------|-----------------------|
| 5                             | 1.40                           | 0.9652             | <b>391.9</b>          |
| 15                            | <b>1.20</b>                    | <b>0.9684</b>      | 368.9                 |
| 25                            | 1.21                           | 0.9678             | 330.5                 |
| 50                            | 1.32                           | 0.9679             | 329.2                 |
| 75                            | 1.32                           | 0.9672             | 258.7                 |
| 100                           | 1.44                           | 0.9627             | 295.3                 |
| Adaptive (k=15, $\alpha=10$ ) | 1.81                           | 0.9544             | 316.94                |



- Outperforms very large k
- Underperforms fixed-15 on some metrics
- $\alpha$  and k need refinement.

<sup>a</sup>[https://en.wikipedia.org/wiki/Mahalanobis\\_distance](https://en.wikipedia.org/wiki/Mahalanobis_distance)

## 1. Locality constrained quantization

Co-variance aware distance for high entropy codeword selection

Addresses **codebook collapse**

## 2. Top-k codeword aggregation

Reduce quantization artifacts, **capture data diversity**

## 3. Retains downstream performance

Lesser computation cost

## 4. Use cases

Low resource settings, federated learning, storage optimization

Medical Image Super-resolution

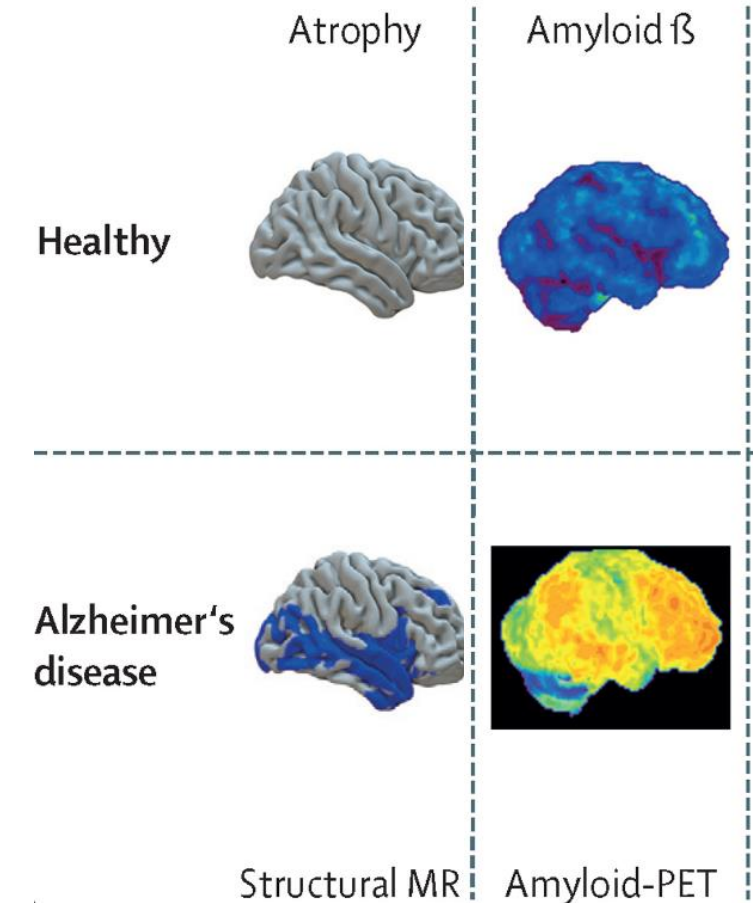
# Improving PET quantification using Deep Learning

## Amyloid PET

1. Measures amyloid beta ( $A\beta$ ) protein deposits in brain
2. Detect pathological changes earlier than clinical symptoms (~15 yrs)

## Comparison

- MRI shows general neurodegeneration  
Amyloid PET is more specific to AD pathology
- Amyloid PET can detect earlier pathological changes than MRI



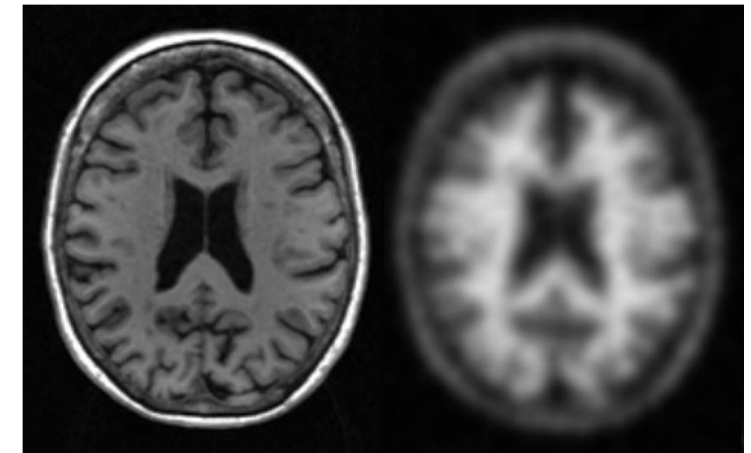
Chételat, Gaël, et al. "Amyloid-PET and 18F-FDG-PET in the diagnostic investigation of AD and other dementias." *The Lancet Neurology* (2020)

## (1) Low Spatial Resolution

Scanners at 4-6 mm FWHM – partial volume effect (PVE)

Size of the object is smaller than twice the FWHM of scanner

1. **Underestimation** of radiotracer uptake  
Especially in small brain structures
2. Spillover between GM, WM, and CSF  
Within tissue variability complicates correction
3. **Longitudinal tracking**  
Hampers monitoring disease progression



T1w MRI

PET (FBP)

## (2) Lack of Standardization

- Multiple PET tracers exist<sup>a</sup>  
florbetapir (FBP), florbetaben (FBB), flutemetamol, and NAV4694
- **Cross-tracer variability**  
Tracer-dependent characteristics leads to inconsistencies  
Lack of consensus in multi-center studies<sup>a</sup>

### *Super-Resolution*

- *To address PVE (due to low-res)*
- *To reduce inter-tracer variability*

<sup>a</sup>Shah, Jay, et al. "Deep residual inception encoder-decoder network for amyloid PET harmonization." *Alzheimer's & Dementia* (2022)



## Partial Volume Correction (PVC)

### 1. Iterative deconvolution methods

- Unblur image by estimating & removing PSF of imaging
- Iteratively deconvolve using the estimated PSF

*Low Spatial Resolution  
of PET Imaging*

### 2. Challenges

- Noise amplification
- Low resolution recovery
- These are region-based approaches  
Ideal is voxel-level resolution recovery

Tohka, Jussi, and Anthonin Reilhac. "Deconvolution-based partial volume correction in Raclopride-PET and Monte Carlo comparison to MR-based method." *Neuroimage* (2008)

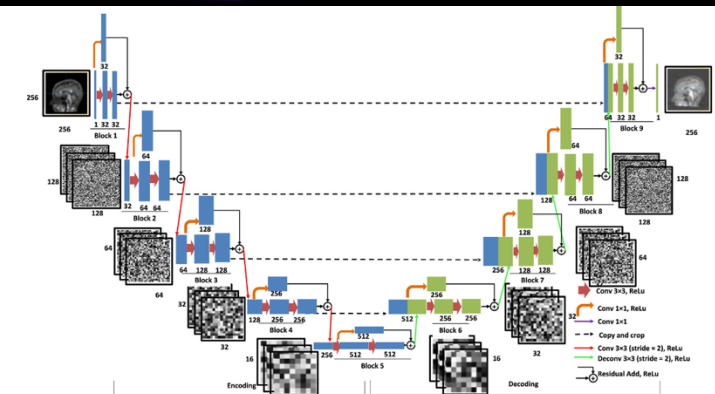
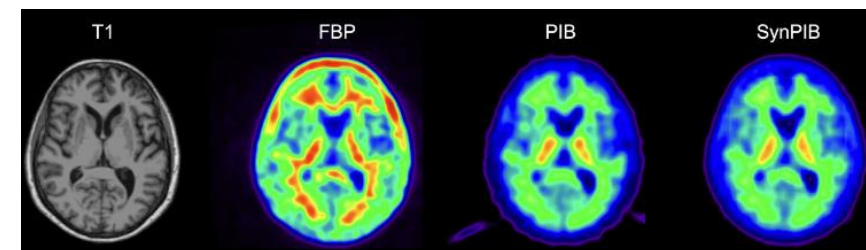
## Cross-tracer Harmonization

1. Paired image-to-image translation
  - Cross-tracer translation

2. Challenges

*Lack of Standardization*

- Can't generalize to other tracers
- Loss of tracer-specific information
- Requires paired datasets
- Bias from imperfect translation



Shah, Jay, et al. "Deep residual inception encoder-decoder network for amyloid PET harmonization." *Alzheimer's & Dementia* 18.12 (2022): 2448-2457.

Phase III

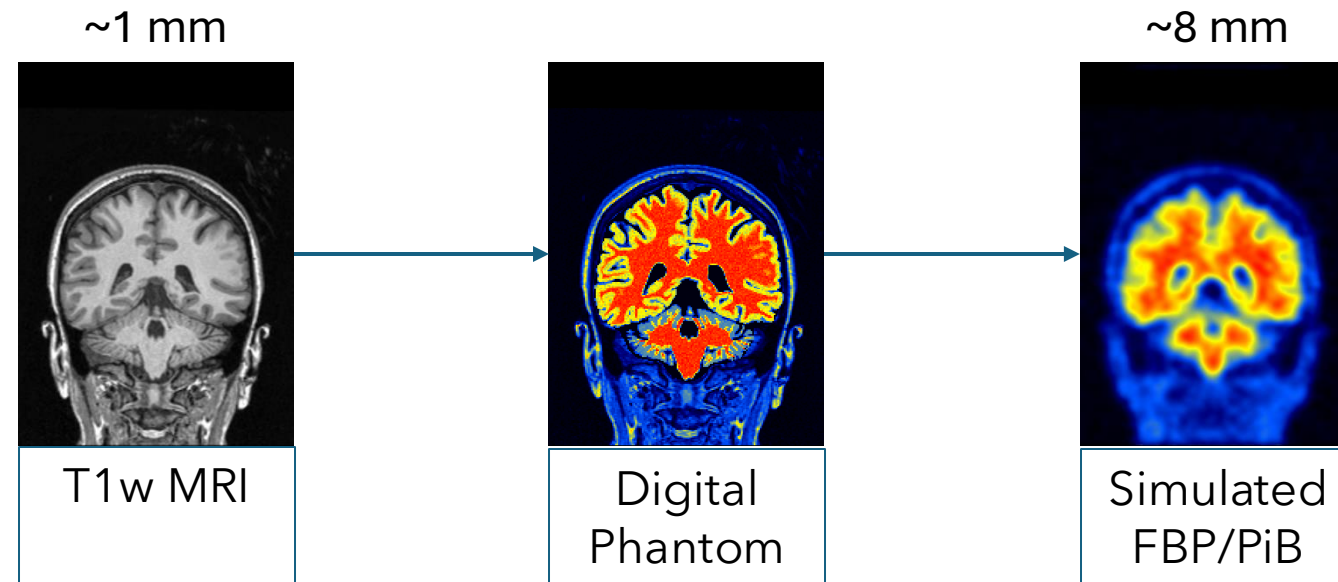
# Improving PET quantification using Diffusion model based Super-resolution

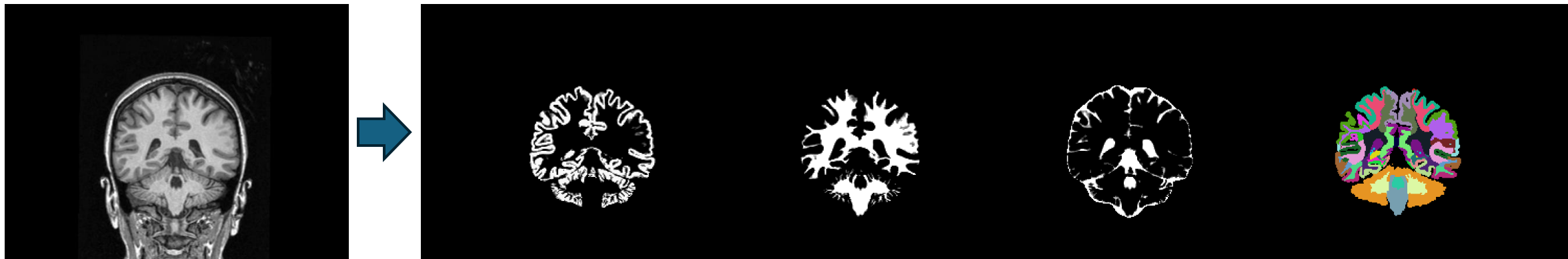
Objectives

1. Improve absolute quantification
2. Detect longitudinal changes (progression)
3. Improve cross-tracer Harmonization

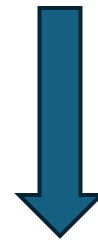
Ground truth high resolution PET does not exist!

Data Simulation - based on PET imaging physics





$$V = f_{gm} * gm_v + f_{wm} * wm_v + f_{csf} * csf_v + f_{bg} * bg_v + f_{gm} * abeta_v$$



## Tracer 1 (PIB)

$gm_v \sim (1, 0.04)$

$wm_v \sim (2.2, 0.066)$

$csf_v \sim (0.05, 0.001)$

$bg_v = nt1_v * .7$

$abeta_v \sim (0.5, 0.1)$

$f_{gm} + f_{wm} + f_{csf} + f_{bg} = 1$

Cerebellum-Cortex  $abeta = 0$

Brain-Stem  $abeta = 0$

Normalize to Cerebellum-Cortex

$MCSUVR = TargetROI / Cerebellum-Cortex$

## Tracer 2 (FBP)

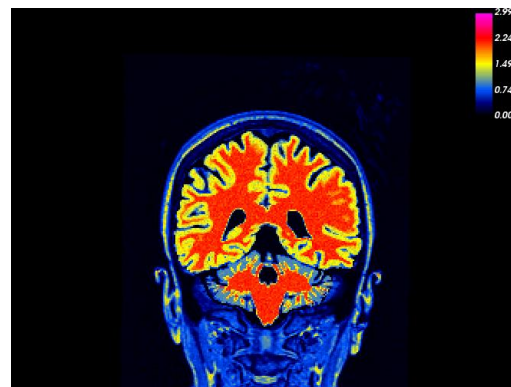
$gm2 = gm1$

$wm2 = 1.2 * wm1$

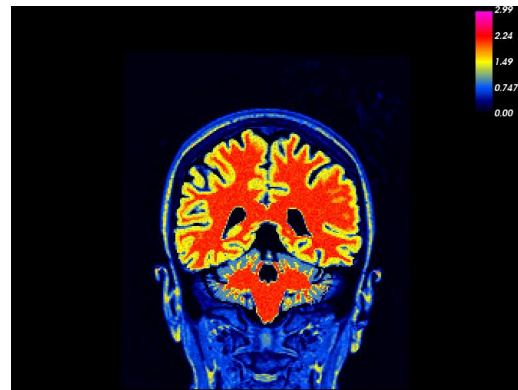
$csf2 = csf1$

$bg2 = 1.2 * bg1$

$abeta2 = 0.75 * abeta1$

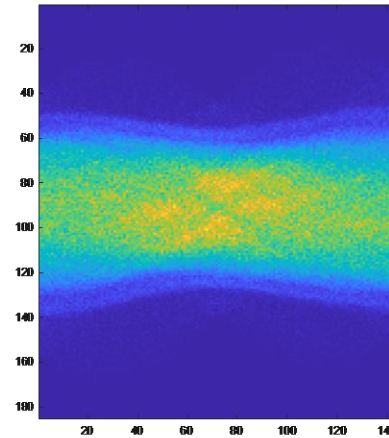


Su, Yi, et al. "Partial volume correction in quantitative amyloid imaging." *Neuroimage* (2015)

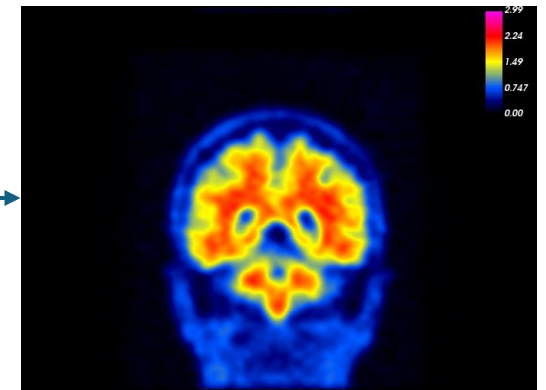


Digital Phantom  
(dpPIB)

smoothing  
forward projection  
add noise

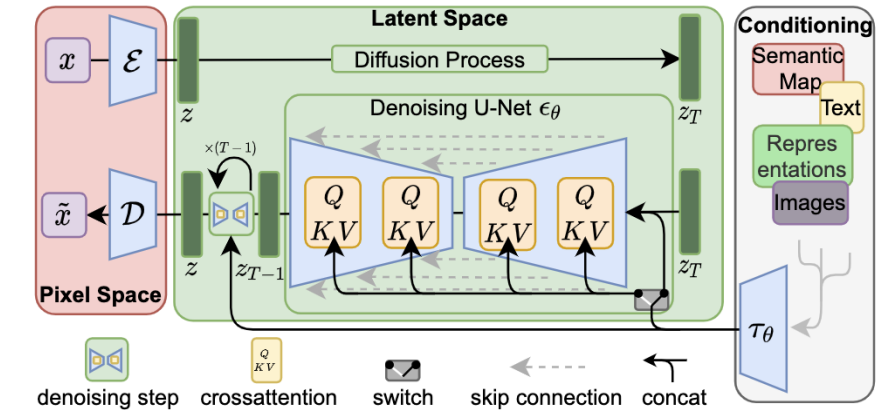


reconstruction  
smoothing

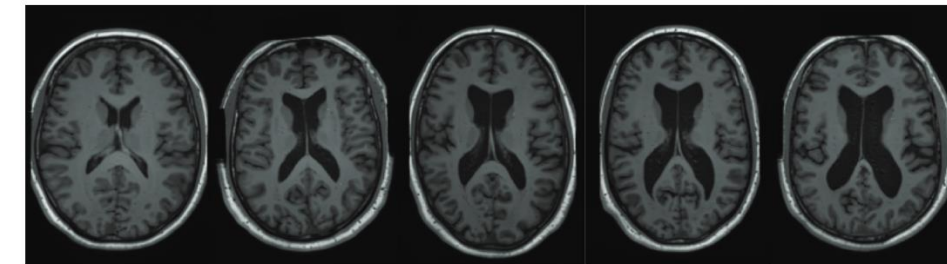


Simulated PET  
(spPIB)

- Diffusion Models outperform GANs in medical imaging synthesis<sup>a</sup>
  - More diversity, stable training, conditioning strategies
  - Limited by computation complexity
- Latent diffusion models
  - Denoising in latent space
  - Ideal for medical imaging ( $256^3$  dim data)
- Ideal for Super-Resolution

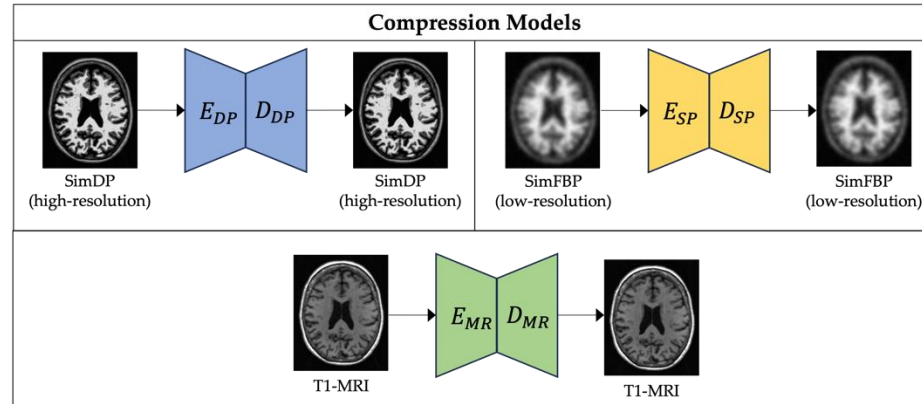


Rombach, Robin, et al. "High-resolution image synthesis with latent diffusion models." *CVPR* (2022)



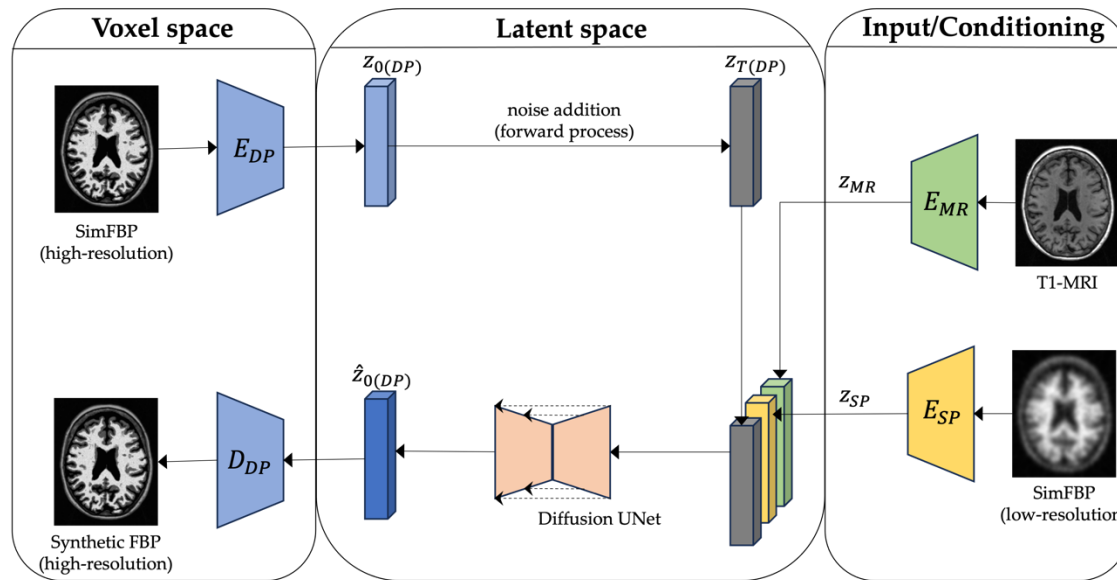
Pinaya, Walter HL, et al. "Brain imaging generation with latent diffusion models." *MICCAI Workshop on Deep Gen Models* (2022)

<sup>a</sup>Khader, Firas, et al. "Denoising diffusion probabilistic models for 3D medical image generation." *Scientific Reports* (2023)



## AutoencoderKL (3D)<sup>a</sup>

- Attention layers only at last level
- 32 base channels, with multiplier of [1,2,2]
- one residual block per level
- latent space [16×16×16], 3 latent channels.
- 80 training epochs, minibatch of 60
- Adam optimizer, base lr=0.0001.
- patch-based discriminator in our adversarial loss with 32 base channels, lr=0.0001.



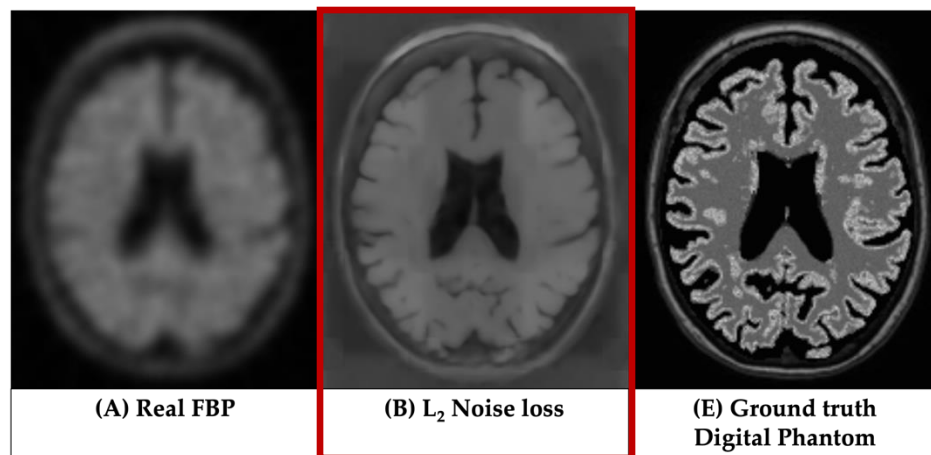
## LDM (3D)

- U-net architecture, 32 base channels, multiplier of [1,2,2]
- one residual block per level
- 9 input channels (3 each for simFBP, simDP, MRI latents).
- Adam optimizer with a base lr=0.0001.
- DDPM scheduler with 1000 timesteps (training), with a linear variance schedule (0.0015, 0.0195)
- DDIM scheduler with 250 timesteps (inference)

<sup>a</sup>Pinaya, Walter HL, et al. "Brain imaging generation with latent diffusion models." *MICCAI Workshop on Deep Gen Models* (2022)



Inputs: low-res PET, T1 MRI  
Diffusion-Unet:  $L_2$  loss on noise scale ( $\epsilon, \hat{\epsilon}$ )



## Observations

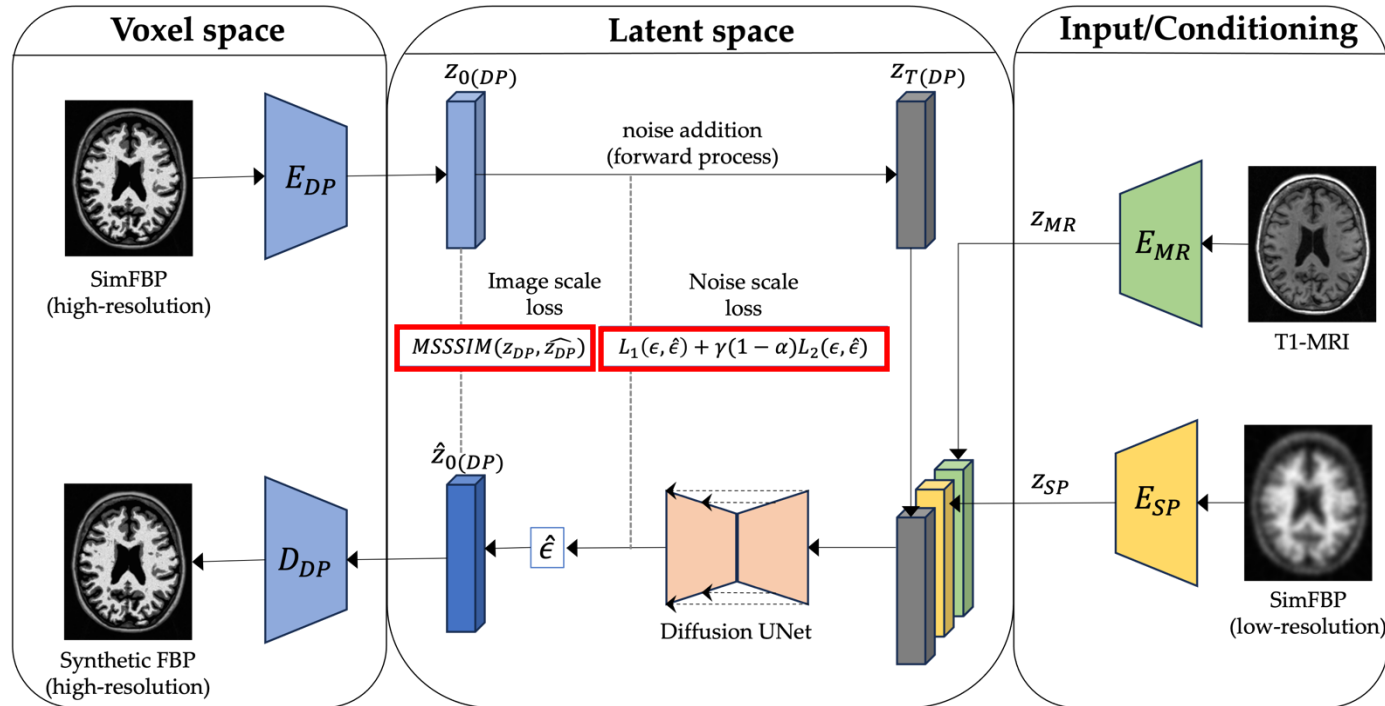
1. Minimizing loss on **noise-scale** does not guarantee accurate **image-scale** reconstruction
2. Cannot retain (brain) structure information
3. Combination of  $L_1/L_2$  and MS-SSIM<sup>b</sup> loss is more suitable for image restoration/super-resolution<sup>a</sup>
  - $L_2$  can be sensitive to outliers
  - $L_1$  suffers non-differentiability at zero

Preserving structure & voxel level intensity is key to PET Quantification accuracy!

<sup>a</sup>Zhao, Hang, et al. "Loss functions for image restoration with neural networks." *IEEE Transactions on computational imaging* (2016)

<sup>b</sup>MS-SSIM=multi scale structural similarity index

## Latent diffusion model for resolution recovery (LDM-RR)



$$\hat{z}_0 = \frac{z_t - \sqrt{1 - \alpha_t} \hat{\epsilon}}{\sqrt{\alpha_t}}$$

$$loss_1 = (1 - \alpha)L_2(z_0, \hat{z}_0) + \alpha MSSSIM(z_0, \hat{z}_0)$$

$$loss_2 = L_1(\epsilon, \hat{\epsilon}) = |\epsilon - \hat{\epsilon}|$$

$$loss_{combined} = \underbrace{L_1(\epsilon, \hat{\epsilon}) + \gamma(1 - \alpha)L_2(\epsilon, \hat{\epsilon})}_{\text{noise-scale}} + \underbrace{\alpha MSSSIM(z_0, \hat{z}_0)}_{\text{image-scale}}$$

Training cohort

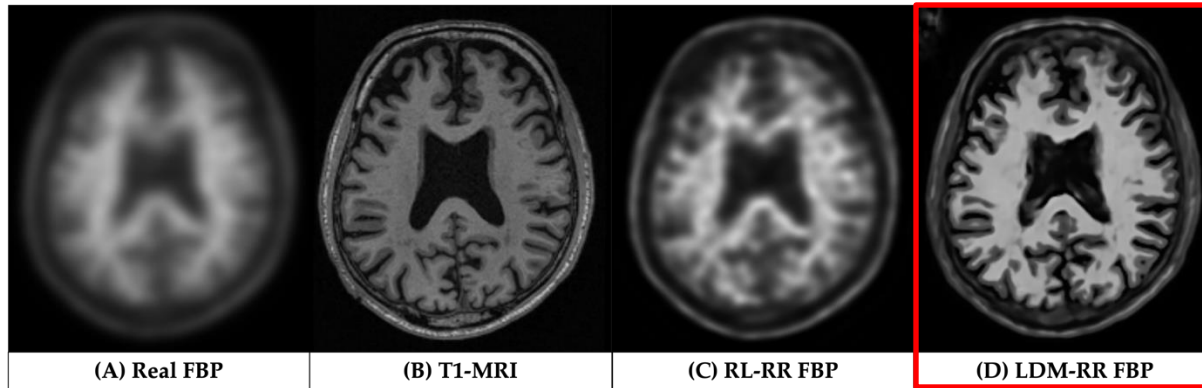
- 3,376 MRI scans from ADNI
- Simulated paired FBP/PiB scans

Longitudinal cohort

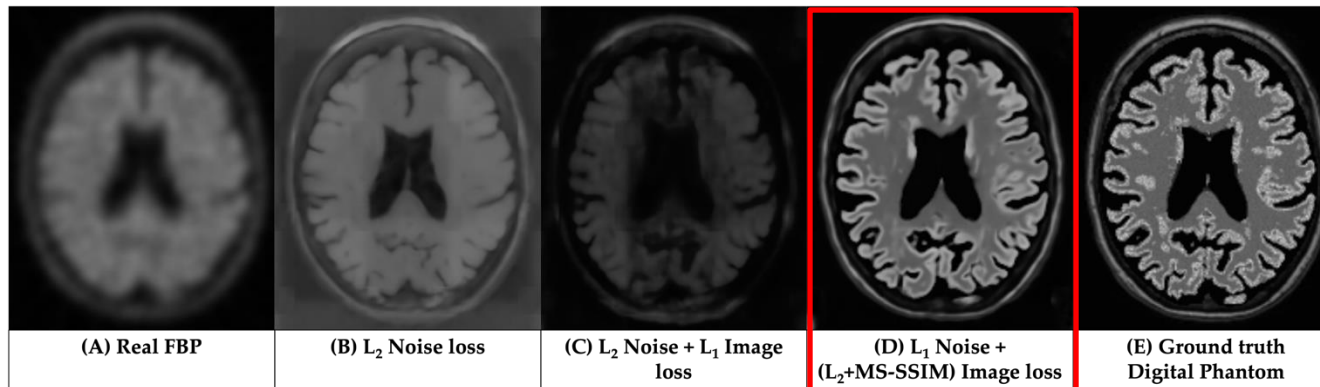
Cross-tracer cohort

| Cohort                   | ADNI                              | OASIS-3                | Centiloid                       |
|--------------------------|-----------------------------------|------------------------|---------------------------------|
| Sample count             | 334 FBPs<br>167 baseline-followup | 113<br>(FBP-PIB pairs) | 46<br>(FBP-PIB pairs)           |
| Age (SD) yrs             | 75.1 (6.9)                        | 68.1 (8.7)             | 58.4 (21.0)                     |
| Education (SD) yrs       | 16.1 (2.7)                        | 15.8 (2.6)             | NA                              |
| Male (%)                 | 182 (54.5%)                       | 48 (42.5%)             | 27 (58.7%)                      |
| Cognitive impairment (%) | 236 (70.6%)                       | 5 (4.4%)               | 24 (52.2%)                      |
| APOE4+ (%)               | 218 (65.3%)                       | 38 (33.6%)             | 15 (46.9*%)<br>[*14/46 unknown] |
| PET interval (SD) yrs    | 2.0 (0.06)                        | NA                     | NA                              |

## Qualitative analysis



Compared to traditional Iterative deconvolution-based correction method<sup>a</sup>



Compared to traditional LDMs with L<sub>2</sub> loss minimization on noise scale

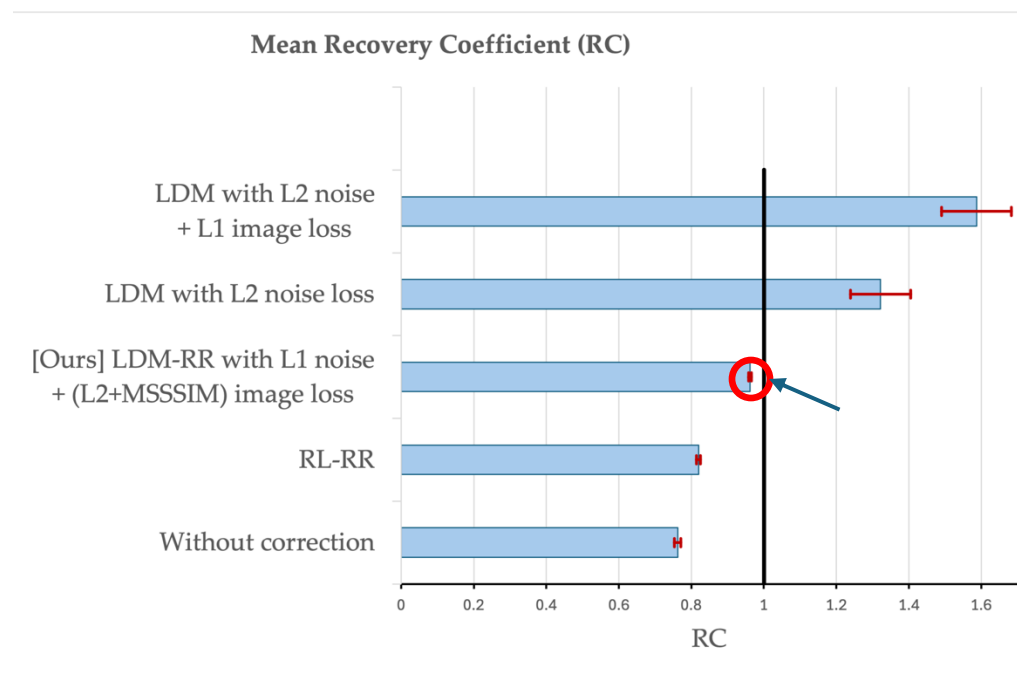
<sup>a</sup>Tohka, Jussi, and Anthonin Reilhac. "Deconvolution-based partial volume correction in Raclopride-PET and Monte Carlo comparison to MR-based method." *Neuroimage* (2008)

## On Simulated dataset

MCSUVR: Mean Cortical Standardized Uptake Value Ratio  
measures amyloid plaque accumulation in brain PET  
normalized measure of radiotracer uptake.

### 1. RC: Recovery Coefficient

- $RC = \frac{MCSUVR (Synthetic DP)}{MCSUVR (Simulated DP)}$
- Synthetic DP = synthetic high-resolution PET  
Simulated DP = simulated digital phantom
- ~1 is ideal



Comparison of mean recovery coefficient (RC) using different methods on a held-out test of 338 samples randomly selected from the simulated dataset.

## On Longitudinal cohort

### 1. Annualized Rate

- $rate = \frac{\Delta MCSUVR (followup - baseline)}{time\ interval\ (yrs)}$
- A **higher rate of change** = higher statistical power to detect longitudinal changes in amyloid deposition

### 2. SS: Sample Size

- # participants per arm needed to detect a 25% reduction in amyloid accumulation rate due to treatment with 80% power and a two-tailed type-I error of  $p=0.05$  in hypothetical anti-amyloid treatment trials.
- A **smaller SS** indicates greater statistical power.

| Annualized rate | Raw     | RL-RR   | LDM-RR        |
|-----------------|---------|---------|---------------|
| Mean            | 0.0278  | 0.0377  | <b>0.0459</b> |
| SD              | 0.0664  | 0.0807  | 0.0881        |
| p-value         | 1.0E-07 | 5.0E-09 | 1.3E-10       |
| SS              | 1431    | 1154    | <b>926</b>    |

Statistical power in detecting longitudinal changes measured

## On Cross-tracer cohort

- Combined dataset (OASIS + Centiloid)
- Agreement of PET-derived global amyloid burden between **FBP** and **PiB**
- Using Pearson correlation & Steiger's t-test p-values

| Method         | Pearson Correlation | Steiger's p-value                         |
|----------------|---------------------|-------------------------------------------|
| w/o Correction | 0.9163              | N/A                                       |
| RL-RR          | 0.9308              | <0.0001<br>(RL-RR vs. without correction) |
| LDM-RR         | <b>0.9411</b>       | 0.0001<br>(LDM-RR vs. without correction) |
|                |                     | 0.0421<br>(LDM-RR vs. RL-RR)              |

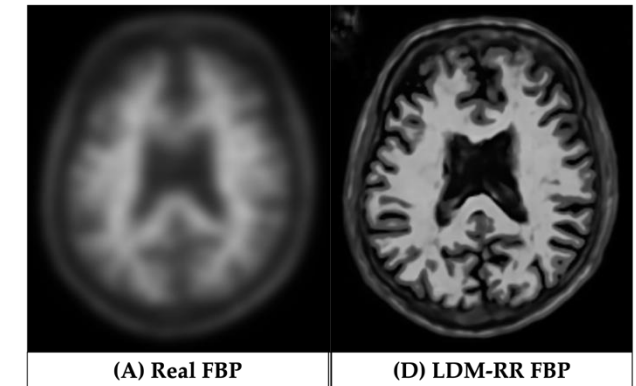
Comparison of RL and LDM-RR methods in improving the MCSUVR agreement between FBP and PIB tracers shown by Pearson correlation and Steiger's test.

## 1. Super-resolution with latent diffusion models

- Adding [image-scale loss](#) penalty can preserve global image structure
- Noise-scale loss does not guarantee accurate reconstruction

## 2. Super-resolution for PET Quantification

- Using [simulated dataset](#) from domain knowledge
- Voxel-level enhancement using MRI
- Better [longitudinal tracking](#)
- Cross-tracer [harmonization](#)



## 3. Deep Learning can address Partial volume effect in PET

- Bettering Early detection and disease monitoring



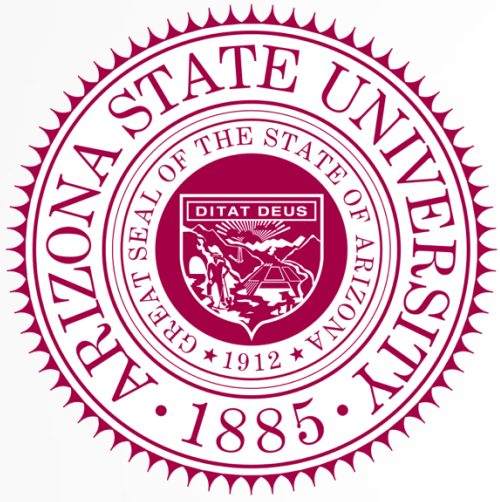
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  - **[Patent]**: Gao, F., Su, Y., Shah, J. and Wu, T., *Banner Health and Arizona State University*, (2025). Deep residual inception encoder-decoder network for amyloid PET harmonization. U.S. Patent 12,186,114.
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13. Shah, J., Chong, C., Schwedt, T., ... & Wu, T. (2021). Interpreting Deep Learning Model Predictions using Shapley Values. *INFORMS Annual Meeting*
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# Thank You

## Questions?

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# Appendix



| $k$      | Method (Loss) | MAE         | Ordinality  | Systematic Bias |             |
|----------|---------------|-------------|-------------|-----------------|-------------|
|          |               |             |             | SB-L            | SB-R        |
| 1/2      | CE            | 6.05        | 0.85        | 5.31            | -5.19       |
| 2/3      | CE            | 18.51       | 0.13        | 30.67           | 28.27       |
| <b>1</b> | <b>CE</b>     | <b>2.56</b> | <b>0.98</b> | <b>0.11</b>     | <b>-2.5</b> |
| 1        | MSE           | 4.66        | 0.95        | 2.19            | -4.98       |
| 2        | CE            | 2.90        | 0.10        | 0.93            | -3.04       |
| 2        | MSE           | 4.57        | 0.95        | 4.83            | -4.13       |

We use Manhattan distance in regularization:

$$\varphi(x_i) = \frac{1}{N-1} \sum_{j=1, i \neq j}^N |i-j| |\bar{x}_i - \bar{x}_j|_{manh}$$

Exploring other  $L_k$  norm distances

$$L_k(x, y) = \sum_{i=1}^d [||x^i - y^i||^k]^{\frac{1}{k}}$$

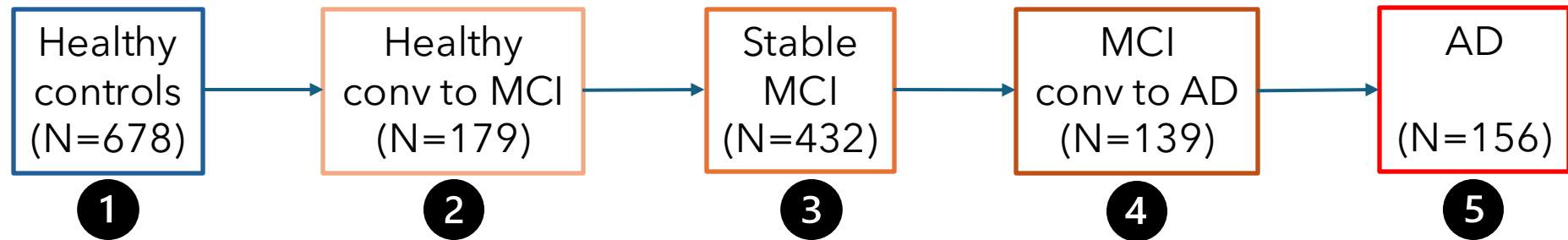
Results align with an established study\*, which suggests Manhattan distance ( $L_1$ ) is more suitable than Euclidean in high dimensional learning

\*Aggarwal, Charu C., et al. "On the surprising behavior of distance metrics in high dimensional space." ICDT (2001).



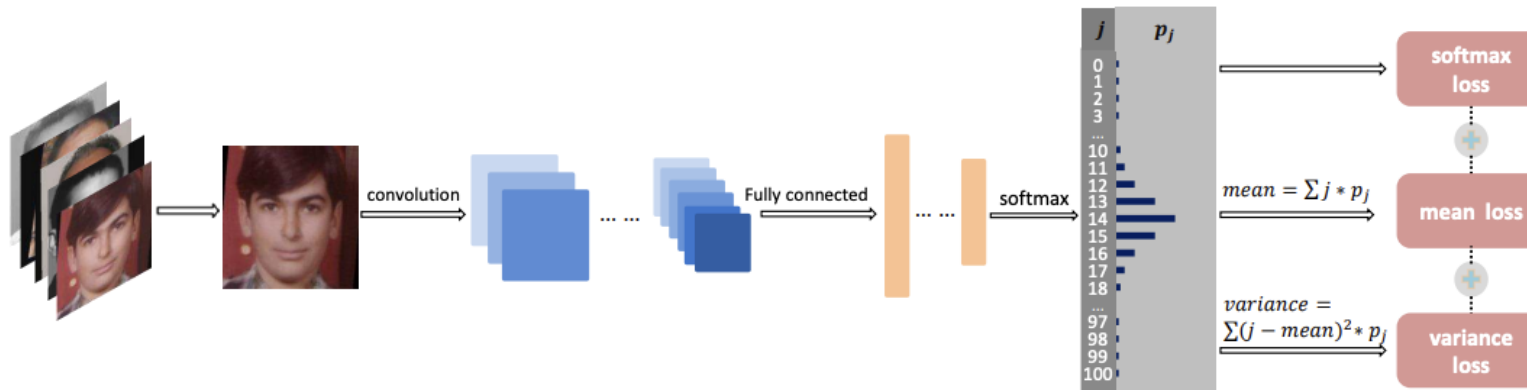
On Discovery (**mixed**) cohort

5 clinical groups with increasing order of severity

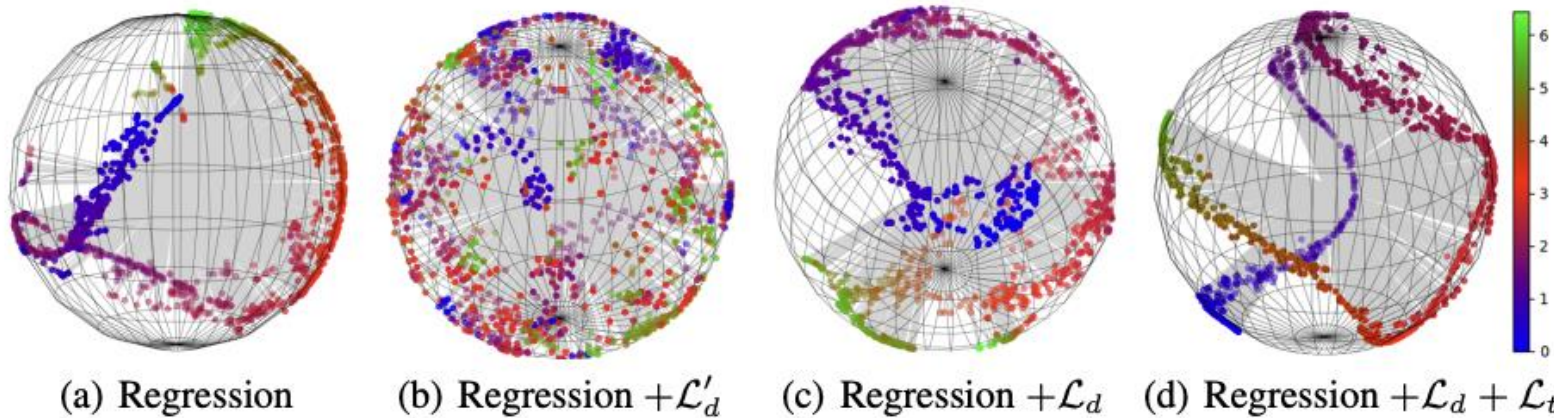


## Definitions

1. HC conv to MCI: normal cognition at baseline, converted to MCI during follow-up.
2. MCI-stable: baseline diagnosis of MCI, unchanged in follow-ups.
3. MCI conv to AD: MCI diagnosis at baseline, subsequently converted to AD.
4. AD: diagnosed with AD at baseline.



Mean-variance Loss



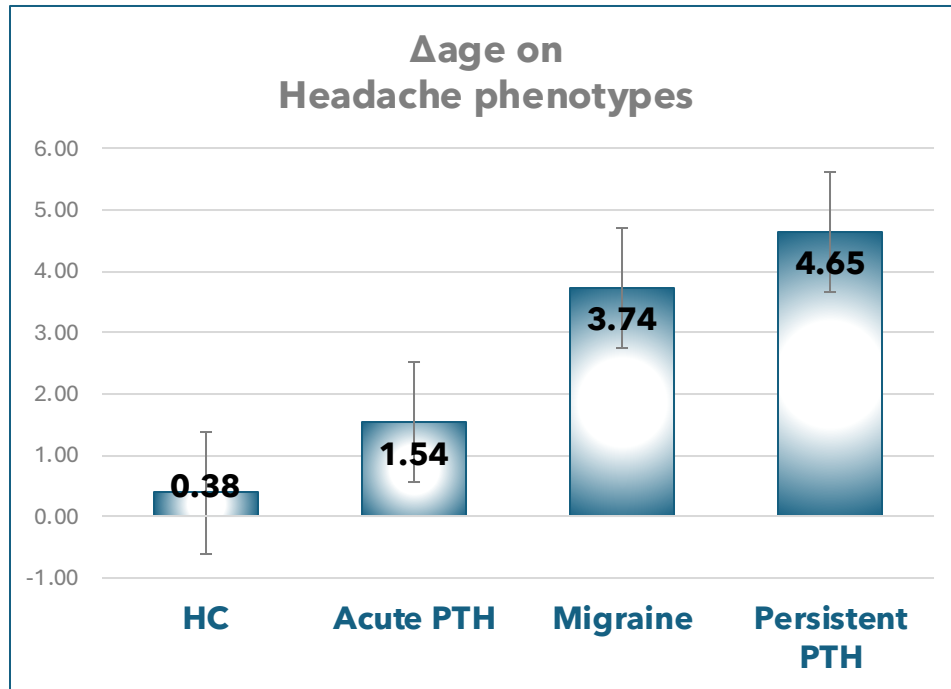
MSE + Euclidean Norm  
(Ordinal entropy Loss)

<sup>a</sup>Zhang, Shihao, et al. "Improving Deep Regression with Ordinal Entropy." ICLR (2023).

<sup>b</sup>Pan, Hongyu, et al. "Mean-variance loss for deep age estimation from a face." CVPR (2018).

## Findings:

- $\Delta\text{age}(\text{P-PTH}) < \Delta\text{age}(\text{A-PTH})$   
suggesting more structural decline related to PTH persistence over time
- Headache frequency associated with structural damage  
 $\Delta\text{age}(\text{P-PTH}) > \underline{\Delta\text{age}(\text{Mig})} > \Delta\text{age}(\text{A-PTH})$
- Early detection potential  
structural decline acutely following TBI at risk for developing persistent PTH

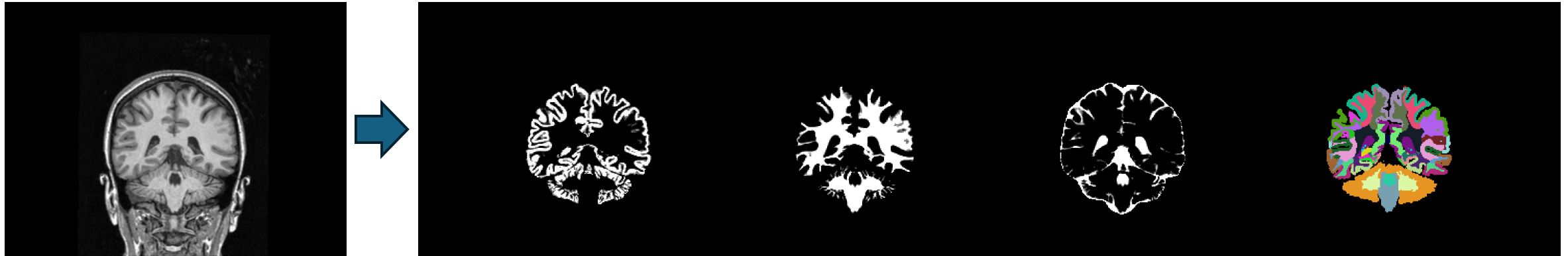


HC = Healthy Controls

PTH = Post Traumatic Headache

\*in-house data collected from Mayo Clinic, Arizona

# Digital Phantoms



$$V = f_{gm} \cdot gmv + f_{wm} \cdot wmv + f_{csf} \cdot csfv + f_{bg} \cdot bgv + f_{gm} \cdot abetav$$

|         |                                                                     |
|---------|---------------------------------------------------------------------|
| V:      | The observed PET signal in a voxel                                  |
| f_gm:   | The true radiotracer concentration in gray matter                   |
| f_wm:   | The true radiotracer concentration in white matter                  |
| f_csf:  | The true radiotracer concentration in cerebrospinal fluid           |
| f_bg:   | The true radiotracer concentration in background (non-brain tissue) |
| gmv:    | The fraction of gray matter in the voxel                            |
| wmv:    | The fraction of white matter in the voxel                           |
| csfv:   | The fraction of cerebrospinal fluid in the voxel                    |
| bgv:    | The fraction of background tissue in the voxel                      |
| abetav: | The fraction of amyloid-beta in the voxel                           |

| Methods                          | Pros                                                                                                                                                       | Cons                                                                                                                                                                                               | For Medical Imaging                                                         |
|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|
| LCVQ                             | <ul style="list-style-type: none"> <li>• Captures anisotropic latent structure</li> <li>• High, <b>organic codebook utilization</b> (no resets)</li> </ul> | <ul style="list-style-type: none"> <li>• Slight extra compute</li> </ul>                                                                                                                           | <b>Best:</b> sharp reconstructions, reproducible latents, ↓ MSE / ↑ MS-SSIM |
| Soft / Stochastic Quantization   | <ul style="list-style-type: none"> <li>• End-to-end differentiable; prevents hard collapse</li> <li>• Minimal extra parameters</li> </ul>                  | <ul style="list-style-type: none"> <li>• Probabilistic sampling → <b>noisy, less deterministic latents</b></li> <li>• Over-softens → blurred details; can hurt subtle pathology signals</li> </ul> | <b>Adequate:</b> for generic images; weak for fine neuro-features           |
| Reset / Regularization           | <ul style="list-style-type: none"> <li>• Simple add-on to VQ-VAE</li> <li>• <b>Rarely-used codes are alive without softness</b></li> </ul>                 | <ul style="list-style-type: none"> <li>• <b>Tuning reset freq &amp; penalty weights needed</b></li> <li>• Still Euclidean; no locality or covariance awareness</li> </ul>                          | <b>Moderate:</b> avoids collapse, but recon detail & task scores plateau    |
| FSQ (Finite Scalar Quantization) | <ul style="list-style-type: none"> <li>• No learnable codebook</li> <li>• <b>Guaranteed non-collapse</b></li> </ul>                                        | <ul style="list-style-type: none"> <li>• Fixed grid <b>can't adapt to data manifold</b></li> </ul>                                                                                                 | <b>Low:</b> coarse, anisotropic errors degrade PET/MRI precision            |