

(MICCAI 2021)

Self-Supervised Longitudinal Neighbourhood Embedding

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Motivation

Longitudinal MRIs are often used to capture the gradual deterioration of brain structure and function caused by aging or neurological diseases. Analyzing this data via machine learning generally requires a large number of ground-truth labels, which are often missing or expensive to obtain. **Reducing the need for labels**, they propose a self-supervised strategy for representation learning named Longitudinal Neighborhood Embedding (LNE).

Method

LNE explicitly models the similarity between trajectory vectors across different subjects. They do so by building a graph in each training iteration defining neighborhoods in the latent space **so that the progression direction of a subject follows the direction of its neighbors.**

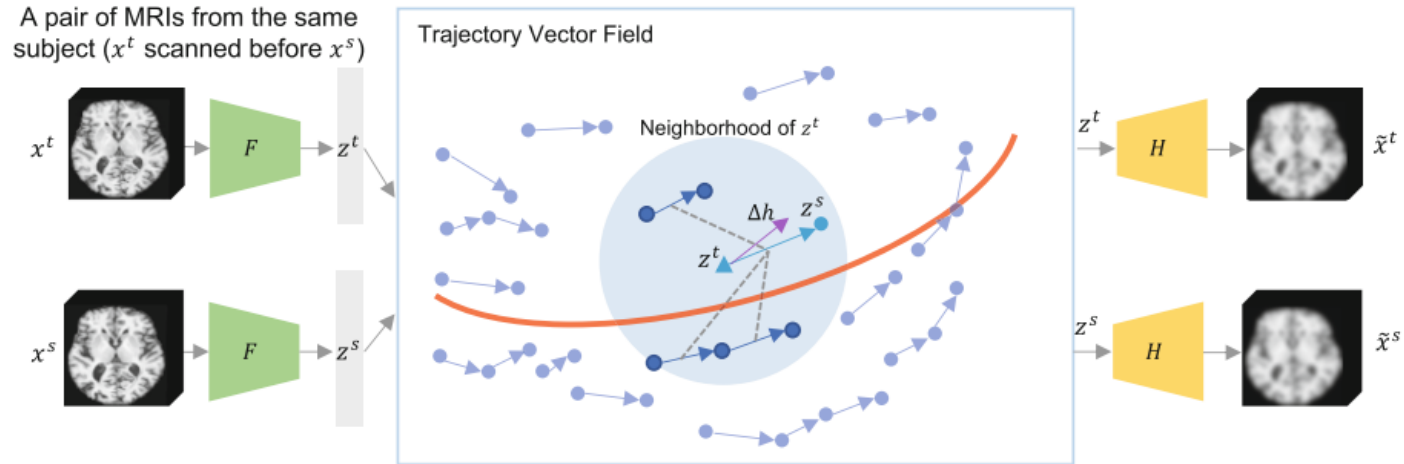
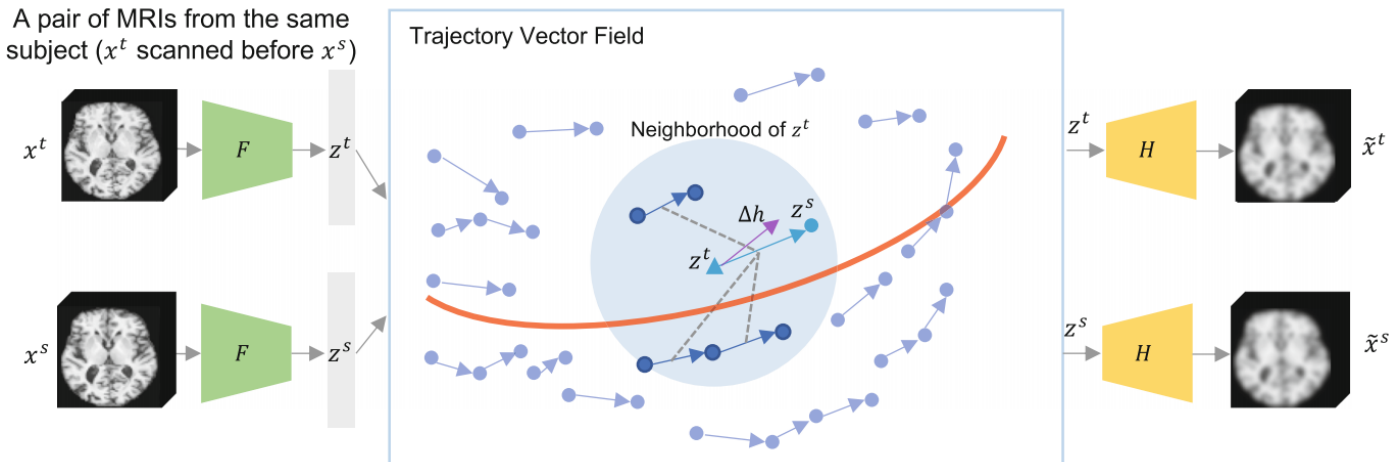


Fig. 1. Overview of the proposed method: an encoder projects a subject-specific image pair (x^t, x^s) into the latent space resulting in a trajectory vector (cyan). We encourage the direction of this vector to be consistent with Δh (purple), a vector pooled from the neighborhood of z^t (blue circle). As a result, the latent space encodes the global morphological change linked to aging (red curve). (Color figure online)

Method

A pair of MRIs from the same subject (x^t scanned before x^s)



Objective Function.

$$L := \mathbf{E}_{(x^t, x^s) \sim \mathcal{S}} \left(\|x^t - \tilde{x}^t\|_2^2 + \|x^s - \tilde{x}^s\|_2^2 - \lambda \cdot \cos(\theta_{\langle \Delta z, \Delta h \rangle}) \right),$$

1. Pairwise Training Strategy.

i. subject-specific image pairs

$$(x^t, x^s)$$

ii. latent representations

$$z^t = F(x^t), z^s = F(x^s)$$

iii. normalized trajectory vector

$$\Delta z^{(t,s)} = (z^s - z^t) / \Delta t^{(t,s)}$$

2. Longitudinal Neighbourhood Embedding.

i. adjacency matrix

$$P_{i,j} = \|z_i^t - z_j^t\|_2$$

$$A_{i,j} := \begin{cases} \exp(-\frac{P_{i,j}^2}{2\sigma_i^2}) & j \in \mathcal{N}_i \\ 0, & j \notin \mathcal{N}_i \end{cases}.$$

$$\text{with } \sigma_i := \max(P_{i,j \in \mathcal{N}_i}) - \min(P_{i,j \in \mathcal{N}_i})$$

ii. longitudinal neighbourhood embedding

$$\Delta h_i := \sum_{j \in \mathcal{N}_i} A_{i,j} D_{i,j}^{-1} \Delta z_j,$$

Experiments

1. Predicting age

Lab data set: 582 MRIs of 274 healthy individuals with the age ranging from 20 to 90. Each subject had 1 to 13 scans with an average of 2.3 scans spanning an average time interval of 3.8 years.

2. Classification

The second data set comprised 2389 longitudinal T1-weighted MRIs (at least two visits per subject) from ADNI, which consisted of 185 NC (age: 75.57 ± 5.06 years), 119 subjects with AD (age: 75.17 ± 7.57 years), 193 subjects diagnosed with sMCI (age: 75.63 ± 6.62 years), and 135 subjects diagnosed with pMCI (age: 75.91 ± 5.35 years). There was no significant age difference between the NC and AD cohorts ($p = 0.55$, two-sample t-test) as well as the sMCI and pMCI cohorts ($p = 0.75$).

Result

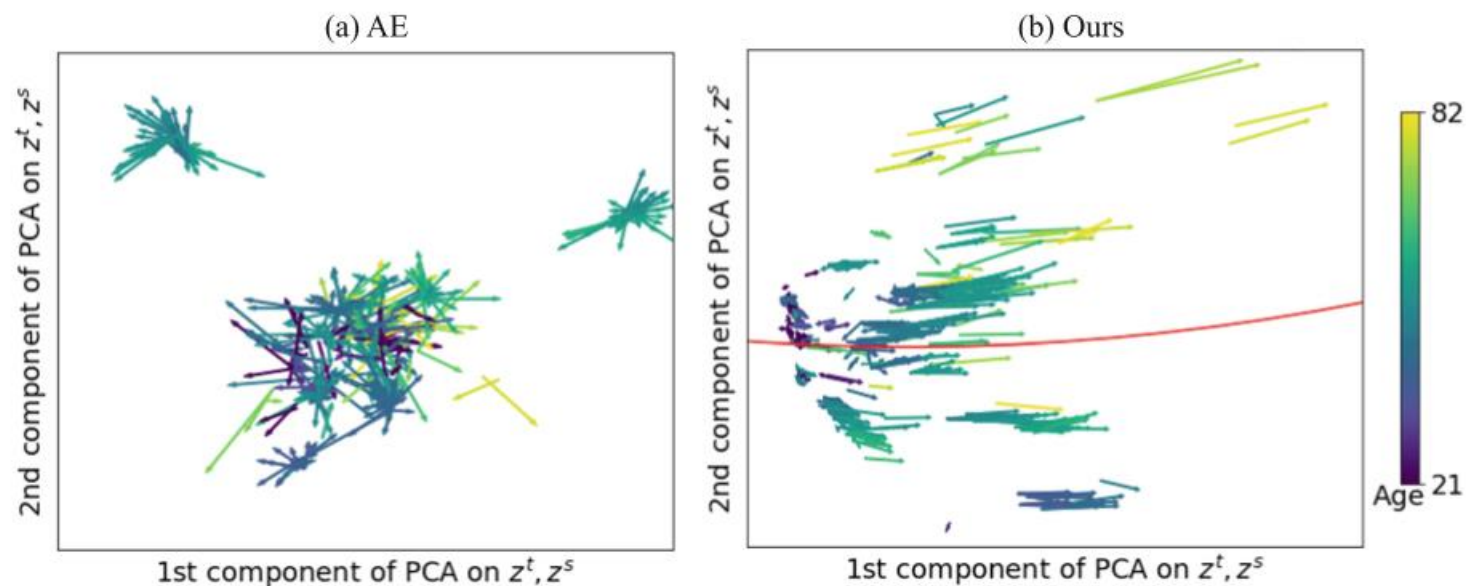


Fig. 2. Experiments on healthy aging: Latent space of AutoEncoder (AE) (a) and the proposed LNE (b) projected into 2D PCA space of z^t and z^s . Arrows represent Δz and are color-coded by the age of z^t . The global trajectory in (b) is fitted by robust linear mixed effect model (red curve). (Color figure online)

Result

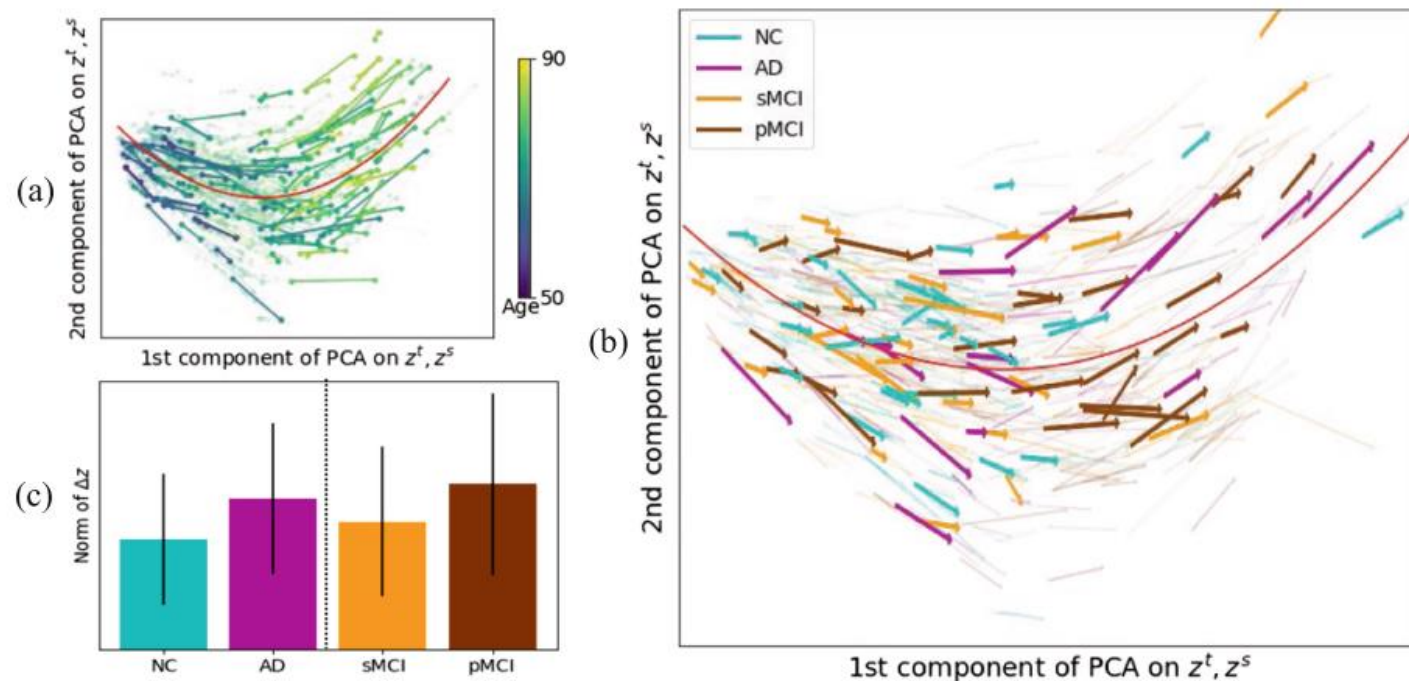


Fig. 3. Experiments on ADNI: (a) The age distribution of the latent space. Lines connecting z^t and z^s are color-coded by the age of z^t ; Red curve is the global trajectory fitted by a robust linear mixed effect model. (b) Trajectory vector field color-coded by diagnosis groups; (c) The norm of Δz encoding the speed of aging for 4 different diagnosis groups. (Color figure online)

Result

Table 1. Supervised downstream tasks in frozen or fine-tune scenarios. Left: Age regression on healthy subjects with R2 as an evaluation metric. Right: classification on ADNI dataset with BACC as the metric.

Methods	Health aging (R2)		ADNI (BACC)			
	Age		NC vs AD		sMCI vs pMCI	
	Frozen	Fine-tune	Frozen	Fine-tune	Frozen	Fine-tune
No pretrain	–	0.72	–	79.4	–	69.3
AE	0.53	0.69	72.2	80.7	62.6	69.5
VAE [12]	0.51	0.69	66.7	77.0	61.3	63.8
SimCLR [6]	0.56	0.73	72.9	82.4	63.3	69.5
LSSL [24]	0.59	0.74	74.2	82.1	69.4	71.2
Ours (LNE)	0.62	0.74	81.9	83.6	70.6	73.4

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Contrastive Learning with Continuous Proxy Meta-Data for 3D MRI Classification

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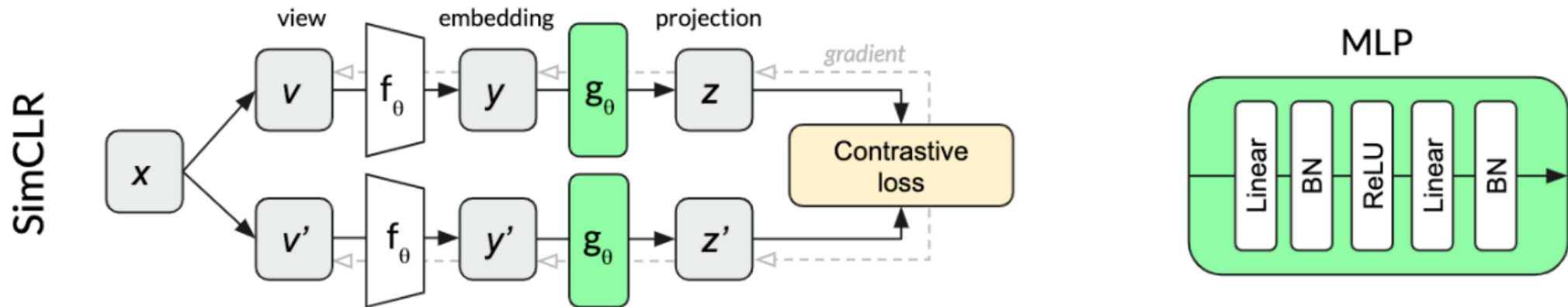
Motivation

Most of recent works do not take advantage of available meta-data, such as participant's age.

Goal

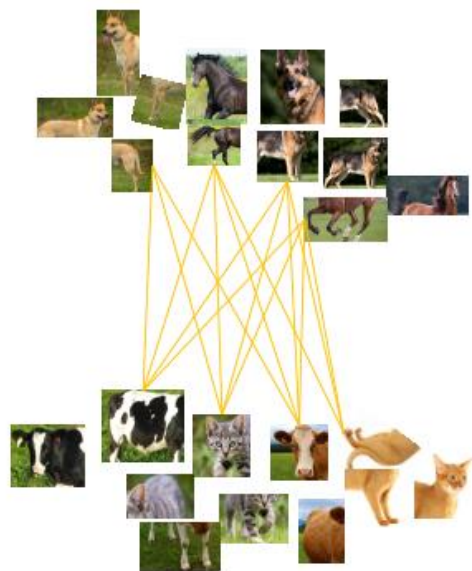
Propose a new **y-Aware InfoNCE loss** inspired from the Noise Contrastive Estimation loss that aims at improving the positive sampling according to the similarity between two proxy meta-data

SimCLR



$$L_N = -\mathbb{E}_X \left[\log \frac{\exp(f(x)^T f(x^+))}{\exp(f(x)^T f(x^+)) + \sum_{j=1}^{N-1} \exp(f(x)^T f(x_j^-))} \right]$$

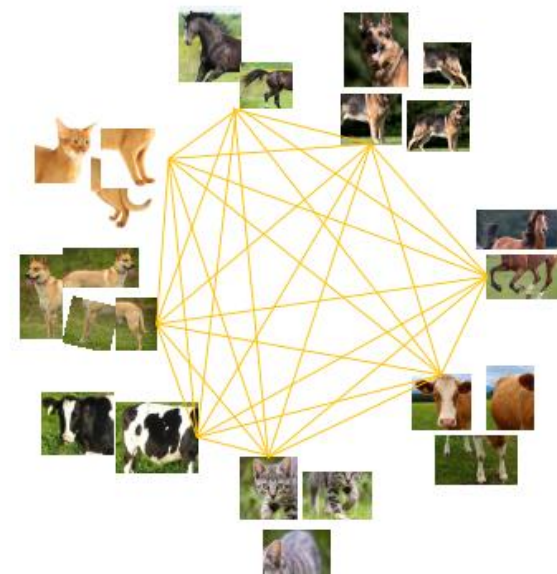
Problems



(a) under-clustering



(b) ideal clustering



(c) over-clustering

Figure 2. Illustration of under-clustering and over-clustering. Each sample pair connected by a yellow line represents a negative pair.

Method

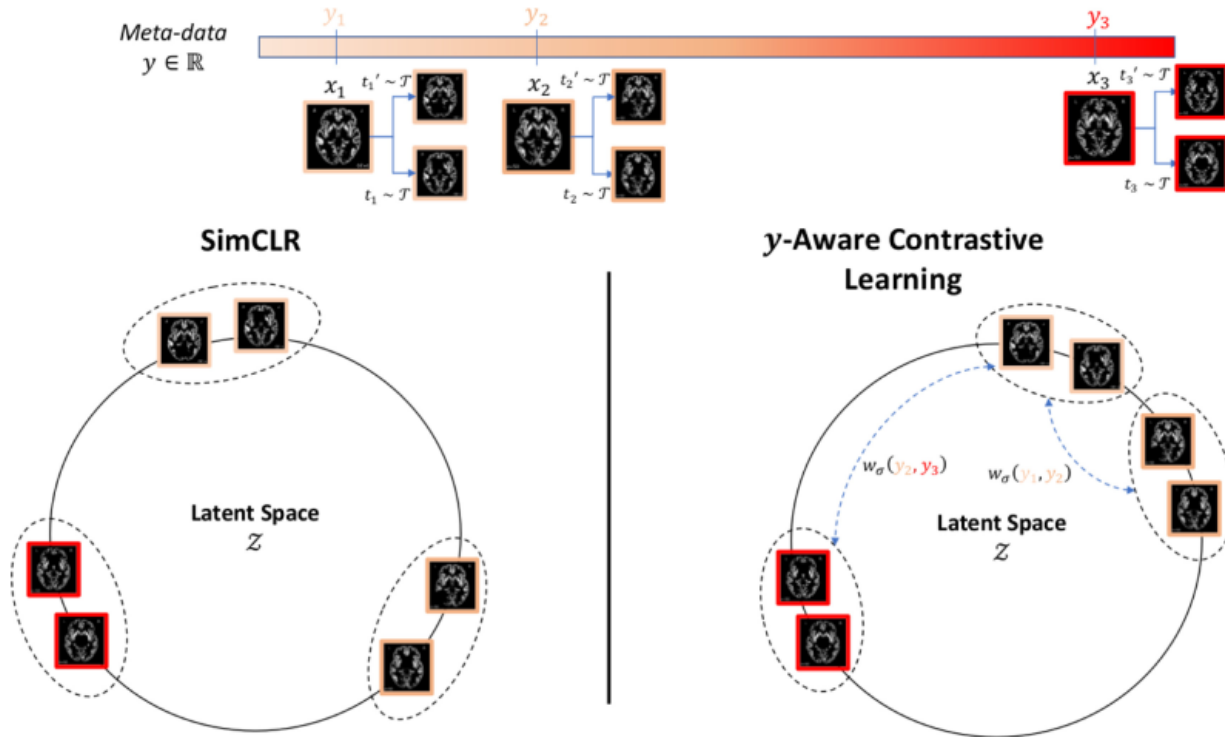


Fig. 1. Differently from SimCLR [5], our new loss can handle meta-data $y \in \mathbb{R}$ by redefining the notion of similarity between two images in the latent space \mathcal{Z} . For an image x_i , transformed twice through two augmentations $t_1, t_1' \sim \mathcal{T}$, the resulting views $(t_1(x_i), t_2(x_i))$ are expected to be close in the latent space through the learnt mapping f_θ , as in SimCLR. However, we also expect a different input $x_{k \neq i}$ to be close to x_i in \mathcal{Z} if the two *proxy* meta-data y_i and y_k are similar. We define a similarity function $w_\sigma(y_i, y_k)$ that quantifies this notion of similarity.

InfoNCE loss:

$$\mathcal{L}_{NCE} = -\log \frac{e^{f_\theta(v_1^i, v_2^i)}}{\frac{1}{n} \sum_{j=1}^n e^{f_\theta(v_1^i, v_2^j)}}$$

y-Aware InfoNCE loss:

$$\mathcal{L}_{NCE}^y = -\sum_{k=1}^n \frac{w_\sigma(y_k, y_i)}{\sum_{j=1}^n w_\sigma(y_j, y_i)} \log \frac{e^{f_\theta(v_1^i, v_2^k)}}{\frac{1}{n} \sum_{j=1}^n e^{f_\theta(v_1^i, v_2^j)}}$$

Radius Basis Function (RBF) kernel

$$w_\sigma = \exp\left(-\frac{\|\mathbf{x} - \mathbf{x}'\|^2}{2\sigma^2}\right)$$

Experiments

- Datasets

- **Big Healthy Brains (BHB) dataset** We aggregated 13 publicly available datasets of 3D T1 MRI scans of healthy controls (HC) acquired on more than 70 different scanners and comprising $N = 10$ samples. We use this dataset only to pre-train our model with the **participant's age as the proxy meta-data**. The learnt representation is then tested on the following four data-sets using as final task a binary classification between HC and patients.
- **SCHIZCONNECT-VIP** It comprises $N = 605$ multi-site MRI scans including 275 patients with strict schizophrenia (SCZ: 精神分裂) and 330 HC.
- **BIOBD** This dataset includes $N = 662$ MRI scans acquired on 8 different sites with 356 HC and 306 patients with bipolar disorder (BD: 躁郁症).
- **BSNIP** [25] It includes $N = 511$ MRI scans with $N = 200$ HC, $N = 194$ SCZ and $N = 117$ BD.
- **Alzheimer's Disease Neuroimaging Initiative (ADNI-GO)** We use $N = 387$ co-registered T1-weighted MRI images divided in $N = 199$ healthy controls and $N = 188$ Alzheimer's patients (AD: 阿兹海默). We only included one scan per patient at the first session (baseline).

Result

Evaluation of the representation

Classification is performed using a linear layer on top of the pre-trained frozen encoders.

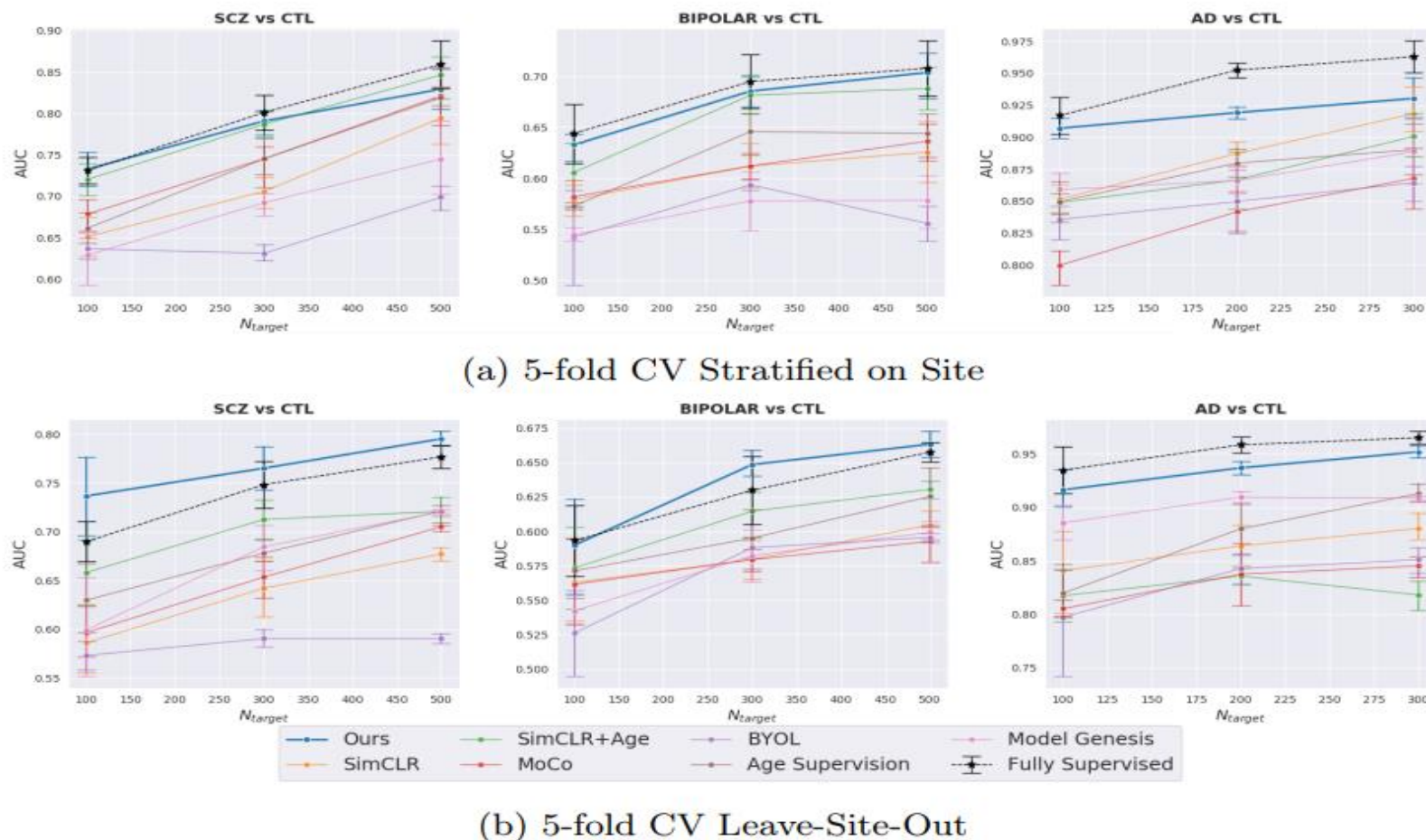


Fig. 2: Comparison of different representations in terms of classification accuracy (downstream task) on three different data-sets (one per column). Classification is performed using a linear layer on top of the pre-trained frozen encoders. (a) Data for training/validation and test come from the the same acquisition sites (b) Data for training/validation and test come from different sites.

Result

Fine-tuning Results

Backbone	Pre-training	SCZ vs HC		BD vs HC		AD vs HC	
		$N_{train} = 100$	$N_{train} = 500$	$N_{train} = 100$	$N_{train} = 500$	$N_{train} = 100$	$N_{train} = 300$
UNet	None	72.62 \pm 0.9	76.45 \pm 2.2	63.03 \pm 2.7	69.20 \pm 3.7	88.12 \pm 3.2	94.16 \pm 3.9
	Model Genesis [29]	73.00 \pm 3.4	81.8 \pm 4.7	60.96 \pm 1.8	67.04 \pm 4.4	89.44 \pm 2.6	95.16 \pm 3.3
	SimCLR [4]	73.63 \pm 2.4	80.12 \pm 4.9	59.89 \pm 2.6	66.51 \pm 4.3	90.60 \pm 2.5	94.21 \pm 2.7
	Age Prediction w/ D.A	<u>75.32\pm2.2</u>	<u>85.27\pm2.3</u>	64.6\pm1.6	70.78\pm2.1	<u>91.71\pm1.1</u>	<u>95.26\pm1.5</u>
	Age-Aware Contrastive Learning (ours)	75.95\pm2.7	85.73\pm4.7	<u>63.79\pm3.0</u>	<u>70.35\pm2.7</u>	92.19\pm1.8	96.58\pm1.6
DenseNet	None	73.09 \pm 1.6	85.92 \pm 2.8	64.39 \pm 2.9	70.77 \pm 2.7	92.23 \pm 1.6	93.68 \pm 1.7
	None w/ D.A	<u>74.71\pm1.3</u>	86.94 \pm 2.8	64.79 \pm 1.3	72.25 \pm 1.5	92.10 \pm 1.8	94.16 \pm 2.5
	SimCLR [5]	70.80 \pm 1.9	86.35 \pm 2.2	60.57 \pm 1.9	67.99 \pm 3.3	91.54 \pm 1.9	94.26 \pm 2.9
	Age Prediction	72.90 \pm 4.6	<u>87.75\pm2.0</u>	64.60 \pm 3.6	72.07 \pm 3.0	92.07 \pm 2.7	<u>96.37\pm0.9</u>
	Age Prediction w/ D.A	74.06 \pm 3.4	86.90 \pm 1.6	65.79\pm2.0	<u>73.02\pm4.3</u>	94.01\pm1.4	96.10 \pm 3.0
	Age-Aware Contrastive Learning (ours)	76.33\pm2.3	88.11\pm1.5	<u>65.36\pm3.7</u>	73.33\pm4.3	<u>93.87\pm1.3</u>	96.84\pm2.3

Table 1: Fine-tuning results using 100 or 500 (300 for AD vs HC) training subjects. For each task, we report the AUC (%) of the fine-tuned models initialized with different approaches with 5-fold cross-validation. For age prediction, we employ the same transformations as in contrastive learning for the Data Augmentation (D.A) strategy. Best results are in **bold** and second bests are underlined.

Thanks for listening