Beyond Euclidean -Hyperbolic Representation Learning

Joakim Bruslund Haurum Assistant Professor Center for Software Technology - SDU Vejle

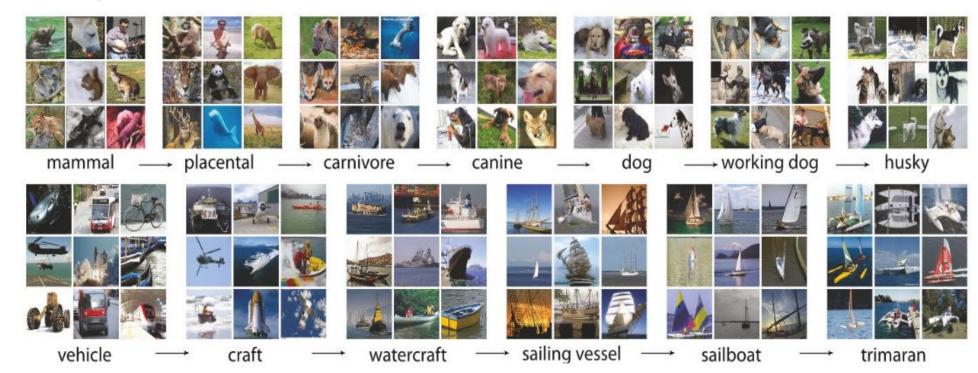




- → Euclidean Geometry is the "default" space for most settings
- → Vast majority of Neural Networks are implemented in Euclidean Geometry



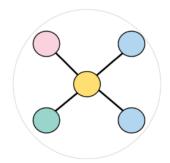
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- → However, our domain knowledge / data is not Euclidean. It is hierarichal!





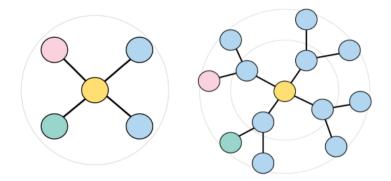
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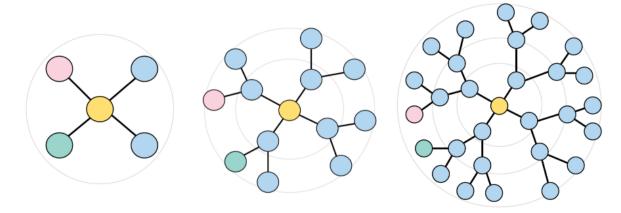


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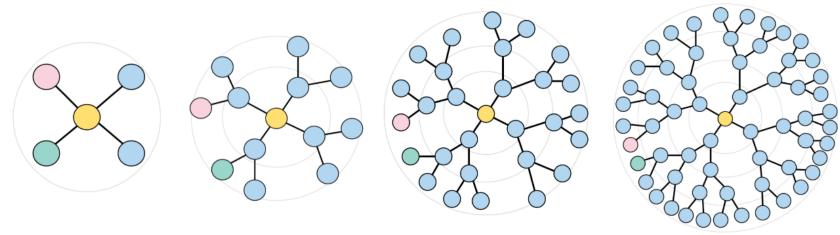


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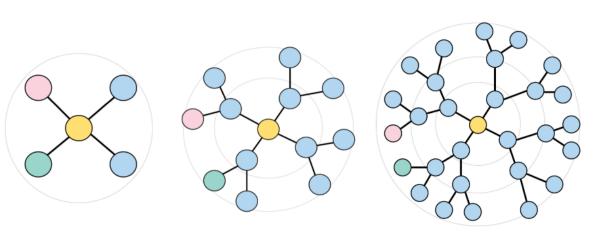


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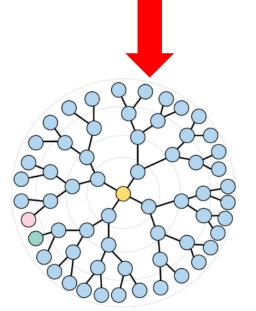




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Leaf nodes should be far apart





Hyperbolic Geometry







- 1. To draw a straight line from any point to any point.
- 2. To produce (extend) a finite straight line continuously in a straight line.
- 3. To describe a circle with any centre and distance (radius).
- 4. That all right angles are equal to one another.



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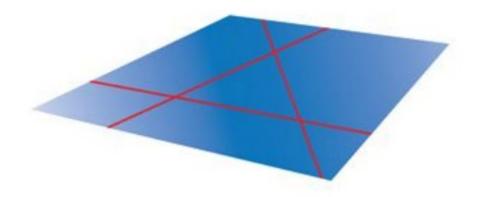
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What if this is not true?



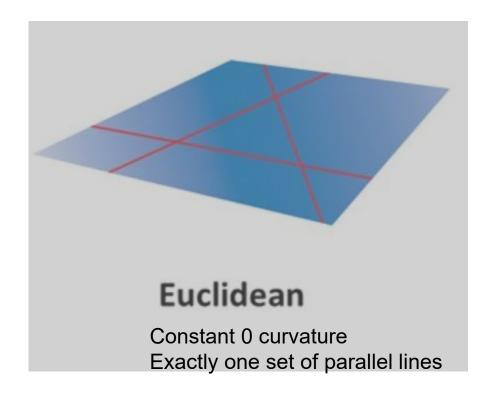
What does Non-Euclidean Geometry look like?





Euclidean

Constant 0 curvature Exactly one set of parallel lines

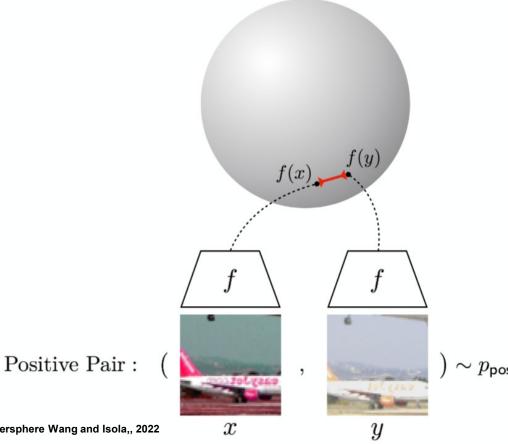




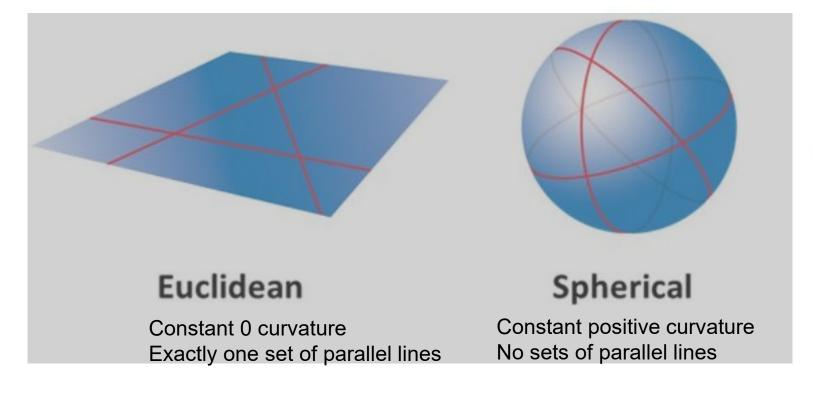
Spherical
Constant positive curvature
No sets of parallel lines

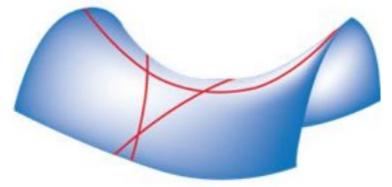
Contrastive Learning is Hyperspherical Learning

- → Contrastive Learning is often applied by measuring cosine similarity of unit vectors
- → All embeddings lie on a unit hypersphere



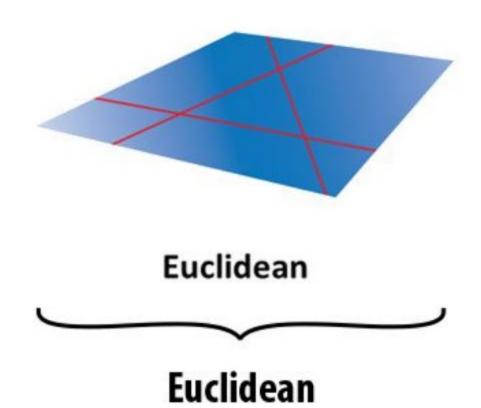


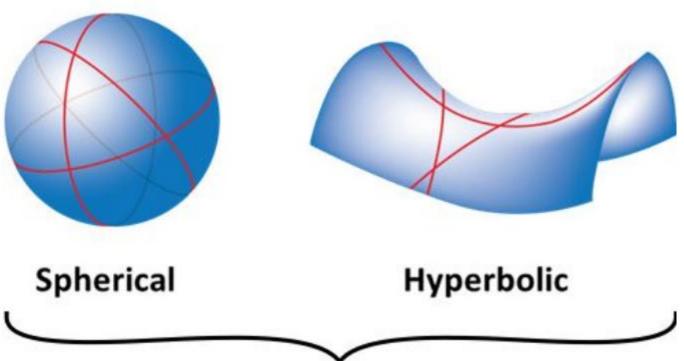




Hyperbolic

Constant negative curvature Infinite sets of parallel lines



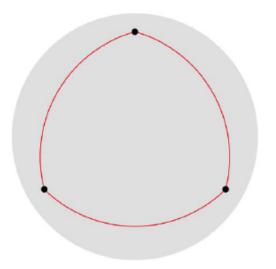


Non-Euclidean



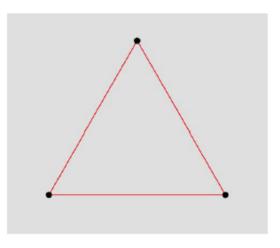
Spherical

$$(\kappa = +1)$$

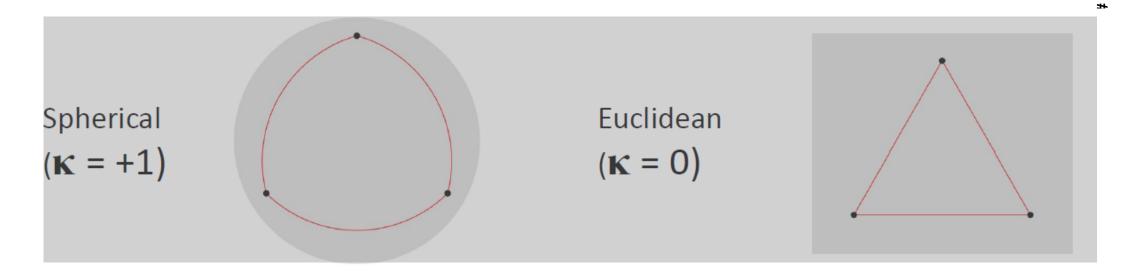


Euclidean

$$(\mathbf{K} = 0)$$



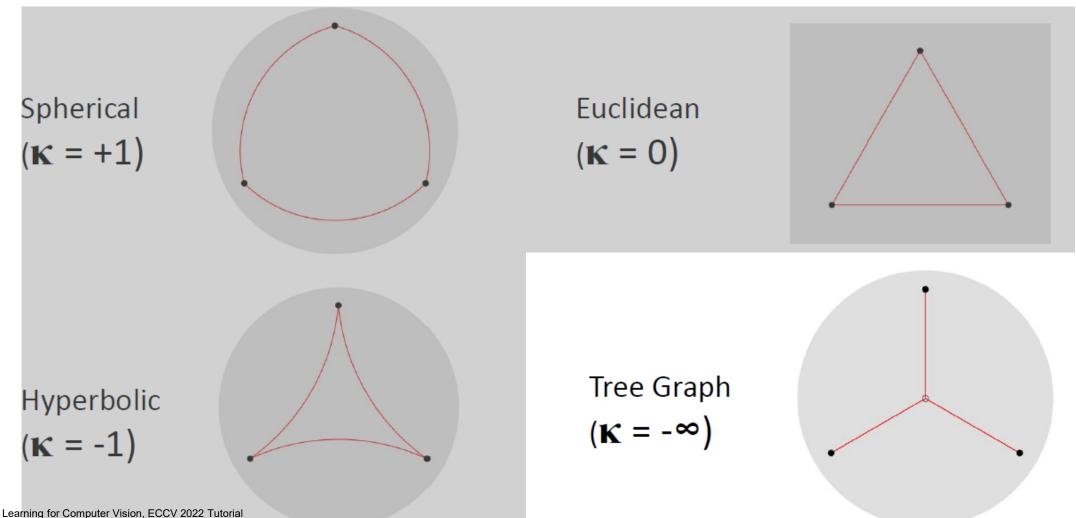




Hyperbolic (K = -1)



Hyperbolic Representation Learning for Computer Vision, ECCV 2022 Tutorial



SDU &

Hyperbolic Representation Learning for Computer Vision, ECCV 2022 Tutorial

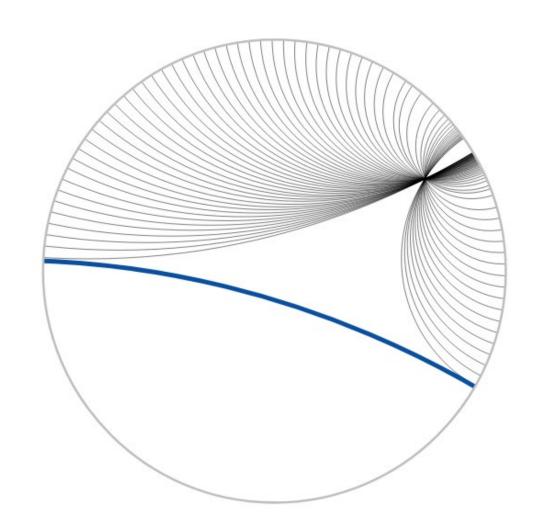


- → There are several options!
- → The two most commonly used are:



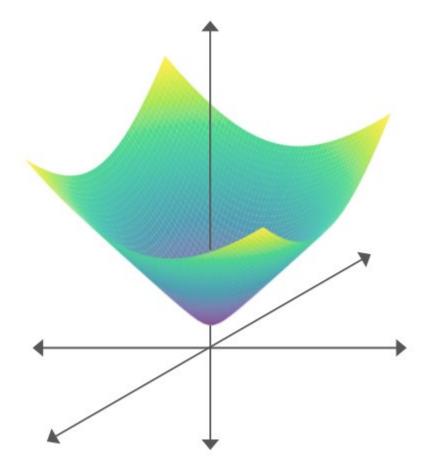
- → There are several options!
- → The two most commonly used are:
- → The Poincaré disk model
 - → Conformal to Euclidean space
 - → Restricted to a unit disc

$$\mathbb{D}_d = \{ p \in \mathbb{R}^d : p_1^2 + \dots + p_d^2 < 1 \}$$



- → There are several options!
- → The two most commonly used are:
- → The Poincaré disk model
- → The Hyperboloid / Lorentzian model
 - → Embeds a d-dimensional Euclidean space into a d+1 hyperbolic space

$$\mathbb{H}_d = \{ x \in \mathbb{R}^{d+1} : x_0^2 - (x_1^2 + \dots + x_d^2) = 1, x_0 > 0 \}$$





Distance: Measure how far two points and are from each other in hyperbolic space.



Distance: Measure how far two points and are from each other in hyperbolic space.

Poincaré

$$d_{\mathbb{D}}(p,q) = \frac{1}{\sqrt{\kappa}} \operatorname{arcosh} \left(1 + \frac{2|p-q|^2}{(1-|p|^2)(1-|q|^2)} \right)$$

Lorentz

$$d_{\mathbb{H}}(x,y) = \frac{1}{\sqrt{\kappa}} \operatorname{arcosh}(x \circ y)$$

$$x \circ y = x_0 y_0 - (x_1 y_1 + \dots + x_d y_d)$$

Distance: Measure how far two points and are from each other in hyperbolic space.

Geodesic arc: The shortest (=distance-minimizing) curve from *x* to *y*.

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This is done by mapping a tangent space vector, v, onto the manifold at point x, with unit speed.



Key concepts of Hyperbolic Geometry

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Poincaré

$$\exp_{x}^{\kappa}(v) = x \bigoplus_{\kappa} \left(\tanh(\frac{\sqrt{\kappa} ||v||}{1 - \kappa ||x||^{2}}) \frac{v}{\sqrt{\kappa} ||v||} \right)$$

Lorentz

$$\exp_{x}^{\kappa}(v) = \cosh\left(\sqrt{\kappa} ||v||_{L}\right) x + \frac{\sinh\left(\sqrt{\kappa} ||v||_{L}\right)}{\sqrt{\kappa} ||v||_{L}} v$$



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This is how you map from Euclidean spaces to Hyperbolic space!

Hyperbolic Representation Learning

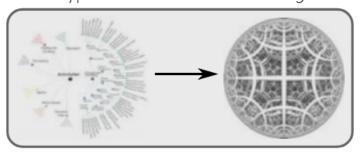


So what has been done?





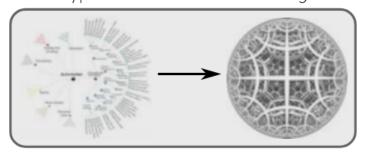
Hyperbolic action embedding



Action hierarchy

Discriminative hyperbolic embedding

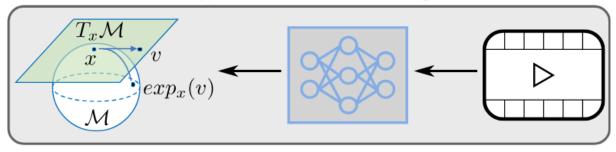
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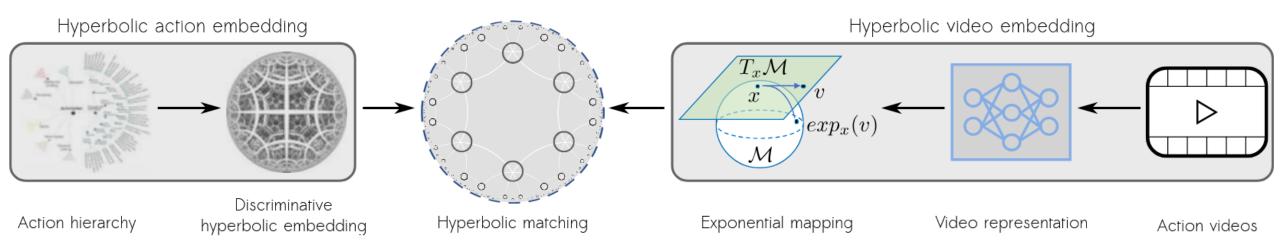
Hyperbolic video embedding



Exponential mapping

Video representation

Action videos

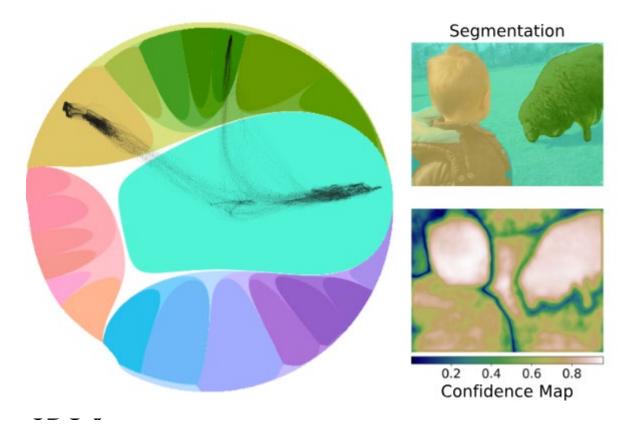




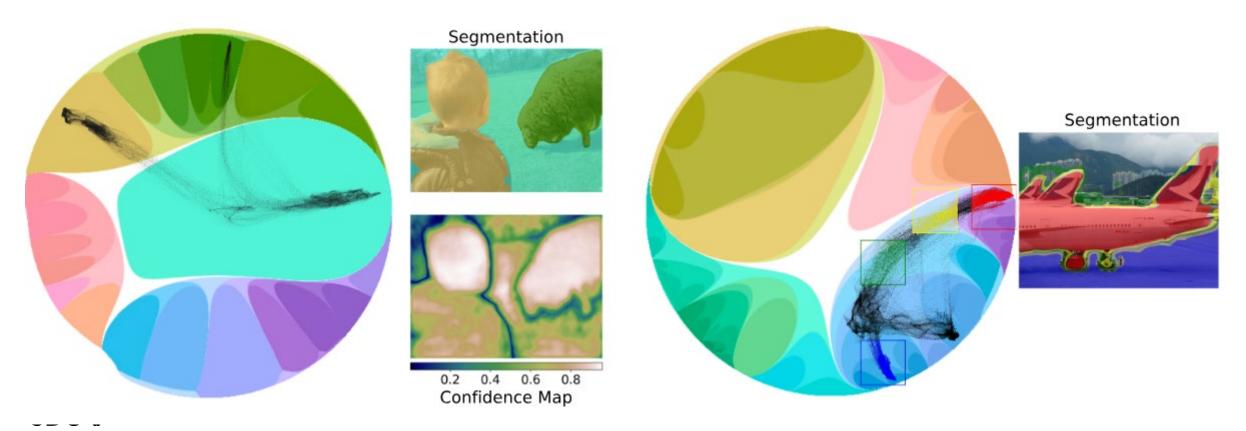
→ Key insight: The closer a Poincaré embedding norm is to 1, the more certain the prediction is



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Hyperbolic Image-Text Representations

Karan Desai ¹ Maximilian Nickel ² Tanmay Rajpurohit ³ Justin Johnson ¹² Ramakrishna Vedantam ⁴

Abstract

Visual and linguistic concepts naturally organize themselves in a hierarchy, where a textual concept "dog" entails all images that contain dogs. Despite being intuitive, current large-scale vision and language models such as CLIP (Radford et al., 2021) do not explicitly capture such hierarchy. We propose MERU, a contrastive model that yields hyperbolic representations of images and text. Hyperbolic spaces have suitable geometric properties to embed tree-like data, so MERU can better capture the underlying hierarchy in image-text datasets. Our results show that MERU learns a highly interpretable and structured representation space while being competitive with CLIP's performance on standard multi-modal tasks like image classification and image-text retrieval. Our code and models are available at: https://github. com/facebookresearch/meru

1. Introduction

Visual-semantic hierarchy. It is commonly said that 'an image is worth a thousand words'—consequently, images contain a lot more information than the sentences which typically describe them. For example, given the middle image in Figure 1 one might describe it as 'a cat and a dog playing in the street' or with a less specific sentence like 'exhausted doggo' or 'so cute <3'. These are not merely diverse descriptions but contain varying levels of detail about the underlying semantic contents of the image.

As humans, we can reason about the relative detail in each caption, and can organize such concepts into a meaningful visual-semantic hierarchy (Vendrov et al., 2016), namely, 'exhausted doggo'

'a cat and a dog playing in the street'

(Figure 1 middle image). Providing multimodal models access to this inductive bias about vision and language has the potential to improve generalization (Radford et al.,

Proceedings of the 40th International Conference on Machine Learning, Honolulu, Hawaii, USA. PMLR 202, 2023. Copyright 2023 by the author(s).

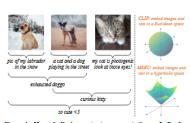


Figure 1. Hyperbolic image-text representations. Left: Images and text depict concepts and can be jointly viewed in a visual-semantic hierarchy, wherein text 'exhausted doggo' is more generic than an image (which might have more details like a cat or snow). Our method MERU embeds images and text in a hyperbolic space that is well-suited to embed tree-like data. Right: Representation manifolds of CLIP (hypersphere) and MERU (hyperboloid) illustrated in 3D. MERU assumes the origin to represent the most generic concept, and embeds text closer to the origin than images.

2021), interpretability (Selvaraju et al., 2017) and enable better exploratory data analysis of large-scale datasets (Radford et al., 2021; Schuhmann et al., 2022).

Vision-language representation learning. Approaches such as CLIP (Radford et al., 2021) and ALIGN (Jia et al., 2021) have catalyzed a lot of recent progress in computer vision by showing that Transformer-based (Vaswani et al., 2017) models trained using large amounts of image-text data from the internet can yield transferable representations, and such models can perform zero-shot recognition and retrieval using natural language queries. All these models represent images and text as vectors in a high-dimensional Euclidean, affine space and normalize the embeddings to unit L² norm. However, such a choice of geometry can find it hard to capture the visual-semantic hierarchy.

An affine Euclidean space treats all embedded points in the same manner, with the same distance metric being applied to all points (Murphy, 2013). Conceptually, this can cause issues when modeling hierarchies – a generic concept (closer to the root node of the hierarchy) is close to many other concepts compared to a specific concept (which is only close to its immediate neighbors). Thus, a Euclidean space can find it hard to pack all the images that say a generic

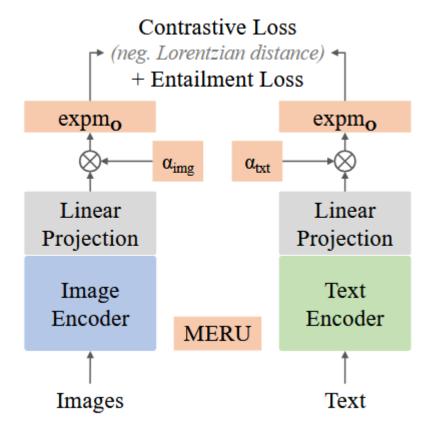


KD and Rama did this work while at Meta. ¹University of Michigan ²Meta Al ³Independent Researcher ⁴New York University. Correspondence to: Karan Desai <kdexd@umich.edu>.

- → Proposes a CLIP style setup in Hyperbolic space
- → Uses the Lorentzian space due to *numerical instabilities* in Poincaré space

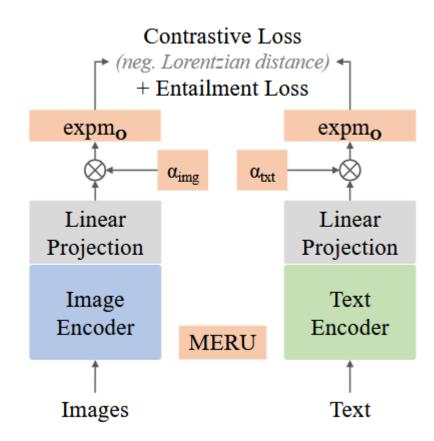


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- → Proposes a CLIP style setup in Hyperbolic space
- → Uses the Lorentzian space due to *numerical instabilities* in Poincaré space
- → Two losses: Contrastive and Entailment loss

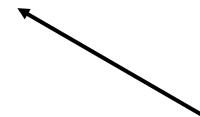




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- \rightarrow Lorentzian inner product: $\langle x,y\rangle_L=x\circ y=x_0y_0-(x_1y_1+\cdots+x_dy_d)$
- → Lorentzian distance: $d_L(x,y) = \sqrt{\frac{1}{c}} \cosh^{-1}(c \langle x,y \rangle_L)$

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Minimize distance for positive pairs Maximize distance for negative pairs

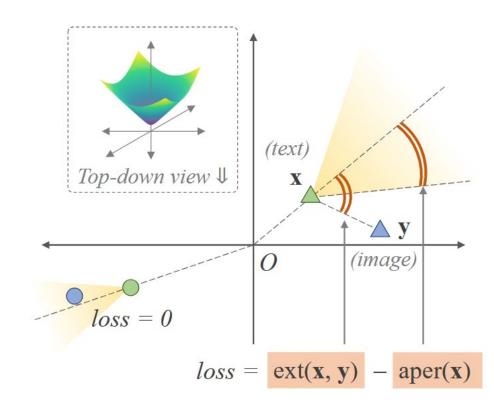
→ Key concept: Fine-grained concepts should be embedded *deeper* into the space



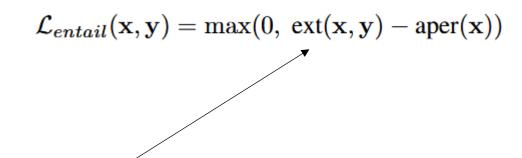
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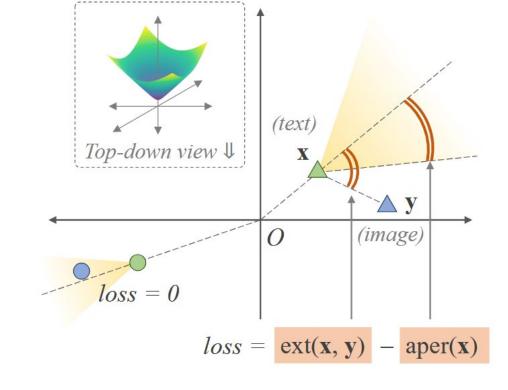
$$\mathcal{L}_{entail}(\mathbf{x}, \mathbf{y}) = \max(0, \operatorname{ext}(\mathbf{x}, \mathbf{y}) - \operatorname{aper}(\mathbf{x}))$$



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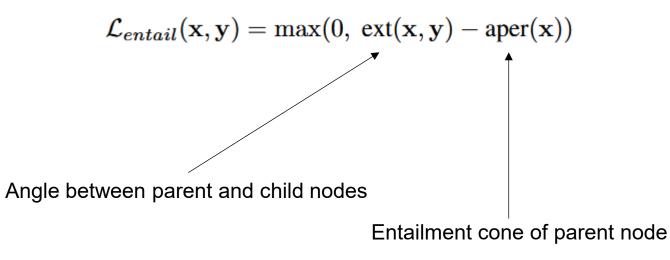


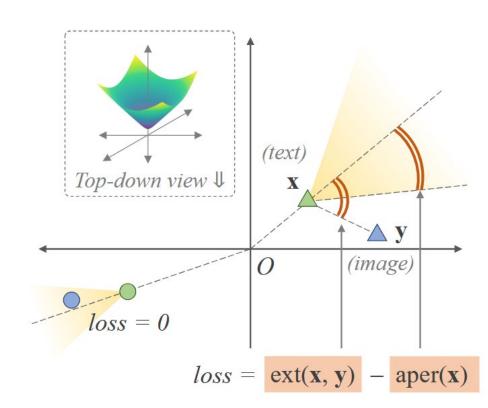
Angle between parent and child nodes





- → Key concept: Fine-grained concepts should be embedded *deeper* into the space
- → Enforced by making sure the fine-grained concept is within the *entailment cone* of a parent concept









MERU	CLIP
brooklyn bridge	
	brooklyn bridge,
	new york
new york city	new york city
city	new york
outdoors	↓
day	↓
[ROOT]	[ROOT]



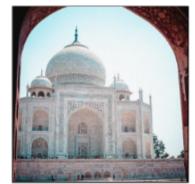
MERU	CLIP
brooklyn bridge	
	brooklyn bridge,
	new york
new york city	new york city
city	new york
outdoors	↓
day	↓
[ROOT]	[ROOT]



MERU	CLIP
taj mahal	taj mahal
	through an arch
monument	travel
architecture	inspiration
travel	↓
day	
[ROOT]	[ROOT]



MERU	CLIP
brooklyn bridge	photo of
	brooklyn bridge,
	new york
new york city	new york city
city	new york
outdoors	↓
day	1
[ROOT]	[ROOT]



MERU	CLIP
taj mahal	taj mahal
	through an arch
monument	travel
architecture	inspiration
travel	↓
day	
[ROOT]	[ROOT]



MERU	CLIP
sydney opera	sydney opera
house	house
opera house	opera house
holiday	gift
day	beauty
[ROOT]	[ROOT]

Stacked Entailment Loss





- → Assume paired multi-modal data, with expert textual labels
- → The textual labels contains the full hierarchy!



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Diptera Psychodidae Psychoda Psychoda grisescens

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Diptera Psychodidae Psychoda Psychoda grisescens

Order Family Genus Species



Stacked Entailment Loss



Hyperbolic Multimodal Representation Learning for Biological Taxonomies

ZeMing Gong¹ Chuanqi Tang¹ Xiaoliang Huo¹ Nicholas Pellegrino²
Austin T. Wang¹ Graham W. Taylor^{3,4} Angel X. Chang^{1,5}
Scott C. Lowe^{3†} Joakim Bruslund Haurum^{6†}

Simon Fraser University¹ University of Waterloo² Vector Institute³
University of Guelph⁴ Alberta Machine Intelligence Institute (Amii)⁵ Aalborg University⁶
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Abstract

Taxonomic classification in biodiversity research involves organizing biological specimens into structured hierarchies based on evidence, which can come from multiple modalities such as images and genetic information. We investigated whether hyperbolic networks provide a better embedding space for such hierarchical models. Our method embeds multimodal inputs into a shared hyperbolic space using contrastive and novel entailment-based objectives. Experiments on the BIOSCAN-1M dataset show that hyperbolic embedding gs achieve competitive performance with Euclidean baselines, and outperforms all other models on unseen species classification using DNA barcodes. However, fine-grained classification and open-world generalization remain challenging. This framework offers a scalable and structure-aware foundation for biodiversity modelling, with potential applications to species discovery, ecological monitoring, and conservation efforts.

1. Introduction

Taxonomic classification is essential for monitoring and mitigating biodiversity loss, requiring accurate identification of specimens across diverse ecosystems. DNA barcodes [1, 7] provide a way to classify specimens to known taxa or identify them as novel to science, but classification to the species level remains challenging when barcodes are unavailable. To tackle this, Gong et al. [5] showed that using contrastive learning to align DNA barcode embeddings to image embeddings can improve classification at the species level even when only using images as input at inference.

However, a key limitation of CLIBD [5] and other recent biodiversity-focused multimodal methods [17] is that the methods do not utilize the known taxonomic hierarchy of the input data. To address this, we explore whether embeddings in hyperbolic space can better capture the hierar-

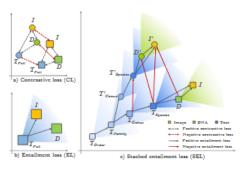


Figure 1. (a) Contrastive loss: instance-level alignment between modalities. (b) Entailment loss: enforces hierarchy within the text modality using entailment cones. (c) Stacked entailment loss: combines EL and cross-modal constraints by aligning image and DNA embeddings to multiple levels of the text hierarchy.

chical structure of taxonomic relationships, enabling better fine-grained classification. While training, the model takes inputs from multiple modalities—DNA barcodes, specimen images, and hierarchical taxonomic labels—and co-aligns their embeddings into a shared hyperbolic space to promote taxonomic alignment across modalities.

Our experimental results show that our hyperbolic multimodal learning framework achieves strong performance in taxonomic classification and retrieval, especially at higher taxonomic ranks. The approach consistently matches or outperforms Euclidean baselines and better preserves the hierarchical relationships among modalities. However, all methods—including ours—face challenges in fine-grained species classification, particularly for previously unseen taxa. These results highlight both the potential of hyperbolic learning for hierarchical biological data, and the ongoing difficulty of open-world classification for biodiversity.

Stacked Entailment Loss

→ Core ideas:

- 1. Enforce entailment loss between consecutive taxonomic ranks
- 2. Also apply a negative entailment loss



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Abstract

Taxonomic classification in biodiversity research involves organizing biological specimens into structured hierarchies based on evidence, which can come from multiple modalities such as images and genetic information. We investigated whether hyperbolic networks provide a better embedding space for such hierarchical models. Our method embeds multimodal inputs into a shared hyperbolic space using contrastive and novel entailment-based objectives. Experiments on the BIOSCAN-IM dataset show that hyperbolic embedding gs achieve competitive performance with Euclidean baselines, and outperforms all other models on unseen species classification using DNA barcodes. However, fine-grained classification and open-world generalization remain challenging. This framework offers a scalable and structure-aware foundation for biodiversity modelling, with potential applications to species discovery, ecological monitoring, and conservation efforts.



Taxonomic classification is essential for monitoring and mitigating biodiversity loss, requiring accurate identification of specimens across diverse ecosystems. DNA barcodes [1, 7] provide a way to classify specimens to known taxa or identify them as novel to science, but classification to the species level remains challenging when barcodes are unavailable. To tackle this, Gong et al. [5] showed that using contrastive learning to align DNA barcode embeddings to image embeddings can improve classification at the species level even when only using images as input at inference.

However, a key limitation of CLIBD [5] and other recent biodiversity-focused multimodal methods [17] is that the methods do not utilize the known taxonomic hierarchy of the input data. To address this, we explore whether embeddings in hyperbolic space can better capture the hierar-

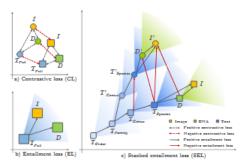


Figure 1. (a) Contrastive loss: instance-level alignment between modalities. (b) Entailment loss: enforces hierarchy within the text modality using entailment cones. (c) Stacked entailment loss: combines EL and cross-modal constraints by aligning image and DNA embeddings to multiple levels of the text hierarchy.

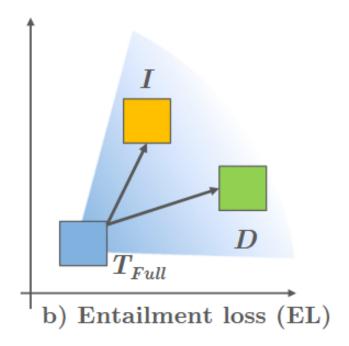
chical structure of taxonomic relationships, enabling better fine-grained classification. While training, the model takes inputs from multiple modalities—DNA barcodes, specimen images, and hierarchical taxonomic labels—and co-aligns their embeddings into a shared hyperbolic space to promote taxonomic alignment across modalities.

Our experimental results show that our hyperbolic multimodal learning framework achieves strong performance in taxonomic classification and retrieval, especially at higher taxonomic ranks. The approach consistently matches or outperforms Euclidean baselines and better preserves the hierarchical relationships among modalities. However, all methods—including ours—face challenges in fine-grained species classification, particularly for previously unseen taxa. These results highlight both the potential of hyperbolic learning for hierarchical biological data, and the ongoing difficulty of open-world classification for biodiversity.

Stacked Entailment Loss

→ Core ideas:

- 1. Enforce entailment loss between consecutive taxonomic ranks
- 2. Also apply a negative entailment loss

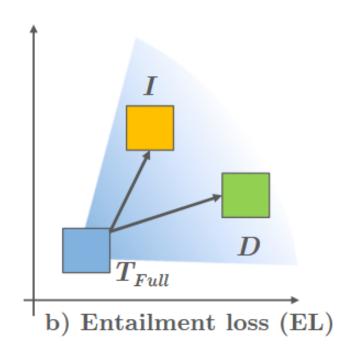


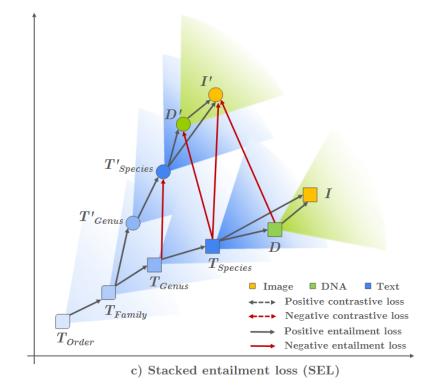


Stacked Entailment Loss

→ Core ideas:

- 1. Enforce entailment loss between consecutive taxonomic ranks
- 2. Also apply a negative entailment loss







Postive and Negative Entailment loss:

$$L_{\text{ent}}^+ = \frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} \max(0, \operatorname{ext}(x_i, y_j) - \operatorname{aper}(x_i))$$

$$L_{\text{ent}}^- = \frac{1}{|\mathcal{N}|} \sum_{(i,j)\in\mathcal{N}} \max(0, \operatorname{aper}(x_i) - \operatorname{ext}(x_i, y_j) + m)$$

Postive and Negative Entailment loss:

$$L_{\text{ent}}^+ = \frac{1}{|\mathcal{P}|} \sum_{(i,j)\in\mathcal{P}} \max(0, \operatorname{ext}(x_i, y_j) - \operatorname{aper}(x_i))$$
 $L_{\text{ent}}^- = \frac{1}{|\mathcal{N}|} \sum_{(i,j)\in\mathcal{N}} \max(0, \operatorname{aper}(x_i) - \operatorname{ext}(x_i, y_j) + m)$
 $L_{\text{ent}} = \frac{1}{2} \left(L_{\text{ent}}^+ + L_{\text{ent}}^- \right)$



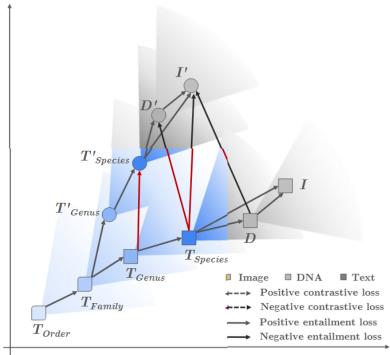
$$L_{\text{SEL-intra}} = \frac{1}{\sum_{r=2}^{R} \mathbb{1}_r} \sum_{r=2}^{R} \mathbb{1}_r \times L_{\text{ent}}(T_r, T_{r-1})$$

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Indicates whether the rank is annotated

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Indicates whether the rank is annotated



c) Stacked entailment loss (SEL)



$$L_{\text{SEL-intra}} = \frac{1}{\sum_{r=2}^{R} \mathbb{1}_r} \sum_{r=2}^{R} \mathbb{1}_r \times L_{\text{ent}}(T_r, T_{r-1})$$

$$L_{\text{SEL-inter}} = \frac{1}{3} \left(L_{\text{ent}}(I, T_{R'}) + L_{\text{ent}}(D, T_{R'}) + L_{\text{ent}}(I, D) \right)$$

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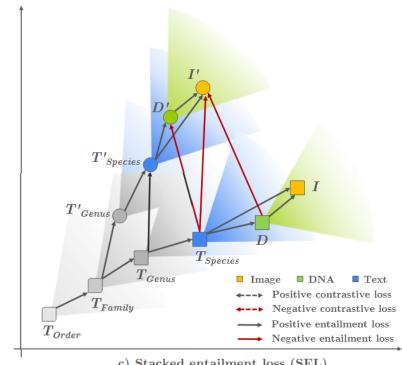
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Deepest annotated taxonomic rank

$$L_{\text{SEL-intra}} = \frac{1}{\sum_{r=2}^{R} \mathbb{1}_r} \sum_{r=2}^{R} \mathbb{1}_r \times L_{\text{ent}}(T_r, T_{r-1})$$

$$L_{\text{SEL-inter}} = \frac{1}{3} \left(L_{\text{ent}}(I, T_{R'}) + L_{\text{ent}}(D, T_{R'}) + L_{\text{ent}}(I, D) \right)$$

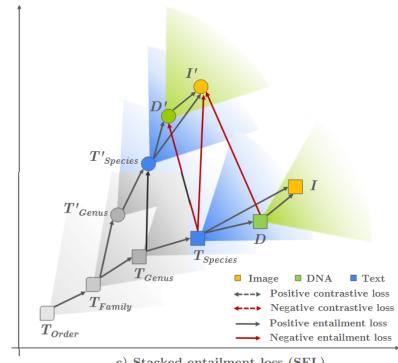
Deepest annotated taxonomic rank



$$L_{\text{SEL-intra}} = \frac{1}{\sum_{r=2}^{R} \mathbb{1}_r} \sum_{r=2}^{R} \mathbb{1}_r \times L_{\text{ent}}(T_r, T_{r-1})$$

$$L_{\text{SEL-inter}} = \frac{1}{3} \left(L_{\text{ent}}(I, T_{R'}) + L_{\text{ent}}(D, T_{R'}) + L_{\text{ent}}(I, D) \right)$$

$$L_{\rm SEL} = L_{\rm SEL-intra} + L_{\rm SEL-inter}$$



c) Stacked entailment loss (SEL)

Preliminary Results



BIOSCAN-1M Results



					DNA-to-DNA			Image-to-Image			Image-to-DNA		
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.
	CLIBD	_	✓	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9
	CL	_	✓	\mathbb{H}^n_L	89.1	85.6	87.3	98.5	61.2	75.5	89.1	47.8	62.2
0-1	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7
Order	SEL	Pos.+Neg.	X	\mathbb{H}_L^n	88.4	90.8	89.6	79.3	62.3	69.8	98.7	48.9	65.4
	SEL+CL	Pos.+Neg.	×	\mathbb{H}_L^n	88.7	86.3	87.5	<u>99.4</u>	65.9	79.3	78.6	48.2	59.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}_L^n	88.9	88.2	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3

					DNA-to-DNA			Ima	ge-to-Ima	age	Image-to-DNA		
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.
	CLIBD	_	√	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9
	CL	_	1	\mathbb{H}^n_L	89.1	85.6	87.3	98.5	61.2	75.5	89.1	47.8	62.2
Ondon	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7
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	SEL+CL	Pos.+Neg.	Х	\mathbb{H}_L^n	88.7	86.3	87.5	<u>99.4</u>	65.9	<u>79.3</u>	78.6	48.2	59.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	88.9	<u>88.2</u>	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3
	CLIBD	_	✓	\mathbb{R}^n	90.8	75.8	82.6	89.2	52.2	65.9	83.6	19.3	31.4
	CL	_	✓	\mathbb{H}^n_L	90.3	76.6	82.9	83.9	<u>48.5</u>	61.4	<u>79.6</u>	18.8	<u>30.4</u>
Esmile.	EL+CL	Pos.	✓	\mathbb{H}_L^n	89.3	74.9	81.4	81.9	37.6	51.5	76.7	16.8	27.6
Family	SEL	Pos.+Neg.	X	\mathbb{H}_L^n	86.8	78.8	82.6	79.0	41.8	54.7	78.9	18.4	29.9
	SEL+CL	Pos.+Neg.	Х	\mathbb{H}_L^n	89.0	76.9	82.5	79.6	46.6	58.8	78.7	17.3	28.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}_L^n	91.2	<u>77.0</u>	83.6	82.4	41.5	55.2	78.1	17.4	28.4



					DNA-to-DNA			Ima	ge-to-Ima	ige	Image-to-DNA		
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.
	CLIBD	_	✓	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9
	CL	_	✓	\mathbb{H}^n_L	89.1	85.6	87.3	98.5	61.2	75.5	89.1	47.8	62.2
Ondon	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7
Order	SEL	Pos.+Neg.	X	\mathbb{H}_L^n	88.4	90.8	89.6	79.3	62.3	69.8	98.7	48.9	65.4
	SEL+CL	Pos.+Neg.	Х	\mathbb{H}_L^n	88.7	86.3	87.5	<u>99.4</u>	65.9	<u>79.3</u>	78.6	48.2	59.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}_L^n	88.9	<u>88.2</u>	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3
	CLIBD	_	√	\mathbb{R}^n	90.8	75.8	82.6	89.2	52.2	65.9	83.6	19.3	31.4
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	SEL+CL	Pos.+Neg.	Х	\mathbb{H}_L^n	89.0	76.9	82.5	79.6	46.6	58.8	78.7	17.3	28.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}_L^n	91.2	<u>77.0</u>	83.6	82.4	41.5	55.2	78.1	17.4	28.4
	CLIBD	_	✓	\mathbb{R}^n	85.2	64.3	73.3	71.3	35.0	47.0	70.8	7.1	12.9
	CL	_	✓	\mathbb{H}^n_L	86.4	64.9	74.1	65.6	32.4	43.4	66.9	6.5	11.8
	EL+CL	Pos.	/	\mathbb{H}_L^n	84.7	63.1	72.3	63.0	22.8	33.5	64.2	6.6	11.9
Genus	SEL	Pos.+Neg.	X	$\mathbb{H}_L^{\widetilde{n}}$	82.7	65.9	73.4	62.1	29.2	39.7	63.1	6.6	12.0
	SEL+CL	Pos.+Neg.	X	\mathbb{H}_L^n	83.6	66.9	74.3	63.3	33.1	43.5	67.6	6.4	11.7
	SEL+CL	Pos.+Neg.	1	\mathbb{H}_L^n	<u>85.8</u>	64.8	73.9	64.8	27.5	38.6	64.8	6.2	11.4



					DNA-to-DNA			Image-to-Image			Image-to-DNA		
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.
	CLIBD	_	✓	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9
	CL	_	✓	\mathbb{H}^n_L	89.1	85.6	87.3	98.5	61.2	75.5	89.1	47.8	62.2
Order	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7
Order	SEL	Pos.+Neg.	Х	$\mathbb{H}_L^{\widehat{n}}$	88.4	90.8	89.6	79.3	62.3	69.8	98.7	<u>48.9</u>	65.4
	SEL+CL	Pos.+Neg.	X	\mathbb{H}^n_L	88.7	86.3	87.5	<u>99.4</u>	<u>65.9</u>	<u>79.3</u>	78.6	48.2	59.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	88.9	<u>88.2</u>	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3
	CLIBD	_	✓	\mathbb{R}^n	90.8	75.8	82.6	89.2	52.2	65.9	83.6	19.3	31.4
	CL	_	✓	\mathbb{H}^n_L	90.3	76.6	<u>82.9</u>	<u>83.9</u>	<u>48.5</u>	<u>61.4</u>	<u>79.6</u>	18.8	<u>30.4</u>
Family	EL+CL	Pos.	✓	\mathbb{H}^n_L	89.3	74.9	81.4	81.9	37.6	51.5	76.7	16.8	27.6
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	SEL+CL	Pos.+Neg.	X	\mathbb{H}^n_L	89.0	76.9	82.5	79.6	46.6	58.8	78.7	17.3	28.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	91.2	<u>77.0</u>	83.6	82.4	41.5	55.2	78.1	17.4	28.4
	CLIBD	_	✓	\mathbb{R}^n	85.2	64.3	73.3	71.3	35.0	47.0	70.8	7.1	12.9
	CL	_	✓	\mathbb{H}^n_L	86.4	64.9	<u>74.1</u>	<u>65.6</u>	32.4	43.4	66.9	6.5	11.8
Genus	EL+CL	Pos.	✓	\mathbb{H}^n_L	84.7	63.1	72.3	63.0	22.8	33.5	64.2	<u>6.6</u>	11.9
Genus	SEL	Pos.+Neg.	Х	\mathbb{H}^n_L	82.7	<u>65.9</u>	73.4	62.1	29.2	39.7	63.1	<u>6.6</u>	12.0
	SEL+CL	Pos.+Neg.	Х	\mathbb{H}^n_L	83.6	66.9	74.3	63.3	<u>33.1</u>	<u>43.5</u>	<u>67.6</u>	6.4	11.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>85.8</u>	64.8	73.9	64.8	27.5	38.6	64.8	6.2	11.4
	CLIBD	_	✓	\mathbb{R}^n	81.8	60.6	69.7	55.1	24.3	33.7	55.8	0.7	1.4
	CL	_	✓	\mathbb{H}^n_L	84.4	61.8	71.4	<u>48.2</u>	22.6	<u>30.8</u>	53.7	0.9	1.7
Species	EL+CL	Pos.	✓	\mathbb{H}^n_L	82.5	60.1	69.6	45.4	14.3	21.8	50.5	0.9	1.8
Species	SEL	Pos.+Neg.	X	\mathbb{H}^n_L	79.5	62.3	69.9	45.5	20.0	27.8	52.0	1.1	2.1
	SEL+CL	Pos.+Neg.	X	\mathbb{H}_L^n	80.5	63.2	<u>70.8</u>	46.8	<u>22.8</u>	30.7	<u>54.2</u>	0.7	1.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>82.6</u>	62.0	<u>70.8</u>	47.8	19.0	27.2	51.4	1.0	2.1



					DNA-to-DNA			Image-to-Image			Image-to-DNA		
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.
	CLIBD	_	✓	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9
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Onder	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7
Order	SEL	Pos.+Neg.	X	$\mathbb{H}_L^{\widetilde{n}}$	88.4	90.8	89.6	79.3	62.3	69.8	98.7	48.9	65.4
	SEL+CL	Pos.+Neg.	×	\mathbb{H}^n_L	88.7	86.3	87.5	99.4	<u>65.9</u>	<u>79.3</u>	78.6	48.2	59.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	88.9	<u>88.2</u>	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3
	CLIBD	_	✓	\mathbb{R}^n	90.8	75.8	82.6	89.2	52.2	65.9	83.6	19.3	31.4
	CL	_	✓	\mathbb{H}^n_L	90.3	76.6	<u>82.9</u>	83.9	<u>48.5</u>	<u>61.4</u>	<u>79.6</u>	18.8	30.4
Family	EL+CL	Pos.	✓	\mathbb{H}^n_L	89.3	74.9	81.4	81.9	37.6	51.5	76.7	16.8	27.6
raility	SEL	Pos.+Neg.	×	\mathbb{H}^n_L	86.8	78.8	82.6	79.0	41.8	54.7	78.9	18.4	29.9
	SEL+CL	Pos.+Neg.	×	\mathbb{H}^n_L	89.0	76.9	82.5	79.6	46.6	58.8	78.7	17.3	28.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	91.2	<u>77.0</u>	83.6	82.4	41.5	55.2	78.1	17.4	28.4
	CLIBD	_	✓	\mathbb{R}^n	85.2	64.3	73.3	71.3	35.0	47.0	70.8	7.1	12.9
	CL	_	✓	\mathbb{H}^n_L	86.4	64.9	<u>74.1</u>	<u>65.6</u>	32.4	43.4	66.9	6.5	11.8
Genus	EL+CL	Pos.	✓	\mathbb{H}^n_L	84.7	63.1	72.3	63.0	22.8	33.5	64.2	<u>6.6</u>	11.9
Ochus	SEL	Pos.+Neg.	×	\mathbb{H}^n_L	82.7	<u>65.9</u>	73.4	62.1	29.2	39.7	63.1	<u>6.6</u>	12.0
	SEL+CL	Pos.+Neg.	×	\mathbb{H}^n_L	83.6	66.9	74.3	63.3	<u>33.1</u>	<u>43.5</u>	<u>67.6</u>	6.4	11.7
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>85.8</u>	64.8	73.9	64.8	27.5	38.6	64.8	6.2	11.4
	CLIBD	_	✓	\mathbb{R}^n	81.8	60.6	69.7	55.1	24.3	33.7	55.8	0.7	1.4
	CL	_	✓	\mathbb{H}^n_L	84.4	61.8	71.4	48.2	22.6	30.8	53.7	0.9	1.7
Chagias	EL+CL	Pos.	✓	\mathbb{H}^n_L	82.5	60.1	69.6	45.4	14.3	21.8	50.5	0.9	1.8
Species	SEL	Pos.+Neg.	X	\mathbb{H}^n_L	79.5	62.3	69.9	45.5	20.0	27.8	52.0	1.1	2.1
	SEL+CL	Pos.+Neg.	X	\mathbb{H}^n_L	80.5	63.2	<u>70.8</u>	46.8	22.8	30.7	<u>54.2</u>	0.7	1.4
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>82.6</u>	62.0	<u>70.8</u>	47.8	19.0	27.2	51.4	<u>1.0</u>	2.1



					DNA-to-DNA			Ima	ige-to-Ima	age	Ima	ge-to-DN	NA				
Rank	Method	EL config.	Full Text	Space	Seen	Unseen	H.M.	Seen	Unseen	H.M.	Seen	Unseen	H.M.				
	CLIBD	_	✓	\mathbb{R}^n	89.1	87.8	88.4	99.5	66.4	79.6	98.7	49.5	65.9				
	CL	_	/	\mathbb{H}^n_L	89.1	85.6	87.3	98.5	61.2	75.5	89.1	47.8	62.2				
Ondon	EL+CL	Pos.	✓	\mathbb{H}_L^n	88.6	86.5	87.5	98.6	56.9	72.1	77.8	48.4	59.7				
Order	SEL	Pos.+Neg.	X	\mathbb{H}_L^n	88.4	90.8	89.6	79.3	62.3	69.8	98.7	48.9	65.4				
	SEL+CL	Pos.+Neg.	X	\mathbb{H}^n_L	88.7	86.3	87.5	99.4	<u>65.9</u>	<u>79.3</u>	78.6	48.2	59.7				
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	88.9	<u>88.2</u>	<u>88.5</u>	99.0	60.9	75.4	78.6	<u>48.9</u>	60.3				
	CLIBD	_	✓	\mathbb{R}^n	90.8	75.8	82.6	89.2	52.2	65.9	83.6	19.3	31.4				
	CL	_	✓	\mathbb{H}^n_L	90.3	76.6	<u>82.9</u>	83.9	<u>48.5</u>	<u>61.4</u>	<u>79.6</u>	18.8	<u>30.4</u>				
Family	EL+CL	Pos.	✓	\mathbb{H}^n_L	89.3	74.9	81.4	81.9	37.6	51.5	76.7	16.8	27.6				
railing	SEL	Pos.+Neg.	×	\mathbb{H}^n_L	86.8	78.8	82.6	79.0	41.8	54.7	78.9	18.4	29.9				
	SEL+CL	Pos.+Neg.	×	\mathbb{H}^n_L	89.0	76.9	82.5	79.6	46.6	58.8	78.7	17.3	28.4				
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	91.2	<u>77.0</u>	83.6	82.4	41.5	55.2	78.1	17.4	28.4				
	CLIBD	_	✓	\mathbb{R}^n	85.2	64.3	73.3	71.3	35.0	47.0	70.8	7.1	12.9				
	CL	_	✓	\mathbb{H}^n_L	86.4	64.9	<u>74.1</u>	<u>65.6</u>	32.4	43.4	66.9	6.5	11.8				
Genus	EL+CL	Pos.	✓	\mathbb{H}^n_L	84.7	63.1	72.3	63.0	22.8	33.5	64.2	<u>6.6</u>	11.9				
Ochus	SEL	Pos.+Neg.	×	\mathbb{H}^n_L	82.7	<u>65.9</u>	73.4	62.1	29.2	39.7	63.1	<u>6.6</u>	12.0				
	SEL+CL	Pos.+Neg.	×	\mathbb{H}^n_L	83.6	66.9	74.3	63.3	<u>33.1</u>	<u>43.5</u>	<u>67.6</u>	6.4	11.7				
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>85.8</u>	64.8	73.9	64.8	27.5	38.6	64.8	6.2	11.4				
	CLIBD	_	✓	\mathbb{R}^n	81.8	60.6	69.7	55.1	24.3	33.7	55.8	0.7	1.4				
	CL	_	✓	\mathbb{H}^n_L	84.4	61.8	71.4	48.2	22.6	<u>30.8</u>	53.7	0.9	1.7				
Cnaciae	EL+CL	Pos.	✓	\mathbb{H}^n_L	82.5	60.1	69.6	45.4	14.3	21.8	50.5	0.9	1.8				
Species	SEL	Pos.+Neg.	X	\mathbb{H}^n_L	79.5	62.3	69.9	45.5	20.0	27.8	52.0	1.1	2.1				
	SEL+CL	Pos.+Neg.	X	\mathbb{H}^n_L	80.5	63.2	<u>70.8</u>	46.8	22.8	30.7	<u>54.2</u>	0.7	1.4				
	SEL+CL	Pos.+Neg.	✓	\mathbb{H}^n_L	<u>82.6</u>	62.0	<u>70.8</u>	47.8	19.0	27.2	51.4	1.0	2.1				



BIOSCAN-1M Results Summary



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- → Across all ranks Hypebolic models match or outperform Euclidean CLIBD
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- → SEL methods consistently perform best at unseen DNA retrieval
- → But Euclidean CLIBD is better at image retrieval tasks
- → This is still ongoing research, so we hope to further improve results within the coming months

