# AI Models for Ultrasound Image Similarity Search: A Performance Evaluation

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Abstract: Querying similar images from a database to a reference image is an important task with multiple possible usecases in healthcare industry, including improving labelling processes, and enhancing diagnostic support to medical professionals. The aim of this work is to measure the performance of different artificial neural networks, comparing their ability to identify clinically relevant similar images based on their generated feature sets. To measure the clinical relevance, metrics using expert labels of organs and diagnoses on the images were calculated, and image similarity was further confirmed by pixel metrics. Images with organ and diagnosis labels were selected from a dataset of early-stage pregnancy and 2<sup>nd</sup> -3<sup>rd</sup> trimester pregnancy ultrasound images respectively for the measurements. The networks were chosen from state-of-the-art foundational models trained on natural images, DINO and DINOv2, SAM2, and DreamSim. The best performing model based on our experiments is DreamSim for organ matches, and DINO for diagnosis matches. A simple ResNet trained on the mentioned early pregnancy dataset for organ classification was also added to the selection. ResNet performs best for early pregnancy organ matches, therefore finetuning a robust encoder on our own dataset is a promising future step to further enhance medically relevant similar image search.

# 1 INTRODUCTION

Image similarity search is a method that is able to list the top N most similar images from a reference database to a query image. The image similarity search methods are widely applicable for different use-cases, for example, image acquisition support, diagnostic support applications, annotation tools (in medical device or during development to label dataset for AI training). These can benefit from presenting a clinically useful reference gallery of medical images to a given query image.

The currently most popular image similarity search methods require the image dataset to be converted into a feature space representation where a robust and fast search algorithm can be applied. This method is also called content-based image retrieval (CBIR), a popular area of research that focuses on developing methods for efficient retrieval processes in large image datasets. In CBIR systems, there are two phases, the offline and online phase. During the offline phase, features are being extracted from a set of reference images, stored as local features, and used to index the whole image database. During the online phase, the features for the query image are generated and compared with those in the database using a similarity- or distance metric. Images that have the lowest distances to the query image are considered as the results of the similarity search (Agrawal, 2022), (Qayyum, 2017).

CBIR systems for image similarity are currently based on CNN, ResNet or Vision Transformer (ViT) models. ViTs tend to be better encoders than ResNets for tasks, where the input data is not structured, or has a high variability in features. ResNets were designed for image recognition, which assumes that images have regularity and structure in their features while ViTs are more flexible, able to encode information from any type of data with less prior knowledge about its structure.

ResNet layers have a limited capacity to process large amounts of data, while ViTs can process longer sequences and higher data dimensionality by using their (self-) attention mechanisms. Self-attention mechanism in ViTs allows them to capture longrange dependencies, while CNNs only have local receptive fields, and they cannot learn long-distance relationships as adequately as ViTs (Vaswani, 2017).

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The ViTs are outstandingly effective for generating high-quality global descriptors, without requiring adjustments in the training data. The ViTmethod outperforms 36 existing state-of-the-art descriptors, which were previously achieved by CNN-based methods in image retrieval tasks. Furthermore, its low computational complexity makes it a promising candidate for replacing traditional and widely used CNN-based approaches in image retrieval techniques (Gkelios, 2021).

The second part of an image similarity task is the search in the extracted feature space of reference images. To be able to effectively and quickly search for similar images in a relatively large dataset size (from a few 1000 samples), structured search methods are recommended. The most popular ones are search trees and vector databases.

Vector databases provide efficient means for storing, retrieving, and managing the highdimensional vector representations in large language model (LLM) operations (Jing, 2024). However, for a smaller dataset, KD Tree search method is quicker to build and use.

Evaluating the similarity search algorithms can happen pixel-wise and using extra information (labels). Measuring how many matching labels (organs with planes, findings, diagnoses) are present compared to the query image can help getting information about how useful the similarity search is for diagnostic support or automatic, AI-based labelling.

Another, novel evaluation method for similarity techniques is DreamSim. The main issue with other popular perceptual similarity metrics is that they operate at the pixel or patch level, analyzing lowerlevel attributes (colours, textures) without considering mid-level similarities (image layout, object poses). DreamSim, a novel perceptual similarity metric fine-tuned to align with human perception can outperform the old metrics by emphasizing foreground objects and semantic content, but also counting with colour and layout (Fu, 2023). Due to its robustness in finding similarities on images, its ability to translate images into feature vectors can also be utilized.

State-of-the-art comparison articles for CBIR methods are available mainly from 1995-2015, evaluating handcrafted techniques (Madugunki, 2011), (Kokare, 2003), (Deselaers, 2008), or comparing text-based models (BERT, XLNet, RoBERTa) only (Yang, 2020). Evaluating CBIR techniques with and without deep learning can be found in (Ahmed, 2024), showing the advantages of using AI.

Based on the mentioned works, the encoders chosen for evaluation are recent state-of-the-art ViTs, DINO and DINOv2, SAM2, and DreamSim. A simple ResNet trained on our dataset for organ classification was also evaluated. The search algorithms used in the CBIR offline stage are KD Tree, Ball Tree and vector database.

The main goal of our experiments was to reach the best possible performance considering clinically relevant similar image search with as small network size and parameter number as possible, remaining fast and easy-to-use.

# 2 METHOD

Four recently published state-of-the-art encoders trained on various image datasets, and a ResNet trained specifically on early pregnancy ultrasound images were evaluated and compared in their abilities of extracting features for medically relevant similarity search on the pregnancy ultrasound database. The encoders chosen for evaluation are detailed below.

## 2.1 Image Encoders

## 2.1.1 DINO

DINO was chosen as the first available, wellperforming pretrained ViT model. From all possible DINO variations (see at Table 1.), ViT-S/8 was chosen with its 21M parameters. The model extracts feature vectors with length of 384. (Vaswani, 2017), (Caron, 2021).

Model	Params
ViT-S/16	21M
ViT-S/8	21M
ViT-B/16	85M
ViT-B/8	85M

#### Table 1: Pretrained DINO weights and parameter numbers.

### 2.1.2 **DINOv2**

DINOv2 is considered to be an improvement over DINO, offering better performance on downstream tasks. The difference between the two models is in their processing details. During training DINO uses cross-entropy loss with soft labels, while DINOv2 uses KL divergence to measure the similarity of two images. The cross-entropy loss in DINO is less efficient computationally and more sensitive to noise than the one used in DINOv2, but it can capture longrange dependencies between pixels better. On the other hand, DINOv2's KL divergence has a lower variance and works well with larger batch sizes. DINOv2 training process incorporates a multi-crop augmentation strategy to improve generalization performance, where multiple views of the same image are used in contrastive learning.

From the available DINOv2 variations, ViT-S/14 distilled was chosen (see at Table 2.), because of the smaller size but comparable performance with the first version of DINO. The model extracts feature vectors with length of 384 (Oquab, 2023), (Darcet, 2023).

Table 2: Pre-trained DINOv2 weights and parameter numbers.

Model	Params (M)		
ViT-S/14	21		
ViT-B/14	86		
ViT-L/14	300		
ViT-g/14	1,100		

### 2.1.3 SAM2

While DINO and DINOv2 were trained for general reconstruction tasks, SAM2 is a foundation model built for solving visual segmentation in images and videos, thus working with matrices instead of vector representations in its feature space. In order to get comparable results with DINO models, the extracted matrix had to be flattened and shortened with averaging. The final feature vector length is 256.

From the available pretrained SAM2 weights (Table 3.), the smallest available network was chosen, similarly to DINO and DINOv2 (Ravi, 2024).

Table 3: Pre-trained SAM2 weights and parameter numbers.

Model	Size (M)
sam2_hiera_tiny	38.9
sam2_hiera_small	46
sam2_hiera_base_plus	80.8
sam2_hiera_large	224.4

## 2.1.4 DreamSim

As mentioned in the introduction, DreamSim has outstanding capabilities measuring similarities among a set of images. Their model was trained by concatenating CLIP (Radford, 2021), Open CLIP (Cherti, 2023), and DINO (Vaswani, 2017) embeddings, and then finetuning it based on human perceptual judgements. This ensembled method outperformed the individual encoders in performance, therefore, its feature extraction abilities were exploited and used besides the final similarity evaluation scores it calculates (Fu, 2023).

The length of a feature vector generated with DreamSim is 1792.

#### 2.1.5 ResNet

A ResNet- based network was trained on the early pregnancy ultrasound images for organ classification. The image features extracted with its encoder are also added to the comparative evaluation, to check the possible effects of using the same ultrasound domain, compared to larger models trained on completely different datasets.

The parameter number of the ResNet trained on early pregnancy is around 1 000 000. The accuracy of the model measured on the same dataset using a completely separated test set (containing 600 images) is 84.81%.

The length of a feature vector generated with ResNet encoder is 256.

#### 2.2 Search Methods

To search among the generated feature vectors effectively, tree-based methods and vector database solutions were applied. The current dataset consists of 4800 early pregnancy and 3300 fetal labelled images, and for this scale KD Tree is the fastest and most efficient method. However, when the size of the labelled dataset scales up, vector database could outperform KD Tree.

#### 2.2.1 Vector Databases (Vector DB)

Vector databases are indexing- and retrieval systems designed for higher dimensional spaces. They use binary search trees for storing vectors in a compressed format allowing efficient querying. Unlike KD Tree or Ball Tree, Vector DB does not divide the dataset into smaller regions, it partitions the data points using a hierarchical clustering algorithm, then stores them as a tree of centroids. The search is performed by finding the closest centroid to the query point, then executing binary searches on its children.

The currently used Vector DB is a Pythonic vector database offering a comprehensive suite of create, read, update, and delete operations and robust scalability options, including sharding and replication. It's easy to deploy in a variety of environments, from local to cloud applications.

## 2.2.2 KD Tree

Tree-based search algorithms work by dividing the dataset into smaller parts, enabling faster access and retrieval of data features in a region of interest. The most common tree-based search algorithm is KD Tree. It divides the dataset along each dimension recursively until it reaches the leaf nodes that contain the data points. KD Tree spatial algorithm was used in our experiments from SciPy library in Python.

### 2.2.3 Ball Tree

Ball Tree is a tree structure designed for K-nearest neighbour search in low dimensional spaces (typically less than 10). It works by partitioning the dataset into hyperspheres of equal size and radius. Each of these balls contain several data points, with the center being the midpoint of the given ball. The algorithm builds a set of overlapping balls, so ball is as large as possible while containing all the nearest neighbours to any point within it. Ball Tree was implemented using scikit- learn Python library.

## 2.3 Experiments and Results

NVIDIA Quadro RTX 5000 was used for the experiments. Generating feature vectors for 10000 images took below 70 minutes in all cases and took around 20 minutes with feature vector length under 400. Inference time of the search algorithms (including building the search structure and querying top 10 images) is below 0.5 seconds.

## 2.3.1 Dataset

Data collection was part of the SUOG research project, conducted by multiple hospitals in Europe. Images were de-identified and managed by Assistance Publique – Hôpitaux de Paris. The data was collected prospectively for SUOG and the image similarity search is a part of this project as well.

The dataset consists of 18000 early pregnancy images from which 4800 is labelled with organs (and planes: axial, coronal, sagittal) and diagnosis (including normal pregnancy), and the other had 130000 fetal images from which 3300 is labelled with organs (and planes) and diagnoses. In this work only the labelled part of the two datasets were used to measure clinical relevance of the methods.

#### 2.3.2 Search Algorithms

To choose between KD Tree, Ball Tree and Vector DB, experiments were made on different data sizes

(5000, 15000 images), comparing the time demand of building the structure and vector querying. For building the tree, the results can be seen in Table 4. For querying the dataset with a vector with length (L) of 10, 20 and 50 the times required are summarized in Table 5.

Table 4: Building times of each structure.

	Building time (s)				
Data size	KD Tree Ball Tree Vector DB				
5000	0.011	0.120	0.042		
15000	0.050	0.540	0.127		

Table 5: Querying times of KD Tree, Ball Tree and Vector DB (in sec).

	Data size	L=10	L=20	L=50
KD T	5000	0.005	0.005	0.004
KD Tree	15000	0.016	0.016	0.015
Doll Tree	5000	0.001	0.001	0.001
Ball Tree	15000	0.004	0.005	0.005
Vector DB	5000	0.015	0.007	0.007
	15000	0.043	0.019	0.019

Considering building times KD Tree performed the best. For querying in a tree Ball Tree seems the quickest by a factor of 2-3, but due to its slower building process, the final chosen algorithm for the dataset is KD Tree.

#### 2.3.3 Pixel Metrics

The main goal is to evaluate the similarity methods based on clinical relevance. To further support this we also compared different pixel-level metrics to assess their ability to distinguish semantically similar and different images. To have an idea of the network's performance on pixel-level similarity different metrics were evaluated and the most distinguishable, quickest, and simplest were selected.

For the pixel- metric evaluation 5-5 visually similar and not- similar images were chosen from our ultrasound dataset. Also 4 non-ultrasound, natural images were chosen to imitate out-of-scope scenarios. This can be seen on Figure 1. with the reference image on the top, the visually similar images from the same ultrasound dataset are in the second row, the visually not-similar images from the same ultrasound dataset are in the third row, and randomly chosen natural images are in the fourth row.

As the number of selected images is limited, if the pixel-metrics would be planned to use for evaluation besides additional confirmation, extended image sets with detailed pixel-metric statistics were needed.

The evaluation of histogram- based image similarity and MSE compared to DreamSim score can be seen in Table 6., 7. and 8. For histogram-based score the range is [0,1], where 1 means the exact same image. For the selected natural images (not similar to ultrasound) the value range is [0.2, 0.6], for ultrasound images it is [0.3, 0.8], for visually similar ultrasound images it is above 0.9. For MSE 0 means the exact same match. For natural images the value range is [5500, 17000], for ultrasound images it is [5000, 7500], for similar ultrasound images it is below 5500. For DreamSim [0,1] is the value range and 0 is the exact same match. For natural images the values are above 0.6, for ultrasound images the value range is [0.25, 0.4], for similar ultrasound images it is below 0.2. AI- based scores performed more robustly and consistently, separating different types of similarities better than pixel-based metrics.

Other traditional CBIR methods were also evaluated (SSIM, SIFT, RMSE, PSNR, UQI, MSSIM, ERGAS, SCC, SAM, VIF) but their results showed high overlaps between similar and not similar cases.

Table 6: Similarity scores of pixel-based metrics for the same reference image and for other natural images.

Metric	Same	Natural images			
Hist. based	1	0.41	0.29	0.68	0.67
MSE	0	16748	10517	7405	5698
DreamSim	0	0.69	0.81	0.8	0.76

Table 7: Similarity scores of pixel-based metrics for notsimilar images from same database.

Metric	Not similar images from same database				
Hist. based	0.59	0.79	0.73	0.38	0.65
MSE	5097	5898	6190	6452	7106
DreamSim	0.32	0.28	0.36	0.35	0.3

Table 8: Similarity scores of pixel-based metrics for similar images from same database.

Metric	Similar images from same database				
Hist. based	0.95	0.95	0.99	0.98	0.87
MSE	1808	3653	4281	5492	4055
DreamSim	0.04	0.07	0.11	0.13	0.16

## 2.3.4 Image Similarity Search

To evaluate the similarity search methods, a random selection of 10 images were chosen from SUOG dataset for comparison. Since the fetal image dataset has significantly more possible organ and diagnosis labels, it was chosen to present the results in detail. The same measurements were done also on the early pregnancy dataset.



Figure 1: Test images for pixel-based similarity metrics.



Figure 2: Image of sagittal cervical fetal spine, in fetal spine group.

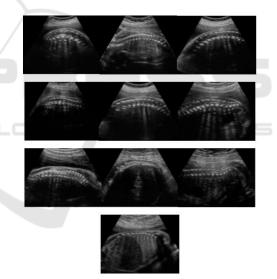


Figure 3: 10 Most similar images for reference image in Figure 2., 8 out of 10 belongs to fetal spine group.

## 2.3.5 Results on Fetal Dataset

To compare the methods, as a first step the top 10 retrieved similar image results were evaluated iterating through all images in our dataset. We measure the relevance of the retrieved similar images by checking how many organ, diagnosis and finding labels match with the original (reference) image. For example, for a reference image labelled as 'sagittal cervical fetal spine' (presented in Figure 2.), the most similar 10 images (based on DreamSim features and

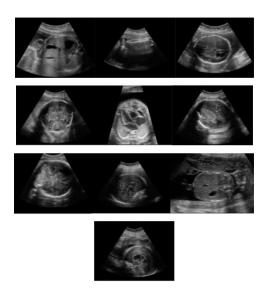


Figure 4: 10 Randomly selected images from the database for comparison to the top 10 images retrieved with similarity search, 0 out of 10 belongs to fetal spine group.

KD Tree search) can be seen on Figure 3., and a random selection of 10 images can be seen on Figure 4. Evaluating the organ labels of the images in both selection of images (Figure 2., 3. and 4.) the superiority of similarity sampling is visible. In the similar selection 8 out of 10 images belongs to the same organ group as the query image (fetal spine), while in the random selection, no image belongs to the same organ group.

Apart from visual similarity, label matches have also been counted to measure clinical relevance of the retrieved similar images. Exact label matches and label group matches are measured separately for organs and for diagnoses. The groups were formed based on consultations with medical experts. Organ groups are created to fuse together organs that belongs together biologically (e.g. different parts of the spine – lumbar, cervical, thoracic), or are very close to each other in space, or are visually similar (left and right part of the same organ).

The following values were measured for the top 10 similar retrieved image for a reference image (note that '#' is used to abbreviate 'number count' in the following tables):

• The organs and organ group match counts in a reference image's top 10 similar image set, with each encoder's features. Table 9. shows an example, measured with DreamSim features.

•Diagnosis match counts in a reference image's top 10 similar image set, with each encoder's features. Table 10. shows an example, measured with DreamSim features.

• Histogram-based pixel similarity, MSE and DreamSim score for each of a reference image's top 10 similar image set, measured with each encoder's features. (Summarized results are presented later.)

• The summarized and averaged label match values for each organ and for each diagnosis, with the total number of labelled images marked for each organ or diagnosis class, and the expected values to get similar images calculated with random sampling for comparison. The summary tables have been generated for each encoder. Table 11., 12., 13., and 14. show an example of a subset of the measured label match values, with 6 organs presented (out of 102 available ones) for simpler visualization.

• The summarized label match values for each organ and diagnosis, calculated with weighted average (with the number of labelled images for each class) to have a final, single value for method comparison (see in Table 15- 17).

Table 9: Organ and organ group label match counts for a reference image's top 10 similar images (using DreamSim features and KD Tree search). Higher counts in the same organ class or organ group class are considered as better results. Reference organ label is 'sagittal cervical fetal spine' in 'fetal spine' group.

Organ	#	Group	#
Sagittal conus medullaris	3	Fetal spine	
Sagittal thoracic fetal spine	3	Fetal spine	8
Sagittal lumbar fetal spine	2	Fetal spine	
Axial middle cerebral artery	1	Fetal brain and skull	1
Sagittal right diaphragmatic dome	1	Fetal abdomen	1

For every labelled image in the dataset with every mentioned encoder (and KD Tree search), the top 10 similar images statistics are calculated to measure organ, organ group, diagnosis, and diagnosis label matches. Not found labels (that are being present in the reference image but not on any of the top 10 similar ones), and extra organ classes/ diagnoses (that are not present among the reference image labels, but present on one or more of the retrieved top 10 similar ones) are also counted and stored. Table 10: Diagnosis label match counts for a reference image's top 10 similar image set (using DreamSim features).

Reference diagnoses:
Left congenital diaphragmatic hernia
# common diagnoses (reference- top 10 similar):
0
# not found diagnoses (at all on top 10 similar):
1
# extra diagnoses (besides reference diagnose(s)):
8

The statistics from Table 9. and 10 are further summarized for image examples belonging to the same organ class and diagnosis, organ group and diagnosis group. As a final step, label match statistics are weighted averaged together based on the amount of image examples belonging to each organ class.

	Image count	Expected number of images with the same organ label in 10 images with random sampling (mean)	Number of images with the same organ label in top 10 images, with similarity search (mean)
Cerebral posterior fossa mid sagittal	24	0.11	0.38
Longitudinal cervix	3	0.01	0.33
Trans-cerebellar axial oblique	74	0.32	3.45
Lateral ventricule para sagittal	29	0.13	2.86
Sylvian fissure para sagittal	15	0.07	1.60
Sagittal cervical fetal spine	20	0.09	1.45

Table 11: Label match statistics for organ classes.

In Table 11. statistics are summarized from single images' top 10 statistics belonging to the same organ class. The 'image count' column is the number of image examples belonging to the given organ class. The next column is the expected label match count with random sampling (the image count in an organ class divided by all labelled images). The last column presents the label match count with similarity search (using DreamSim). The third row in Table 11. shows that with randomly sampling 10 images, we get 0.32 image examples with the same label in average, and querying top 10 similar images, we get 3.45 image examples with the same label (for an organ class having a total number of 74 image examples. With less image examples in an organ class (total of 3 for example – like 'Longitudinal cervix') the expected number of images is 0.01 in average with random sampling, and 0.33 with image similarity. That means if we randomly select 10 images, we will have very little chance of seeing even one image example from the same organ class, with or without image similarity, so we need about 20-30 images minimum in the reference dataset (for every organ and diagnosis) to use our methods effectively.

Table 12: Label match statistics for organ groups.

Organ	Group	Expected # images with the same organ group label in 10 images with random sampling (mean)	<pre># images with the same organ group label in top 10 images, with similarity search (mean)</pre>
Cerebral posterior fossa mid sagittal	Fetal brain and skull	3.14	8.13
Longitudinal cervix			1.00
Trans- cerebellar axial oblique	Fetal brain and skull	3.14	8.68
Lateral ventricule para sagittal	Fetal brain and skull	3.14	9.17
Sylvian fissure para sagittal	Fetal brain and skull	3.14	7.73
Sagittal cervical fetal spine	Fetal spine	0.79	3.95

In Table 12. the calculation analogy is similar to Table 11. but the organ groups are summarized together instead of calculating with separate organ classes. For example, 'Cerebral posterior fossa mid sagittal', 'Trans-cerebellar axial oblique' and 'Lateral ventricule para sagittal' and 'Sylvian fissure para sagittal' belongs to the same, 'Fetal brain and skull' group, so all the image examples retrieved belonging to 'Fetal brain and skull' is being considered as a match, not just the exact same organ classes.

Organ	# Reference diagnoses (mean)	# Common diagnoses (mean)	# Not-found diagnoses (mean)	# Extra diagnoses (mean)
Cerebral posterior fossa mid sagittal	1.15	0.28	0.87	7.44
Longitudinal cervix	1.33	0.33	1.00	8.00
Trans-cerebellar axial oblique	1.16	0.25	0.90	8.13
Lateral ventricule para sagittal	1.17	0.31	0.86	7.58
Sylvian fissure para sagittal	1.00	0.20	0.80	7.47
Sagittal cervical fetal spine	1.05	0.50	0.55	7.40

Table 13: Diagnosis label match statistics. The values in the columns are averaged through all the single image statistics belonging to the given organ class.

Table 14: Pixel metric statistics. The pixel metric values in the columns are averaged through all the single image statistics belonging to the given organ class.

Organ	Hist. Sim. (mean)	MSE (mean)	DreamSim (mean)
Cerebral posterior fossa mid sagittal	0.9653	2171.54	0.89
Longitudinal cervix	0.9792	2787.11	0.80
Trans-cerebellar axial oblique	0.9674	2557.68	0.90
Lateral ventricule para sagittal	0.9872	1874.36	0.89
Sylvian fissure para sagittal	0.9881	1451.74	0.90
Sagittal cervical fetal spine	0.9592	1565.04	0.87

In Table 13. the number of diagnosis label match counts are summarized for images belonging to the given organ class (presented in rows). This means that separate similar image set statistics like the example in Table 10. (for top 10 retrieved similar images for a single reference image) have been averaged for all reference images in an organ class.

For example, in 'Cerebral posterior fossa mid sagittal' there are 1.15 diagnoses on the reference images in average, 0.28 common diagnoses in average (diagnosis of the reference image that is also found on at least one of the top 10 retrieved images), 0.87 diagnoses from reference images are not found in average, and there are 7.44 diagnoses being present on the similar images, but not on the reference image in average (extra diagnoses).

Table 14. shows pixel-level similarity metrics averaged out similarly as in Table 13.

Table 15: Final summary of image similarity search experiments. Weighted average of organ and organ group label match statistics. Expected value for random sampling and best performing model is highlighted for comparison.

Model	Average number of similar images in top 10 (With same organ label)	Average number of similar images in top 10 (With same organ group label)
Random	0.42	1.93
Sampling	0.12	1.50
DINO	2.14	5.88
DINOv2	2.10	5.69
ResNet	1.10	4.15
DreamSim	2.68	6.41
SAM2	1.18	4.42

In the final summary tables (Table 15., 16., 17.) statistics were counted for organ classes with sufficient amount of image examples (> 20-25). This currently means 30 organ classes from the available 102 ones, and similarly, 30 diagnose classes from the 67 available ones.

Table 15. presents the results with organ label match counts. With randomly sampling 10 images the expected organ label match count is 0.42 (most probably we will not see any image belonging to the same organ label), and with DreamSim and KD Tree search, the organ label match count goes up to 2.68 (we will probably see 2-3 images belonging to the same organ label). Because of the weighted average summary, this means that the organ classes with more image examples will perform even better, while organ classes with fewer image examples are expected to give less meaningful results. The next column shows the similar statistics calculated with organ groups.

Table 16. summarizes diagnosis and diagnosis group statistics. The best performing model on fetal dataset for single and grouped organs is DreamSim, for single and grouped diagnoses it is DINO.

For diagnoses and diagnosis groups the average label match increment is not significant. Based on consultation with medical experts the conclusion is that organs and planes do not correlate well with diagnoses from 2<sup>nd</sup> trimester of pregnancy, because from that point multiple organs must be checked thoroughly to set up a proper diagnosis. However, findings, organs and planes tend to correlate well in every stage of a pregnancy, and findings can help in setting up the diagnosis.

Averaged and summarized pixel-level similarity metrics tend to be quite close to each other for every encoder, but all of them performs better than random sampling, as Table 17. presents.

Table 16: Final summary of image similarity search experiments for diagnoses. Weighted average of diagnoses and diagnosis group label match statistics. Expected value for random sampling and best performing model is highlighted for comparison.

Model	Average number of similar images in top 10 (With same diagnosis label)	Average number of similar images in top 10 (With same diagnosis group label)	
Random Sampling	0.50	1.49	
DINO	0.75	2.29	
DINOv2	0.68	1.98	
ResNet	0.68	1.93	
DreamSim	0.74	2.12	
SAM2	0.64	2.03	

Table 17: Final summary of pixel metrics in image similarity search experiments. DreamSim encoder's DreamSim score is biased but marked for comparison (\*).

	Pixel sim.			
Model	Hist. Sim.	MSE	DreamSim Score	
<b>Random Sampling</b>	0.87	3246.89	0.75	
DINO	0.95	2325.61	0.87*	
DINOv2	0.94	2463.29	0.85	
ResNet	0.93	2437.70	0.82	
DreamSim	0.95	2247.93	0.88*	
SAM2	0.96	2262.52	0.84	

DreamSim scores are one of the best evaluation metrics for similarity search when labels are not available. As DreamSim encoder were used as an encoder as well, its own score is biased and expected to get higher scores than other encoders (as it contains DINO features, it was also marked as a biased result), however it still functions as a good comparison for the other encoders.

#### 2.3.6 Results on Early Pregnancy Dataset

We have performed the same analysis on our early pregnancy dataset, and in that case, finding label match statistics can also be measured (labelling the fetal dataset with findings is still in progress). Due to length constraints, only a brief summary of the final results is provided here.

For early pregnancy data, the performance of the models are very similar, but due to less variability of organs at early stages of the pregnancy, the increments tend to be less than on the fetal dataset.

Table	18:	Final	summary	of	image	similarity	search
experi	ment	s for o	rgans and o	rgai	1 groups	s.	

Model	Average number of similar images in top 10 (With same organ label)	Average number of similar images in top 10 (With same organ group label)
Random Sampling	0.88	3.12
DINO	3.00	7.08
DINOv2	2.81	6.68
ResNet	3.64	8.19
DreamSim	3.20	7.30
SAM2	2.61	6.12

Table 19: Final summary of image similarity search experiments for diagnoses and diagnosis groups.

Model	Average number of similar images in top 10 (With same diagnosis label)	Average number of similar images in top 10 (With same diagnosis group label)
Random Sampling	2.36	2.83
DINO	3.83	4.39
DINOv2	3.45	3.95
ResNet	3.23	3.84
DreamSim	3.76	4.27
SAM2	3.23	3.77

The best performing model on early pregnancy dataset for single and grouped organs is ResNet (which was trained on the very same dataset for organ classification), for single and grouped diagnoses it is DINO, and for findings it is DreamSim. The pixellevel metrics shows that comparing to random sampling, AI- based similarity search methods perform consistently better. These results are being presented in Table 18-21.

Table 20: Final summary of image similarity search experiments for findings.

Model	Average number of similar images in top 10 (With same finding label)
Random Sampling	1.24
DINO	3.43
DINOv2	3.18
ResNet	3.01
DreamSim	3.58
SAM2	2.75

Table 21: Final summary of pixel metrics in image similarity search experiments. DreamSim encoder's DreamSim score is biased but marked for comparison (\*).

	Pixel sim.			
Model	Hist. Sim. MSE DreamSim		DreamSim Score	
Random Sampling	0.57	6234.12	0.70	
DINO	0.92	3553.05	0.87*	
DINOv2	0.91	3777.70	0.86	
ResNet	0.90	3697.85	0.83	
DreamSim	0.93	3397.69	0.89*	
SAM2	0.93	3524.69	0.85	

## **3** CONCLUSIONS

In general, we proved that employing AI models for ultrasound similarity search resulted in reliable performance, offering several usage possibilities in medical applications.

In this image similarity task considering diagnosis label match statistics, DINO features performed best, and for organ label match statistics DreamSim encoder performed best for fetal dataset. Our ResNet was outstanding for early pregnancy organ label matches. One likely explanation for this is that the model's training task was to separate the organs in early pregnancy cases.

From this we can hypothesize that training an encoder model on the whole ultrasound dataset using general target (e.g. reconstruction) could enhance the similarity search performance. This can be realized by training a model from scratch, or finetune an already evaluated encoder model using specific techniques developed to tailor these models to custom datasets.

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