



Topics in Machine Learning Machine Learning for Healthcare

Rahul G. Krishnan Assistant Professor Computer science & Laboratory Medicine and Pathobiology

Outline

- Machine learning thus far
 - Supervised learning
 - Unsupervised learning
 - Semi-supervised learning
- Self-supervised learning
- Case study : Histopathology



• Given a dataset, the model parameters are learned via maximum likelihood estimation

$$\mathcal{L}(y,x) = \log p(y|x;\theta)$$
Score function (high is good, low is bad)

$$\theta = \arg \max_{\theta} \sum_{i=1}^{N} \mathcal{L}(y_i, x_i)$$
Solve this optimization problem to learn the model. Often formulated as a minimization of the negative of the log-likelihood function

Deep neural networks typically learned using tools that leverage automatic differentiation



Deep residual neural networks



Researchers found that deep networks had a hard time learning the identity function.

They added a skip-connections between layers:

$$h_k = \phi(\operatorname{conv}(h_{k-1})) + \sum_{j < k-1} h_{k-j}$$

Deep Residual Learning for Image Recognition, He et. al, 2015

Limitations of supervised learning

- Deep neural networks have proven very successful in learning useful representations of image data from large datasets
- Models like AlexNet, ResNet trained on imagenet capture features useful for multiple different tasks
- For a new task:
 - Need fine-grained labels associated with each example
 - Standard approach: Use a pre-trained imagenet model and fine-tune on new dataset
- Self-supervised learning:
 - What if we do not need labels to learn good representations?

Unsupervised learning



$$\mathcal{L}(x) = \log p(x;\theta)$$
Score function (high is good, low is bad)
$$\theta = \arg \max_{\theta} \sum_{i=1}^{N} \mathcal{L}(x)$$
Solve this optimization problem to learn
the model. Often formulated as a minimization
of the negative of the log-likelihood function



$$\theta = \arg \max_{\theta} \sum_{i=1}^{3} \mathcal{L}(x;\theta) + \mathcal{L}(y_1|x_1;\theta_2) + \mathcal{L}(y_3|x_3;\theta_2)$$

• Have a combination of labelled and un-labelled data in your dataset

Unsupervised and semi-supervised learning of high-dimensional images is hard

- Even if there is a small space of concepts unsupervised models of image data are challenging to build
- Need a good model of each pixel in the image.
- Recently there has been a lot of work in leveraging generative adversarial networks for this problem
- Idea: Can we build representations without labels and without modeling each pixel as a random variable?

Self-supervised learning

- Recent (last 4-5 years) development in machine learning
- **Principle**: Leverage domain knowledge about what kinds of information the representation should contain when building it
- Learn about self-supervised learning by examples

Notation

$$\mathcal{T}: x \to \tilde{x}$$

 \mathcal{O}

$$\sin(k,k')$$

- Feature function [Resnet]
- Transformation of an image [random crop, rotation, jittering, color normalization]
 - Preserves the identity of the image
- Similarity function
 - Measure of similarity of two vectors
 - Mean squared error, cosine similarity

SSL 1 - Learning with contrastive examples

- <u>A Simple Framework for Contrastive Learning of Visual</u> <u>Representations, Chen et. al, ICML 2020</u>
- Builds upon earlier work: Unsupervised Feature Extraction by Time-Contrastive Learning and Nonlinear ICA, Hyvarinen et. al

SIMCLR: Self-supervised learning with contrastive examples



Randomly sample a mini-batch of datapoints.

Minimize loss below

Goal: Learn representations that recognize that the class of transformations in T preserve identity.

Note: No labels used.

$$\ell_{i,j} = -\log \frac{\exp(\operatorname{sim}(\boldsymbol{z}_i, \boldsymbol{z}_j)/\tau)}{\sum_{k=1}^{2N} \mathbb{1}_{[k\neq i]} \exp(\operatorname{sim}(\boldsymbol{z}_i, \boldsymbol{z}_k)/\tau)}, \quad (1)$$

How good are the representations?

	Food	CIFAR10	CIFAR100	Birdsnap	SUN397	Cars	Aircraft	VOC2007	DTD	Pets	Caltech-101	Flowers
Linear evaluation:												
SimCLR (ours)	76.9	95.3	80.2	48.4	65.9	60.0	61.2	84.2	78.9	89.2	93.9	95.0
Supervised	75.2	95.7	81.2	56.4	64.9	68.8	63.8	83.8	78.7	92.3	94.1	94.2
Fine-tuned:												
SimCLR (ours)	89.4	98.6	89.0	78.2	68.1	92.1	87.0	86.6	77.8	92.1	94.1	97.6
Supervised	88.7	98.3	88.7	77.8	67.0	91.4	88.0	86.5	78.8	93.2	94.2	98.0
Random init	88.3	96.0	81.9	77.0	53.7	91.3	84.8	69.4	64.1	82.7	72.5	92.5

A Simple Framework for Contrastive Learning of Visual Representations

Table 8. Comparison of transfer learning performance of our self-supervised approach with supervised baselines across 12 natural image classification datasets, for ResNet-50 ($4\times$) models pretrained on ImageNet. Results not significantly worse than the best (p > 0.05, permutation test) are shown in bold. See Appendix B.8 for experimental details and results with standard ResNet-50.

SSL 1 - Learning without contrastive examples

- In the above examples, the quality of representations will depend on the choice of negative examples used.
- Can we learn without negative examples?
- <u>DINO: Emerging Properties in Self-Supervised Vision Transformers,</u> <u>Caron et. al, 2021</u>
 - Key idea: Instead of comparing the representations with respect to random negative examples, compare the representation to a different crop of itself

DINO



Case study : Deep learning for histopathological image data

- Research by Richard J. Chen
- 3rd year Ph.D. Candidate, Harvard University / BWH, Broad Institute

Histopathological images in the clinical workflow

- Histopathology: Microscopic examination of tissue to study diseases and their different presentations,
- Pipeline:
 - Surgery, biopsy or autopsy for excision of tissue
 - Placed in a fixative to stabilize tissue
 - Investigated under a microscope
- Histopathological images are routinely used for clinical diagnoses of cancer
 - Key question: How can we use machine learning to build representations of histopathological image data?

Slide-Level Supervised Learning (Weak Supervision)



Lipkova et al. 2021, In Review

Weakly-Supervised Learning: Finding Needles in Haystacks via Attention



Lu et al. 2021, Nature BME

Current Paradigm is limited by: Clinical Domain Knowledge

- Requires clinical domain knowledge to:
 - label image regions in WSIs with known morphological phenotypes (patch-level tasks)
 - 2. Make prognostic decisions from subjective interpretation of the entire WSI (slide-level tasks)
- How can we identify new phenotypic biomarkers?
- What are we missing in current decisionmaking that can guide prognosis?



Current Paradigm is limited by: Clinical Domain Knowledge



Current pipelines for creating representations of whole slide images make use of ResNet50 architectures pretrained on imagenet.





Lipkova et al. 2021, In Review, Ciga et. al

We build upon recent work [Resource and data efficient self supervised learning, Ciga et. al, 2021] who show that self-supervision yields general purpose representations of histopathological images

DINO-based Knowledge Distillation for Patch-based Representations

Loss Function: p1 log (p2)



Chen et al. 2021, In Preparation

DINO

- We wanted to study the use of non-contrastive self-supervised learning for creating representations
- Input:
 - Two crops with color contrasts from the same image
- Goal of self-supervised learning:
 - Teach the network that these two crops are from the same image
 - Output of student network is trained to match the distribution of teacher network via minimizing cross-entropy loss
 - Avoid network collapse by having two networks
 - Train the student via gradient descent
 - Teacher is **not trained**, weights are updated via exponential moving average from students
- Does not require negative samples
 - Data inductive biases in natural images may not hold in H&E pathology slides

DINO: Emerging properties in self-supervised vision transformers, Caron et. Al, 2021

DINO-based Knowledge Distillation for Patch-based Representations



H&E Image Patch X

Chen et al. 2021, In Preparation

DINO

- Output of student network is trained to match the distribution of teacher network via:
 - minimizing cross-entropy loss
 - EMA to update teacher network
- Does not require negative samples
 - Data inductive biases in natural images may not hold in H&E pathology slides
- Vision Transformer (ViT) used as encoder
 - 256 x 256 H&E tissue patches are further patched as 16 x 16 patch embeddings

Study Design



Results [1]: TCGA Lung Subtyping (LUAD vs. LUSC)

Lung Adenocarcinoma (LUAD)

Lung Squamous Cell Carcinoma (LUSC)



	Model Architecture	Training Source	Epochs	100%	75%	50%	25%
Method							
ImageNet Transfer	ResNet-50	ImageNet	100	0.945 ± 0.018	0.943 ± 0.019	0.917 ± 0.024	0.888 ± 0.031
SimCLR SimSiam DINO	ResNet-50 ResNet-50 ViT	Lung Only Lung Only Lung Only	100 100 100	$\begin{array}{c} 0.950 \pm 0.026 \\ 0.952 \pm 0.017 \\ 0.948 \pm 0.021 \end{array}$	$\begin{array}{c} 0.947 \pm 0.017 \\ 0.944 \pm 0.018 \\ 0.942 \pm 0.019 \end{array}$	$\begin{array}{c} 0.934 \pm 0.025 \\ 0.935 \pm 0.026 \\ 0.937 \pm 0.021 \end{array}$	$\begin{array}{c} 0.897 \pm 0.028 \\ 0.897 \pm 0.029 \\ 0.928 \pm 0.024 \end{array}$
SimCLR SimSiam DINO	ResNet-50 ResNet-50 ViT	Pan-Cancer Pan-Cancer Pan-Cancer	100 100 100	$\begin{array}{c} 0.951 \pm 0.016 \\ 0.493 \pm 0.085 \\ \textbf{0.957} \pm \textbf{0.019} \end{array}$	$\begin{array}{c} 0.948 \pm 0.017 \\ 0.534 \pm 0.072 \\ 0.949 \pm 0.019 \end{array}$	$\begin{array}{c} 0.930 \pm 0.023 \\ 0.508 \pm 0.085 \\ \textbf{0.941} \pm \textbf{0.022} \end{array}$	$\begin{array}{c} 0.898 \pm 0.026 \\ 0.603 \pm 0.040 \\ \textbf{0.931} \pm \textbf{0.024} \end{array}$

• Self-supervised feature extractors from DINO are more data-efficient than pretrained ResNet-50 on ImageNet for subtyping

Results [2]: TCGA Lung Subtyping (LUAD vs. LUSC) + Mutation Prediction (TP53 + KRAS)

Lung Adenocarcinoma (LUAD)

Lung Squamous Cell Carcinoma (LUSC)

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Method	Model Architecture	Training Source	Epochs	100%	75%	50%	25%	TP53	KRAS
ImageNet Transfer	ResNet-50	ImageNet	100	0.945 ± 0.018	0.943 ± 0.019	0.917 ± 0.024	0.888 ± 0.031	$\textbf{0.756} \pm \textbf{0.053}$	0.761 ± 0.073
SimCLR SimSiam DINO	ResNet-50 ResNet-50 ViT	Lung Only Lung Only Lung Only	100 100 100	$\begin{array}{c} 0.950 \pm 0.026 \\ 0.952 \pm 0.017 \\ 0.948 \pm 0.021 \end{array}$	$\begin{array}{c} 0.947 \pm 0.017 \\ 0.944 \pm 0.018 \\ 0.942 \pm 0.019 \end{array}$	$\begin{array}{c} 0.934 \pm 0.025 \\ 0.935 \pm 0.026 \\ 0.937 \pm 0.021 \end{array}$	$\begin{array}{c} 0.897 \pm 0.028 \\ 0.897 \pm 0.029 \\ 0.928 \pm 0.024 \end{array}$	$\begin{array}{c} 0.694 \pm 0.073 \\ 0.698 \pm 0.084 \\ 0.751 \pm 0.041 \end{array}$	$\begin{array}{c} 0.737 \pm 0.044 \\ 0.681 \pm 0.117 \\ \textbf{0.771} \pm \textbf{0.059} \end{array}$
SimCLR SimSiam DINO	ResNet-50 ResNet-50 ViT	Pan-Cancer Pan-Cancer Pan-Cancer	100 100 100	$\begin{array}{c} 0.951 \pm 0.016 \\ 0.493 \pm 0.085 \\ \textbf{0.957} \pm \textbf{0.019} \end{array}$	$\begin{array}{c} 0.948 \pm 0.017 \\ 0.534 \pm 0.072 \\ 0.949 \pm 0.019 \end{array}$	$\begin{array}{c} 0.930 \pm 0.023 \\ 0.508 \pm 0.085 \\ \textbf{0.941} \pm \textbf{0.022} \end{array}$	$\begin{array}{c} 0.898 \pm 0.026 \\ 0.603 \pm 0.040 \\ \textbf{0.931} \pm \textbf{0.024} \end{array}$	$\begin{array}{c} 0.687 \pm 0.100 \\ 0.516 \pm 0.073 \\ 0.746 \pm 0.051 \end{array}$	$\begin{array}{c} 0.711 \pm 0.127 \\ 0.612 \pm 0.051 \\ 0.740 \pm 0.052 \end{array}$

• Self-supervised feature extractors from DINO are more data-efficient than pretrained ResNet-50 on ImageNet for subtyping

• No difference found in gene mutation prediction

Results [3]: DINO Attentions to Cellular Identities



Questions?