## Generalized Multiple-Instance-Learning and its applications in biomedical imaging

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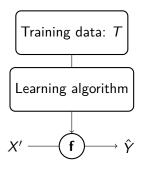




## Overview

- Standard MIL
  - formulation and algorithms
- Generalized MIL
  - formulation and algorithms
  - applications
- MIL in deep learning

## Supervised learning



Input Data

$$X = \{x_1, x_2, \dots, x_N\}, x_i \in \mathcal{X}$$
  

$$Y = \{y_1, y_2, \dots, y_N\}, y_i \in \mathcal{Y}$$
  

$$T = \{(x_i, y_i)\}$$
  

$$\mathcal{Y} = \{-1, +1\} \text{ (binary case)}$$

 $\begin{array}{l} \text{Classifier} \\ \mathbf{f}: \mathcal{X} \rightarrow \mathcal{Y} \end{array}$ 

• limited by (pixel-wise) label availability

#### Get more labels...

• hire a crowd, f.i. Google's re-CAPTCHA



C (i) (i) Report a problem





Verify

# 50 MUCH OF "AI" IS JUST FIGURING OUT WAYS TO OFFLOAD WORK ONTO RANDOM STRANGERS.

ANSWER QUICKLY-OUR SELF-DRIVING CAR IS ALMOST AT THE INTERSECTION.



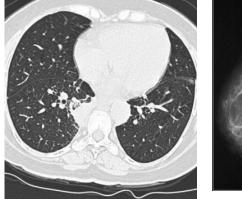


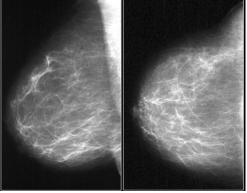
#### TO COMPLETE YOUR REGISTRATION, PLEASE TELL US WHETHER OR NOT THIS IMAGE CONTAINS A STOP SIGN:

## Get more labels...

#### CT Lung

#### Mammography





## Labels in BioMed

#### In clinical routine:

- labels available on patient-level
  - healthy/diseased
  - diagnostic staging
- detailed annotations time consuming
- requires a medical expert

#### **General applications:**

- molecule polymorphism (MUSK)<sup>1</sup>
- content-based image retrieval (semantic annotation)

#### $\rightarrow$ weakly-supervised learning

<sup>&</sup>lt;sup>1</sup>Dietterich et al.

## Definition

#### Standard Multiple-Instance Learning (MIL)

1

The building blocks are *bags*  $B_I$ ,  $I \in \mathcal{I}$ , each denotes a group of instances  $x_i$ , i.e.  $B_I = \{x_i, i \in I\} \subset \mathbb{R}^m$ . Furthermore, each bag is assigned a label  $y_I \in \{-1, +1\}$ . Instance labels  $y(x_i)$  are not given. A standard MIL problem is defined if it holds:

1) 
$$y_l = +1 \Leftrightarrow \exists x_i$$
, s.t.  $y(x_i) = +1$  (positive identifiability)

2  $y_l = -1 \Leftrightarrow \forall x_i \ y(x_i) = -1$  (negative exclusion)

## **MIL** Classification

For classification, we want either

• an instance classifier

$$f(X): \mathcal{X} \to \mathcal{Y}$$

• a bag classifier

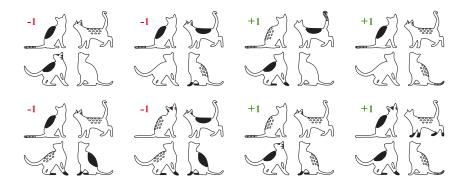
$$F(X^m): \mathcal{X}^m \to \mathcal{Y}$$

#### Note

Each instance classifier f(X) induces a bag classifier  $F(X^m)$  by

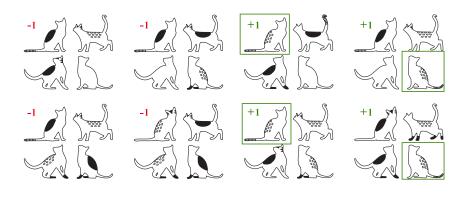
$$F(X^m) = \max\{f(x_1), ..., f(x_m)\},\$$

# MIL Example (1)



#### from Cheplygina, V: PhD Thesis

# MIL Example (2)



## MIL Approach Illustration

Support Vector Machine classifier:

$$\min \frac{1}{2} \|w\|_2^2 + C \sum_{ij} \xi_{ij}$$
  
s.t.  $y_{ij}(w \cdot x_{ij} + b) \ge 1 - \xi_{ij}$   
 $\xi_{ij} \ge 0$ 

Construction of a MIL classifier:

- MI-SVM (bag-level)
- mi-SVM, MI-RF: (instance-level)
- further approaches<sup>2</sup>

<sup>&</sup>lt;sup>2</sup>Carbonneau et al., J PatRec'2017, Review article

## SVM-based MIL algorithms

Solution through iterative heuristics:<sup>3</sup>

#### MI-SVM

- start with bag labels
- 2 while labels change:
  - select bag witness s(j)
  - train\_SVM( $X^- \cup \{s(j)\}$ )

#### mi-SVM

- $1 \quad \text{set } y(x_{ij}) = Y_i$
- 2 while labels change:
  - train\_SVM $(X^- \cup X^+)$
  - ensure MIL-conditions

<sup>&</sup>lt;sup>3</sup>Andrews et al.

## MIL Random Forests

- use deterministic annealing(DA) with random forests (RF)<sup>4</sup>
- DA-formulation of the loss function:

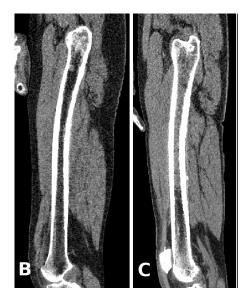
$$\mathcal{L}(\mathsf{F},\hat{p}) = \sum_{i,j}\sum_{k}\hat{p}(k|x_i^j)\ell(\mathsf{F}_k(x_i^j)) + T\sum_i \mathcal{H}(\hat{p}_i).$$

- **1** find minimal  $\hat{p}$  for fixed confidences  $F_k(x_i)$
- Pre-train the RF with sample distribution p̂ (ensure at least one positive instance in positive bags prior to training phase)

<sup>4</sup>Leistner et al., ECCV'2010

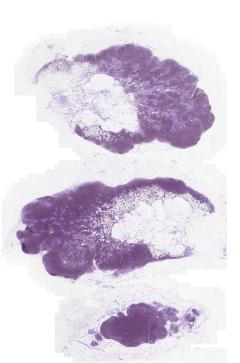
#### Example I

Detection of bone-marrow infiltrations in low-dose CT images of femurs. Scans of both femurs are provided, labels are available only at patient-level.



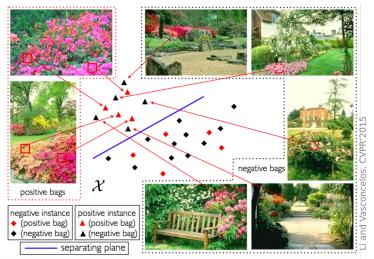
#### Example II

Detect tumorous histo-pathology sections. The tumor annotations may not be complete or may be missing completely (i.e. only image-level labels).



## Weak labels

#### Concept (flowers) present also in negative bags:



## Standard MIL

#### Weak points of standard MIL

- robustness impact of a single false detection
- weak labels other concepts present in the input image
- counting the number of positive instances is decisive ("traffic jam")

## Definition

#### Standard Multiple-Instance Learning (MIL)

The building blocks are *bags*  $B_I$ ,  $I \in \mathcal{I}$ , each denotes a group of instances  $x_i$ , i.e.  $B_I = \{x_i, i \in I\} \subset \mathbb{R}^m$ . Furthermore, each bag is assigned a label  $y_I \in \{-1, +1\}$ . Instance labels  $y(x_i)$  are not given. A standard MIL problem is defined if it holds:

1 
$$y_l = +1 \Leftrightarrow \sum_{i \in I} \llbracket y(x_i) > 0 \rrbracket \ge 1$$
 (positive identifiability)  
2  $y_l = -1 \Leftrightarrow \sum_{i \in I} \llbracket y(x_i) > 0 \rrbracket < 1$  (negative exclusion)

## Definition

#### Generalized Multiple-Instance Learning (gMIL)

The building blocks are bags  $B_I$ ,  $I \in \mathcal{I}$ , each denotes a group of instances  $x_i$ , i.e.  $B_I = \{x_i, i \in I\} \subset \mathbb{R}^m$ . Furthermore, each bag is assigned a label  $y_I \in \{-1, +1\}$ . Instance labels  $y(x_i)$  are not given. A bag is said to be  $\zeta$ -positive, if it holds

$$y_{l} = +1 \Leftrightarrow \sum_{i \in I} \llbracket y(x_{i}) > 0 \rrbracket \ge \zeta \text{ (positive identifiability)}$$

 $2 \ y_I = -1 \Leftrightarrow \sum_{i \in I} [ [y(x_i) > 0 ] ] < \zeta \text{ (negative exclusion)}$ 

# gMIL Algorithms

# **Common principle**: With an instance-classifier *C*

- While labels change
  - predict labels with C
     ensure at least k positive instance in each positive bag
  - 3 retrain C with current labels y(x<sub>ij</sub>)

#### **First approach:** introduce a (hyper-)parameter k

**Q**: How to **learn** the threshold k (resp.  $\zeta$ ).

- *k*-mi-SVM
- k-MI-SVM
  - *k*-top-MI-SVM<sup>5</sup>
- *k*-MIL-RF

<sup>&</sup>lt;sup>5</sup>Li and Vasconcelos, CVPR'2015

# gMIL Algorithms (cont'd)

While labels change:

- 1 predict labels with C
- **2**  $\hat{k} \leftarrow \text{get}_k \text{hat}(X^-, X^+)$
- **3** ensure **at least**  $\hat{k}$  positive instance in each positive bag
- **4** retrain C with current labels  $y(x_{ij})$

get\_k\_hat

estimate count pos. instances in pos. and neg. bags,  $\hat{k}$  their average optimize take  $\hat{k}$  that minimizes bag-level classification error

## Experiments

Applied to detection of multiple myeloma infiltrations (Example I)  $^{6}$ .

#### Classification features

Split femur into segments  $I, t, \phi$  and compute intensity-based features. Each instance is then  $\mathbf{x}_i = [I, t, \phi, \mu, \sigma, h_1, \dots, h_{N_h}]$ .

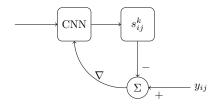
	k	mi-SVM <sup>8</sup>	$\mathrm{MI}\text{-}\mathrm{SVM}^8$	MIL-ARF <sup>9</sup>
AUC	$rac{1}{\zeta_{ m est}}$	$\begin{array}{c} 0.747 \pm 0.065 \\ 0.867 \pm 0.049^{\ddagger} \\ 0.823 \pm 0.066^{\ddagger} \end{array}$	$\begin{array}{c} 0.751 \pm 0.053 \\ 0.774 \pm 0.068^{\dagger} \\ 0.764 \pm 0.058 \end{array}$	$\begin{array}{c} 0.854 \pm 0.055 \\ 0.874 \pm 0.048^{\dagger} \\ \textbf{0.876} \pm \textbf{0.048}^{\ddagger} \end{array}$

(Convolutional) Neural Networks

## Weakly supervised networks

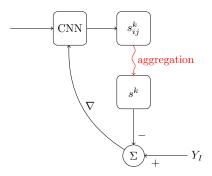
#### **CNN** backpropagation

feature map pixels:  $s_{i,i}^k$ 

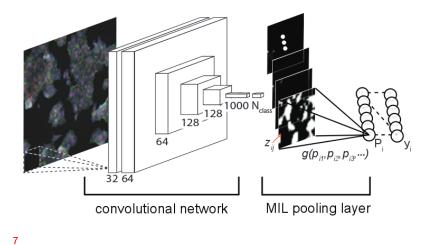


MIL-CNN

need to aggregate  $s_{i,i}^k$ 



## MIL-CNN



<sup>7</sup>Kraus et al., J BioInf 2016

## **MIL-CNN** Aggregation

• global sum

$$s^k = \sum_{i,j} s^k_{ij}$$

global max pooling<sup>8</sup>

$$s^k = \max_{i,j} s^k_{ij}$$

• LSE (log-sum-exp)<sup>9</sup>

$$s^{k} = \frac{1}{r} \log[\frac{1}{wh} \sum \exp(r \cdot s_{ij}^{k})]$$

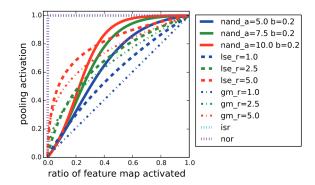
<sup>8</sup>Oquab et al., CVPR'2015 <sup>9</sup>Pinheiro et al., CVPR'2015

## **MIL-CNN** Aggregation II

• Noisy-AND<sup>10</sup>

$$s = \frac{\sigma(a(\bar{s_{ij}} - b_i)) - \sigma(-ab_i)}{\sigma(a(1 - b_i)) - \sigma(-ab_i)}$$

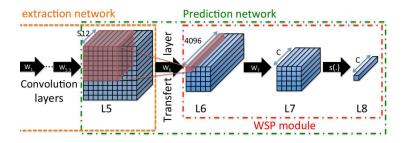
activation once the mean of the instance probabilities  $\bar{s_{ij}}$  surpasses a threshold.



<sup>10</sup>Kraus et al., J BioInf 2016

## gMIL-CNN Aggregation

**Two-stage network**: feature extraction + weakly-sup. module<sup>11</sup>



• select *top-k* and *m-low* instances

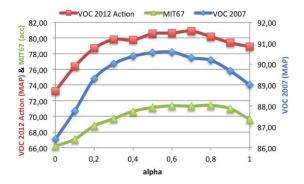
$$\mathbf{L8}(c) = s_{top} \left( \mathbf{L7}(c) \right) + s_{low} \left( \mathbf{L7}(c) \right) = \sum_{t_c^*=1}^{k} \mathbf{l}^{\mathbf{7}}_{t_c^*} + \sum_{l_c^*=1}^{m} \mathbf{l}^{\mathbf{7}}_{l_c^*}$$

<sup>11</sup>Durand et al., CVPR'2016

## gMIL-CNN Aggregation

• weight the contribution of *low* instances<sup>12</sup>

$$s^{c} = \max_{\mathbf{h} \in \mathcal{H}_{k^{+}}} \frac{1}{k^{+}} \sum_{i,j} h_{i,j} \bar{z}^{c}_{i,j} + \alpha \left( \min_{\mathbf{h} \in \mathcal{H}_{k^{-}}} \frac{1}{k^{-}} \sum_{i,j} h_{i,j} \bar{z}^{c}_{i,j} \right)$$



<sup>12</sup>Durand et al. CVPR'17

## Summary

- generalization approaches in both traditional and deep learners
- gMIL formulation better suited in multiple scenarios

#### gMIL - Addressed issues

- robustness impact of a single false detection
- weak labels multiple concepts are present
- counting the number of positive instances is decisive

## Thank you for your attention!

