

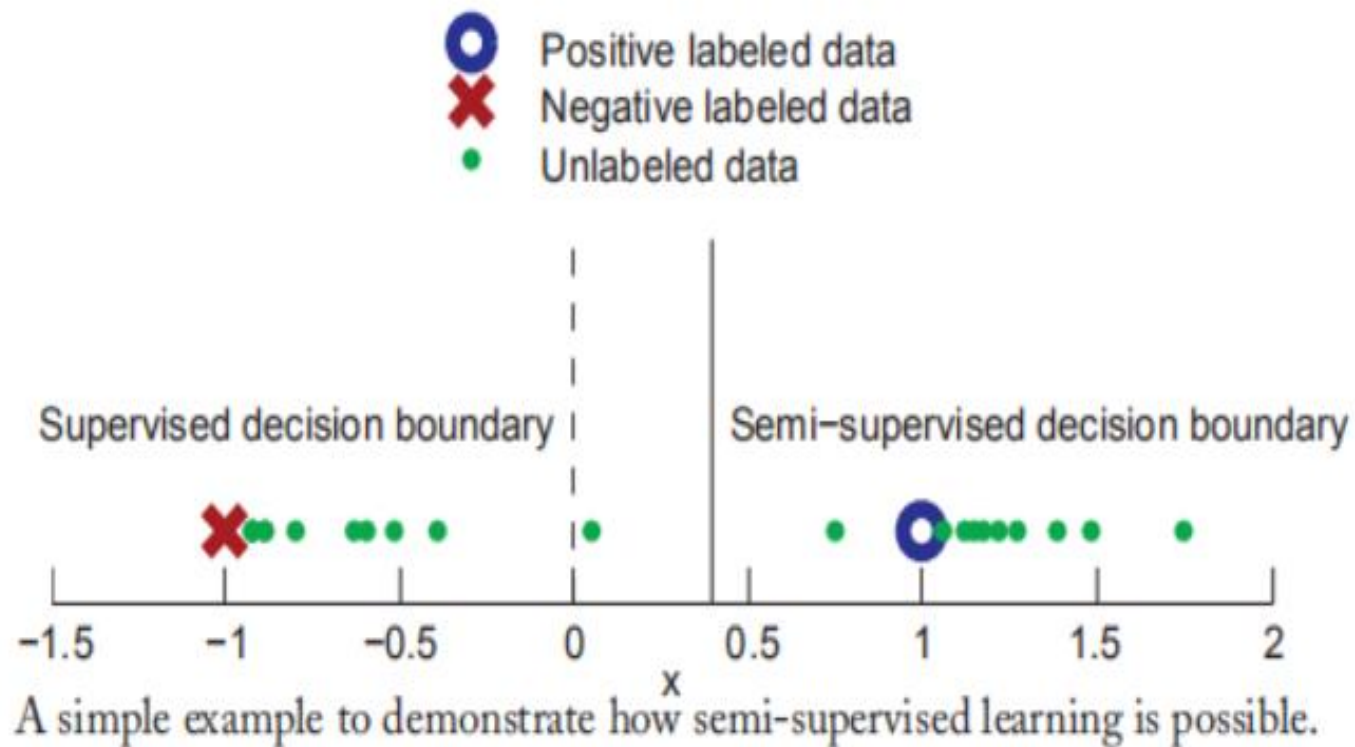


面向医疗图像的半监督学习

Semi-supervised learning based on medical images

半监督学习

将有标签数据与无标签数据混成成的训练数据，送入深度学习框架中进行学习的一种算法



半监督学习算法

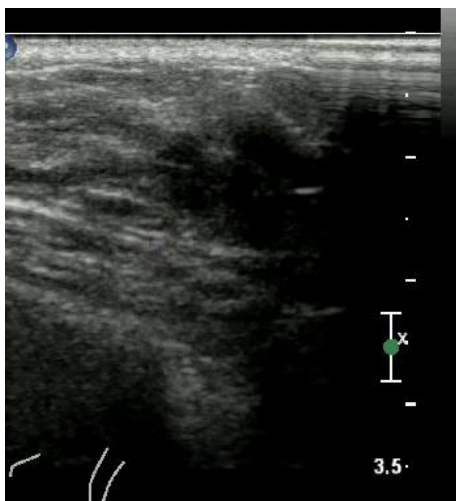
1. 无标签数据预训练，有标签数据微调

<https://blog.csdn.net/hjimce/article/details/49106869>

2. 利用从网络中得到的深度特征来做半监督算法

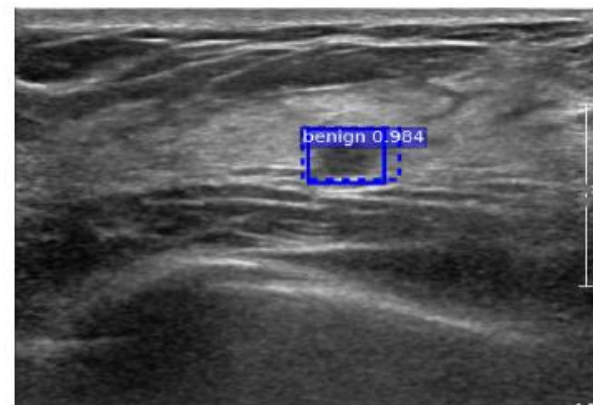
3. 让网络自身进行半监督学习

医学图像



1 / 数据稀少

医学图像属于个人隐私，
因此极少有公开的数据
集



2 / 标注困难

医学图像的标注需要一
个经验丰富的专家花费
较多时间去进行标注

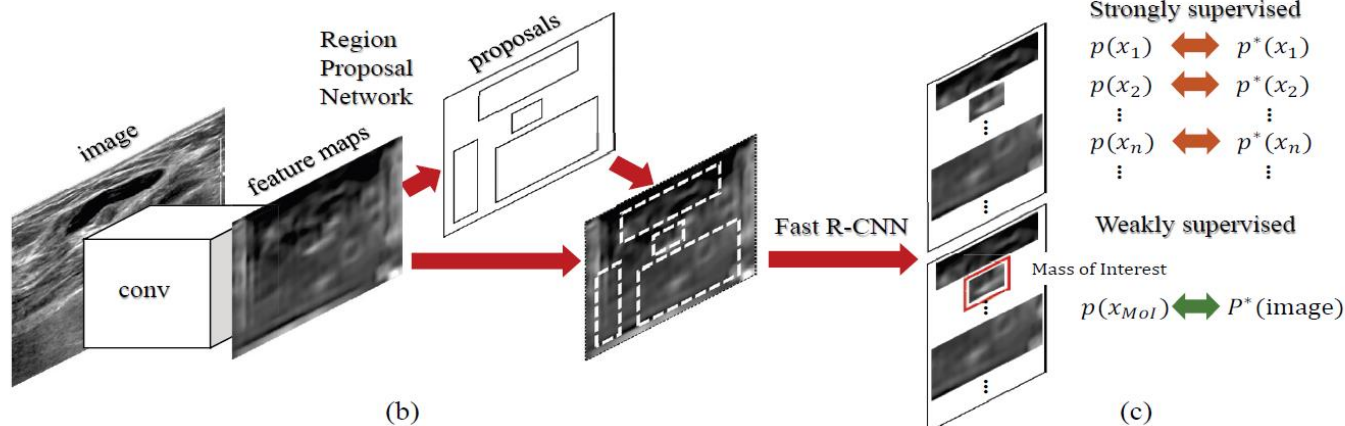
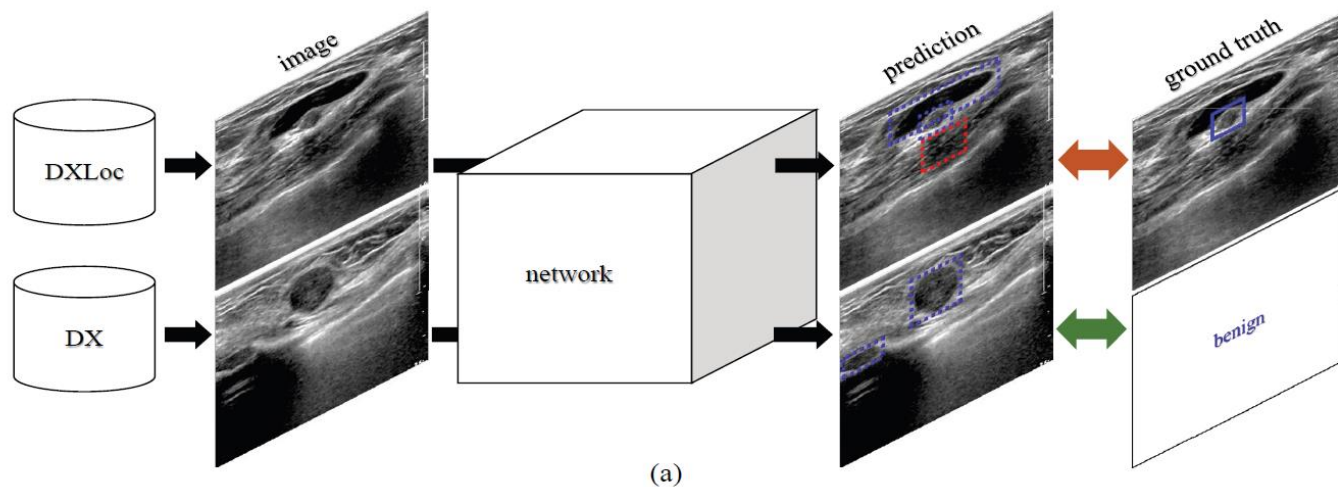
提出问题

1. 使用大量的无标签的数据集送入基于CNN的mass Detector会导致训练精度低，无法正确标记出病灶区
2. 使用少量的标注完善的数据集会造成过拟合问题



提出方法

强标注与弱标注混合训练效果更好



Strongly supervised
 $p(x_1) \leftrightarrow p^*(x_1)$
 $p(x_2) \leftrightarrow p^*(x_2)$
 \vdots
 $p(x_n) \leftrightarrow p^*(x_n)$
 \vdots

Weakly supervised

Mass of Interest
 $p(x_{Moi}) \leftrightarrow P^*(\text{image})$

DXLoc: 标注出病灶区域以及知道超声图像良恶性的数据

DX: 仅知道超声图像良恶性

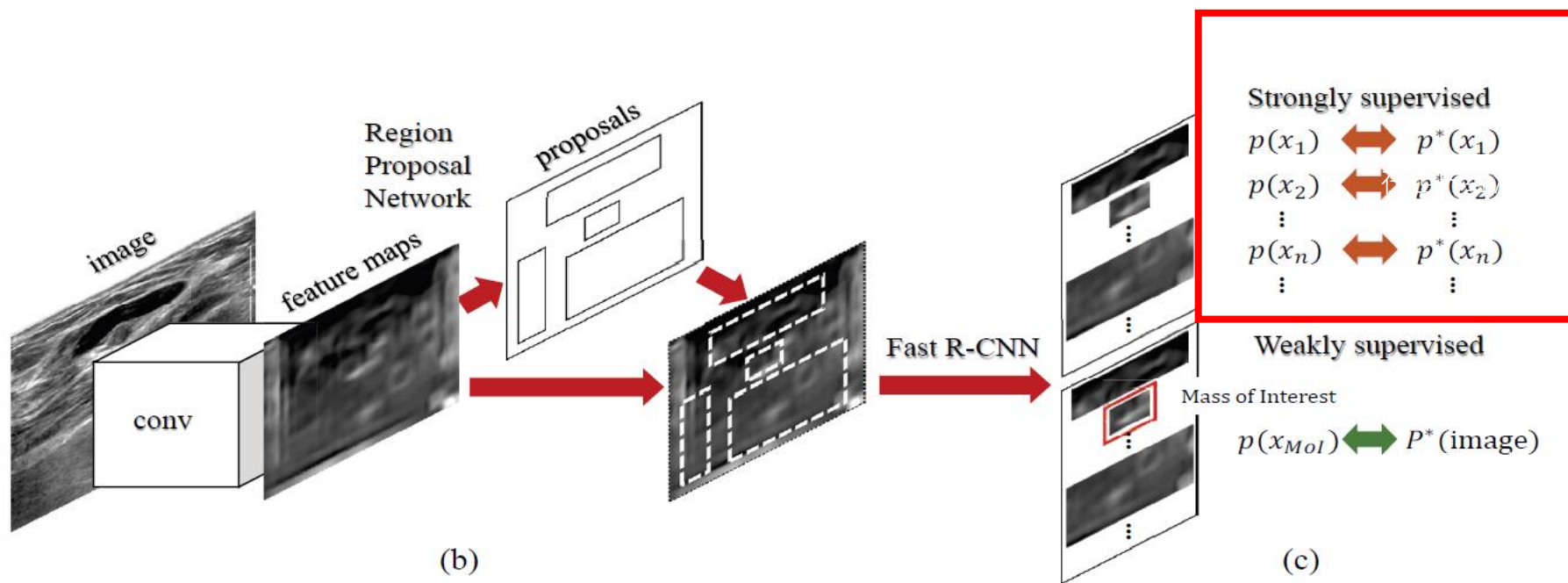
数据集

TABLE I
CARDINALITY OF SNUBH AND UDIAT DATASETS

Dataset		SNUBH				UDIAT		
Role	Supervision	Nor.	Ben.	Mal.	Total	Ben.	Mal.	Total
Training	Strong (DXLoc)	0	400	400	800	90	33	123
	Weak (DX)	0	3291	933	4224	-	-	-
Test	Strong (DXLoc)	200	200	200	600	20	20	40
Total		5624				163		
Cases/Patients		3123/2578				163/163		

Each dataset is further split by patients into subsets according to the role and the amount of supervision. Nor., Ben., and Mal. denote normal, benign, and malignant, respectively.

Strongly Supervised Learning Using the DXLoc Subset



损失函数

$$L(p_i, t_i) = \frac{1}{N_{cls}} \sum_i L_{cls}(p_i, p_i^*) + \lambda \frac{1}{N_{reg}} \sum_i p_i^* L_{reg}(t_i, t_i^*)$$

p_i : $Anchor[i]$ 的预测概率

$$L_{cls}(p_i, p_i^*) = -\log[p_i p_i^* + (1 - p_i)(1 - p_i^*)]$$

p_i^* : $Anchor[i]$ 是正样本时, $p_i^* = 1$; $Anchor[i]$ 是负样本时, $p_i^* = 0$;

t_i : $Anchor[i]$ 预测的Bounding Box的参数化坐标

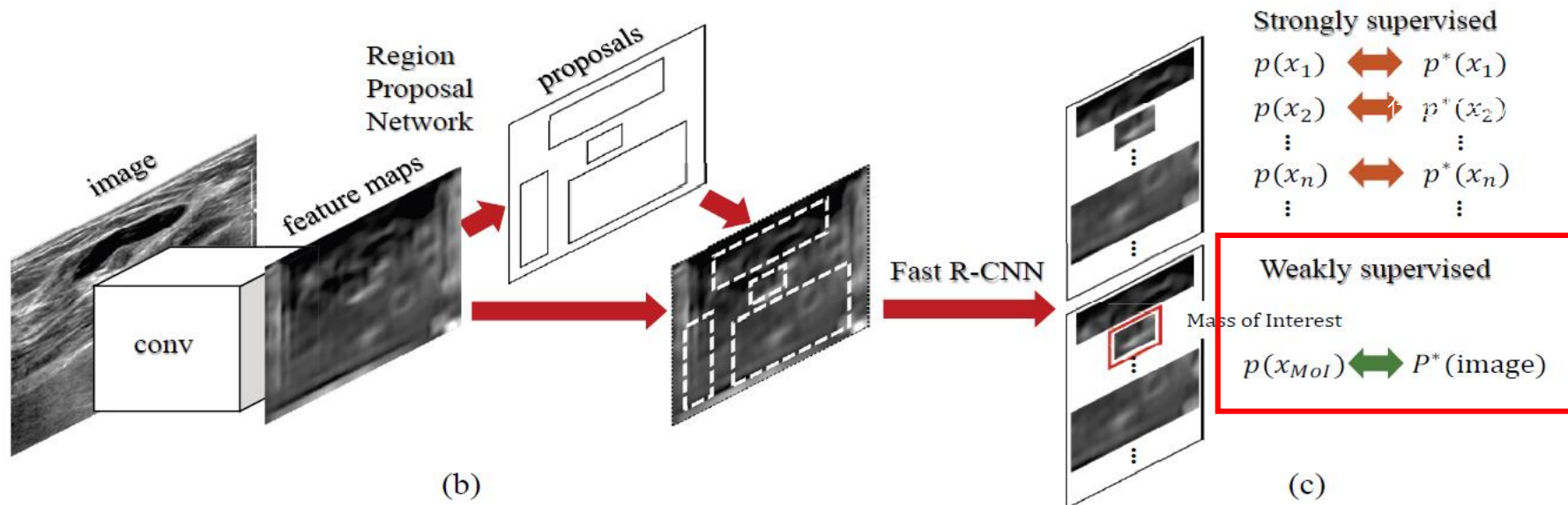
t_i^* : $Anchor[i]$ 的Ground Truth的Bounding Box的参数化坐标

N_{cls} : *mini - batch size*

N_{reg} : *Anchor Location*的数量

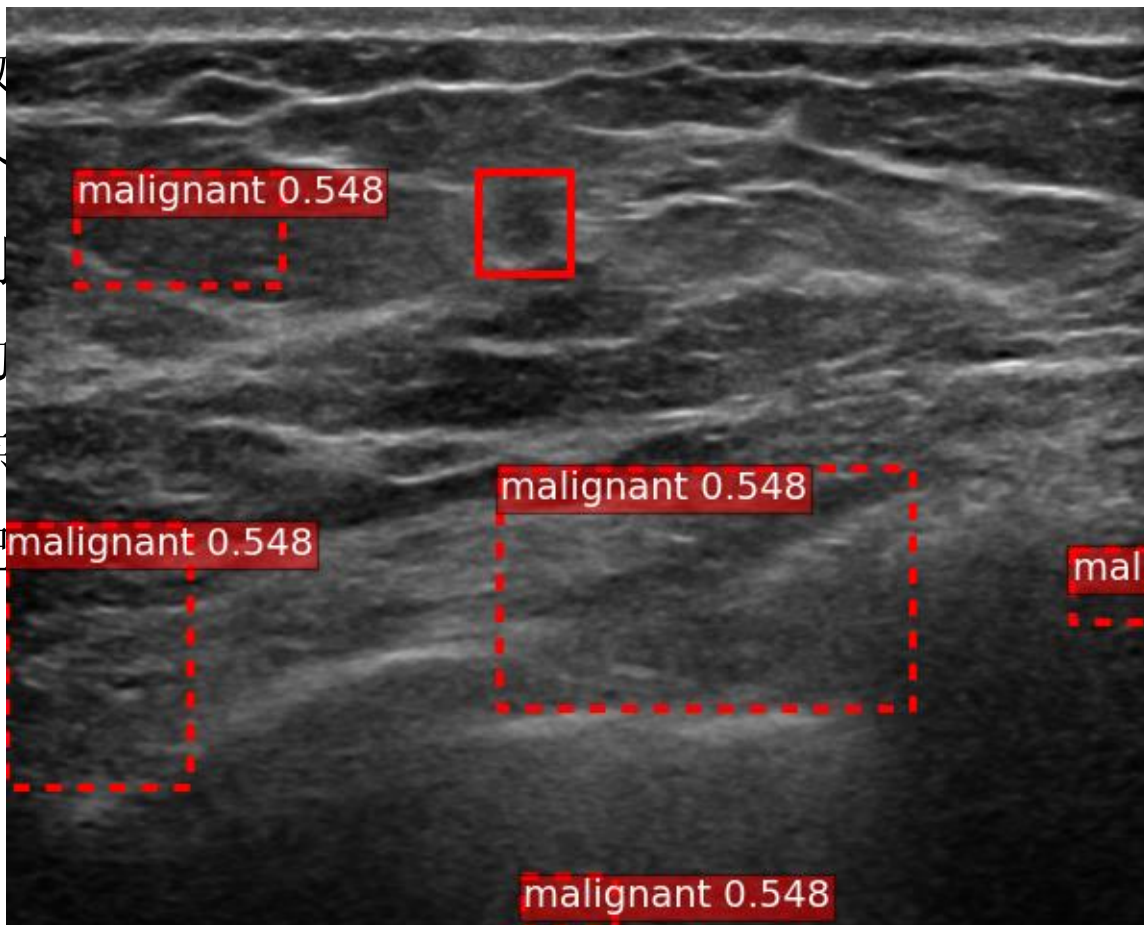
L_{reg} : $L_{reg}(t_i, t_i^*) = R(t_i - t_i^*)$, R 是Smooth L1函数; $p_i^* L_{reg}(t_i, t_i^*)$ 表示只有在正样本时才回归Bounding Box

Weakly Supervised Learning Using the DX Subset



多实例学习

假设训练数据中每个包都有一个正标记的示例，则（这里说包中的包，是相对训练包，是相对训练包，但是示例的标记



instance) 的集合，
E 一个正
三例均为负标记。
例时包为正标记
含了包的标记，

损失函数

$L_{ws}(I_i) = -\sum_{l \in \mathcal{L}} P_l^*(I_i) \log(p_l(I_i))$, 表示第i张图像GT label P^* 和预测值P的交叉熵

$$\mathcal{L} = \{N, B, M\}$$

$$P_l(I_i) = p_l(x_{Mol}), \forall l \in \mathcal{L}$$

$$x_{Mol} = \underset{x_n \in R(I_i)}{\operatorname{argmax}} p_B(x_n)$$

$$x_{Mol} = \underset{x_n \in R(I_i)}{\operatorname{argmax}} \max_{l \in \{B, M\}} p_l(x_n)$$

$$x_{Mol} = \underset{x_n \in R(I_i)}{\operatorname{argmax}} p_M(x_n)$$

$$x_{Mol} = \underset{x_n \in R(I_i)}{\operatorname{argmin}} p_N(x_n)$$

Joint Weakly and Semi-Supervised Learning Using the DXLoc and DX Subsets

$$\theta = \theta_{conv} \cup \theta_{rpn} \cup \theta_{frcnn}$$

the two data streams can be used in two ways:

(1) combining respective data instances into a single mini-batch (combined mini-batch)

(2) alternating between mini-batches of data from either stream(alternating mini-batch).

$$L = L_s + \alpha L_{ws}$$

$$L_s = L_{cls}^{RPN} + L_{reg}^{RPN} + L_{cls}^{FRC} + L_{reg}^{FRC}$$

实验结果对比

TABLE II

ABLATION STUDY SHOWING ALGORITHMIC VARIANTS OF THE PROPOSED METHOD ON THE SNUBH DATASET

Aspect	Variant	CorLoc [%]	95% Confidence Interval (CI) [%]
MIL definition of MoI for images labeled B / M	most benign region / most malignant region	79.50	75.75-83.50
	most discriminative region / most malignant region	80.50	76.50-84.25
	most abnormal region / most malignant region	82.00	78.25-85.75
MIL scale factor	static value (0.5)	82.25	78.25-86.00
Combining weakly and strongly supervised data	alternating mini-batches from each set	82.50	78.75-86.25
Proposed		84.50	81.00-88.00
MIL definition of MoI for images labeled B / M	most malignant region / most malignant region		
MIL scale factor	gradual increase		
Combining weakly and strongly supervised data	combined single mini-batch		

Bootstrapping by randomly sampling test images with replacement is used to generate subset CorLoc values. From these sampled CorLoc values, 95% confidence intervals (CI) are computed.

Joint Weakly and Semi-Supervised Deep Learning for Localization and Classification of Masses in Breast Ultrasound

TABLE IV

RESULTS OF THE PROPOSED METHOD WITH SELF-TRAINING ON THE SNUBH DATASET

Model		Initial	Retrained (50%)	Retrained (75%)	Initial	Retrained (50%)	Retrained (75%)
CorLoc [%]		70.50	82.25	80.75	63.25	81.00	79.25
CI [%]		66.00–75.00	78.50–86.00	76.75–84.75	58.25–67.75	77.00–84.75	75.25–83.00
# of training images	#Strong	50	50+4974*0.5	50+4974*0.75	10	10+5014*0.5	10+5014*0.75
	#Weak	4974	4974*0.5	4974*0.25	5014	5014*0.5	5014*0.25

The initial network is applied to the images in the weakly supervised set and images with the highest classification probabilities coincident with the image-level label are automatically selected and moved to the strongly supervised set, along with the most confident detection as the GT MoI. Retraining is conducted with the reconfigured strongly and weakly supervised sets. Bootstrapping is used to sample subset CorLoc values from which 95% confidence intervals (CI) are computed.

TABLE V

QUANTITATIVE RESULTS OF FULLY WEAKLY SUPERVISED (WEAK), FULLY SUPERVISED (STRONG), AND THE PROPOSED JOINT WEAKLY AND SEMI-SUPERVISED (WEAK AND SEMI) METHODS ON THE SNUBH DATASET

Method		[43]	SS+MIL	[34]	Proposed		Proposed+Self training (retrained 50%)
CorLoc [%]		10.25	21.25	80.00	84.50	83.50	83.50
CI [%]		7.50–13.25	17.25–25.50	76.00–83.75	81.00–88.00	79.75–87.00	79.75–87.00
p-value		<0.0001	<0.0001	<0.0001	-	0.0032	0.0018
# of training images	#Strong	-	-	800	800	800	800
	#Weak	5024	5024	-	4224	5024	2000
Level of supervision		Weak		Strong	Weak & Semi		

Bootstrapping is used to sample subset CorLoc values from which 95% confidence intervals (CI) and p-values for indicating statistical significance of improvement are computed. P-values are obtained using a paired t-test for each comparable method.

论文源码地址: https://github.com/syshin1014/wssdl_bus