Active Bayesian meta-learning for brain cell classification

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MICCAI 2021

Outline

- What is meta-learning?
 - Problem of supervised-learning
 - Model-agnostic meta-learning (MAML)
- tAsk-auGmented actIve meta-LEarning (AGILE)
 - Problems of MAML
 - Task augmentations
 - Active-learning in real-task
- Experiments and results





What is meta-learning?







Problem of supervised-learning

- It often requires large & diverse data to train a good model.
- The human, on the other hand, can learn new concept or skills more efficiently.



Russakovsky et al. '14

GPT-2

Radford et al. '19



Figure 1: The Transformer - model architecture.

Vaswani et al. '18

Source: Finn & Levine, Meta-learning tutorial



Meta-learning

• Supervised learning

 $\begin{aligned} \phi^* &= \arg \max_{\phi} \log p(\phi | \mathcal{D}) \\ \phi &= \{ (\mathbf{x}_q, \mathbf{y}_q) \}_{q=1}^Q \end{aligned} : Observed dataset (Contains Q samples) \\ \phi &: Model parameters \end{aligned}$

• Incorporate additional data (to reduce Q)

$$\phi^* = rg\max_{\phi} \log p(\phi | \mathcal{D}, \mathcal{D}_{ ext{meta}})$$

 $\begin{aligned} \mathcal{D}_{\text{meta}} &= \{\mathcal{D}_1, \mathcal{D}_2, ..., \mathcal{D}_n\} & : \text{Additional datasets (From meta tasks)} \\ \mathcal{D}_i &= \{\left(\mathbf{x}_q^i, \mathbf{y}_q^i\right)\}_{q=1}^{Q_i} & : \text{One meta dataset} \end{aligned}$

• Meta learning

 $\phi^* = \arg \max_{\phi} \log p(\phi | \mathcal{D}, \theta^*)$ $\theta^* = \arg \max_{\theta} \log p(\theta | \mathcal{D}_{\text{meta}}) \qquad \qquad \theta$

:Meta-learning parameters



Meta-learning

Supervised learning

 $\begin{aligned} \phi^* &= \arg \max_{\phi} \log p(\phi | \mathcal{D}) \\ \phi &= \{ (\mathbf{x}_q, \mathbf{y}_q) \}_{q=1}^Q \end{aligned} : Observed dataset (Contains Q samples) \\ \phi &: Model parameters \end{aligned}$

• Incorporate additional data (to reduce Q)

$$\phi^* = \arg \max_{\phi} \log p(\phi | \mathcal{D}, \mathcal{D}_{\text{meta}}) \qquad \qquad \mathcal{D}_{\text{meta}} = \{\mathcal{D}_1, \mathcal{D}_2, ..., \mathcal{D}_n\} \qquad \text{:Additional datasets (From meta tasks)} \\ \mathcal{D}_i = \{(\mathbf{x}_q^i, \mathbf{y}_q^i)\}_{q=1}^{Q_i} \qquad \text{:One meta dataset} \end{cases}$$

• Meta learning



Brain cell classification example

- Real task
 - $\mathcal{D} = \{(\mathbf{x}_q, \mathbf{y}_q)\}_{q=1}^Q$



Meta tasks

$$egin{split} \mathcal{D}_{ ext{meta}} &= \left\{\mathcal{D}_1, \mathcal{D}_2, ..., \mathcal{D}_n
ight\} \ \mathcal{D}_i &= \left\{\left(\mathbf{x}_q^i, \mathbf{y}_q^i
ight)
ight\}_{q=1}^{Q_i} \end{split}$$



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Model-agnostic meta-learning (MAML)





tAsk-auGmented actIve meta-LEarning (AGILE)







Problem of MAML

- It requires a lot of meta-task to train the meta-parameters
- There is no uncertainty for the classification results
- It doesn't use the most important samples for adaptation
- It is not dynamic enough

Task augmentations

- Not enough meta-tasks \rightarrow meta-overfitting
- Task augmentations:
 - 1. Flipping the label

 $y' = z(1-y) + (1-z)y_{z}$

where $z \sim \text{Bernoulli}(p_f)$

2. Shuffling the order of input channels

 $\mathbf{x}' = \mathbf{x} * \mathbf{s}_{ij}, \quad i, j = 1, 2, 3 \dots c$

where $\{\mathbf{s}_{ij}\}_{i=1}^c \in \mathbb{R}^{1 \times 1 \times c}$

3. Rotating the images



Comparison of (a) transfer learning and (b) task-augmented meta-learning.



Active-learning in real-task

• Active-learning:

Use the most valuable samples for adaptation

• Valuable:

High uncertainty obtained from Monte-Carlo Dropout

$$H\left(\mathbf{y}^{\text{te}}|\mathbf{x}^{\text{te}}, \mathcal{D}^{\text{train}}\right) = -\sum_{\mathbf{y}^{\text{te}} \in \mathcal{Y}} p(\mathbf{y}^{\text{te}}|\mathbf{x}^{\text{te}}, \mathcal{D}^{\text{train}}) \log p(\mathbf{y}^{\text{te}}|\mathbf{x}^{\text{te}}, \mathcal{D}^{\text{train}})$$

• Dynamic:

Random number of training samples for each task during meta-training



Randomly dropout neurons at different iterations equivalent to sampling from a distribution.

Source: Nguyen et al, Bayesian deep learning tutorial





Datasets





FIGURE 1.3 Rat brain cell samples. There are five cell types: neurons, astrocytes, oligodendrocytes, microglia, and endothelial cells and seven biomarkers: DAPI, Histones, NeuN, S100, Olig 2, Iba1, and RECA1. 2 samples are shown here for each of the cell type. DAPI and Histones are used to indicate the location of the cells while others are biomarkers for classification of specific cell types. High correlation can be found between NeuN and neurons, Iba1 and microglia, S100 and astrocytes, Olig2 and oligodendrocytes, RECA1 and endothelial cells.

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- Settings:
 - Five cell types:
 - 3 meta-tasks: neurons , oligodendrocytes, microglia
 - 2 real-tasks: astrocytes and endothelial cells

or

- 3 meta-tasks: neurons , astrocytes, endothelial cells
- 2 real-tasks: oligodendrocytes and microglia
- Seven biomarkers: DAPI, Histones, NeuN, S100, Olig 2, Iba1 and RECA1
- Network: CNN
- Baselines:
 - lower bound (supervised training with a small dataset)
 - upper bound (fully supervised training)
 - a pretrained model (transfer learning)
 - a state-of-the-art method (MAML)

Table 1. Methods configuration comparison which differ mainly in the data they use and the training framework. Meta-learning methods are supposed to perform well with few training samples and little training time. (# means the number of)

Methods	Use data			in Real-train		# Moto
	Meta-train	Meta-test	Real-train	# samples	# gradient updates	$\frac{\#}{\text{tasks}}$
Vanilla_limit	-	-	\checkmark	16 (1%)	100	0
Vanilla_full	-	-	\checkmark	960 (60%)	100	0
Transfer	 ✓ 	-	\checkmark	16 (1%)	100	3
MAML	\checkmark	\checkmark	\checkmark	16(1%)	1	3
AGILE(phase I)	\checkmark	√	√	16 (1%)	1	many
AGILE(phase II)	\checkmark	\checkmark	\checkmark	16(1%)	1	many
AGILE(phase II)	\checkmark	\checkmark	\checkmark	160 (10%)	1	many



• Few shot classification results:

TABLE 1.2 Quantitative results of different methods in rat brain cell classification experiments with first task split. Vanilla method use all available training data (60%) and act as the upper bound while AGILE method get the highest accuracy using very few training data (1%).

Methods (Size %)	Precision	Recall	F1-score	Accuracy(± Std)	Cl ₉₅
Vanilla_limit (1%)	0.642	0.622	0.632	0.637(±0.062)	0.632 - 0.642
Vanilla_full (60%)	0.937	0.965	0.951	0.950 (±0.021)	0.948 - 0.952
Transfer (1%)	0.447	0.433	0.440	0.449(±0.085)	0.449 - 0.456
MAML (1%)	0.408	0.402	0.405	0.409(±0.030)	0.406 - 0.412
AGILE(phase I) (1%)	0.791	0.790	0.791	0.791(±0.054)	0.786 - 0.796
AGILE(phase II) (1%)	0.883	0.926	0.904	0.902(±0.048)	0.898 - 0.906
AGILE(phase II) (10%)	0.950	0.951	0.951	0.950 (±0.044)	0.946 - 0.954

TABLE 1.3 Quantitative results of different methods in rat brain cell classification experiments with second task split.

Methods (Size %)	Precision	Recall	F1-score	Accuracy(± Std)	Cl ₉₅
Vanilla_limit (1%)	0.745	0.711	0.728	0.738(±0.084)	0.715 - 0.761
Vanilla_full (60%)	0.948	0.958	0.952	0.952(±0.011)	0.946 - 0.960
Transfer (1%)	0.713	0.710	0.712	0.708(±0.089)	0.700 - 0.716
MAML (1%)	0.669	0.678	0.674	0.675(±0.108)	0.666 - 0.684
AGILE(phase I) (1%)	0.929	0.892	0.910	0.913(±0.055)	0.908 - 0.918
AGILE(phase II) (1%)	0.896	0.874	0.885	0.888(±0.088)	0.861 - 0.915
AGILE(phase II) (4%)	0.939	0.965	0.952	0.952 (±0.053)	0.936 - 0.968

Task split2

Task split1

• Fast adapting ability:

(a) AGILE method learns faster compared with other baselines.

Fewer updates

• Adapt with few samples: (b) AGILE method can get a much better performance with smaller training size.

Fewer samples

Few is enough



Task split1

• Fast adapting ability:

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Task split2





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