A New Ensemble Learning Framework for 3D Biomedical Image Segmentation

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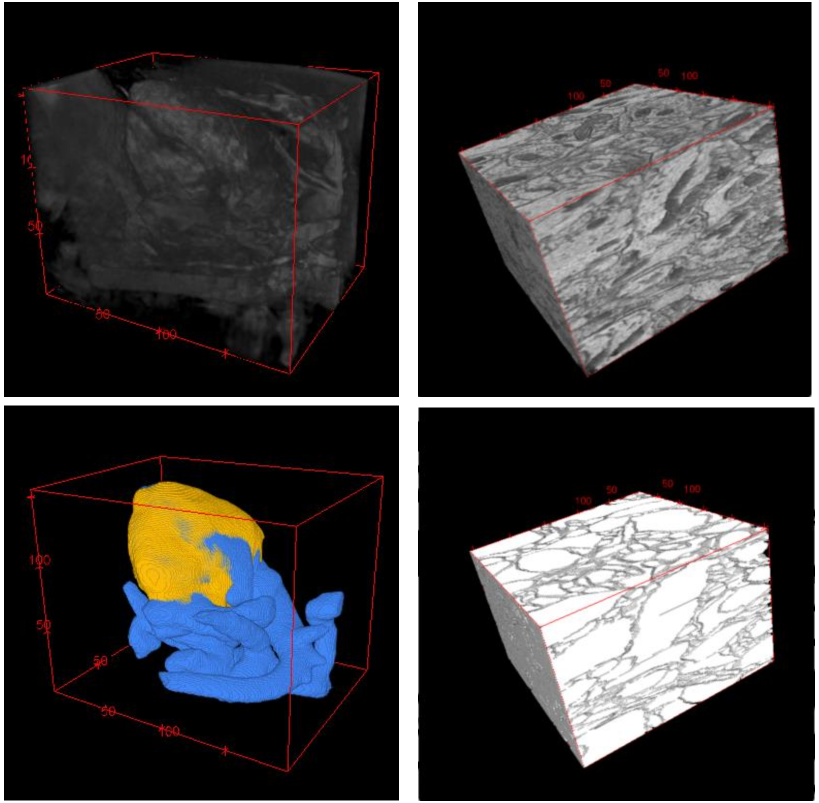
3D biomedical image segmentation

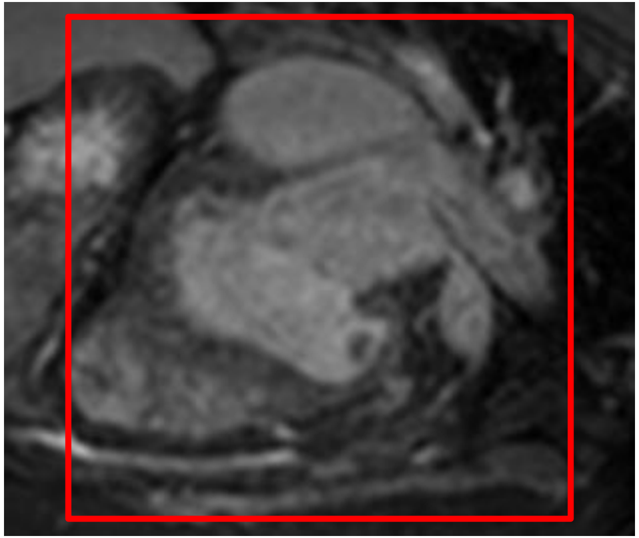
400x400



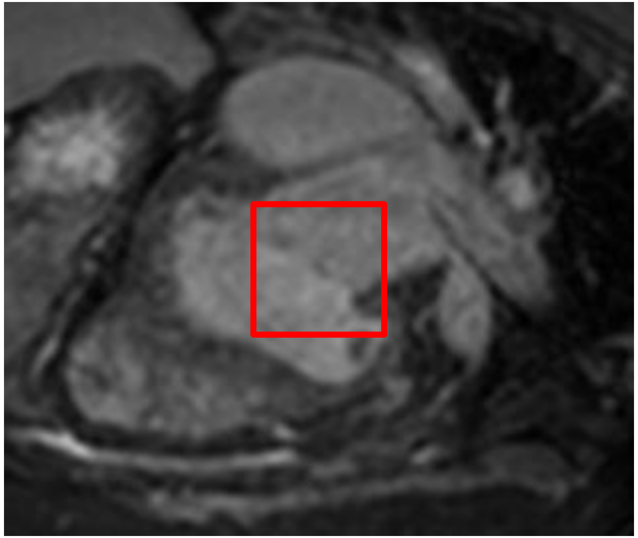
200x150x120 512x512x200

Challenges in 3D image segmentation

- Large image size in 3D and limited GPU memory
- Trade-off between inter-slice information and the size of field of view



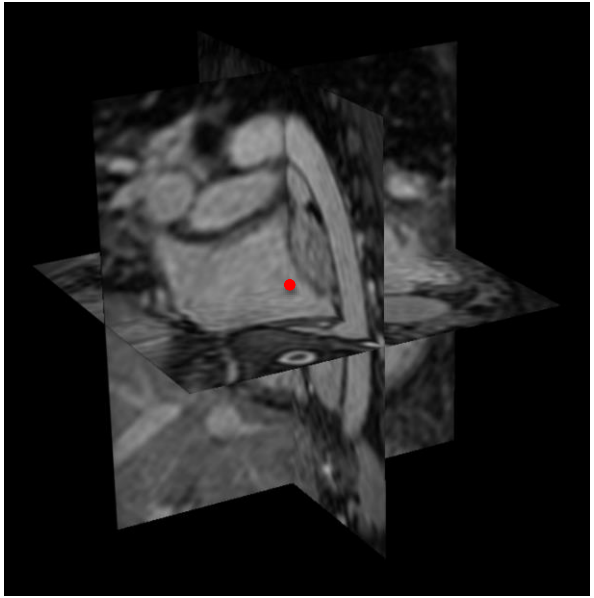
2D: 572 x 572 x 1



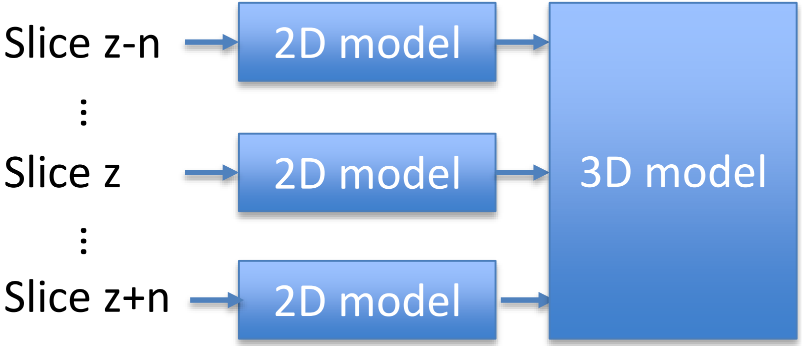
3D: 64 x 64 x 64

Previous methods to circumvent this trade-off

Triplanes



Multi-stage 2D + 3D



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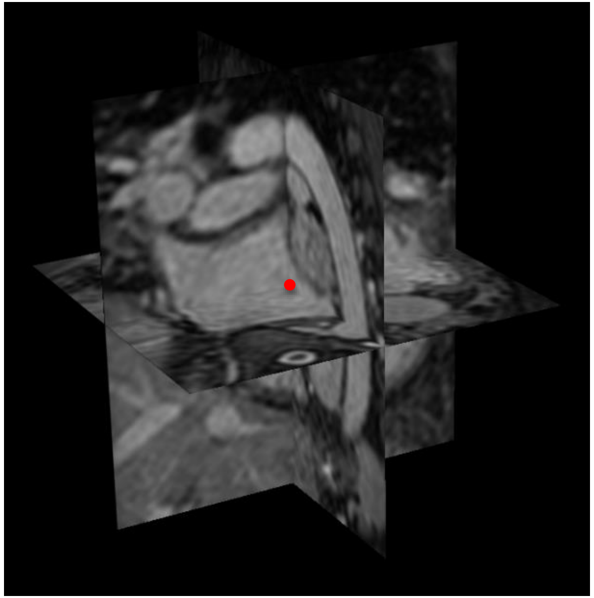
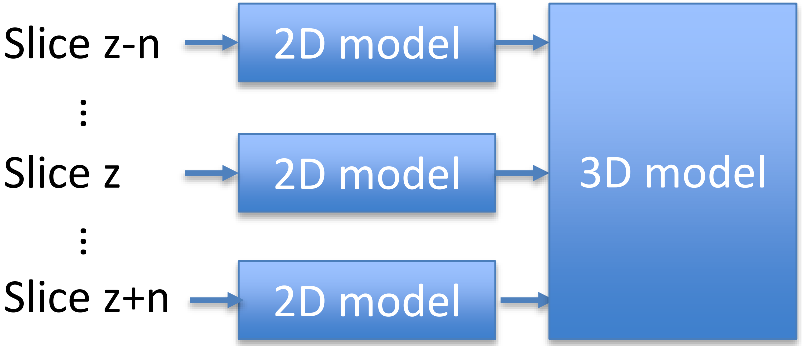


Still not full 3D

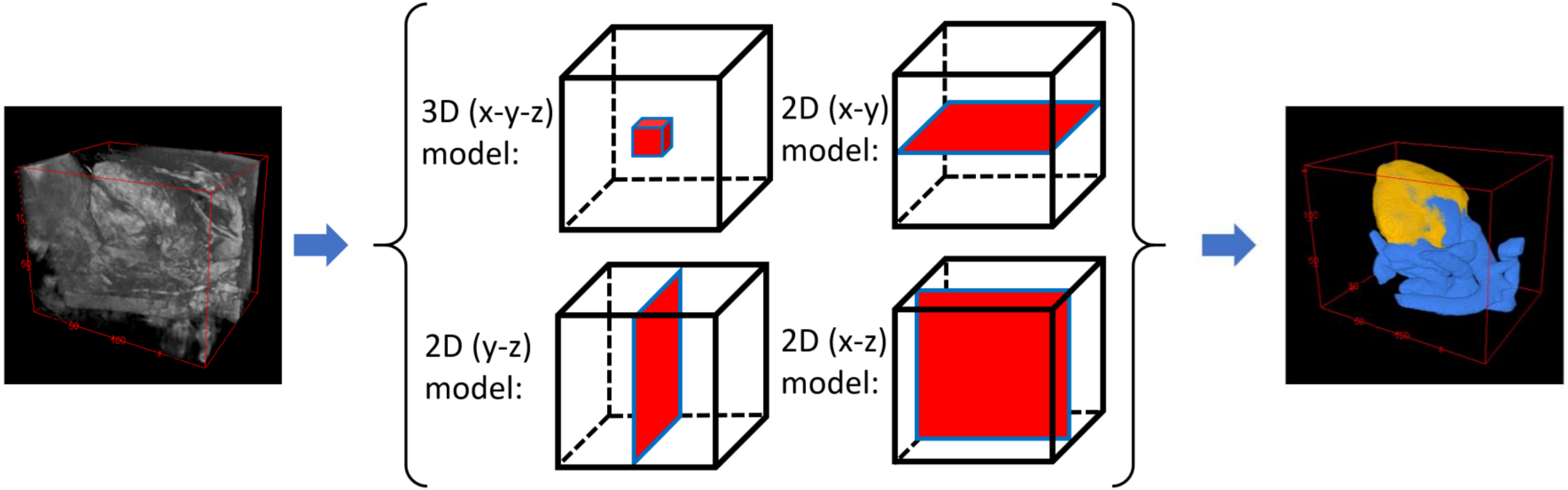
Multi-stage 2D + 3D



2D results may dominate

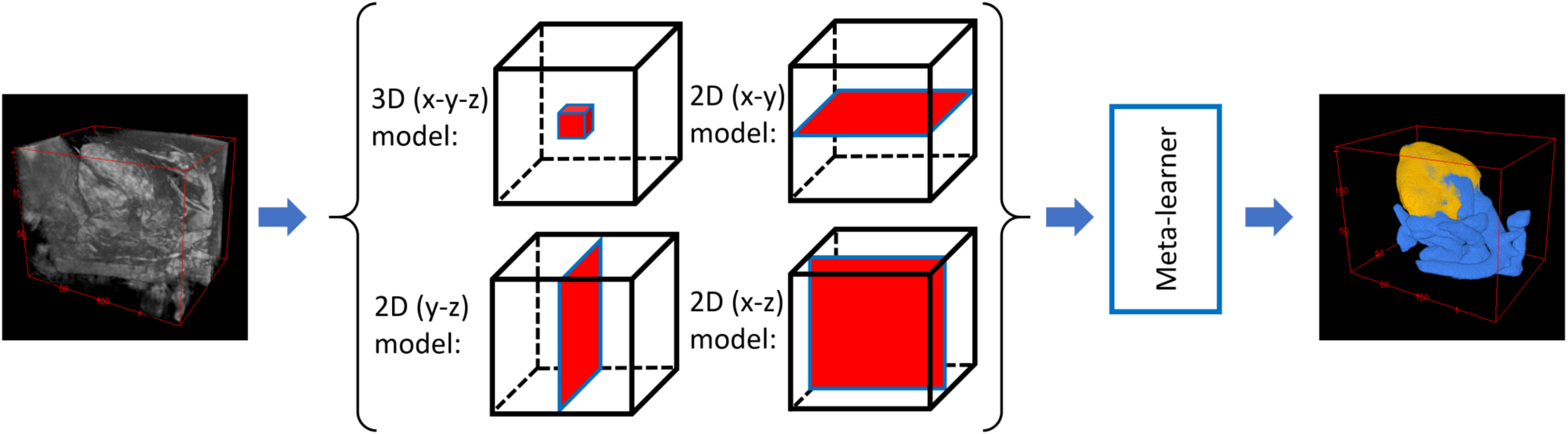
Our idea: Ensemble learning

- Ensemble learning: Unifying the merits of multiple **base-learners**
  - 2D models (large field of view)
  - 3D models (inter-slice information)



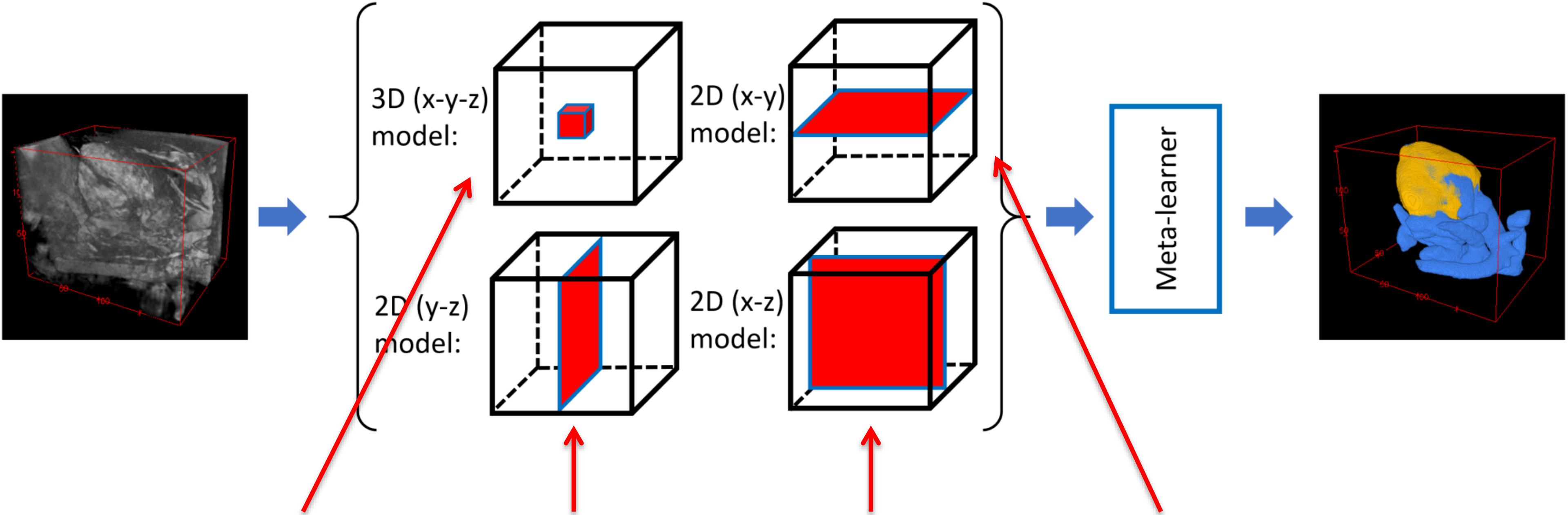
Base-learners

Our approach: Diverse base-learners + meta-learner



- Diverse base-learners: Each has a unique geometric view of the 3D data
- Meta-learner: Learn how to combine base-learners (instead of simple averaging/voting)

Our approach: Diverse base-learners



- Diverse base-learners: Each has a unique geometric view of the 3D data
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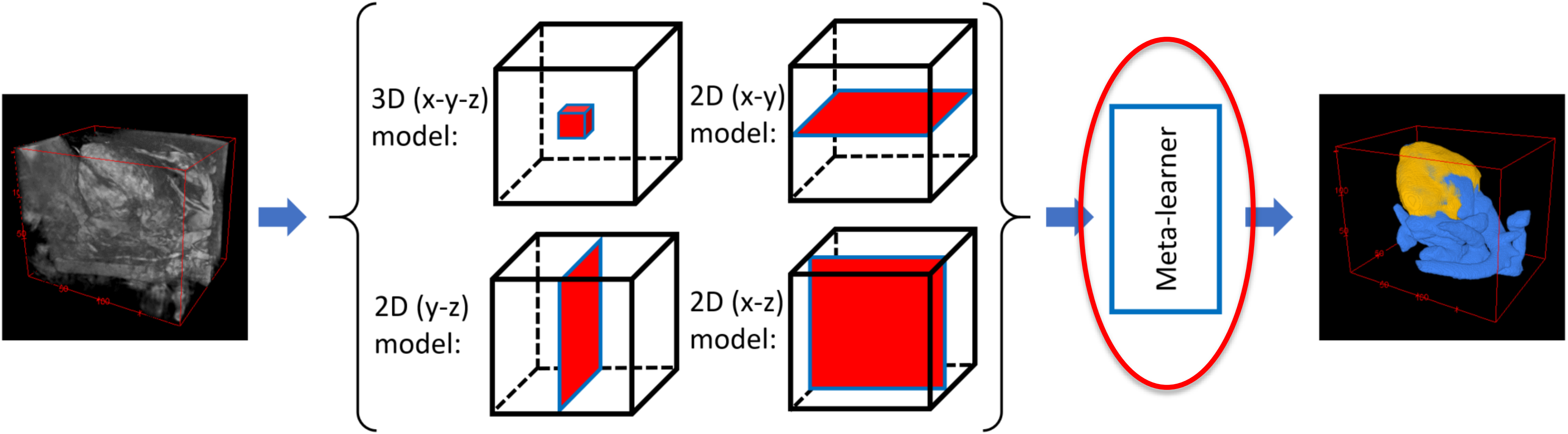
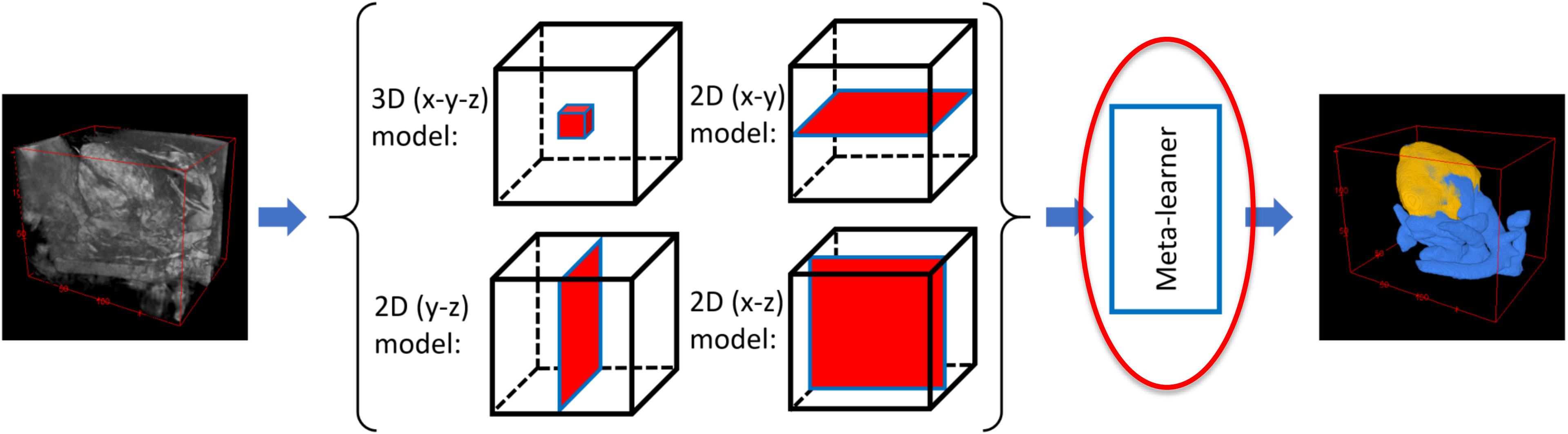
Our approach: Meta-learner



- Diverse base-learners: Each has a unique geometric view of the 3D data
- Meta-learner: Learn how to combine base-learners (instead of simple averaging/voting)

Our approach: We focus on the meta-learner



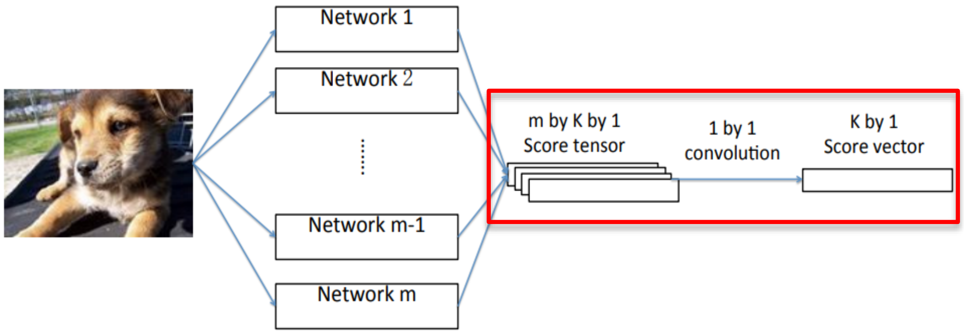
- Diverse base-learners: Each has a unique geometric view of the 3D data
- Meta-learner: Learn how to combine base-learners (instead of simple averaging/voting)
- In our study, we focus on how to design a best possible meta-learner

Previous meta-learners

Learning via fitting the ground truth $$\ell(\theta_{\mathcal{H}})=\sum_{i=1}^{n}\ell_{mce}(\theta_{\mathcal{H}}(x_i,S(PL_i)),GT_i)$$

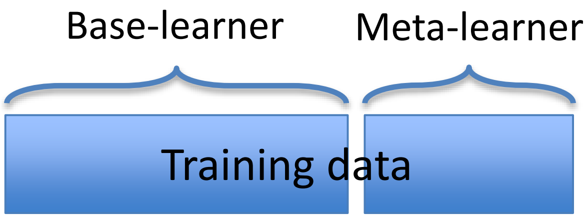
A key issue: Overfitting

Linear combination [1]



Limited capability

Super learner [2]



Not practical when training data are scarce

Our need: A powerful meta-learner with a new scheme to reduce overfitting

[1] The relative performance of ensemble methods with deep convolutional neural networks for image classification
[2] Super learner. Statistical applications in genetics and molecular biology

Previous meta-learners

Learning via fitting the ground truth

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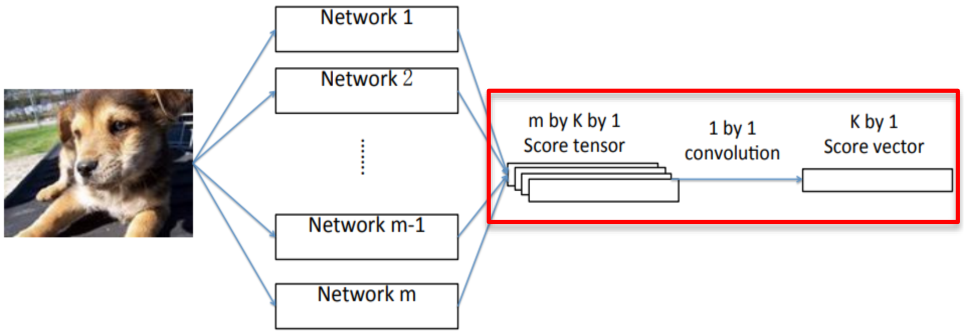

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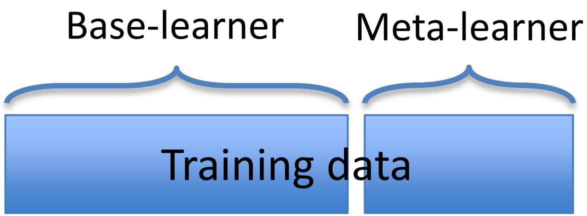

Not practical when training data are scarce

Our need: A $\boxed{\text{powerful meta-learner}}$ with a new scheme to reduce overfitting

Part I

Previous meta-learners

Learning via fitting the ground truth $$\ell(\theta_{\mathcal{H}})=\sum_{i=1}^{n}\ell_{mce}(\theta_{\mathcal{H}}(x_i,S(PL_i)),GT_i)$$

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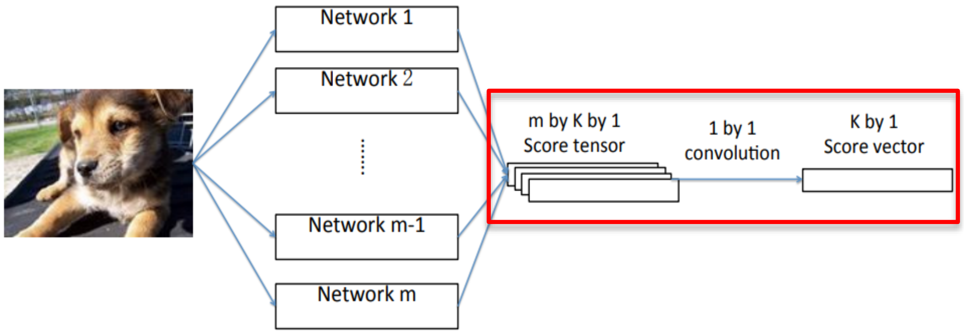

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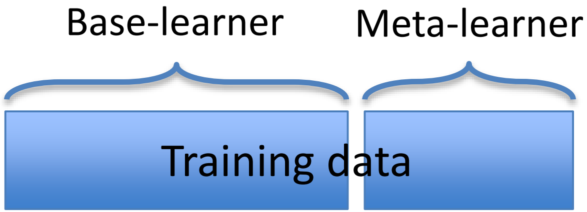

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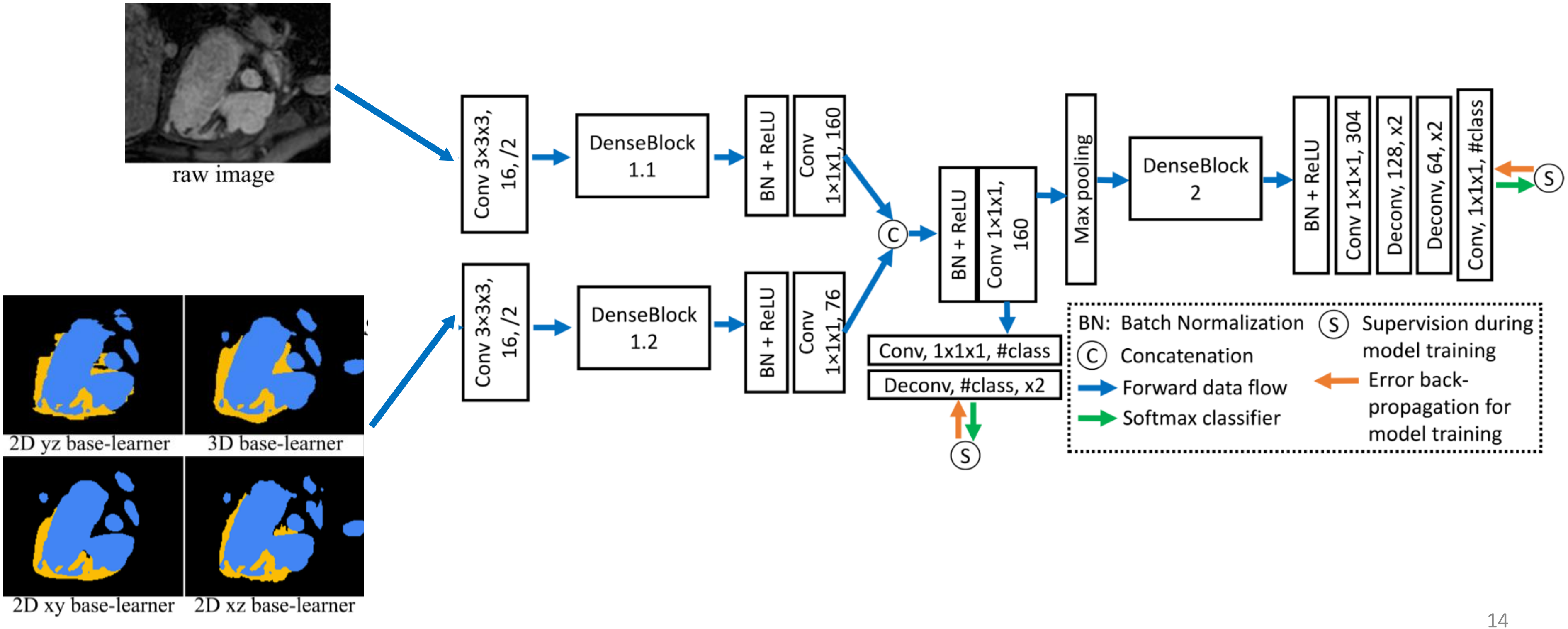
Our need: A powerful meta-learner with a $\boxed{\text{new scheme to reduce overfitting}}$

Part II

Part I: Our meta-learner structure

- To capture knowledge of each base-learner, we design an FCN based meta-learner



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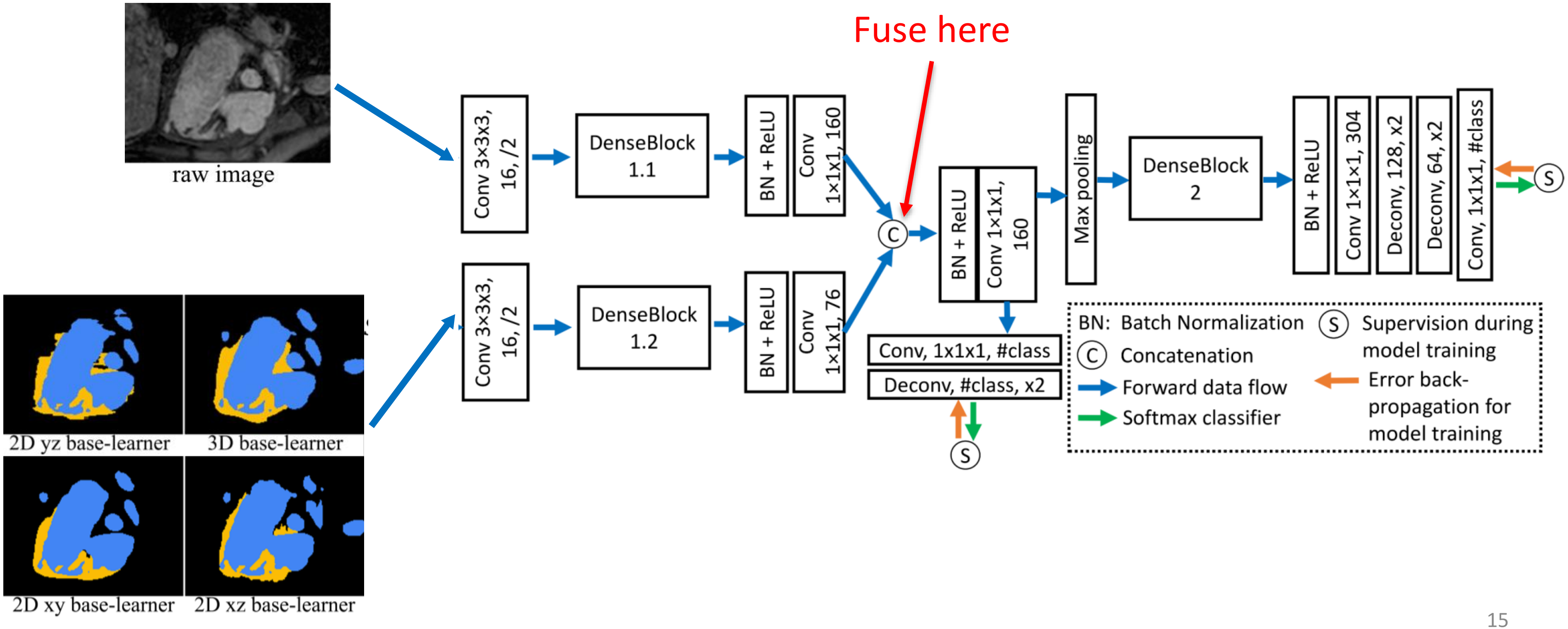

Part II: A new unsupervised training scheme

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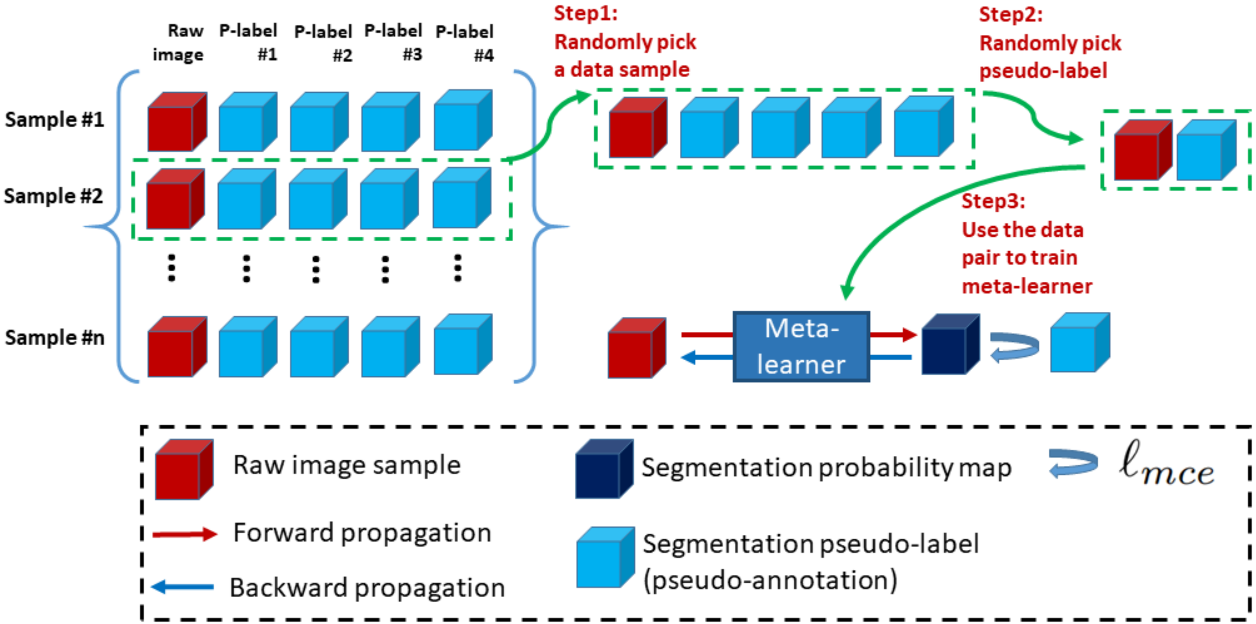
- Key ideas to **reduce overfitting**
  - Achieve ensemble by finding a balance among base-learners' results (instead of directly fitting the ground truth)
  - Utilize abundant unlabeled raw images
- Our solution:
  - View base-learners' results as pseudo-labels ("fake" ground truth)
  - Find a balance via network training

$$\ell(\theta_{\mathcal{H}}) = \sum_{i=1}^{n} \ell_{mce}(\theta_{\mathcal{H}}(x_i, S(PL_i)), \cancel{GT_i})$$

$$\ell(\theta_{\mathcal{H}}) = \sum_{i=1}^{n} \sum_{j=1}^{m} \ell_{mce}(\theta_{\mathcal{H}}(x_i, S(PL_i)), f_j(x_i))$$

Part II: Training scheme 1 — Random fit



Algorithm 1: Random-fit

Input: $(x_i, PL_i = \{f_1(x_i), f_2(x_i), \ldots, f_m(x_i)\}, S(PL_i))$, $i = 1, 2, \ldots, n$

Output: A trained meta-learner $\mathcal{H}$

initialize a meta-learner $\mathcal{H}$ with random weights;

mini-batch = $\emptyset$

while *stopping condition not met* **do**

  for k = *1 to batch-size* **do**

    $p = rand\text{-}int(1, n)$

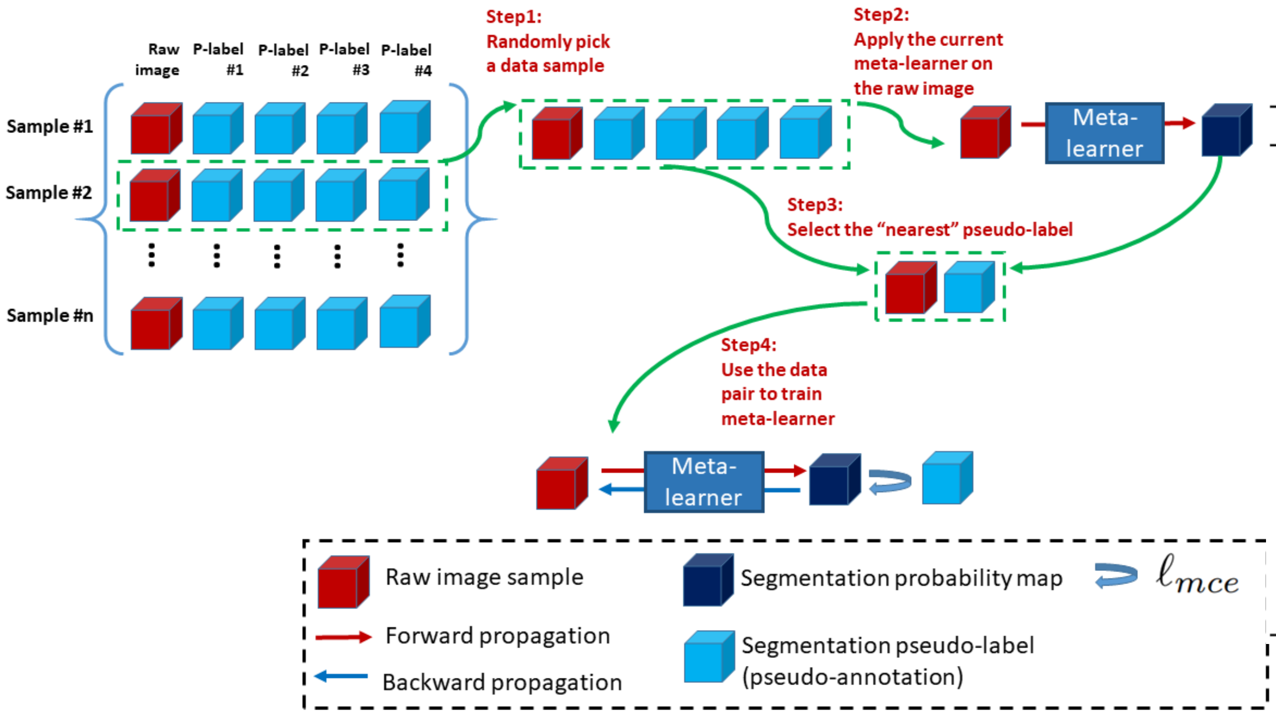
    $q = rand\text{-}int(1, m)$

    add training sample $\{(x_p, S(PL_p)), f_q(x_p)\}$ to the mini-batch

  update $\mathcal{H}$ using training samples in the mini-batch with forward and backward propagation

  mini-batch = $\emptyset$

Part II: Training scheme 2 — Nearest neighbor fit (NN-fit)



Algorithm 2: Nearest-neighbor-fit (NN-fit)

Input: $(x_i, PL_i = \{f_1(x_i), f_2(x_i), \dots, f_m(x_i)\}, S(PL_i))$, $i = 1, 2, \dots, n,$ meta-learner $\mathcal{H}$ (obtained from random-fit)

Output: A refined meta-learner $\mathcal{H}$

mini-batch = $\emptyset$

while *stopping condition not met* **do**

  for k = *1 to batch-size* **do**

    $p = rand\text{-}int(1, n)$

    $\hat{y} = \mathcal{H}(x_p, S(PL_p))$

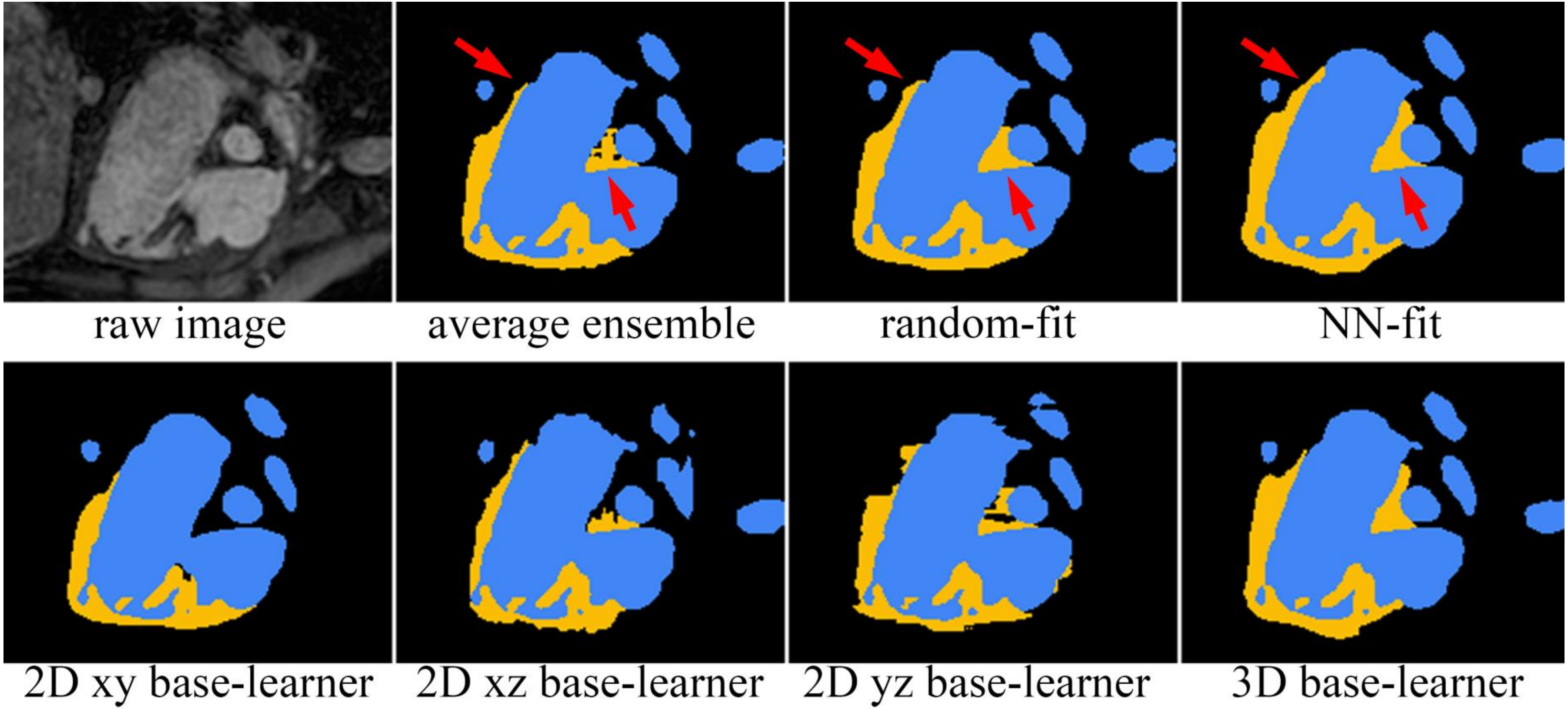
    $\hat{q} = \arg\min_{q=1,2,\dots,m} \mathcal{L}_{mce}(\hat{y}, f_q(x_p))$

    add training sample $\{(x_p, S(PL_p)), f_{\hat{q}}(x_p)\}$ to the mini-batch

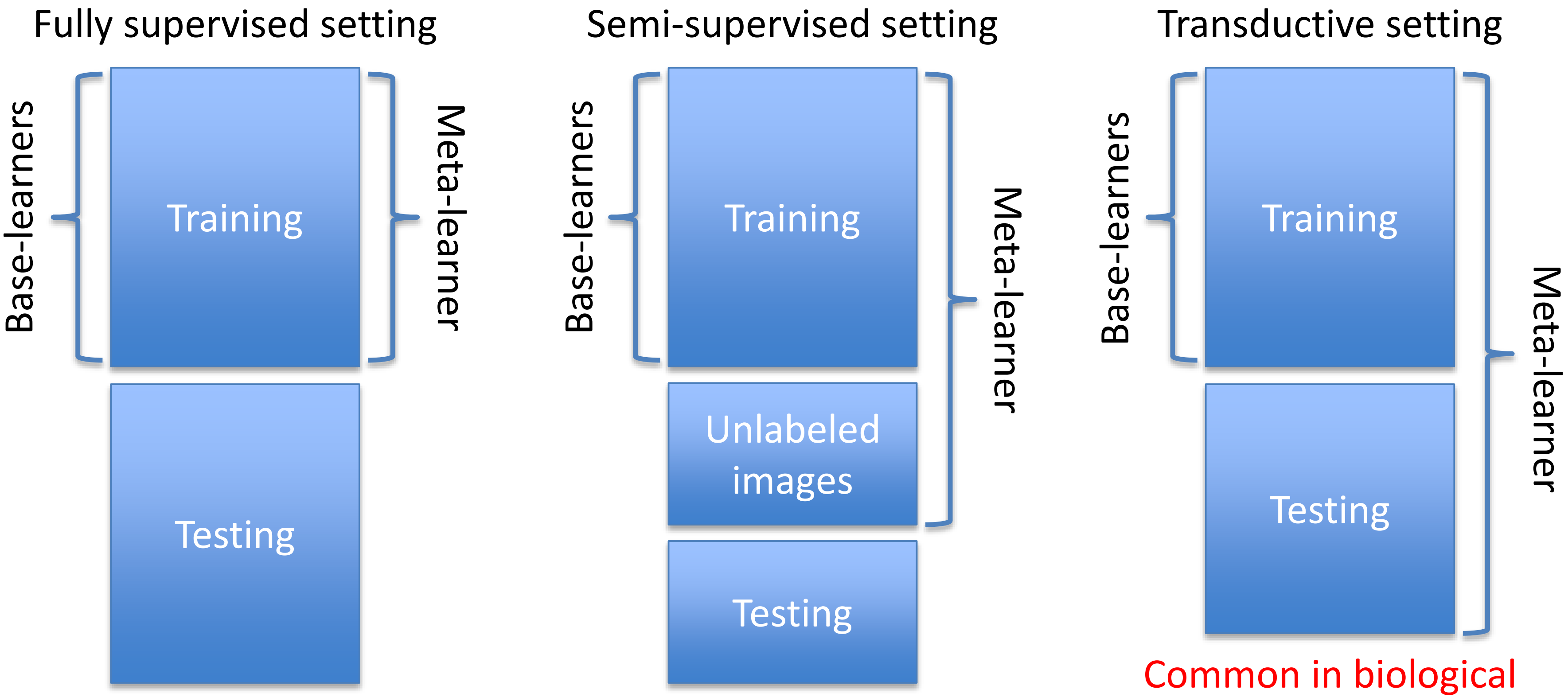
  update $\mathcal{H}$ using training samples in the mini-batch with forward and backward propagation

  mini-batch = $\emptyset$

Visual comparison



Applications



Common in biological discovery applications

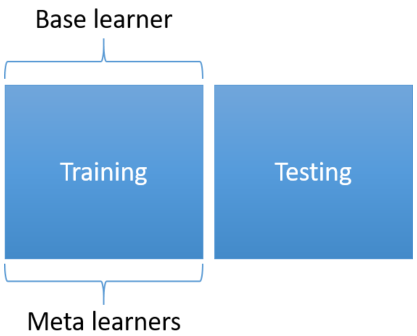
Quantitative comparison — Fully supervised setting

HVSMR 2016 Challenge Dataset

Method	Overall score	
3D U-Net (Çiçek et al. 2016)	-0.419	← 3D models
VoxResNet (Chen et al. 2017)	-0.202	
DenseVoxNet (Yu et al. 2017)	-0.161	
Wolterink *et al.*(Wolterink et al. 2016)	-0.036	← Tri-planar
VFN* (Xia et al. 2018)	0.108	← Multi-stage 2D+3D
Base learner 2D (xy)	0.13	
Base learner 2D (xz)	-0.098	
Base learner 2D (yz)	0.108	
Base learner 3D	0.13	
Average ensemble	0.2	
Our meta-learner (only training data)	0.215	

Mouse Piriform Cortex Dataset

Method	V^{Rand}_{Fscore}
N4 (Ciresan et al. 2012)	0.9304
VD2D (Lee et al. 2015)	0.9463
VD2D3D (Lee et al. 2015)	0.9720
M^2FCN (Shen et al. 2017)	0.9866
Our 2D base-learner	0.9948
Our 3D base-learner	0.9956
Average ensemble of 2D and 3D	0.9959
Random-fit (only training data)	0.9963
NN-fit (only training data)	0.9967



Quantitative comparison — Transductive setting

HVSMR 2016 Challenge Dataset

Method	Overall score
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Base learner 2D (yz)	0.108
Base learner 3D	0.13
Average ensemble	0.2
Our meta-learner (only training data)	0.215
Our meta-learner (transductive)	**0.234**

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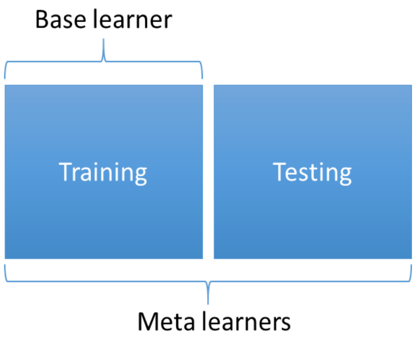
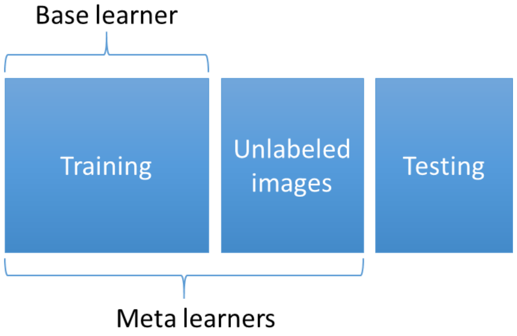
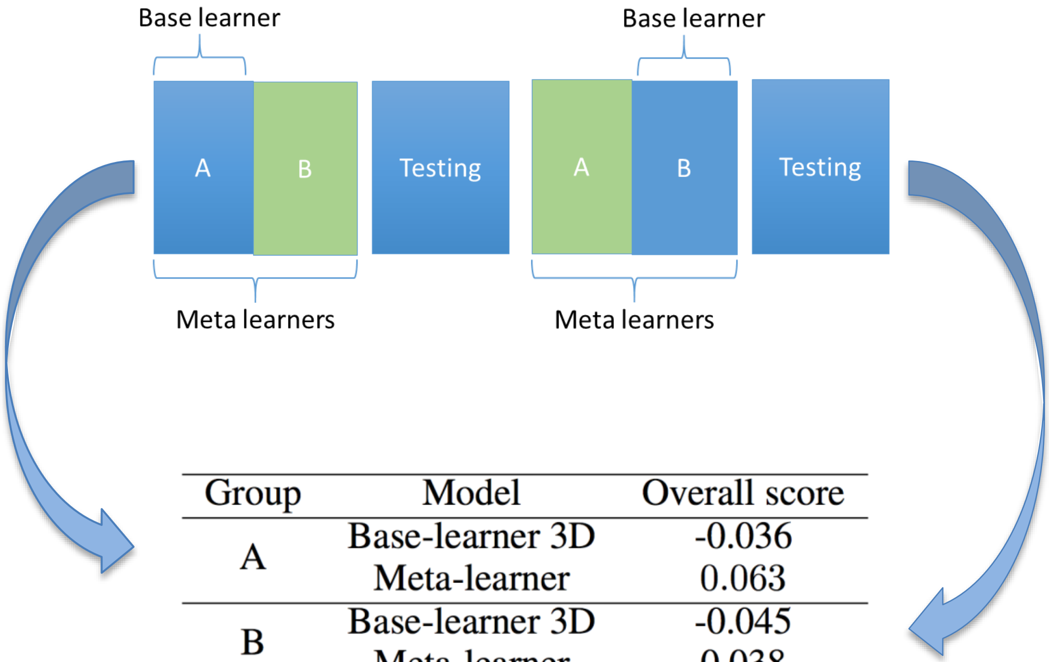
Our 3D base-learner	0.9956
Average ensemble of 2D and 3D	0.9959
Random-fit (only training data)	0.9963
NN-fit (only training data)	0.9967
Random-fit (transductive)	0.9967
NN-fit (transductive)	**0.9970**



Quantitative comparison — Semi-supervised setting



HVSMR 2016 Challenge Dataset



Group	Model	Overall score
A	Base-learner 3D	-0.036
	Meta-learner	0.063
B	Base-learner 3D	-0.045
	Meta-learner	0.038

Quantitative comparison — Ablation study

- HVSMR 2016 Challenge Dataset

Setting	Inputs		Supervision of training set	Transductive learning	Supervision of testing set	Training		Overall score
	raw image (x_i)	$S(PL_i)$				random fit	NN fit	
S1		✓	GT					0.075
S2	✓	✓	GT					0.192
S3	✓	✓	GT	✓	PL	✓		0.217
S4	✓	✓	GT + PL	✓	PL	✓		0.205
S5	✓	✓	GT + PL	✓	PL	✓	✓	0.224
S6	✓	✓	PL			✓		0.199
S7	✓	✓	PL			✓	✓	0.215
S8	✓	✓	PL	✓	PL	✓		0.218
S9	✓	✓	PL	✓	PL	✓	✓	**0.234**

- Random-fit + NN-fit vs. Random-fit alone (S7 > S6, S5 > S4, S9 > S8)
- Meta training using pseudo-labels vs. ground truth
  - Only training data (S7 > S2)
  - Transductive settings: (1) only GT (S3); (2) GT + PL (S4 & S5); (3) only PL (S8)

Summary & conclusions

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- Introduce a new **ensemble learning framework** to segment 3D biomedical images
- Propose to use **heterogeneous base learners** with different geometric views of 3D data
- Propose to use **pseudo labels** and design a **sophisticated meta learner** to distillate knowledge from base learners
- Propose two optimization strategies (**Random-fit & NN-fit**) for training the meta learner
- Empirical experiments demonstrate that overfitting is alleviated considerably

Thank you!

Q & A