Multi-class boosting with adversarial multi-arm bandits on incomplete views Andrea Simeon (Mihajlović)

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TOPIC OUTLINE









MOTIVATION





CONCLUSION

MOTIVATION









MCROBIONE

- Sequence data analysis
- Choose:

a. Sequencing technique: amplicon vs shotgun

b. Preprocessing technique: different pipelines

- Associate with diseases and conditions (ML classification)
- Dan et al. (2020) doi: 10.1080/19490976.2020.1747329
- Multi-view learning (fusion)
- Peng et al. (2018) doi: 10.1109/TNNLS.2016.2637881





PROBLEM STATEMENT



PROBLEM 1: MULTIPLE INCOMPLETE VIEWS

- Multiple measurements on the same data
- Incomplete in terms of samples across views

PROBLEM 2: MULTI-CLASS

• More than two classes

data s views



EXAMPLE

Complete views

	$f_{1,1}$	$f_{1,2}$	$f_{1,3}$
s_1	5	10	2
s_2	1	1	2
s_3	7	4	1
s_4	5	4	3

	$f_{2,1}$	$f_{2,2}$	$f_{2,3}$
s_1	10	7	2
s_2	1	2	2
s_3	3	4	7
s_4	5	4	6

	$f_{1,1}$	$f_{1,2}$
s_1	5	10
s_2	1	1
s_4	5	4

Incomplete views



	$f_{2,1}$	$f_{2,2}$	$f_{2,3}$
s_1	10	7	2
s_3	3	4	7



Peng et al. (2018) doi: 10.1109/TNNLS.2016.2637881

sample weight



prediction

Adversarial MAB

- Multiarmed bandits (MAB)
- Player vs k slot machines
- Maximize total reward
- Adversaries
- EXP3.P
- Very good in finding expected





Peng et al. (2018) doi: 10.1109/TNNLS.2016.2637881

sample weight





prediction









irBoost.SH

- Extension to rBoost.SH
- Incomplete views
- Multi-class setting
- Edge and prediction changes





	$f_{2,1}$	$f_{2,2}$	$f_{2,3}$
s_1	10	7	2
s_2	1	2	2
s_3	3	4	7
s_4	5	4	6

Incomplete views

	$f_{1,1}$	$f_{1,2}$	$f_{1,3}$
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	$f_{2,1}$	$f_{2,2}$	$f_{2,3}$
s_1	10	7	2
s_3	3	4	7

rBoost.SH

 $h_t(x_i)$ classifier's prediction

time t $y_i, h_t(x_i) \in \{1, -1\}$ samples

edge
$$\theta_i$$

$$\theta_t = 2 \sum_{i \in \mathcal{N}} w_{t,i} y_i h_t(x_i)$$

edge weight $\alpha_t = \frac{1}{2} \ln \frac{1 + \theta_{t,j^*}}{1 - \theta_{t,i^*}}$ chosen view i^*

reward

$$r_t = 1 - \sqrt{1 - \theta_t^2}$$

irBoost.SH

$y_i, h_t(x_i) \in \mathbb{N}$

edge

$\theta_t = 2\sum_{i=2}^{\infty} w_i \left(\mathbb{I}[y_i = h_t(x_i)] - \frac{1}{2} \right)$

rBoost.SH

weight update

$$w_{t+1,i} = \frac{w_{t,i}}{Z_t} \times e^{-\alpha_t y_i h_t(x_i)}$$

normalization factor

prediction

$$H(\mathbf{x}) = sign\left(\sum_{t} \alpha_{t} h_{t,*}(x_{i,*})\right)$$

irBoost.SH

weight update $w_{t+1,i} = \frac{w_{t,i}}{Z_t} \times e^{-2\alpha_t \left(\mathbb{I}[y_i = h_t(x_i)] - \frac{1}{2} \right)}$

prediction

$$H(\mathbf{x}) = \arg\max_{c} \frac{1}{Z} \left(\sum_{t} \alpha_{t} \widehat{\boldsymbol{h}}_{t}(x_{i,*}) \right)$$

RESULTS



DATA

ASD

- 2 incomplete views
- amplicon and shotgun data
- 2 classes (ASD vs noASD)

ASD-16S

- 40 views from 16s sequences
- varying clustering similarity and filtration method





- 44 views from 16s sequences
- same pipeline like ASD-16s
- 3 classes (C, A, H)
- •Normal •Adenoma •Small adenoma •Large adenoma •Cancer

251		
228		

DATA PRE-PROCESSING

- Using QIIME 2
- SILVA taxonomy database
- Different similarity measures
- Filtering strategies:
 - filtering features by minimum frequency
 - filtering features by
 minimum samples in
 which feature must be
 represented
 - no filtering



ASD EXPERIMENTS ASD-1 ASD-2

ONLY 16S SAMPLES

- Single view
- Baseline multi-view
- irBoostSH

ONLY SHOTGUN SAMPLES

- Single view
- Baseline multi-view
- irBoostSH

ASD-3

INTERSECTION SAMPLES

- Baseline multi-view
- irBoostSH

RESULTS





ASD-16S Single-view ir







Predicted label



Single-view



irBoost.SH





VIEW STATISTICS



CONCLUSION

- Diversity necessary
- Extended:
 - multi-class case
 - view-based missing samples
- Learning rate?
- How much heterogeneous?
- Regression?
- Weight initialization? • Semi-supervised?

• Efficient multi-view framework

THANK YOU FOR LISTENING!

Q & A

