Bi-directional semi-supervised domain adaptation via gradient and class centroid alignment

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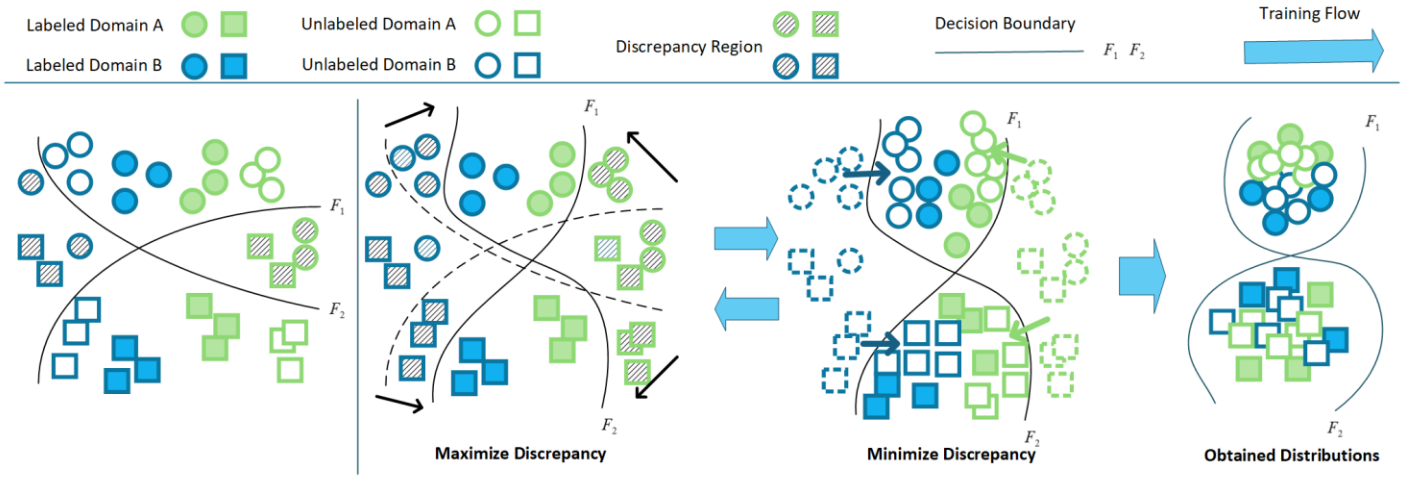
Problems & Ideas

- Motivations:
  - If the source domain has a much larger number of labeled samples than the target domain, performing supervised learning using labeled samples across domains will lead to the features of labeled target domain samples do not have the same level of diversity as those of source domain samples, or bias feature extractor and classifier towards the source domain, impairing their discriminability.
  - If the source and target domains are roughly matched and semi-supervised, both the source and target domains may have a strong motivation to engage in domain adaptation to each other.
- Ideas: A method of Gradient discrepancy minimization and labeled Class Centroid Align-ment (GCCA) for BiSSDA is proposed.

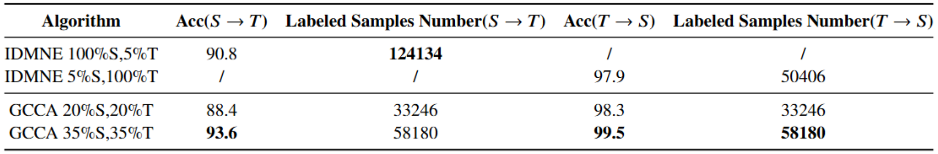


The overview of the proposed GCCA method. Discrepancy refers to the inconsistency between the predictions of twoclassifiers. Initially, it can be observed that the unlabeled samples in domains A and B, which lie outside the support of the labeled samples in both domains, can be assessed using twoclassifiers (as shown on the far left). Subsequently, in the training process, we identify two classifiers that maximize the discrepancy among the unlabeled samples in domains A and B,and then generate features that minimize this discrepancy, thereby addressing the alignment issue between two domains.

Main Contributions

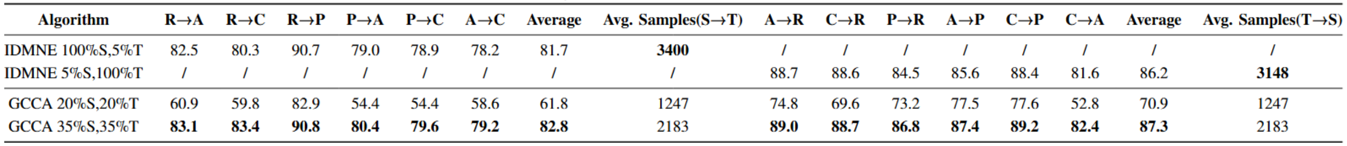
- Contributions:
  - This is the first time that the problem of bi-directional semi-supervised domain adaptation (BiSSDA) has been proposed;
  - A method of Gradient discrepancy minimization and labeled Class Centroid Alignment (GCCA) for BiSSDA is proposed, which may be a novel paradigm for transfer learning or domain adaptation in future;
  - The experimental results can give us an intuition that for a semi-supervised domain which needs to get help from another domain, it is not necessary to find a strong source domain which has enough labeled samples, but to find a semi-supervised domain that is comparable to itself to cooperate for bi-directional domain adaptation while the total number of labeled samples for both domains can be significantly reduced.

Table 6 Accuracy on VisDA-2017 for GCCA versus IDMNE.



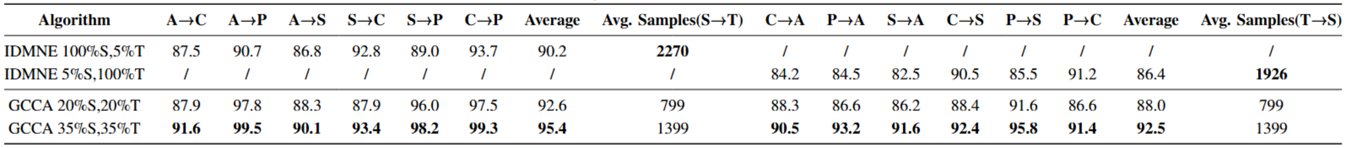
Algorithm	Acc($S \rightarrow T$)	Labeled Samples Number($S \rightarrow T$)	Acc($T \rightarrow S$)	Labeled Samples Number($T \rightarrow S$)
IDMNE 100%S,5%T	90.8	**124134**	/	/
IDMNE 5%S,100%T	/	/	97.9	50406
GCCA 20%S,20%T	88.4	33246	98.3	33246
GCCA 35%S,35%T	**93.6**	58180	**99.5**	**58180**

Table 7 Accuracy on Office-Home for GCCA versus IDMNE.



Algorithm	R→A	R→C	R→P	P→A	P→C	A→C	Average	Avg. Samples(S→T)	A→R	C→R	P→R	A→P	C→P	C→A	Average	Avg. Samples(T→S)
IDMNE 100%S,5%T	82.5	80.3	90.7	79.0	78.9	78.2	81.7	**3400**	/	/	/	/	/	/	/	/
IDMNE 5%S,100%T	/	/	/	/	/	/	/	/	88.7	88.6	84.5	85.6	88.4	81.6	86.2	**3148**
GCCA 20%S,20%T	60.9	59.8	82.9	54.4	54.4	58.6	61.8	1247	74.8	69.6	73.2	77.5	77.6	52.8	70.9	1247
GCCA 35%S,35%T	**83.1**	**83.4**	**90.8**	**80.4**	**79.6**	**79.2**	**82.8**	2183	**89.0**	**88.7**	**86.8**	**87.4**	**89.2**	**82.4**	**87.3**	2183

Table 8 Accuracy on PACS for GCCA versus IDMNE.



Algorithm	A→C	A→P	A→S	S→C	S→P	C→P	Average	Avg. Samples(S→T)	C→A	P→A	S→A	C→S	P→S	P→C	Average	Avg. Samples(T→S)
IDMNE 100%S,5%T	87.5	90.7	86.8	92.8	89.0	93.7	90.2	**2270**	/	/	/	/	/	/	/	/
IDMNE 5%S,100%T	/	/	/	/	/	/	/	/	84.2	84.5	82.5	90.5	85.5	91.2	86.4	**1926**
GCCA 20%S,20%T	87.9	97.8	88.3	87.9	96.0	97.5	92.6	799	88.3	86.6	86.2	88.4	91.6	86.6	88.0	799
GCCA 35%S,35%T	**91.6**	**99.5**	**90.1**	**93.4**	**98.2**	**99.3**	**95.4**	1399	**90.5**	**93.2**	**91.6**	**92.4**	**95.8**	**91.4**	**92.5**	1399