INFO5993/4990, CS Research Methods, 2023-Semester 2

Assignment 1 (15%)

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Task 1

[20 marks] Identify the list of top conferences and journals in your research area. While the length of this list can vary greatly depending on your research area, you may use a guideline of 8-12. Justify your selection, using a range of ranking systems and metrics such as CORE, ERA, SCOPUS, Web of Science, Scimago etc.. or other relevant evidence.

Our research encompasses major research topics such as image processing, image segmentation, the application of deep learning in medical image analysis and domain adaptation. Therefore, here is a summary of top conferences and journals in these fields based on my research:

Top conferences:

1. **The IEEE / CVF Computer Vision and Pattern Recognition Conference (CVPR)**
   1. CORE Ranking: CVPR holds an "A*" ranking in CORE2023, which is the highest rank.
   2. Scopus: CVPR boasts a CiteScore of 40.7 for 2019-22, placing it in the 99th percentile, with a citation count of 264,109 from 6,487 documents during the same period, of which 86% were cited.
   3. Scimago Journal & Country Rank: CVPR conference has an SJR of 5.952 and an H-index of 470 in 2022.

   CVPR is one of the top conferences in the field of computer vision. Not only does CVPR cover fundamental research in deep learning, but it also delves into its performance in various application scenarios, with medical image analysis being a particularly important subfield. Every year, CVPR receives high evaluations in the aforementioned ranking systems and metrics.

2. **The International Conference on Computer Vision (ICCV)**
   1. CORE Ranking: ICCV holds an "A*" ranking in CORE2023, which is the highest rank.
   2. Scopus: ICCV boasts a CiteScore of 33.9 for 2019-22, placing it in the 99th percentile, with a citation count of 103,692 from 3,055 documents during the same period, of which 93% were cited.
   3. Scimago Journal & Country Rank: ICCV conference has an SJR of 5.662 and an H-index of 313 in 2022.

   ICCV is one of the top conferences in the field of computer vision. While ICCV covers a broad spectrum of topics in computer vision, it holds significant relevance to medical computer vision.

3. **Medical Image Computing and Computer Assisted Intervention (MICCAI)**
   1. CORE Ranking: MICCAI holds an "A" ranking in CORE2023, which is a relatively high ranking.
   2. Scimago Journal & Country Rank: The MICCAI conference has an H5 index of 89.

   MICCAI is one of the most recognized conferences in the field of medical image processing and is also one of the top conferences in the field. UNet, which has a profound impact on the field of segmentation, was published on MICCAI in 2015.

4. **International Symposium on Biomedical Imaging (ISBI)**
   1. Scimago Journal & Country Rank: ISBI conference has an H5-index of 59.

   ISBI is a top conference in medical computer vision because it covers a wide range of topics and methods related to this field. It publishes high-quality papers that address the challenges and solutions of medical image processing, such as segmentation, registration, reconstruction, enhancement, etc.

5. **International Conference on Image Processing (ICIP)**
   1. CORE Ranking: ICIP holds a "B" ranking in CORE2023.
   2. Scopus: ICIP boasts a CiteScore of 33.9 for 2019-22, placing it in the 99th percentile, with a citation count of 103,692 from 3,055 documents during the same period, of which 93% were cited.
   3. Scimago Journal & Country Rank: ICIP conference has an SJR of 5.662 and an H-index of 108 in 2018.

   Although ICIP’s rankings are not relatively high, People still regard ICIP as a top conference because it is the world’s largest and most comprehensive technical conference focused on image & video processing and computer vision. ICIP covers a wide range of topics and applications in image processing, such as deep learning, medical imaging, video coding, biometrics, face recognition, etc. These are some of the reasons why ICIP has a good reputation in the research community.

Top journals:

6. **IEEE Transactions on Medical Imaging (TMI)**
   1. CORE Ranking: TMI holds an "A*" ranking in CORE2020, which is the highest rank.
   2. Scimago Journal & Country Rank: MedIA conference has an SJR of 2.872 and an H-index of 246 in 2022.
   3. Journal Citation Reports (JCR) database: It has an impact factor of 11.56.

7. **Medical Image Analysis (MedIA)**
   1. Scopus: MedIA boasts a CiteScore of 19.9 for 2019-22, placing it in the 99th percentile, with a citation count of 18,812 from 946 documents during the same period, of which 88% were cited.
   2. Scimago Journal & Country Rank: MedIA conference has an SJR of 3.195 and an H-index of 159 in 2022.
8. **IEEE Transactions on Image Processing**
   1. CORE Ranking: It holds an "A*" ranking in CORE2020, which is the highest rank.
   2. Scimago Journal & Country Rank: It has an SJR of 2.359 and an H-index of 311 in 2022.
   3. Journal Citation Reports (JCR) database: It has an impact factor of 10.50.
9. **IEEE Transactions on Multimedia**
   1. CORE Ranking: It holds an "A*" ranking in CORE2020, which is the highest rank.
   2. Scimago Journal & Country Rank: It has an SJR of 1.638 and an H-index of 144 in 2022.
   3. Journal Citation Reports (JCR) database: It has an impact factor of 7.08.

Task 2

[10 marks] Identify a list of the main research groups working in your research topic.

Based on my research, I found some research groups and individuals who have been working on topics related to cross-domain mitochondria segmentation in electron microscopy images:

1. Ryan Conrad and Kedar Narayan have developed a generalist deep learning model for instance segmentation of mitochondria in electron microscopy (EM) images. They have trained a model, MitoNet, on a highly heterogeneous unlabeled cellular EM dataset and segmented mitochondrial instances therein.
2. A group of researchers from the University of Missouri have proposed a 3D deep convolutional neural network for mitochondria instance segmentation in EM image volumes. They extended the classical U-Net semantic segmentation network with a convolutional long-short-term memory (3D CLSTM U-NET).
3. Daniel Franco-Barranco, Arrate Muñoz-Barrutia & Ignacio Arganda-Carreras have conducted an extensive study of the state-of-the-art architectures and compared them to different variations of U-Net-like models. They found very stable architectures and training configurations that consistently obtained state-of-the-art results in the well-known EPFL Hippocampus mitochondria segmentation dataset.

4. A research group from the Scientific Computing and Imaging Institute, University of Utah and the National Center for Microscopy and Imaging Research, University of California, San Diego has proposed a fully automated method that exploits both shaped information and regional statistics to segment irregularly shaped intracellular structures such as mitochondria in electron microscopy (EM) images. They used algebraic curves to extract shape features together with texture features from image patches.
5. A research group from the Xiamen Key Laboratory of Computer Vision and Pattern Recognition, and the Fujian Key Lab of Big Data Intelligence and Security has achieved cross-domain segmentation by integrating geometrical cues provided by the annotated labels and the visual cues latent in images of both domains in a framework of adversarial domain adaptive multi-task learning.

In addition to these relatively relevant research groups and individuals, I have also found some of the major research groups in medical image analysis：

1. Harvard Medical School
2. The Oxford Biomedical Image Analysis (BioMedIA) cluster
3. Seung Lab at Princeton University

Task 3

[20 marks] Give two exemplary papers in your research area, with a small paragraph explaining why you think each one is exemplary (methodology evaluation, writing style, structure, etc.). Think about papers you could use as a model for the research you are planning to do.

Here are two exemplary papers in my research area.

1. **EM-Net: Centerline-Aware Mitochondria Segmentation in EM Images Via Hierarchical View-Ensemble Convolutional Network in ISBI, 2020**

   This paper serves as an exemplary model in the field of Cross-domain Mitochondria Segmentation in Electron Microscopy Images for the following reasons. Firstly, from a methodological standpoint, the paper introduces a novel approach by jointly performing segmentation and centerline detection in a single network, emphasizing efficiency by introducing the hierarchical view-ensemble convolution (HVEC). This innovation ensures reduced computational costs without sacrificing accuracy, which is especially relevant in deep learning models. In addition, the research demonstrates thorough evaluation by testing the model on the EPFL public benchmark. Their rigorous comparative analyses against state-of-the-art methods offer a clear indication of the method's robustness and superiority. The paper’s structure is nicely organized, guiding the reader seamlessly from problem statement to solution, followed by evaluations and conclusions. The writing style is clear and concise which makes the complex topic more easy to understand. Lastly, the inclusion of tables and figures enhances the comprehensibility of their findings. Therefore, I think this paper could serve as an exemplary model for my research topic.

2. **Deep learning-based domain adaptation for mitochondria segmentation on EM volumes in *Computer Methods and Programs in Biomedicine* 222 (2022)**

   This paper stands out due to its innovative methodology, robust evaluation, and clear writing. It introduces state-of-the-art models, particularly U-Net convolutional networks and addresses the complex case of deep learning-based domain adaptation for mitochondria segmentation across different tissues and species. The authors propose three unsupervised domain adaptation strategies, including style transfer, self-supervised learning, and multi-task neural network architectures. They conducted comprehensive cross-dataset experiments using three publicly available EM datasets and found that their methods outperformed baseline methods. The paper is written in a clear and concise manner and provides a detailed description of their methodology. This allows other researchers to replicate their work and validate the results. Furthermore, the results are also presented in a clear and organized manner, with sufficient data to support their thoughts which includes all possible cross-dataset experiments. Therefore, I think this paper could serve as an exemplary model for my research topic.

Task 4

[20 marks] Identify two or three research problems that have not been answered/addressed appropriately or at all in the field of research study. you need to show a deep (within reason) understanding of the research field, well-chosen research problems, and good insights into the research questions to address.

Here are the two main questions I summarized through reading the literature:

Heterogeneity Across Modalities and Domain Variations:

Obtaining images from electron microscopes involves various parameters and settings. Differences in labs, devices, or settings can produce varied images, not just at the pixel level but more importantly in structure and texture. For instance, two images might both depict mitochondria but look quite different, posing challenges for automatic segmentation algorithms. In cross-domain contexts, this variation becomes more pronounced. A model effective in one dataset might underperform in another due to factors like microscope resolutions, sample preparation, or imaging conditions. This heterogeneity can hinder a model's performance, particularly when trained in one domain and tested in another. Therefore, the central challenge is finding improved methods to seamlessly integrate data from different modalities or to allow models to be trained on one modality and tested on another without compromising performance.

Limited Training Data and Annotation Challenges:

Annotating electron microscope images is a meticulous and specialized task. Unlike conventional image annotation, this demands in-depth biological knowledge, especially an understanding of the morphology and structure of mitochondria. Thus, acquiring substantial annotated data is both costly and time-consuming. This data scarcity poses a significant challenge for machine learning and deep learning models, which typically rely on vast amounts of data to learn and generalize. Moreover, the morphology and function of mitochondria can differ due to varying biological states or experimental conditions. This means that even if we possess some annotated data, it might only represent a fraction of possible mitochondrial morphologies. This diversity and complexity make annotation even more challenging and can potentially lead to overfitting in models. Therefore, the central challenge is finding ways to maximize the use of limited annotated data or leveraging unlabeled data to aid model learning.

Task 5

[30 marks] Provide an annotated bibliography of core relevant articles and books that are potentially very relevant to the research problems/questions identified in the previous step (about 5 per research problem) containing:
(i). a summary and evaluation of the content of the publication
(ii). how its content is relevant to the research problem/question(s)

Heterogeneity Across Modalities and Domain Variations:

1. Domain adaptation for Alzheimer's disease diagnostics from Neuroimage in 2016

Summary:

This paper focuses on the challenges of computer-aided diagnosis for Alzheimer's disease. The study emphasizes the importance of early diagnosis using MRI scans to understand the disease process, determine risk factors, and explore preventive therapies. The paper introduces a compact classification approach that combines volume, thickness, and anatomical shape features from MRI scans. The main contribution of this work is the introduction of a method for supervised domain adaptation based on instance weighting. This method addresses the challenge of variations between source and target datasets, which can significantly influence classification accuracy.

Evaluation of the Content:

This paper provides a comprehensive approach to Alzheimer's disease diagnostics using domain adaptation. The authors combine various MRI features, including volume, thickness, and anatomical shape, to achieve high classification accuracy. The introduction of instance weighting for domain adaptation is particularly noteworthy. This method allows for better integration of data from different sources, addressing the challenge of dataset variations. This paper also highlights the importance of domain adaptation for the successful deployment of computer-aided diagnostic systems in clinical settings.

Relevance to the Research Problem:

This problem revolves around the heterogeneity across modalities and domain variations, especially in the context of electron microscope images. This paper addresses the issue of domain variations, albeit in the context of Alzheimer's disease diagnostics using MRI scans. The challenges faced in this paper are similar to the challenges in this research problem, i.e. variations between source and target datasets. The method of supervised domain adaptation based on instance weighting introduced in the paper can potentially be applied or adapted to address the heterogeneity in electron microscope images. The emphasis on ensuring that models trained on one dataset perform well on another dataset is directly in line with your research problem's focus on training models on one modality and testing them on another without compromising performance.

2. Domain adaptive segmentation in volume electron microscopy imaging from ISBI 2019

Summary:

This paper discusses the challenges of automated segmentation in volume electron microscopy (EM) imaging. Traditional techniques have relied on fully supervised encoder-decoder CNNs, which require a significant amount of annotated images. The paper introduces the concept of Domain Adaptation (DA) to reduce the annotation burden. DA adapts networks trained on existing ground truth data (source domain) to work on a different (target) domain with minimal additional annotation.

The paper extends classification DA techniques to an encoder-decoder layout and proposes a novel method that adds a reconstruction decoder to the classical encoder-decoder segmentation. This is done to align source and target encoder features. The method has been validated on segmenting mitochondria in EM volumes, and the results indicate that the proposed method outperforms other recent techniques.

Evaluation of the Content:

This paper provides a comprehensive approach to address the challenges of domain variations in electron microscopy imaging. By introducing the concept of Domain Adaptation and extending it to encoder-decoder layouts, the authors offer a solution that can potentially reduce the need for extensive annotations. When validated on segmenting mitochondria in EM volumes, the results indicate that the proposed method outperforms other recent techniques, especially in challenging domain shifts like the HeLa data and the Drosophila data.

Relevance to the Research Problem:

This paper addresses the problem of heterogeneity across modalities and domain variations by proposing a method to integrate data from different modalities seamlessly. This paper's approach to training models on one modality and testing on another without compromising performance aligns with the central challenge of our research problem to some extent.

3. Semi-supervised learning with generative adversarial networks for chest X-ray classification with ability of data domain adaptation from ISBI 2018

1. Summary and Evaluation of the Content:

This paper focuses on the challenges posed by the scarcity of labeled medical imaging data and the overfitting of models to specific data domains. The authors propose a semi-supervised learning approach using Generative Adversarial Networks (GANs) to address these issues. They demonstrate that their approach requires significantly fewer labeled samples compared to traditional supervised learning methods to achieve comparable results. Moreover, the GAN-based model showcased robustness when tested across different datasets for similar classification tasks.

2. Relevance to the Research Problem:

Our research problem revolves around the heterogeneity in images obtained from electron microscopes, where differences in labs, devices, or settings can produce varied images. This variation can hinder a model's performance, especially when trained in one domain and tested in another. This paper addresses a similar challenge but in the context of medical imaging, specifically chest X-rays. The paper highlights the difficulty of obtaining large amounts of labelled data and the challenges of domain variations. By using GANs in a semi-supervised learning architecture, the authors tackle the problems of labelled data scarcity and data domain overfitting, which aligns with the key challenge of our research problem. Therefore, the methods from this paper may provide some insights that could be adapted for addressing heterogeneity in EM images.

4. Supervised domain adaptation of decision forests: Transfer of models trained in vitro for in vivo intravascular ultrasound tissue characterization from Medical Image Analysis Journal in 2016

Summary and Evaluation of the Content:

This paper introduces a supervised domain adaptation (DA) framework. This framework adapts decision forests in the presence of distribution shifts between training (source) and testing (target) domains, especially when there are limited labelled examples. The paper presents a novel method for DA that corrects distribution shifts through an error-correcting hierarchical transfer relaxation scheme. The method is applied to adapt in vitro-trained forests for in vivo applications, specifically for characterizing atherosclerotic tissues using intravascular ultrasound signals. The results demonstrate improved tissue characterization performance, reducing annotation costs and enhancing computational efficiency over traditional retraining approaches.

Relevance to the Research Problem:

This paper addresses the challenge of heterogeneity across modalities and domain variations, especially in the context of electron microscope images. By introducing a domain adaptation framework for decision forests, this paper also offers a solution to seamlessly integrate data from different modalities. This is relevant for situations where images from one domain need to be effectively used in another domain, ensuring consistent and accurate segmentation and characterization.

5. Multi-domain Adaptation in Brain MRI Through Paired Consistency and Adversarial Learning from the first MICCAI workshop in 2019

Summary and Evaluation of the Content:

This paper addresses the challenge of supervised learning algorithms failing to generalize across changes in acquisition parameters in medical imaging. The authors introduce a novel method for domain adaptation that leverages a consistency loss combined with adversarial learning. This method aims to adapt from one source domain to multiple target domains, provided there are paired data covering all domains. The study focuses on white matter lesion hyperintensity segmentation from brain MRIs. The proposed method demonstrated significant outperformance over other domain adaptation baselines, especially in the context of white matter hyperintensity segmentation.

Relevance to the Research Problem:

This paper solves the heterogeneity problem in medical imaging, where algorithms trained on one domain may not generalize well to another due to variations in acquisition parameters. By introducing a method that integrates data from different modalities seamlessly, it offers a solution to the challenge of training models on one modality and testing on another without compromising performance which is relevant to our research problem.

Limited Training Data and Annotation Challenges:

1. Automatic segmentation of mitochondria and endolysosomes in volumetric electron microscopy data from Computers in Biology and Medicine Journal in 2020

Summary and Evaluation of the Content:

This paper focuses on the automatic segmentation of intracellular compartments, specifically mitochondria and endolysosomes, in electron microscopy (EM) data. The authors highlight the challenges of manual segmentation due to the intricacies of EM data and the need for high-throughput techniques. They introduce the UroCell dataset, a novel publicly available dataset of urothelial cells. The paper evaluates various state-of-the-art segmentation methods and presents a new segmentation pipeline based on supervised deep learning. This approach effectively addresses issues like data dependencies, artifacts, and annotation errors, outperforming other baseline methods on the proposed dataset.

Relevance to the Research Problem:

This paper addresses the challenge of annotating electron microscope images, especially mitochondria. It emphasizes the difficulties of manual segmentation and the importance of specialized knowledge for accurate annotation. By introducing an automatic segmentation method and a new dataset, the study offers a solution to the problem of limited annotated data. The deep learning approach proposed can potentially reduce the need for extensive annotated data, which is relevant to our research problem.

2. Fast Mitochondria Segmentation for Connectomics from arXiv in 2018

Summary and Evaluation of the Content:

This paper focuses on the automatic detection of mitochondria in EM images, crucial for understanding the wiring diagram of the mammalian brain. The authors introduce a fully automatic mitochondria detector based on a modified U-Net architecture. This detector achieves high accuracy and rapid processing times, with results showing a Jaccard index of up to 0.90 and inference speeds below 16ms for a 512 × 512 image tile, which outperforms real-time methods. The authors also present updated versions of benchmark datasets and re-annotated by experts.

Relevance to the Research Problem:

This paper addresses the challenge of annotating electron microscope images, specifically mitochondria. The introduced automatic detector alleviates the need for extensive manual annotation, which is time-consuming and requires specialized knowledge. By achieving real-time detection, the method offers a solution to the problem of data scarcity and the potential for overfitting. The updated datasets provide a more accurate foundation for training and evaluating machine learning models in this domain which could be helpful for our research topic.

3. DenseUNet: densely connected UNet for electron microscopy image segmentation from IET Image Processing in 2020

Summary and Evaluation of the Content:

This paper addresses the challenge of EM image segmentation. Traditional EM image segmentation is labour-intensive and requires expert knowledge. This paper introduces DenseUNet, a novel method that combines the strengths of UNet and DenseNet for efficient EM image segmentation. This approach not only reduces the number of parameters but also alleviates the vanishing-gradient problem, encouraging feature reuse and reducing overfitting. The method was tested on the ISBI 2012 EM dataset and achieved state-of-the-art results without any post-processing or pre-training.

Relevance to the Research Problem:

The research problem emphasizes the challenges of annotating electron microscope images due to their complexity and the need for specialized knowledge. The DenseUNet method directly addresses this by offering an efficient and effective solution for EM image segmentation. Its design reduces overfitting, which is particularly crucial given the limited annotated data available. Furthermore, its high performance on a standard dataset demonstrates its potential to maximize the use of limited annotated data.

4. Sparse Object-level Supervision for Instance Segmentation with Pixel Embeddings from CVPR in 2022

Summary and Evaluation of the Content:

This paper addresses the challenge of training instance segmentation models on sparsely annotated images. Traditional methods require densely annotated images, especially in biomedical fields where domain expertise is essential. The authors introduce a proposal-free segmentation approach based on non-spatial embeddings, leveraging the structure of the learned embedding space to extract individual instances. They also present a novel self-supervised consistency loss for unlabeled parts of training data. Evaluations on various datasets, including 2D and 3D microscopy images, showed promising results, with significant performance improvements even with limited annotated data.

Relevance to the Research Problem:

This paper addresses the challenge of limited training data and annotation in electron microscopy images. By proposing a method that can be trained on sparsely annotated images, it offers a solution to the costly and time-consuming process of acquiring densely annotated data. The approach's ability to leverage unlabeled data aligns with the need to maximize the use of limited annotated data, which is relevant to the research problem.

5. A domain-adaptive two-stream U-Net for electron microscopy image segmentation from ISBI in 2018

Summary and Evaluation of the Content:

This paper addresses the challenge of segmenting EM images, especially when limited annotated data is available for a specific domain. The authors introduce a Domain Adaptation approach using a two-stream U-Net architecture. One stream is trained on a source domain with abundant data, while the other adapts to a target domain with scarce data. The method also incorporates a novel loss function based on a differentiable version of the Jaccard index. Experimental results demonstrate the superiority of this approach over other state-of-the-art Domain Adaptation methods, especially in segmenting organelles in EM images.

Relevance to the Research Problem:

This paper addresses the research problem of limited training data and annotation challenges in electron microscopy images. By introducing a Domain Adaptation approach with a two-stream U-Net, the method leverages existing annotations from a well-represented domain to assist in segmenting images from a less-represented domain. This approach effectively maximizes the use of limited annotated data and potentially mitigates the overfitting issue, which is relevant to our research problem.

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