Transfer Learning in Imaging Genomics: A Survey

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Abstract

Transfer learning has become an instrumental technique in imaging genomics, particularly for enhancing the diagnostic precision and treatment strategies of colorectal cancer and liver metastasis. This survey paper delves into the utilization of pre-trained convolutional neural networks (CNNs) for feature extraction, addressing the pervasive issue of data scarcity and variability in medical imaging datasets. By leveraging extensive datasets and applying domain adaptation techniques, transfer learning improves model performance and generalization across diverse clinical settings. The integration of synthetic data further enhances model robustness, enabling accurate classification and predictive modeling despite limited labeled datasets. Successful applications in colorectal cancer imaging underscore the transformative potential of transfer learning, showcasing significant improvements in diagnostic accuracy and model adaptability. The paper also highlights the role of interdisciplinary collaborations and technological advancements in driving innovation within imaging genomics. Future research directions emphasize the need for sophisticated data augmentation techniques, optimized computational frameworks, and the integration of advanced AI methods to refine predictive models. Overall, transfer learning in imaging genomics not only enhances diagnostic processes but also supports personalized treatment strategies, ultimately leading to improved patient outcomes. These advancements promise to revolutionize medical imaging, offering new avenues for effective cancer diagnosis and treatment.

1 Introduction

1.1 Significance of Transfer Learning in Imaging Genomics

Transfer learning has become essential in imaging genomics, significantly improving the diagnostic and treatment processes for complex diseases such as colorectal cancer and liver metastasis. The challenge of limited high-quality annotated data in medical image analysis, compounded by the high costs of expert annotations [1], is effectively addressed through transfer learning. This approach utilizes pre-trained models that can be fine-tuned for specific medical imaging tasks, enhancing model performance even with minimal data [2].

A key advantage of transfer learning is its ability to reduce inconsistencies in feature distributions between training and testing datasets from diverse sources, such as different endoscopic equipment [3]. This capability is critical for maintaining robust classification performance across various medical imaging datasets. Typically, transfer learning in medical imaging involves leveraging convolutional neural networks (CNNs) pre-trained on large-scale datasets like ImageNet, which are adapted to extract pertinent features from medical images [4]. This strategy not only mitigates data scarcity but also enhances the generalization of machine learning models across different medical imaging cohorts [5].

Moreover, integrating synthetic image data has been shown to boost transfer learning effectiveness, thereby improving diagnostic accuracy and treatment strategies in imaging genomics [6]. The transfer of knowledge from large-scale natural image datasets to specialized tasks, such as microscopy, underscores the necessity of domain-specific features for precise classification [4]. In histopathology,

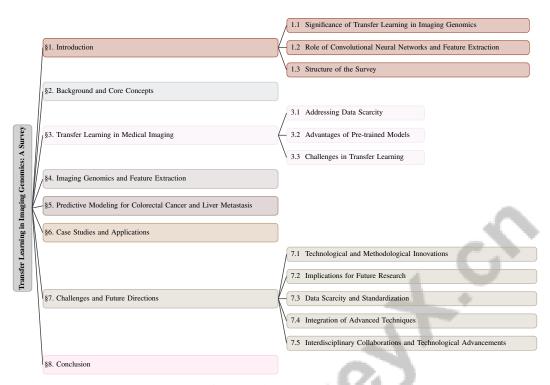


Figure 1: chapter structure

particularly for binary classification of colorectal polyps, established benchmarks facilitate model performance evaluation, emphasizing transfer learning's critical role in this field [7].

Ultimately, transfer learning is vital in imaging genomics, effectively addressing data scarcity while enhancing diagnostic and treatment processes by leveraging pre-trained models. This technique not only improves model performance through feature reuse but also optimizes resource utilization, facilitating medical image analysis despite limited data availability. Ongoing research highlights the necessity of selecting appropriate models and transfer learning strategies to maximize effectiveness, enabling practitioners to navigate the complexities of domain differences and varying data characteristics in medical applications [8, 9, 10]. The ability to apply existing knowledge from extensive datasets to specific medical imaging tasks not only enhances model performance but also reduces the need for exhaustive labeling efforts, ultimately leading to improved patient outcomes.

1.2 Role of Convolutional Neural Networks and Feature Extraction

Convolutional Neural Networks (CNNs) have revolutionized medical image analysis by serving as powerful feature extractors, particularly within imaging genomics. Their layered architecture effectively captures complex patterns from raw image data, essential for developing predictive models that accurately diagnose diseases such as colorectal cancer and liver metastasis [11]. The success of CNNs in natural image classification has influenced their application in medical domains, facilitating automatic extraction of hierarchical features crucial for accurate diagnosis and treatment planning [12].

However, the effective training of CNNs typically requires large datasets, often unavailable in medical imaging due to high data annotation costs and the scarcity of labeled images [13]. Transfer learning has emerged as a viable solution, allowing the adaptation of pre-trained CNN models like ResNet or Inception for specific medical imaging tasks [8]. This approach alleviates data scarcity issues and enhances the generalization capabilities of CNNs across various medical imaging domains [14].

Furthermore, integrating transfer learning techniques with CNNs has been shown to significantly enhance predictive model performance. Factors such as the choice of loss network architecture and specific feature extraction layers critically influence model efficacy, as demonstrated in systematic analyses of deep learning frameworks [15]. Innovative methods, including surrogate supervision

schemes, enable pre-training of models directly within the medical domain, optimizing the utility of CNNs in medical image analysis [14].

In the broader context of transfer learning, distinguishing between homogeneous and heterogeneous approaches is essential, as these frameworks offer varied strategies for leveraging pre-trained models in new domains [16]. By employing sparse discriminant models trained on reference databases, CNNs can effectively adapt to select relevant features for new but related tasks, thereby enhancing the predictive power of medical imaging models [12].

1.3 Structure of the Survey

This survey is structured into several key sections, each addressing distinct aspects of transfer learning in imaging genomics, particularly concerning colorectal cancer and liver metastasis. Following the introduction, which highlights the significance of transfer learning and the crucial role of convolutional neural networks (CNNs) in feature extraction, the paper provides a comprehensive overview of the fundamental principles of transfer learning, imaging genomics, and predictive modeling, elucidating their interconnections and relevance to the study.

Subsequent sections explore the application of transfer learning in medical imaging, focusing on its benefits and challenges. This includes discussions on leveraging pre-trained CNNs for feature extraction to mitigate data scarcity in medical datasets. The section on imaging genomics and feature extraction further examines the impact of these techniques on cancer diagnosis and treatment, emphasizing their role in predictive modeling for colorectal cancer and liver metastasis.

The development of predictive models utilizing transfer learning and feature extraction techniques is scrutinized, with an emphasis on modeling challenges and solutions specific to colorectal cancer and liver metastasis. Case studies and applications highlight successful implementations of transfer learning in imaging genomics, showcasing outcomes and benefits, such as improved performance in tasks with limited annotated data by leveraging knowledge from related domains, as evidenced by recent research examining factors influencing transfer learning effectiveness in medical imaging [17, 10].

The survey identifies current challenges in transfer learning and proposes future research directions, emphasizing the importance of leveraging technological advancements and fostering interdisciplinary collaborations. These strategies aim to address limitations of existing methodologies, enhance the effectiveness of knowledge transfer across diverse domains, and ultimately improve the performance of machine learning models in scenarios with scarce labeled data [18, 17, 19, 16, 5]. This structured approach ensures a comprehensive understanding of transfer learning's potential in enhancing diagnostic accuracy and treatment strategies in imaging genomics. The following sections are organized as shown in Figure 1.

2 Background and Core Concepts

2.1 Colorectal Cancer and Liver Metastasis

Colorectal cancer represents a significant global health challenge, being one of the top causes of cancer-related deaths. It often originates in the colon or rectum and frequently metastasizes to the liver, complicating treatment and worsening prognosis. This progression necessitates the integration of genomic data with advanced imaging techniques to better understand tumor biology and heterogeneity, crucial for precise disease classification and prognosis [20]. Such integration is essential for developing accurate diagnostic and therapeutic strategies.

Imaging challenges in colorectal cancer and liver metastases arise from variability in imaging protocols and patient demographics, which impede the development of robust predictive models [5]. Limited sample sizes for specific cancer types exacerbate these issues, often resulting in nongeneralizable outcomes [21]. Consequently, variability in imaging modalities and data distributions demands advanced analytical techniques to enhance diagnostic accuracy and treatment efficacy.

Differences in histopathological image stain styles notably affect tumor classification network performance, highlighting the need for effective transfer learning strategies to ensure consistent diagnostic outcomes [20]. Resources like the CytoImageNet dataset, with 890,737 microscopy images across 894 classes, are invaluable for training models in bioimage analysis, aiding in the development of

predictive models capable of handling diverse imaging data [4]. Similarly, the Petri Dish dataset, derived from colorectal polyp whole-slide images, is critical for evaluating histopathology image analysis model performance [7].

Current research often lacks a comprehensive theoretical framework to address complexities arising from varying data distributions between source and target problems, creating a gap that must be filled to enhance imaging genomics models' accuracy and reliability [22]. Estimating polygenic risk scores (PRS) using genome-wide genotype data faces challenges due to numerous genetic variants and limited sample sizes, necessitating innovative solutions [23].

2.2 Predictive Modeling in Medical Imaging

Predictive modeling in medical imaging has advanced significantly through the integration of transfer learning and feature extraction techniques, addressing challenges related to data scarcity and domain variability. Transfer learning enables models pre-trained on extensive datasets to be adapted for specific medical imaging tasks, enhancing performance in scenarios with limited labeled data [17]. This adaptation is critical in medical contexts where obtaining annotated datasets is costly and time-consuming [1].

Managing distribution shifts between training (source) and test (target) data is a critical aspect of developing predictive models, as unaddressed shifts can impair generalization [24]. Techniques like Multi-source Adversarial Transfer Learning (MSATL) extract transferable local features between similar source and target domains through adversarial training and attention mechanisms, enhancing adaptability and performance [25].

Benchmarks comparing transfer learning and self-supervised learning methods in medical image classification provide insights into their respective strengths and weaknesses, optimizing predictive models [9]. The Few-Shot Efficient Fine-Tuning (FSEFT) framework employs parameter-efficient fine-tuning and black-box Adapters to adapt models in clinical scenarios, demonstrating potential for efficient customization in resource-limited settings [26].

Addressing out-of-distribution (OOD) detection is crucial for trustworthy AI practices in digital pathology. Benchmarks evaluating various OOD detection methods enhance the reliability of deep neural networks (DNNs) in clinical applications [27], essential for maintaining high accuracy when applying predictive models to new datasets with distinct characteristics.

Smaller, well-annotated datasets, such as the Petri Dish dataset for histopathology image analysis, provide accessible resources for researchers to assess model performance and improve predictive accuracy [7]. These datasets, combined with innovative modeling frameworks, contribute to the ongoing enhancement of predictive modeling in medical imaging.

The integration of transfer learning and feature extraction techniques significantly elevates predictive model development in medical imaging. These strategies enhance accuracy and efficiency while promoting robustness and adaptability to the unique challenges posed by medical imaging datasets. Parameter-Efficient Fine-Tuning (PEFT) has shown substantial performance improvements—up to 22

3 Transfer Learning in Medical Imaging

Transfer learning has significantly advanced medical imaging by addressing challenges associated with data scarcity. This section delves into methods that overcome limitations of limited labeled datasets, focusing on innovative strategies enhancing model performance and adaptability. As illustrated in Figure 2, the hierarchical structure of transfer learning in medical imaging highlights key strategies for addressing data scarcity. This figure outlines the advantages of pre-trained models and the challenges faced in their implementation. It specifically details methods and techniques that enhance model performance and adaptability, underscoring the benefits of leveraging pre-trained models for improved accuracy and efficiency, while also acknowledging the obstacles posed by domain discrepancies and model limitations. The following subsection discusses the critical issue of data scarcity and how transfer learning leverages existing knowledge to improve medical imaging outcomes.

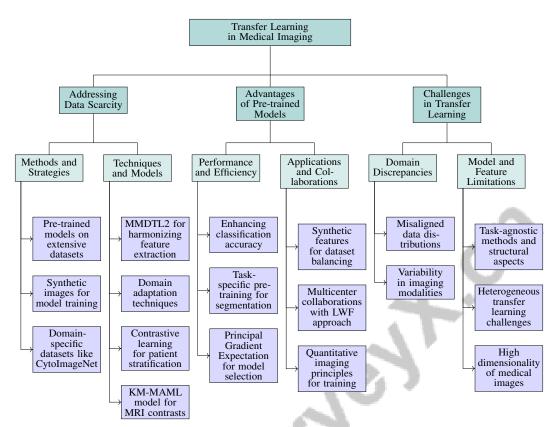


Figure 2: This figure illustrates the hierarchical structure of transfer learning in medical imaging, highlighting key strategies for addressing data scarcity, the advantages of pre-trained models, and the challenges faced in implementation. It outlines methods and techniques that enhance model performance and adaptability, the benefits of leveraging pre-trained models for improved accuracy and efficiency, and the obstacles posed by domain discrepancies and model limitations.

3.1 Addressing Data Scarcity

Data scarcity in medical imaging, driven by high costs and privacy concerns, poses a significant challenge. Transfer learning mitigates this by employing pre-trained models on extensive datasets, thus reducing the dependency on large labeled datasets in target domains [26, 9]. Innovative methodologies, such as synthetic images, further enhance transfer learning by supplementing real data and improving model training [6]. The CytoImageNet dataset exemplifies the benefits of large-scale, domain-specific datasets in improving feature extraction for microscopy tasks [4]. Such augmentation is crucial in medical fields where acquiring annotated datasets is costly and time-consuming [7].

Methods like MMDTL2 address inconsistent feature distributions across imaging systems, harmonizing feature extraction across diverse datasets [3]. Domain adaptation techniques, demonstrated by MRI analysis benchmarks, overcome distribution shifts affecting model performance and enhance generalization [28, 27]. Contrastive learning techniques achieve high performance in patient stratification without extensive labeled datasets, maintaining accuracy while addressing data scarcity [23]. The KM-MAML model, which generates mode-specific weights, illustrates adaptation to various MRI contrasts, improving performance in heterogeneous datasets and tackling data scarcity effectively [29].

Efficient transfer of core knowledge is critical, avoiding negative transfer by selectively transferring relevant information [30]. This selective transfer enhances efficiency and accuracy in medical imaging tasks. By leveraging pre-trained models and innovative strategies, transfer learning provides a robust framework for overcoming data scarcity, fostering predictive model development with high performance and adaptability even in data-limited environments [5].

Figure 3 illustrates the strategies to address data scarcity in medical imaging, highlighting transfer learning, domain adaptation, and contrastive learning as key approaches. It emphasizes the use of pre-trained models, synthetic images, and domain-specific datasets, alongside methods like MMDTL2 and KM-MAML for domain adaptation, and contrastive learning for efficient patient stratification and knowledge transfer.

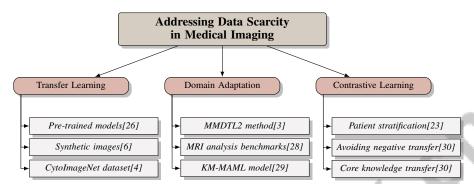


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3.2 Advantages of Pre-trained Models

Pre-trained models in medical imaging offer numerous advantages by enhancing model performance through existing knowledge from extensive datasets. These models, often trained on large-scale datasets like ImageNet, provide robust feature representations that can be fine-tuned for specific medical imaging tasks, thereby improving classification accuracy and computational efficiency [3]. The GTL approach exemplifies the transfer of core knowledge, enabling faster adaptation and improved performance with fewer parameters [30].

Pre-trained models can generate synthetic features, aiding in dataset balancing and enhancing classification accuracy, crucial in medical imaging where annotated data is scarce [2]. In segmentation tasks, models with segmentation-pretrained encoders outperform those with classification-pretrained encoders, highlighting the importance of task-specific pre-training [31]. The Principal Gradient Expectation (PGE) method evaluates the transferability of pre-trained models by calculating first-order gradients and their expectation, optimizing model selection for specific tasks [32].

Pre-trained models also facilitate multicenter collaborations in medical imaging, as demonstrated by the LWF approach, which enables effective knowledge transfer between centers while maintaining high sensitivity and precision in tasks such as breast mass detection [33]. These advantages include improved computational efficiency, enhanced predictive accuracy, and adaptability to various tasks. By leveraging large-scale datasets, pre-trained models provide robust initial conditions for fine-tuning on specific medical tasks, leading to improved performance in clinical applications. Incorporating quantitative imaging principles during training enhances image quality and biological accuracy, maximizing model effectiveness in real-world medical scenarios [9, 34, 8, 35, 36]. These benefits underscore the pivotal role of pre-trained models in addressing data scarcity and domain variability, advancing effective and efficient medical imaging solutions.

3.3 Challenges in Transfer Learning

Transfer learning in medical imaging encounters several challenges that can hinder the development of effective predictive models. A significant issue is the domain discrepancy between source and target domains, which existing methods often fail to bridge effectively [24]. This discrepancy can lead to suboptimal performance due to misaligned data distributions, posing a critical obstacle to robust transfer learning outcomes [22]. Variability in imaging modalities and inter-modality heterogeneity further complicates this process, as models must adapt to diverse imaging characteristics and patient demographics without sacrificing accuracy.

The reliance on task-agnostic methods may result in high regret by failing to identify optimal models within heterogeneous model pools, exacerbated by the high costs of obtaining sufficient labeled data, which often bottleneck deep learning applications in medical imaging [22]. Many approaches focus predominantly on weight tuning while neglecting structural model aspects, potentially leading to suboptimal transfer performance.

Heterogeneous transfer learning demands effective feature mapping between disparate domains, a task that current studies often struggle to address adequately [22]. This limitation can restrict the exploration of interrelatedness between target domains, resulting in partial knowledge transfer and diminishing the potential benefits of transfer learning in medical imaging. Additionally, the high dimensionality of medical images presents challenges concerning computational efficiency and model scalability.

Innovative approaches and frameworks are needed to manage domain discrepancies, optimize model selection, and enhance structural aspects of transfer learning models. By addressing challenges such as differences in data characteristics between natural and medical images, model architecture influences, and feature reuse complexities, transfer learning implementation can be significantly improved. This enhancement is likely to yield more robust and accurate predictive models, effectively utilizing limited medical datasets, and advancing diagnostic capabilities and patient outcomes in healthcare [10, 9, 8, 35, 36].

4 Imaging Genomics and Feature Extraction

The fusion of imaging data with genomic information in imaging genomics is crucial for advancing diagnostic accuracy and guiding treatment strategies. Machine learning and large-scale data analytics facilitate the extraction of valuable insights from complex datasets, encompassing diverse modalities like MRI scans and genetic profiles. This integration enhances disease detection precision and supports personalized medicine through quantitative imaging principles and innovative datasets, such as CytoImageNet, which provide robust features for classification tasks [34, 5, 4, 27]. A comprehensive examination of imaging genomics' contributions to cancer diagnosis underscores feature extraction's pivotal role in predictive modeling, essential for optimizing imaging genomics' effectiveness.

4.1 Role of Imaging Genomics in Cancer Diagnosis

Imaging genomics significantly enhances cancer diagnosis by merging imaging data with genomic information, improving cancer subtyping accuracy and supporting advanced methodologies such as meta-learning. This integration effectively utilizes gene expression profiles, even with limited samples, optimizing machine learning models for superior predictive outcomes. It also addresses digital pathology challenges, including out-of-distribution detection, through robust evaluation protocols and diverse machine learning techniques, ultimately refining treatment strategies and patient management [37, 27]. This interdisciplinary approach captures tumor phenotypic expressions, providing a comprehensive understanding of tumor biology and heterogeneity, crucial for developing precise diagnostic and therapeutic strategies, particularly in complex diseases like colorectal cancer and liver metastasis.

Frameworks such as Bayesian Multi-Domain Learning (BMDL) illustrate imaging genomics' integration in cancer diagnosis by employing a generative framework that learns domain-dependent latent representations of overdispersed count data, thereby enhancing cancer subtyping accuracy [21]. This approach systematically addresses variability in imaging protocols and patient demographics, boosting predictive model reliability.

Continual learning methods are vital for advancing imaging genomics, allowing models to adapt to new data without forgetting previously acquired knowledge, thus maintaining high diagnostic accuracy over time [20]. This adaptability is essential in cancer diagnosis, where continuous data influx can shift distributions, requiring adaptive learning strategies to sustain model performance.

4.2 Impact of Feature Extraction on Predictive Modeling

Feature extraction is a cornerstone in developing predictive models within imaging genomics, significantly influencing model accuracy and reliability. This process enhances diagnostic precision by generalizing models across diverse datasets. Recent advancements in transfer learning underscore feature extraction's importance, especially in data-scarce and heterogeneous scenarios. Transfer learning leverages knowledge from related source domains to improve target task performance, addressing challenges arising from differing training and testing data distributions, particularly in medical image analysis [8, 38, 17].

Innovatively, features extracted from inadequately pre-trained models may outperform those from fully trained models, challenging the assumption that extensive training always enhances performance [39]. This insight is crucial for optimizing feature extraction processes, ensuring high accuracy and reliability.

Integrating metadata with pathology labels has been shown to enhance TB detection and patient metadata prediction accuracy, demonstrating how enriched feature sets improve predictive modeling outcomes [40]. The DVME approach illustrates the impact of effective feature extraction on predictive modeling, enhancing performance across various tasks [1]. Additionally, the MMDTL2 method improves predictive modeling accuracy by enforcing similarity between transformed target features and source features, despite variations in imaging conditions [3]. Domain adaptation techniques, achieving a Dice score of 0.63 with only two training examples, further highlight feature extraction's critical role in predictive modeling [28]. The utilization of synthetic data within a bridged transfer framework has also shown to enhance model performance, underscoring synthetic features' value in predictive modeling [6].

4.3 Challenges in Feature Extraction and Knowledge Transfer

Feature extraction and knowledge transfer in imaging genomics face significant challenges, particularly when adapting pre-trained models from established domains like ImageNet to new medical imaging contexts. The success of transfer learning in this domain relies on factors such as dataset size, model capacity, inductive bias, and the similarity between source and target domains. Although transfer learning generally proves beneficial, the assumption that features from the source domain are directly reusable is being reevaluated, highlighting the need for careful model selection and transfer learning strategies to optimize medical image classification performance [8, 10]. A primary challenge is selecting optimal layers for knowledge transfer, as mismatches can lead to significant prediction errors. This issue is exacerbated by variability in imaging data, complicating feature space alignment across domains.

In continual learning scenarios, where models are pre-trained on specific datasets, transfer learning methods may struggle to achieve optimal performance due to entrenched knowledge from initial training phases, which may not align with new task requirements. Consequently, the model's adaptability to new domains can be hindered, particularly with significant discrepancies between source and target domains. While transfer learning enhances performance in various applications, its effectiveness can vary based on the relevance of pre-trained knowledge to new tasks, necessitating structural modifications to better align with target task characteristics [17, 38, 41, 42, 39]. This limitation emphasizes the need for adaptive strategies that can dynamically adjust to evolving data distributions.

The Pairwise Similarity Transfer approach offers a promising solution for transfer learning, enabling the transfer of pairwise similarity properties from a source to a target domain, even when their predictive functions differ. This method assumes that if the source model predicts similar outcomes for a pair of instances, the target model is likely to do the same. By incorporating pairwise similarity into a flexible graph-based regularization framework, this approach enhances standard supervised learning algorithms' effectiveness, integrating domain knowledge and improving performance in scenarios with scarce labeled data [43, 17, 16, 18]. However, like other methods, it relies on a sufficient number of labeled samples to guide the alignment process, which may not always be feasible.

Distribution shifts pose substantial challenges to effective knowledge transfer, disrupting the assumption of consistent probability distributions between training and testing data. This necessitates advanced transfer learning techniques to facilitate learning in label-scarce target domains and en-

hance model performance across diverse applications [44, 18, 17, 45]. Methods that incorporate prior knowledge regarding shape restrictions can improve parameter estimation despite these shifts, contingent on the relevance and accuracy of that prior knowledge. This underscores the importance of robust domain adaptation techniques that accommodate diverse task distributions.

Meta-transfer learning (MTL) encounters difficulties when faced with extremely diverse task distributions, where pre-trained knowledge may lack relevance. This limitation necessitates developing adaptable learning frameworks that effectively manage a wide array of tasks, particularly in contexts with scarce labeled data or significant discrepancies between source and target domains. Innovative approaches like Multi-Relevance Transfer Learning and model optimization techniques such as TransTailor can leverage existing related data to enhance performance across various applications, facilitating efficient knowledge transfer and improving overall model efficacy [18, 17, 45, 41, 46].

Domain mismatches between expert models and downstream tasks can hinder performance, especially in structured tasks with specific domain requirements. The quality and relevance of reference databases are crucial for accurate predictions in transfer learning; insufficient commonalities between reference data and the target experiment can yield unreliable outcomes, as effective knowledge transfer relies heavily on data distribution alignment and shared latent factors between domains [17, 18, 47, 12, 44].

The challenges in feature extraction and knowledge transfer are further exacerbated by distribution shifts affecting model performance, particularly when transferring knowledge across different imaging cohorts. These shifts necessitate reevaluating existing transfer learning conventions to develop more robust and adaptable models. The limitations of GTL in scenarios with significant architectural differences between networks complicate the compatibility of learnable genes, impacting knowledge transfer efficacy [30].

To address the challenges associated with transfer learning, innovative methodologies must be developed to manage discrepancies between domains, optimize model selection, and refine transfer learning framework structural components. This includes leveraging knowledge from related source domains to enhance target learner performance, addressing domain shifts through strategies like importance-weighting and feature augmentation, and utilizing techniques such as Multi-Relevance Transfer Learning (MRTL) to simultaneously transfer knowledge across multiple target domains. Approaches like TransTailor, which fine-tunes pre-trained model structures to better align with specific target tasks, can significantly improve transfer performance while reducing computational costs [18, 17, 24, 41, 16]. By overcoming these obstacles, the implementation of transfer learning in imaging genomics can be substantially enhanced, leading to more reliable and effective predictive models.

5 Predictive Modeling for Colorectal Cancer and Liver Metastasis

5.1 Model Robustness and Efficiency

Benchmark	Size	Domain	Task Format	Metric
DVME[1]	220,025	Medical Imaging	Image Classification	AUC, Kappa
OODD4DP[27]	272,000	Histopathology	Out-of-Distribution Detection	AUROC, PPR
HistoKT[48]	176,680	Histopathology	Image Classification	Top-1 accuracy
Transfusion[35]	200,000	Ophthalmology	Image Classification	AÚC
TL-MI[10]	327,680	Medical Imaging	Image Classification	ROC-AUC, Quadratic
				Cohen Kappa
OSBORN[49]	1,000,000	Image Classification	Ensemble Learning	PCC, KT
SSL-SCV[50]	400	Surgical Computer Vision	Phase Recognition	F1 Score, mAP
TransNAS-Bench-	120,000	Image Classification	Multi-task Evaluation	Accuracy, SSIM

Table 1: This table presents a comprehensive overview of representative benchmarks utilized in the evaluation of model robustness and efficiency within the medical imaging domain. It details the size, domain, task format, and performance metrics for each benchmark, highlighting their relevance to tasks such as image classification and out-of-distribution detection. These benchmarks are instrumental in assessing the adaptability and accuracy of predictive models in diverse clinical settings.

Ensuring robustness and efficiency in predictive models for colorectal cancer and liver metastasis is vital for accurate diagnostics and prognostics. These models must generalize across diverse datasets, which often exhibit variability in imaging modalities and patient demographics [5]. Addressing this variability is crucial, particularly given the scarcity of annotated datasets in the medical domain [1]. Transfer learning frameworks that incorporate domain adaptation techniques, such as adversarial training and attention mechanisms, effectively align feature distributions between source and target domains, enhancing model adaptability and robustness [25]. The use of synthetic data further augments real-world datasets, improving robustness by capturing a broader range of variability, which is especially beneficial in balancing datasets and enhancing classification accuracy in medical imaging [6, 2].

Handling out-of-distribution (OOD) data is also crucial for model robustness. Table 1 provides a detailed overview of the representative benchmarks used to assess model robustness and efficiency in the context of medical imaging for colorectal cancer and liver metastasis diagnostics. Benchmarks for OOD detection provide insights into model performance in clinical settings, ensuring high accuracy with novel data [27]. Efficiency can be enhanced through parameter-efficient fine-tuning frameworks, such as Few-Shot Efficient Fine-Tuning (FSEFT), which allow rapid model adaptation with minimal computational overhead [26]. These frameworks leverage pre-trained models to maintain high performance with fewer parameters, reducing computational burdens and facilitating the deployment of predictive models in clinical environments.

Advanced methodologies, including transfer learning, synthetic data augmentation, and domain adaptation techniques, collectively enhance predictive models' effectiveness and efficiency for colorectal cancer and liver metastasis. These approaches accelerate model convergence and improve performance, particularly in medical imaging contexts where precision and recall are critical for accurate diagnosis [52, 17, 24, 16, 8]. By addressing data variability and distribution shifts, these strategies ensure accurate and reliable predictive model outcomes, ultimately improving patient care and treatment planning.

5.2 Domain Adaptation and Generalization

Domain adaptation and generalization are essential for maintaining high performance in predictive models across diverse datasets, especially in medical imaging where data variability is common. The challenge is to adapt models trained on specific source domains to perform effectively on target domains with differing characteristics, often with limited labeled data [17]. Adversarial training techniques, such as Multi-source Adversarial Transfer Learning (MSATL), align feature distributions between source and target domains, enhancing model adaptability and performance [25]. MSATL emphasizes transferable local features through attention mechanisms, ensuring effective generalization across various medical imaging datasets.

Synthetic data generation plays a crucial role in enhancing domain generalization by augmenting existing datasets, providing a comprehensive training set that captures a wider range of variability [6]. This is particularly beneficial where acquiring labeled data is challenging, enabling models to learn robust feature representations that generalize well to new domains. Parameter-efficient fine-tuning frameworks, like Few-Shot Efficient Fine-Tuning (FSEFT), further improve generalization by facilitating rapid adaptation of pre-trained models with minimal computational overhead [26]. By leveraging pre-trained knowledge, FSEFT enables model deployment across different domains while maintaining high accuracy and efficiency.

Developing benchmarks for out-of-distribution (OOD) detection is essential for evaluating model generalization in clinical settings. These benchmarks provide insights into the trustworthiness of deep neural networks (DNNs) when applied to novel data, ensuring models maintain high performance even with previously unseen datasets [27]. Such evaluations are crucial for verifying predictive models' reliability in medical applications.

6 Case Studies and Applications

Transfer learning represents a pivotal advancement in medical imaging, notably for colorectal cancer. This section delves into case studies and applications showcasing the integration of transfer learning techniques, which enhance diagnostic precision and treatment strategies. By exploring

these applications, we gain insights into transfer learning's potential to improve patient outcomes and address challenges in colorectal cancer imaging. The following subsection examines successful applications, highlighting methodologies and their clinical implications.

6.1 Successful Applications of Transfer Learning in Colorectal Cancer Imaging

Transfer learning has markedly enhanced diagnostic accuracy and treatment strategies in colorectal cancer imaging. Noteworthy is the use of pre-trained convolutional neural networks (CNNs) for histopathological image analysis of colorectal polyps, significantly improving classification of cancer subtypes and addressing data scarcity, thereby enhancing model generalization across diverse cohorts [7].

The use of synthetic image data further underscores transfer learning's success. Advanced augmentation techniques generate synthetic images that bolster CNN training, enhancing model robustness in colorectal cancer classification [6]. This approach is critical for creating balanced datasets, essential for reliable predictive model development in medical imaging.

Large-scale, domain-specific datasets like CytoImageNet have also advanced transfer learning in colorectal cancer imaging. These datasets provide extensive resources for bioimage analysis, facilitating the fine-tuning of pre-trained models and optimizing their diagnostic performance [4]. Their availability enhances model customization and diagnostic capabilities.

Innovative frameworks such as Multi-source Adversarial Transfer Learning (MSATL) address variability in imaging protocols and patient demographics. By aligning feature distributions across domains, these techniques improve model adaptability to new data while maintaining accuracy and efficiency [25]. Attention mechanisms focus on transferable local features, ensuring robust performance across varied contexts.

Comparative studies of pre-trained models like Densenet161 and Resnet101 reveal transfer learning's transformative potential in enhancing diagnostic accuracy and optimizing treatment planning. Leveraging knowledge from related tasks, transfer learning accelerates model convergence, addresses data scarcity, and facilitates precise cancer detection processes. This approach empowers clinicians to choose models aligned with diagnostic priorities, whether emphasizing precision or recall, revolutionizing oncology imaging [8, 52]. Through pre-trained models, synthetic data augmentation, and domain-specific datasets, transfer learning significantly enhances robust predictive model development, improving patient outcomes in colorectal cancer management.

6.2 Comparative Analysis of Case Studies

A comparative analysis of case studies in colorectal cancer imaging highlights the efficacy of various transfer learning approaches in enhancing diagnostic accuracy and treatment planning. A prominent example involves CNNs pre-trained on extensive datasets like ImageNet, fine-tuned for specific colorectal cancer diagnostic tasks. Recent deep learning advancements in histopathological image classification have improved clinical and research performance, addressing data scarcity and variability challenges through continual learning and transfer learning techniques that enhance adaptability and convergence rates [27, 20, 52].

The integration of synthetic image data through advanced augmentation techniques has notably improved model training outcomes. By generating synthetic features, researchers create balanced datasets that enhance predictive model robustness, particularly in scenarios with limited annotated data [6]. This approach not only boosts classification accuracy but also ensures effective generalization across diverse imaging cohorts.

Domain adaptation techniques, such as MSATL, effectively align feature distributions between source and target domains. Utilizing adversarial networks and attention mechanisms, these techniques enhance model adaptability to new data, crucial for maintaining diagnostic accuracy in clinical settings with prevalent data variability [25].

Comparative studies emphasize the importance of large-scale, domain-specific datasets like CytoImageNet in training predictive models. These datasets serve as comprehensive resources for bioimage analysis, facilitating the fine-tuning of pre-trained models and optimizing their performance for

specific colorectal cancer imaging tasks [4]. Their availability allows for precise model customization, ultimately improving patient outcomes.

This comparative analysis underscores the effectiveness of combining pre-trained models, synthetic data augmentation, and domain adaptation techniques in advancing colorectal cancer imaging. These methodologies collectively contribute to developing highly effective predictive models, significantly improving diagnostic accuracy and streamlining treatment planning. By leveraging continual learning, out-of-distribution detection, and meta-learning strategies, researchers address challenges such as data variability and limited sample sizes, enhancing the robustness and adaptability of machine learning models in clinical applications. Additionally, standardized datasets and innovative training approaches facilitate the integration of diverse histopathological data, ensuring models remain current with evolving patient demographics and diagnostic criteria [48, 37, 27, 7, 20].

7 Challenges and Future Directions

7.1 Technological and Methodological Innovations

Advancements in transfer learning for imaging genomics demand innovative technologies to overcome existing challenges and enhance model robustness. Recent progress in domain adaptation has addressed data shifts effectively [24]. Future research should focus on advanced data augmentation to improve model performance amid data scarcity and variability, creating diverse training datasets for better generalization across imaging cohorts. Exploring various GAN architectures, such as InfoGANs, may address feature generation and classification challenges in medical imaging.

Optimizing computational efficiency is critical. Enhancing frameworks like MMDTL2 to handle larger datasets and complex features is necessary [3]. Additionally, refining hyperparameter optimization and leveraging more datasets can improve models trained on CytoImageNet [4], optimizing configurations for medical imaging applications.

Integrating real-time applications and one-shot learning presents a promising research avenue, requiring innovative designs for rapid data processing with minimal training data. Addressing extreme class imbalances and refining alignment processes are essential for model robustness across diverse datasets. The Weighted Balanced Distribution Adaptation (W-BDA) algorithm highlights the potential of adaptively adjusting distribution discrepancies to improve class imbalance handling. Effective out-of-distribution detection methods can further enhance reliability in digital pathology applications [53, 27].

Future research should also optimize mutation processes and extend learngenes' applicability to diverse network architectures and tasks [30]. Refining these processes can enhance predictive model precision and efficiency, contributing to robust solutions in imaging genomics.

7.2 Implications for Future Research

Recent advancements in transfer learning and imaging genomics offer substantial opportunities for further exploration. A promising area is integrating hybrid methods that combine various transfer learning techniques to enhance model performance in complex scenarios, effectively addressing data scarcity and domain variability [54].

Developing sophisticated domain adaptation techniques is crucial, focusing on aligning feature distributions between source and target domains to improve model generalization across diverse data distributions. Addressing discrepancies in marginal and conditional distributions while leveraging knowledge from related domains can significantly enhance machine learning models' effectiveness [18, 17, 24, 16, 53]. Novel adversarial training frameworks and attention mechanisms are vital for achieving these objectives, ensuring consistent model performance across medical imaging datasets.

Integrating synthetic data into training processes enhances existing datasets, creating robust resources for model development. This is advantageous in transfer learning contexts, where real images are challenging to acquire due to privacy concerns. While synthetic images can enhance model performance when aligned with real data, naive inclusion can lead to suboptimal results. Strategies like the bridged transfer framework and dataset style inversion have shown improvements in classification tasks, highlighting the importance of careful implementation [16, 6, 17]. Future research should

refine data augmentation techniques to generate high-quality synthetic images reflecting real-world clinical variability, enhancing model robustness and accuracy.

Exploring real-time applications and one-shot learning scenarios is an exciting frontier for imaging genomics research. Developing models for rapid data processing with minimal training data could transform clinical workflows. Reliable performance in time-sensitive medical environments requires innovative architectural designs balancing computational efficiency with predictive accuracy. Techniques like Parameter-Efficient Fine-Tuning (PEFT) have shown promise in enhancing medical image analysis, especially with limited data. Addressing challenges like out-of-distribution detection in digital pathology and utilizing specialized datasets like MHIST can further optimize model performance while ensuring robust evaluation across diverse medical imaging tasks [27, 7, 55].

These findings highlight the need for ongoing research and innovation in transfer learning and imaging genomics. Investigating hybrid methodologies merging transfer learning and self-supervised learning, refining domain adaptation techniques to address data imbalance and scarcity, and effectively incorporating synthetic data can significantly enhance model performance and clinical applicability, ultimately improving patient care and treatment strategies [24, 9, 10].

7.3 Data Scarcity and Standardization

Data scarcity remains a significant challenge in imaging genomics, exacerbated by the high costs and logistical difficulties of acquiring large, annotated datasets. This issue is compounded by variability in imaging protocols and patient demographics, complicating robust predictive model development [28]. Existing benchmarks often focus on single-source models, overlooking complexities introduced by domain mismatches and ensemble model cohesiveness, limiting their applicability in diverse clinical settings [49].

The iterative self-transfer learning method has shown promise in enhancing model performance on small datasets, yet underscores the advantages of larger datasets for optimal outcomes, highlighting the necessity of data accumulation in imaging genomics [56]. This need is echoed in histopathology, where future research could prioritize developing extensive datasets and tackling complex classification tasks to improve model generalization and accuracy [7].

Standardization in imaging genomics is vital to address data variability challenges and ensure consistent model performance across different datasets. Unanswered questions regarding best practices for estimating importance weights and understanding the implications of various domain shifts on classifier performance underscore the need for standardized methodologies [24]. Establishing standardized protocols and benchmarks that account for real-world variability can significantly enhance the generalizability and reliability of predictive models in imaging genomics.

7.4 Integration of Advanced Techniques

Integrating advanced AI and machine learning techniques is crucial for enhancing predictive modeling in imaging genomics. Exploring self-supervised learning techniques, which improve model performance without extensive labeled datasets, represents a promising research direction [1]. By utilizing unlabeled data, self-supervised methods extract valuable features that bolster model generalization and robustness across diverse medical imaging tasks.

AI-driven approaches, especially those employing deep learning frameworks, enhance predictive model efficiency and accuracy by automating feature extraction and classification processes. This automation alleviates the burden of manual feature design and leverages transfer learning to improve model performance in scenarios with limited labeled data. Deep neural networks can identify complex patterns within imaging data, providing crucial insights for accurate diagnosis and treatment planning [57, 19, 17]. Additionally, machine learning algorithms focusing on unsupervised and semi-supervised learning can further enhance model adaptability to evolving data distributions, ensuring consistent performance across various clinical settings.

Developing hybrid models that combine multiple machine learning techniques offers a comprehensive approach to predictive modeling. By leveraging the complementary strengths of diverse methodologies, hybrid models effectively address the inherent challenges of heterogeneity and variability in medical imaging datasets. This integration enhances diagnostic reliability and precision, improves model generalization and robustness, particularly in the face of data imbalance and scarcity. Further-

more, these models can capitalize on advanced techniques like transfer learning and self-supervised learning, optimizing performance across medical domains while providing valuable insights for future research and application strategies [27, 9, 10].

Integrating advanced AI and machine learning techniques into imaging genomics is essential for advancing the field. Investigating cutting-edge self-supervised learning techniques and creating hybrid models that leverage both transfer learning and surrogate supervision can significantly enhance the accuracy, adaptability, and robustness of predictive models in medical imaging. Addressing critical challenges such as data scarcity and imbalance will ultimately lead to improved patient care and more effective treatment strategies tailored to individual medical needs. Additionally, incorporating quantitative imaging principles during model training can optimize image quality and enhance model performance in downstream tasks, validating their clinical applicability [34, 14, 9].

7.5 Interdisciplinary Collaborations and Technological Advancements

Interdisciplinary collaborations and technological advancements are crucial for advancing imaging genomics, particularly in transfer learning applications. Integrating expertise from fields such as biology, computer science, and economics fosters innovative methodologies and tools to address complex challenges in medical imaging. The Residual Importance Weighted Transfer method exemplifies the potential of interdisciplinary approaches, demonstrating applicability across domains and highlighting the value of cross-disciplinary insights in refining transfer learning techniques [58].

Technological advancements in AI and machine learning have transformed imaging genomics. The development of sophisticated algorithms and computational frameworks, particularly in out-of-distribution detection, parameter-efficient fine-tuning, and self-supervised learning, enhances the ability to extract meaningful patterns from complex imaging data. This progress improves diagnostic accuracy and treatment planning in digital pathology and facilitates better performance in medical image analysis by leveraging diverse datasets and incorporating quantitative imaging principles, ultimately leading to more effective healthcare solutions [34, 55, 27]. Collaborative efforts that unite domain experts are crucial for developing comprehensive solutions tailored to specific clinical needs.

Moreover, integrating advanced imaging technologies with genomic data analysis tools enables a nuanced understanding of tumor biology and heterogeneity. Techniques such as meta-learning, transfer learning, and continual learning enhance personalized medicine by creating treatment strategies tailored to individual patients' unique genomic and phenotypic profiles. These methodologies address challenges associated with limited data availability in medical research, such as rare diseases and evolving patient populations, by optimizing machine learning models and facilitating knowledge transfer across diverse datasets. Consequently, personalized medicine approaches can leverage comprehensive insights derived from various data sources, ultimately improving patient outcomes through more precise and effective treatment plans [48, 37, 27, 59, 20].

8 Conclusion

The exploration of transfer learning in imaging genomics underscores its pivotal role in advancing diagnostic and therapeutic approaches for colorectal cancer and liver metastasis. The strategic use of pre-trained convolutional neural networks (CNNs) for feature extraction effectively addresses the challenges of data scarcity and variability inherent in medical imaging, thereby enhancing both model performance and generalizability. The integration of synthetic data and domain adaptation techniques further strengthens the predictive models, ensuring consistent diagnostic accuracy across diverse clinical environments.

Transfer learning's application in medical imaging not only optimizes diagnostic workflows but also supports the creation of personalized treatment plans, ultimately improving patient care. The potential for growth in this field is substantial, with opportunities to incorporate advanced AI and machine learning techniques to refine predictive modeling. Continued research and interdisciplinary collaboration are essential to overcoming existing hurdles and driving innovation in imaging genomics, thereby contributing to more effective cancer diagnostic and treatment methodologies.

These advancements are particularly evident in applications like MRI reconstruction, where transfer learning has significantly improved image quality, highlighting the transformative impact of these methods in clinical settings. Future research should focus on enhancing these techniques and

exploring new applications to ensure that the benefits of transfer learning continue to propel the field

of imaging genomics forward.

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