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BACKGROUND AND THEORETICAL FOUNDATIONS OF A 2.5D DEEP LEARNING FRAMEWORK FOR COVID-19 CT DIAGNOSIS

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Аннотация. В данном исследовании представлены теоретические основы лёгкой, эффективной и интерпретируемой 2.5D-архитектуры глубокого обучения для автоматической классификации КТ-изображений лёгких при COVID-19. Обоснована необходимость разработки таких систем из-за высокой нагрузки на здравоохранение и ограничений ПЦР-диагностики. Рассмотрены ключевые компоненты: сверточные нейронные сети, трансферное обучение, стратегия 2.5D, традиционные методы пулинга и их недостатки при работе с разреженными очагами. Предложен адаптивный механизм Top-K пулинга, основанный на L2-норме векторов признаков, который автоматически отбирает наиболее информативные срезы КТ и агрегирует их для классификации. Описаны преимущества смешанного обучения (AMP) для снижения потребления памяти GPU и ускорения вычислений. Метод Grad-CAM в сочетании с визуализацией отобранных Top-K срезов обеспечивает интерпретируемость решений модели. Работа закладывает теоретический фундамент для практической реализации системы, проверенной в следующих главах диссертации.

Ключевые слова: COVID-19, компьютерная томография грудной клетки, глубокое обучение, 2.5D фреймворк, DenseNet-121, объединение Top-K, трансферное обучение, смешанное прецизионное обучение, Grad-CAM, интерпретируемость, агрегация поражений

Annotatsiya. Ushbu tadqiqotda COVID-19 tashxisida o‘pka KT tasvirlarini avtomatik tasniflash uchun yengil, samarali va izohlanadigan 2.5D chuqur o‘rganish arxitekturasining nazariy asoslari keltirilgan. Sog‘liqni saqlash tizimlariga yuqori yuklanish va PZR tashxisining cheklovlari tufayli bunday tizimlarni yaratish zarurligi asoslangan. Asosiy komponentlar ko‘rib chiqilgan: konvolyutsion neyron tarmoqlar, transfer learning, 2.5D strategiyasi, an’anaviy pooling usullari va ularning kam uchraydigan zararlanishlarda ishlashdagi kamchiliklari. L2-normaga asoslangan adaptiv Top-K pooling mexanizmi taklif qilingan bo‘lib, u eng informativ KT qatlamlarini avtomatik tanlaydi va ularni tasniflash uchun birlashtiradi. Aralash aniqlikda o‘qitish (AMP) GPU xotirasini tejash va hisoblashlarni tezlashtirish imkonini beradi. Top-K tanlangan qatlamlarga qo‘llangan Grad-CAM usuli model qarorlarining izohlanishini ta’minlaydi. Ushbu ish dissertatsiyaning keyingi boblarida amaliy sinovdan o‘tkazilgan tizim uchun nazariy asosni yaratadi.

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Kalit so'zlar: COVID-19, ko'krak qafasining kompyuter tomografiyasi, chuqur o'rganish, 2.5D ramka, DenseNet-121, Top-K birlashmasi, uzatishni o'rganish, aralash aniqlikdagi trening, Grad-CAM, talqin qilish, lezyonlarni yig'ish

Abstract. This paper presents the theoretical foundations of a lightweight, efficient, and interpretable 2.5D deep learning framework for automated COVID-19 classification using chest CT images. The need for such systems is motivated by the high burden on healthcare systems and the limitations of RT-PCR diagnostics. Key components are reviewed: convolutional neural networks, transfer learning, the 2.5D strategy, traditional pooling methods and their shortcomings for sparse lesions. An adaptive Top-K pooling mechanism based on the L2 norm of feature vectors is proposed, which automatically selects the most informative CT slices and aggregates them for classification. Mixed precision training (AMP) is introduced to reduce GPU memory consumption and accelerate computation. Grad-CAM applied to the Top-K selected slices provides model interpretability. This work lays the theoretical groundwork for a practically validated system presented in subsequent chapters of the dissertation.

Keywords COVID-19, chest CT, deep learning, 2.5D framework, DenseNet-121, Top-K pooling, transfer learning, mixed precision training, Grad-CAM, interpretability, lesion aggregation

INTRODUCTION.

1. Research Background and Motivation

The outbreak of Coronavirus Disease 2019 (COVID-19) placed unprecedented pressure on healthcare systems worldwide. Caused by SARS-CoV-2, the disease spreads rapidly through respiratory transmission and can be asymptomatic. Real-time polymerase chain reaction (RT-PCR) is the standard diagnostic method, but during peak infection periods it suffers from delays, kit shortages, and false-negatives due to low viral load or improper sampling [1].

Chest CT imaging has proven uniquely valuable for COVID-19 diagnosis. The virus primarily attacks the respiratory system, producing distinct patterns on CT: ground-glass opacities (GGOs), reticular shadows, consolidations, and the “cobblestone” sign. These changes appear early, often before RT-PCR becomes positive, and correlate with disease progression [2]. However, manual reading of CT volumes is labour-intensive, suffers from inter-observer variability, and becomes impractical during surges.

Deep learning, particularly convolutional neural networks (CNNs), has revolutionised medical image analysis. For COVID-19 CT classification, two main approaches exist: 2D CNNs process individual slices, losing inter-slice spatial continuity; 3D CNNs preserve volumetric information but demand high GPU memory and computational power, making them difficult to deploy on

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consumer-grade hardware [3]. Moreover, most models lack interpretability – clinicians need not only accurate predictions but also understandable evidence for decision-making.

These challenges motivate this research: to design a lightweight, efficient, and interpretable 2.5D deep learning framework that balances accuracy and computational cost for automated COVID-19 CT classification. As highlighted by Topol [21], the convergence of human and artificial intelligence in medicine offers unprecedented opportunities, but only if AI systems are transparent and trustworthy.

2. Literature Review and Theoretical Foundations

2.1 Convolutional Neural Networks and DenseNet-121

CNNs are the dominant architecture for image analysis, using local receptive fields, weight sharing, and spatial pooling. Since AlexNet's breakthrough in 2012, networks have grown deeper and more efficient. ResNet introduced skip connections to solve vanishing gradients and degradation, enabling ultra-deep networks. DenseNet takes this further by densely connecting each layer to every later layer via concatenation. For a dense block with L layers, the l-th layer receives the concatenation of all previous feature maps: $x_l = H_l([x_0, x_1, \ldots, x_{l-1}])$ [4]. This design yields extreme parameter efficiency, enhanced gradient flow, implicit regularisation, and natural fusion of low- and high-level features – ideal for small-sample medical imaging tasks [5, 6]. DenseNet-121 (growth rate $k = 32$) outputs a 1024-dimensional feature vector per slice, serving as the backbone in this study.

2.2 Transfer Learning and Pre-trained Models

Medical datasets are small and expensive to annotate. Transfer learning – fine-tuning a model pre-trained on a large source dataset (e.g., ImageNet) – dramatically improves performance and convergence [7]. Early CNN layers learn universal features (edges, textures), while deeper layers become task-specific [8]. DenseNet-121 is chosen for its strong generalisation on small datasets and proven reliability in medical imaging. For small medical datasets, transfer learning consistently outperforms training from scratch, and fine-tuning fewer layers is often beneficial [9, 10].

2.3 2.5D Deep Learning Strategy

"2.5D" refers to methods that use 2D modules but inject 3D spatial information. This study adopts a slice-sequence approach: eight consecutive CT slices are processed in parallel by a shared DenseNet-121, producing slice-level feature vectors. These vectors are then aggregated into a single global representation. The aggregation step is critical – it must preserve discriminative lesion information while discarding irrelevant slices. 2.5D representations have

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been successfully applied to CT-based diagnosis of various diseases, including kidney tumor segmentation and COVID-19 detection [11, 12, 13].

2.4 Limitations of Traditional Pooling and the Top-K Mechanism

Let $\{f_1, f_2, \ldots, f_N\}$ be slice feature vectors $(d = 1024)$. Common aggregation methods have severe drawbacks for sparse lesions:

Average pooling $F_{avg} = \frac{1}{N}\sum f_i$ assumes every slice is equally important. Normal slices dilute the signal from the few abnormal slices, reducing sensitivity [14].

Max pooling $F_{\max}[j] = \max_i f_i[j]$ retains only the strongest activation per dimension. It fragments complementary information from multiple slices and is sensitive to noise.

The proposed Top-K pooling adaptively selects the most informative slices based on their L2 norm. Steps:

Extract features: $f_i = F(x_i)$.

Compute anomaly score: $s_i = \| f_i \|_2$.

Select indices of the K largest scores: $I = \text{argTopK}(s_i)$.

Aggregate: $F_{global} = \frac{1}{K}\sum_{i \in I} f_i$.

Classify via dropout + fully connected layer + softmax.

For $N = 8$ (dataset fixed length), $K = 4$ gives the best balance – filtering background noise while preserving complementary lesion evidence. Top-K pooling is computationally light $(O(N))$, dynamically adaptive, and provides selective gradient propagation. Compared with attention-based pooling [15], Top-K pooling performs hard selection, which is more decisive for sparse lesions.

2.5 Mixed Precision Training

Mixed precision training (AMP) stores most weights, activations, and gradients in FP16 while keeping a master copy in FP32 and using loss scaling [16]. On an NVIDIA RTX 4070 laptop GPU (8 GB), AMP reduces memory usage by ~40% (from 7.6 GB to 4.8 GB) and speeds up training by ~1.37×, enabling the entire pipeline to run on consumer hardware without accuracy loss.

2.6 Interpretability: Grad-CAM and Top-K Slice Visualisation

For clinical trust, models must explain their decisions. Grad-CAM produces heatmaps by weighting the last convolutional feature maps with gradients of the target class score: $L^c_{Grad-CAM} = \text{ReLU}(\sum_k \alpha_k^c A^k)$ [17]. Applied to the Top-K selected slices, these heatmaps show which lung regions drove the prediction. Moreover, the explicit slice selection itself is an intrinsic explanation – clinicians can directly inspect the K slices that the model found most informative, bridging

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the gap between black-box AI and radiological reasoning. The importance of such interpretability in radiology has been emphasised in recent literature [18].

2.7 Evaluation Metrics

Binary classification metrics include: accuracy, precision (PPV), sensitivity (recall, TPR), specificity (TNR), F1-score, and area under the ROC curve (AUC) [19]. Sensitivity is prioritised for public health screening; AUC provides a threshold-independent global measure. The use of AUC is particularly well-established in machine learning evaluation [20].

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