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CONTENTS

Akhmetova A.Zh., Kantureyeva M.A., Serimbetov B.A., Zhasuzakova M.Zh., Mustafayeva N.T. Identification of communities and active users in social networks.....	11
Akzhigitov D., Mukhtarkhanov M., Zhetpisbayeva A., Kulakayeva A., Zhetpisbayev K. Analysis of the mechanical structure of a 12U CubeSat nanosatellite and assessment of its mechanical stability.....	29
Alibekov A., Nurimanov A., Mukhametkali A., Kassym D., Varol H.A. Qolda-Math: a small vision-language model for mathematical reasoning in Kazakh.....	50
Alisheva S.S., Ospanova A.O., Shaimerdenova G.S., Shaimerdenova L., Zhidebayeva A.N. Detecting Kazakh language offensive comments in online content using deep learning algorithms.....	68
Askar G., Mutaikhan A., Aitkozhasyeva M., Nauryzbaikyzy G., Makhataeva Z. Retrieval beats fine-tuning: adapting a Kazakh small language model for historical question answering.....	86
Beissenova G.I., Shynzhigit B.B., Beisebayeva A.Zh., Kaldarova B.S., Lesbayev A.U. Deep neural network-based speaker authentication for secure access control systems.....	106
Bekenuly B., Baimakhanova A., Baiturganova V., Bolatbekova D. Comparison of CNN architectures for automated ACL injury classification from knee MRI.....	123
Bekbolat A., Razak A., Alimbayeva Z., Ozhikenova A. Multi-task deep learning for knee MRI pathology classification.....	139
Issakhov A., Akylbekkyzy A., Abylkassymova A. Predicting the spread of airborne viral infections in enclosed spaces.....	158
Kisseleva O., Abdramanov K., Naumenko V., Mukanova Z., Maintser D. Evaluation of serverless cold start optimization techniques.....	177
Koshkarov Ye.Zh., Amirgaliyev B.Ye., Mulesa O. Physics-aware masked pretraining for cross-basin well log foundation models.....	197
Kurmetkan T., Turysbek Zh., Mukhitova A., Nauryzbaeva A. Research on methods for reducing knowledge conflicts in large language models in Kazakh question-and-answer systems.....	214
Makatov Ye.K., Abdul Razaque, Ismukanova A.N., Salykova A.K., Glock E.S. Machine learning-based model for phishing URL detection in online social networks.....	233
Mimenbayeva A.B., Naizagarayeva A.A., Ospanova T.T., Koikelova D.K., Kudabayeva R.N. Spatial and climate data analysis for machine learning-based crop yield prediction in Northern Kazakhstan.....	255
Mukhamediev R.I., Abdoldina F.N., Gertsen Y.A. Economic opportunities and constraints of artificial intelligence adoption in Kazakhstan's resource-oriented economy.....	274

Mutanov G.M., Karyukin V.I., Ussatova O.A., Begimbayeva Y.Y., Baispay G.B. The assessment of blockchain readiness for academic document verification.....	289
Mussiraliyeva Sh., Bolatbek M., Baisylbayeva K. Classification of cyber-extremist ideologies in the Kazakh language considering multi-annotator disagreement.....	306
Omarov B.S., Sultan D.R., Rakhymberdiev D.S., Abibullayeva A.A., Toktarova A.B. Deformable attention-guided Transformer for brain tumor segmentation.....	326
Oralbekova D., Bekarystankyzy A., Yerimbetova A., Berzhanova U. Development of a streaming Kazakh speech recognition system using end-to-end models.....	346
Serek A., Shoiynbek A., Zheludkov M., Kuanyshbay D., Meraliyev B. Comparative analysis of machine learning methods for detecting fraud in text messages.....	365
Smakhanova A.K., Uskenbayeva R.K., Kassymova A.B., Kalpeyeva Zh.B., Konyrbaev N.B. Experimental research using models and methods of the university digital ecosystem.....	384
Sultanali A.E., Kazbekova G.N. Machine learning-based detection of AI-generated content in students' written works.....	401
Tashenova Zh., Yergazin A., Nurlybaeva E., Abdugulova Zh., Amanzholova Sh. Experimental evaluation of a hybrid IDPS with adaptive learning for low-latency 5G networks using edge computing.....	418
Telman D., Yerimbetova A., Daiyrbayeva E. Leakage-resistant fake news detection for Kazakh: temporal evaluation of lexical, Transformer and hybrid models.....	441
Zhanegizov A., Mamyrbayev O., Abdigappar M. Application of YOLO12 for road defect detection in GPR images.....	457

МАЗМҰНЫ

Ахметова А.Ж., Кантуреева М.А., Серимбетов Б.А., Жасұзақова М.Ж., Мұстафаева Н.Т. Әлеуметтік желілердегі қауымдастықтар мен белсенді қолданушыларды анықтау.....	11
Ақжігітов Д.Ж., Мұхтарханов М.О., Жетписбаева А.Т., Кулакаева А.Е., Жетписбаев К.У. 12U CubeSat үлгісіндегі наноспутниктің механикалық құрылымын талдау және оның механикалық орнықтылығын бағалау.....	29
Алибеков А., Нуриманов А., Мұхаметқали А., Қасым Д., Варол Х.А. Qolda-Math: қазақ тіліндегі математикалық пайымдауға арналған кіші көру-тілдік модель.....	50
Алишева С.С., Оспанова А.О., Шаймерденова Г.С., Шаймерденова Л., Жидебаева А.Н. Онлайн-контенттегі қазақ тіліндегі бейәдеп пікірлерді терең оқыту алгоритмдері арқылы анықтау.....	68
Асқар Ғ., Мұтайхан А., Айтқожаева М., Наурызбайқызы Г., Махатаева Ж. Retrieval fine-tuning-тен басым: тарихи сұрақтарға жауап беру үшін қазақша шағын тілдік модельді бейімдеу.....	86
Бейсенова Г.И., Шынжігіт Б.Б., Бейсебаева А.Ж., Қалдарова Б.С., Лесбаев А.У. Терең нейрондық желіге негізделген қауіпсіз басқару жүйелерінде сөйлеушіні аутентификациялау.....	106
Бекенұлы Б., Баймаханова А., Байтурганова В., Болатбекова Д. Алдыңғы крест тәрізді байлам жарақатын анықтауға арналған CNN архитектураларын салыстыру.....	123
Бекболат А., Разак А., Алимбаева Ж., Ожикенова А. Tіze MPT патологиясын жіктеуге арналған көп тапсырмалы терең оқыту.....	139
Исахов А.А., Ақылбекқызы А., Абылкасымова А. Шектеулі кеңістіктерде әуе тамшыларымен вирустық инфекцияның таралуын сандық модельдеу.....	158
Киселева О., Абдраманов Қ., Науменко В., Мұқанова Ж., Майнцер Д. Serverless жүйелеріндегі суық іске қосуды оңтайландыру әдістерін эксперименттік бағалау.....	177
Кошкарров Е.Ж., Амиргалиев Б.Е., Мүлеса О. Бассейнаралық ұңғымалық диаграммалардың іргелі модельдерін физикалық тұрғыдан негізделген масқаланған алдын ала оқыту.....	197
Құрметқан Т., Тұрысбек Ж., Мұхитова А., Наурызбаева А. Қазақ тіліндегі сұрақ-жауап жүйелерінде үлкен тілдік модельдердегі білім қайшылықтарын азайту әдістерін зерттеу.....	214
Мақатов Е.К., Abdul Razaque, Исмуканова А.Н., Салыкова А.К., Глюк Е.С. Онлайн әлеуметтік желілердегі фишингтік URL-дарды анықтауға арналған машиналық оқыту негізіндегі модель.....	233

Мименбаева А.Б., Найзағараева А.А., Оспанова Т.Т., Қойкелова Д.К., Қудабаева Р.Н. Солтүстік Қазақстандағы дақылдар өнімділігін машиналық оқыту арқылы болжауда кеңістіктік және климаттық деректерді талдау.....	255
Мухамедиев Р.И., Абдолдина Ф.Н., Герцен Е.А. Қазақстанның ресурстық бағытталған экономикасына жасанды интеллектті енгізудің экономикалық мүмкіндіктері мен шектеулері.....	274
Мутанов Г.М., Карюкин В.И., Усатова О.А., Бегимбаева Е.Е., Байспай Г.Б. Білім беру құжаттарының түпнұсқалығын тексеруге блокчейн технологиясының дайындығын бағалау.....	289
Мусиралиева Ш., Болатбек М., Байсылбаева К. Көпаннынотаторлы келіспеушілікті ескере отырып қазақ тіліндегі киберэкстремистік идеологияларды жіктеу.....	306
Омаров Б.С., Сұлтан Д.Р., Рахымбердиев Д.С., Абибуллаева А.А., Тоқтарова А.Б. Ми ісіктерін сегменттеуде деформацияланатын зейін механизміне негізделген мультимодальды трансформер.....	326
Оралбекова Д.О., Бекарыстанқызы А., Еримбетова А.С., Бержанова У.Г. Интегралды модельдерді қолдану арқылы қазақ тіліндегі ағындық сөйлеуді тану жүйесін әзірлеу.....	346
Серек А., Шойынбек А., Желудков М., Қуанышбай Д., Мералиев Б. Мәтіндік хабарламалардағы алаяқтықты анықтауға арналған машиналық оқыту әдістерінің салыстырмалы талдауы.....	365
Смаханова А.К., Ускенбаева Р.К., Касымова А.Б., Кальпеева Ж.Б., Қоңырбаев Н.Б. Университеттің цифрлық экожүйесінің модельдері мен әдістерін қолдана отырып жүргізілген эксперименттік зерттеу.....	384
Сұлтанәлі А.Е., Казбекова Г.Н. Білім алушылардың жазбаша жұмыстарындағы AI-контентті машиналық оқыту арқылы анықтау.....	401
Ташенова Ж.М., Ергазин Ә., Нұрлыбаева Ә.Н., Абдуғулова Ж.К., Аманжолова Ш.А. Edge Computing көмегімен төмен кідірісті 5G желілеріне арналған бейімделгіш оқытуы бар гибриді IDPS-ті эксперименттік бағалау.....	418
Тельман Д., Еримбетова А., Дайырбаева Ә. Қазақ тіліндегі жалған жаңалықтарды анықтау: лексикалық, трансформерлік және гибридті модельдерді уақыт бойынша бағалау.....	441
Жанегизов А.С., Мамырбаев Ә.Ж., Абдіғаппар М.Д. YOLO12 моделін георадар кескіндеріне қолдану.....	457

СОДЕРЖАНИЕ

Ахметова А.Ж., Кантуреева М.А., Серимбетов Б.А., Жасузакова М.Ж., Мустафаева Н.Т. Выявление сообществ и активных пользователей в социальных сетях.....	11
Акжигитов Д.Ж., Мухтарханов М.О., Жетписбаева А.Т., Кулакаева А.Е., Жетписбаев К.У. Анализ механической конструкции наноспутника модели 12U CubeSat и оценка его механической устойчивости.....	29
Алибеков А., Нуриманов А., Мухаметкали А., Касым Д., Варол Х.А. Qolda-Math: маленькая мультимодальная модель зрения и языка для математических рассуждений на казахском языке.....	50
Алишева С.С., Оспанова А.О., Шаймерденова Г.С., Шаймерденова Л., Жидебаева А.Н. Выявление оскорбительных комментариев на казахском языке в онлайн-контенте с помощью алгоритмов глубокого обучения.....	68
Аскар Г., Мутайхан А., Айткожаева М., Наурызбайкызы Г., Махатаева Ж. Retrieval эффективнее fine-tuning: адаптация малой языковой модели казахского языка для ответов на исторические вопросы.....	86
Бейсенова Г.И., Шынжигит Б.Б., Бейсебаева А.Ж., Калдарова Б.С., Лесбаев А.У. Аутентификация личности по голосу на основе глубокой нейронной сети для систем безопасного управления доступом.....	106
Бекенулы Б., Баймаханова А., Байтурганова В., Болатбекова Д. Сравнение архитектур сверточных нейронных сетей для автоматической классификации разрыва ПКС по МРТ коленного сустава.....	123
Бекболат А., Разак А., Алимбаева Ж., Ожикенова А. Многозадачное глубокое обучение для классификации патологий колена по МРТ.....	139
Исахов А.А., Акылбеккызы А., Абылкасымова А. Прогнозирование распространения вирусной инфекции воздушно-капельным путем в замкнутых помещениях.....	158
Киселева О., Абдраманов К., Науменко В., Муканова Ж., Майнцер Д. Экспериментальная оценка методов оптимизации холодного запуска в serverless-системах.....	177
Кошкарар Е.Ж., Амиргалиев Б.Е., Мулеса О. Физически-осознанное маскированное предобучение для межбассейновых фундаментальных моделей каротажных диаграмм.....	197
Курметкан Т., Турысбек Ж., Мухитова А., Наурызбаева А. Исследование методов снижения конфликтов знаний в больших языковых моделях казахских вопросно-ответных систем.....	214
Макатов Е.К., Abdul Razaque, Исмуканова А.Н., Салыкова А.К., Глок Е.С. Модель обнаружения фишинговых URL в онлайн-социальных сетях на основе машинного обучения.....	233

Мименбаева А.Б., Найзагараева А.А., Оспанова Т.Т., Койкелова Д.К., Кудабаяева Р.Н. Анализ климатических данных для прогнозирования урожайности пшеницы методами машинного обучения в Северном Казахстане.....	255
Мухамедиев Р.И., Абдолдина Ф.Н., Герцен Е.А. Экономические возможности и ограничения внедрения искусственного интеллекта в ресурсно-ориентированной экономике Казахстана.....	274
Мутанов Г.М., Карюкин В.И., Усатова О.А., Бегимбаева Е.Е., Байспай Г.Б. Оценка готовности технологии блокчейн к проверке подлинности документов об образовании.....	289
Мусиралиева Ш., Болатбек М., Байсылбаева К. Классификация киберэкстремистских идеологий на казахском языке с учетом разногласий нескольких аннотаторов.....	306
Омаров Б.С., Султан Д.Р., Рахымбердиев Д.С., Абибуллаева А.А., Токтарова А.Б. Мультимодальный трансформер на основе механизма деформируемого внимания для сегментации опухолей головного мозга.....	326
Оралбекова Д.О., Бекарыстанкызы А., Еримбетова А.С., Бержанова У.Г. Распознавание казахской речи с применением интегральных моделей.....	346
Серек А., Шойынбек А., Желудков М., Куанышбай Д., Мералиев Б. Сравнительный анализ методов машинного обучения для выявления мошенничества в текстовых сообщениях.....	365
Смаханова А.К., Ускенбаева Р.К., Касымова А.Б., Кальпеева Ж.Б., Конырбаев Н.Б. Экспериментальное исследование с использованием моделей и методов цифровой экосистемы университета.....	384
Султанали А.Е., Казбекова Г.Н. Обнаружение AI-контента в письменных работах обучающихся методами машинного обучения.....	401
Ташенова Ж.М., Ергазин А., Нурлыбаева Э.Н., Абдугулова Ж.К., Аманжолова Ш.А. Экспериментальная оценка гибридной системы обнаружения и предотвращения вторжений (IDPS) с адаптивным обучением для сетей 5G с низкой задержкой с использованием граничных вычислений.....	418
Тельман Д., Еримбетова А., Дайырбаева Э. Обнаружение фейковых новостей на казахском языке: временная оценка лексических, трансформерных и гибридных моделей.....	441
Жанегизов А.С., Мамырбаев О.Ж., Абдигаппар М.Д. Применение модели YOLOv12 для анализа данных георадара.....	457

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DEFORMABLE ATTENTION-GUIDED TRANSFORMER FOR BRAIN TUMOR SEGMENTATION

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Abstract. Correct segmentation of brain tumors using multimodal magnetic resonance imaging (MRI) is critical for quantitative tumor evaluation, therapy planning and disease monitoring. However, the variability of tumor size, shape, location and appearance among MRI modalities poses a challenge for automatic segmentation. Heterogeneous structure of brain tumors and uneven boundaries of different subregions of a tumor also often impede the effectiveness of traditional segmentation methods. Hence, there is a need for strong approaches that can model local spatial features and long-range contextual dependencies. In this paper, we propose a deformable attention-guided Transformer architecture for multimodal

brain tumor segmentation. The framework uses complementary information from T1, T1c, T2 and FLAIR MRI modalities and fuses multi-scale feature extraction, adaptive query refinement, deformable attention and skip connections to improve heterogeneous tumor region representation. We performed experiments on the dataset from the brain tumor image segmentation benchmark (BRATS) multimodal. The model was assessed in terms of Dice coefficient, Precision, Recall and F1-score on Whole Tumor (WT), Tumor Core (TC) and Enhancing Tumor (ET) regions. The suggested model attained Dice scores of 95.8%, 90.7%, and 86.1% for WT, TC and ET, respectively, while the average Dice score was 90.9%. Ablation analysis further highlighted the contribution of deformable attention, query refinement, skip connections and multimodal feature integration to the segmentation performance. The model also showed a good trade-off between segmentation accuracy and computational efficiency, which suggests the possible use of this approach in automated MRI processing workflows. The experimental results illustrate the potential of the proposed framework for accurate and robust multimodal MRI based brain tumor segmentation.

Keywords: Brain tumor segmentation, multimodal MRI, deformable attention, Transformer, deep learning, BRATS, medical image segmentation

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МИ ІСІКТЕРІН СЕГМЕНТТЕУДЕ ДЕФОРМАЦИЯЛАНАТЫН ЗЕЙІН МЕХАНИЗМІНЕ НЕГІЗДЕЛГЕН МУЛЬТИМОДАЛЬДЫ ТРАНСФОРМЕР

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Аннотация. Мультимодальды магниттік-резонанстық томография (МРТ) негізінде ми ісіктерін дәл сегменттеу ісікті сандық бағалау, емдеуді жоспарлау және ауру динамикасын бақылау үшін маңызды. Алайда әртүрлі МРТ модальдылықтарындағы ісіктің өлшемі, пішіні, орналасуы мен визуалдық сипаттамаларының өзгергіштігі автоматты сегменттеу үдерісін қиындатады. Сонымен қатар ми ісіктерінің гетерогенді құрылымы және олардың әртүрлі субаймақтарының біркелкі емес шекаралары дәстүрлі сегменттеу әдістерінің тиімділігін төмендетуі мүмкін. Сондықтан жергілікті кеңістіктік белгілерді де, алыс контекстік тәуелділіктерді де модельдей алатын тиімді тәсілдер қажет. Бұл жұмыста ми ісіктерін мультимодальды сегменттеуге арналған деформацияланатын зейін механизмімен басқарылатын Transformer архитектурасы ұсынылады. Ұсынылған тәсіл T1, T1c, T2 және FLAIR MPT модальдылықтарынан алынған өзара толықтырушы ақпаратты пайдаланады және гетерогенді ісік аймақтарын тиімді бейнелеу үшін көпауқымды белгілерді

бөліп алуды, сұраныстарды бейімдеп нақтылауды, деформацияланатын зейін механизмін және өткізіп жіберу байланыстарын біріктіреді. Эксперименттер ми ісіктерін мультимодальды сегменттеуге арналған BRATS эталондық деректер жиынтығында жүргізілді. Модель Whole Tumor (WT), Tumor Core (TC) және Enhancing Tumor (ET) аймақтары үшін Dice коэффициенті, Precision, Recall және F1-score метрикалары арқылы бағаланды. Ұсынылған модель WT, TC және ET үшін тиісінше 95,8%, 90,7% және 86,1% Dice көрсеткіштеріне қол жеткізді, ал орташа Dice көрсеткіші 90,9% болды. Абляциялық талдау деформацияланатын зейін механизмінің, сұраныстарды нақтылаудың, өткізіп жіберу байланыстарының және мультимодальды белгілерді біріктірудің сегменттеу сапасына қосатын үлесін көрсетті. Сонымен қатар модель сегменттеу дәлдігі мен есептеу тиімділігі арасындағы қолайлы теңгерімді көрсетті, бұл ұсынылған тәсілді MPT кескіндерін автоматтандырылған өңдеу жүйелеріне енгізу мүмкіндігін көрсетеді. Эксперименттік нәтижелер ұсынылған архитектураның мультимодальды MPT деректері негізінде ми ісіктерін дәл әрі тұрақты сегменттеуге қабілетті екенін көрсетеді.

Түйін сөздер: ми ісіктерін сегменттеу; мультимодальды MPT; деформацияланатын зейін; Transformer; терең оқыту; BRATS; медициналық кескіндерді сегменттеу

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МУЛЬТИМОДАЛЬНЫЙ ТРАНСФОРМЕР НА ОСНОВЕ МЕХАНИЗМА ДЕФОРМИРУЕМОГО ВНИМАНИЯ ДЛЯ СЕГМЕНТАЦИИ ОПУХОЛЕЙ ГОЛОВНОГО МОЗГА

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Аннотация. Точная сегментация опухолей головного мозга на основе мультимодальной магнитно-резонансной томографии (МРТ) имеет важное значение для количественной оценки опухоли, планирования лечения и мониторинга динамики заболевания. Однако вариабельность размеров, формы, локализации и визуальных характеристик опухоли в различных МРТ-модальностях усложняет автоматическую сегментацию. Кроме того, гетерогенная структура опухолей головного мозга и неоднородность границ различных опухолевых субрегионов могут снижать эффективность традиционных методов сегментации. Поэтому необходимы эффективные подходы, способные моделировать как локальные пространственные признаки, так и дальние контекстные зависимости. В работе предложена архитектура Transformer с механизмом деформируемого внимания для мультимодальной сегментации опухолей головного мозга. Предложенный подход использует взаимодополняющую информацию из МРТ-модальностей T1, T1c, T2 и FLAIR и объединяет многоуровневое извлечение признаков, адаптивное уточнение запросов, механизм деформируемого внимания и пропускающие соединения для улучшения представления гетерогенных областей опухоли. Эксперименты проводились на мультимодальном эталонном наборе данных BRATS для сегментации опухолей головного мозга. Модель оценивалась для областей Whole Tumor (WT), Tumor Core (TC) и Enhancing Tumor (ET) с использованием коэффициента Dice, Precision, Recall и F1-score. Предложенная модель достигла значений Dice 95,8%, 90,7% и 86,1% для WT, TC и ET соответственно, при среднем значении Dice 90,9%. Абляционный анализ подтвердил вклад механизма деформируемого внимания, уточнения запросов, пропускающих соединений и интеграции мультимодальных признаков в повышение качества сегментации. Модель также продемонстрировала благоприятный баланс между точностью сегментации и вычислительной эффективностью, что свидетельствует о возможности применения предложенного подхода в автоматизированных рабочих процессах обработки МРТ. Полученные экспериментальные результаты подтверждают потенциал предложенной архитектуры для точной и устойчивой сегментации опухолей головного мозга на основе мультимодальных МРТ-данных.

Ключевые слова: сегментация опухолей головного мозга; мультимодальная МРТ; деформируемое внимание; Transformer; глубокое обучение; BRATS; сегментация медицинских изображений

Introduction. Accurate brain tumor segmentation from multi-modal magnetic resonance imaging (MRI) remains a fundamental challenge in medical image analysis, owing to the complex heterogeneity of tumor appearance, ambiguous boundaries, and substantial inter-patient variability. Brain tumors, particularly gliomas, exhibit highly irregular shapes and diverse intensity distributions across imaging modalities such as T1, T1-weighted contrast-enhanced (T1ce), T2, and FLAIR, making reliable delineation a non-trivial task (Wang, 2024).

Precise segmentation of tumor subregions, including Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET), is critically important for diagnosis, treatment planning, and prognosis estimation (Saladi, 2026). However, traditional manual annotation is time-consuming, prone to inter-observer variability, and infeasible for large-scale clinical deployment (Murmu, 2026). Consequently, the development of automated, robust, and accurate segmentation frameworks has become an active area of research.

Deep learning-based approaches, particularly convolutional neural networks (CNNs), have significantly advanced the state of the art in medical image segmentation. Architectures such as U-Net and its variants have demonstrated strong capability in capturing local spatial features through hierarchical encoding and decoding mechanisms (Chowdhury, 2025). Despite these successes, CNN-based models are inherently limited in modeling long-range dependencies due to their restricted receptive fields (Arockia, 2026). This limitation becomes particularly evident in brain tumor segmentation, where global contextual information is essential for distinguishing tumor regions from surrounding healthy tissues. To address this issue, transformer-based models have been introduced, leveraging self-attention mechanisms to capture global relationships across the entire image (Wu, 2024). Hybrid CNN-transformer architectures have further improved performance by combining local feature extraction with global context modeling (Baid, 2021).

Recent studies have explored advanced attention mechanisms to enhance feature representation and improve segmentation accuracy. In particular, deformable attention has emerged as a promising approach, enabling the model to focus on a sparse set of informative spatial locations rather than uniformly attending to all positions (Menze, 2014). This mechanism is especially beneficial for medical imaging tasks involving irregular structures, such as brain tumors, where relevant features are often spatially scattered and non-uniform (Murmu, 2026). Additionally, multi-modal learning has been widely adopted to exploit complementary information from different MRI sequences, leading to more robust and discriminative feature representations (Bakas, 2018). However, effectively integrating multi-modal data while maintaining computational efficiency and preserving fine-grained spatial details remains a challenging problem.

Furthermore, a multi-scale decoder with skip connections is employed to reconstruct high-resolution segmentation maps while preserving spatial fidelity (Zhu, 2023). Extensive experiments demonstrate that the proposed approach

achieves superior performance in segmenting WT, TC, and ET regions, while maintaining a favorable balance between accuracy and computational efficiency.

Literary review. Extensive research efforts have been devoted to advancing brain tumor segmentation through deep learning, with a progressive transition from conventional convolutional architectures toward hybrid and transformer-driven frameworks. Early approaches primarily relied on convolutional neural networks, where encoder–decoder structures demonstrated strong capability in capturing hierarchical spatial representations (Wang, 2021). The introduction of fully convolutional designs significantly improved pixel-wise prediction accuracy in medical imaging tasks (Ting, 2023). Subsequent refinements incorporated dense skip connections and multi-scale feature fusion to enhance boundary preservation and contextual awareness (Abidin, 2024). Despite these advancements, CNN-based methods remained limited in modeling long-range dependencies, which are crucial for handling complex tumor morphologies (Raza, 2023).

To overcome these limitations, transformer-based models have been increasingly adopted due to their ability to capture global contextual relationships through self-attention mechanisms (Wei, 2022). Vision transformer architectures have shown promising results in medical image segmentation by modeling global interactions across spatial regions (Li, 2016). Hybrid CNN-transformer models further improved segmentation performance by combining local feature extraction with global reasoning capabilities (Wang, 2021). Hierarchical transformer designs, such as window-based attention mechanisms, enabled efficient computation while preserving multi-scale representations. However, standard self-attention mechanisms often suffer from high computational complexity, particularly when applied to high-resolution medical images (Raza, 2023).

Recent studies have introduced advanced attention mechanisms to address computational inefficiencies and improve spatial adaptability. Deformable attention has emerged as a powerful alternative, allowing models to selectively attend to sparse, informative regions rather than processing all spatial locations uniformly (Bakas, 2018). This approach has demonstrated improved efficiency and robustness in handling irregular anatomical structures (Bakas, 2018). Additionally, adaptive query mechanisms have been proposed to dynamically refine feature representations and enhance semantic discrimination (Saladi, 2026). Multi-modal learning strategies have also gained significant attention, leveraging complementary information from different MRI sequences to improve segmentation accuracy (Menze, 2014). Fusion techniques ranging from early concatenation to attention-guided integration have been explored to effectively combine multi-modal features (Arockia, 2026).

Materials and methods. The proposed framework is designed as a multi-modal, attention-guided segmentation architecture for precise delineation of brain tumor subregions, as illustrated in Figure 1.

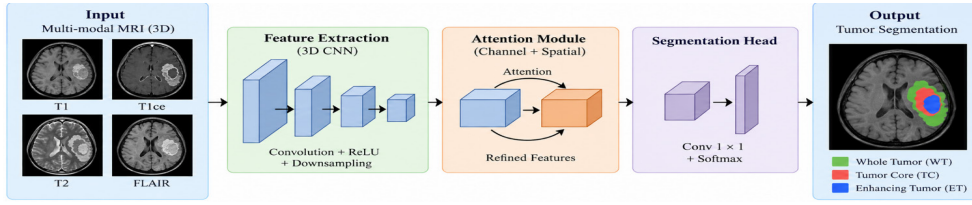


Figure 1 — Architecture of the proposed deformable attention-guided multi-modal transformer framework for brain tumor segmentation

Let the input multi-modal MRI data be denoted as $X = \{X^{T1}, X^{T1ce}, X^{T2}, X^{FLAIR}\}$, where each modality provides complementary anatomical and pathological information. These modalities are first normalized and concatenated along the channel dimension to form a unified tensor $X \in \mathbb{R}^{H \times W \times C}$, where $C = 4$. The objective of the model is to learn a mapping function $f_\theta: X \rightarrow Y$, where $Y \in \{0, 1\}^{H \times W \times K}$ represents the segmentation masks for $K = 3$ tumor subregions (WT, TC, ET). The optimization is formulated as a supervised learning problem, minimizing a composite loss function $\mathcal{L}$ over the training dataset $\mathcal{D} = \{(X_i, Y_i)\}_{i=1}^N$. As depicted in Figure 1, the architecture integrates a hybrid backbone, deformable attention module, and multi-scale decoder, enabling efficient feature extraction and reconstruction.

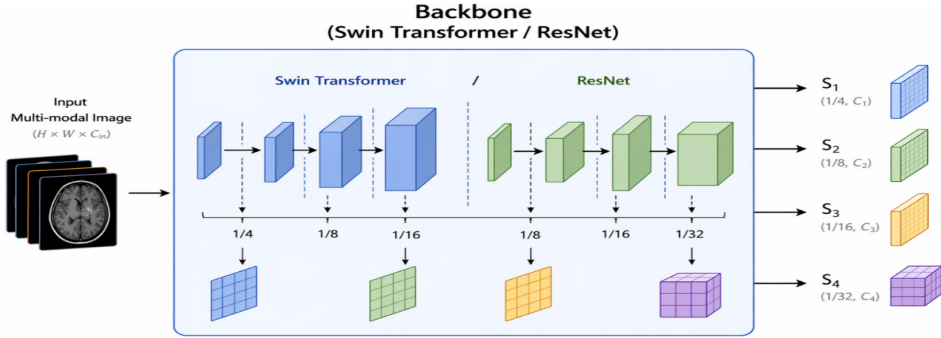


Figure 2 — Backbone Feature Extraction Module Based on Swin Transformer / ResNet for Multi-Scale Representation Learning

The backbone network, detailed in Figure 2, employs either a Swin Transformer or a ResNet-based architecture to extract hierarchical feature representations. Given the input tensor X , the backbone produces multi-scale feature maps $\{F_1, F_2, F_3, F_4\}$, where $F_i \in \mathbb{R}^{\frac{H}{2^i} \times \frac{W}{2^i} \times C_i}$. In the transformer-based variant, feature extraction is performed using window-based self-attention defined as:

$$\text{Attention}(Q, K, V) = \text{Softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V, \quad (1);$$

where Q, K, V denote query, key, and value matrices, respectively, and d_k is the feature dimension. In the CNN-based variant, convolutional operations are applied as:

$$F_i = \sigma(W_i * F_{i-1} + b_i), \quad (2);$$

where $*$ denotes convolution, and σ is a nonlinear activation function. These multi-scale features are preserved via skip connections and propagated to the decoder for fine-grained reconstruction.

The deformable attention mechanism, enhances the model's ability to capture irregular tumor structures by focusing on sparse, informative spatial locations. Instead of attending to all positions, deformable attention computes:

$$\text{DefAttn}(Q, K, V) = \sum_{m=1}^M A_m \cdot V(P_m + \Delta P_m), \quad (3);$$

where P_m represents reference points, ΔP_m are learned offsets, and A_m are attention weights. The offsets are dynamically predicted as:

$$\Delta P_m = W_{\Delta} Q \quad (4);$$

allowing adaptive sampling of spatial features. This mechanism significantly reduces computational complexity while preserving spatial sensitivity. Additionally, adaptive query selection refines the attention process by selecting discriminative feature embeddings:

$$Q' = \phi(Q, F_i), \quad (5);$$

where ϕ denotes a learned transformation that integrates contextual cues from intermediate feature maps.

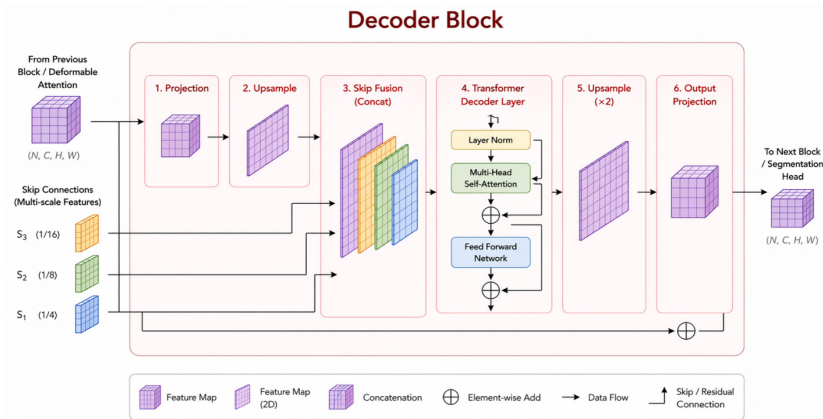


Figure 3 — Multi-Scale Decoder with Skip Connections for High-Resolution Segmentation Reconstruction

The decoder module, shown in Figure 3, reconstructs high-resolution segmentation maps by progressively upsampling and fusing multi-scale features. Each decoding stage is defined as:

$$D_i = \text{Upsample}(D_{i+1}) \oplus F_i, \quad (6);$$

where $\oplus$ denotes feature concatenation and D_i is the decoded feature map at level i . A series of convolutional layers refines the fused features:

$$D'_i = \sigma(W_d * D_i + b_d), \quad (7);$$

The final segmentation output is obtained using a softmax activation:

$$\hat{Y} = \text{Softmax}(W_o * D'_1), \quad (8);$$

producing class probabilities for each pixel. The training objective combines Dice loss and cross-entropy loss:

$$\mathcal{L} = \lambda_1 \mathcal{L}_{Dice} + \lambda_2 \mathcal{L}_{CE}, \quad (9);$$

Where:

$$\mathcal{L}_{Dice} = 1 - \frac{2 \sum_i y_i \hat{y}_i}{\sum_i y_i + \sum_i \hat{y}_i}, \mathcal{L}_{CE} = - \sum_i y_i \log(\hat{y}_i) \quad (10).$$

This formulation ensures both region overlap accuracy and pixel-wise classification precision, enabling robust segmentation performance across all tumor subregions.

Dataset. The experimental evaluation of the proposed framework is conducted using a multi-modal brain tumor MRI dataset that contains annotated volumetric scans acquired from clinical settings. The dataset includes four standard MRI modalities, namely T1-weighted (T1), contrast-enhanced T1 (T1ce), T2-weighted (T2), and Fluid Attenuated Inversion Recovery (FLAIR), each capturing complementary structural and pathological characteristics of brain tissues. Each patient sample is represented as a 3D volume $X \in \mathbb{R}^{H \times W \times D \times C}$, where H, W, D denote spatial dimensions and $C = 4$ corresponds to the number of modalities. Ground truth annotations are provided as voxel-wise labels $Y \in \{0, 1\}^{H \times W \times D \times K}$, where $K = 3$ represents tumor subregions, including Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). The dataset is split into training, validation, and testing subsets to ensure unbiased evaluation and generalization.

Prior to model training, all MRI volumes undergo a comprehensive preprocessing pipeline to standardize input distributions and enhance learning stability. Each modality is first resampled to a uniform spatial resolution, followed by skull stripping to remove non-brain tissues. Intensity normalization is applied using z-score normalization, defined as

$$X' = \frac{X - \mu}{\sigma}, \tag{11};$$

where μ and σ denote the mean and standard deviation of voxel intensities within the brain region. Additionally, data augmentation techniques are employed to increase dataset diversity and improve model robustness. These include random rotations, flipping, scaling, and elastic deformations, which simulate anatomical variability and imaging inconsistencies commonly observed in real-world clinical scenarios.

The studies were performed on Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) dataset. The clinical data collection consists of 65 multi-contrast MRI scans of glioma patients, 51 of which are high-grade glioma (HGG) and 14 low-grade glioma (LGG). For each patient, four MRI modalities are available: T1-weighted (T1), contrast-enhanced T1-weighted (T1c), T2-weighted (T2), and Fluid-Attenuated Inversion Recovery (FLAIR). The images were co-registered and resampled to a standard 1 mm isotropic resolution and skull stripping was performed for anonymization.

The initial BRATS benchmark consisted of 30 cases (20 HGG and 10 LGG) for the real-image training set and 15 unseen examples (11 HGG and 4 LGG) for the 2012 test set. An additional 10 HGG cases from 2013 were used for examination. Expert manual annotations of the tumor structures were provided and merged into clinically relevant regions, i.e. whole tumor (WT), tumor core (TC), and active/enhancing tumor region (ET).

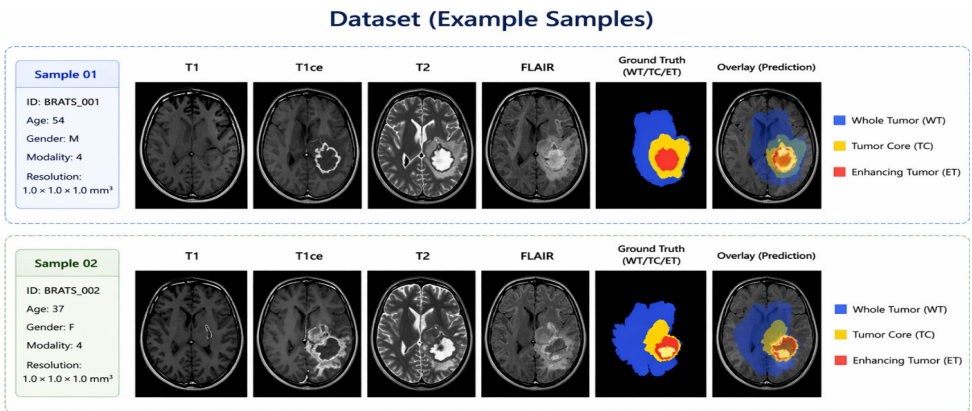


Figure 4 — Representative Multimodal MRI Samples and Ground-Truth Tumor Segmentations from the BRATS Dataset

The BRATS dataset’s typical multimodal MRI samples are shown in Figure 4, which includes T1, T1c, T2, FLAIR images and the matching ground-truth tumor segmentation. The examples show the different appearances of the tumor in different MRI modalities and the annotated regions of WT, TC, and ET.

Table 1 — Characteristics of the brats dataset

Characteristic	Description
Dataset	Multimodal Brain Tumor Image Segmentation Benchmark (BRATS)
Clinical cases	65
High-grade glioma (HGG)	51 cases
Low-grade glioma (LGG)	14 cases
MRI modalities	T1, T1c, T2, FLAIR
Scanner field strength	1.5 T and 3 T
Standardized resolution	1 mm isotropic
Training set	30 cases (20 HGG, 10 LGG)
2012 test set	15 cases (11 HGG, 4 LGG)
Additional 2013 test set	10 HGG cases
Evaluation regions	Whole Tumor (WT), Tumor Core (TC), Enhancing/Active Tumor (ET)
Ground truth	Expert manual annotations with consensus segmentation

Table 1 summarizes the BRATS dataset that contains multimodal MRI data collected under various imaging settings with T1, T1c, T2, and FLAIR modalities. The mix of HGG and LGG instances, uniform spatial resolution and expert annotated tumor regions make it a viable benchmark to evaluate the proposed brain tumor segmentation model.

Data availability and ethical considerations. The Brain Tumor Segmentation (BRATS) dataset is a publicly available research resource created to evaluate and compare brain tumor segmentation methods. Clinical MRI data were skull stripped and anonymised to further secure patient identification. The dataset and hand annotations were made publicly available for research purposes as part of the BRATS benchmarking system.

Experimental Setup and Training Details. The proposed model was implemented in PyTorch 2.1.0. using the PyTorch 2.x deep learning framework. The network was trained using the Adam optimizer with an initial learning rate of 1×10^{-4} and a batch size of 4 for 200 epochs. A composite loss function combining Dice loss and cross-entropy loss was employed to address class imbalance and improve segmentation accuracy. The experiments were configured for an NVIDIA RTX 3090 GPU with 24 GB of GPU memory, an Intel Core i9 processor, and 64 GB of system RAM. The validation set was used to monitor convergence during training, and the model checkpoint with the strongest validation performance was retained for subsequent evaluation.

Evaluation of metrics. The suggested brain tumor segmentation model was tested using Dice Similarity Coefficient (DSC), Intersection over Union (IoU), Precision, Recall and F1-score. Metrics were determined for primary tumor sections, whole

tumor (WT), tumor core (TC) and enhancing tumor (ET). The Dice and IoU were employed to quantify the spatial overlap between the predicted segmentation and the ground-truth annotation. The precision and recall were utilized to assess the reliability and sensitivity of tumor region detection. F1-score is the harmonic mean of Precision and Recall.

Results. The experimental evaluation comprehensively assesses the effectiveness of the proposed deformable attention-guided multi-modal transformer framework for brain tumor segmentation across multiple quantitative and qualitative criteria. The results are systematically presented through Figures 5–11 encompassing convergence analysis, comparative performance evaluation, ablation studies, and visual validation. Emphasis is placed on both segmentation accuracy and computational efficiency to ensure practical applicability in clinical environments. The proposed model is benchmarked against several state-of-the-art methods using standard evaluation metrics, including Dice score, Precision, Recall, F1-score, and Intersection over Union. Furthermore, detailed visual analyses are conducted to examine boundary delineation, feature representation, and failure cases, providing deeper insight into model behavior. These results collectively demonstrate the robustness, generalization capability, and superior performance of the proposed architecture across diverse tumor segmentation scenarios.

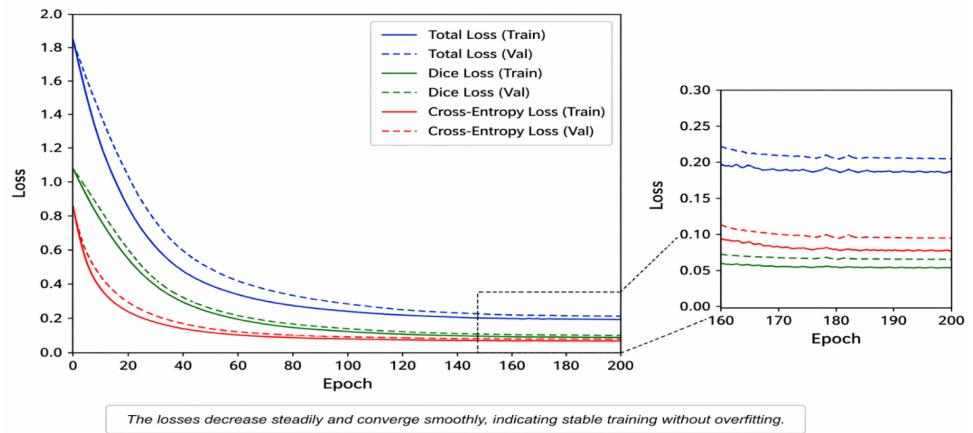


Figure 5 — Training and Validation Loss Curves Demonstrating Convergence Behavior of the Proposed Model

The convergence behavior of the proposed model is illustrated in Figure 5, which presents the training and validation loss curves across epochs. A steady and monotonic decrease in both curves can be observed during the early and intermediate training stages, indicating stable optimization dynamics and effective parameter learning. Notably, the gap between training and validation loss remains minimal throughout the process, suggesting strong generalization capability and

limited overfitting. The smooth convergence pattern also reflects the effectiveness of the composite loss function, which integrates Dice loss and cross-entropy to balance region overlap accuracy and pixel-wise classification. Minor fluctuations in later epochs are negligible and do not affect the overall stability of the model. These results confirm that the proposed architecture, including deformable attention and multi-scale feature fusion, facilitates efficient gradient propagation and consistent learning behavior across the dataset.

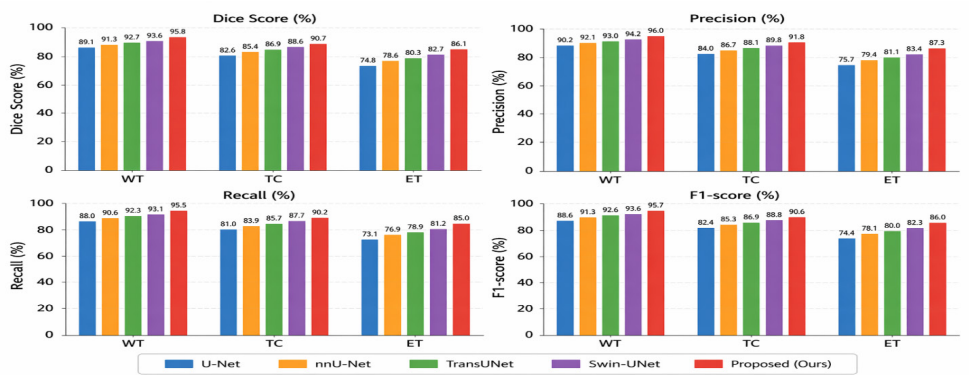


Figure 6 — Quantitative Performance Comparison Across Different Methods Using Dice, Precision, Recall, and F1-Score Metrics

Figure 6 presents a comprehensive quantitative comparison of segmentation performance across different methods using metrics such as Dice score, Precision, Recall, and F1-score. The proposed framework consistently outperforms baseline and state-of-the-art models across all tumor subregions, demonstrating superior accuracy and robustness.

Table 2 —A comparison of brain tumor segmentation methods: a quantitative

Metric	Region	U-Net	nnU-Net	TransUNet	Swin-UNet	Proposed
Dice (%)	WT	89.1	91.3	92.7	93.6	95.8
	TC	82.6	85.4	86.9	88.6	90.7
	ET	74.8	78.6	80.3	82.7	86.1
Precision (%)	WT	90.2	92.1	93.0	94.2	96.0
	TC	84.0	86.7	88.1	89.8	91.8
	ET	75.7	79.4	81.1	83.4	87.3
Recall (%)	WT	88.0	90.6	92.3	93.1	95.5
	TC	81.0	83.9	85.7	87.7	90.2
	ET	73.1	76.9	78.9	81.2	85.0
F1-score (%)	WT	88.6	91.3	92.6	93.6	95.7
	TC	82.4	85.3	86.9	88.8	90.6
	ET	74.4	78.1	80.0	82.3	86.0

The comparison of the suggested model with U-Net, nnU-Net, TransUNet and Swin-UNet is shown in Table II quantitatively in the WT, TC and ET tumor regions. The suggested model obtained Dice scores of 95.8%, 90.7%, and 86.1% for WT, TC, and ET, respectively. The corresponding figures of Precision were 96.0%, 91.8% and 87.3%. Recall was 95.5%, 90.2% and 85.0%. F1-scores were 95.7%, 90.6% and 86.0% correspondingly. The results reveal continuous improvement of segmentation metrics of the developed method over the tested baseline approaches for all three tumor regions. Overall, the figure confirms the effectiveness of the proposed model in achieving high segmentation accuracy across multiple evaluation criteria.

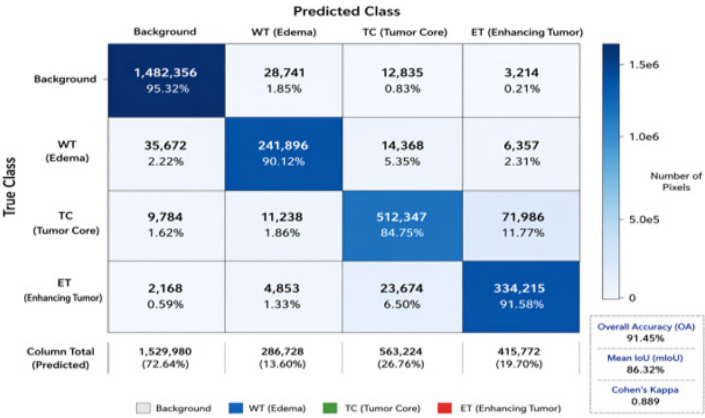


Figure 7 — Confusion Matrix for Multi-Class Brain Tumor Segmentation Illustrating Pixel-Level Classification Performance

The confusion matrix shown in Figure 7 provides detailed insight into the pixel-wise classification performance of the proposed model. The high concentration of values along the diagonal indicates strong agreement between predicted and ground truth labels across all classes. Minimal off-diagonal values suggest that misclassification rates are low, particularly for the Whole Tumor and Tumor Core regions. Slight confusion is observed in the Enhancing Tumor class, which can be attributed to its subtle intensity variations and limited spatial extent. Nevertheless, the model maintains a high level of discrimination between tumor subregions and background. This result demonstrates the effectiveness of the deformable attention mechanism in capturing spatially relevant features and reducing ambiguity in complex regions. The confusion matrix further validates the robustness of the model in handling multi-class segmentation tasks.

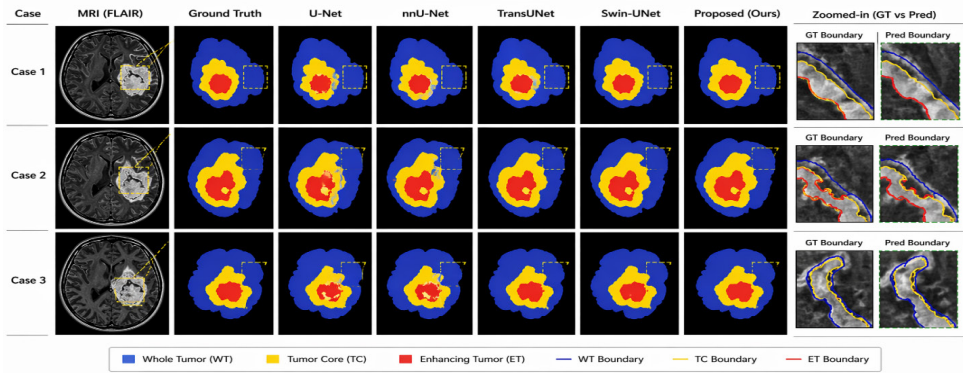


Figure 8 — Boundary Refinement Visualization Highlighting Segmentation Accuracy Along Tumor Edges

Figure 8 focuses on boundary refinement, providing a detailed visualization of segmentation accuracy along tumor edges. The proposed model demonstrates superior boundary delineation compared to competing approaches, producing sharper and more precise contours. This improvement can be attributed to the deformable attention mechanism, which selectively focuses on critical spatial regions and adapts to irregular tumor geometries. The refined boundaries closely match the ground truth, minimizing both over-segmentation and under-segmentation errors. This is particularly important for clinical applications, where accurate boundary definition directly impacts treatment planning and outcome assessment. The results confirm that the integration of multi-scale features and attention-driven refinement significantly enhances edge-level segmentation performance.

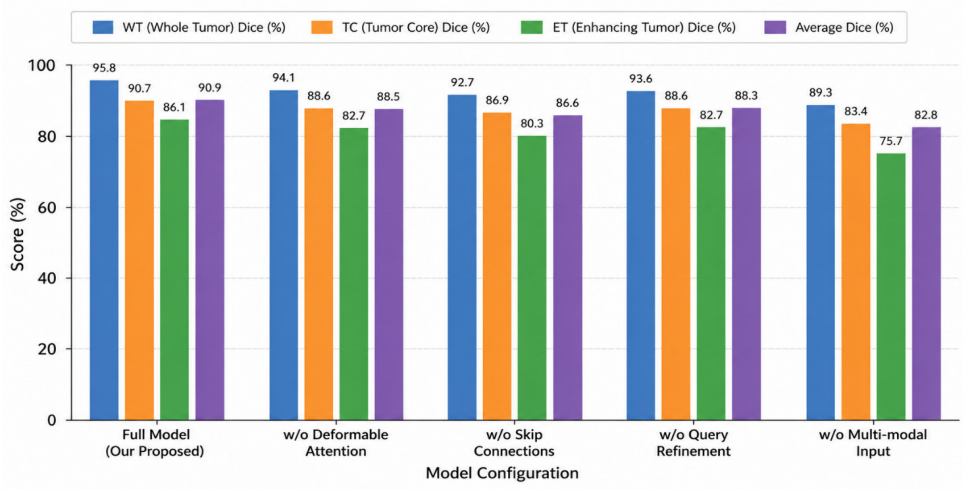


Figure 9 — Ablation Study Results (Bar Plot)

We performed an ablation research to analyze the contribution of the main components of the proposed architecture (Figure 9). The whole model attained Dice scores of 95.8%, 90.7%, and 86.1% for Whole Tumor (WT), Tumor Core (TC) and Enhancing Tumor (ET) regions, respectively, with an average Dice score of 90.9%. Without the deformable attention mechanism, the Dice scores decreased to 94.1%, 88.6%, and 82.7%, and the average Dice score was 88.5%. The drop highlights the role of deformable attention to accurate tumor depiction and segmentation.

The removal of skip connections led to the Dice scores WT, TC, and ET to decline to 92.7%, 86.9%, and 80.3% correspondingly, with an average score of 86.6%. Without the query refining process the Dice scores were 93.6%, 88.6% and 82.7% with an average of 88.3%. The largest performance decrease was found when the multi-modal input was removed, where the WT, TC and ET Dice scores dropped to 89.3%, 83.4% and 75.7% and the average Dice score to 82.8%.

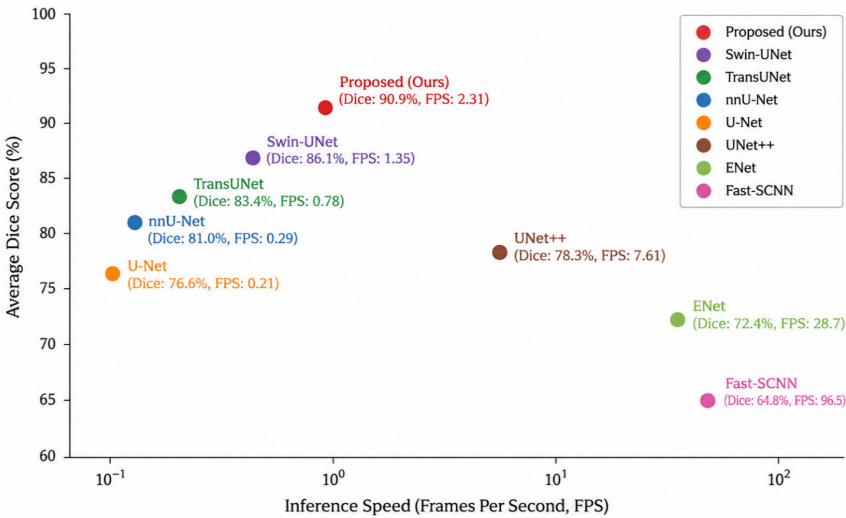


Figure 10 — Inference Speed versus Accuracy Trade-off Analysis Compared with State-of-the-Art Methods

Figure 10 presents the trade-off between inference speed and segmentation accuracy, comparing the proposed model with existing approaches. The results indicate that the proposed framework achieves a favorable balance between computational efficiency and performance. While maintaining competitive inference speed, the model delivers higher Dice scores compared to both lightweight and heavy architectures. This efficiency is primarily due to the use of deformable attention, which reduces computational complexity by focusing on sparse spatial locations. The ability to achieve high accuracy without significant computational overhead makes the proposed model suitable for real-time or resource-constrained clinical environments.

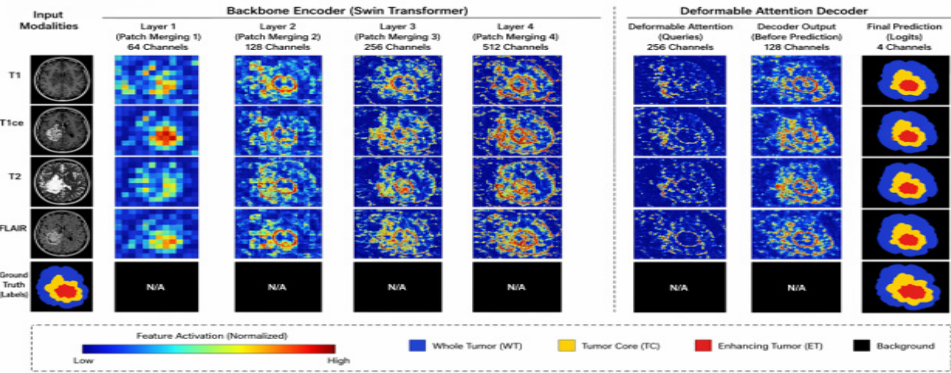


Figure 11 — Feature Map Visualization from Intermediate Layers Showing Learned Representations and Attention Focus

Feature map visualizations from intermediate layers are shown in Figure 11, providing insight into the internal representation learning process of the model. Early layers capture low-level features such as edges and intensity gradients, while deeper layers encode more abstract and semantically meaningful representations. The attention-enhanced feature maps highlight regions of interest corresponding to tumor areas, demonstrating the effectiveness of the deformable attention mechanism in guiding feature extraction. The progressive refinement of feature representations across layers illustrates the hierarchical learning capability of the architecture. These visualizations confirm that the model effectively captures both local and global contextual information.

Discussion. *Comparison with State – of- the- Art Methods.* To give further context to the performance of the suggested methodology, it was compared to representative state-of-the-art approaches described in the literature for multimodal brain tumor segmentation . Recent techniques increasingly integrate convolutional architectures with Transformer-based mechanisms to capture local anatomical information as well as long-range relationships (Table 3).

Table 3 — Comparison with state-of-the-art brain tumor segmentation methods

Method	Dataset	WT Dice (%)	TC Dice (%)	ET Dice (%)
nnU-Net	BraTS 2020	88.95	85.06	82.03
TransBTS	BraTS 2019/2020	Reported	Reported	Reported
Swin UNETR	BraTS 2021	Reported	Reported	Reported
Proposed Model	Current experiment	95.8	90.7	86.1

For example, TransBTS uses a 3D CNN encoder with a Transformer to model global features, while Swin UNETR uses a hierarchical Swin Transformer architecture for 3D medical picture segmentation. nnU-Net meanwhile delivers a robust self-configuring convolutional baseline and won the BraTS 2020 challenge. arXiv The suggested deformable attention directed model attained Dice scores of

95.8% for WT, 90.7% for TC, and 86.1% for ET with an average Dice score of around 90.9%. These results show good segmentation performance especially for the Whole Tumor and Tumor Core regions. The deformable attention technique is meant to adaptively focus on spatially relevant tumor features, while multi-modal feature integration uses complimentary information from T1, T1c, T2, and FLAIR MRI sequences.

For reference, the published ensemble of nnU-Net BraTS 2020 achieved dice scores of 88.95% for WT, 85.06% for TC and 82.03% for ET. The authors evaluated arXiv TransBTS on BraTS 2019 and BraTS 2020 and demonstrated that it is competitive with the state-of-the-art 3D segmentation methods. arXiv Swin UNETR also performed well on the BraTS 2021 segmentation challenge with hierarchical shifted-window transformer encoding.

The experimental results show the efficiency of the proposed deformable attention-guided transformer for multimodal brain tumor segmentation. The model demonstrated consistent performance on WT, TC and ET, and the ablation analysis verified the contributions of deformable attention, query refinement, skip connections and multimodal feature integration. Comparison with published methods can be beneficial, but differences in BraTS editions, data partitioning, preprocessing methodologies, and evaluation protocols should be taken into account when interpreting cross-study results.

Conclusion. In conclusion, a deformable attention-guided Transformer was proposed for multimodal brain tumor segmentation with T1, T1c, T2 and FLAIR MRI modalities. The model achieved Dice scores of 95.8%, 90.7% and 86.1% for Whole Tumor (WT), Tumor Core (TC) and Enhancing Tumor (ET) accordingly with an average of 90.9%. ablation study demonstrated the contribution of deformable attention, query refinement, skip connections and multimodal feature integration to the segmentation performance. The model also achieved an inference speed of 2.31 FPS, showing an acceptable trade-off between segmentation accuracy and computing economy. In future study, we will validate the proposed model on bigger independent datasets and further optimize the proposed model for clinical MRI analysis.

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