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POLYTECHNIQUE MONTRÉAL

affiliée à l'Université de Montréal

Détection, prédiction et classification des tumeurs cérébrales basées sur les modèles formels et l'apprentissage en profondeur

LAHCEN EL FATIMI

Département de génie informatique et génie logiciel

Thèse présentée en vue de l'obtention du diplôme de *Philosophiæ Doctor*

Génie informatique

Avril 2023

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POLYTECHNIQUE MONTRÉAL

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Cette thèse intitulée:

Détection, prédiction et classification des tumeurs cérébrales basées sur les modèles formels et l'apprentissage en profondeur

présentée par Lahcen EL FATIMI

en vue de l'obtention du diplôme de *Philosophiæ Doctor*

a été dûment acceptée par le jury d'examen constitué de :

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RÉSUMÉ

Les tumeurs cérébrales sont parmi les maladies les plus meurtrières de ces dernières années avec environ 70 000 nouveaux cas chaque année aux États-Unis seulement et seulement environ 25% des personnes diagnostiquées avec une tumeur cérébrale survivent pendant cinq ans ou plus après le diagnostic. Le taux de mortalité des tumeurs cérébrales est extrêmement élevé, la plupart des patients succombent à la maladie moins de deux ans après le diagnostic. Avec un taux de survie aussi faible, il est urgent d'améliorer notre compréhension des tumeurs cérébrales afin de les détecter le plus tôt possible et de les traiter efficacement. Devant ces besoins pressants, la communauté scientifique s'est engagée à développer des techniques d'analyse visant à mieux comprendre, détecter et traiter les tumeurs cérébrales. Ces dernières années, les progrès des technologies de séquençage génomique ont permis aux chercheurs de commencer à démêler les complexités des tumeurs cérébrales au niveau moléculaire, cela a permis l'identification de différents types et sous-types de tumeurs cérébrales, qui peuvent désormais être ciblées avec un traitement plus précis et a également permis aux chercheurs de découvrir les changements génétiques complexes qui entraînent la croissance et la progression tumorale. Il s'agit d'une avancée majeure dans la lutte contre les tumeurs cérébrales, et avec l'espoir d'émergence de nouvelles options de traitement qui permettront de réduire la morbidité et la mortalité associées à cette forme de cancer. Et, aussi, conduire à de meilleurs de traitement des patients atteints.

Dans ce contexte, la détection des tumeurs et l'analyse de la croissance des tumeurs cérébrales sont devenues nécessaires afin de mieux comprendre comment les cibler et les traiter plus efficacement, et avec l'avènement des techniques d'imagerie modernes telles que l'Imagerie par Résonance Magnétique (IRM) et la tomodensitométrie, il est désormais possible de visualiser les tumeurs et de les détecter en temps réel. Cela a permis aux professionnels de la santé de mieux évaluer la gravité des tumeurs et de déterminer le meilleur plan d'action pour le traitement. Cependant, même avec ces progrès dans les techniques d'imagerie, il est encore difficile de déterminer la cause et l'effet biologiques exacts d'un modèle de croissance tumorale, ainsi que les interactions cellulaires sous-jacentes qui entraînent la croissance tumorale.

Cette thèse porte sur la détection, la prédiction et la classification des tumeurs cérébrales. Elle vise à concevoir et développer des techniques automatiques et plus efficaces de détection, de

classification et de prédiction de l'évolution des tumeurs cérébrales. Ces techniques s'appuient sur des approches existantes de segmentation d'images IRM et d'apprentissage automatique combinées avec des formalismes de haut niveau comme le modèle de Markov et les automates cellulaires.

Le modèle de Markov est utilisé pour la prédiction de tumeurs cérébrales. Il est généré à partir de jeux de données disponibles (ensembles d'images IRM). La prédiction est, notamment, basée sur le calcul de probabilités de présence de tumeurs cérébrales.

Les automates cellulaires, quant à eux, sont utilisés pour détecter des tumeurs cérébrales. Il s'agit de représenter une image par un automate cellulaire où une cellule correspond à une région, un pixel ou un voxel de l'image et où l'évolution de l'état d'une cellule dépend de ceux de son voisinage. La détection des tumeurs est basée sur l'analyse du comportement des cellules dictée par la sémantique des automates cellulaires.

En ce qui concentre la classification des tumeurs cérébrales, cette thèse montre comment utiliser et configurer adéquatement MobileNet, afin de réduire, tout en conservant la même précision de classification, les temps d'inférence, par rapport aux modèles traditionnels d'apprentissage. Ce gain a pour conséquence d'accélérer le processus de diagnostic des tumeurs cérébrales.

L'ensemble des techniques proposées, dans le cadre de cette thèse ont été testés, validés et évalués sur des ensembles de données. Les résultats obtenus confirment leur efficacité et leur précision.

Enfin, le dernier volet de cette thèse porte sur l'apport des techniques de model-checking dans la segmentation d'images médicales ainsi que dans la validation et la mise au point de techniques de détection des tumeurs cérébrales.

ABSTRACT

Brain tumors are among the deadliest diseases in recent years with approximately 70,000 new cases each year in the United States alone and only about 25% of people diagnosed with a brain tumor survive for five years or more after diagnosis. The mortality rate of brain tumors is extremely high, with most patients succumbing to the disease within two years of diagnosis. With such a low survival rate, there is an urgent need to improve our understanding of brain tumors in order to detect them as early as possible and treat them effectively. In response to this pressing need, the scientific community is committed to developing analytical techniques to better understand, detect and treat brain tumors.

In recent years, advances in genomic sequencing technologies have allowed researchers to begin to unravel the complexities of brain tumors at the molecular level; this has allowed the identification of different types and subtypes of brain tumors, which can now be targeted with more precise treatment, and has also allowed researchers to discover the complex genetic changes that drive tumor growth and progression. This is a major advance in the fight against brain tumors and with it the hope of emerging new treatment options that will reduce the morbidity and mortality associated with this form of cancer. And also lead to better treatment of affected patients.

In this context, tumor detection and growth analysis of brain tumors have become necessary to better understand how to target and treat them more effectively, and with the advent of modern imaging techniques such as Magnetic Resonance Imaging (MRI) and CT scans, it is now possible to visualize tumors and detect them in real time. This has allowed medical professionals to assess the severity of tumors better and determine the best course of action for treatment. However, even with these advances in imaging techniques, it is still difficult to determine the exact biological cause and effect of a tumor growth pattern, as well as the underlying cellular interactions that drive tumor growth.

This thesis focuses on the detection, prediction, and classification of brain tumors. It aims to design and develop automatic and more efficient techniques for detecting, classifying, and predicting brain tumors. These techniques are based on existing MRI image segmentation and machine learning approaches combined with high-level formalisms such as the Markov model and cellular automata.

The Markov model is used for brain tumor prediction. It is generated from available data sets (MRI image sets). The prediction is, in particular, based on calculating probabilities of the presence of brain tumors.

Cellular automata are used to detect brain tumors. It consists in representing an image by a cellular automaton where a cell corresponds to a region, a pixel, or a voxel of the image and where the evolution of the state of a cell depends on those of its neighborhood. Tumor detection is based on the analysis of cell behavior dictated by the semantics of cellular automata.

Focusing on brain tumor classification, this thesis shows how to use and configure MobileNet appropriately, in order to reduce training and inference times, while keeping the same classification accuracy compared to traditional learning models. This gain results in accelerating the diagnosis process of brain tumors. All the techniques proposed in this thesis have been tested, validated, and evaluated on data sets. The results were obtained to confirm their efficiency and accuracy.

Finally, the last part of this thesis deals with the contribution of model-checking techniques in the segmentation of medical images as well as in the validation and development of brain tumor detection techniques.

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LISTE DES SIGLES ET ABRÉVIATIONS

AIM	Analyse d'images médicales
IRM	Imagerie par résonance magnétique
CM	Chaine de Markov
MMC	Modèle de Markov cache
CA	Automate cellulaire
TC	Tumeur cérébrale
DL	Apprentissage en profondeur
TL	Logique temporelle
LTL	Logique temporelle linéaire
KNN	K-nearest neighbors
DTMC	Chaîne de Markov à temps discret
AP	Propositions atomiques
PF	Faux positifs
FN	Faux négatifs
TP	Vrais positifs
TN	Vrais négatifs
GLCM	Matrice de cooccurrence de niveaux de gris
FCM	Clustering flou C-Means
ASM	Deuxième moment angulaire
IDM	Moment de Différence Inverse

CHAPITRE 1 INTRODUCTION

Ce premier chapitre est dédié au contexte, à la problématique, aux objectifs de recherche, ainsi qu'au plan de cette thèse.

1.1 Contexte et problématique

Cette thèse s'intéresse à la détection, la classification et la prédiction automatiques de tumeurs cérébrales. Une tumeur cérébrale est une masse anormale de tissu, dans le cerveau, dans laquelle les cellules se développent et se multiplient de manière incontrôlable [1, 2, 3, 4, 5]. Plus de 150 tumeurs cérébrales différentes ont été identifiées et documentées [6,7], mais les tumeurs cérébrales primaires et métastatiques, et les tumeurs cérébrales carcinoïdes comptent parmi les maladies sournoises les plus mortelles. L'une des principales raisons du taux de mortalité élevé est le retard dans la détection et le traitement à temps de ces maladies. Il est donc impératif de se doter de tous les moyens matériels et logiciels permettant de les détecter et de les traiter le plus tôt possible [1, 2, 3, 4, 5].

Généralement, la détection de tumeurs se base sur des technologies d'imagerie qui comprennent, mais sans s'y limiter, l'imagerie par résonance magnétique (IRM), les rayons X et la tomodensitométrie (CT). Les données brutes fournies par ces technologies d'imagerie sont traitées manuellement ou automatiquement, afin de détecter une tumeur (son type, sa taille, son emplacement, etc.) et de la traiter adéquatement. Les techniques de traitement automatique d'images, de plus en plus précises et efficaces, s'imposent actuellement comme un impératif inéluctable afin de déceler des anomalies y compris celles qui sont non visibles à l'oeil humain. Elles permettent ainsi une détection plus précoce de tumeurs. La principale limitation des techniques automatiques existantes reste la non-fiabilité à 100% de leurs résultats comme, par exemple, une détection d'une tumeur inexistante, une classification erronée d'une tumeur ou encore un échec de détection d'une tumeur existante. Ce manque de fiabilité peut être lié à l'emplacement, la taille, le type d'une tumeur, le processus d'apprentissage. En effet, l'emplacement de la tumeur peut rendre difficile sa détection. Par exemple, les tumeurs situées dans le cerveau ou la moelle épinière peuvent être difficiles à détecter en raison de la complexité de la structure de leurs tissus.

Les petites tumeurs peuvent être également difficiles à détecter à l'aide de techniques d'imagerie, en particulier si elles sont situées dans des zones avec beaucoup de tissus environnants. Certains types de tumeurs peuvent être également plus difficiles à détecter, si, par exemple, elles ne produisent pas, en quantités suffisantes, de protéines servant à les détecter. La précision de la détection des tumeurs peut également être affectée par le manque d'expérience et l'expertise des professionnels de la santé impliqués dans le processus de dépistage. Il faut aussi mentionner que certaines techniques d'imagerie, telles que la mammographie, ont des limites en termes de capacité à détecter des tumeurs dans certaines populations, telles que les femmes ayant un tissu mammaire dense.

Enfin, certaines tumeurs évoluent dangereusement sans produire aucun symptôme, ce qui les rend plus difficiles à détecter à un stade précoce. Ainsi, la problématique abordée dans cette thèse concerne l'automatisation des processus de détection, de classification et de prédiction des tumeurs cérébrales et l'amélioration de leur fiabilité par rapport aux méthodes traditionnelles, ce qui peut conduire à une meilleure prise en charge des patients atteints de tumeurs cérébrales et à de meilleurs résultats pour ces patients

1.2 Objectifs et contributions

L'objectif général de cette thèse est de concevoir et développer un cadre méthodologique plus fiable pour la détection, la classification et la prédiction automatiques des tumeurs cérébrales. L'atteinte de cet objectif s'appuie sur des modèles de représentation d'images, tels que les automates cellulaires et le modèle de Markov, les techniques d'analyses associées aux modèles combinées avec des techniques d'apprentissage. Les questions de recherche adressées le long de cette thèse en relation avec cet objectif général sont :

1. Comment utiliser et adapter les automates cellulaires pour détecter automatiquement et avec plus de précision des tumeurs cérébrales ?
2. Comment utiliser et adapter l'architecture MobileNet pour améliorer la classification des tumeurs cérébrales ?

3. Comment utiliser le modèle de Markov pour la prédiction avec précision de la progression des tumeurs cérébrales ?
4. Comment appliquer et adapter les techniques de model-checking pour la validation de la détection de tumeurs cérébrales ?

1.2.1 Première contribution

La première contribution de notre recherche est la conception et le développement d'une technique de prédiction de la progression des tumeurs cérébrales basée sur le modèle de Markov et l'algorithme KNN. Cette technique consiste à calculer un modèle de Markov à partir de données cliniques et d'imagerie de tumeurs cérébrales. La prédiction de la progression des tumeurs cérébrales est calculée sous forme de probabilités. Cette technique a fait l'objet d'un article, intitulé « Tumor growth prediction and classification based on the KNN algorithme and Discrète-time Markov Chains (DTMC) », présenté au chapitre 3 de cette thèse.

1.2.2 Deuxième contribution

La deuxième contribution de notre recherche est la conception et le développement d'une technique de détection des tumeurs cérébrales basée sur les automates cellulaires. Les automates cellulaires sont utilisés pour spécifier le comportement des cellules individuelles (pixels, voxels ou régions d'une image) ainsi que leurs interactions, et déduire ensuite les éventuelles dégénérescences tumorales. Cette technique a fait l'objet d'un article, intitulé « Brain Tumor Detection using Cellular Automata based image Segmentation techniques », présenté au chapitre 4 de cette thèse.

1.2.3 Troisième contribution

La troisième contribution de notre recherche concerne la classification des tumeurs cérébrales à l'aide des modèles MobileNet. Cette contribution a fait l'objet d'un article, intitulé « Brain Tumors Classification using the Mobile Net Models », présenté au chapitre 5. Cet article montre comment utiliser et configurer adéquatement les modèles MobileNet afin d'améliorer la précision et le temps de la classification des tumeurs cérébrales.

1.2.4 Quatrième contribution

Cette contribution montre comment utiliser les techniques formelles de model-checking pour valider la détection des tumeurs. Ces techniques permettent de vérifier si un modèle, représentant un système ou un objet, satisfait certaines propriétés et de fournir, dans le cas échéant, des contre-exemples. Il s'agit, dans le cas de cette thèse, de représenter une image par un espace discret et de spécifier les propriétés qui caractérisent les régions tumorales au moyen d'une logique spatio-temporelle. Le model-checking consiste à déterminer les régions d'une image qui satisfont les propriétés ou encore à vérifier si une région de l'image satisfait les propriétés. Cette contribution a fait l'objet d'un article, intitulé « Validation of Tumor Detection using Model Checking », présenté au chapitre 7 de cette thèse. Un autre article dédié à la revue de littérature portant sur l'emploi des techniques de model-checking dans l'analyse d'images médicales.

1.3 Plan de la thèse

Cette thèse, par articles, est composée de 9 chapitres au total. Ce présent chapitre est dédié au contexte, à la problématique, aux objectifs, aux contributions et au plan de cette thèse. Le chapitre 2 présente quelques concepts de base, formalismes et une revue de littérature portant sur la détection, la prédiction et la classification automatiques de tumeurs cérébrales. Les chapitres 3, 4, 5, 6 et 7 sont dédiés à la présentation, sous forme d'articles, des contritions de cette thèse. Le chapitre 8 est consacré à une discussion générale des travaux et les résultats obtenus dans le cadre de cette thèse. Enfin, le chapitre 9 présente la synthèse et les limites des solutions proposées ainsi qu'un aperçu des travaux futurs.

CHAPITRE 2 REVUE CRITIQUE DE LA LITTÉRATURE

Ce chapitre a pour objectif de présenter succinctement quelques concepts de base, formalismes, ainsi qu'une revue de littérature portant sur la détection, la prédiction et la classification des tumeurs cérébrales.

2.1 Tumeurs cérébrales

Une tumeur est l'une des nombreuses pathologies qui affectent les cellules d'un tissu et acquièrent la capacité de proliférer anormalement, d'envahir d'autres tissus au fil du temps et de provoquer une myriade de complications [9]. Elle est également connue sous le nom de tumeurs malignes ou de néoplasmes, et a été indirectement responsable d'environ 10 millions de décès en seulement 2020 [9, 10]. Les tumeurs se développent généralement à partir d'une seule cellule maligne et ont des qualités similaires et des caractéristiques génétiques partagées, quelle que soit leur emplacement dans le corps [11, 12].

Détecter une tumeur cérébrale et suivre sa croissance à l'aide d'une IRM du cerveau est l'une des méthodes les plus populaires et bien établies. Des informations concernant le développement de tumeurs cérébrales peuvent être obtenues grâce à la numérisation d'images cérébrales de la structure interne du cerveau humain. Cependant, il peut être difficile d'identifier manuellement les tumeurs cérébrales à partir d'une IRM car certaines tumeurs provoquent également des altérations importantes des structures internes et externes du cerveau [13]. Des modèles et techniques mathématiques ont été progressivement utilisés pour étudier les phénomènes oncologiques, contribuant ainsi au développement de nouvelles approches diagnostiques et thérapeutiques ainsi qu'à une meilleure compréhension de l'évolution des maladies associées [14, 15, 16]. La création et l'utilisation de modèles pour décrire des processus tels que la croissance néoplasique et le traitement individualisé font tous partie de l'oncologie mathématique [17]. En raison de leur capacité à tester et à reproduire une variété de scénarios qui sont soit peu pratiques, soit impossibles à tester in vitro, les modèles mathématiques ont un avantage stratégique qui en fait des outils d'analyse importants [18] car les tests cliniques sur les humains demandent beaucoup de temps et de ressources. Cela a été une percée dans le domaine de la recherche médicale car les modèles mathématiques peuvent simuler une variété de scénarios rapidement et efficacement. En effet, en

s’appuyant sur la puissance des modèles mathématiques pour simuler des tests cliniques de manière beaucoup plus efficace, les chercheurs sont en mesure de mieux comprendre comment un cancer progresse, comment certains traitements peuvent l'affecter et quelle approche individualisée peut être utilisée, afin de maximiser l'efficacité du traitement et potentiellement améliorer les résultats des traitements à long terme.

Les types de tumeurs cérébrales peuvent être classées selon le lieu de leur création et la malignité [7]:

- **En fonction de la localisation, les tumeurs cérébrales sont classées comme suit :**
    a. **Tumeurs cérébrales primaires :** Ces tumeurs prennent naissance dans les cellules cérébrales et se propagent parfois à d'autres parties du cerveau ou à la colonne vertébrale. Mais la propagation à d'autres organes ne se produit que rarement.
    b. **Tumeurs cérébrales métastatiques (ou secondaires) :** Ces tumeurs prennent naissance dans d'autres parties du corps et se propagent ensuite au cerveau.
- **Sur la base de la malignité, les tumeurs cérébrales sont classées comme suit :**
    a. **Tumeurs cérébrales bénignes :** Du nom lui-même, on peut comprendre que ces tumeurs sont les moins agressives. Elles proviennent de cellules du cerveau ou de parties associées au cerveau et ne contiennent pas de cellules cancéreuses. Elles ne se développent que lentement et ont également des frontières claires, c'est-à-dire que leur croissance est auto-limitée et qu'elles ne se propageront pas à d'autres tissus.
    b. **Tumeurs cérébrales malignes :** Ces tumeurs contiennent des cellules cancéreuses et leur croissance n'est pas auto-limitée. Souvent, leurs frontières ne sont pas claires. De plus, elles se développent rapidement et envahissent les tissus cérébraux environnants. Par conséquent, elles deviendront potentiellement mortelles si aucun traitement approprié n'est prescrit à temps.

Différents types de techniques d'imagerie telles que l'imagerie par résonance magnétique (IRM), la tomodensitométrie (CT), etc. existent pour le diagnostic de tumeur cérébrale.

L'IRM est la plus recommandée car elle n'utilise pas de rayonnement ionisant et elle offre également un plus grand contraste entre les différents tissus mous du corps humain, ce qui rend plus facile l'identification des tumeurs. En effet les images IRM (Imagerie par Résonance Magnétique) sont des images médicales produites à l'aide d'un équipement d'IRM qui utilise des ondes électromagnétiques pour produire des images en 3D de l'intérieur du corps humain. Les images IRM sont souvent utilisées pour visualiser les tissus mous et les organes internes tels que le cerveau, le cœur, le foie, les reins et les articulations. Les images IRM sont très utiles pour aider les médecins à diagnostiquer les maladies et les affections [19], car elles fournissent des images très détaillées de l'intérieur du corps sans utiliser de rayonnement ionisant, contrairement aux images radiographiques ou scanographiques. Les images IRM peuvent être utilisées pour diagnostiquer une variété de conditions médicales, y compris les maladies cardiaques, les tumeurs cérébrales, les accidents vasculaires cérébraux, les troubles de la colonne vertébrale, les maladies rénales et hépatiques, et bien d'autres encore. Les images IRM peuvent également être utilisées pour surveiller la progression d'une maladie et évaluer l'efficacité d'un traitement. En général, les images IRM sont considérées comme très sûres et ne présentent pas de risques significatifs pour la santé, bien qu'il y ait des précautions à prendre pour certains patients, comme ceux portant des implants métalliques ou ayant des problèmes rénaux.

2.2 Détection de tumeurs cérébrales

La détection fait référence au processus d'identification de la présence d'une tumeur cérébrale. Cela se fait généralement à l'aide de techniques d'imagerie médicale telles que l'imagerie par résonance magnétique (IRM), la tomodensitométrie (TDM) ou la tomographie par émission de positrons (TEP). L'objectif principal de la détection est de confirmer la présence d'une tumeur et de déterminer son emplacement et sa taille.

2.3 Classification de tumeurs cérébrales

La classification fait référence au processus de détermination du type de tumeur cérébrale qui a été détecté. Il existe de nombreux types différents de tumeurs cérébrales, chacune avec ses propres caractéristiques uniques et ses options de traitement spécifiques. La classification se fait généralement à l'aide d'une combinaison d'études d'imagerie et d'échantillons de tissus obtenus par

biopsie. L'objectif principal de la classification est d'identifier le type spécifique de tumeur afin que le plan de traitement le plus approprié puisse être développé.

2.4 Prédiction de la progression de tumeurs cérébrales

La prédiction fait référence au processus d'estimation du comportement futur d'une tumeur cérébrale. Cela peut inclure la prédiction de la vitesse à laquelle la tumeur est susceptible de croître ou de se propager, ainsi que la façon dont elle est susceptible de répondre à différentes options de traitement. La prédiction se fait généralement à l'aide d'une combinaison d'études d'imagerie, de tests de laboratoire et d'observations cliniques. L'objectif principal de la prédiction est d'aider à orienter les décisions de traitement et de fournir aux patients et à leur famille des informations sur ce à quoi s'attendre à l'avenir.

En résumé, la détection consiste à identifier la présence d'une tumeur, la classification consiste à identifier le type de tumeur, et la prédiction consiste à estimer le comportement futur de la tumeur. Les trois aspects sont importants pour le diagnostic et le traitement des tumeurs cérébrales et sont généralement utilisés en combinaison pour fournir les informations les plus précises et utiles possibles.

2.5 Analyse d'images médicales (AIM)

L'objectif de l'analyse d'images médicales est d'extraire des informations cliniquement pertinentes à partir d'images médicales dans le but de faciliter le diagnostic, la planification du traitement et la surveillance de la progression de maladies. Plusieurs banques d'images médicales recueillies dans divers établissements de santé sont disponibles pour tester et évaluer des méthodes de détection de maladies [18]. Dans le but d'aider les chercheurs, ces images médicales sont rassemblées, analysées et cataloguées sous forme d'ensembles de données annotées d’informations importantes. Par exemple, les images médicales de radiographies pulmonaires peuvent être annotées par les caractéristiques, tels que les nodules pulmonaires, les fractures des côtes et les épanchements pleuraux, qui peuvent aider au diagnostic du cancer du poumon, des fractures des côtes et des épanchements pleuraux, respectivement, ainsi que d'autres maladies. Les banques d’images médicales sont aussi exploitées pour, notamment, développer et tester des techniques automatiques de détection de maladies.

Il existe plusieurs techniques différentes d'analyse d'images médicales, notamment [19, 20, 21]:

- Segmentation d'images : il s'agit du processus de partitionner une image en plusieurs segments ou régions en fonction de certaines caractéristiques, telles que la couleur, l'intensité ou la texture. La segmentation d'images est souvent utilisée pour isoler et identifier des structures ou des tissus spécifiques dans une image, tels que des tumeurs ou des vaisseaux sanguins.
- Recalage d'images : il s'agit du processus d'alignement de deux images ou plus du même sujet prises à des moments différents ou avec des modalités d'imagerie différentes. L'enregistrement d'images est utile pour surveiller les changements de l'état d'un patient au fil du temps ou pour combiner différents types d'images afin de créer une image plus complète de l'anatomie du patient.
- Classification et reconnaissance : cela implique le développement d'algorithmes pour reconnaître automatiquement des caractéristiques spécifiques dans les images médicales. Par exemple, un algorithme peut être conçu pour reconnaître les signes d'une maladie particulière dans une radiographie pulmonaire.
- Diagnostic assisté par ordinateur (DAO) : il s'agit d'utiliser des algorithmes pour aider les radiologues ou d'autres professionnels de la santé à établir des diagnostics basés sur des images médicales. Les systèmes de DAO peuvent aider à identifier des anomalies qui pourraient être difficiles à détecter pour un observateur humain.

L'analyse d'images médicales est un domaine important et en croissance, avec de nombreuses applications. Elle a le potentiel d'améliorer la précision et l'efficacité des diagnostics et des traitements médicaux, et d'aider à identifier de nouveaux traitements et thérapies pour diverses maladies.

2.6 Ensembles de données (Dataset) utilisés

Plusieurs ensembles de données d'images cérébrales IRM sont disponibles pour le développement et le test de méthodes de détection de tumeurs cérébrales. L’ensemble de données BRATS (multimodal brain tumor image segmentation benchmark), qui inclus BRATS 2012, BRATS 2013,

BRATS 2015, BRATS 2016, BRATS 2017 et BRATS 2018, est le plus souvent utilisé pour développer et tester des techniques de détection de tumeurs cérébrales.

Pour atteindre nos objectifs discutés au chapitre 1, nous avons utilisé 3 jeux de données accessibles au public.

Le premier ensemble de données contient 2000 images de sujets nouvellement diagnostiqués avec un glioblastome primaire [22]. Ces sujets ont été traités par chirurgie et radiothérapie standard (RCT) concomitante. Cet ensemble de données a été utilisé pour évaluer les performances des techniques de classification et de prédiction de la progression tumorale.

Le second ensemble de données est sélectionné à partir de Kaggle. Il a été créé en 2021 par Kanchan S et al. et a été téléchargé plus de 13980 fois [22], en raison de son efficacité à évaluer la qualité des algorithmes de classification et de détection de tumeurs cérébrales. De plus, il est organisé sous forme de classes de tumeurs cérébrales, où chaque classe contient plusieurs cas de tumeurs qui diffèrent en termes d'emplacement, de taille, de vitesse de propagation, etc. Il inclut, en plus, une classe saine (aucune présence de tumeurs). Chaque classe est, à son tour, composé de données d'apprentissage et de données de test. Parmi les différentes classes, dans le cadre de cette thèse, nous avons utilisé la classe saine et les classes liées aux tumeurs malignes.

Le troisième ensemble de données est sélectionné à partir de Kaggle. Il a été créé en 2019 par Anshu S et al. Il contient deux catégories de données : une catégorie tumorale contenant plusieurs cas de tumeurs et une catégorie saine. La catégorie tumorale comprend 1550 images et la catégorie sain comprend 980 images. Plus de 38 440 personnes ont téléchargé cet ensemble pour son efficacité à évaluer la qualité des algorithmes de classification et de détection.

La section suivante montre comment représenter les images sous forme de modèles et disposer ainsi des techniques d'analyse associées aux modèles.

2.7 Modèles de représentation des images

La modélisation d'image fait référence au processus de création d'un modèle qui représente une image. L'objectif de cette modélisation est de capturer la structure sous-jacente et les caractéristiques de l'image afin qu'elles puissent être analysées, manipulées ou utilisées à d'autres fins. L'utilisation de modèles de représentation formels, comme les systèmes de transitions, les automates cellulaires et les modèles de Markov, est motivée par leurs capacités, d'une part, à capturer les caractéristiques complexes des images médicales de manière précise et rigoureuse et, d'autre part, exploiter adéquatement les techniques d'analyse associées, afin de détecter, prédire la progression et classifier les tumeurs cérébrales.

En effet, les tumeurs cérébrales peuvent varier considérablement en termes de taille, de forme et de localisation, et il est important d'avoir des modèles qui puissent identifier ces variations avec précision tout en offrant des techniques d'analyse intéressantes. Certains modèles, comme les automates cellulaires, offrent la possibilité de spécifier les interactions entre les tumeurs et les tissus environnants, de simuler leur propagation et, en fin, déterminer les zones à traiter. D'autres modèles, comme les modèles de Markov, permettent d'exploiter les données existantes pour calculer les probabilités de progression des tumeurs.

Par ailleurs, les modèles de représentation des images permettent également de combiner les données d'imagerie avec des données cliniques et génétiques pour améliorer la précision de la détection et de la classification des tumeurs cérébrales. Il serait alors possible d'analyser les données à plusieurs échelles et de découvrir des corrélations complexes entre les caractéristiques de la tumeur et les facteurs de risque ou les résultats cliniques. Les résultats de ces analyses peuvent, notamment, aider à déterminer le type de thérapie le plus approprié pour chaque patient en fonction de ses caractéristiques uniques.

2.7.1 Systèmes de transitions

Dans ce contexte, une image est généralement représentée par un espace composé de pixels et d'une relation d'adjacence entre pixels. Chaque pixel est identifié par sa position et un ensemble d'attributs (niveau de gris et luminosité). La grille 3x3 de pixels est un exemple de représentation d'image qui indique pour chaque pixel sa position, son niveau de gris et ses pixels voisins :

```
1 2 3
4 5 6
7 8 9
```

Il est possible représenter cette image par un système de transitions où l'état est un pixel défini par son niveau de gris et sa position dans la grille :

```
State 1: Pixel (1,1), Grayscale Value 1
State 2: Pixel (1,2), Grayscale Value 2
State 3: Pixel (1,3), Grayscale Value 3
State 4: Pixel (2,1), Grayscale Value 4
State 5: Pixel (2,2), Grayscale Value 5
State 6: Pixel (2,3), Grayscale Value 6
State 7: Pixel (3,1), Grayscale Value 7
State 8: Pixel (3,2), Grayscale Value 8
State 9: Pixel (3,3), Grayscale Value 9
```

La relation de transitions entre états est généralement basée sur la relation d'adjacence entre pixels. Partant d'un état de départ (un pixel de départ), il possible d'explorer cette grille en se déplaçant d'un état vers un état voisin. La relation de transitions entre états peut aussi comporter d'autres conditions comme exiger que les états source et destination aient des niveaux de gris différents. Par exemple, si l'état courant est State 1, une transition vers l'état State 4 est possible et fait basculer l'état courant vers l'état State 4 :

```
State 1 -> State 4
```

Les systèmes de transitions peuvent être aussi utilisés pour représenter les relations entre les différents segments d'une même image ou entre images d'une partie du corps produites, par exemple, à des dates différentes. Dans ce cas, un état est, selon le cas, un segment ou une image et

la relation de transitions définit les liens entre les segments ou les images. Cette relation de transitions peut être munie de conditions ou encore de probabilités de transitions entre états pour obtenir des systèmes de transitions probabilités comme le modèle de Markov.

2.7.2 Modèle de Markov

Le modèle de Markov, utilisé dans le cadre de cette thèse, est un système de transitions probabiliste où la relation de transitions est définie par une matrice de probabilités de transitions P. Cette matrice donne pour chaque couple d'états *(i, j)*, la probabilité d'atteindre l'état j à partir de l'état i en réalisant une seule transition[23, 24, 25, 26]. Le produit *PxP* donne pour chaque couple d'états (i, j), la probabilité d'atteindre l'état j à partir de l'état i en réalisant deux transitions [27, 28, 30, 31]. D'une manière générale, le produit P^n donne pour chaque couple d'états (i, j), la probabilité d'atteindre l'état j à partir de l'état i en réalisant n transitions.

Par exemple, supposons qu'un pixel est identifié par sa position, dans une grille représentant une image, et par l'un des 4 attributs suivants : sain, tumoral, œdème et nécrose. La matrice P peut être, d'ordre 4, calculée en considérant, par exemple, la règle suivante : La probabilité de transitions de l'attribut i à l'attribut j est égale au nombre de transitions de i vers j, dans la grille, divisé par le nombre total de transitions de i, dans la grille.

Nous avons montré, dans le chapitre 3, comment utiliser le modèle de Markov, en combinaison avec les algorithmes de classification d'images KNN, pour prédire l'évolution des tumeurs cérébrales.

2.7.3 Automates cellulaires

À partir du moment où une image est abstraite pour être représentée par une grille de pixels, il est naturellement envisageable d'utiliser les automates cellulaires pour représenter et analyser des images [32, 33, 34, 35, 36]. En effet, un automate cellulaire consiste en une grille de cellules définie chacune par sa position dans la grille et un ensemble d'attributs qui caractérisent son état. L'état d'une cellule peut évoluer au cours du temps. Cette évolution dépend de son état courant ainsi que ceux de cellules voisines. Le voisinage d'une cellule est défini comme l'ensemble des

cellules qui interagissent avec elle. Il peut être défini à l'aide de différentes configurations telles que le Von Neumann, où seuls les quatre voisins immédiats (haut, bas, gauche et droite) sont pris en compte, ou le quartier Moore, où les huit voisins environnants sont pris en compte.

La modélisation d'une image à l'aide d'un automate cellulaire consiste à représenter cette image sous la forme d'une grille de cellules, où chaque cellule représente un pixel avec comme attributs le niveau de gris et éventuellement tout autre qualifiant d'un pixel. Les règles de l'automate cellulaire dictent alors l'évolution de l'état de chaque cellule (pixel) dans le temps, en fonction de son état et ceux de ses voisines [37, 83, 39, 40, 41, 42, 43]. Ces règles peuvent tenir compte d'autres facteurs tels que le taux de croissance de la tumeur, la résistance des tissus environnants à l'invasion tumorale [44, 45, 46, 47, 48, 49].

La première étape consiste à définir la grille, qui représente l'image. La taille de la grille est déterminée par la résolution de l'image, et chaque cellule est représentée par un pixel. L'état de chaque cellule peut être représenté par une valeur en niveaux de gris, où 0 représente un tissu sain et des valeurs plus élevées représentent un tissu tumoral.

Par exemple, supposons qu'une image est représentée par une grille bidimensionnelle de cellules, où chaque cellule peut être dans l'un des états sémantiques suivants : SAIN, TUMEUR, ŒDÈME et NÉCROSE correspondant à des valeurs différentes de niveaux de gris. Nous pouvons définir des règles de transition qui précisent pour chaque cellule comment calculer son état sémantique à l'instant t+1 en fonction de son propre état et ceux de ses huit voisines à l'instant t. Un exemple de règle pourrait être : Si à un instant t, une cellule (i, j) est dans l'état Sain et exactement deux cellules voisines (sur huit) sont dans l'état TUMEUR alors l'état de la cellule (i, j) à l'instant t+1 est TUMEUR.

Ces règles visent à spécifier comment la tumeur pourrait se propager d'une cellule à une autre et, également, déterminer comment les tissus environnants pourraient devenir œdémateux ou nécrotiques.

Le chapitre 4 montre comment utiliser les automates cellulaires pour détecter les tumeurs cérébrales.

2.7.4 Logiques temporelles

Les logiques temporelles ont été introduites [50, 51, 52, 53, 54, 55, 56] dans le but de décrire comment les propriétés d'un système évoluent avec l'évolution de son état. Elles sont, notamment, utilisées dans les techniques de vérification, comme le *model checking*, pour spécifier les propriétés à vérifier. Elles étendent la logique propositionnelle avec des opérateurs temporels et éventuellement des quantificateurs de chemin.

Les **propositions** servent à qualifier les états par des conditions sur les attributs des états. Une proposition est soit vraie ou fausse dans un état. Pour la détection des tumeurs cérébrales, ***Tumeur_présente*,** et ***Taille_tumeur>seuil*** sont des exemples de propositions.

Les **opérateurs temporels** spécifient comment les propositions se succèdent le long d'une évolution de l'état (un chemin). Ils permettent de spécifier des propriétés de chemin. Les principaux opérateurs temporels sont :

a. **« X » (next)** qui fait référence à l'état suivant de l'état courant, et est utilisé pour spécifier la propriété qui doit être dans l'état qui suit l'état actuel. Par exemple, la formule *"**X Tumeur_présente**"* signifie que la tumeur est présente dans l'état suivant.

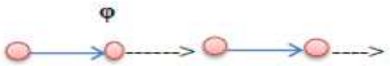
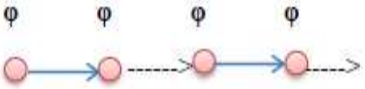
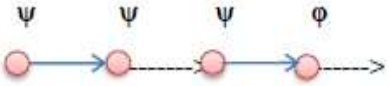
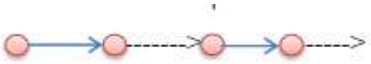
b. **« F » (Fatally)** qui fait référence à un certain état dans le futur et est utilisé pour spécifier qu'une propriété finira par être atteinte. Par exemple, la mention "***F Tumeur_présente**"* signifie que la tumeur est présente dans l'état courant ou dans un état futur.

c. **« G » (Globally)** qui permet de spécifier qu'une propriété est vraie dans l'état courant et tous les états futurs. Par exemple, la mention *" **G not tumeur_présente**"* signifie que la tumeur n'est présente ni dans l'état courant ni dans les états futurs.

d. **« U » (Until)** utilisé pour spécifier qu'une propriété est vraie tant qu'une autre ne l'est pas. Par exemple, la mention *" **not Tumeur_présente U Taille_tumeur>seuil**"* signifie que la tumeur n'est pas présente tant que sa taille n'a pas dépassée un certain seuil.

Le tableau 1 suivant résume la sémantique des opérateurs principaux temporels :

Tableau 1. Sémantique des opérateurs temporels.

Opérateur	**Explication**	**Diagramme**
X **ψ**	ψ doit être satisfaite dans l'état suivant.	
G **ψ**	**ψ** doit être satisfaite dans l'intégralité des états futurs.	
ψ U φ	**ψ** doit être satisfaite dans tous les états tant que **φ** n'est pas satisfaite.	
F ψ	**ψ** doit être satisfaite dans l'état courant ou dans au moins l'un des états futurs.	

Les **quantificateurs** de chemin A et E servent à spécifier qu'une propriété de chemin est vraie pour toutes les évolutions ou pour au moins une évolution de l'état courant.

Parmi les logiques temporelles, nous considérons les logiques temporelles linéaires LTL et à branchements CTL. La logique LTL interdit les quantificateurs de chemin alors que CTL impose que les opérateurs temporels soient utilisés en combinaison avec un quantificateur de chemin [57, 58, 59, 60, 61].

Tableau 2. Sémantique de certains opérateurs de base de CTL.

EX φ	-Vrai dans l'état actuel si la formule φ est vraie dans au moins l'un des états suivants.
EF φ	-Vrai dans l'état actuel s'il existe un chemin partant de l'état actuel qui satisfait la formule F φ.
EG φ	-Vrai dans l'état actuel s'il existe un chemin partant de l'état courant qui satisfait la formule G φ.
AX φ	-Vrai dans l'état actuel si la formule φ est vraie dans chacun des états suivants.
AF φ	-Vrai dans l'état actuel s'il existe un état dans chaque chemin partant de l'état courant, qui satisfait la formule φ.
AG φ	- Si tous les chemins partant de l'état courant satisfont la formule G φ.
ψ EU φ	-Vrai dans l'état actuel s'il existe un chemin partant de l'état actuel qui satisfait la formule **ψ U φ**.
ψ AU φ	-Vrai dans l'état actuel si tous les chemins partant de l'état courant satisfont la formule **ψ U φ**.

Certaines formules CTL sont illustrées par la figure 1.

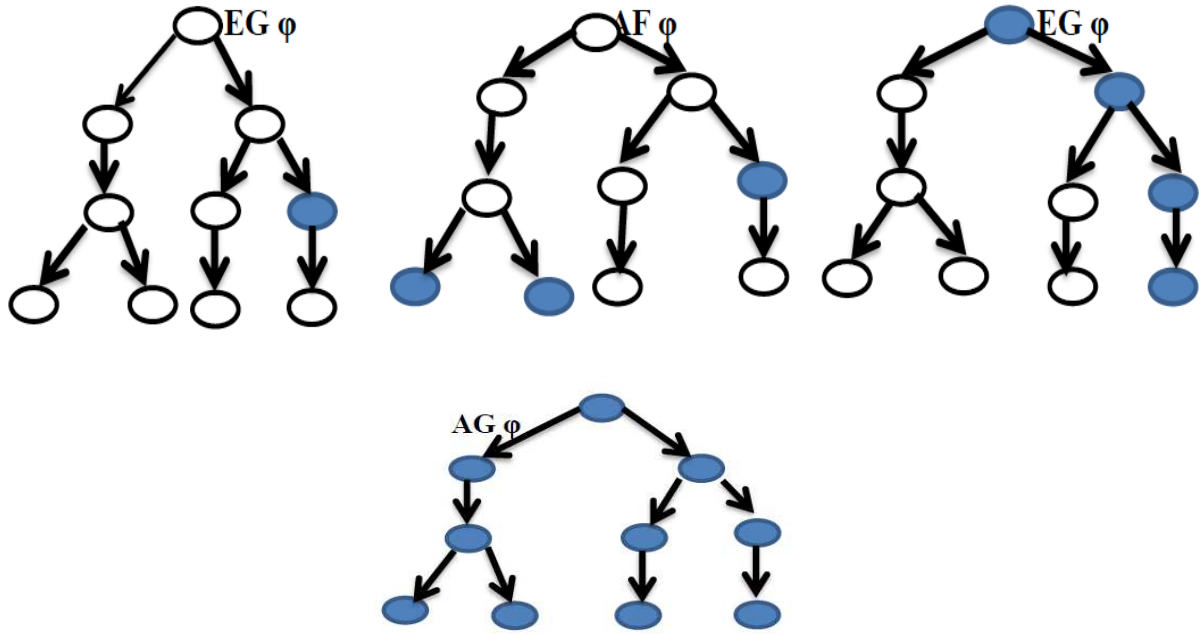


Figure 1 Illustration de certaines formules CTL

Les logiques LTL et CTL peuvent être utilisées pour décrire un large éventail de propriétés attendues d'un système de transitions. Leurs sémantiques permettent de calculer l'ensemble des chemins et d'états qui satisfont respectivement des propriétés LTL et CTL. Pour plus de détails concernant la logique temporelle CTL et LTL, se référer à [8].

Dans le cadre de la détection des tumeurs cérébrales, les logiques LTL et CTL peuvent être utilisées pour spécifier des propriétés des chemins ou des états des modèles précédents de représentation des images cérébrales. Par exemple, dans le contexte des automates cellulaires, la propriété CTL suivante :

- *"**not Tumeur_présente → EF Tumeur_présente**" est vraie pour toutes les cellules qui ne sont pas dans l'état **Tumeur_présente** mais qui peuvent atteindre dans le futur l'état **Tumeur_présente**. Dans le cas des systèmes de transitions,*

- *La propriété "* **EX-Tumeur_*présente*** *" est vraie pour tout pixel de la grille qui a au moins un voisin où la tumeur est présente.*

2.8 Prédiction, Détection et Classification de Tumeurs Cérébrales

La littérature propose diverses approches qui visent à détecter, prédire ou classifier automatiquement des tumeurs cérébrales. Ces approches se basent généralement sur l'analyse des images IRM et des techniques d'apprentissage automatique [62, 63, 64, 65, 66, 67, 68].

Détection de tumeurs cérébrales : L'une des méthodes les plus importantes pour la détection automatique des tumeurs est [69] qui repose sur des réseaux de neurones convolutifs (CNN), explorant de petits noyaux 3×3. L'utilisation de petits noyaux permet une conception d'architecture plus profonde, ainsi que l'effet positif contre le surajustement, compte tenu de la diminution du nombre de poids dans le réseau. Cet article a également étudié l'utilisation de la normalisation de la densité comme étape de prétraitement, qui, bien que peu courante dans les méthodes de segmentation basées sur CNN, ainsi que l'augmentation des données, s'est avérée très efficace pour segmenter les tumeurs cérébrales dans les images IRM.

D'autre part, l'article [70] présente une méthode de segmentation entièrement automatique des tumeurs cérébrales basée sur les réseaux de neurones profonds (DNN). Les grilles proposées sont adaptées aux glioblastomes (bas et haut grade) représentés sur les images IRM. Cet article explore diverses architectures basées sur des réseaux de neurones convolutifs (CNN), c'est-à-dire des réseaux de neurones convolutifs spécialement adaptés aux données d'image. Les résultats ont révélé l'efficacité de la méthode proposée et son application sur l'ensemble de données de test BRATS 2013.

Dans l'article [71], le cadre proposé comporte cinq phases qui sont le prétraitement, le décapage du crâne, la segmentation tumorale basée sur CNN, le post-traitement et la classification binaire des tumeurs cérébrales basée sur l'apprentissage. Le modèle GoogleNet est utilisé dans trois

ensembles de données accessibles au public. Les résultats expérimentaux ont montré que la méthode proposée atteignait une précision moyenne de 96,50 %, 97,50 % et 98 % pour la segmentation et de 96,49 %, 97,31 % et 98,79 % pour la classification des tumeurs cérébrales dans les ensembles de données BRATS2018, BRATS2019 et BRATS2020, respectivement.

Prédiction de la progression des tumeurs cérébrales: Parmi les travaux les plus importants qui prédisent la croissance tumorale, nous en trouvons [72]. Ce travail se concentre sur le modèle d'interaction-diffusion, qui suggère que le coefficient de diffusion et le taux de diffusion peuvent être liés à des informations cliniquement pertinentes. Cette approche d'allocation a été comparée à deux méthodes couramment utilisées basées sur l'analyse asymptotique sphérique du modèle d'interaction-diffusion et sur un algorithme d'optimisation. La performance de la méthode a été démontrée sur des données ultra structurales, et sur sept patients atteints de glioblastome, la tumeur cérébrale primitive la plus agressive. Cette affectation bayésienne donne des résultats plus informatifs. En particulier, il fournit des échantillons de régions d'intérêt et met en évidence la présence de plusieurs positions pour certains patients.

L'article [73] vise à introduire de nouvelles fonctionnalités d'imagerie qui peuvent être automatiquement calculées à partir d'images RM et introduites dans des modèles d'apprentissage automatique pour prédire la survie des patients. Les caractéristiques proposées par cet article ont une explication fonctionnelle-anatomique directe : elles mesurent la déformation induite par la tumeur des structures cérébrales environnantes et comparent la forme de différentes structures dans le cerveau d'un patient à celle attendue chez les individus en bonne santé. À l'aide d'expériences incorporant des données pré- et postopératoires, les caractéristiques proposées dans cet article ont une valeur prédictive en termes de survie globale et sans progression, en plus des caractéristiques d'imagerie non traditionnelles.

Classification des tumeurs cérébrales : La classification des tumeurs cérébrales est un problème important dans le diagnostic assisté par ordinateur pour des applications médicales. L'article [74] se concentre sur un problème de classification en trois catégories pour différencier les gliomes, les méningiomes et les adénomes hypophysaires, qui constituent trois types distincts de tumeurs

cérébrales. Le système de classification proposé adopte le concept d'apprentissage profond par transfert et utilise Google Net pré-entrainé pour extraire les caractéristiques des images IRM du cerveau. Le système proposé obtient une précision de classification moyenne de 98 %, surpassant toutes les méthodes récentes. Les autres mesures de performance utilisées dans l'étude sont l'aire sous la courbe (AUC), la précision, le rappel et un score F.

La recherche [75] fournit un modèle hybride d'apprentissage en profondeur (DeepTumorNetwork) pour la classification binaire des BT et surmonte les problèmes ci-dessus. L'approche hybride proposée pour l'architecture GoogLeNet avec le modèle CNN en éliminant les 5 couches de GoogLeNet et en ajoutant 14 couches de modèle CNN qui extrait automatiquement les fonctionnalités. Dans le même jeu de données Kaggle (Br35H), le KPI du modèle proposé a été comparé avec le modèle d'apprentissage (TL) (ResNet, VGG-16, SqeezNet, AlexNet, MobileNet V2) et divers ML/DL. Les méthodes proposées ont montré des mesures de performance de classification élevées, l'exactitude (99,51%), l'exactitude (99%), le retrait (98,90%) et le score F1 (98,50%).

Dans l'article [76], un modèle de classification de réseau neuronal profond avec prétraitement de la technique de suréchantillonnage synthétique a été utilisé dans l'ensemble de données Rembrandt Images accessible visuellement. Le modèle proposé de classification des tumeurs cérébrales se composait de 1319 paramètres entraînables et la méthode proposée a atteint un taux de précision de 95,0 %. Les valeurs de précision, de rappel et de F1 mesurées sont respectivement de 95,4 %, 95,0 % et 94,9 %.

Dans ce qui suit, nous discuterons en détail des méthodes d'apprentissage en profondeur et d'apprentissage automatique dans la classification, la détection et la prédiction des tumeurs cérébrales.

2.8.1 Approches d'apprentissage automatique

Les algorithmes d'apprentissage automatique sont des algorithmes d’analyse de données qui ont la capacité d’apprendre de leurs expériences pour améliorer continuellement leurs résultats [77]. Ils sont, de plus en plus, utilisés pour identifier une tumeur cérébrales à partir d’une image IRM [78, 79, 80, 81]. Ils sont avérés plus pratiques et fournissent des prédictions avec un haut degré de

précision, par rapport aux méthodes conventionnelles. De plus, ils sont capables d'analyser un grand ensemble de données [82] et d'améliorer continuellement la précision de leurs prédictions au fur et à mesure qu'ils reçoivent de nouvelles données, sans que l'utilisateur n'ait besoin de les ajuster. La figure 2 montre le schéma fonctionnel typique des modèles d'apprentissage automatique utilisés dans l'identification des tumeurs cérébrales.

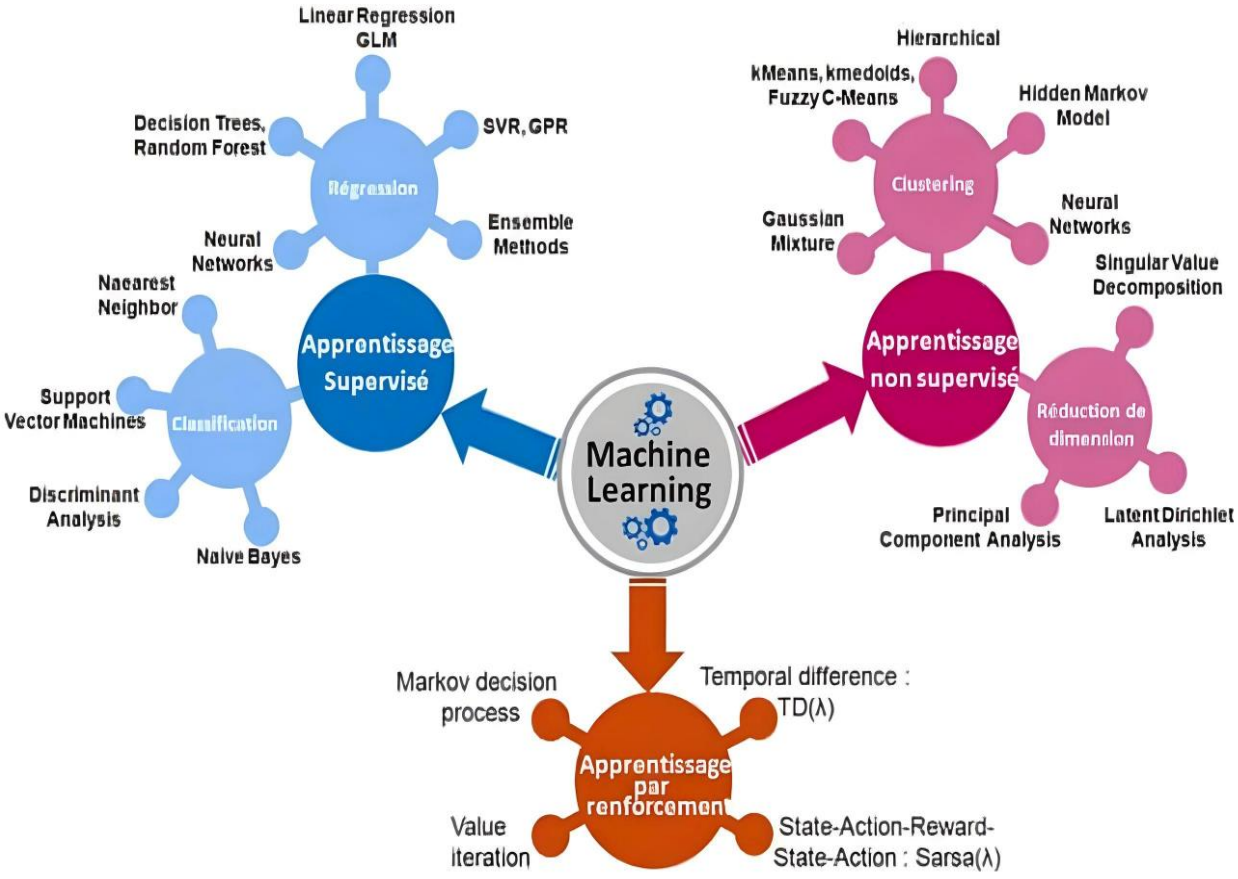


Figure. 2 Apprentissage automatique pour la détection de tumeurs cérébrales [83].

En général, les processus, de détection de tumeurs cérébrales, basés sur les algorithmes d'apprentissage automatique comportent les étapes suivantes :

1. Collection d'un grand ensemble de données d'images IRM concernant les tumeurs cérébrales. L'ensemble de données doit être diversifié et inclure différents types et tailles de tumeurs.
2. Prétraitement des scans IRM pour s'assurer qu'ils sont de haute qualité et standardisés. Cela peut inclure la suppression de bruit, la correction des artefacts et la normalisation des niveaux d'intensité.
3. Extraction des caractéristiques pertinentes des scans IRM, telles que la texture, la forme ou l'intensité. Cela peut être réalisé manuellement par un expert du domaine ou automatiquement à l'aide d'algorithmes d'extraction de caractéristiques.
4. Répartition des données en ensembles d'entraînement, de validation et de test. L'ensemble d'entraînement est utilisé pour former l'algorithme ML, l'ensemble de validation est utilisé pour surveiller ses performances et ajuster les hyperparamètres, et l'ensemble de test est utilisé pour évaluer les performances finales.
5. Sélection d'un algorithme d'apprentissage automatique, tel que les arbres de décision, les forêts aléatoires ou les machines à vecteurs de support, et entraînement de cet algorithme sur l'ensemble des données d'entraînement.
6. Ajustement des hyperparamètres de l'algorithme d'apprentissage sélectionné si nécessaire pour améliorer ses performances sur l'ensemble de validation. Les hyperparamètres courants à ajuster incluent le taux d'apprentissage, le nombre d'arbres ou la fonction noyau.

2.8.2 Approaches d'apprentissage en profondeur

L'apprentissage en profondeur est un sous-ensemble des techniques d'apprentissage automatique qui combinent l'apprentissage par représentation avec les réseaux de neurones artificiels [84, 85]. L'apprentissage en profondeur peut être supervisé, semi-supervisé ou non supervisé. L'apprentissage supervisé utilise des données annotées (une base de connaissance) ce qui n'est pas le cas de l'apprentissage non supervisé.

Les algorithmes d'apprentissage en profondeur sont organisés en couches. Chaque couche reçoit des données en entrée, leur applique des fonctions mathématiques et produit des données qui sont ensuite transmises à la couche suivante et ainsi de suite jusqu'à atteindre la sortie.

Les algorithmes d'apprentissage en profondeur sont avérés nettement meilleurs pour établir des diagnostics que les techniques d'apprentissage automatique traditionnelles [86]. Avec le développement d'algorithmes d'apprentissage en profondeur, les professionnels de la santé sont en mesure de diagnostiquer plus rapidement et plus précisément que jamais et de prendre des décisions plus éclairées concernant les traitements et les interventions médicales pour de nombreuses maladies, telles que le cancer, tout en réduisant le temps nécessaire pour diagnostiquer les patients, et améliorer les résultats pour les patients Pour cette raison, les algorithmes d'apprentissage en profondeur deviennent de plus en plus importants pour l'industrie médicale et ont apporté des avantages sans précédent aux médecins et aux patients.

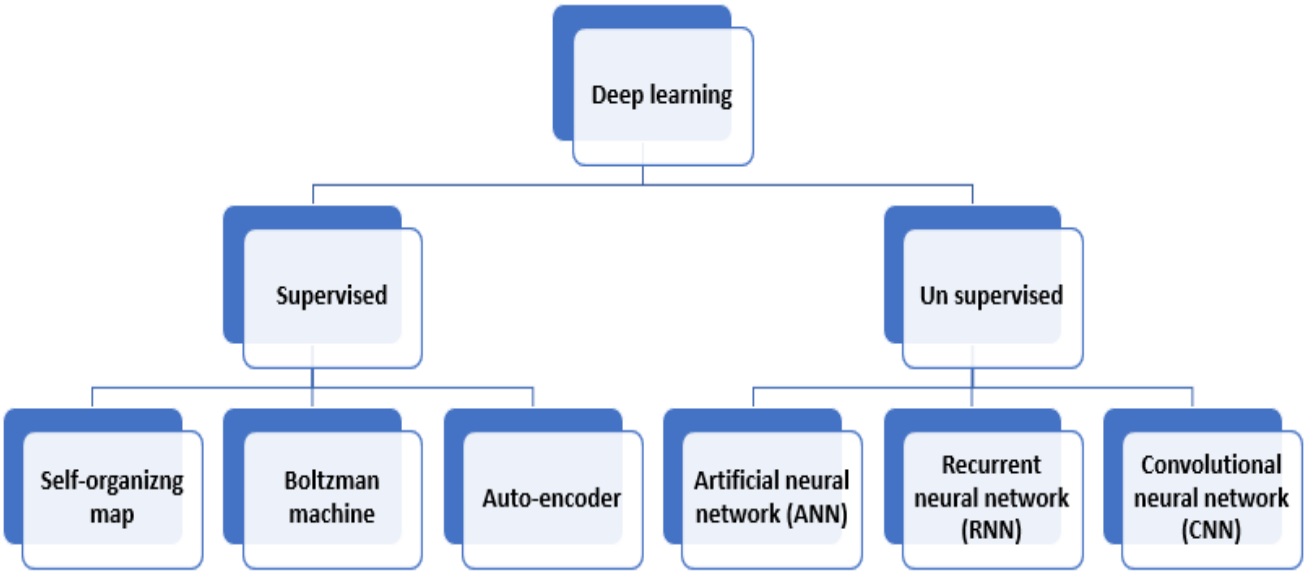


Figure 3 Apprentissage en profondeur pour la détection des tumeurs cérébrales.

Les processus, de détection de tumeurs cérébrales, basés sur les algorithmes d'apprentissage en profondeur diffèrent de ceux basés sur l'apprentissage automatique, par les algorithmes et les

librairies d'apprentissage utilisés. En effet, comme TensorFlow et PyTorch sont utilisés pour créer un réseau de neurones convolutifs (CNN) qui peut apprendre à détecter les tumeurs cérébrales à partir d'images IRM.

L'apprentissage automatique et l'apprentissage en profondeur sont tous deux des sous-ensembles de l'intelligence artificielle (IA) qui impliquent des algorithmes de formation pour construire des modèles à partir de données. Bien qu'ils partagent certaines similitudes, il existe plusieurs différences entre les deux approches de détection des tumeurs cérébrales comme illustré à la figure 4.

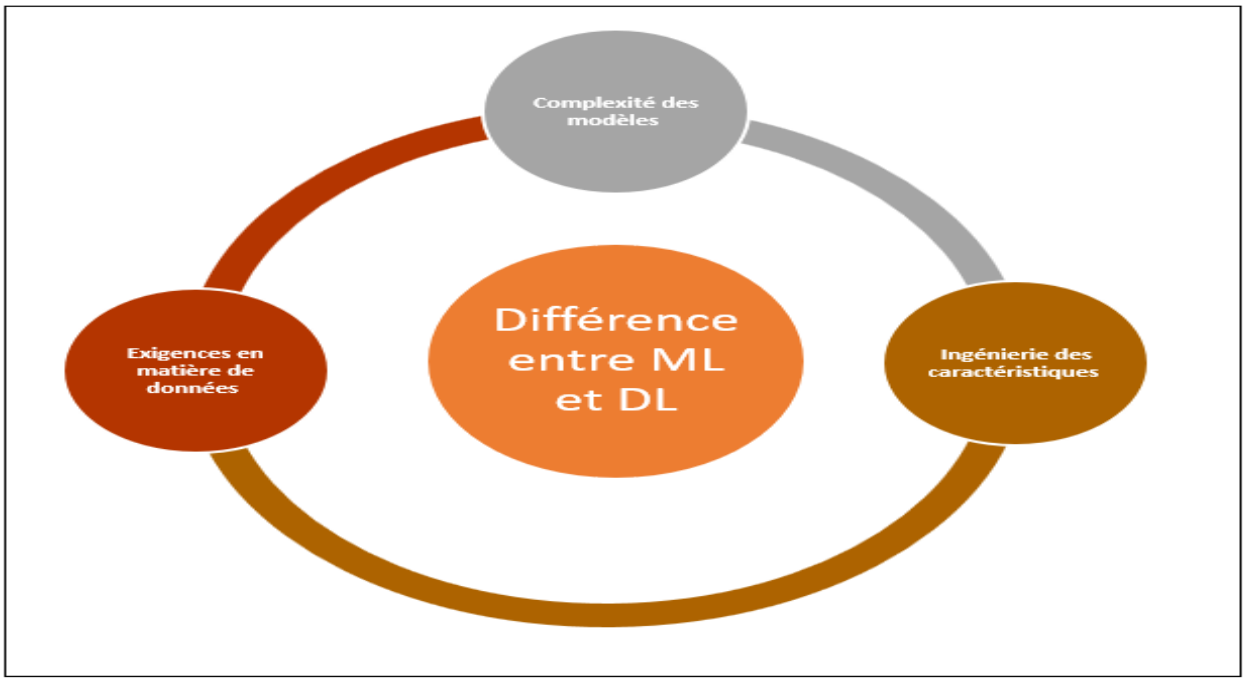


Figure 4 Différence entre l'apprentissage en profondeur et l'apprentissage automatique pour la détection des tumeurs cérébrale.

1. **Complexité des modèles :** les algorithmes d'apprentissage automatique utilisent généralement des modèles plus simples tels que des arbres de décision, des forêts aléatoires ou des machines à vecteurs de support, tandis que les algorithmes d'apprentissage en profondeur utilisent des réseaux de neurones complexes, tels que des réseaux de neurones convolutifs (CNN) ou des réseaux de neurones récurrents (RNN).

2. **Extraction des caractéristiques :** les algorithmes d'apprentissage automatique nécessitent souvent une extraction manuelle des caractéristiques, ce qui implique de sélectionner et d'extraire les caractéristiques pertinentes des données que l'algorithme va utiliser pour entraîner des modèles. En revanche, les algorithmes d'apprentissage en profondeur peuvent automatiquement apprendre les fonctionnalités à partir des données brutes, ce qui élimine le besoin d'une ingénierie manuelle des caractéristiques.
3. **Exigences en matière de données** : les algorithmes d'apprentissage automatique peuvent fonctionner avec des ensembles de données plus petits et peuvent souvent bien se généraliser à de nouvelles données. En revanche, les algorithmes d'apprentissage en profondeur nécessitent généralement de grandes quantités de données pour obtenir de bonnes performances et peuvent ne pas bien se généraliser aux nouvelles données sans ajustement supplémentaire.
4. **Configuration matérielle requise** : les algorithmes d'apprentissage en profondeur nécessitent un matériel plus puissant, tel que des GPU, pour entraîner et exécuter les modèles. En revanche, les algorithmes d'apprentissage automatique peuvent souvent être entrainés et exécutés sur du matériel moins puissant.

En résumé, les algorithmes d'apprentissage en profondeur peuvent offrir de meilleures performances mais nécessitent de plus grandes quantités de données et un matériel plus puissant. De plus, ils nécessitent moins d'ingénierie manuelle des caractéristiques, ce qui peut économiser du temps et des efforts. Cependant, le choix entre les deux types d'apprentissage dépendra de l'application et des ressources disponibles.

Parmi les architectures de réseaux de neurones profonds pour le traitement des images, cette thèse s'est aussi intéressée à MobileNet.

2.8.3 MobileNet

MobileNet a été proposé pour la première fois par les chercheurs de Google en 2017 [87], et il est rapidement devenu un choix populaire pour les applications mobiles de vision par ordinateur, telles que la classification d'images, la détection d'objets et la segmentation sémantique. L'objectif

principal de MobileNet est d'atteindre une grande précision tout en minimisant le nombre de paramètres et le coût de calcul du modèle.

L'architecture de MobileNet est basée sur des convolutions séparables en profondeur, qui décomposent l'opération de convolution standard en deux couches distinctes : une convolution en profondeur et une convolution ponctuelle. Cette approche réduit le nombre de calculs requis par le modèle et lui permet d'être plus léger et efficace que les réseaux de neurones convolutifs traditionnels.

La classification des tumeurs cérébrales à l'aide de MobileNet est une tâche d'apprentissage automatique qui implique l'entrainement d'un modèle d'apprentissage en profondeur pour classer les images de tumeurs cérébrales en différentes catégories telles que bénignes ou malignes.

Pour entraîner un modèle de classification des tumeurs cérébrales à l'aide de MobileNet, nous avons besoin d'un ensemble de données d'images de tumeurs cérébrales avec leurs étiquettes correspondantes. L'ensemble de données doit être divisé en ensembles d'entraînement, de validation et de test utilisés pour respectivement entraîner, ajuster les hyperparamètres, et évaluer les performances finales du modèle. L'image ci-dessous montre la méthodologie de classification des tumeurs cérébrales basée sur MobileNet.

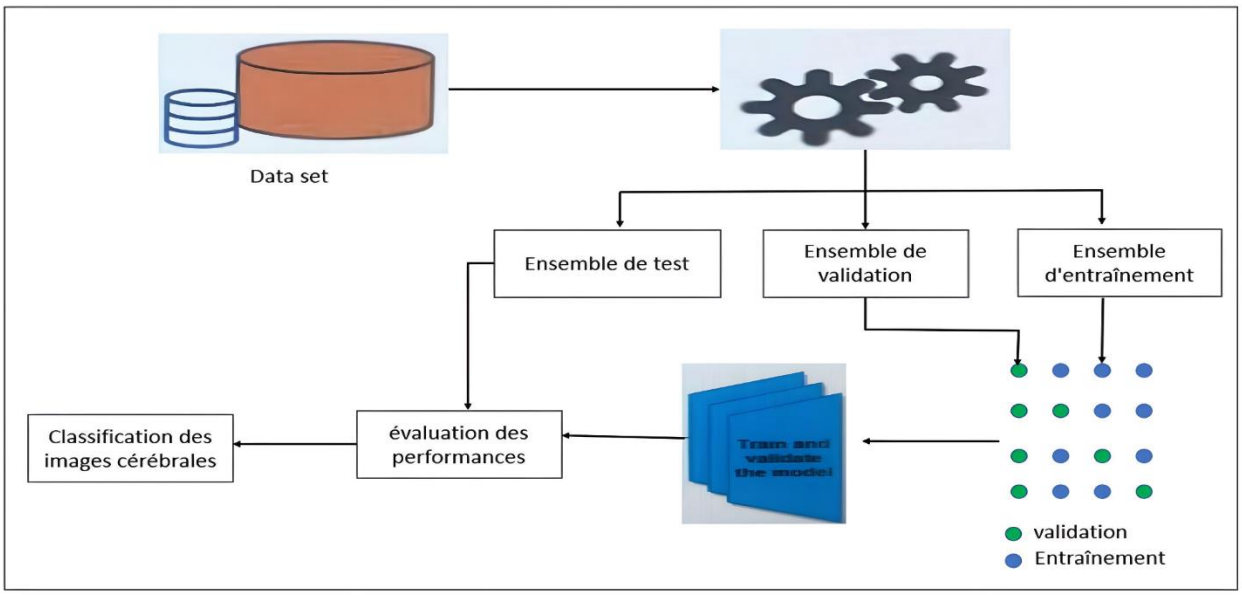


Figure 5 Classification des tumeurs cérébrales en utilisant MobileNet

Les étapes de classification des tumeurs cérébrales à l'aide de MobileNet :

1. Collection des images cérébrales IRM de patients avec et sans tumeurs cérébrales : Ces données peuvent être obtenues à partir, par exemple, d'ensembles de données accessibles au public.
2. Prétraitement des données afin de pouvoir les utiliser pour entrainer le modèle : Cela implique de redimensionner les images à une taille fixe, de les convertir au format niveaux de gris et de normaliser les valeurs de pixel.
2. Création de modèles : MobileNet peut être facilement importée depuis TensorFlow ou Keras. La dernière couche du modèle MobileNet, qui est une couche entièrement connectée, doit être remplacée par une nouvelle couche capable de générer le nombre de classes souhaité.
3. Entraînement du modèle en utilisant l'ensemble de données d'entraînement et des techniques telles que l'augmentation des données, la régularisation et l'arrêt précoce pour éviter le sur-ajustement.
4. Validation : Pendant l'entraînement, le modèle est évalué sur l'ensemble de données de validation distinct pour s'assurer qu'il ne sur-adapte pas les données d'entrainement. Si le modèle est sur-ajusté, des ajustements peuvent être apportés à l'architecture du modèle ou aux hyperparamètres pour améliorer les performances.
5. Évaluation du modèle entraîné à l'aide de l'ensemble de données de test : Cela consiste à calculer des mesures telles que l'exactitude et la précision.
6. Déploiement du modèle formé : Le modèle de classification des tumeurs cérébrales formé peut être déployé sur un appareil mobile ou intégré pour la classification en temps réel des images de tumeurs cérébrales.

Nous montrons dans cette thèse qu'avec une sélection rigoureuse des hyperparamètres et un ensemble de données suffisamment volumineux, un modèle de classification des tumeurs cérébrales basé sur MobileNet peut atteindre une grande précision.

2.9 Positionnement des travaux

Dans le cadre de cette thèse, nous proposons de combiner des techniques d'apprentissage automatique avec des formalismes tels que le modèle de Markov, les automates cellulaires et les systèmes de transitions pour effectuer la prédiction, la détection, la classification et la validation de tumeurs cérébrales.

Pour la prédiction de la croissance des tumeurs cérébrales, le chapitre 3 propose une technique basée sur l'algorithme d'apprentissage supervisé non paramétrique KNN et le modèle de Markov.

Pour la détection de tumeurs cérébrales, le chapitre 4 montre comment employer les techniques de segmentation d'images basée sur les automates cellulaires pour améliorer la précision de la détection.

Pour la classification des tumeurs cérébrales, le chapitre 5 propose d'utiliser l'architecture MobileNet pour améliorer la précision de la classification.

Enfin, pour valider un processus de détection des tumeurs cérébrales, le chapitre 7 propose de combiner l'algorithme d'apprentissage supervisé non paramétrique KNN avec des techniques formelles de model-checking.

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CHAPITRE 3 ARTICLE 1: TUMOR GROWTH PREDICTION AND CLASSIFICATION BASED ON THE KNN ALGORITHM AND DISCRETE-TIME MARKOV CHAINS (DTMC)

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Abstract: In recent years, brain tumors have become one of the most common fatal diseases. Despite the existence of an important number of research studies on tumors, the proportion of research on predicting the growth of tumors remains insufficient due to the intricate nature of this research domain. Therefore, the presence of any application able to predict the growth of the tumor may have a role in eliminating the tumor by finding the appropriate treatment for it before it grows. This paper investigates tumor growth and presents a technique for tumor growth prediction based on the Discrete Time Markov Chain (DTMC) and K-Nearest Neighbor (KNN) algorithms. The design and development of this technique consists of a proposition of a stochastic model of tumor progression. This is followed by an extension of the mode to several cases that allow the derivation of new cases based on the study of predictive probabilities. The aim of this paper is to develop a model based on the KNN and DTMC algorithms that can classify tumors and predict the future state based on the current state of the tumor without the knowledge of the past state. In other words, all relevant information about the past and the present that would be useful in making predictions is available in the current state. In terms of performance evaluation metrics, the results show that the proposed method exceeds the existing methods with 97.65% accuracy, 71.65% specificity and 99.087% sensitivity.

Keywords: Tumor growth prediction, Probabilities, DTMC, KNN algorithm

3.1 Introduction

A tumor is a mass of tissues that results from the accumulation of abnormal cells due to abnormal tissue growth [88]. Tumors grow and act unexpectedly, depending on whether they are cancerous. Each type of tumor looks more like a particular case, and as a tumor grows new changes

occur that differ from case to case; for this reason, treatment for a particular tumor may not cure all tumors. The constantly changing tumor is one of the biggest challenges in treatment, especially since the tumor often grows into more drug-resistant forms [89]. However, if specialists can predict how the tumor will grow, they could intervene early to stop the tumor from growing before it has a chance to develop resistance, thus, increasing the patient's chances of survival. More importantly, a link could also be found between specific sequences of repeated tumor mutations and survival outcomes, indicating that well-developed methods could be used as a predictor, helping to shape future treatment. Professor Paul Workman, executive director of ICR, said: "Tumor growth is the biggest challenge physicians face in creating treatments that will work successfully for patients. If the doctor can predict the progression of the tumor, treatment can be changed before adaptation and drug resistance, which allows us to quickly bring the tumor under control" [90]. Generally, there are two types of tumors: benign and malignant. These will be discussed in subsequent sections before design and development of prediction of tumor growth is investigated. A malignant tumor is a cancerous growth that has the ability to metastasize and spread from the effected organ to any other organ in the body. Unlike benign tumors, whose cells are non-cancerous and do not spread to surrounding cells; benign tumors grow slowly and do not return to the body again after removal. Table 1 shows some differences between benign and malignant tumors [91].

Table 1 Difference between benign and malignant tumors

Parameter	**Malignant**	**Benign**
Rate of growth	Malignant tumors usually have a relatively rapid growth rate.	Most benign tumors have a slow growth rate.
Boundaries	These tumors may recur after their removal. Furthermore, they may also recur in regions other than the original site.	Benign tumors tend to have clear boundaries.
Secretion of substances	Malignant tumors can secrete certain substances that result in weight loss and fatigue	These tumors do not secrete hormones and other substances. Furthermore, anotable exception, is pheochromocytomas

It is critical to understand the stages of tumor growth sequence where tumorous cells initially show a dependence on available nutrients for their growth. However, once these nutrients are depleted, these cells must find a way for their growth, redirecting their focus toward the normal body cells [92].

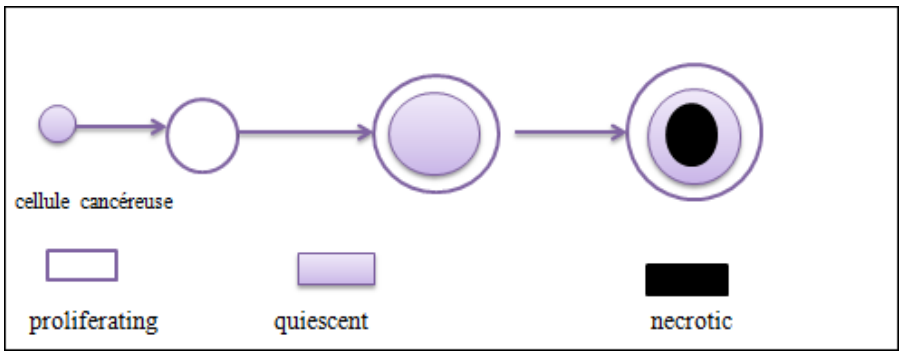


Fig.1 Cancer cell growth.

In the same context, the objective of the tumor growth prediction in [93] is to model the tumor growth process, which could be accomplished through collaboration in theoretical mathematical modeling with the customization of the model from the clinical evaluation, through the participation to conclude the final relationship between the experimental and theoretical approaches. These lead to a modeling of the pathway to predict tumor growth. The basic model of tumor growth associated with normal differential equations should be investigated at the outset to extend the problem to models of interaction propagation [94]. With the recent advances in scientific development, there is a need for a more robust and efficient approach to developing and validating these models. Tumor prediction, however, remains a challenge that has not yet been fully realized, owing to the complexity of the tumor structure and drug response prediction in tumors. Mostly, the research in these intricate domains is theoretical in nature [95], resulting in rare applications of predicting tumor progression.

This work aims to develop a method for predicting tumor progression using DTMC and KNN algorithms to predict the future state of a brain tumor. It also aims to provide a comprehensive methodology that combines all that is theoretical and practical. This paper relies on studying the

probabilities of moving from one state to another in the growth of the tumor. Therefore, tumor's behavior is already known before its impact.

This work aims to develop a method for predicting tumor progression using DTMC and KNN algorithms to predict the future state of a brain tumor. It also aims to provide a comprehensive methodology that combines all that is theoretical and practical. This paper relies on studying the probabilities of moving from one state to another in the growth of the tumor. Therefore, tumor's behavior is already known before its impact.

The rest of this paper is coordinated as follows. Section 5.2 provides some related works. The application of the Markov model to predict tumor growth is given in section 5.3. Section 5.4 shows the proposed methodology. The results and discussion are introduced in section 5.5 Finally, a conclusion and future works are given in section 5.6.

3.2 Related Works

Regarding tumor growth prediction, a rich and diverse body of excellent theoretical works has been proposed in this discipline. One of the most influential works on tumor prediction has been recently published [96] by a research team from the Department of Medicine at the University of Waterloo in Canada, suggesting that a form of mathematical analysis called "evolutionary dynamics" can be used with the goal to examine how cancer mutations develop in colorectal and bowel cancers. The study found that by utilizing mathematics, prediction of cell behavior can be improved as it helps to understand the process of cancer growth movement from one organ to another. The experiments confirmed that the new cells created could differ fundamentally from the original cell when the cancer stem cells divide and multiply. On the other hand, in terms of deep learning, according to another study in the journal [105], Byun et al. compared DeepSurv models with the CPH model to predict recurrence free survival (RFS) by performing survival analyzes of malignancies, including Renal cell carcinoma (RCC), the result is DeepSurv performance for RFS and CSS (C-index = 0.802 and 0.834, respectively) and performance of the CPH model (C-index = 0.794 and 0.831, respectively). Thus, the DeepSurv model was superior to the CPH model.

Regarding the improvement of the prediction of tumor progression, in the article [98], Yifeng et al. have worked to improve the diagnostic prognosis of cancer using clonal evolution models to

determine and predict how well the phenotypes of different cancer mutations are successful, however, the reported results were inaccurate. Concerning the 3-D tumor growth prediction, Pinjian et al. worked on the Finite-element method (FEM)-based 3-D tumor growth prediction [102]. The preliminary results demonstrated the limitations of the proposed method, where the effect of mass was not taken into account and did not include the surrounding tissues. From another perspective, Hope et al. have worked on the study of COPD prediction through the context of a COPD domain-related prediction model using a Bayesian belief network and the performance rate for COPD prediction with an accuracy of 81.5%. It is an acceptable ratio, even if the general validation method used for the proposed model is not convincing because of its poor effectiveness with other models [103].

Machine learning and deep learning approaches have also shown promising results in the areas of tumor detection, and analysis [99–101], especially in areas where large and reliable data sets are available. Among these works, there are applications of machine learning in cancer diagnosis and prediction. To that end, Ourou et al used artificial neural networks (ANNs) and Bayesian networks (BNs) to identify potential flaws in using experimental design to extract clinical decisions. The best performance was with an accuracy of 69% [104]. Using machine learning, Pragya et al. worked on lung cancer prediction and classification, and it lists all major research that has been done over the past years. Artificial neural network (ANN) predicted the presence of lung cancer with 96.67% [105].

One of the most important works on the prediction and detection of tumors is [106] where Mobarakol et al. used the (CNN) algorithm and the artificial neural network (ANN), where Hypercolumn Convolutional Neural Network (CNN) was used for tumor segmentation, while an artificial neural network (ANN) was used to predict the number of days of survival by performing regression on the extracted features, the result was a mean accuracy of 87.31% and 70.22% for the whole tumor. As for predicting other types of cancer, the authors worked on diagnosing and predicting bladder cancer in [109] using the Intelligent Firefly and helped to discover the genes causing cancer. This work uses the tested artificial neural network technique to collect experimental data, the accuracy of the results was not enough to highlight this technique, but it is the beginning of the way to go deeper into such research. As for the prediction of other diseases, for example, heart disease prediction, the authors in [110] proposed a method called Cardio Help that predicts

the probability of developing cardiovascular disease using CNN, and the experimental results showed that the accuracy achieved is 97%.

Although most of these articles have had limited results, they contribute to scientific research related to the study of tumors. By explaining several methods of studying tumors, any work in the study of tumor prediction would be a great addition to this field. Table 2 summarizes the examples explained above along with a comparison of additional literature in terms of their reported results, limitations, and techniques.

Table 2 Comparison of existing techniques.

Ref	Year	Author	Technique	Result	Performance
[10]	2021	Byun et al.	-DL prediction algorithm.	-Compared DeepSurv models with the CPH model, the DeepSurv model was better than the CPH model.	Accuracy=79.4% -80.2 %
[11]	2019	Yifeng et al.	Phylogenetic tree inference algorithms	-Suggest a strategy for enhancing the predictive power of conventional clinical.	Accuracy=60%
[12]	2019	Arvid et al.	-ANNs -CNN	Explain how we can apply deep learning to the entire MRI processing chain.	Accuracy= 70%
[13]	2021	Maria et al	-Transfer learning	Provide a thorough critique of the studies done to detect and classify brain tumors.	Accuracy=70%-87%
[14]	2018	Sohail et al.	-ANNs -SVM	Predicting cancer and comparing cancer survival rates.	Accuracy= 71%
[15]	2012	Xinjian et al.	-Finite-element method (FEM).	-The preliminary experimental results proved the efficacy of the proposed system. However, the mass effect was not taken into consideration and did not include the surrounding tissues.	Accuracy=91.4%

[103]	2017	Mcheick et al.	Bayesian network algorithm	-The general validation method for the proposed model is not effective.	Accuracy=81.5%
[104]	2014	Kourou et al.	-ANNs. -Bayesian Networks (BNs). -SVM.	-The identification of potential drawbacks including the experimental design, and the validation of the classified results,	Accuracy=96%
[105]	2021	Pragya et al.	-KNN,-MLP, SVM	-Comparing most major research that has been done over the past years.	Accuracy =96,67%
[106]	2019	Mobarakol et al.	-Neural network (CNN) with hypercolumn technique. -ANN	-Prediction is done by extracting features (Geometric, Fractal, and Histogram) from the segmented brain tumor data	Accuracy =70.22%-87.31%
[107]	2019	Rupal et al	Convolutional neural network(CNN).	-Testing local structure prediction approach for 3D segmentation tasks	Accuracy=80%
[108]	2016	Tawfeeq et al	-Intelligent Firefy. -Artificial neural network	-predicting bladder cancer using the Intelligent Firefly, and helping to discover the genes causing cancer	Accuracy=97%
[109]	2021	Awais et al	-CNN	-Predicting the likelihood of developing cardiovascular disease	Accuracy=97%
		Our work	-DTMC, -KNN, -Patterns, -FCM.	-Predicting tumor growth. -Studying the possibility of moving from one state to another	Accuracy=97.65%

However, predicting tumor growth remains a major challenge that requires further work. In this context, methodologies based on the Markov models can also be helpful to improve tumor prediction for several reasons:

Adoption of the discrete-time Markov chain (DTMC) in the current situation without the need to study the history of the tumor;

1. Tumor growth prediction with high accuracy;
2. Calculate the probability of transition from one state to another;

3. Verify that the probabilities are correct;
4. To facilitate the work of researchers in this field through the abundance of information, and thus the development of techniques that are more accurate in predicting tumors.

From the human perspective where we see daily dozens or even hundreds of people dying in different parts of the world because of malignant tumors, any scientific work in this specialty, will be a strong addition to researchers and doctors so that they can make the scientific applications that help eliminate malignant tumors.

In this study, the authors rely on a new methodology that depends mainly on accuracy and ease of understanding. This methodology depends, in particular, on studying the expected possibilities to predict tumor growth and applying them in practice so that a linkage between theoretical and practical aspects can be established, thus, highlighting the role of the Markov model, especially DTMC, in the prediction process.

3.3 Application of the Markov model to predict tumor growth.

In this section, the focus is on the explanation of the Markov model application in order to predict tumor growth. Since Markov modeling is a stochastic model in nature [111–113], it allows for tumor growth predictions to be made based solely on the current state rather than the prior events. This is made possible by the computation of state transition probabilities. This technique is contrary to contemporary techniques that require a history of the tumor before predicting its growth. Therefore, as a first step, the proposed logic is defined for studying the predictability of states. This is followed by the definition of the state classification method that is adopted in this work.

Definition 1 Let $\{x_n, n = 0, 1, 2, ...\}$ be a sequence of a random process used to store the state evolution at discrete time-steps of a system, i.e., X_k gives the system state observed at the time-step k.

Let S be the set of states of the system, and i and j are two states of S. The probability of the system reaching in one time-step the state j from the state i is denoted by P_{ij},

$$P_{ij} = P(xn + 1 = j/xn = i) \quad (1)$$

In particular:

$$P_{ij} = P(x1 = j/x0 = i) \quad (2)$$
$$= P(x2 = j/x1 = i)\ldots..$$

Where P is called the state transition probability matrix that gives the probabilities of transitioning from one state to another.

Definition 2 The state j is accessible from the state i, denoted by $i \rightarrow j$, if $P^n > 0$ for some $n \in N$, every state is accessible from itself since $P^n > 0$, P^n is the n^{th}power

of the state transition probability matrix P.

Definition 3 States i and j are communicated if they are accessible from each other, which means $i \rightarrow j$ and $j \rightarrow i$.

After formally defining 1, 2, and 3, state determination is explained using them in the next section.

3.3.1 Classification of states

This section uses the definitions 1, 2 and 3 to build on the classification of states. In addition to that, the understanding of transitions from states i to state j is also developed. In Fig. 2, the extracted states from the data set can be seen, as described in 4.1.1. These are the common states for all patients i.e., a patient will always be in one of these stat.

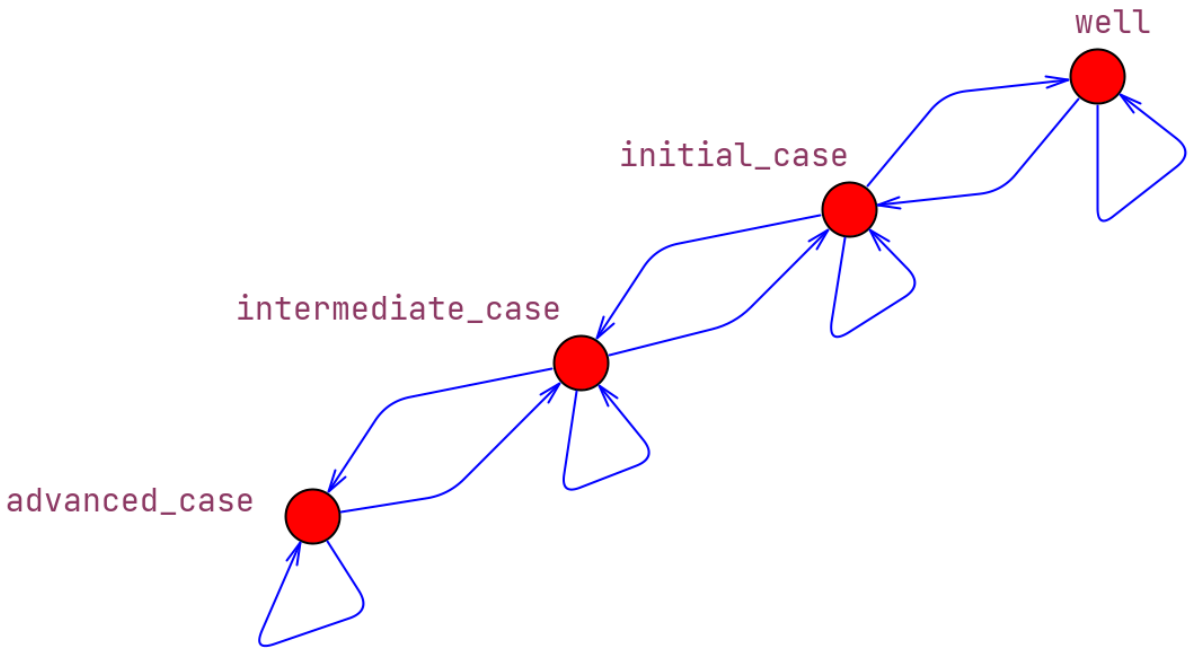


Fig. 2 Transition state diagram.

Four states are chosen that are the most common states in the stages of tumor growth, and a patient can be in one of these states after a careful examination. In this study, the predictors of tumor growth are carefully studied. Here, possible states are further discussed before their use in prediction is examined.

Well: In this state, the patient is in good health but suffers from symptoms that require regular monitoring of his condition, this state helps us to identify if the person will continue to be in a good health condition or will enter the beginning of the disease as a result of the emergence of some factors.

Initial case: The tumor is in its first stage; this stage is the actual beginning of tumor growth. In this state, which is considered the nucleus for the beginning of tumor growth, the future stage is predicted using a study of probability between states.

Intermediate case: In this state, it is determined if the tumor growth is increasing or decreasing.

Advanced case: This is the last case of tumor growth, as the tumor has reached its maximum growth as a result of the growth of tumor cells. This state is considered too late when the tumor has great resistance to treatment, and therefore it is expected that the possibility of eliminating cancer

cells will be very weak. However, if this stage is predicted before the patient enters the danger stage; the possibility of treatment is possible by finding an appropriate treatment for the tumor.

3.3.2 Determining the probabilities of predictions

Here, the focus is on understanding the probabilities of tumor growth predictions based on the prediction of the future state in two steps:

Step 1: After the precision of states, the initial transition matrix is calculated that is composed of transition probabilities which give the probability of P_{ij} passing from state i to j, in each step:

$$\sum_{j=1}^{n} \boldsymbol{P_{ij}} = \mathbf{1} \qquad \textit{(3)}$$

For any couple (i, j) $0 \leq P_{ij} \leq 1$

The transition probability matrix is obtained from the information extracted directly from the data set. This data set consists of 20 subjects with newly diagnosed Glioblastoma. Each patient can go through one or more health conditions (*well, initial state, intermediate state, advanced state*), which means that the disease takes different stages of progression in tumor growth.

Fig. 3, shows the expected states in which patient (Di) may be in one of them, and thus the future state of tumor growth should be predicted. However, if the patient is in a certain state i.e.

based on the information of the current state, knowing the next state as shown in the figure is the fundamental problem, for example, if the tumor is in the initial state, it can develop into an advanced state that may worsen the patient's condition along with the growth of the malignant tumor, or the patient's condition may improve, thus, reducing the growth of the malignant tumor

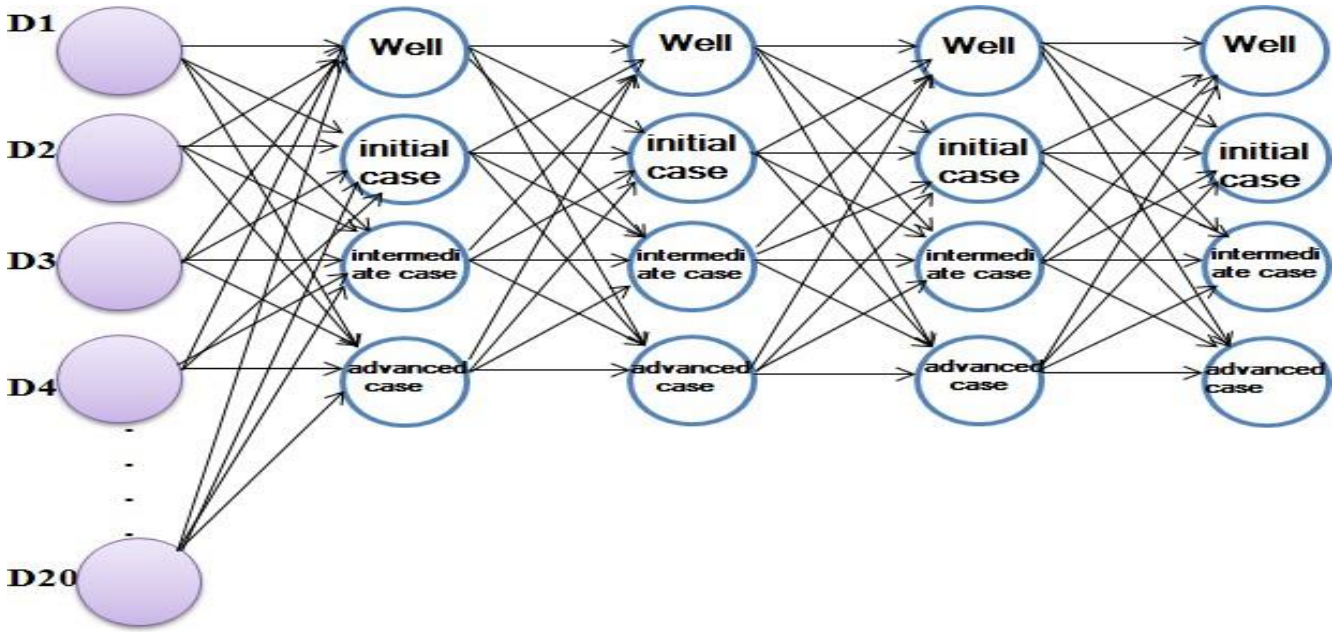


Fig. 3 Expected cases for each patient.

In essence, it is difficult to predict the future state given the rapid change in the structure of the tumor, however, in this study possible expected cases are included in order to accurately know the growth of the tumor, whether it is increasing or decreasing in size. So, the goal of this step is to define the states and extract the initial transition matrix in order to apply it in the second step.

Step 2: This step describes the basic interpretations of DTMC containing the probabilities of tumor development at the location defined by the equation:

$$\overrightarrow{\boldsymbol{W}}_{\boldsymbol{k+1}} = \overrightarrow{\boldsymbol{W}}_{\boldsymbol{k}}\boldsymbol{P}; (\boldsymbol{k} = \boldsymbol{0}, \boldsymbol{1}, \dots.) \qquad (\boldsymbol{4})$$

P is a transition matrix, and $\overrightarrow{W}_k$ is a state vector that contains the probabilities of tumors developing at specific locations at a given time step j. Then:

$$\overrightarrow{\boldsymbol{W}}_{\boldsymbol{k+1}} = \overrightarrow{\boldsymbol{W}}_{\boldsymbol{0}}\boldsymbol{P}^{\boldsymbol{k}}; (\boldsymbol{k} = \boldsymbol{0}, \boldsymbol{1}, \dots.) \qquad (\boldsymbol{5})$$

$\vec{W}_0(k=0)$ is an initial state vector. The position of the primary tumor site is represented by a 1 and 0's elsewhere.

3.4 Proposed methodology

This work will focus on predictive analysis of tumor growth; figure 4 shows the methodology followed in this work.

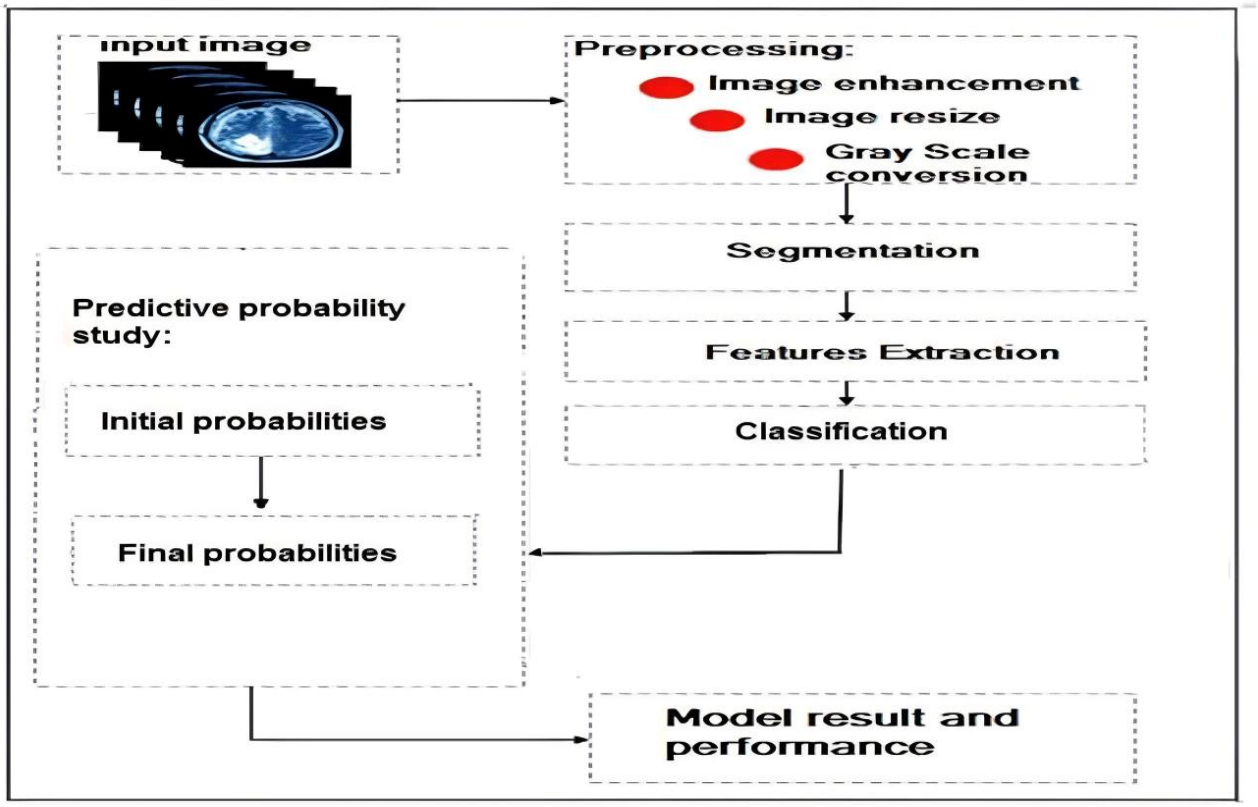


Fig. 4 Overall block diagram of proposed methodology.

The proposed methodology consists of the following main steps:

1. ***Input image:*** Firstly, the dataset Brain MRI medical images are used as input images. The input image must be in the.jpg or.png format.

2. ***Preprocessing:*** Preprocessing is applied to the collected input images. It is implemented in the following steps:

    a) Image enhancement or

    b) Image resizing or

    c) Gray Scale conversion.

3. ***Segmentation:*** In this step, the segmentation is done by using FCM Clustering.

4. ***Feature extraction:*** Feature extraction is a data reduction procedure to find a subset of useful variables based on an image. In this work, seven textural features based on gray level co-occurrence matrix (GLCM) are extracted from each image and are as follows: Invers, Dissimilarity, Maximum Probability, Contrast, Angular Second Moment (ASM), Inverse Difference Moment (IDM), Homogenety and Entropy

The GLCM is used for extracting features of the MRI brain image and those features were fed as the input to the classifier for the classification of the tumor.

5. ***Classification and Prediction:*** In this classification step, the KNN algorithm is used, which is one of the best machine learning algorithms. KNN is used in a variety of applications such as healthcare, handwriting detection, image recognition, and video recognition. The KNN algorithm is used for both classification and regression problems. In this study, the KNN algorithm is used to classify the image as a tumor or non-tumor. If a tumor is detected, the growth of the tumor will be predicted, which requires the following steps:

    a) Briefly describes the basic characteristics and interpretations of a DTMC.

    b) Calculate the probabilities of tumor growth at specific sites in a given time step.

6. ***Model result and performance:*** Evaluate the results and performance parameters of the proposed and existing method.

3.4.1 Brain tumor progression dataset and data classification

In this section, the focus is on brain tumor progression dataset and data classification.

3.4.1.1 Brain tumor progression dataset

This paper used a publicly available dataset containing 2000 images of subjects newly diagnosed with primary glioblastoma [114]. They were treated with surgery and concomitant standard radiotherapy (CRT). All image sets contain FLAIR, T1w, T2w, and ADC. The purpose of this data set is to evaluate the performance of the KNN algorithm and Markov model, in particular DTMC, for predicting tumor progression.

3.4.1.2 Data classification

The normal probability plot technique was used to identify substantial deviations from normality in order to assess whether the dataset is distributed normally and to identify cases with an abnormal distribution so as to study each case separately. The following figure 5 shows the classification of the dataset, which allows us to classify the data for each person to study and calculate the current and normal probabilities.

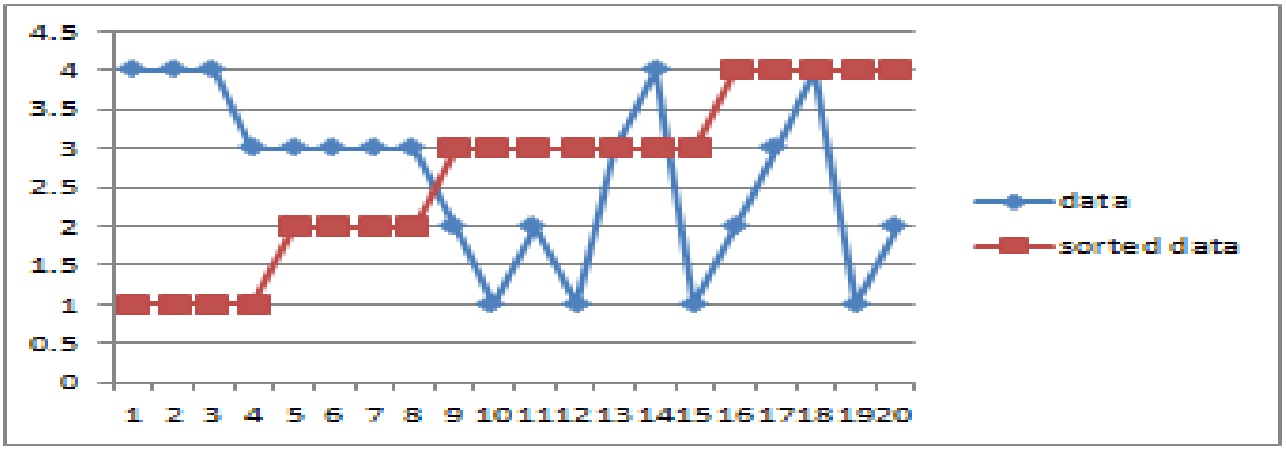


Fig. 5 Data classification.

After classifying the data, the probabilities for each case are calculated so that all the cases can be studied in order to see if the tumor probabilities are distributed naturally. This is critical so as to apply an accurate parallel with the study of the possibilities and come up with an integrated work

that combines what is theoretical and practical. Graph 6 shows the probabilities that have been calculated based on databases.

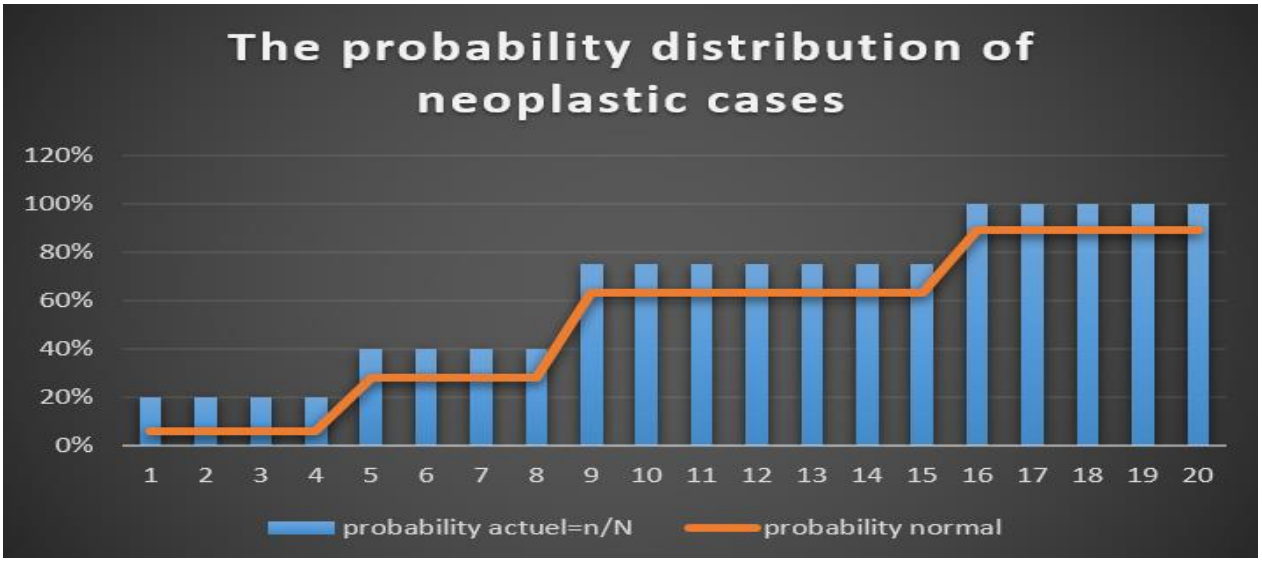


Fig.6 The probability distribution of neoplastic cases.

The normal probability plot points form a roughly linear pattern, indicating that the normal distribution is a good model for the data set.

3.5 Result and Discussion

The most important result of this work is the automatic predictor of tumor growth that is a consequence of the design and development of a methodology for predicting tumor growth based on the study of probabilities. This technique allows the possibility of discovering regions of the tumor and predicting its growth, in addition to studying all possible probabilities to move from one stage to another in the growth of the tumor and extracting all the details. The proposed models are trained with the collection, which includes datasets from 20 subjects with primary newly diagnosed glioblastoma (section 4.1). The collected input images are subjected to preprocessing. In the preprocessing step, image enhancement, image resize, and grayscale conversion are implemented.

- The image is resized into the dimension of Row = 256 and Column = 256 (Fig 7.a).
- The range of filtering is batch size = 3 and then the filtering level = 0.5 (Fig 7.b).

- The smoothing level will depend upon the filtering level. Hence, if the noise is present in the image, it will be removed (Fig 7.c).

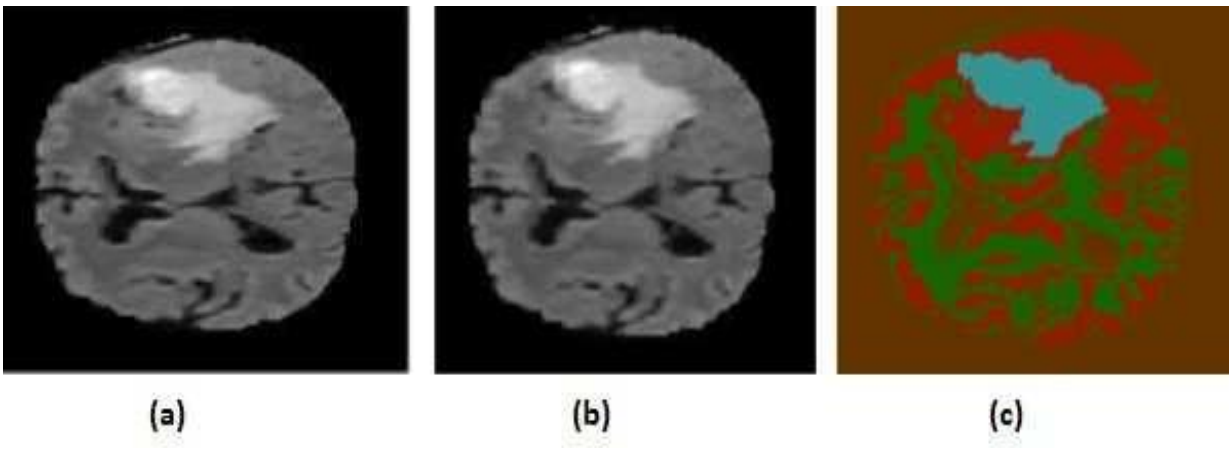


Fig. 7 (a) Resize image, (b) Filtered image, (c) Clustering segmentation.

The tumor is segmented using FCM Clustering. In this portion, clustering is done to cluster the region's interest separately from the background. Then color-based segmentation is applied to segment the area. The number of clusters mentioned in the code is 4, which results in partitioning the image into four regions.

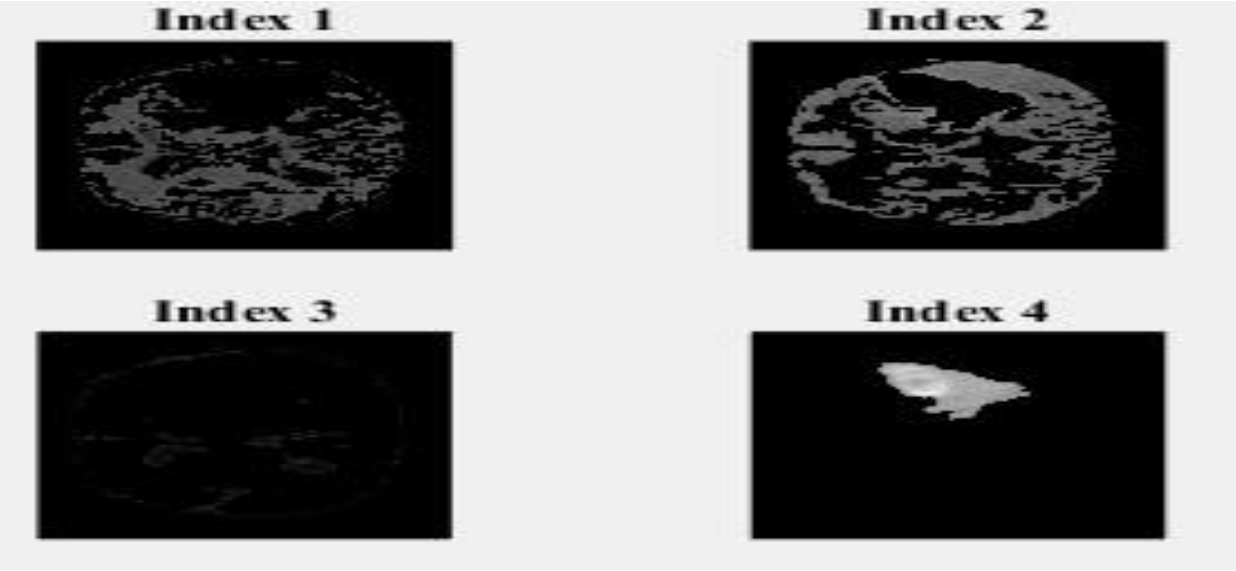


Fig. 8 Select the appropriate region.

Among those four regions, the appropriate region needs to be selected. Then that region will be the segmented image (for the above Fig. 8, Index 4 is applicable). Fig. 9 below show the tumor segmentation and tumor localization.

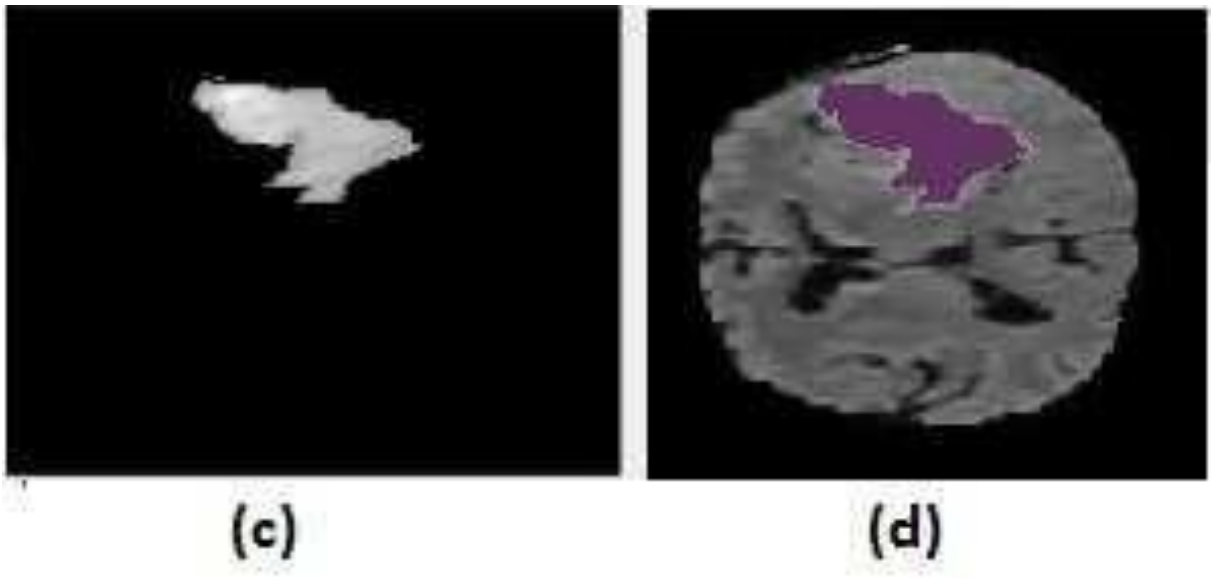


Fig. 9 (c) Tumor segmentation, (d) Tumor localization.

After Tumor segmentation and image feature extraction, the KNN algorithm is used to classify the image as Tumor or non-Tumor (Fig. 10). The classification result is then displayed, as shown in Fig. 10.

The inputs of the classification algorithm are the test feature, the train feature, and the target/ label:

1. Test features, represent the features of the input image.
2. Train features, represent the features of the overall dataset images.
3. Labels, represent the image category, like mild or moderate.

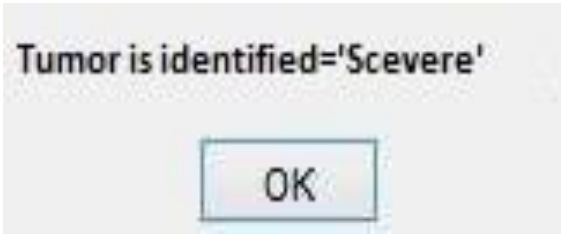


Fig. 10 Classification of images as Tumor or non-Tumor.

If a tumor is detected, the prediction of tumor growth is demonstrated using the DTMC and KNN algorithm (5.1). Furthermore, the exponential cell growth rate is used to clarify tumor growth among people in this experiment. It is noted that the percentage of cells increases incrementally in people with time, which explains the tumor growth during the specified period of the experiment growth.

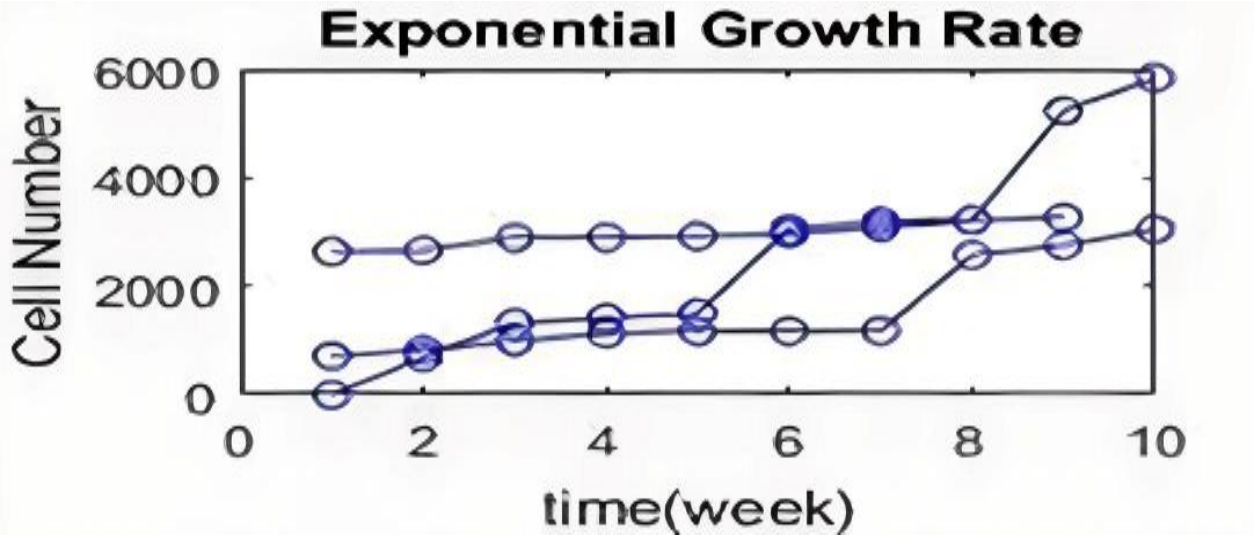


Fig. 11 Exponential growth rate.

It is also noted that the percentage of cells increases incrementally in people with time, which explains the growth of the tumor during the specified period of the experiment.

3.5.1 Tumor growth prediction results based on probabilities study

Based on the study of the probabilities, the results of predicting tumor growth from one case to another are reported as follows:

```
ans  =  4×4

    0.8824    0.1176         0         0
    0.2222    0.3704    0.4074         0
         0    0.2800    0.2400    0.4800
         0         0    0.8667    0.1333

ans  =  4×1

     1
     1
     1
     1
```

Fig. 12 Tumor growth prediction results based on probabilities study.

Thus, the tumor transmission rate from one case to another can be predicted.

If a person is healthy but has symptoms that require follow-up with their doctor, the probability of staying healthy is 89%, compared to only 11%, which is an initial state (tumor onset) of tumor growth.

If the patient is in the first stage of the disease, the probability that his condition will be stable is 22%, and the probability of his condition getting better is 37%, in contrast, the probability that his condition will worsen in the future is 41%.

If the patient is in the intermediate case of the disease, then the probability that his condition will be stable is 24%, and the probability of his condition getting better is 28%, in contrast, the probability that his condition will worsen in the future is 48%.

if the patient is in an advanced case of the disease, the probability of stabilizing his condition is 13%, and the probability of his condition moving to an advanced state is 87%.

Given the reported results of the probability of tumor growth from one case to another and the calculation of the probability matrix between cases, the following Graph 13 clearly shows the expected cases of the tumor and the chances of its potential growth in each case.

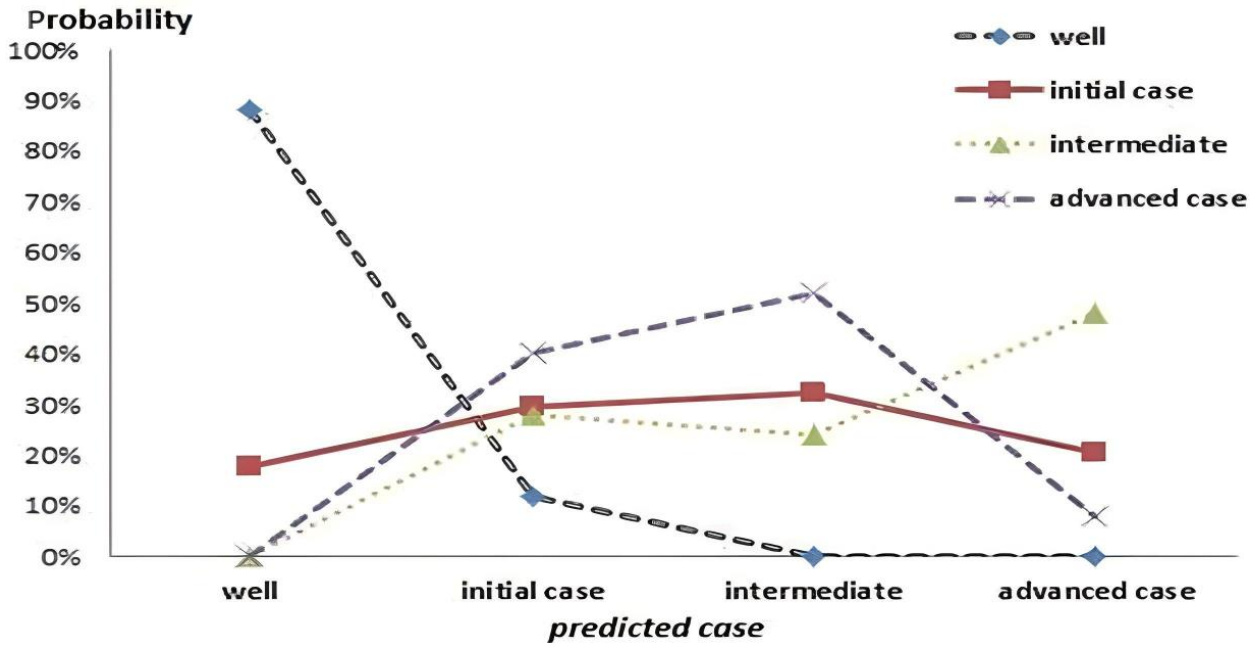


Fig. 13 Predict possible states of tumor growth.

In the above chart, the prognosis of the disease in the initial case limits the progression of the tumor to the advanced case, and therefore the success rate in treating the tumor is very high. On the contrary, tumor growth prediction in the advanced case may be challenging to treat, and this is noticeable in the `advanced case because it requires a long period of treatment time, or it may not be treated, and the patient's condition can possibly deteriorate. Therefore, the patient has a great role in maintaining his safety through early tumor detection, while the doctor and the prediction process have a decisive role in treatment.

3.5.2 Tumor growth prediction performance evaluations

To assess the results, a confusion matrix was used which is a matrix that measures the quality of the classification system. One of the advantages of the confusion matrix is that it can quickly show the predicted and actual classification and also evaluate the performance parameters. These include accuracy, sensitivity, specificity, and F1-measure [115]. Therefore, the performance evaluation equations are given in Equations to calculate measures and evaluate results. 6, 7 and 8 are used.

Precision performance: Among all positive predictions, precision is expressed as a truly positive percentage.

$$\boldsymbol{Precision} = \frac{TP}{(TP+FP)} \quad (6)$$

Recall: Also called Sensitivity: the ratio of correct positive predictions to the total positives:

$$\boldsymbol{Recall} = \frac{TP}{(FN+TP)} \quad (7)$$

Accuracy: From all the classes (positive and negative), How many of them were correctly predicted:

$$\boldsymbol{Accuracy} = \frac{(TP+TN)}{(TP+FN+TN+FP)} \quad (8)$$

True Negatives (TN) are cases in which tumor growth is not present and negative predictions of tumor growth are correct.

False Positives (FP) are cases in which there is no tumor growth and incorrect positive predictions of tumor growth.

False Negatives (FN) are cases in which tumor growth and baseline fact image data are correctly classified as not tumor growth in the sense of incorrect negative predictors of tumor growth.

True Positives (TP) are cases in which a base truth image data point is correctly classified as true positive predictors of tumor growth.

Using Equations 6, 7, and 8 it is found that the accuracy ranged from 95% to 97.65% for ten periods, and it achieved a verification accuracy of 97.65%, a sensitivity of 99.87%, and specificity of 71.65%. Figure 14 shows the overall performance comparison of the model at the end of each period.

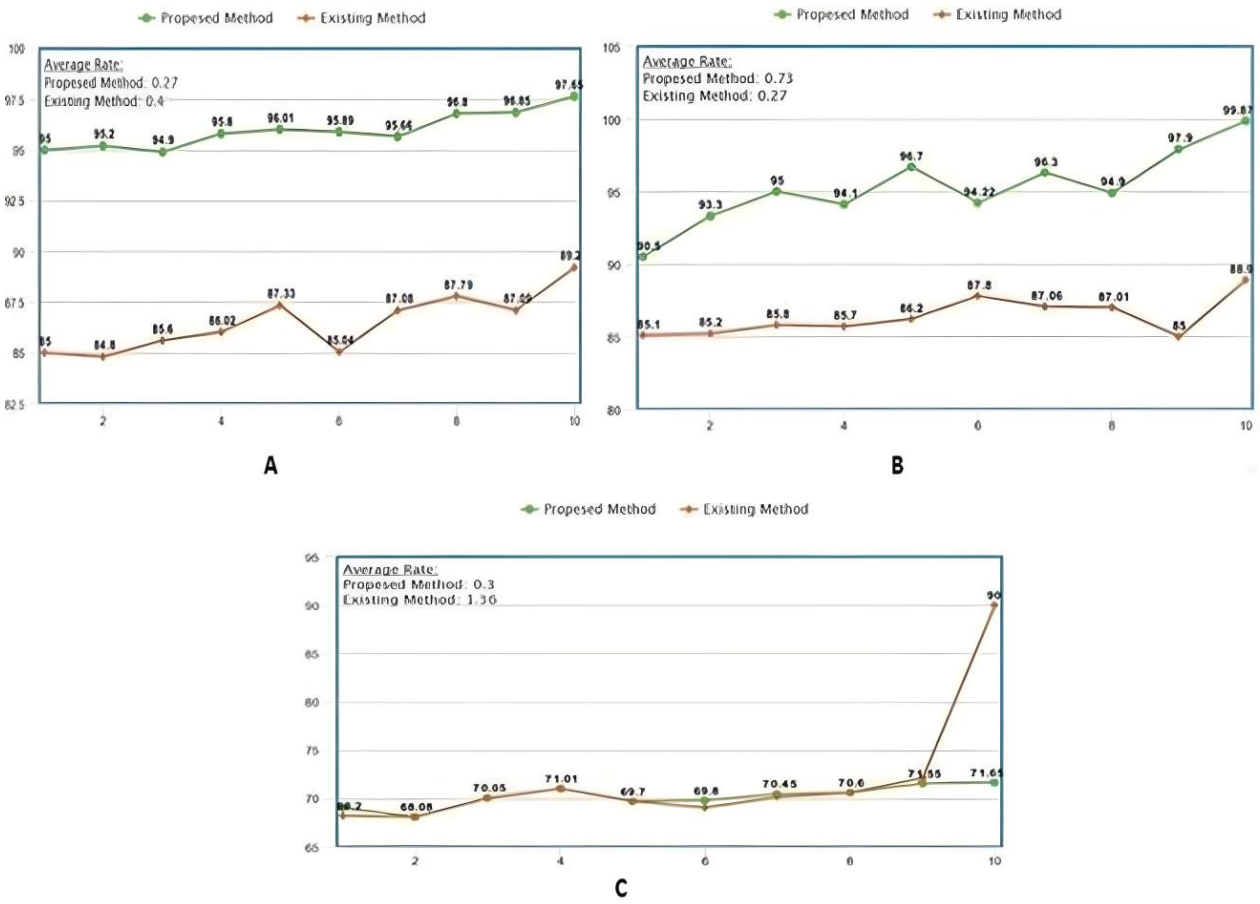


Fig. 14. Overall performance comparison: A: Accuracy, B: Sensitivity, C: Specificity

Thus, it reports the best results of this study for the evaluation performance in the overall periods and show them as a comparison to the best results of the existing methods for the same period in table 3.

Table 3 Performance parameters of the existing [29] and proposed method.

Performance Parameters	**Proposed method**	**Existing method**
Accuracy	97.65%	89.2%
Sensitivity	99.87%	88.9%
Specificity	71.65%	90%

By comparing the performance results obtained with the previous existing results shown in Fig. 14. It is found that the results obtained in this work are better than the existing results [116] that represent the performance of the morphological segmentation algorithm. However, due to the morphological segmentation, the feature stability is low. So the classification performance will be low when compared to the proposed work. In the proposed system, clustering is used to improve the segmentation accuracy and then improve the classification and prediction performance.

3.6 Conclusion and Future Works

In recent years, it has become clear that new methods must be found to predict the future state of the tumor in order to reduce its risk and find the appropriate treatment for it. To that end, it is necessary to focus on what is practical and theoretical and to explore new methods that are more precise and usable in different cases. This paper proposed a new method to predict the future state of a brain tumor. Through both applied and theoretical analysis tumor growth possibilities were studied and the accuracy and reliability of prediction along with their validity were discussed and compared with several methods, keeping practical considerations for evaluation in view. The core focus was to improve the performance of tumor prediction models. The experimental results of this work showed that the proposed method outperforms the existing method in terms of performance evaluation measures; the accuracy rate is 97.65% compared to the existing method 89.2%, the specificity is 71.65% and the sensitivity is 99.87%.

However, with all these results, there are limitations to this work, which will be among the future goals. The most important of these limitations is that this technique cannot be generalized to all datasets for other tumors.

In future work focus will be on the presentation of another case study, which is the segmentation and prediction of a tumor in a more advanced way. This method can also be generalized and applied to the prediction of other tumors located in other parts of the body and create a specification language for tumor prediction where images can be treated as a model and can be studied in detail. This will highlight the role of the Markov model in highly advanced functions.

CHAPITRE 4 ARTICLE 2: BRAIN TUMOR DETECTION USING CELLULAR AUTOMATA BASED IMAGE SEGMENTATION TECHNIQUES

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Abstract: A quick and effective diagnosis is critical to the treatment of any disease. In the case of cancer related diseases, the success of the treatment is typically correlated to the time of accurate diagnosis of the disease. Thus, it is important to make a quick and accurate diagnosis. This work presents a cellular automata-based system capable of diagnosing tumors in medical data from various imaging techniques, including MRI and X-ray. This system is an Automated Cellular (CA) that uses the Moore neighborhood algorithm to detect the area of cancer cells in the image, by segmenting areas of abnormality from the background. We also present an analysis of different parameters of the Moore neighborhood algorithm for optimal detection of cancerous cells; the results of this analysis confirm the proposed method effectiveness on all data sets, with an accuracy of more than 93\% and 95\% precision.

Keywords: Cellular Automata; Tumor Detection; Magnetic Resonance Imaging; Segmentation.

4.1 Introduction

Malignant tumors are among the most deadly diseases. Within the next two decades, it is expected that the cancer burden will double. In turn, this is expected to have a worldwide impact on both human and financial resources. However, these developments are tied to the global capability of timely detection and treatment of cancerous lesions [117]. The leading type of cancer that causes death in women is breast cancer. Its prevalence is increasing with time. Diagnosed as abnormal tissue in the breast, it may be classified as benign or malignant. Malignant tumors are deadly and must be excised from the body after a biopsy. Since there is no official cure for cancer, an early diagnosis is a key to the right course of action, be it treatment or ablation of the abnormal mass.

Various imaging methods, such as X-ray and MRI, are frequently used to pinpoint the growth of the tumor.

Further analysis of these images is done using medical image processing techniques. Another type of cancer that is very common. A general classification of lung cancer cells is based on the cell size and is typically referred to as small and non-small-cell lung disease [118], the assured survival rate in lung cancer is 15%; however, if the diagnosis is made at a very early stage, this survival rate can increase to 70% [119]. A major cause of lung cancer's high death rate is the delayed detection and subsequent treatment of the disease. In that regard, it is of paramount importance that a timely detection is made. Various imaging methods including MRIs and X-rays are used to diagnose different diseases. Their primary goal is to aid in the monitoring and detection of abnormalities using image processing, the raw data available from these imaging modalities can be transformed into meaningful information for clinical use [120]. To that end, Cellular Automata (CA) is one stream of information processing that is efficient, accurate, and used for detecting boundaries and edges and thus finds its application in multiple areas [121]. By leveraging CA, tumor detections can be made to assist timely diagnosis of potential cancer patients. In that regard, this study is very important as it serves as a tool to facilitate the clinicians.

CA can be represented in a regular and uniform pattern. This preserves heterogeneity, particularly concerning the dependency on the neighborhood and the structure of the overall lattice. CA comprises a cellular grid where each cell can take a particular state. The overall number of possible states is finite. A cell’s state is periodically updated based on previous states of neighborhood cells [122]. A transition rule does this state change. One, two, or three dimensions can be CA models. One dimensional CAs consist of a linear set of cells. In 2D CA, the arrangement of cells is grid-like:

Rectangular or hexagonal. Importantly, the connections between the neighborhood cells are maintained by the grids [123]. 2D CAs are solved as digital image processing problems because cells are represented as digital images. In order to leverage cellular automata to design solutions, mathematical techniques such as lattice geometry, neighborhood size, and initial condition boundary problems, as well as cell states and their accompanying rules of transition, must be

understood and carefully studied with reference to the problem at hand [124]. All adjacent cells are referred to as a cell adjacent to the reference (central) cell.

In this work, we show how to use the CA formalism to detect the presence or absence of abnormal cells in MRI images, for cancer diagnosis, tumor detection is absolutely critical, and this study is a step in that direction to facilitate and automate the detection of tumors. The CA-based image segmentation algorithm is deployed to isolate the tumor region from the normal background image. Due to the variate nature of the cell images, successful deployment of segmentation is difficult to achieve with reasonable accuracy. The kind of image segmentation approach one must take depends on the characteristics of the area of interest. Segmentation typically makes use of thresholding pixel values to differentiate pixels that are beyond a threshold value. Tuning the right threshold value greatly affects the kind of segmentation success one gets.

Cellular automata-based image segmentation rules can be modified depending on the image type to suit the application's needs. In cellular automata, operations based on neighborhood cell states are typical for processing images. In this work, we apply a 24-point neighborhood operation to isolate the abnormal cells from the background image.

The importance of this work in the application of cellular automata in tumor modeling lies in the ability to formalize tumor cells and monitor the dynamics of the tumor boundary level, where the study of tumors using cellular automata is like the study of tumor cell models in the laboratory. In addition to being a successful method for interpreting medical images, cellular automata are also computationally efficient, this method is useful for specialists in detecting the area of abnormal cells, and among the main contribution of this study is cellular automata based 24-point Moore neighborhood segmentation algorithm that leverages cellular automata to update the cell states as it traverses to subsequent cells, using updated states of the prior cells. It is also an application on brain tumor detection on MRI dataset.

The remainder of this work is structured as follows. We go over related work and explain the work concerned with CA-based techniques in section 6.2. Section 6.3 proposes a methodology to segment cancerous areas from the background. In section 6.4, we evaluate the proposed methodology and discuss the results in light of our experiment. Conclusion and Discussion are made in section 6.5.

4.2 Background

This section expands on the basics of cellular automata, the cancer detection techniques used, and cellular automata based image segmentation.

4.2.1 Cellular automata basics

Cellular automata is a grid of cells and is considered as a computational model [122]. Each cell functions as finite automata having a particular state, and the state transitions happen with respect to a transition rule. CA exhibit uniform as well as dynamic and complex behavior. The complex behavior is determined by the various properties that constitute the CA transition rules. by observing cellular automata outputs collectively acquired in continuous actions, a pattern is generated. We denote a CA with a fairly simple expression.

$$\mathbf{CA = \{L, N, \ P, \ \delta, \ p0\}} \qquad \mathbf{(1)}$$

L: Is a reference to the normal cell.

P: represents a limited number of states.

$\boldsymbol{P_0}$: The starting state, and $P_0 \in$ P.

N: With regard to neighborhood indices, N: is a finite set and r ∈ L and $\boldsymbol{a \in N: \ r + a \in L.}$

$\boldsymbol{\delta}$***: is*** the process stage such that $\boldsymbol{P_m \rightarrow P}$ [124].

Different CA structures have different applications depending on the problem under consideration. Typically, 1D, 2D, and 3D CAs are used. 1D CA may be represented as infinite cells in an array where two states are possible for each cell: 0 or 1. A 2D CA may have a rectangular or a hexagonal grid structure; however, for the representation of images, a rectangular grid is considered to assign each cell to an image pixel with the cell state as the pixel's intensity. The difference between 1D and 2D CA structures is evident in Fig. 1 and Fig. 2. As cells change their state, image transformations can be visualized. These image transformations can be implemented by performing

operations based on the neighborhood in a CA. A reference cell's neighborhood is made up of the cells that are right next to it.

The convention for one-dimensional CA entails that a reference cell has two neighbors along each of its sides. In two-dimensional CA, based on the algorithm, there are certain variations to categorize a cell as a neighbor. For example, the reference cell of a Von Neumann neighborhood CA has four neighbors, i.e., the horizontal and vertical cells surrounding the reference cell; Moore neighborhood CA has eight adjacent cells in its neighborhood [124].

Fig. 2 is in fact Von Neumann CA, whereas Fig. 3 shows a 2D CA structure using the Moore neighborhood. The difference between Von Neumann and Moore algorithms in terms of neighborhood classification is shown in Fig. 2 and Fig. 3 where it can be seen that with respect to the reference (R) cell, the Moore neighborhood structure takes all adjacent cells into account.



Fig.1: 1D CA structure

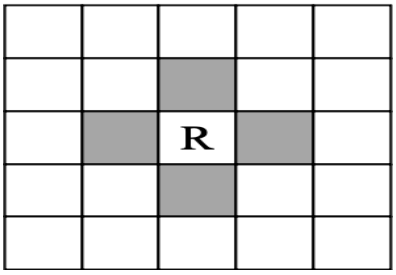


Fig.2: 2D CA Von Neumann structure

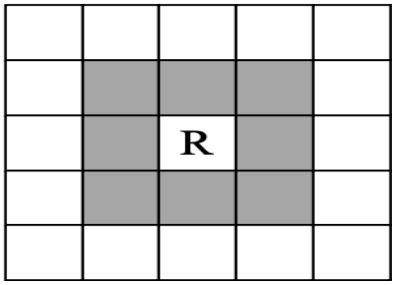


Fig.3: 2D CA Moore structure

4.2.2 Cancer Detection Techniques

The importance of early cancer diagnosis cannot be stressed enough. Due to the effectiveness of early cancer diagnosis, image processing and deep learning technologies help in rapid tumor detection. In this paper, we do research on tumor detection. Where we find one of the most prominent techniques in detecting tumors, x-ray imaging is imaging through which any signs of a tumor can be identified. Unfortunately, the radiographic image contains a lot of noise, and only the lighter pixels in the image can indicate a cancer cell. For the detection of breast cancer, R. Ramani et al. proposed a preprocessing mechanism for radiographs. [126], which has been successful in improving the quality of mammograms. It also reduces noise to help further detect abnormal cells, cancerous or otherwise. region splitting, growing, and the Watershed algorithm-helps identify regions with abnormal mass growth. The classic algorithm called the watershed algorithm [129] is a morphological technique for segmenting images related to specific regions. In this algorithm, the Watershed transformation considers images as topographic maps of each point standing out by its brightness. In order to perform watershed transformation [127], a computation is made for the distance transform over a binarized image before the gradient value marker-controlled method can be applied. Another approach for identifying breast tumors from a mammogram was proposed by A. Singh et al. [128]. First, the tumor region is extracted after smoothing and choosing a threshold. Then, the important outcomes image is created by making a box and enclosing the tumor region, brain tumor is yet another terrible illness. It is possible to detect it by analyzing the CT image of a brain. An automated approach for brain tumor diagnosis was presented by S.Sazzad et al. [129]. This approach started with an image enhancement technique to counteract the effects of variations

in grayscale colors in the image. This was followed by filtering to get rid of the noise. Since grayscale images were used, OTSU-based segmentation was done. Using feature information from pathology experts, tumor regions were marked and identified. It is possible to detect lung cancer using different imaging techniques such as CT scans or X-rays of S.Tarawneh et al. [130] proposed an approach where the authors used the OTSU method for thresholding after cleaning the image. Segmentation allowed for certain features to be extracted, which was followed by binarization and masking. A clustering-based segmentation technique was presented by K. Senthil et al. [131]. Multiple filters were used for the enhancement of input images quality. The segmentation was then implemented using K-means, optimization techniques are then used. to distinguish the focus region and collect crucial tumor characteristics.

4.2.3 Image segmentation using cellular automata.

One of the major concerns in medical imaging is robust and accurate detection of diseases that could include tumors or fractures. For an efficient detection of tumors in brain and other parts of the body, segmentation of image is typically employed to segregate an image into various parts and eventually extract a region of interest. The core objective of segmentation is to represent the abnormality in a simple way for analysis. Typically, segmentation detects edges or boundaries in the image [132]. Another important process in image processing is thresholding, as it directly affects the clarity of resulting image and contributes directly in determining the regions of interest. Utilizing cellular automata-based techniques for segmentation provides robustness and accurate detection of abnormal cells [133]. To that end, different methods have been applied in the past to detect edges in the image that facilitate isolating the tumor in the original image. These include leveraging CA to find edges on binary images of hand X-rays, brain tumor images [133], as well as brain, lung, and breast images [134].

4.3 Related works

Malignant tumor is a mass of tissue in which cells grow abnormally. Therefore, brain tumors are one of the most critical areas to be studied. There are more than 150 types of brain tumors that differ from each other, and brain tumors are among the causes of death for many people; in 2021, more than 83,570 people in the United States were diagnosed with brain tumors, of which 59,040

were benign, and 24,530 were malignant [135]. Due to the importance of the topic, many methods have been suggested over the past four years to study brain tumors.

In paper [135], an automated system was used to detect brain tumors, which helps to detect the area of abnormalities, and this method also enables to improve the X-ray image quality. The outcomes, particularly those related to enhancing the X-ray image's quality, supported the suggested approach's effectiveness.

M. Diwakar et al [136], focused on Edge-Detection; this paper proposed Edge-Detection through the use of cellular automata. The result of this work was good in terms of accuracy, in addition to the use of large database.

In the same context, Paper [137] presents a cellular-automata-based method to identify and segment the damaged area through MRI treatment, whereas the proposed method concluded that in order to achieve better outcomes, the method should be included for the outer cells of the next level.

In paper [138], the effect of treatment on the development of vascular carcinoma was investigated using a random cellular model. The findings demonstrated that taking the medication consistently as prescribed by a doctor is more effective at halting the spread of cancer cells, as demonstrated by simulation results based on in vivo data.

In the same context, Paper [139], studied skin cancer such as melanoma, which is the most aggressive skin cancer. The study concluded that early detection has a significant role in the high rate of survival. This study relied on spatial domain analysis and feature extraction using statistical techniques. The percentages of accuracy, sensitivity, and specificity reached 0.978, 0.944, 0.987, respectively; this makes the proposed method more effective.

In the paper [140], a new method for treating tumors based on CA was presented, where this method depends in the first stage on naturally growing of tumor, and then the treatment is done by reducing the settings of the model, where the results are that with the decrease in the parameters of the model, there is no change in contrast to the increase in the parameters, so the inactivity of the tumor was resolved and thus it was possible to eradicate it.

This paper [141] focuses on tumor detection using CNN techniques and CA, where CNN is considered one of the most prominent techniques in tumor detection and classification, and several applications have demonstrated the effectiveness of this method, and when it is combined with cellular automata, the simulation of cancer cells resembles the behavior of cells in reality, and this is due to the power of cellular automata in tumor simulation, as the study was also applied to the magnetic resonance imaging data set, and the results were generally satisfactory.

In paper [142] segmentation and detection was discussed utilizing fuzzy logic, and CA, where the proposed method was implemented on the BraTS data set, where the density of each pixel is relied on by feeding it to label each pixel, and the same process continues several times, where the accuracy rate in the stage before the improvement was 85.8%, while in the second stage, after analyzing the image, the accuracy reached 99.8%.

In paper [143] edge-detection was studied using Cellular-Automata, where the suggested technique shown success in terms of analyzing and clarity compared to other methods such as prewitt, sobel, and canny, which have some disadvantages.

In paper [144] a three-dimensional cellular-automated model was developed that works mainly on tumor modeling by relying on parameters, as this model simulates the growth of the tumor, and this model also enables the prediction of tumor motility over time, the work principal goal is to develop a novel model of the tumor, and the results of this method were acceptable.

The paper [146] focuses on tumor detection using electromagnetism and watersheds, where it focuses on the behavior of the tumor and the importance of detecting it at an early stage, several methods were discussed in this paper and among these methods, the suggested method yielded good results that demonstrate the effectiveness of the presented approach compared to other techniques.

The paper [147] aims to study tumor segmentation with high accuracy, and this paper also presented a set of works in order to compare and test the suggested method, and the results of partitioning confirmed the effectiveness of the proposed method.

In order to further clarify the relevant work, we have extracted the most important characteristics of the discussed works as shown in Table 1, where we define the objective of each study and the techniques used.

Table 1 shows the objective of each study and the techniques used in the relevant work

Ref	**Year**	**Author**	**Objective**	***-Techniques used***
[134]	2022	R. Barik et al	Cancer Detection using Cellular Automata	*-Cellular automata* *- Edge detection*
[135]	2022	M. Diwakar et al	Segmentation of brain tumors using cellular automata	*-Cellular Automata* *- Edge Detection*
[136]	2022	K. Anil et al	Segmentation of brain tumors using outer totality cellular automata	*-OTCA* *-Cellular automata*
[137]	2019	P. Fateme et al	Targeting cancer and immune cells by using cellular automata	*-Cellular automata*
[138]	2022	L .B. Benjamín et al	Dermoscopic Image Melanoma Detection Using a Cellular Automata Classifier	*-Pattern recognition* *-Cellular Automata Classifier*
[139]	2018	S Shiva et al	Modeling the growth of an avascular tumor using stochastic cellular automata and immunotherapy	*-Cellular automata* *-Immunotherapy*
[141]	2019	R Kalantari et al	Brain Tumor Detection Using CNN and CA	*-CNN* *- Cellular Automata*
[142]	2022	K Roqaie et al	Segmentation of Brain Tumor Using Fuzzy Logic	*-Fuzzy Logic* *-Cellular Automata*
[143]	2021	B Rupashri et al	Analysis and application to biomedical using cellular automata	*-Edge detection* *- Cellular automata*
[144]	2022	A. R. Kansa l et al	Brain Tumor Simulation Using 3D and CA	*-Cellular Automata*

[146]	2018	A.C. Motagi et al	using watershed for brain tumor Detection	*-Watershed*
[147]	2021	P. Jain et al	Detection of brain tumor	*-Morphological*

The key components of the suggested literature are presented in Table 1. Among these features are the goals and techniques used, it also shows the great role of cellular automata in the study of tumors, in addition to the possibility of combining it with other techniques, which makes the study of the tumor more detailed. Moreover, cellular automata simulate the real reality of cancer cell development and transition from one state to another, and this highlights the effective role of cellular automata in the study of tumors compared to other techniques.

4.4 Materials and methods

The suggested methodology for detecting tumors with CA is detailed together with the dataset and tools used.

4.4.1 Dataset Used

The dataset used for this investigation contains MRI images of human brain segregated into two sets of images: those containing brain tumors and those without it. We have considered 40 images from each segregation for our work as beyond this number, the results do not vary significantly. Some samples in our dataset are presented in Fig.4.

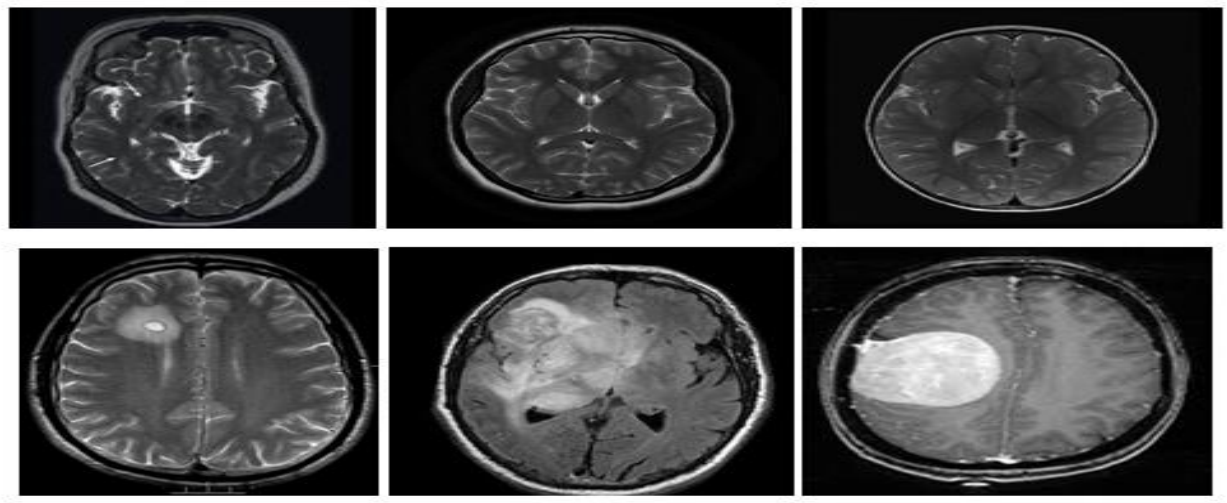


Fig.4: Some samples from the used dataset

4.4.2 Tools used

For all work, licensed software MATLAB has been used. Due to its ease of use and robustness in processing image data, MATLAB was the preferred software.

4.5 Proposed Methodology

In this work, we focused on detecting brain tumors. Figure 5 illustrates the methodology used.

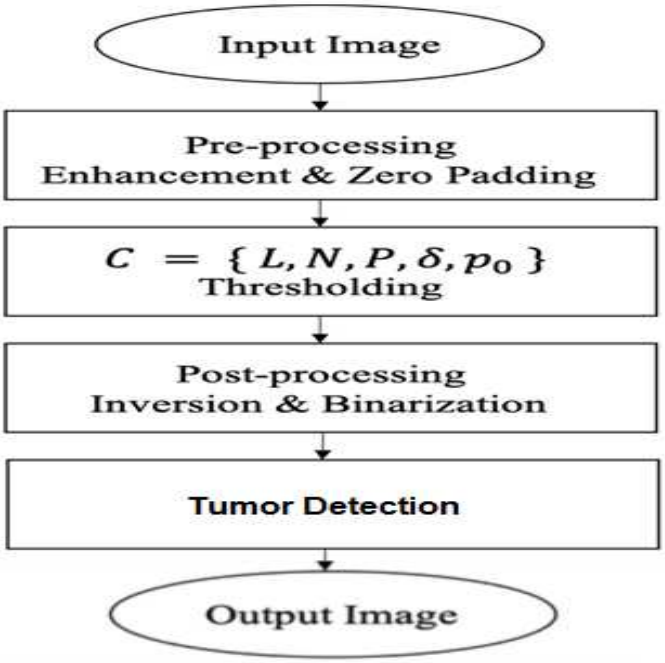


Fig.5: The diagram illustrates the suggested methodology.

The main steps of the proposed methodology are as follows:

1. ***Input image:*** Firstly, the dataset Brain MRI is used as an input images.
2. ***Preprocessing:*** This step is to improve input image for further operations. Any noise in the image can affect the segmentation process; thus, smoothing operations are first done. This is achieved by using a Gaussian bilateral smoothing filter that preserves the edges when smoothing the image. Once this is done, the smoothened image is zero-padded to ensure that the reference cells at the boundary of the image have a suitable number of cells as their neighbors. Zero-padding ensures we have sufficient pixels as neighbors for the boundary reference cells. An illustration of cellular automata based 8 points Moore neighborhood

algorithm at the boundary pixel location is shown in Fig. 6 where 'R' corresponds to the reference pixel, shown here at the boundary of the original image, and 'N' corresponds to a neighbor pixel. The black squares in the figure correspond to the zero-padded pixels in the image, and the white squares correspond to the original image. Thus, zero-padding ensures that the boundary pixels in the original image are not void of any neighbors.

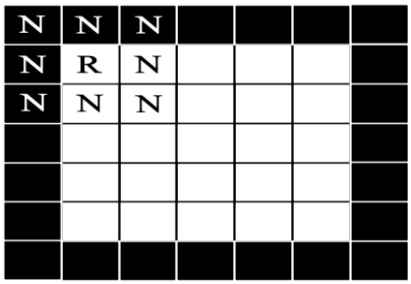


Fig.6: Illustration of zero-padding on 8-point neighbors

3. ***Threshold and implementation of cellular automata****:* After this pre-processing, we then perform cellular automata-based Moore neighborhood segmentation technique that entails taking 24 adjacent points around the reference cells to compute their differences. A 24 point Moore neighborhood structure is shown in Fig. 7.

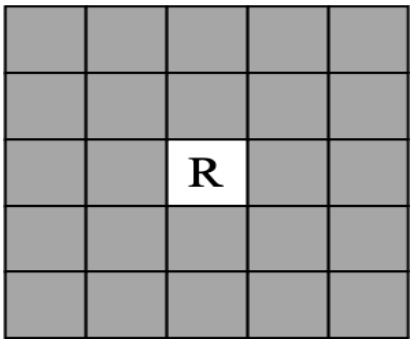


Fig.7: 2D CA 24-point Moore structure

The means to traverse from one cell to another, which in the case of an image is essentially a movement from one pixel to another, is done sequentially, row by row by keeping track of the indices of the image. We can refer to index locations for a particular reference cell as (i, j) refers to a row and column number, respectively. Any increments or decrements in these locations allow us to access the neighborhood cells, as shown in Fig. 8.

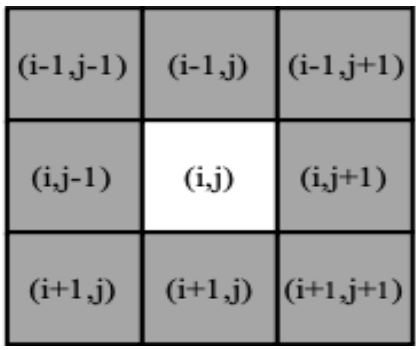


Fig.8. Reference cell and neighbor locations

With respect to Equation (1), our lattice of cells, L, is in fact the size of the image (512x512) since we are implementing CA on 2D images with N = 24 as there are 24 neighbors for each cell; P = 256 as we work on 8-bit images and P_0, the initial state is considered to be the input image's pixel value. The transition rule δ for this cellular automata implementation is such that if all differences of the reference cell from its neighbors are below a pre-set threshold value, we assign the reference cell a zero value. Otherwise, the reference cell value remains unchanged. This is done for all pixels in the image. This is the major step in implementing cellular automata based segmentation on 2D images: selecting neighbors according to Moore's algorithm to select cells adjacent to a given cell state $Y_{i,j}$ of the cell by:

$$\mathbf{M}_{(\mathbf{y_{0,0}})}{}^{\mathbf{N}} = \{(\boldsymbol{Y}_{(i,j)}) : |\boldsymbol{Y}_{(i,j)} - \mathbf{y_{0,0}}| \leq \mathbf{r}\}$$

For r=0, 1, 2, and 3, moore neighborhoods are odd squares that make up the amount of cells in the Moore neighborhood of range r.$(2r+1))^2$.

state $Y_{(i,j)}{}^{t+1}$of the cell at time (t + 1) can also be specified by the native rule procedure f : $(Z_3{}^9)$ → Z3 as follows:

$$\mathbf{Y_{(i,j)}}^{\mathbf{t+1}} = \mathbf{f}(\mathbf{Y_{(i,j)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j-1)}}^{\mathbf{t}}, \mathbf{Y_{(i-1,j-1)}}^{\mathbf{t}},$$

$$\mathbf{Y_{(i-1,j)}}^{\mathbf{t}}, \boldsymbol{Y_{(i,j-1)}}^{\boldsymbol{t}}, \mathbf{Y_{(i-1,j+1)}}^{\mathbf{t}}, \mathbf{Y_{(i,j+1)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j+1)}}^{\mathbf{t}})$$

$$= \boldsymbol{b_0 Y_{(i,j)}}^{\boldsymbol{t}} + \boldsymbol{b_1 Y_{(i+1,j)}}^{\boldsymbol{t}} + \boldsymbol{b_2 Y_{(i+1,j-1)}}^{\boldsymbol{t}} + \boldsymbol{b_3 Y_{(i-1,j-1)}}^{\boldsymbol{t}}$$

$$+ \quad b_4 Y_{(i-1,j)}{}^{t} + b_5 Y_{(i,j-1)}{}^{t} + b_6 Y_{(i-1,j+1)}{}^{t} + b_7 Y_{(i,j+1)}{}^{t} + b_8 Y_{(i+1,j+1)}{}^{t}$$

Where $b_0, b_1 \ldots \in Z3$ each cell's value for the following state, and then deciding threshold values based on the computed differences from each neighbor.

4. ***Post-processing and detection:*** The resultant image is then fed to the post-processing block where it is inverted and binarized for simpler viewing. The inversion of image subtracts the pixel value from 255 which is the maximum pixel value. The zero pixels become 255 and the 255 valued pixels become 0, hence the name inversion. Essentially, this is done for a better visualization as the image is now meant to show only the tumor mass in dark black pixels in image. We also perform binarization on this image, thus the image on contains 0s and 1s. This binary image is an even better visualization of the tumor. Thus, the result is the process of detecting the tumor using cellular automata.
5. ***Output image:*** It is the result of the model and performance, where we evaluate the results and performance parameters of the proposed methodology.

4.6 Results and Discussion

In this section, we present a demonstration of proposed algorithm using cellular automata-based segmentation on a publicly available brain tumor MRI image dataset. The pseudo-code below shows the algorithm used in this paper.

Procedure 1 CA based Segmentation

Require: *image, threshold*

```
procedure TUMOR DETECTION()
    Image enhancement via filtering
    Image padding with zeros
    Initialize threshold
    for each reference pixel do
        Neighborhood determination
        Difference computation
        Thresholding
        Update reference pixel value if needed
    end for
    Image inversion
    Image binarization
    Tumor Detection
end procedure
```

The proposed algorithm is shown to work on a brain tumor image to focus on the desired area i.e., the tumorous cells. The input image is shown in Fig. 9.a. Notice the tumor in the left center of the brain MRI image, which is the target area of segmentation and needs to be isolated for the physician. We apply a bilateral filter that performs Gaussian blurring while maintaining edges in the image. It smoothens the image as shown in Fig. 9.b.

This is followed by zero padding to ensure the cellular automata-based segmentation has neighbor pixels for the boundary pixels in the image. The zero-padded image looks the same as the smoothened image except that its size is now 516x516 since two pixels are added on each side of the image as padding because we consider two pixels in each direction of the reference pixel for neighbor determination. The zero-padded image is also shown below in Fig. 9.c The CA-based segmentation is done on this padded image to determine pixel values according to the CA transition rules discussed in Section III-C. When the CA rules are applied, they take into account a rectangular subset of pixels. The pixels on the border of the image do not have any neighbors. In order to provide neighbors to the bordering pixels, zero padding is done. The resulting image is shown in

Fig. 9.d where it can be seen that tumor is successfully segmented. However, areas other than tumors are also evident in the image as unwanted artifacts. These additional areas show up because of the nature of the algorithm where it is focusing on determining the edges. Hence, the artifacts correspond to the edges of features in the brain image. A well-tuned threshold value can aid in the image to reducing these artifacts.

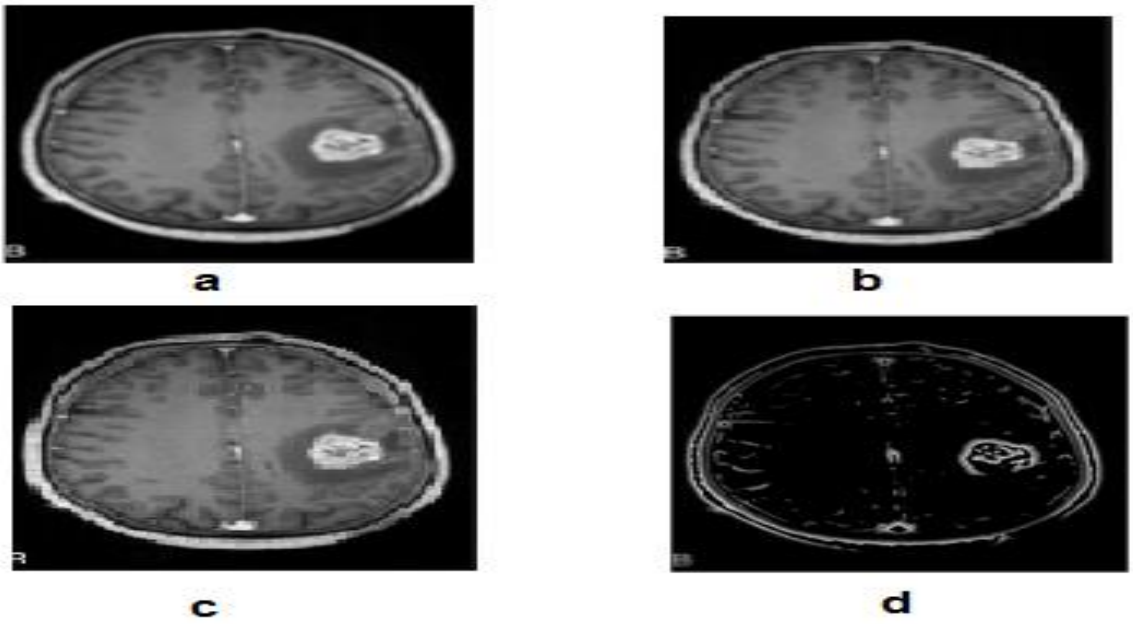


Fig.9: a: Brain input image, b: Smoothened image, c: Zero padded image, d: Image after CA based segmentation.

In order to make the tumor more visually apparent, we invert the image. This inverted image is shown in Fig. 10.

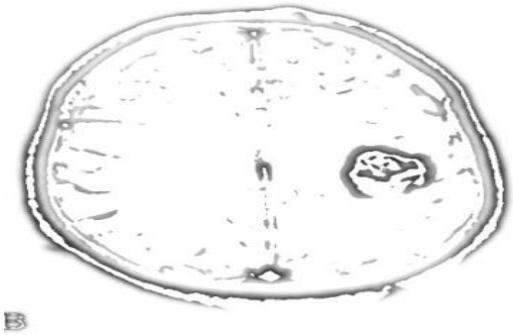


Fig.10: Inverted image

The inverted image is then binarized, which serves as an even better visual to exactly locate the tumor location in the image. This output binary image of the CA-based approach is presented in Fig. 11, where it is visible through visual inspection that the algorithm has successfully detected the tumor in the original image Fig 12. e. It is noteworthy that thresholding values have a significant impact on the segmentation outcome. Thus, they need to be fine-tuned for successful results. In addition, the final image Fig 12. e, also gives a good result from MRI image with segmented tumor as shown in Fig12. f using CA in segmentation.

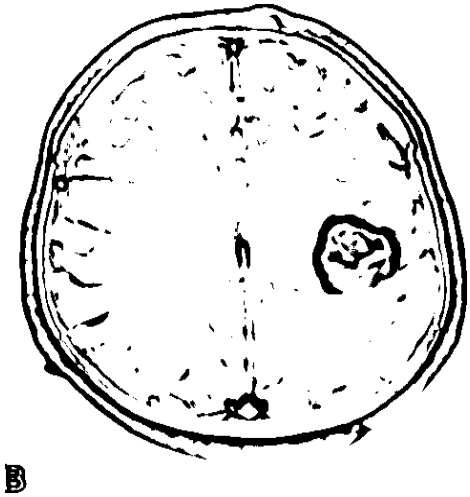
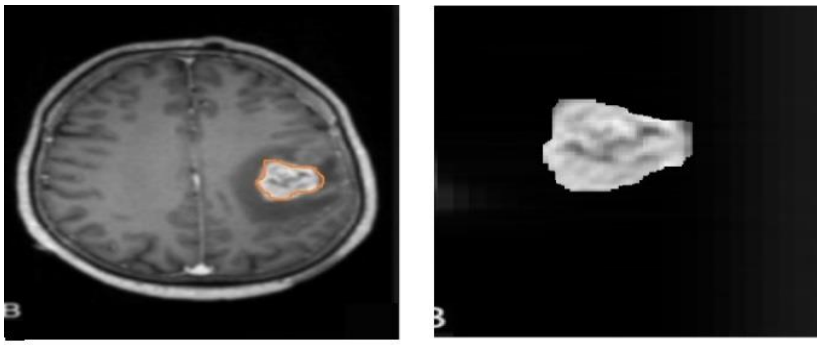


Fig. 11: Binarized image



e f

Fig.12: e: Tumor detection region, f: Segmented Tumor

4.6.1 Evaluation of results

We apply this CA-based segmentation technique on 40 tumors and 40 non-tumor images and visually confirm the presence or absence of the tumor detection, resulting in a confusion matrix shown in Fig. 13. From this confusion matrix, and by using four statistical indices, namely (FN: False_negative, TP: True_positive, FP : False_positive, TN True_negative).

We derive important evaluation measures like: F1-score, recall, accuracy, and precision. The results are assessed using several equations, including:

$$\boldsymbol{Precision} = \frac{TP}{(TP+FP)} \quad (1)$$

$$\boldsymbol{Recall} = \frac{TP}{(FN+TP)} \quad (2)$$

$$\boldsymbol{Accuracy} = \frac{(TP+TN)}{(TP+FN+TN+FP)} \quad (3)$$

$$\boldsymbol{F\,1-score} = \frac{2(precision*recall)}{precision+recall} \quad (4)$$

Therefore, the results of the performance measure evaluation are as shown in the chart below.

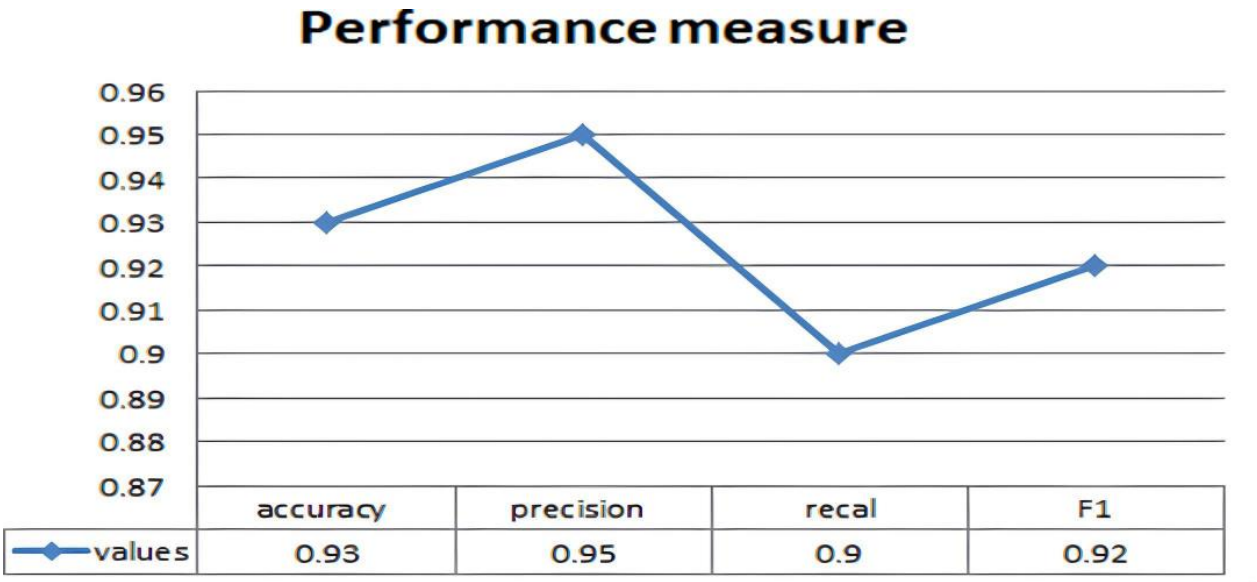


Fig.13: Performance measure

An accuracy of 93% confirms this proposed algorithm to be very respectable.

4.7 Conclusion and future work

Malignant tumors are considered one of the most deadly tumors, and many techniques have been discussed in this field, especially between 2018 and 2022. However, their results were limited, and we have discussed some of these techniques in the related works. Early tumor detection is important, as early diagnosis greatly increases the chances of survival. For this reason, an efficient and robust cytosolic-based methodology was presented in this study to detect tumors in the brain through the use of CA-based segmentation. The approved method is able to successfully isolate tumor areas from the background with an accuracy of 93%. It is a good result compared to several other methods, and this method has many benefits, especially in terms of accuracy, clarity, and speed of implementation. However, there is still room for improvement, especially since the algorithm can also be extended to 3D, and better preprocessing steps can be put in place for image optimization before CA-based segmentation, which we will work on in the future. In addition, we will also focus on integrating CA with deep learning in order to detect other tumors, giving CA a very advanced role in medical image analysis.

CHAPITRE 5 ARTICLE 3: BRAIN TUMORS CLASSIFICATION USING THE MOBILENET MODELS

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Abstract: Brain tumors are among the most dangerous diseases, as thousands of people die annually due to malignant brain tumors. Early detection of brain tumors is of great importance for surviving death, especially for malignant brain tumors. Therefore, the automatic classification of brain tumors is of great importance too because it allows specialists to determine the type of Tumor quickly and, as a result the best brain tumor treatment option. This paper proposes a method for classifying brain tumors based on MobileNet with the open-source library TensorFlow. The proposed method was trained and tested using the Kaggle Brain Tumor Classification (MRI) dataset, which contains 2363 images divided into three categories (glioma, meningioma, and healthy image). In order to assess the viability of the proposed method, we compared the outcomes of MobileNet and MobileNetV2 by checking if we can get shorter training times, simpler retraining, and higher accuracy. Indeed, the results confirmed the effectiveness of the proposed method on all data sets, with an accuracy of more than 96, 09%.

Keywords: MobileNet, Brain Tumor, Classification, Dataset, MobileNetV2.

5.1 Introduction

Brain tumors are considered one of the most deadly tumors or the cause of death for many people, and this is a result of the lack of early detection of the tumor or perhaps due to the strength of the tumor's resistance to treatment when it is difficult to save the patient's life. A large percentage of patients suffer from brain tumors, according to the national brain tumor website, an estimated 700,000 people in the United States live with a primary brain tumor, and approximately 88,970 others will be diagnosed in 2022 [148]. More than 120 different types of brain tumors vary according to their location. Certain types of brain tumors are benign as well as malignant [149, 150]. Among the essential types of benign tumors, we find Meningioma, Pituitary Adenoma,

Craniopharyngioma, Schwannoma, and Choroid Plexus Tumor, and we also find brain tumors with varying degrees from benign to malignant, for example, Glioma, Ependymal Tumors, Hemangiopericytoma, and Pineal Tumors. One of the most important research topics that must be studied extensively in order to save many lives is the study of tumor detection and classification in order to know the type of tumor and its degree of severity in order to facilitate the work of doctors in determining the classification of tumors and thus finding early treatment that helps to eliminate tumors.

Several techniques have been proposed to classify brain tumors on MRI. Among the most important of these techniques are Deep Neural Networks, in particular, the three types of neural networks; Multi-Layer Perceptrons (MLP), Convolutional Neural Networks (CNN), and Recurrent Neural Net-works (RNN) We will focus in particular on Convolutional Neural Networks (CNN), which is one of the most prominent techniques in the classification of brain tumors [151]. Convolutional Neural Network (CNN) is a class of Artificial Neural networks [152]; CNN is also known as Non-Variable Artificial Neural Net-work (SIANN), CNN has made a noteworthy contribution in many areas such as image classification and recognition. As for the main structure of CNN, there are two main parts; a convolution tool and a fully connected layer, and there are three types of layers that make up a CNN: pooling layers, fully connected layers, and convolutional layers.

1. Convolutional Layer: We use this layer to extract various features from the input images.
2. Pooling Layer: This layer is used to reduce the size of the included feature map to reduce computational costs.
3. Fully Connected Layer: used to connect neurons between two different layers. These layers are usually placed before the output layer and make up the last few layers of the CNN architecture [153].

Among the most important CNN models are LeNet, AlexNet, ZFNet, GoogleNet, VGGNet, and other models that cannot be detailed in this paper. In this work, we will focus on MobileNet, and for more information about other CNN models, we refer the reader to the following surveys [154–156], where they are described in detail. In the next section, we briefly describe MobileNet and the motivation for choosing MobileNet, as well as the objectives and contribution of this study.

5.1.1 MobileNet

This paper presents a new method for classifying brain tumors using MobileNet, a Convolutional Neural Network (CNN) architecture, which uses depth-wise separable convolution layers instead of standard convolution layers. There are other models as well [154–156], but what makes us use MobileNet unlike other models is that MobileNet has fewer parameters and higher classification accuracy and is a class of small, low-power, and low-latency models that are suitable for detection, classification, and other typical Convolutional neural network tasks [155]. MobileNets introduces two new global hyperparameters, the width, and resolution multiplier, allowing model developers to trade off latency or resolution for speed and reduce size according to their requirements.

The high number of deaths due to malignant tumors around the world and the multiplicity of tumors, in addition to the need for a large number of researches that facilitate the work of specialists in the identification and classification of tumors is one of the motivations of this study. The major goal of this study is to create an automated model that can classify brain tumors using MoblieNet and an effective network architecture in order to create precise models that make tumor classification simple, fast, and with high accuracy. In order to delve deeper into our reclassification, we trained the model using the MobileNetV2 architecture under the same controlled settings as MobileNet to see if we might achieve high performance.

In this study, we used a publicly available data set that includes two types of malignant tumors (Glioma tumor and Meningioma tumor) and one healthy category that does not contain tumors, with 500 images in the healthy classes, 926 images in the malignancy (Glioma Tumor) and 937 images in the meningioma tumor. The main purpose of using this data set is the availability of adequate metrics to evaluate the proposed method and compare the performance of different structures to construct an effective model that can readily classify tumors. Among the contributions this work makes is the design and development of a new method based on the MobileNet model capable of classifying brain tumor types with shorter training times, easier retraining, and higher accuracy. In addition to evaluating the model through various experiments on the brain tumor MRI dataset and improving the overall accuracy and validity of the results.

In order to be able to highlight the proposed method and establish its effectiveness, we focused on evaluating the results and performance based on the comparison of several parameters such as

training loss, validation loss, training and validation accuracy. The rest of this paper is organized as follows. Section 7.2 is devoted to the related work. Section 7.3 describes method and materials; result and discussion are introduced in section 7.4. Finally, a Conclusion and Future work is presented in section 7.5.

5.2 Related work

A brain tumor is an abnormal tissue mass in which cells grow and multiply uncontrollably. More than 150 different brain tumors have been documented [139], but the two main groups of brain tumors are called primary and metastatic tumors. Due to the presence of many types of tumors, many techniques have been proposed to classify tumors in order to study the treatments of each class to determine the degree of its severity. The paper [157] proposed a CNN-based dense EfficientNet to classify 3260 brain magnetic resonance images into four categories (meningioma, pituitary, glioma, and no tumor). The results proved that the accuracy of the proposed model is 99.97% for training and 98.78% during testing.

The investigation of a convolutional neural network (CNN) to identify brain tumors from X-ray images is described in the paper [158], where the proposed method was more significant. The presented model focuses on improving accuracy while using the transfer learning strategy, where three models are adopted: VGG19, InceptionV3, and MobileNetV2. Results Shown MobileNetV2 provides higher accuracy of 92%, InceptionV3 has an accuracy of 91%, and VGG19 has an accuracy of 88%.

The paper [159] proposed a Mobile Network architecture to classify brain tumor types using a data set of 2475 images. The data set was split into three sections: 10% was used for testing, 80% for training, and 10% was used for validation. In this experiment, the test accuracy was 94%.

From another side, we find that paper [160] studies the classification of brain tumor images based on several classifiers such as (AIFC), (SIFC), (ASIFC), (AIC), (SIC), (ASIC), and finally CFIC. The Kaggle Brain Tumor Detection 2020 dataset was also used to train and test the proposed classifiers; CFIC performed better than all other suggested approaches, with an accuracy rate of 98.9794%.

Assigning the output layer of the Inception ResNet v2 to a deep dense network and a softmax layer, the paper [161] studied the classification of brain tumours into three classifications. The aim was to improve the classification accuracy of the proposed model. The performance rate of the proposed method on a data set that contains 3064 images is 99.69%.

In paper [162], a new classification algorithm for the MRI is proposed. Initially, MobileNetV2 was used to extract features from the input brain images. After that, three different feeding networks were trained: Schmidt neural network, random vector functional-link net, and extreme learning machine. The verification result reveals that the proposed method can perform well, with an accuracy ratio of 96%.

In this paper [163], the tumor was segmented using (FCPPN). The proposed classification technique was used to track down the specific location of the tumor or the type of tumor, the Multiple Attention Channel Convolutional Neural Network (MTCACNN). After grading the tumor, the overall prediction of survival is the task of testing. The overall prediction is named Multi-Tier Zernike (MTZR) and is implemented by handcrafted features; the results showed that the proposed method might be useful in classifying tumors with an accuracy of 98.18%.

This paper [164] proposes an automatic classification of brain tumor using a classification of convolutional neural networks (CNN). Small kernels were used to secure the implementation of the deeper architectural design. This method showed good results, as the accuracy rate reached 97.5%.

For optimizing CNN weights using the Genetic Algorithm (GA), the paper [165] proposes a method to design a CNN model to facilitate the classification process, and various experiments on the BreakHis dataset evaluate the model. Since the model was trained with three different optimizers (dam, mini-batch gradient descent, and GA), the results obtained in this paper show that the accuracy of the CNN model trained through GA is 85%.

This paper [166] proposes an approach called DenseNet121-AnoGAN to classify histopathological images of the breast into benign and malignant categories. The performance of the proposed approach was evaluated on the publicly available BreaKHis dataset, and the best accuracy of 99.13% and a best F1 score of 99.38% were obtained. The results of this work also showed that classification networks with AnoGAN have better performance than those without AnoGAN.

The paper [167] aims to perform multiple classifications of brain tumors for early diagnosis using a convolutional neural network (CNN). Three different CNN models have been proposed for three various classification tasks. The proposed CNN models are compared with other latest popular CNN models such as GoogleNet, ResNet-50, Inceptionv3, VGG-16, and AlexNet. As a result, brain tumors are detected with an accuracy of 99.33% based on publicly available clinical data sets.

Ohata, E. F.et al. [168] propose the automatic identification of eight tissue types found in the histopathological evaluation of CRC. These tissues are Support Vector Machine (SVM), k-Nearest Neighbors, Naive Bayes, Multilayer Perceptron, and Random Forest; the evaluation results of this work were good, with the evaluation accuracy reaching 92.083% and F1-Score 92.17%.

Javaria A et al. [169] explained several methods used to detect brain tumors through magnetic resonance imaging to help researchers. The most important things discussed in this paper are data sets, segmentation, techniques, classification, and deep learning. The results of the majority of the methods discussed have good accuracy.

The paper [170] looks at how some models of breast cancer applied to ultrasound images are classified. Whereas the proposed model shows 100% accuracy, the previously trained model shows 92% accuracy.

Krizhevsky A et al. in paper [171] proposes to train a convolutional neural network to classify 1.2 million images in the ImageNet LSVRC-2010 competition into 1000 different classes [172]. It used an organization method called “dropout” which proved effective in the test data; the results were perfect, which is much better than the previous latest methods.

Transfer learning is introduced in this study [173] as a means of reusing previously trained exemplary information for a different task. In categorization difficulties, transitional learning can be applied to classify images, this article also uses VGG-16 in conjunction with a deep convolutional neural network.

Table 1: Comparison of existing techniques.

Ref	Year	Author	Dataset	Architecture	Objective	Performance
[157]	2021	Dillip et al	Brats dataset 2018	EfficientNet	BrainTumor Classification	Accuracy=97%-99.97%
[158]	2021	Tahia et al	Kaggle database	CNN	BrainTumor Classification	Accuracy= 91%-92%
[159]	2021	Tsamara H	Brats dataset 2015	Mobilenet	BrainTumor Classification	Accuracy=94%.
[160]	2022	Srinath et al	Kaggle dataset	CNN	BrainTumor Classification	Accuracy=98.97%
[161]	2021	Srinath k ,et al	BTDS dataset	ResNet v2	BrainTumor Classification using CNN	Accuracy=99.69%
[162]	2020	Siyuan et al	ImageNet dataset	MobileNet and Feedforward	BrainTumor Classification using MobilNet	Accuracy=96%
[163]	2021	Fathima s et al	BRATS dataset 2015	CNN	BrainTumor Classificatio and syrvival prediction	Accuracy=98.18%
[164]	2018	Seetha J et al	BRATS dataset 2015	CNN	BrainTumor Classification using CNN	Accuracy=97.5%
[165]	2021	KhatereH et al	BreakHis dataset	CNN	Evolving convolutional neural networkparameters throughthe genetic algorithmfor the breast cancerclassification problem	Accuracy=85%
[166]	2020	RUIM et al	BreaKHis dataset	AnoGAN	Classification of Breast Cancer Histopathological Images	Accuracy=99.13-99.30%
[167]	2021	Emrah I et al	RIDER dataset	CNN	Multi-Classification of Brain Tumor MRI Images	Accuracy=98.14%

[168]	2021	Elene F et al	Colorectal Histology dataset	CNN	classification of histological images of colorectal cancer	Accuracy=92.083 %
[169]	2020	Javaria A et al	Benchmark datasets	CNN	Brain tumor detection and classification	Accuracy=92.083 %
[170]	2020	Mehedi M et al	BUSI datase	CNN	Diagnosis of breast cancer	Accuracy=92%
[171]	2020	Krizhevsky A et al	ImageNet dataset.	CNN	ImageNet Classification with Deep Convolutional Neural Networks	Accuracy=96%
[172]	2019	Taranjit K et al	Harvard repository dataset.	VGG-16	Automated brain image classification Neural Networks	Accuracy=96%
[173]	2021	Bansal M et al	Benchmark dataset	VGG19	image classification using VGG19	Accuracy=93.73 %
[174]	2019	Tammina S et al	imagenet dataset	VGG 16	Images Classification	Accuracy=95.40 %
		Our work	Kaggle dataset.	MobileNet	Brain Tumors Classificatio	Accuracy=96,09 %.

Table 1 reports the main features of the various classification techniques proposed in the literature.

Among these features, we have the used dataset and architecture, the objective and the accuracy, where we noticed a variation in the performance ratio from one technique to another. On the other hand, in the papers in which MobileNet was used [13] and [16], The performance accuracy of the two studies was 94% and 96%, respectively, on the training data set, which is lower than the result of the proposed method as described in the results and discussion section. The overall accuracy of the models in Table 1 also generally decreases when the size and total number of parameters are reduced. We used a new method to classify tumors by relying on an efficient network architecture to build very small and low latency models that allow easy classification of tumors and in the fastest time to implement, where improving latency and improving accuracy were among our goals, We have improved accuracy along with reduced size, fewer layers, lower average computation time, and lower processing compared to the methods listed in the table. We evaluated the MobileNet architecture for its effectiveness in classifying tumors; In addition, we trained our model using the MobileNetV2 architecture under the same conditions as MobileNet in order to verify and learn

more about the highest attainable performance; the results showed the effectiveness of the proposed method.

5.3 Method and Materials

The data set, tools, and methods used in our work are discussed in this section.

5.3.1 Dataset

This paper used a public data set available to all and selected from Kaggle. This data set was created in 2021 by Kanchan S et al. and was downloaded by more than 13980 people [174], due to its effectiveness in evaluating the quality of the algorithms whose effectiveness is to be studied, in addition to its availability on three classes of brain tumors, where each class contains several cases of tumor that differ in terms of location, size, speed of spread, in addition to a healthy class that does not include tumors, this data set distributed between training and testing. Our work will focus only on two classes of malignant tumors, the first type of malignant tumor studied is the glioma tumor, where the training set for this class consists of 826 images and 100 images as a test set. The second type is meningioma tumor. The training set for this type consists of 822 images. The test set consists of 115 images. Finally, the class that does not contain a tumor consists of 395 images as a training set and 105 as a test set. Table 2 describes the data set used.

Table 2: Description of the selected data set.

	Training	**Testing**
Glioma_tumor	826	100
Meningioma_tumor	822	115
No_tumor	395	105

We trained the dataset using MobileNet architectures and evaluated the results according to four performance evaluations: Precision, Accuracy, Recall, and F1-score. Some samples in our dataset are presented in Figure 1.

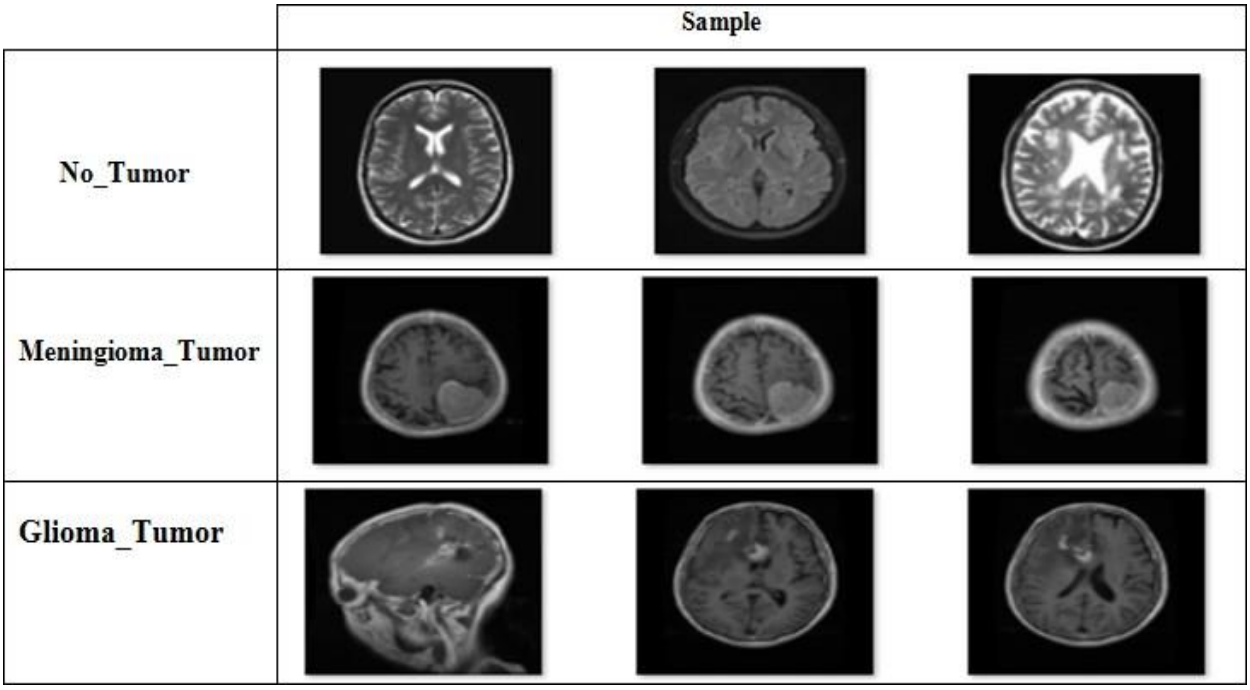


Fig. 1: Brain tumor and healthy image.

5.3.2 Tools

In order to investigate the proposed approach, we used three tools in this work:

- ***Python***: is suitable for data processing, especially when dealing with deep learning algorithms.
- ***Google Collab:*** is particularly suitable for machine learning and data analysis as it allows anyone to write and execute Python code through the browser.
- ***MobileNet model*** with the open-source python library and TensorFlow.

5.3.3 Training process and implementation

This section describes the steps for training a MobileNet model and performing an experimental setup of a brain tumor model using MobileNet architectures and the TensorFlow framework. Moreover, since the learning method in the MobileNet architecture is compatible with deep learning, we tried to define the input data and add additional detailed labels to train, prepare and

label the data, which will help the MobileNet model to learn and understand what the output predictions are. Classified data sets are always required to train and evaluate a particular model in order to classify brain tumor images accurately (see Figure 2).

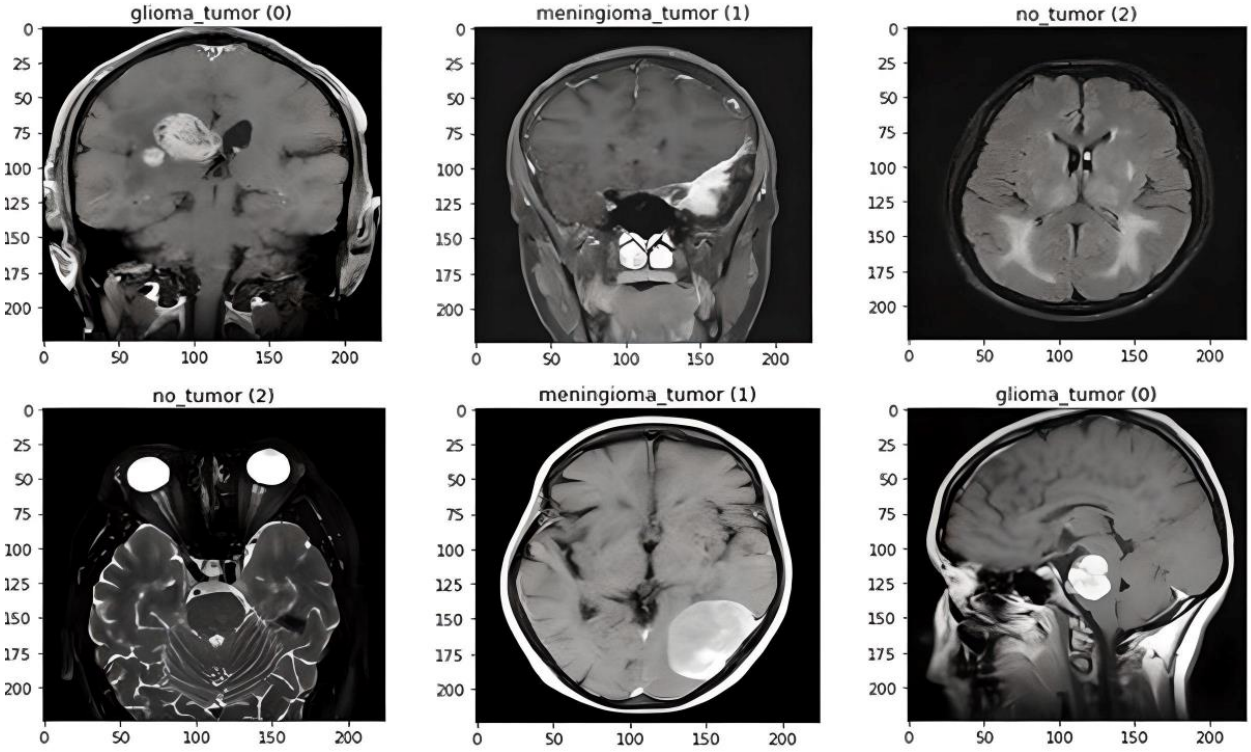


Fig. 2: Example of labeled Brain Tumor data set.

In the current study, MobileNet uses eight convolutional layers designed to classify images, and each image is used multiple times during the training process. Therefore, the learning algorithm will thoroughly test each training batch while training the model. The dataset is split into several batches, consisting of three classes: meningioma, healthy category, and glioma.

The proposed model's system configuration is based on a learning rate of 0.001, a correlation of 0.8, a filter size number of 10, a batch size of 32, and the optimizer utilized for this approach is Adam's optimizer, which does not suffer from any performance decreases in accuracy, which mean we should see less training loss and validation loss with each period.

In addition, the current experiment structures' hyperparameter settings were used to evaluate and rely on classification results under similar scenarios. Furthermore, the hyperparameter settings of the current experiment structures relied on similar conditions to evaluate and rely on the

classification results. For the time being, we have defined the number of epochs at 100, and the accuracy may vary at the end of each epoch, which means the model will rate its performance from the training set to the validation set at the end of each epoch. Finally, the model should be terminated once the accuracy and loss have stabilized. The following sections will go into more detail about the proposed model.

5.4 Results and discussion

In this study, we worked on designing and developing a MoblieNet model for classifying and recognizing classes of brain tumors. We also tested the proposed method on a data set of 2363 images distributed in three classes (glioma tumor, meningioma tumor, healthy) between testing and training (see section 7.3.1). We used the same data set to prove the impact of different architectures and controlled all variables under the same conditions (hyperparameters, methodologies, architecture). We also looked at how to choose an optimizer. Performance varies based on the image selected, with the image selection process being random, and each parameter being tested separately to find the ideal setting for the architecture. The results obtained for classifying brain tumors and evaluating the performance of the proposed method are discussed in the following sections.

5.4.1 MobileNet model implementation on Brain Tumor Dataset

In this section, we examined the performance rate for classifying brain tumors using MobileNet to perform prognostic testing on Brain Tumor Datasets. We also used the Adam optimizer as requiring fewer parameters to adjust and a faster computation time and is generally better than all other optimization algorithms [175]. We focused on working on comparing and studying the outcomes throughout 100 epochs. As a result, and as shown in Figure 3, where we compared the results based on model accuracy and model loss using the training and validation sets, the usefulness of the proposed method has been proved as follows:

1. Model loss: The result proves that the training loss is 0.0069, and validation loss is 0.1652.
2. Model accuracy: The result proves that the training accuracy is 0.9980 and validation accuracy is 0.9323.

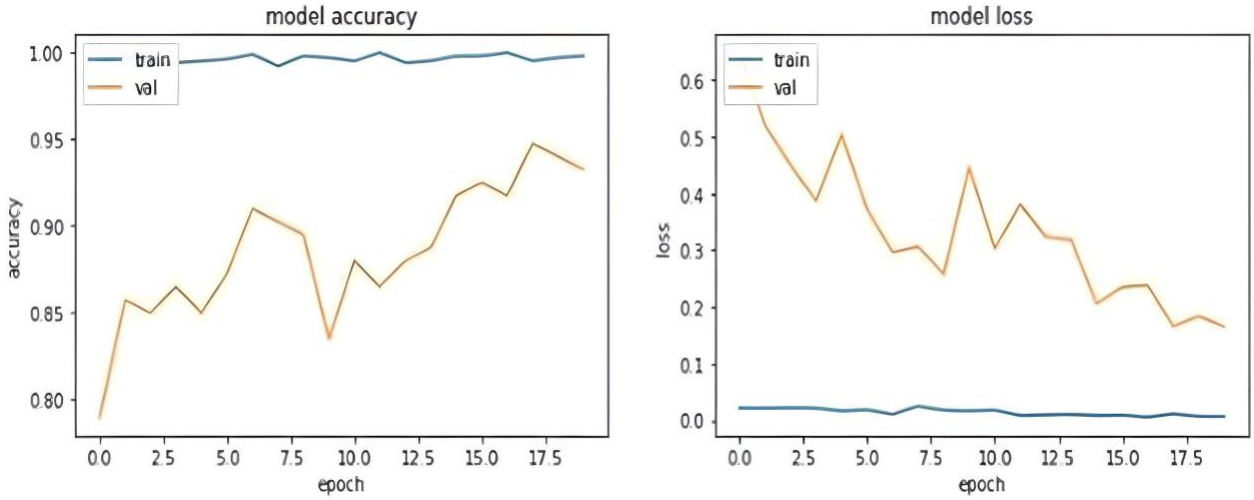


Fig. 3: Comparison of accuracy and loss curve based on model accuracy and model loss

After checking the outcomes of model loss and model accuracy, we will now attempt to analyse the validity and performance of our MobileNet model architecture over 100 epochs with the same hyperparameters as before, where we focused on four elements: accuracy, validation accuracy, loss and validation loss, for a comprehensive study from all aspects. The accuracy of the proposed method using the data set has reached a very high rate of 100%, and the validation accuracy has reached 0.9323. As for loss, its rate did not exceed 0.0069. In the same context, we found that the validation loss was less than 0.1652% (see Figure 4). All of these results validate and demonstrate the utility of our MobileNet model architecture.

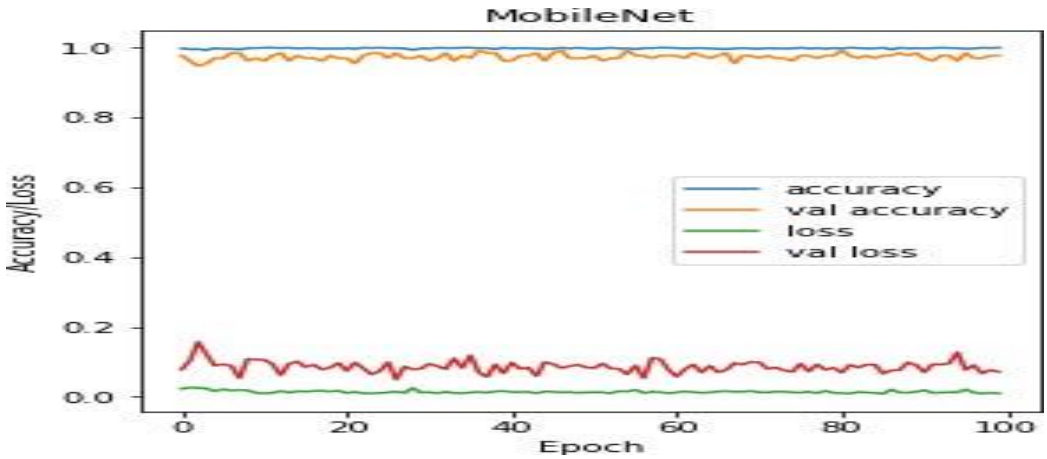


Fig. 4: The proposed method's accuracy and loss curve utilizing the MobileNet model

In order to further confirm the correctness of our model, we used MobileNetv2 under the same conditions as MobileNet to check and learn more about the highest accessible performance and get faster training times, and we compared its results with MobileNet, given that MobileNetV2 uses inverted residual blocks to improve performance on multiple tasks and criteria. In addition, it also has a much less number of parameters than the original MobileNet. Furthermore, we used 100 epochs and a learning rate of 0.001 in this comparison investigation. As illustrated in Figure 5, our MobileNet model architecture achieved 100% training accuracy and 98.20% validation accuracy. However, we found that MobileNetV2 was similarly effective in classifying brain tumors, with a training accuracy of 100% and a validation accuracy of 99.87%, which were higher than the validation accuracy of the MobileNet model.

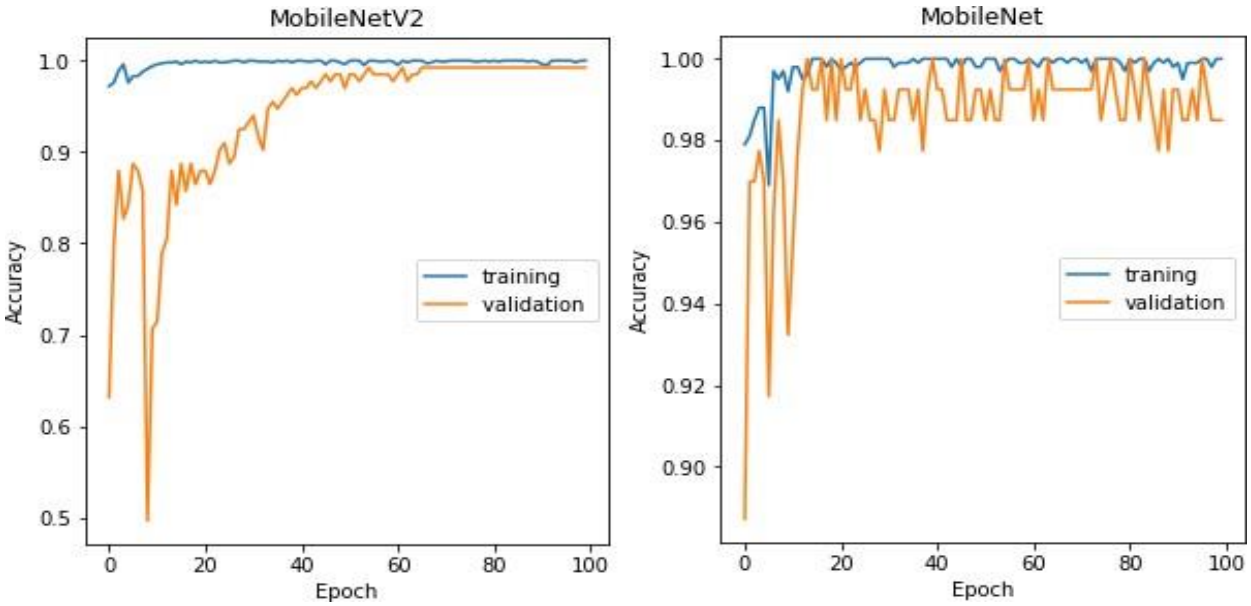


Fig. 5: Training and validation accuracy using MobileNet and MobileNetV2 Structure.

On the other hand, to give a clear idea of the accuracy and ways in which predictions are made in classifying brain tumors, we describe the details in the following section.

5.4.2 Performance mesure of classification

To evaluate the results, we focused on the confusion matrix, which is a matrix that measures classification quality and highlights prediction outcomes for a classification problem. We therefore

summarized the results of a classifier test that distinguishes between three classes (Glioma tumor, Meningioma tumor and No tumor). A feature of the confusion matrix is to evaluate mostly performance measures such as Precision, Accuracy, Recall, and F1-score. Several equations are used to evaluate the outcomes:

$$\boldsymbol{Precision} = \frac{\boldsymbol{TP}}{(\boldsymbol{TP+FP})} \quad (1)$$

$$\boldsymbol{Recall} = \frac{\boldsymbol{TP}}{(\boldsymbol{FN+TP})} \quad (2)$$

$$\boldsymbol{Accuracy} = \frac{(\boldsymbol{TP+TN})}{(\boldsymbol{TP+FN+TN+FP})} \quad (3)$$

$$\boldsymbol{F\,1\,-\,score} = \frac{\boldsymbol{2(precision*recall)}}{\boldsymbol{precision+recall}} \quad (4)$$

Figure 6 illustrates the confusion matrix that generates a reminder of the classification model, and as shown, the model reached 98.20% as validation accuracy of brain tumors and 99.87% training accuracy.

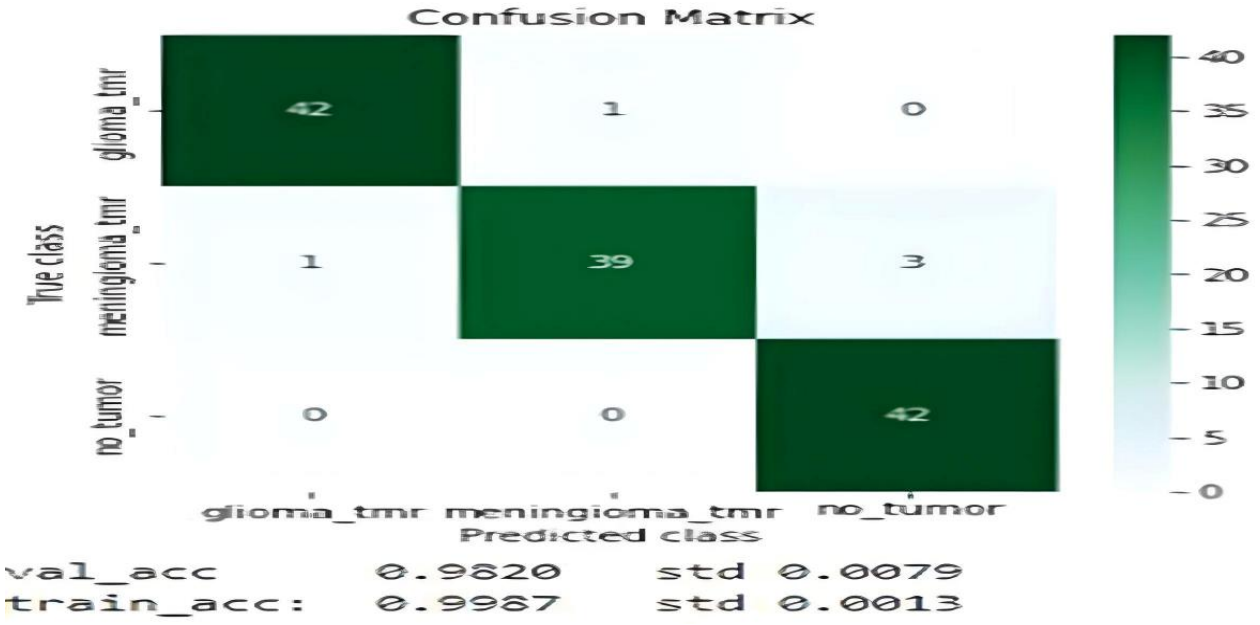


Fig. 6: confusion matrix

The proposed method was also proven to be effective, with an accuracy of 96.09% on the total images of the data set and a very high percentage on all performance measures on the three classes of the data set. The acquired results are shown in Figure 7 below.

	precision	recall	f1-score	support
0	0.9767	0.9767	0.9767	43
1	0.9750	0.9070	0.9398	43
2	0.9333	1.0000	0.9655	42
accuracy			0.9609	128
macro avg	0.9617	0.9612	0.9607	128
weighted avg	0.9619	0.9609	0.9606	128

Fig. 7: The proposed method's accuracy and loss curve utilizing the Mobilenet model.

As shown, Figure 7 illustrates the high Precision ratio, which ranged between 93.33% and 97.67% on the data set, as well as the high Recall ratio, which ranged between 96.12% and 97.67%, and the high F1-score ratio, which was also 97.67%.

As a conclusion, our proposed model for classifying brain tumors was effectively implemented, evaluated, and a great performance classification result was achieved.

5.5 Conclusion and future work

Many malignant brain tumors require careful studies to identify and find the appropriate treatment. In this context, the issue of tumor classification is significant for its importance in classifying the tumor and facilitating the process of identifying it. In the proposed method, we initially relied on two models, the accuracy model and the loss model, by studying the training accuracy and the validation accuracy rate, and the results were very satisfactory, as the validation accuracy rate for an accuracy model reached 0.9323 and the training accuracy percentage in the same model is

0.9980, either As for the loss model, the validation accuracy ratio is 0.1652, and the training accuracy rate is 0.0069. Then we compared the results using the MobileNet and MobileNetV2 architecture to highlight the proposed method's effectiveness. Actually, the results showed the effectiveness of the proposed method over 100 epochs, where the training ratio for both MobileNet and MobileNetV2 reached 100%, while the validation rate knew a slight increase for MobileNetV2 Compared with MobileNet, where the validation ratio for MobileNetV2 and MobileNet was 98.20% and 99,87% respectively. We believe this study will be a rich reference for those wishing to search for the classification of brain tumors, as it facilitates the work of researchers in this field. In addition, it will also help in solving many problems related to the study of brain tumors. In our future work, we will generalize this method to other tumors as well as use new methods based on the current method, whose goal will be to classify and predict tumor growth and compare it with the latest methods.

CHAPITRE 6 ARTICLE 4: MODEL CHECKING ON MEDICAL IMAGING - A REVIEW

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Abstract: Recent works on the use of model checking have shown great promise for a diverse set of applications, particularly for signal and image analysis. Medical imaging is an area of keen interest for researchers where model checking can be utilized effectively to develop and analyze frameworks. These frameworks allow for automatic and semi-automatic contouring on regions of interest in an image. In this paper, we analyze recent works that build on spatial logic to develop and derive operators and tools in order to identify regions of interest that can be tumorous regions or non-tumorous regions. We also review potential challenges associated with spatial model checking techniques for segmentation in medical images, including variability in truth data and procedural easiness for everyday use in clinical setting.

Keywords: Model Checking, Segmentation, medical images, Tumor.

6.1 Introduction

Model checking is the method involved with checking whether a given construction is a model of a given legitimate formula. The idea is general and applies to a wide range of rationales and reasonable designs. A straightforward model-checking issue is trying to determine whether a given equation in the propositional rationale is fulfilled by a given structure.

Model checking is most frequently applied to equipment plans. For programming, in light of undecidability, the methodology can't be completely algorithmic; normally, it might neglect to demonstrate or refute a given property.

Model checking finds its role in a wide variety of applications. is used for various purposes, including ensuring the correctness of the property and reducing the errors of programs that are in the process of development; traditional model checking is composed of three major steps:

• Formal model of the system; that is dependent upon confirmation by making a model of the framework in a language that fits the model checker's feedback language.

• Give a specific system property; that ought to be demonstrated. In other words, an inquiry regarding the system's way of behaving is figured out that ought to be replied by the model checker.

• The model checker indicates to the device whether a specified system feature is satisfied. If the system property cannot be checked, a counterexample is produced to indicate error source in the simulation of the model.

The figure below shows a typical model checking work-flow

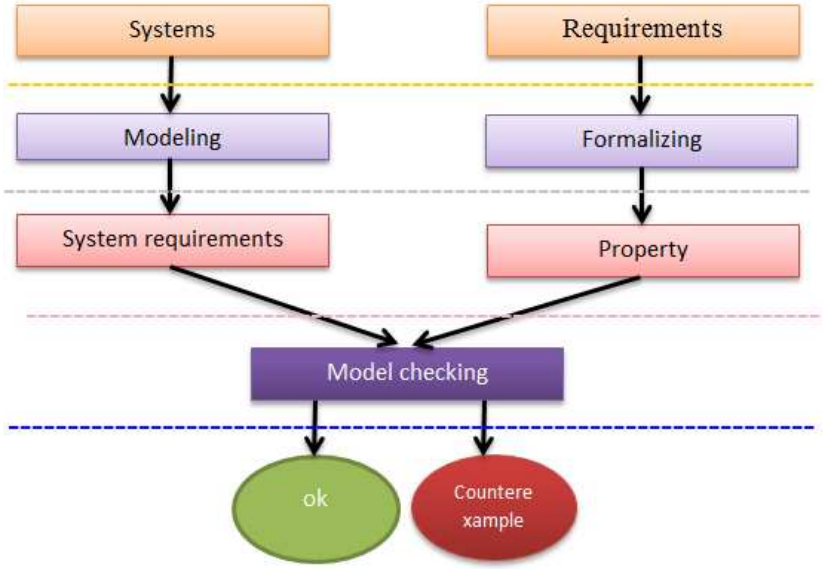


Fig. 1 A typical model checking work-flow

There are also countless examples of applications in Model Checking, especially in the domain of image processing on medical images, including image segmentation, image contouring, image filtering, and image classification. These kinds of computations are associated with the spatial features of the image. For example, diagnosis with the assistance of a computer is aimed at the classification of certain regions in an image which could correlate to a disease perhaps [176]. Similarly, image segmentation methods are aimed at identifying certain areas in an image that exhibit a particular feature within an image [177]. Typically,

this is with the underlying goal of segmenting out the region of interest. These regions could correspond to tumors or lesions for instance, based on the nature of application. Another way is to automatically form contours on the target areas that could correspond to organs in the body with the underlying goal of identification of such organs that are at risk. Such methodologies find their applications in radiotherapy [178]. In addition to these, there are many other methods that include indicator-based schemes where computation is done on the acquired images to compute the indicators that not only facilitate diagnostic procedures but also aid in understanding disease-specific characteristics. These indicators may then also be extended to the monitoring of any treatment and thereby, predict treatment outcomes accordingly [178]. Example of one such indicator is mean diffusivity [179]. This review paper is primarily aimed at comprehensively understanding and assessing the past works for model checking on medical images. While that encompasses a large spectrum of research areas, the focus will mainly be on segmentation-based approaches. Medical imaging constitutes multiple modalities. Typically, in clinical setting and as well as in routine checks, the magnetic resonance (MR) images are

qualitatively assessed. This is done mostly by looking into the contrast in the image which is essentially a marker for the presence of any hyperintense tissue [180]. The core idea is to realize segmentation. However, manually finding these regions of interest is laborious, time intensive as well as error prone. This also becomes subjective in nature. Thus, in order to overcome such limitations, segmentation techniques have evolved over time, particularly with the development of algorithms that are both automatic and semi-automatic in nature. Such methods are considered more accurate and reliable for isolating tumorous regions in an image. These algorithms, since they are independent of human judgment for tumor delineation, are also reproducible [181]. Brain segmentation is in fact one of the research areas that has realized a newfound importance. Segmentation of these kinds of medical images has now seen many applications, particularly in neuroimaging. Recent studies confirm this as an active area of research [183, 187]. It is customary to divide the segmentation methods into two major categories, known as generative models and discriminative models [181]. The models that are generative in nature rely particularly on prior information about appearance of specific brain tissues whereas the models that are discriminative find their dependence on extraction of a huge number of image features that are low-level, for instance, local texture features or histograms [181]. The fundamental principle of segmentation,

widely used in a range of techniques, is to exploit the changes in intensity and texture in different pixels in the image [188]. This is mostly used in the diverse range of semi and fully automatic segmentation techniques that include, for instance, thresholding, region growing, and clustering. Several such techniques can also be combined to form hybrid methods. Neural networks and support vector machines are examples of semi-automatic techniques. However, automated segmentation techniques constitute the current gold standard [181], [189]. A challenge, however, in the segmentation of brain tumors is that the areas are defined only through the variations in the luminosity of image pixels with respect to the luminosity of the surrounding tissue background. This is a great challenge for automated systems since even manual segmentation experts reflect significant variation. In addition to the subjective assessment of experts, such variations are also due to the variations in the images of different patients owing to different imaging modalities.

6.2 Datasets used for brain tumor detection.

There are many data sets that have been used in brain tumors, especially with the model checking, the most important of which is BRATS, which identified shifts from 2017 to 2019, where we find BRATS 2012, BRATS 2013, BRATS 2015, BRATS 2016, BRATS 2017, BRATS 2018, and there are other types of datasets such as DICOM, TCIA, MICCAI in the table Below we find the most important datasets.

Sr	Datasets	Description
1	***ISLES***	A total of 103 stroke patients' brain images from this dataset are provided.
2	***Local Har-vard***	This is a collection of distinct brain MRI scans from a clinical image segmentation dataset.
3	Figshare	It serves as a repository for publishing citeable and shareable datasets.
4	***BRAINIX***	This dataset for segmenting brain images includes the T1, T2, and flair images.
5	***ABIDE***	Images from MRI scans taken from autistic patients make up this dataset.

6	***BRATS 2012***	a sizable collection of brain MRI scans with the tumor and edoema locations manually identified
7	***BRATS 2013***	Two class labels are included in this dataset to distinguish between high and low-grade gliomas
8	***BRATS 2015***	a segmentation dataset for brain tumors with 220 high-grade and 54 low-grade gliomas
9	***BRATS 2016***	dataset for segmenting brain tumors using the same BRATS 2015 training data
10	***BRATS 2017***	285 images of brain tumors are in this dataset.
11	***BRATS 2018***	285 The collection consists of multimoda 4 modality 3D brain MRI images.

The rest of this paper is organized as follows. Section 2 is devoted to the related work. Section 3 describes the Methodology. Result and Discussion are introduced in section 4. Finally, a Conclusion and Future Work are presented in section 5.

6.3 Related Work

There is a lot of literature on model checking as a technique for various applications. In [190], the author survey and present a historical account of algorithmic requirements of directed model checking. A broad range of areas is explored in [190], including bug-hunting techniques for mitigation of state explosion problem, prioritization of successor selection, as well as adaptation of algorithms to time based automata and probabilistic domains. In [191], the review is primarily aimed at algorithmic verification of probabilistic model checking where different probabilistic models along with their algorithms are discussed. The reliability and dependability of these models are also discussed. Extensive work in [192] reviews model-checking technology as a technique that has emerged as a powerful approach for the automatic verification of hardware systems. The work identifies other areas of application to translate the verification problems in proper model-checking questions [192] and also presents a taxonomy of model, property and model checking as an approach. In the survey by [193], formal verification of state charts with model checking is

reviewed where a key observation among many different state charts used is that the different approaches find their reliance on the translation of hierarchical structures onto flat representations of the input language, thereby, making it difficult to scale to industrial models. This is fundamentally due to the state space growing exponentially with flattening. [194] presents a classic overview of programmable logic controllers software in terms of verification using model-checking practices. With programmable logic controller systems, the constraint is real time functionality, particularly in production; thus, an assessment of the software using model checking for verification is critical. A very sound theoretical overview is presented by [195] regarding the practical application of model-checking schemes to verify multi-threaded software systems. The focus is mainly on the automata theoretic method of verification along with its problems. Another survey on automata theoretic approaches is done by [196], but the primary focus is on the correctness of probabilistic systems (finite-state) with respect to the linear time properties.

[197] presents a comprehensive review with regards to the critical system design in light of symbolic model checking. A detailed review of model-checking techniques is discussed along the domains of information sciences. The review by [198] incorporates verification of web service using model checking to better understand data flow, requirements, and quality of service. This systematic review takes fifteen years of literature on web service into account. In [199], the authors review their experiences on applying model checking for verification of arbitration logic of a vehicle control system.

6.3.1 Spatio-temporal model checking for medical imaging.

Utilizing model checking framework in a spatial setting for medical imaging is a relatively recent area of research. This is also reflected by only a small number of publications in the field. However, the existing works, although few, are comprehensive. For tumor detection, machine learning has been leveraged on features of images for validation with Spatio-temporal model [100, 101].

In [102] spatio-temporal model checking has been utilized for biological processes analysis with a strong focus on multi-scale aspects. However, when it comes to fully automated approaches, it is pertinent to mention the resounding impact of machine learning-based techniques where deep

learning is effectively utilized to model the non-linearity's in the data so as to draw meaningful conclusions [103].

For in vivo images, the segmentation done manually is still considered a standard but it has some associated disadvantages. Manual segmentation takes the clinician's focus and attention, rendering the entire process time consuming. In addition to that, the skill level needed as well as the working hours required for careful identification, also makes the entire process expensive in nature. Furthermore, the subjectivity involved in the judgment between one clinician, and another makes the manual segmentation process very difficult to reproduce and introduces unwanted human errors in the pipeline. Although deep learning and machine learning techniques have delivered remarkable results for detection, classification, and pattern recognition based tasks, a precursor to the success of such techniques is in fact the reliability and quality of the datasets. Similarly, deep learning based frameworks require that the datasets are very large and are able to capture sufficient variations. The advantage of deep learning-based techniques is that from raw data, it is able to extract features in different layers and then make key inferences. One point of consideration when employing these techniques in a supervisory framework is the requirement of ground truth labeling of the data. This is important and sensitive as it involves the annotation of data based on the clinician's inference of the ground truth which brings subjectivity in the assessment between different annotators. According to a study [188], this intra-expert and interexpert variability could be as high as 35% and 30%, respectively, for manually segmenting tumor regions in brain MRI images [104]. Therefore, it is of great importance that interactive model-checking methods are utilized in order to drastically enhance the generation of these ground truth annotations in a way that is relatively more reproducible and efficient.

The area of Spatio-temporal model checking is a relatively recent area of research and thus, does not have significant literature available on it. Nonetheless, some works are important to mention as part of the discussion such as the works in [105] where a spatial extension of the signal temporal logic, that is linear and time-bounded, is implemented, providing a framework for stochastic population models. The framework is valid for situations where agents lives and can exhibit movement in a discrete representation of space. This signal temporal logic is in effect, a graph based approach with finite cost based weighted graphical connections with the framework having a single spatial operator that is similar to the operator defined in the work of [106]. This is then

followed by an extension that included the bounded surrounded operator which essentially extends the surrounded operator in the works of [107] but with additional requirements. In [198], the bounded surrounded operator has been alternatively characterized as a derivation from a basic operator.

In [108], the author takes a different approach where instead of model checking using purely spatial logics, the author focuses on a mixture of approaches taking spatial, statistical, and algorithmic frameworks. This entails that distance as well as texture operators are also introduced along with the spatial operators. The distance based operators may be appended to the spatial logic in a multitude of ways. Typically, these are represented by real numbers and are defined on certain semantics satisfying a particular constraint. One instance of a distance operator is a 'doughnut operator' that meets the distance criterion between two distance limits. [108] also considers closure models that are quasi discrete as a starting point, defining such a model by a binary relation on a set of points. However, it is also noted that such a model does not include information on distances. Thus, there is a proposition to add a distance operator [108]. Distances in medical imaging are typically based on Euclidean distances or symmetric graphs. The idea of focusing on shortest path distance in weighted graph is very intuitive. In addition to that, there are other notions that include sampling the spatial grid initially that can be done in Euclidean space on a regular grid, with some connections on edges based on a connectivity scheme. For example, considering a two-dimensional space, it is customary to consider four or eight neighbors. However, regardless of the connectivity and sampling scheme, there is always a complexity and a challenge in medical imaging due to the nature of variation in the voxel in each dimension of the image. The operators related to texture analysis are primarily designed for finding and analyzing patterns in medical images. It is often the case that these patterns are imperceptible to the human visual system, own to their subtle characterization with respect to brightness, color, or size [209]. That is the reason texture analysis based schemes find their applications in a wide variety of applications, even within medical imaging [210]. These have been proven to be instrumental in application in diagnosing prostate cancer [211] as well as analyzing tumor heterogeneities [212].

6.3.2 Techniques used with model checking for analyzing the medical image.

Many techniques are used with Model Checking in the analysis of medical images, the most important of which is Texture analysis, which has also found its application in dynamic contrast enhanced MRI of breast imaging for the detection of and segmentation of malignant lesions [213]. In addition to that, there is extensive work on computer aided diagnosis and segmentation using texture based analysis [214], including diagnosis of pulmonary nodules [215]. Classification and segmentation using texture primitive features in medical imaging have historically been an area of in depth exploration. Extensive works of [216–217] have demonstrated the use of texture analysis for classification. Texture analysis requires that the image textures be characterized by some quantitative measure. For that reason, certain descriptors are estimated to quantify these textural features [217]. A typical classification of these types of features includes syntactic, spectral and statistical.

In [217] the authors focused on first order statistical features primarily which entails extracting certain descriptors that are statistically derived from the feature distribution of each voxel. These first order statistical features mainly consisted of statistics that are dependent on probability density functions of the intensity of voxels in the image. These could then be estimated as histograms by binning voxels values of the same intensities. Statistical features on the first order include the mean, variance, skewness, kurtosis, and entrop. The advantage of using these statistical features, specifically in medical imaging is that they are invariant to transformations of the image. By construction, these first order statistical operators are invariant to affine transformations that consist of rotation and scaling. This kind of transformation is critical in medical applications due to the variance involved in different image acquisition conditions. However, while this variance of first-order statistical descriptors is plausible, they also have a critical limitation which is their lack of spatial coherence. The features assume a degree of independence by ignoring the relative spatial placement of the voxels in the image. In the experimentation done in [208], the authors defined a logical operator to compare the areas of the image with a degree of statistical similarity to a predetermined area. The idea is to search for sub-areas in the image with an empirical distribution similar to the predetermined area. For that purpose, some surrounding areas are also considered

and a threshold is applied so as to obtain a Boolean value that confirms the voxel's statistical similarity to the sub-region. A measure for comparison for a statistical distribution used is cross-correlation [209]. As a result, the authors generalize the classical texture analysis making use of some spatial information owing to the examination of neighborhood distribution when investigating a particular voxel. The framework is implemented by the authors on an MR image slice of a brain affected by glioblastoma tumor [209]. In [188], the authors proposed an approach for segmentation based on a spatial logic method. The goal was to identify a region of interest in MR images for the analysis of glioblastoma as well as other tumors. The authors employed a texture-based method along with local histograms to create a hybrid approach for segmentation, maintaining relative spatial information. This is primarily inspired by a topological approach interwoven with spatial logic. In this domain of research, works of [218] have been significant as they developed the theory to enhance the use of arbitrary graphs as models of space, particularly by utilizing a generalized form of topological spaces model called 'closure spaces' [212]. As a consequence of this, the spatial logic for closure spaces was formally defined along with a model-checking algorithm associated with it. Another important application of model checking in medical imaging is the contouring of nevus images. Nevus is a visible, circumscribed lesion of the skin. Typically, it is small and benign. However, these are very difficult to distinguish from the malignant counterpart [220] which is medically known as a melanocytic nevus. Melanoma is an advanced form of this. As with most types of cancers, this too requires early detection and diagnosis for effective disease management and treatment. In the case that melanoma is not recognized at an early stage, it can become lethal and life threatening. Reportedly, there are over 20,000 deaths due to melanoma in Europe each year [221]. Another critical factor that is the number of biopsies needed. This number can be cut down if automated systems are present to detect and diagnose melanoma. In the work of [220], the authors focused specifically on the contouring of the 2D images of nevi. This is generally considered to be a challenging problem since there is a lot of homogeneity in the texture, size, color, and shape of the nevi. Adding to the variance of the types of nevus, there are often extraneous elements that include patches, rulers, or hair. In [220], the authors take up this challenge by leveraging texture similarity operators along with spatial logic operators. Altogether, the feasibility of such a technique on the dermoscopic images from a public database is investigated in [220]. Usually, in the diagnosis of melanoma, segmentation of nevi is

considered a part of the overall bigger problem. In the literature, [221, 222] there is evidence that techniques that include automatic contouring with spatial model checking for brain tumors have in fact shown quality comparable to the current state-of-the-art. However, in the case of nevi segmentation and model checking, the additional challenges make it relatively complex, largely due to the optical effects that are associated with it. For instance, the type of lesions and contrast and the variance within the types of lesions. Certain spatial model checkers essentially utilize specifications that are typically high-level but written in a logical language in order to describe certain spatial properties so as to identify spatial patterns of interest in an automatic and efficient way. These spatial patterns are key in the identification of spatial structures of [220]. The images are conveniently described by their voxels. In [220], the authors investigate the feasibility of a technique that is based on spatial logic for closure spaces for the analysis of nevi images from a public data set. The authors show that despite the homogeneity in the nature of nevi, ranging from variance in shape, color, texture, and size to inclusion of extraneous elements like rulers, patches, and hair, the authors were able to demonstrate the analytic ability in a semi-automatic way. This is credited to the intrinsic rigor of a logic-based approach, utilizing the efficient implementation of spatial model-checking algorithms. The comparison is then drawn against the ground truth that is provided along with the public dataset. The dataset used is the one provided by the Skin Lesion Analysis toward Melanoma Detection challenge 2016 [223]. The composition of the data set includes highresolution annotated dermoscopic images. The ground truth segmentation data is done manually by the experts and are separately available as ground truth mask images.

[220] also reports variance not only in the different nevi but also within one nevus. The change of texture and color within a nevus poses a great segmentation challenge. This is even more complicated with the presence of any sebaceous follicle. Since the inter and intra variations in the nexus pose a great challenge in segmentation, the approach is then tailored to focus primarily on the differentiation between any type of nevus tissue and skin tissue. This is done with the help of texture analysis as well as spatial operators to isolate the nevus tissue from the skin tissue. To that end, the authors employ a statistical texture analysis operator to approximate a nevus. This is done by using a statistical heuristics approach to distinguish between background skin and likely parts of nevus. There is an underlying assumption that the likely part of nevus is centered in the image so that the area at the periphery of the image belongs to the background healthy skin cells [221].

This allows for the algorithm to take a sample of the background. Here, only the intensities are considered while hue or saturation is ignored. Using these intensities only, a histogram of the distribution of intensities is computed with a suitable number of bins. While there is a global histogram, one that takes into account all the pixels in the image, a smaller, more localized histogram is also constructed for each pixel where intensities of surrounding pixels in a specific radius are considered. Comparison of these local histograms with the global histogram in the form of a Pearson correlation coefficient allows for a comparison of the nature of the localized areas. This texture operator serves as a good first approximation method to identify the area covered by the nevus. However, this is still an approximation and requires adjustments to be made, which are subsequently performed using derived operators with metrics like relative distance and similarity indexes. The spatial model checking techniques can be used with the spatial model checking tool VoxlogicA developed in [224] to efficiently segment nevi. The segmentation based on thermoscopic images is important in automatic routines for the diagnosis of malign skin tumors including but not limited to melanoma. Spatial model checkers make use of high-level logic languages to identify certain spatial properties. In conclusion, [48] presented a novel segmentation method to combine spatial operators, that were inspired by closure spaces, and domain-based operators such as the texture similarity operator. As a result, achieving a dice score of 0.9 validates the segmentation quality. One of the outcomes of employing such a technique is that it is explainable in its methods, and it is mostly high-level [221]. There is room to advance this work by increasing the number of classes of images for which the segmentation has shown remarkable accuracy. It is pertinent to mention the scale of homogeneity between the nevi and within the nevi as well. Such variations reflect artifacts in the image and pose a tremendous challenge for accurate segmentation.

6.3.3 The Spatial Logic Framework

One of the most important frameworks for image analysis using model Checking is VoxLogic, which is a framework for image processing that incorporates user-oriented expression languages into the logic ImgQL to edit images [224], this tool takes advantage of the library of computational imaging algorithms alongside distinct combinations of the declarative specification to deliver optimized execution inherent to the spatial logic model checking. Consequently, the methodology

developed is considered to be rapid. Testing this methodology on existing brain tumor segmentation benchmark images shows that the accuracy can reach state of the art. The additional advantage is the explain ability and replicability of the approach [224].

The fundamental idea of Spatio-temporal model checking is to use the specifications in a relevant logical language in order to describe the spatial characteristics so that patterns and structures of key importance can automatically be identified. In [224], the main focus is on medical imaging for radiotherapy, particularly brain tumor segmentation. A challenge in this domain is that the tumorous regions or lesions are only defined distinctively from the normal tissue, owing to any changes in the intensities of the pixels in the gray-scale images. This relativity of pixel intensity as a marker of tumor presence makes it a complex challenge to isolate the lesions from normal tissue pixels. In addition to that, there is a considerable variation in the ground truth images of these segmented images. This is due to the variance in the manual segmentation by the experts. When there are intensity gradients between adjacent tissue structures, the experts have shown significant subjectivity in the assessment of ground truth for segmenting tumors [224]. This adds to the already challenging constraint of isolating tumors from normal tissues in gray-scale images based on intensities as a metric. Furthermore, the inconsistency in the data complicates things further as different MRI scanners also show considerable variation in the image quality. However, for demonstration of the approach, the authors use the publicly available BraTS 2017 dataset [181] where ground truth data is available for any objective deductions; reporting accuracies competitive with the state-of-the-art techniques for glioblastoma segmentation. The authors build on the image query language(ImgQL) that was proposed in [188]. This was in turn based on the spatial logic for closure spaces [226]. It is from [226] that the authors in [224] derive their kernel for their framework. The work in [224] is closely related to the spatial logic for closure spaces presented in [181] particularly with regard to the distancebased operator formed therein. For the digital image analysis, a statistical similarity operator is used that quantifies the similarity of an area around a point with that of a given region. This is achieved by the computation of respective histograms and then finding cross-correlation between them. This operator allows checking to what end an area near a point of interest is similar to a given region statistically. Another operator introduced is the percentile operator which takes a numeric value based image and its binary mask in order to return an image that shows how each point is related to the percentile rank of its pixel intensity with

regard to the pixel intensity of the surrounding population voxels. This allows for the same segmentation specification on images that have different intensity distributions. This also allows for avoiding the need to use absolute values in constraints on the intensity of points. In terms of its functionality, the VoxLogicA tool specializes for spatial analysis for multidimensional images. The pipeline for VoxLogicA is fairly simple as it interprets a particular specification that is written in the image query language and produces a set of multidimensional images representing the valuation of user specified expressions. However, when it comes to medical images, the images are boolean valued for logical operators, thus, the regions of interest may be overlaid on top of the original images for better viewing. On the other hand, the nonlogical operators will yield number valued images. The tool was used in [224] for evaluation in two ways. First, the evaluation was done for VoxLogicA for the segmentation of Glioblastoma in medical images obtained from MRI scans where the clinical target volume of the whole tumor is considered. This is different from the gross tumor volume which corresponds to what is actually visible on an image. Secondly, the evaluation was done on the BraTS 2017 dataset which serves as a quality measure of the proposed technique. The Dice similarity metric serves as a means to quantify the segmentation accuracy by computing a numeric value for the overlap between the manually segmented ground truth and the ones achieved by the VoxLogicA tool. The Dice result of 0.9 reflects the tool is sufficiently accurate [224].

The evaluation of VoxLogicA involved sets of 3D images of size 240 ×240 × 155 which is about 9 million voxels. Using a variant of [221] a comparison is made to assess the performance of VoxLogicA and another model, topochecker. The specifications consist of two human authored text files of about 30 lines each, identifying the oedema. The machine used for testing is a desktop computer equipped with a 7th-generation Intel Core I7 processor and 16GB of RAM. In the 2D case (image size: 512 × 512), topochecker takes 52 seconds to complete the analysis, whereas VoxLogicA takes 750 milliseconds. In the 3D case (image size: 512 × 512 × 24), topochecker takes about 30 minutes, whereas VoxLogicA takes 15 seconds. This huge improvement is due to the combination of a specialized imaging library, new algorithms such as statistical similarity of regions, parallel execution, and other optimizations. In other studies, [223] reiterates that model checking in medical imaging is mostly related with building visual representations of human body parts for analysis as well as preparedness for medical intervention. A key step in radiotherapy

planning includes contouring tissues and organs accurately. This, in conjunction with automatic contouring simplifies diagnostic procedures and eventually contributes to the reduction of time and cost as compared to manual contouring. The automated software that is used for contouring is typically highly specific in its application, for instance, having the ability only to contour the human brain. Such software offers little flexibility and transparency for the users and often does not deliver satisfactory accuracy [223]. Deep learning based approaches have recently become popular for medical image analysis. These are computationally efficient and mostly deliver decent results. However, they do require sufficiently large data sets that are accurately labeled by experts. Such large datasets are often not available, thus, posing as a limiting factor to these deep learning based techniques. In addition to that, there is inter and intra variability between the labelers who annotate the data for ground truth. In the above discussed literature, the works are aimed at reviewing model checking as a verification tool set in a multitude of domains. However, at the time of writing this work, there is no review or survey that explores the specific application of medical imaging with model checking as a means of verification, particularly with spatial logic design. This paper is a first of its kind reviewing different model-checking approaches taken to understand segmentation and identification of regions of interest in medical images.

6.4 Methodology

In this work, the discussion includes recent research papers that perform model checking on medical images. In this study, a list of papers is compiled to perform an analysis of the nature of model checking done on medical images. To that end, multiple web-based scientific databases were accessed. The keywords used included model checking and medical imaging. We also review key methodologies used in the papers that utilize model checking to verify proposed techniques. A key focus has been on the segmentation of tumors in medical images. Model checking for medical images is an active area of research with a lot of potential and promise. In this study, we aim to understand and discuss all recent studies that employ model checking for segmentation.

6.5 Results and Discussion

In this section, we review the findings of some of the works on model checking in medical imaging and build our discussion on top of these works. An analysis of these works in the form of a

compilation is also shown in this section so as to discuss these works in detail. While there are conclusive advantages to using spatial model-checking methods for medical imaging, it is imperative to understand the associated challenges. Logic based techniques in model checking have a strong reliance on basic set of logical operators. These logical operators allow for the definition of more expressive derived operators that resonate with the domain specific reasoning of the user. The idea is to exploit the compositionality of the basic operators so as to build more complex operators. A benefit for using very basic building blocks is the underlying efficiency for the verification and correctness of the algorithms. It is also expected that the approach has some degree of flexibility and generalization so that it does not unnecessarily be coupled with a particular application. Furthermore, a lot of focus in medical imaging and diagnosis has been on deep learning based techniques where hierarchical features are extracted and a model is trained to fit under plenty of hyper-parameters to give desired results. However, this requires large datasets and with significant variability in inter and intra experts on contours of segmentation, not only is deep learning implementation time consuming for manual segmentation help improve as well. To that end, interactive approaches based on spatial model checking may be of help in terms of improving the generation of manual ground truth annotations in a more efficient, transparent, and reproducible way. The explaining ability aspect is also an under explored problem when it comes to deep learning methods as deep learning approaches suffer from a lack of reasonable explanations on human insight as to why a certain area is classified as a tumor by the model, particularly when the models do not always provide correct results. The results in [223] are obtained by utilizing the VoxLogicA based model checking approach with the integration of the above discussed derivative operators. The quantitative metrics used for evaluation included the dice coefficient, specificity, and sensitivity. Sensitivity quantifies the fraction of pixels correctly identified as the ground truth whereas specificity quantifies the fraction of pixels identified as true negatives. The dice index encapsulates the similarity. The authors were able to achieve dice, sensitivity, and specificity scores as high as 0.90, 0.91, and 0.98, respectively for grey matter in the brain MRI image and 0.89, 0.85, and 1.0, respectively for white matter. In [221] work on nevus segmentation, the authors achieved dice, sensitivity, and specificity scores of 0.81, 0.81, and 0.96, respectively. While some variation in scores is evident owing to the difference in applications, the objectivity in the strong performance of model checking as a tool for segmentation, in general, is appreciable nonetheless. [223] also

identified the need for extended ability and openness of the annotation procedures by the experts for the segmentation since the experts have vast experience in marking the ground truths on the data; it warrants the need to encapsulate that expertise in terms of high-level operations with formal specifications that can be exchanged, published and discussed by the domain experts. There is also a strong case for ensuring device independence in the long run, as there are certain factors that hinder the adoption of academically significant research for everyday use in clinical practice. These include academic research outcomes that lack integration with existing hardware as well as hardcoded dependence on execution environments. Therefore, for successful technology transfer, it is crucial to overcome the fragmentation of academic research outcomes and work towards open standards and protocols to facilitate the intermediaries like imaging device vendors who can convert novel ideas into clinical practice. There is also a challenge of the privacy of data and procedures; however, the need is to set up open standards to enable users to exchange analysis procedures for establishing common knowledge. We summarize the results of the relevant literature contributions with respect to model checking in Table 1

Table 1 Comparison of existing techniques

SN	Studies	Application	Innovation/ PaperType	Result	year
1	Karmakar et al.[297]	System Design	Review	-Algorithmic verification of probabilistic finite-state systems with respect to linear-time properties.	***2022***
2	Belmont et al.[2]	Nevus Segmentation	Spatial MC	-Determination of the contour of the two-dimensional images of nevi.	***2021***
3	Gopal et al.[198]	Web Service	Review	-A systematic review of the current research work on web service validation-based model validation that emerged during the period 2002-2017.	***2021***
4	Jonas et al.[199]	Vehicle Control	Review	-Report on model check application trials to check the arbitration logic of the vehicle control system. Identify the pros and cons of different modelchecking techniques and tools	***2020***

5	Vincenzo et al.[224]	Glioblastoma	VoxLogicA	-Automatic segmentation of glioblastoma in MR flair for radiotherapy	***2019***
6	Massink et al. [223]	Glioblastoma	Spatial MC	Providing an open platform introducing declarative medical image analysis.	***2019***
7	Buonamici et al. [208]	Glioblastoma	ImgQL	Introducing the logical language ImgQL (”Image Query Language”). ImgQL extends SLCS with Boolean operators that describe distance and area similarity.	***2018***
8	Belmont et al.[223]	Glioblastoma	Automatic Segmentation	-Automatic segmentation of glioblastoma	***2017***
9	Nenzi et al. [205]	Reaction Diffusion	Spatiotemporal Logic	-Introducing the Signal SpatioTemporal Logic (SSTL), a modality that may be utilised to characterise the spatiotemporal characteristics of linear time and discrete space models.	***2016***
10	Katoen et al. [200]	Probabilistic MC	Review	Algorithmic verification of probabilistic models, in particular probabilistic model checking.	***2016***
11	Ovidiu et al.[202]	Biological Systems	Meta MC	A New Approach to Multiscale SpatioTemporal Meta Model Checking for Multilevel Computational Models of Biological Systems	***2016***
12	Ovatman et al[194]	PLC	Review	Model checking practices on verification of PLC software,” Software and Systems Modeling	***2016***
13	Ciancia et al.[189]	Spatial Operato	Topological Generalization	Defining and confirming space attributes	***2016***
14	Edelkamp et al.[190]	State-explosion	Review	Using Histological Image Processing Techniques, Chronic Tumor Hypoxia is Quantitatively Characterized	***2008***
15	Gerard et al.[195]	Software systems	Review	Explaining the theoretical underpinnings and practical applications of logic model-	***2005***

				checking methods for the verification of multi-threaded software	
16	Bhaduri [194]	State-chart models	Review	Recommending a variety of approaches to deal with the issue of state space explosion as well as some future research topics.	***2004***
17	Vardi et al.[196]	Probabilistic MC	Review	Being able to reduce probabilistic model checking for ergodic analysis of Markov chains.	***1999***
18	Reif and al. [206]	Packet Routing	Spatio temporal Operators	spatial and temporal modalities in a multiprocess network logic	***1985***

The table results show that most of the publications we studied focused primarily on segmentation and analysis of medical images. This is to confirm the effectiveness of the model checking in the analysis of medical images, as the accuracy of most of these works exceeded 90%, which is a percentage that shows the importance of model checking in the analysis of medical images, in order to learn more about the areas of use of model checking (computer science, engineering, Medicine Public Health, medicine), figure 1 shows the results of the top 5 areas where the model checking was applied by relying on Spring Nature statistics.

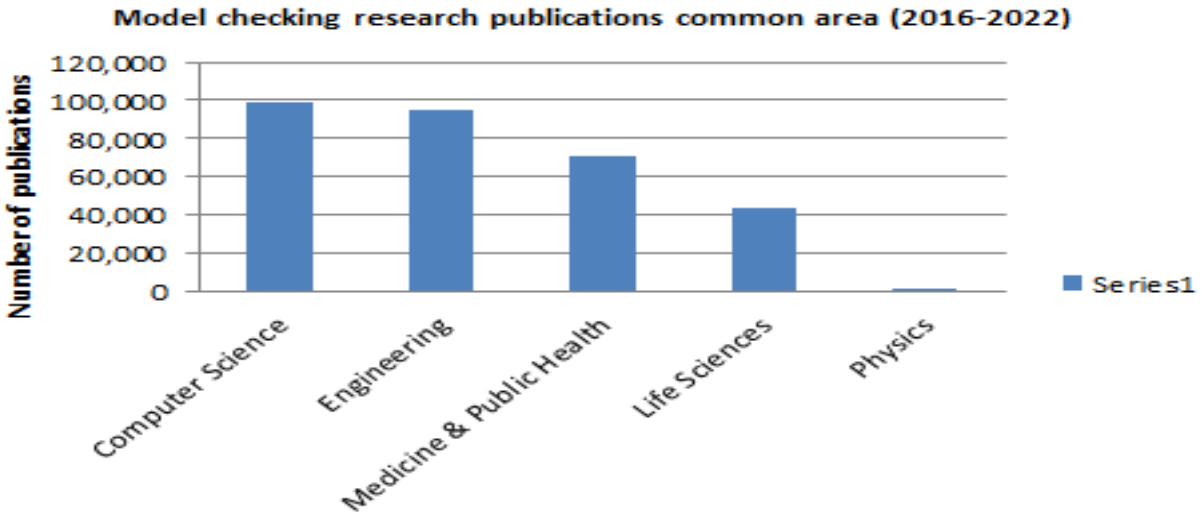


Fig. 2 Model checking research publications common area.

In order to be more precise, we calculated the percentage for each field in terms of the number of Model Checking publications by relying on Spring Nature statistics.

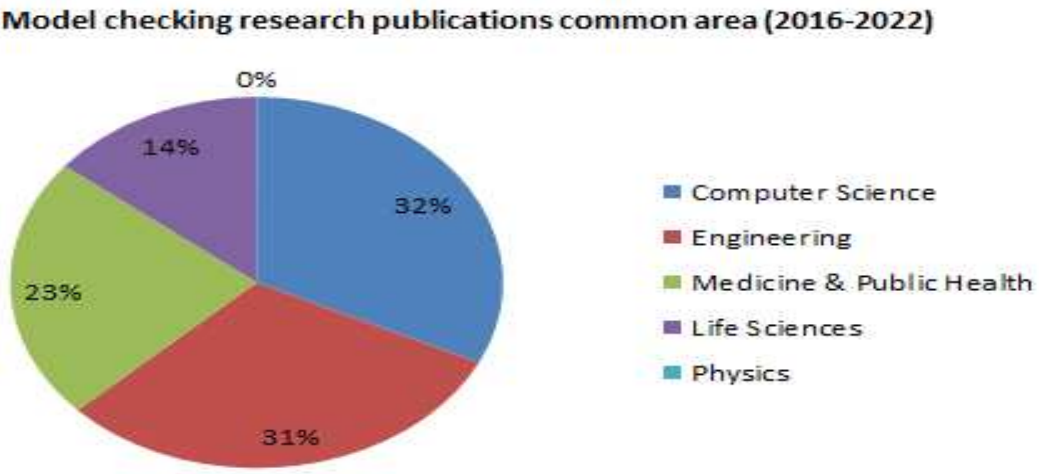


Fig. 3 Model Checking research publications common area

It is clear from the above diagram that the strength of model checking is the ability to apply it in different areas, unlike some other methods, and it is clear that most applications of model checking are in computer engineering sciences due to the need for computer engineering to verify the correctness of the characteristics in order to avoid errors in the development of programs. we used the systematic review to draw the historical publication chart of model-checking research publications per year.

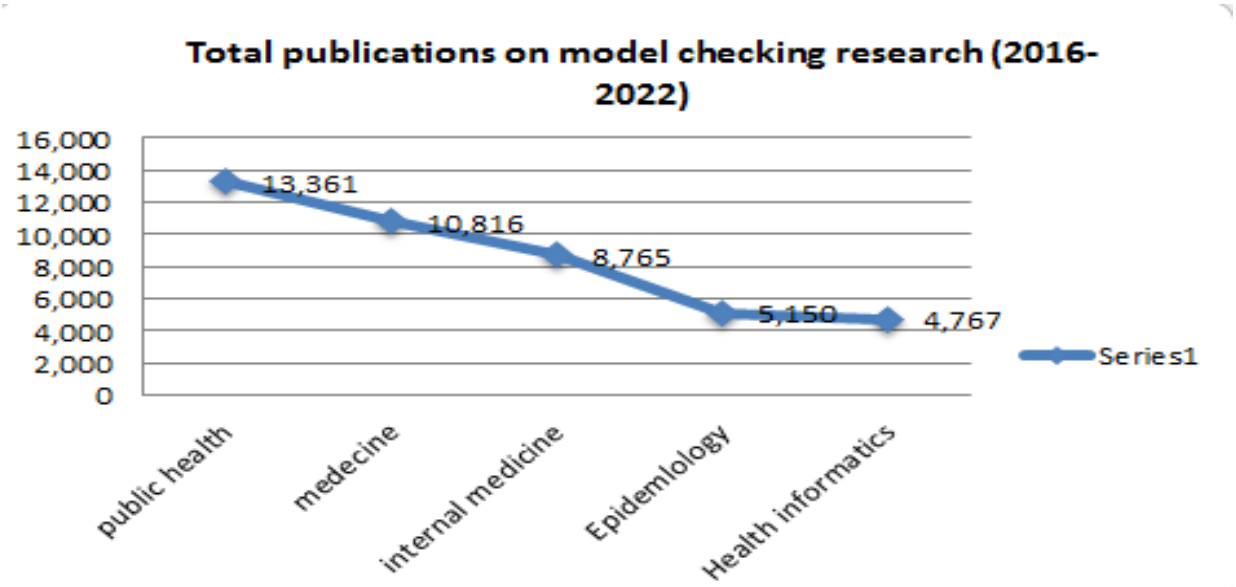


Fig. 4 Total publications on model checking research (2016–2022)

We note that the importance of model checking in the health field is being studied due to the ability of the model checking to identify and avoid errors, in addition to its low cost compared to deep learning technique.

6.6 Conclusion and future work

Model checking in medical imaging is still a very active area of research. Using spatial model checking for verification of and confirmation of spatial logic design is instrumental in identifying and segmenting various natures of tissues in the body. There are still many challenges in terms of the technical development of the framework as well as the explainability and reproducibility of methodologies in the model-checking domain. The literature suggests that model checking is a valid tool of detection for not just tumorous tissues but is also extendable to understand and differentiate distinct healthy tissues in the body. These are achieved with appreciable accuracies in the literature. However, there is still much room for improvement as most of the literature focuses on particular applications. In this context, we will work in the future to develop the techniques of Model checking in analyzing medical images by applying Model checking to 3D images.

CHAPITRE 7 ARTICLE 5: VALIDATION OF TUMOR DETECTION USING MODEL-CHECKING

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submitted to: Neural Computing and Application, on 23 March 2023

Abstract: Model-checking is a formal verification technique for figuring out whether a formal model of a system satisfies the expected requirements. This technique has a wide range of application areas and, recently, it gained a great interest in medical image analysis domain. In this context, its main idea is to represent an image by a discrete space and to specify, by means of a spatial temporal logic, the structural characteristics of regions of interest. The verification process consists in identifying, in the image, the regions of interest, leading to some segmentation of the image. This paper shows how to apply the model-checking technique to verify whether a segmentation provided by a brain tumor detection meets some specific requirements. To this end, we define some spatial logical operators useful to specify the requirements related to the detection of tumors. The test of the proposed approach confirms its effectiveness in verifying the detection of the tumors, as the accuracy, Precision, and Recall reached 98%, 96.15%, and 100%, respectively.

Keywords: Model checking, Tumor Detection, Segmentation technique,

7.1 Introduction

Model checking is an automatic technique for verifying whether a system meets the expected properties. This technique has a wide range of application domains, among which large-scale distributed systems [225–227], signal 222], and medical images analysis [229–232], and showed its effectiveness to find subtle errors in complex systems. The research related to the last domain is still ongoing looking for the perfect (precise, complete, simple) approach for analyzing medical images. In this domain, model-checking in medical images has shown that it is a promising application that can greatly facilitate the work of specialists, by verifying, for example, the detection of tumors provided by a brain segmentation.

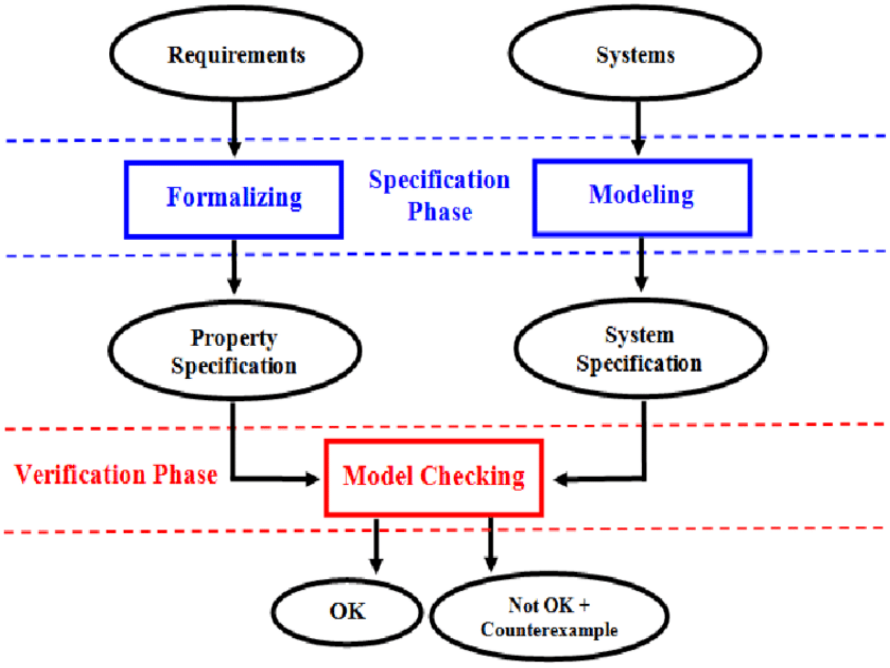


Fig. 1 Schematic view of model-checking approach

A Brain segmentation, or the process of identifying and separating different structures or regions within a brain image, has recently gained significant traction in the research area. Segmentation techniques have a variety of applications in neuroimaging, including the analysis of brain scans to identify abnormalities or track the progression of conditions such as brain tumors or neurological disorders. There have been numerous studies on brain segmentation in recent years, and it is considered an active and growing area of research. Automatic or semi-automatic segmentation methods, which use algorithms to identify and distinguish different structures in brain images, are often used to improve the accuracy and reliability of brain image analysis. These methods may have a range of applications in the medical field, including diagnosis, treatment planning, and monitoring of treatment response [234, 235].

In [236], the authors suggest a method that involves combining region growing and mathematical morphology to distinguish and separate various structures within the brain. Segmentation techniques are typically categorized into two groups: generative and discriminative models. Generative models are based on past knowledge of the anatomy of particular brain tissues. In contrast, the discriminative models rely on extracting many low-level features in images, including texture features and local histograms [238].

Segmentation methods may use various techniques to analyze the intensity and texture characteristics of the pixels in an image, such as thresholding, clustering, region growing, or machine learning algorithms [239]. These methods separate the pixels into groups or segments based on intensity and texture characteristics. Each group corresponds to a different structure or region in the image. Segmentation can be challenging, particularly in medical images, due to the complexity and variability of the structures being segmented and the presence of noise or other artifacts in the image. However, it is a crucial step in different tasks for image analysis. Several techniques can also be combined to form hybrid methods. For example, support vector machines and neural networks, are examples of semi-automatic techniques. However, automated segmentation techniques constitute the current gold standard [238, 240]. One challenge in developing automated methods for brain tumor segmentation is that tumor regions are often only categorized by subtle changes in the brightness of image pixels relative to the surrounding normal tissue [238]. This can make it difficult for automated systems to identify and distinguish tumor regions accurately, as even manual expert segmentation can exhibit significant variation. This variation may be due to subjective expert interpretation or differences in the images of different patients due to the use of different imaging modalities [238].

The main challenge of this paper consists of four parts: segmentation, feature extraction, tumor detection and finally tumor detection validation.

This paper proposes to use the model-checking technique to verify the correctness of the

results provided by a detection process of brain tumors. The contributions of this paper are:

1. Introduction of a new logical temporal operators useful to identify tumor regions in a medical image.
2. Development of a model-checking technique to verify whether the correctness of a detection process of brain tumors.
3. Test and evaluation of the proposed technique on some available datasets.

The remainder of this paper is organized as follows; section 9.2 provides some related works. The proposed approach is presented in section 9.3. Some experimental results are reported in section 9.4. Finally, a conclusion and future works are given in Section 9.5.

7.2 Related work

The use of model-checking in medical imaging is a relatively new research area, as evidenced by the small number of published works in this field. However, the current studies that have been published are promising. For example, [243] have used machine learning and model- checking techniques to learn and detect emerging behavior in networks of cardiomyocytes. Where the finite model examination was used to find the beginning of the spiral wave, a new spatial logic based on spatial superposition was developed to identify the emerging behavior and to devise a new way to learn the formulas of this logic from the studied traits. The effectiveness of this approach has been demonstrated by applying EMERALD to scalar electric fields produced by the CELLEXCITE simulator.

The Paper [244] presents a new method for validating multilevel computational models of biological systems using multiscale spatial and temporal descriptive model inspection. This methodology and software will enable computational biologists to efficiently develop reliable multilevel computational models of biological systems by translating insights gained from multilevel computational models of biological systems into real-world applications.

On another side, when it comes to fully automated approaches, it is worth noting the significant impact of machine learning techniques that utilize deep learning to model non-linearities in data in order to draw meaningful conclusions [248]. Manually segmenting in vivo images is currently considered the standard practice but has several disadvantages. First, the process is time consuming and requires a high level of skill and attention from the clinician, which makes it costly [240].

Additionally, the subjectivity of manual segmentation can lead to differences in judgment between clinicians and make it difficult to reproduce, introducing the possibility of human error [234]. Deep learning and machine learning approaches have demonstrated impressive results in detection, classification, and pattern recognition tasks. However, the success of these techniques depends on the reliability and quality of the datasets used. Deep learning approaches require large datasets that capture a wide range of variations. One major advantage of deep learning is its ability to extract features from raw data and make inferences across multiple layers. However, using deep learning in a supervisory framework requires using ground truth labels, which can be subjective and vary significantly between annotators. According to [240], the intra-expert and inter-expert variability

for manually segmenting tumor regions in the brain MRI images can be as high as 35% and 30%, respectively. To address this issue, it is important to use interactive model-checking methods to improve the reproducibility and efficiency of ground truth annotation. Among notable works in this field include [256], who developed a spatial extension of signal temporal logic for stochastic population models in a discrete representation of space. The framework uses a graph based approach with weighted, cost based graphical connections and a single spatial operator similar to the one defined in [246].

[240] Extended this approach with a bounded surrounded operator, which builds upon the surrounded operator described in [247] with additional requirements. [248] alternatively characterized the bounded surrounded operator as a derivation from a basic operator [247], [249] made significant contributions to the research on Spatial model checking as well as spatial logic in medical imaging by developing the theory of models of space utilizing arbitrary graphs, specifically by using a generalized form of topological spaces called ‘closure spaces’ [250]. This led to the formal definition of spatial logic strictly defined for closure spaces and the development of a model-checking algorithm. These works have had a significant impact on this field of research. Spatial Model checking has also been applied to the contouring of nevus images, which are benign skin lesions that can be hard to identify from melanoma, deadly skin cancer. For effective disease management and treatment, early detection and diagnosis are crucial.

In [251], the authors used texture similarity operators and spatial logic operators to tackle the challenges of contouring 2D nevus images, which can vary in texture, size, color, and shape, and may contain extraneous elements. They tested the effectiveness of their technique on a public dataset. While Spatial model checking has shown comparable quality to the current gold standard for brain tumor segmentation, additional challenges such as optical effects and variance within types of lesions make nevus segmentation and model checking more complex. Often model checkers utilize specifications that are high level and written in logic language to model spatial properties to identify specific patterns, which in turn are key in the identification of structures [249, 252, 253].

In [251], the authors investigate the feasibility of a technique that is based on spatial logic for closure spaces for analysis of nevi images from a public dataset. Authors use spatial model

checking techniques to analyze nevi images from a public dataset. They show that these techniques can effectively identify spatial patterns in the images, even with the presence of inhomogeneity and extraneous elements. The results of the analysis are compared to the manually annotated ground truth data from the dataset. The authors suggest that the use of Spatial model checking and the effective implementation of validation algorithms tumor detection. in this context, the dataset is provided for the analysis of the melanoma detection [254]. The inter and intra variations in the nexus, as reported in [240] pose a great challenge in segmentation. Thus, the approach is to distinguish between nevus tissue and skin tissue. The authors use a statistical texture analysis operator to approximate a nevus. The algorithm takes local histograms into account to determine between background pixels and target pixels. The texture operator used for this serves as a good first approximation but requires adjustments, such as in the form of the use of derived operators with metrics like similarity indexes.

In [253], the focus is on using Spatial model checking in imaging to create representations of human body parts for possible medical intervention planning as well as clinical analysis, with a particular emphasis on accurate contouring tissues and organs in the healthy brain. Automated software tools that are commonly used for this purpose are often highly specialized and lack flexibility and transparency and may not always produce accurate results.

In complement to the state of art, this paper proposes a model-checking technique to quantify the quality of a brain tumor detection process. As in all related work, the image is represented as a discrete space and the requirements are specified by means of a spatial temporal logic. The verification technique consists in identifying the regions of the image that meet the requirements. The brain tumor detection process is based on the KNN algorithm, and, in this context, the input image of the model-checking technique is the classification result of this algorithm. The purpose is the verify whether this classification meets the requirements of the detection of tumors.

7.3 Model-checking of tumor detection

Model-checking of tumor detection, methodology, dataset, and tools are discussed in this section.

One of the biggest challenges of model-checking in analysis of medical image is to define its input formalisms used to represent medical images and to specify useful requirements, respectively.

Once the input formalisms are fixed, their associated analysis algorithms can be exploited to verify whether the model of an image meet the requirements.

7.3.1 . Input model

As in [226], the input model is an extension of a closure space with attributes and is relied on the following definitions.

Definition 1 [254]: A closure space is a pair (X, C) composed of a set X of elements and a closure function $C : 2^X \rightarrow 2^X$, which assigns to every subset of X a corresponding closure that satisfies the following axioms (called Kuratowski Closure Axioms) [255]:

1. **$C(\emptyset) = \emptyset$,**
2. **$C(Y) \subseteq Y$, for all $Y \subseteq X$,**
3. **$C(Y \cup Z) = C(Y) \cup C(Z)$, for all $Y, Z \subseteq X$,**
4. **$C(C(Y)) = C(Y)$, for all $Y \subseteq X$.**

In the context of medical images, X is the set of pixels, voxels or regions of an image and C is generally derived, from a reflexive and symmetric adjacency relation R over X, as follows: $C(Y) = Y \cup \{x \in X \mid \exists\, y \in Y, y\ R\ x\}$. Different adjacency relations can be used such as the orthogonal adjacency relation and orthodiagonal adjacency relation [261]. In the former relation, only elements which share an edge count as adjacent, while, in the latter relation, elements of X are adjacent if they share at least either an edge or a corner.

A closure space (X, C) can be enriched with attributes used to qualify the element of X.

Definition 2: The input model Γ is a tuple ((X, C), A, V) consisting of a closure space (X, C) based on such that C is based on adjacency relation, a set of attributes A, and a valuation function $V: X \rightarrow 2^A$ that assigns to each element of X, the set of attributes it satisfies. For any element x of X, V(x) is the set of attributes.

From a semantics point of view, X is considered as a set of states labelled with attributes and the transition relation between states is given the adjacency relation used to derive C.

7.3.2 Input spatial temporal logic

The used spatial temporal logic ECTL, we use in this paper, is a subset of the CTL temporal logic [252] given below:

Any atomic proposition p is a ECTL formula and if φ and ψ are ECTL formulae, then so are:

$\neg\varphi$, $\varphi \wedge \psi$, $\varphi \vee \psi$, EX φ, EG φ, and **φ EU ψ,** where:

EX φ means that φ holds in some next state of the current state.

EG φ means that along some path of the current state, **φ** holds in every state of the path.

φ EU ψ means that along some path of the current state, **φ** holds until reaching a state holding **ψ**.

Other abbreviated formulas can be also used such as **EF φ,** which means that in some path of the current state, there is at least a state holding φ. **EF φ** is equivalent to true **EU φ**.

Definition 3: The semantics of **ECTL** on the model **Γ = ((X, C), A, V)** is defined by induction from the formula structure. Let x ∈ X and φ a ECTL formula. The satisfaction of φ at point x ∈ X in Γ, denoted by **Γ, x |= φ**, is defined as follows:

Γ, x |= p	⇔	p ∈ V(x)
Γ, x |= ¬ Φ	⇔	Γ, x |= Φ does not hold
Γ, x |= Φ1 ∧ Φ2	⇔	Γ, x |= Φ1 and Γ, x |= Φ2
Γ, x |= EX Φ	⇔	for some successor x' of x, Γ, x' |= Φ
Γ, x |= EG Φ	⇔	for some path y1 y2 … of x, Γ, yi |= Φ, for all i>0
Γ, x |= (Φ1 EU Φ2)	⇔	Γ, x |= Φ2 or (for some path y1 y2 … of x, for some k > 0 y_k |= Φ2 and for all i<k, Γ, y_i |= Φ1).

Based on this semantics, it is possible to compute recursively the set of elements of X that satisfy a ETCL formula **φ: sat(φ) = {x ∈ X | Γ, x |= φ}.**

Example 1: Suppose that an image is represented by the space in Fig.2.and the attribute color is associated with its elements. The sets sat (¬ (Orange ∨ Blue)), sat (Blue), sat (Orange), sat(Orange ∨ Blue), sat(¬ Orange), and sat(¬ Blue) are shown in green color in Fig.2.b, Fig,2.c, Fig.2.d, Fig.2.e, Fig.2.f and Fig.2.g, respectively.

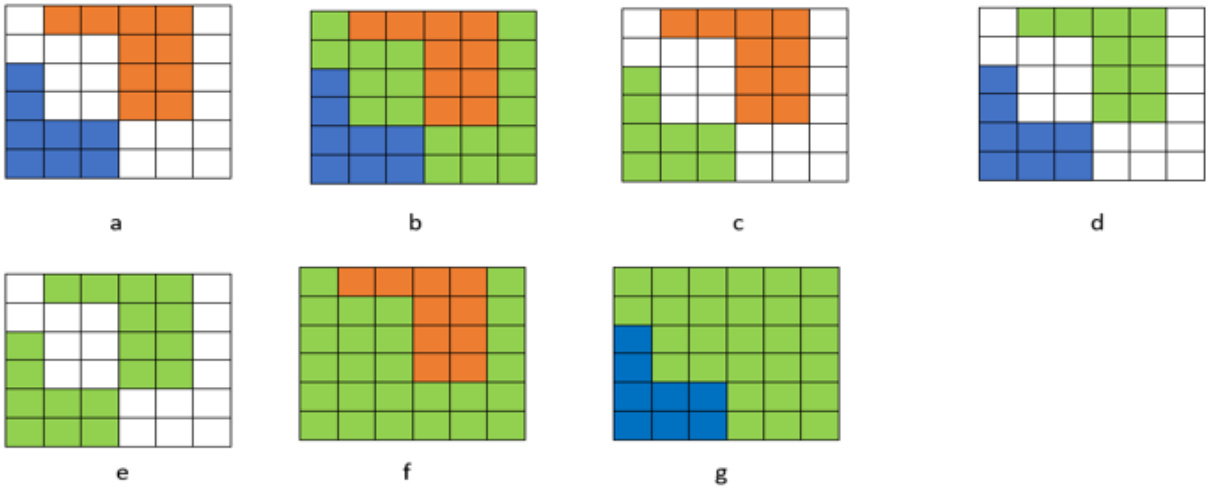


Fig.2 Model checking: **a.** Input model; **b.** sat (¬ (Orange ∨ Blue); **c.** sat (Blue); **d.** sat (Orange); **e.** sat (Orange ∨ Blue); **f.** sat (¬ (Orange)); **g.** sat (¬ (Blue))

In the context of this paper, we have used some atomic propositions and some operators defined as follows:

Let Γ = ((X, C), A, V) be a model representing an image and φ *an ECTL formula. The set Sat(φ)* = *{x*∈ X | Γ, x |= φ} yields a partition of the image into regions that satisfy φ and regions that do not satisfy φ.

- Γ, x |= *border* φ is true iff x lie on the boundary of a region of the image that satisfies φ. The property *border* φ is equivalent to ¬ φ ∧ EX φ.
- Γ, x |= *brain* φ is true iff x is located inside a region holding φ.
- Γ, x |= *background* φ is true iff x is outside the brain and the boundary. Then, background φ is equivalent to: ¬ φ ∧ ¬ border φ.

- Let $\phi 1$, $\phi 2$ be two *ECTL formulas,* Γ, x |= *connect* ($\phi 1$, $\phi 2$) is true iff x satisfies $\phi 1$, does not satisfy $\phi 2$ and some of its successors satisfy $\phi 2$. Then, *connect* ($\phi 1$, $\phi 2$) is equivalent to $\phi 1 \wedge \neg \phi 2 \wedge EX\ \phi 2$.

- Let $\phi 1$, $\phi 2$ be two *ECTL formulas.* Γ, x |= *str* (d, φ1, φ2) iff for some elementary path of x, all elements that are at a distance less than d from x satisfy φ1, and the one at distance d from x satisfies φ2. The distance between two elements x and y along a path is the number of transitions made to reach y from x.

Example 2.

Suppose that an image is represented by the space in Fig.3.a and the attribute color is associated with its elements. Then, the background of orange can be specified by the ECTL formula: ¬ orange Λ ¬ EX orange. The border of orange can be specifying by the ECTL formula ¬ orange Λ EX orange. The brain is equivalent to the ECTL formula: orange. The sets sat (Background orange), sat (Border orange) and sat (Brain) are shown in blue color in Fig.3.b, Fig,3.c and Fig.3.d, respectively.

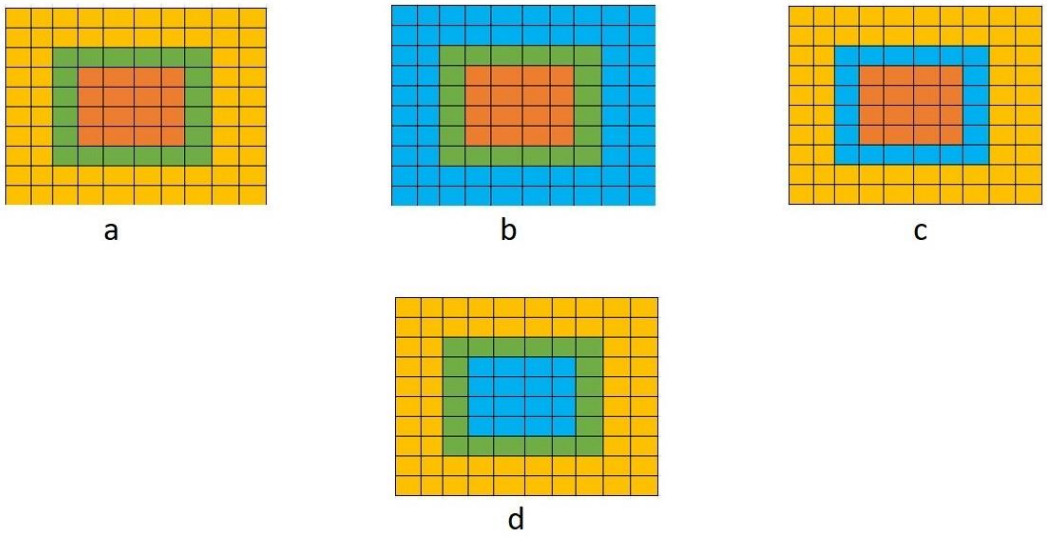


Fig.3 Model checking: a. Input model; b. sat (Background orange); c. sat (Border orange); d. sat(Brain).

7.4 Methodology

This work will focus on analyzing the effectiveness of the model-checking algorithm in quantifying the quality of brain tumor detection using the KNN algorithm. In addition to determining whether the tumor detection was done correctly, the study of whether the model satisfies the properties. Fig 4 is shown the methodology we follow in our work.

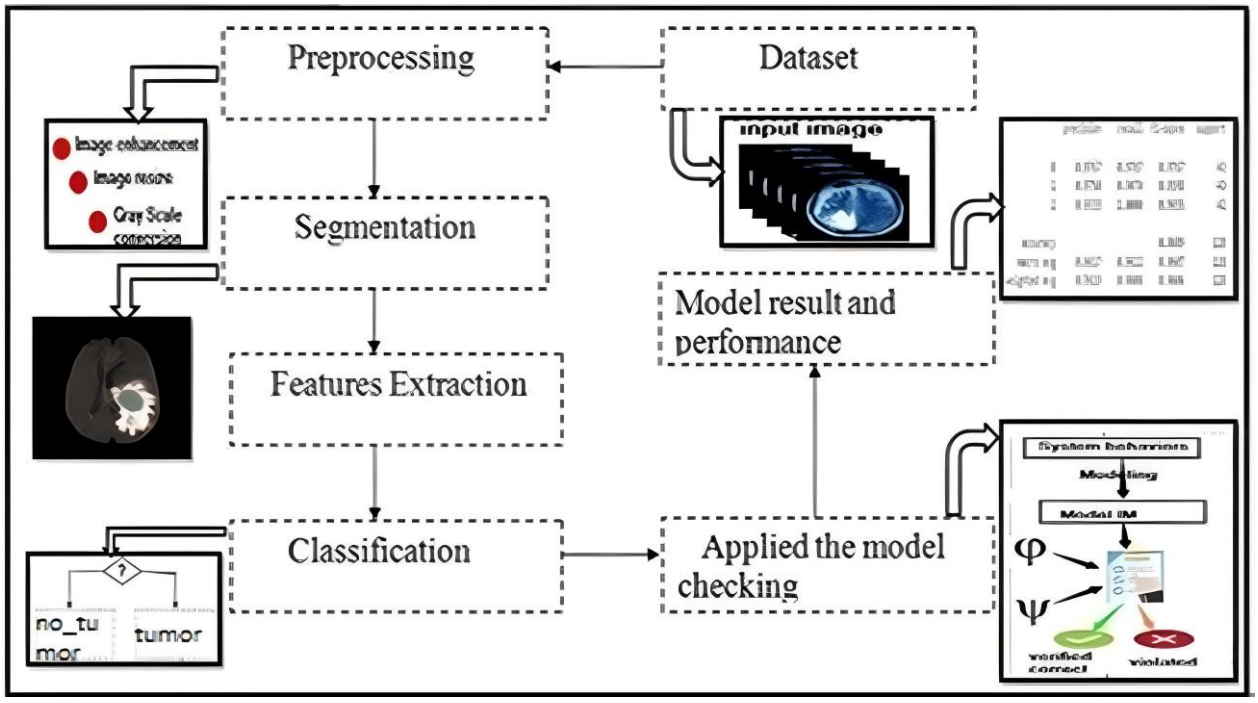


Fig.4 Overall block diagram of proposed methodology

The methodology of this work is mainly concerned with performing a model check based on the implemented segmentation of the input image and detecting the tumor using the KNN algorithm. The essential steps in this methodology are as follows:

1. **Input Image:** Input images are implemented using the medical Brain MRI images dataset.
2. **Preprocessing:** The combined input images are subject to pre-processing. In the preprocessing step, we can perform image enhancement and image resize conversion, as well as grayscale conversion, is performed.

3. **Segmentation:** FCM Clustering is used to segment the data in this step. Then, a cluster is chosen from among the others that are appropriate.
4. **Feature Extraction**: Feature extraction has been performed using Pattern and texture such as- Energy, Homogeneity, Dissimilarity, Correlation.
5. **Classification and detection:** In this step, the KNN algorithm is used, which is one of the best machine learning algorithms. The KNN algorithm is a simple and effective algorithm used for classification and regression tasks. It works by finding the k nearest neighbors of a given data point and using their labels to make a prediction. In this study, the KNN algorithm is used to classify the image as a tumor or non-tumor.
6. **Applied the model checking:** Analysis of the detection effectiveness of the model checking in determining the quality of brain tumor through a specially derived operators for medical image analysis. So that we can verify that the tumor has been detected correctly.
7. **Model result and performance: In** this section, the performance metrics like Accuracy, Sensitivity, and Specificity will be estimated. This performance will be compared by means of the performance parameters.

7.5 Data set

This study used a publicly available dataset selected from Kaggle. It contains two categories: a tumor category with several cases of tumors that differ in location, size, and speed of spread, and a healthy category that does not include tumors. The tumor category comprises 1550 images, and the non-tumor category comprises 980 images. This data set was generated in 2019 by Anshu S et al. More than 38,440 people downloaded it for its effectiveness in evaluating the quality of the algorithms to be studied. The image below shows some samples from the data set.

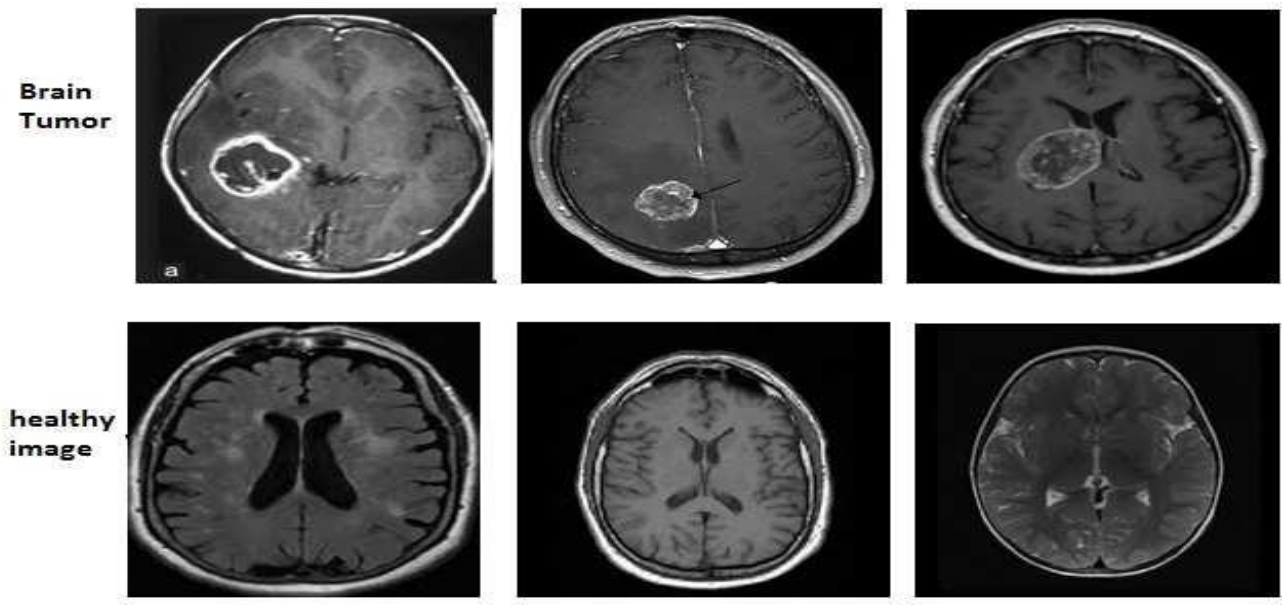


Fig. 5 Brain tumor and healthy image.

7.6 RESULTS

The most important result of this work is the use of model checking to study the detection of tumors, where we took the model checking from its usual roles to play advanced roles in medical imaging by developing a methodology that enables us to know whether the detection of tumor regions is correct, in addition to studying the satisfaction of possible properties And extract all the details. The proposed models included a data set of 2530 images. First, we insert the input image where the row of the input image = 1427 and its column= 1275, where the input images are subject to pre-processing. In this step, we can perform image resizing where the resized image row = 256, its column = 256 and has a grayscale transformation, and a filter where Filter Size = 3 x 3 and Smoothing Level = 0.5, as shown in Figure 6.



Fig. 6 Preprocessing steps:

We segment the tumor using K-FCM Clustering. In this portion, clustering is done to cluster the region's interest separately from the background. Then color-based segmentation is applied to segment the area. The number of clusters mentioned in the code is 4, which results in partitioning the image into four regions.

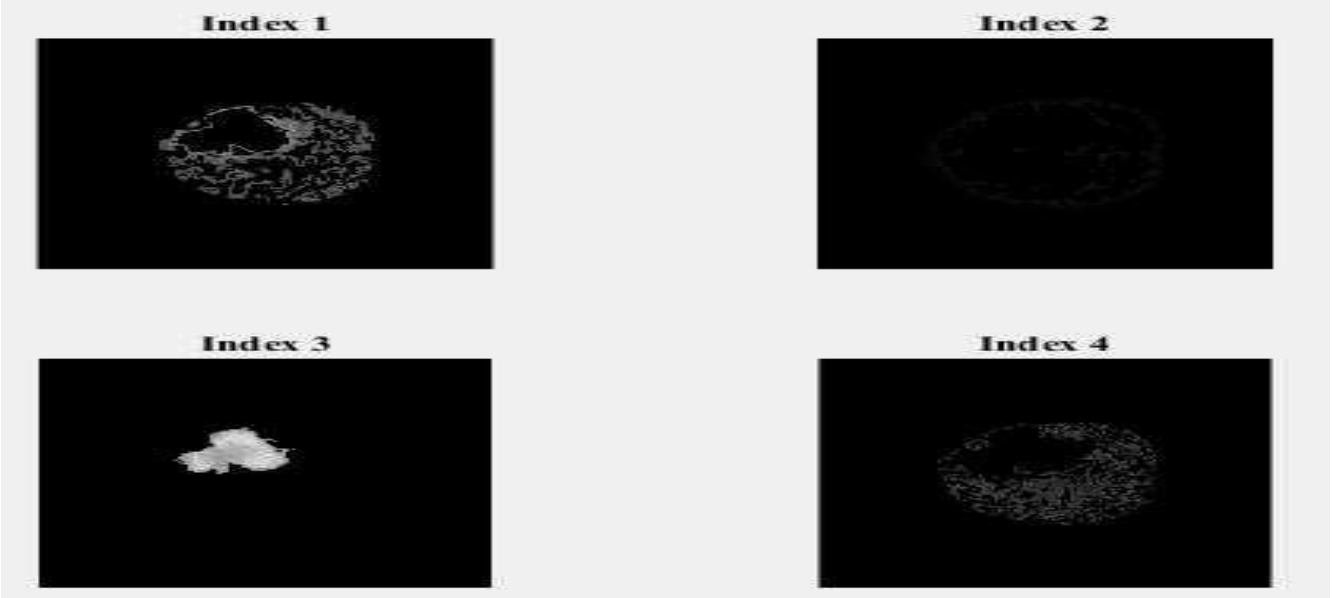


Fig. 7 Select the appropriate region.

Algorithm 2 is a switch that enables us to choose the case that is closest to the tumor and the most obvious from among the four images, and among those four regions, we have to select the appropriate region, then that region will be the segmented image.

Algorithm 2 select the applicable Tumor image Require:

```
INPT = input('Enter the Index num :: ');
1: procedure SELECT REGION()
2:     switch INPT
3:     case 1
       SEG = Segmented1;
4:     case 2
       SEG = Segmented2;
5:     case 3
       SEG = Segmented3;
6:     case 4
       SEG = Segmented4;
       end
7: end procedure
          Output :selcted image
   end procedure
```

The result is a trace as shown below, where we can enter the most obvious case number to segment it.

```
Iteration count = 1, obj. fcn = 130738752.442221
Iteration count = 2, obj. fcn = 101233315.647825
Iteration count = 3, obj. fcn = 101028357.292125
Iteration count = 4, obj. fcn = 98824526.226355
Iteration count = 5, obj. fcn = 87246159.498379
Iteration count = 6, obj. fcn = 64942715.789979
Iteration count = 7, obj. fcn = 50294485.599759
Iteration count = 8, obj. fcn = 43571128.971012
Iteration count = 9, obj. fcn = 34130654.776338
Iteration count = 10, obj. fcn = 25372817.199223
Iteration count = 11, obj. fcn = 21506791.474057
Iteration count = 12, obj. fcn = 20363031.608788
```

```
Iteration count = 13, obj. fcn = 20094601.506415
Iteration count = 14, obj. fcn = 20039248.495941
Iteration count = 15, obj. fcn = 20028426.511818
Iteration count = 16, obj. fcn = 20026348.823408
Iteration count = 17, obj. fcn = 20025952.298998
Iteration count = 18, obj. fcn = 20025876.786704
Iteration count = 19, obj. fcn = 20025862.419908
Iteration count = 20, obj. fcn = 20025859.687728
Iteration count = 21, obj. fcn = 20025859.168260
Iteration count = 22, obj. fcn = 20025859.069505

        Enter the Index num ::      3
```

So, for Figure 4 above, index 3 is applicable. We also used KNN to classify index 3 as a tumor or non-tumor. If there is a tumor, we will initially receive a message, as shown in algorithm 3.

Algorithm 3 Check for tumor

```
Require: global Featuresrresult, global TestfeaLabel, load Trainfea1
1: procedure MESSAGE ()
2:      for ijk = 1:size(Trainfea1,1) do
3:      temp = Trainfea1(ijk,:);
4:      Dist val(ijk) = mean(temp - Testfea);
5:      end for
6:      if result(1) == 1 then
7:      msgbox(' Normal');
8: else result(1) == 2
9:      msgbox(' Abnormal');
10: end procedure
```

Then we check the validity of the detection by using the model checking based on the proprieties satisfaction study; if the model satisfies the proprieties, then there is a tumor, as shown in algorithm 4. Where we enter the input ϕ, and a finite model Γ the objectif is checking the set of points satisfying ϕ.

Algorithm 4 Validation of Tumor Segmentation

```
% initialization
Close all
clear
addpath('Lib') // Appeler la fonction de chaque opérateur
load(strcat('Data\', num2str(i)))
flair = mat2gray(cjdata.image);
% Extraction of the brain region
[m,n,k] = size(flair);
temp = regionprops(~(flair < 0.1));
border = zeros([m, n]);
border = insertShape(border, 'FilledRectangle',temp(1).BoundingBox,...  'color', 'white');
border = border(:, :, 1) > 0.5;  <=> border\= φ1
Background = connect (border, flair < 0.1) ;
Brain=! background
brain_roi = str(2, imerode(bwfill(brain > 4e-2, 'holes'), ...
strel('disk', round(length(brain)/20))));
% Preparing the percentage fliar
pflair = mat2gray(imadjust(flair .* brain_roi, stretchlim(flair .* brain_roi), [], 0.8));
flt_pflair = imfilter(pflair, fspecial('average', round(length(pflair)/20)));
% The initial tumor location
initial_tumor_location = str (2, (flt_pflair > 0.95 * max(flt_pflair(:))));
% Final tumor segmentation
tumFinal = increase (pflair, initial_tumor_location, 50);
```

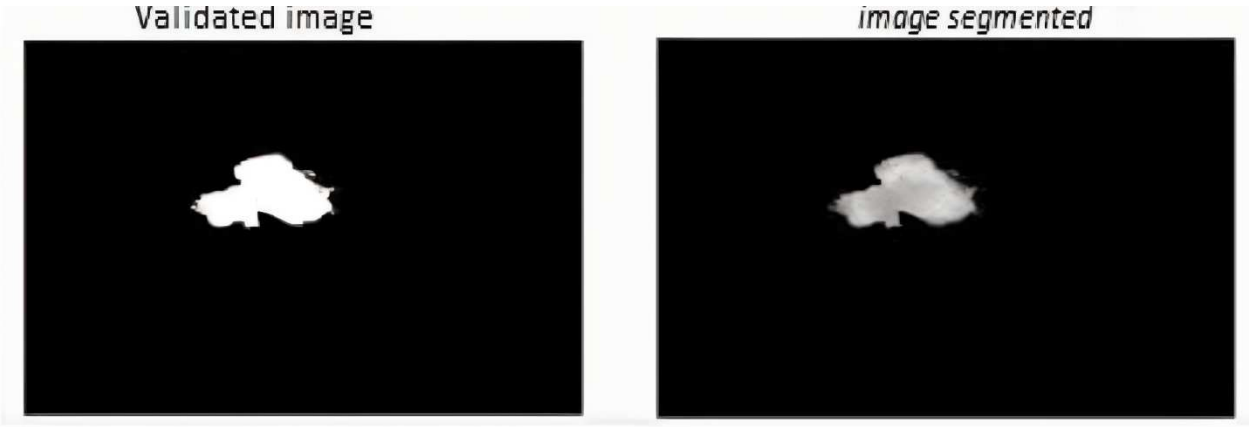


Fig. 8 validated image and Segmented image

7.7 Performance evaluations

We used the confusion matrix, which is a matrix that measures the effectiveness of a rating system. One of the benefits of a confusion matrix is that it may immediately show whether the classification process can be classified correctly. Tumor segmentation outcomes are evaluated against a variety of indicators used to compare the effectiveness of different methodologies. These indicators are True positives (TP), True negatives (TN), False positives (FP), and False negatives (FN).

$$\boldsymbol{Precision} = \frac{TP}{(TP+FP)} \tag{1}$$

$$\boldsymbol{Recall} = \frac{TP}{(FN+TP)} \tag{2}$$

$$\boldsymbol{Accuracy} = \frac{(TP+TN)}{(TP+FN+TN+FP)} \tag{3}$$

$$\boldsymbol{F1-score} = \frac{2(precision*recall)}{precision+recall} \tag{4}$$

By using the confusion matrix and calculating the performance criteria for the current and proposed methods, we were able to obtain good results where the accuracy reached 98% compared to previous works that did not exceed 97%, as indicated in table 1, where we were able to integrate the model checking with machine learning approaches to obtain good results, which confirms The role of model checking in the analysis of medical images.

Table 1 Performance parameters of the existing and proposed methods.

Technique	**Accuracy**	**Precision**	**Recall**
MobileNet [254]	96.17%	96.17%	96.12%
Markov model(DTMC) [256]	97.65%	71.65%	99.87%
Cellular Automata [251]	93 %	95%	90%
Model Checking	98%	96.15%	100%

In order to clarify the results, the chart below compares our previous work in this area with our most recent work. Where we relied on the same data set and reliance on different techniques, such as the Markov model, the cellular automata, and MobileNet, but in the current work, we relied on a combination of machine learning approaches and model checking, as it became clear that this technique helps in reducing errors in addition to improving the quality of tumor detection.

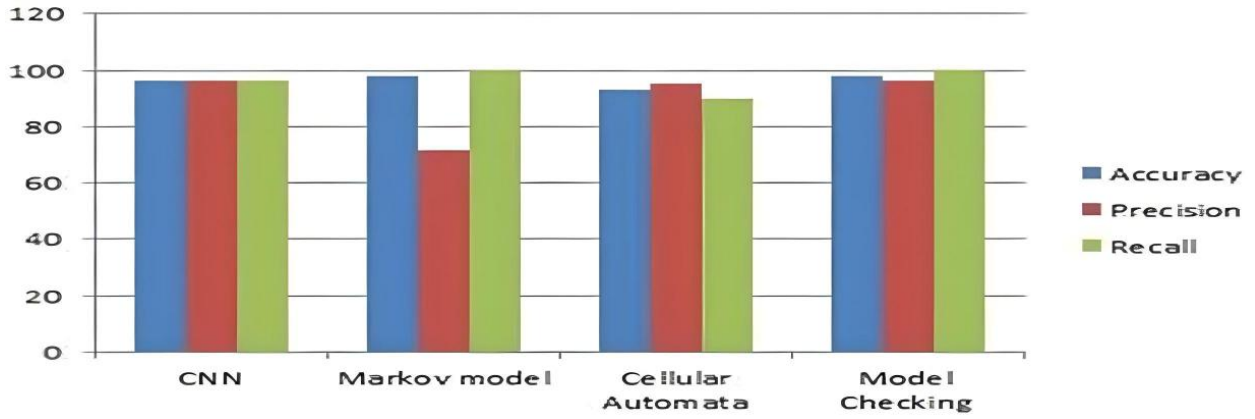


Fig. 8 Comparison between existing and proposed methods

7.8 Conclusion and Future Works

In this work, we verified the detection of tumors using model checking, where the results confirmed the effectiveness of the proposed method, as the accuracy rate reached 98 %, and this proves the role of model checking in the field of medical image analysis. This is done by integrating it with other techniques, such as deep learning, machine learning, the Markov model, and cellular automata. Moreover, model checking helps to reduce the percentage of errors in addition to improving the quality of tumor detection.

In our future work, we will focus on the presentation of another case study, which is the segmentation of a tumor in a more advanced way; this method can also be generalized and applied to the segmentation of other tumors located in other parts of the body. Which will highlight the role of Model Checking in the highly advanced roles, creating a specification language for tumor segmentation, where we will treat the images as a model that can be studied in detail. In addition, we will work on creating an algorithm to detect similar regions of tumors using Model Checking techniques and identify similarities in detail.

CHAPITRE 8 DISCUSSION GÉNÉRALE

Dans ce chapitre, nous présentons une revue succincte des contributions de cette thèse en précisant leurs apports et leurs limites. L'évaluation des contributions s'appuie sur la matrice de confusion, Une caractéristique de la matrice de confusion est d'évaluer principalement des mesures de performance telles que la précision, l'exactitude, le rappel et le score F1.

8.1 Prédiction de la croissance des tumeurs

La première contribution, de cette thèse, consiste en une technique de prédiction de la croissance tumorale, basée sur le modèle de Markov (DTMC) et les algorithmes d'apprentissage KNN. En utilisant un ensemble de données de 20 sujets atteints de glioblastome primaire nouvellement diagnostiqué, un modèle a été entraîné pour extraire toutes les informations liées à la croissance des tumeurs cérébrales et déterminer ensuite les probabilités de transition d'un état d'avancement d'une tumeur à un autre. En termes d'évaluation des performances, les résultats de tests montrent son efficacité dans la prédiction de la croissance tumorale avec une précision d'environ 97.65%. Le tableau ci-dessous présente les résultats de la méthode proposée par rapport à celle présentée dans [262].

Tableau 3. Paramètres de performance de la méthode décrite dans [256] et de celle proposée

Paramètres de performance	**Méthode proposée**	**Méthode existante**
Exactitude	97.65%	89.2%
Sensibilité	99.87%	88.9%
Spécificité	71.65%	90%

Ce gain en précision pourrait s'expliquer par les avantages de l'utilisation du modèle de Markov pour la prédiction de la croissance tumorale. En effet, ce modèle permet de capturer la nature stochastique du processus de croissance. En effet, la croissance tumorale est un processus

complexe et imprévisible qui peut être influencé par de nombreux facteurs, notamment, les mutations génétiques, les facteurs environnementaux et les interventions thérapeutiques. Le modèle de Markov peut intégrer ces facteurs et fournir une estimation probabiliste de la croissance future de la tumeur plus précise.

8.2 Détection des tumeurs cérébrales

La deuxième contribution est une technique de détection de tumeurs cérébrales basée sur les automates cellulaires et leur algorithme de voisinage de Moore. Les automates cellulaires servent à représenter une image sous forme d'un espace discret composé de cellules (pixels, voxels ou régions) et à spécifier l'état de chaque cellule sous forme d'attributs. L'état successeur d'une cellule dépend, non seulement de l'état courant de la cellule, mais aussi de ceux des cellules voisines. La détection des zones de cellules cancéreuses dans l'image s'appuie sur l'analyse de l'évolution de l'automate cellulaire. Les résultats de cette analyse confirment l'efficacité de la méthode proposée sur tous les jeux de données considérés, avec une exactitude de plus de 93% et une précision de 95%, comme le montre le graphique suivant :

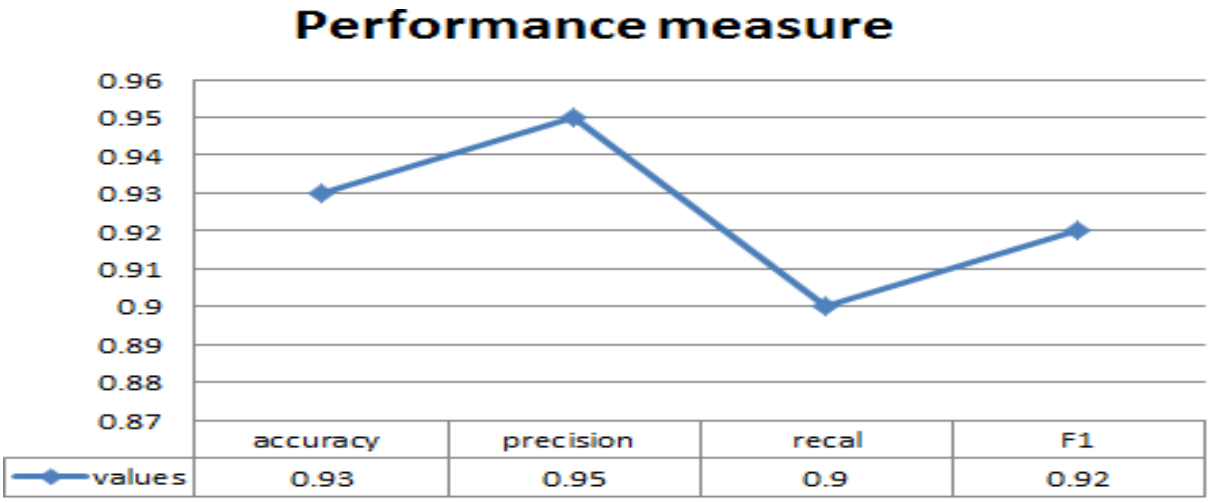


Figure 6 Mesure du rendement.

Le gain Les automates cellulaires permettent la modélisation du comportement de cellules individuelles en réponse à différents stimuli environnementaux, tels que la disponibilité des nutriments ou la présence d'autres cellules. Cela peut aider à mieux comprendre le comportement des cellules cancéreuses et leur interaction avec les cellules saines. Le modèle d'automates

cellulaires est capable de simuler efficacement différents scénarios concernant la détection et la croissance tumorale.

8.3 Classification des tumeurs cérébrales

La troisième contribution propose une technique de classification des tumeurs cérébrales basée sur l'architecture MobileNet. Cette technique a été testée sur l'ensemble de données Kaggle Brain Tumor Classification (MRI), qui est composé de 2363 images de trois catégories (gliome, méningiome et saine). Les résultats obtenus ont été comparés avec ceux obtenus en utilisant MobileNetV2, afin de vérifier si nous pouvions obtenir des temps d'entrainement plus courts, et une plus grande précision. Avec une précision supérieure à 96,09 %, la comparaison a confirmé l'efficacité de la méthode proposée sur l'ensemble de données utilisée. Les résultats obtenus sont présentés dans la figure 7 ci-dessous.

	precision	recall	f1-score	support
0	0.9767	0.9767	0.9767	43
1	0.9750	0.9070	0.9398	43
2	0.9333	1.0000	0.9655	42
accuracy			0.9609	128
macro avg	0.9617	0.9612	0.9607	128
weighted avg	0.9619	0.9609	0.9606	128

Figure 7 Exactitude de la méthode proposée et la courbe de perte utilisant le modèle MobileNet

Comme indiqué, la figure 7 illustre le ratio de précision élevé, qui varie entre 93,33 % et 97,67 % pour les ensembles de données utilisés, ainsi que le ratio de rappel élevé, qui varie entre 96,12 % et 97,67 %, et enfin le ratio de score F1 élevé, qui varie de 93,98 et 97,67 %.

Le choix de MobileNet a permis de réduire le nombre de paramètres à gérer et d'augmenter la précision, sans affecter considérablement le temps de classification.

8.4 Validation de la détection des tumeurs cérébrale

La quatrième contribution est une nouvelle approche pour valider la détection des tumeurs cérébrales en utilisant la technique du model-checking. Cette méthode consiste à modéliser le système de détection de la tumeur et à vérifier son comportement. Cette étude a utilisé un ensemble de données accessible au public sélectionné à partir de Kaggle. Il contient deux catégories : une catégorie de tumeurs avec plusieurs cas de tumeurs qui diffèrent par leur emplacement, leur taille et leur vitesse de propagation, et une catégorie saine qui n'inclut pas les tumeurs. La catégorie tumorale comprend 1550 images et la catégorie non tumorale comprend 980 images. En utilisant cette approche, les résultats obtenus ont montré une grande précision, avec un taux d'exactitude de 98%, un taux de précision de 96,15% et un rappel de 100%. Cela signifie que la méthode de validation proposée est très fiable et peut être utilisée pour améliorer la précision et la fiabilité de la détection des tumeurs cérébrales dans les images médicales.

CHAPITRE 9 CONCLUSION

Ce chapitre récapitule les travaux réalisés, dans le cadre de cette thèse, ainsi que leurs limites et les améliorations futures.

Ces dernières décennies, il est devenu urgent et impératif de mettre à contribution tous les moyens matériel et logiciel pour classer, détecter et prédire le pronostic des tumeurs cérébrales, afin de réduire leur fort et inquiétant taux de mortalité. Le centre d'intérêt doit convoiter de nouvelles techniques plus efficaces et plus fiables.

C'est dans ce sens que cette thèse a proposé et testé de nouvelles approches pour la détection, la classification et la prédiction des tumeurs cérébrales, basées sur des techniques d'apprentissage automatique et des modèles formels, comme le modèle de Markov, les automates cellulaires et les systèmes de transition. Les tests comparatifs, sur un ensemble de données vaste et diversifié d'examens IRM et de leurs images pathologiques associées, montrent un gain en précision et en efficacité. En effet, le taux de précision passe de 89,2 % à 97,65 % pour la prédiction de la croissance tumorale. En ce qui concerne la détection et la classification, la précision atteint 98 %, pour l'ensemble des données testés. D'autres tests sont cependant nécessaires pour confirmer et améliorer les apports de ces approches.

L'une des principales limites de ces approches est qu'elles ne peuvent pas être généralisées et appliquées systématiquement à d'autres ensembles de données qui ont des types d'informations et d'annotations différents, de plus, le rôle de certains modèles, tels que le model checking, se limite à vérifier le modèle selon les spécifications ou exigences spécifiques qui ont été identifiées pour le système ou le modèle en cours de vérification. Cela signifie que s'il existe d'autres facteurs non inclus dans la spécification, l'analyse du modèle peut ne pas être en mesure de vérifier avec précision la détection de la tumeur.

Dans nos futurs travaux, nous travaillerons à résoudre les limites de cette thèse à travers deux points importants :

Premièrement, nous nous concentrerons sur la création d'un algorithme pouvant être intégré à la méthode existante afin que la méthode actuelle puisse être généralisée et appliquée systématiquement à d'autres ensembles de données contenant différents types d'informations et d'annotations. Cette méthode peut également être généralisée et appliquée à la segmentation d'autres tumeurs situées dans d'autres parties du corps ou autres objets [263].

Deuxièmement, pour améliorer la validation de model checking et garantir sa capacité à valider la détection des tumeurs avec une grande précision, il est important d'effectuer des tests approfondis pour vérifier la précision de la détection de la tumeur. Cela peut inclure des tests d'erreur pour vérifier la robustesse du système et des tests d'interopérabilité pour vérifier que le formulaire fonctionne correctement avec les autres systèmes.

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