DEPARTMENT OF

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MASTER IN MSC PROGRAM NAME

A VERY LONG AND IMPRESSIVE

THESIS TITILE WITH A FORCED LINE BREAK

SOME THOUGHTS ON THE LIFE, THE UNIVERSE,

AND EVERYTHING ELSE

JOHN VERY LONGNAME DOE

BSc in name of previous degree

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A VERY LONG AND IMPRESSIVE

THESIS TITLE WITH A FORCED LINE BREAK

SOME THOUGHTS ON THE LIFE, THE UNIVERSE,

AND EVERYTHING ELSE

**JOHN VERY LONGNAME DOE**

BSc in name of previous degree

**A Very Long and Impressive Thesis Title with a Forced Line Break**

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Acknowledgments

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However, without any intention of conditioning the form or content of this text, I would like to add that it usually starts with academic thanks (instructors, etc.); then institutional thanks (Research Center, Department, Faculty, University, FCT / MEC scholarships, etc.) and, finally, the personal ones (friends, family, etc.).

But I insist that there are no fixed rules for this text, and it must, above all, express what the author feels.

“You cannot teach a man anything; you can only help him  
discover it in himself.” (Galileo).

Abstract

The identification of cancer cells is a critical task in biomedical research and clinical practice, with significant implications for disease diagnosis, treatment, and prognosis. However, current methods often rely on manual annotation and interpretation of large datasets, which can be time-consuming, labor-intensive, and prone to human error.

This thesis explores the potential application of **Large Language Models (LLMs)** to identify cancer cells from various data sources, more specifically ultrasound, mammogram and thermogram images, tomosynthesis 3D images and histopathology slides. While LLMs are typically trained on text-based data, their ability to learn patterns and relationships within language can be leveraged in conjunction with other methods to analyze images and signals associated with cancer cells and masses. The challenge lies in finding ways to integrate these different approaches effectively, and to develop novel methods that can take advantage of the unique strengths of each technique. By exploring the potential applications of LLMs in image analysis, we may uncover new insights into the possibilities for combining language-based and visual-based approaches to solve complex problems in biomedical research.

The proposed research is interesting and challenging because it pushes the boundaries of what is possible using LLMs. By investigating the feasibility of applying LLMs to this problem, we aim to contribute to a deeper understanding of the potential applications of language models in biomedical research. This thesis can bring new insights into the strengths and limitations of LLMs for breast cancer identification and has the potential to contribute to the development of novel diagnostic tools and approaches.

**Keywords**: Breast Cancer, Large Language Models, Deep Learning, Artificial Inteligence.

Resumo

A identificação de células cancerígenas é uma tarefa crítica na investigação biomédica e na prática clínica, com implicações significativas no diagnóstico, tratamento e prognóstico da doença. No entanto, os métodos actuais baseiam-se frequentemente na anotação e interpretação manual de grandes conjuntos de dados, o que pode ser moroso, trabalhoso e propenso a erros humanos.

Esta tese explora a potencial aplicação de modelos de linguagem de grande dimensão (LLM) para identificar células cancerígenas a partir de várias fontes de dados, mais especificamente imagens de ultra-sons, mamografias e termogramas, imagens 3D de tomossíntese e lâminas histopatológicas. Embora os LLMs sejam normalmente treinados em dados baseados em texto, a sua capacidade de aprender padrões e relações dentro da linguagem pode ser aproveitada em conjunto com outros métodos para analisar imagens e sinais associados a células e massas cancerígenas. O desafio reside em encontrar formas de integrar eficazmente estas diferentes abordagens e desenvolver novos métodos que possam tirar partido dos pontos fortes únicos de cada técnica. Ao explorar as potenciais aplicações de LLMs na análise de imagens, podemos descobrir novas perspectivas sobre as possibilidades de combinar abordagens baseadas na linguagem e visuais para resolver problemas complexos na investigação biomédica.

A investigação proposta é interessante e desafiadora porque ultrapassa os limites do que é possível fazer com LLMs. Ao investigar a viabilidade da aplicação de LLMs a este problema, pretendemos contribuir para uma compreensão mais profunda das potenciais aplicações de modelos de linguagem na investigação biomédica. Esta tese pode trazer novos conhecimentos sobre os pontos fortes e as limitações dos LLMs para a identificação do cancro da mama e tem o potencial de contribuir para o desenvolvimento de novas ferramentas e abordagens de diagnóstico.

(Traduzido com a versão gratuita do tradutor - DeepL.com)

**Palavras chave**: Cancro da mama, *Large Language Models*, *Deep Learning*, Inteligência Artificial.

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Glossary

|  |  |
| --- | --- |
| **Computer** | A programmable usually electronic device that can store, retrieve, and process data. |
| **Cell phone** | A portable usually cordless telephone for use in a cellular system. |

.

Acronyms

|  |  |
| --- | --- |
| **LLM** | Large Language Model |
| **UI** | User Interface |

Symbols

|  |  |
| --- | --- |
| **π** | The ratio of the circumference of a circle to its diameter, having a value rounded to eight decimal places of 3.14159265 (symbol: π). |
| ***r*** | The radius of a circle. |

# Introduction

The accurate identification of cancer cells is a critical task in biomedical research and clinical practice, with significant implications for disease diagnosis, treatment, and prognosis. The exponential growth of medical imaging technologies has led to an overwhelming volume of image data, which must be analyzed and interpreted by clinicians and researchers. However, current methods for analyzing these images often rely on manual annotation and interpretation, a time-consuming process that is prone to human error [1].

The limitations of traditional image analysis methods have been compounded by the increasing demand for precision medicine and personalized healthcare. The development of targeted therapies and immunotherapies requires a deep understanding of individual patient biology, which can only be achieved through detailed analysis of large-scale imaging data. However, the manual annotation of these images is often a significant bottleneck in research and clinical settings.

Researchers have been exploring various solutions to overcome the challenges of image analysis, including the development of novel algorithms and techniques that leverage advances in machine learning and computer vision. However, more work is needed to develop practical and effective methods for analyzing complex imaging data. This thesis aims to contribute to this effort by investigating the potential application of **Large Language Models (LLMs)** in analyzing images of cancer cells and masses [1] [2].

## The problems

The process of identifying cancer cells from medical images is a complex and time-consuming task, often requiring extensive expertise and specialized knowledge. Clinicians and researchers are faced with the daunting challenge of analyzing vast amounts of imaging data, which can be overwhelming even for experienced professionals. The consequences of inaccurate or delayed diagnoses can be severe, highlighting the need for more effective and efficient image analysis methods [3].

One of the primary limitations of current image analysis approaches is their rigid structure and reliance on standardized protocols. While these methods have been refined over time, they can struggle to adapt to emerging trends and technologies in medical imaging. The increasing availability of high-resolution images and advanced imaging modalities has created a need for more flexible and dynamic analysis techniques that can accommodate the diverse range of data being generated [4].

The potential integration of LLMs into image analysis presents both opportunities and challenges. On one hand, these models have been successfully applied to a wide range of natural language tasks and may offer new insights into visual data representation. However, their adaptation to image analysis requires significant modifications to address the unique characteristics of visual information. For instance, language-based models must be able to interpret complex spatial relationships and patterns within images, which can be difficult to articulate in textual form [5].

Furthermore, the implementation of language-based models in medical imaging raises important questions about bias, accuracy, and transparency. It is essential that these models are designed with careful consideration of the potential pitfalls associated with their use, such as perpetuating existing biases or introducing new ones through their training processes. Additionally, the need for clear and interpretable results cannot be overstated, particularly in high-stakes medical decision-making environments [6].

## Proposed Solution

To address the challenges of image analysis in cancer cell identification, we propose a multi-modal approach that leverages the strengths of various Large Language Models (LLMs) to analyze different types of medical images. Specifically, we will utilize a combination of publicly available LLMs trained on natural language processing tasks to extract relevant features from mammograms, ultrasounds, thermograms, tomosynthesis images, and histopathology slides. To facilitate the integration of these models with visual data, we will convert the image pixels into base64-encoded strings, enabling the LLMs to process and analyze the images in a textual format [7].

We will utilize a combination of pre-trained LLMs and adapt them to our specific task by fine-tuning them on publicly available medical imaging datasets [8] [9]. This approach allows us to leverage the strengths of each LLM architecture while also ensuring that they are optimized for our particular application.

Then, to evaluate the effectiveness of our proposed solution, we will conduct an extensive analysis of the models’ accuracy, precision, recall, and F1-score on various image types. We will also investigate the impact of different hyperparameters, such as learning rates and batch sizes, on model performance and select the most suitable settings for each LLM architecture.

Our proposed multi-modal approach using LLMs offers a promising framework for analyzing medical images and identifying cancer cells. By leveraging the strengths of multiple models, we can develop a more robust and reliable system that improves upon existing methods. While our study focuses on comparing the performance of several different LLM architectures, it also highlights the need for further research into this area. Future work could involve exploring other LLM architectures or developing more sophisticated methods for combining multiple models to improve overall performance [10].

## Context and Motivation

Traditional machine learning and deep learning methods have been widely used for medical image analysis, but they often require extensive technical expertise to implement and interpret. In contrast, LLMs offer a more accessible and user-friendly approach that can be easily integrated into existing clinical workflows. By representing images as text using base64 encoding through a front-end UI, we can leverage the strengths of LLMs in processing sequential data, while also making it easier for clinicians to interact with the system.

The ease of use is particularly important in medical image analysis, where doctors and clinicians may not have extensive technical knowledge or experience with machine learning algorithms. With traditional deep learning methods, clinicians often require significant training and support to accurately interpret results and fine-tune models to their specific needs. In contrast, LLMs can be easily fine-tuned using a user-friendly interface, allowing clinicians to quickly adapt the system to their workflow without requiring extensive technical expertise [11].

Furthermore, LLMs are pre-trained on vast amounts of natural language data, allowing them to learn complex patterns and relationships that may not be apparent through traditional feature engineering. This means that clinicians can focus on interpreting results rather than spending hours fine-tuning models or hand-crafting features [12].

By making medical image analysis more accessible and user-friendly, we can empower clinicians to make more accurate diagnoses and improve patient outcomes.

## Document Structure

The current chapter 1 is an introductory text to contextualize the reader and present the currrent challenges at hand, as well as the brief solution to implement our work.

On chapter 2 we will present the research made by other researchers in this regard, as well as the state-of-the-art technologies that are currently used regarding this subject.

Next, on chapter 3 we will dive a bit deeper in the technical details of the implementation of our system while also presenting a work schedule and the work that is alrready beign developed.

Finally, on chapter 4 we will analyze our results and take our conclusions from it, deciding on the acccurracy (mostly) of the different models in all the situations considered durring the study.

# State of the art

Image analysis has long been an area of active research in the field of medical examination, more specifically breast cancer detection. In recent years, the use of AI techniques has revolutionized the field, enabling the development of highly accurate models for tasks such as tumor segmentation, lesion detection, and image classification.

However, despite these advances, there is still much work to be done in developing robust and reliable medical image analysis systems that can be widely adopted in clinical settings. This chapter provides an overview of the current state of the art in medical image analysis, highlighting recent advances and challenges in areas such as deep learning architectures, data augmentation techniques, and model interpretability.

## Conventional exam methods

The detection of breast cancer relies heavily on a combination of conventional examination techniques, including mammography, ultrasound, digital breast tomosynthesis (DBT), and thermography. While these modalities have revolutionized the field of breast imaging, they all share one common limitation: the reliance on human interpretation [13]. Each modality requires specialized training and expertise to accurately interpret results, which can lead to variability in diagnosis and treatment recommendations between healthcare providers. Furthermore, even with the aid of advanced technology, these methods are inherently limited by their inability to provide a comprehensive view of the breast tissue, leaving some cancers undetected or misdiagnosed.

This chapter explores the conventional examination methods currently used in clinical practice, highlighting both their strengths and limitations.

### Mammography

Mammography has been the primary screening tool for breast cancer since its introduction in the 1960s [14]. It involves the use of low-energy X-rays to produce images of the breast tissue. The technique is based on the principle that dense breast tissue absorbs more X-ray energy than fatty tissue, resulting in a higher contrast between normal and pathological tissues.

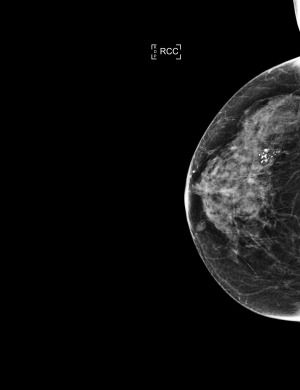


Figure 2.1: Example of a mamogram image (Adapted from [15])

When a radiologist examines a mammogram, they are searching for subtle clues that may indicate the presence of breast cancer. The interpretation process is both nuanced and complex, requiring a deep understanding of the various features that can be present within the image.

One key area of focus is the detection of calcifications - small deposits of calcium that can accumulate within the breast tissue. These tiny formations can often be indicative of cancer, particularly when they appear in a characteristic pattern or are associated with other suspicious findings. In addition to calcifications, radiologists also look for masses - solid or cystic lesions that may indicate the presence of a tumor. Densities - areas of increased breast density - can also be an area of concern, as these can be caused by fibrosis (scarring), inflammation, or even cancer. Finally, radiologists will examine the symmetry and shape of the breasts, searching for any signs of asymmetry that may indicate an underlying issue.

While mammography has been a powerful tool in the detection of breast cancer, it is not without its limitations. One major concern is the issue of false positives - benign lesions are often identified as suspicious, leading to unnecessary biopsies and subsequent anxiety for patients.

Conversely, some cancers may be missed altogether due to their small size or location within the breast. This can be particularly problematic in women with dense breast tissue, who may be at higher risk for false negatives [16]. Furthermore, mammography sensitivity can vary by age and ethnicity, with younger women and those of African descent being at higher risk for false negatives [14]. It is also important to consider the factor of human error in the analysis of these sets of images.

### Ultrasound

Ultrasound imaging has become an increasingly important tool in the assessment of breast lesions, particularly in conjunction with mammography and other diagnostic modalities. Ultrasound uses high-frequency sound waves to create images of structures within the body, allowing for real-time visualization of the breast tissue [17].

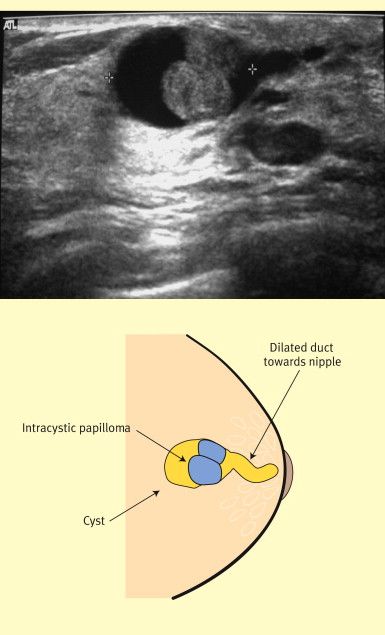


Figure 2.2: Example of a Mammogram (Adapted from [18])

One of the key strengths of ultrasound is its ability to characterize lesions, distinguishing between benign and malignant growths. This enables clinicians to develop targeted treatment plans that maximize patient outcomes. Moreover, ultrasound provides precise measurements of tumor size, which is essential for determining the most effective course of treatment. In addition to these benefits, ultrasound can also guide biopsy procedures, ensuring that tissue samples are obtained with precision and accuracy. By reducing the risk of complications and improving diagnostic yield, ultrasound plays a critical role in the early detection and treatment of breast cancer [19].

Despite its many advantages, ultrasound is not without limitations. The quality of ultrasound images depends heavily on the skill and experience of the operator, which can lead to variations in image interpretation. Furthermore, ultrasound waves have limited penetration depth, making it challenging to image deeper structures within the breast [20].

### Thermogram

## The Types of Text

The template defines five text styles:

* + **Normal** — for the main text, using the Palatino font, with paragraph indentation and line spacing of 1.2x.
  + **Heading 1** — style for the chapter title.
  + **Heading 2** — style for the sections.
  + **Heading 3** — style for the subsections.
  + **Heading 4** — style for the sub-subsections.

## The Table of Contents and other Lists

The document will have several indexes, all of them starting on a unique page, namely:

1. **Table of contents** [required]
2. **List of Figures** [if you have more than three figures]
3. **List of Tables** [if you have more than three tables]
4. **List of Equations** [if you have more than three equations/formulas]
5. **List of Listings** (code/programs) [if you have more than three listings]
6. **Other lists** [glossary, acronyms, symbols, etc]

## References to Chapters, Sections, Figures, Tables, etc.

Whenever you refer to a numbered object present in the text, you should not insert the number as text, but insert a cross-reference using the appropriate menu. In this way, if the objects are renumbered (for example, because inserting a new figure in the middle of two existing figures), the curated references will also be updated automatically.

## The Bibliography

The bibliography appears after the main body of the text and before the Appendices and Annexes.

There are many bibliographic standards and styles. Each scientific area has its own way of presenting both citations and bibliographic references. The most common styles are the APA (American Psychological Association - author/date), now in its 7th edition, and the IEEE (Institute of Electrical and Electronics Engineers - numerical).

There is more than one way to cite/quote other authors in a text, however these can be divided in 2 big classes:

• **Indirect or conceptual citations**, in which we reproduce someone else's ideas in our own words through paraphrases;

• **Direct or formal quotations**, in which we transcribe exactly the words of an author using quotation marks.

The citation models follow 3 systems:

• **Author-date system**, in which the citation appears like this: (Santos, 2003), if there are two authors (Santos and Correia, 2003) and if there are more than 5 authors (Santos, et al., 2003), of which the best known and most used is the [APA style](https://apastyle.apa.org/);

• **Numerical system**, in which each citation is identified with a number [1] and the list of bibliographic references is compiled at the end of the work (bibliography), of which the best known and used style is the [IEEE](https://ieeeauthorcenter.ieee.org/wp-content/uploads/IEEE-Reference-Guide.pdf).

There are also **mixed systems**, in which the citation/quotation in the text is numeric, but the bibliography is sorted alphabetically by the author's surname. Examples of mixed styles are: Springer Lecture notes in Computer Science (alphabetically sorted) and the Council of Science Editors, Citation-Name (numeric alphabetically sorted), amongst others.

The most used styles, in general, are APA and IEEE, FCT is no exception, however you should always define with your advisor the standard or style to use.

The Library of FCT-NOVA provides training on these subjects, as well as support in the use of bibliographic management tools such as Mendeley and Zotero.

# Let’s Create Another Chapter

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Figure 3.1 — Looks list the April’s 25 bridge in Lisbon but it is not. It is the Golden Gate, in S. Francisco in California, USA.

#### Yet another sob-subsection

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Table 3.1 — Portuguese population by age range.

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| --- | --- | --- | --- | --- |
|  | 1971 | 1980 | 1990 | 2000 |
| 0–24 | 3 861 916 | 4 131 825 | 3 660 978 | 3 176 450 |
| 25–49 | 2 658 361 | 3 015 450 | 3 312 011 | 3 705 865 |
| 50–74 | 1 851 909 | 2 245 875 | 2 482 266 | 2 718 007 |
| +75 | 271 575 | 373 125 | 527 967 | 689 581 |
| Total | 8 643 756 | 9 766 275 | 9 983 218 | 10 289 898 |

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Figure 3.1 — And another figure with a caption.

Table 3.2 — This table is identical to the previous one, but it is here so that we have not only one but rather two tables in our docuemnt. And as this caption is very long, it should be justified and not centered.

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|  | 1971 | 1980 | 1990 | 2000 |
| 0–24 | 3 861 916 | 4 131 825 | 3 660 978 | 3 176 450 |
| 25–49 | 2 658 361 | 3 015 450 | 3 312 011 | 3 705 865 |
| 50–74 | 1 851 909 | 2 245 875 | 2 482 266 | 2 718 007 |
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1. An Appendix

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