NOVA SCHOOL OF
SCIENCE & TECHNOLOGY

DEPARTMENT OF
COMPUTER SCIENCE

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BSc in Computer Science and Engineering

LEARNING TO MAP MICRORNA BIOMARKERS SIGNATURES TO BREAST CANCER SUBTYPES

MASTER IN COMPUTER SCIENCE AND ENGINEERING

NOVA University Lisbon
Draft: *June 23, 2025*

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ABSTRACT

Regardless of the language in which the dissertation is written, usually there are at least two abstracts: one abstract in the same language as the main text, and another abstract in some other language.

Keywords: One keyword, Another keyword, Yet another keyword, One keyword more, The last keyword

Resumo

Independentemente da língua em que a dissertação está escrita, geralmente esta contém pelo menos dois resumos: um resumo na mesma língua do texto principal e outro resumo numa outra língua.

Palavras-chave: Primeira palavra-chave, Outra palavra-chave, Mais uma palavra-chave, A última palavra-chave

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Acronyms

AI	Artificial Intelligence *(p. 3)*
BC	Breast Cancer *(pp. 1–3, 5)*
DL	Deep Learning *(pp. 3, 5)*
DNA	Deoxyribonucleic Acid *(pp. iv, 6, 7)*
miRNAs	microRNAs *(pp. 2–5)*
ML	Machine Learning *(pp. 3, 5)*
RNA	Ribonucleic Acid *(pp. 6–8)*

1

Introduction

1.1 Motivation & Problem Statement

1.1.1 Breast Cancer - A Global Health Challenge

Breast Cancer (BC) is currently one of the biggest public health challenges worldwide. In 2022, more than 2.3 million new cases of BC were diagnosed, resulting in around 665,000 global deaths (Bray et al. [9]). Other studies estimate that BC will continue to not only bethe most commonly diagnosed cancer but also to increase in incidence, with projections indicating that by 2040, the number of deaths will almost double and the number of new cases will be around 3.2 million (Arnold et al. [5]). These figures underline the high incidence and mortality associated with the disease, highlighting the ongoing need to develop more effective strategies for its diagnosis and treatment.

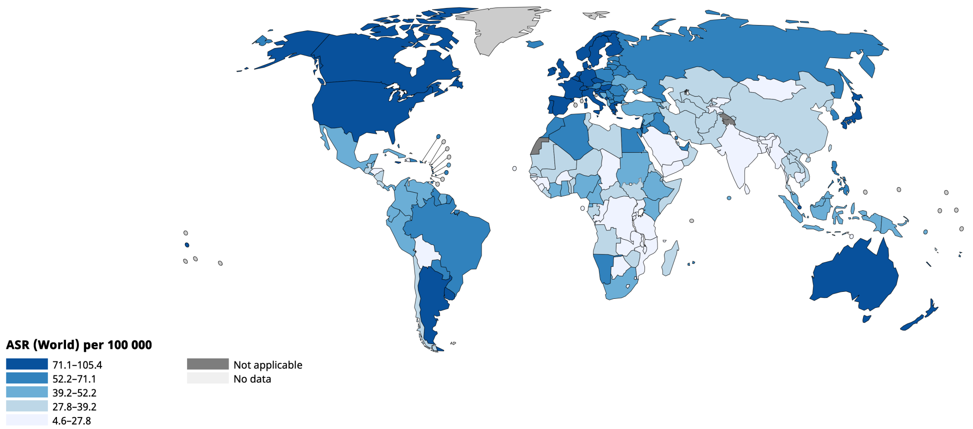
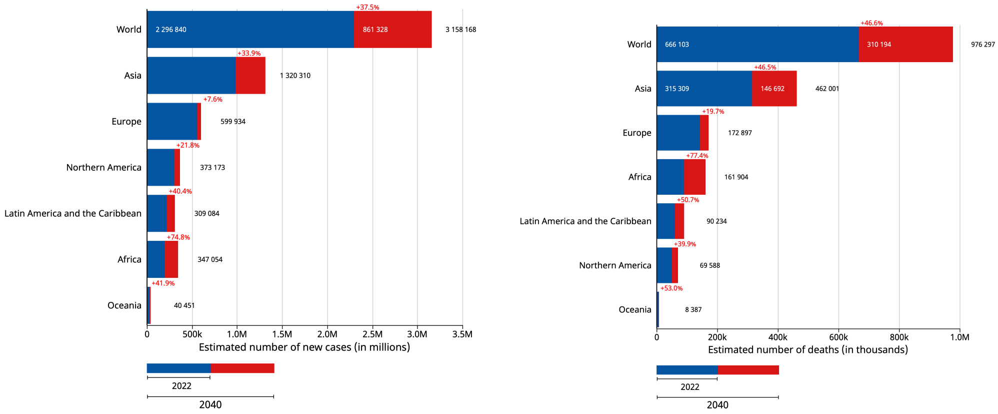


Figure 1.1: Age-standardized incidence rate (ASR, per 100,000 inhabitants) of breast cancer in both sexes in 2022. The data represent global estimates based on International Agency for Research on Cancer [17], highlighting significant geographical variations in disease burden.



(a) Estimate number of new cases of Breast Cancer

(b) Estimate number of deaths caused by Breast Cancer

Figure 1.2: Visual comparison of the estimated number of new cases and deaths caused by Breast Cancer in 2020 (in blue) and 2040 (in red). (International Agency for Research on Cancer [17])

BC is characterized by marked biological heterogeneity, manifested in multiple molecular subtypes that exhibit distinct clinical behaviors (Perou et al. [25]). Each subtype exhibits substantial differences in terms of tumor aggressiveness, metastatic potential, and behavior to specific therapies (Prat et al. [27]). Thus, accurate classification of these subtypes is essential to enable personalized therapeutic approaches, with a direct impact on treatment efficacy and patient prognosis (Testa, Castelli, and Pelosi [32]).

1.1.2 Can we improve the classification of Breast Cancer subtypes?

Among the emerging candidates for robust biomarkers for the classification of BC subtypes are microRNAs (miRNAs), small non-coding RNA molecules that play a crucial regulatory role in gene expression. They are estimated to modulate the expression of about one-third of the genes in the human genome (Hammond [13]) and are implicated in the regulation of multiple physiological and pathological processes, including various human diseases (Ho, Clark, and Le [14]).

Given their regulatory nature, several studies have demonstrated a significant association between miRNAs expression profiles and relevant clinical characteristics in the context of BC, including processes such as tumor progression and metastasis development (Ho, Clark, and Le [14] Muñoz et al. [22]). In addition to these aspects, a seminal study by Blenkiron et al. [8] demonstrated that miRNAs expression profiles can effectively distinguish between different molecular subtypes of BC, highlighting their potential as a precise subtyping tool. This ability to discriminate between subtypes reinforces the value of miRNAs as promising clinical biomarkers.

1.1.3 How to identify the most relevant miRNAs?

The identification of the most relevant miRNAs for BC subtyping represents a major analytical challenge due to the complexity of these high dimensional regulatory molecules, non-linearity interactions between and clinical phenotypes require advanced computational approaches to be effectively modelled. Recent advances in Artificial Intelligence (AI), particularly in Machine Learning (ML) and Deep Learning (DL), have demonstrated remarkable potential in extracting meaningful patterns from high-dimensional and heterogeneous (data from distinct nature) biomedical data (Luo et al. [20]). These approaches enable not only the accurate classification of BC subtypes but also the identification of discriminative miRNAs signatures, supporting their integration as actionable biomarkers in clinical workflows.

In this context, ML and DL models are particularly well suited for the task of robustly characterizing and explaining the profiles of miRNAs-based biomarkers — should such biomarkers exist — with the potential to effectively discriminate between different BC subtypes, as already seen in a study done by Azari et al. [6] where ML algorithms identified potential diagnostic and prognostic miRNAs in gastric cancer, showing high accuracy in the identification of reliable biomarkers for this disease.

This reality reinforces the urgency of developing advanced computational tools that can enable more precise molecular characterization and guide personalized therapeutic decisions, ultimately improving clinical outcomes for patients with aggressive and hard-to-treat BC subtypes.

1.2 Challenges and research hypothesis

Based on the assumption that it is possible to use microRNA expression values and clinical data to map BC subtypes (Ho, Clark, and Le [14] and Muñoz et al. [22]), this dissertation proposes to explore several complementary directions for this pathology where the application of AI techniques is still growing.

First, we intend to assess whether discriminative linear models perform better than latent representation models (in a context where there are two different data sources and many dimensions) - such as DIABLO (Singh et al. [30]), a widely used model. At the same time, we will investigate the impact of patient clinical information (such as age, presence or absence of metastases, hormone levels, among others) on the classification performance of the models, where we will be able to gain valuable insights into possible relationships between these features and BC subtypes.

If substantial results are obtained by any of the models, we will be able to conduct a more extensive study on our main point: whether or not there are miRNAs that are potential biomarkers for BC subtypes. In a more advanced approach, I will be able to explore the applicability of *Conformal Prediction* (Angelopoulos and Bates [4]), which provides statistically based confidence intervals for each prediction (which is widely used in areas where risk must be justified and well-founded, such as finance and healthcare). The latter is an approach that is still gaining ground in healthcare and, considering our problem, it makes sense to be able to give a prediction based on a confidence interval, giving our model greater transparency and reliability, something particularly relevant in clinical contexts where error must be minimized and uncertainty well characterized.

Even though the base seems promising, there are several challenges to overcome in order to achieve the desired results such as:

1. Biological heterogeneity:

Biological heterogeneity is characterized by the diversity of living organisms, including species, genotypes, and populations, which exhibit a variety of biological characteristics, such as morphology, physiology, genetics, and biogeography. The human body is a highly complex system in which the behavior of each component depends on its interaction with countless other parts. Exposure to the same treatment by two bodies can result in completely different reactions.

2. Functional complexity of microRNAs:

The role of miRNAs in biological regulation and cancer progression is extremely complex and still relatively new from a scientific point of view. The action of a single microRNA is not isolated, but rather part of a network of interactions with dozens (or hundreds) of other miRNAs and contextual factors. This highly interdependent behavior raises questions about the effectiveness of overly simplistic or linear models. The application of non-linear models allows for the discovery of complex relationships and cross-interactions between different miRNAs or between them and clinical variables. These relationships and interactions would be invisible to more traditional approaches.

3. No control set:

Another relevant challenge is the absence of a control set that includes data from healthy individuals. Since this type of analysis (miRNAs expression profiling) is not routinely performed in individuals without cancer, it is difficult to define what would be a "normal level" of expression. The implementation of a control group would not only broaden the scope of the model's task (e.g., distinguishing between the presence and absence of cancer before predicting the subtype), but also optimize the robustness of biomarker identification. An illustrative example of this phenomenon is presented in the study Azari et al. [6] where the implementation of a control set was fundamental to the identification of discriminative markers.

The data for this study were previously selected by Dr. Bárbara Mendes and her team based on purely biological selection criteria. These criteria included the scientific interest of the group and molecular characteristics that were considered relevant in the context of the research (CONFIRMAR NA REUNIÃO). Consequently, the dataset I was given consists of 256 samples and 888 miRNAs features, as well as 38 clinical data features. This presents a scenario of high dimensionality with a limited number of examples on which to train.

The morphology of this dataset limits the choice of approaches to be used and requires extra caution in how we work with certain models, such as nonlinear ones, given their high adaptability in high dimensions, which, in a context of limited data, can easily lead to overfitting. This requires careful selection of algorithms and attention to the pipeline that is set up to ensure that the results obtained are robust and relevant.

Furthermore, this problem cannot be addressed with data augmentation techniques used in the field of ML, such as *SMOTE* (Synthetic Minority Over-sampling Technique - Blagus and Lusa [7]). As discussed earlier in the topic 1.2, the nature of this data makes reliable synthetic generation unfeasible, which can lead to artificially inconsistent samples (”Extra-terrestial beings”, in other words).

Having a control set would be an important step toward increasing the generalizability of our model. This data set would not only allow us to expand the problem to include the distinction between healthy and sick individuals, but also improve the identification of discriminative biomarkers. The latter has already been successfully tested in other types of cancer, and a key step in the pipeline used is precisely the comparison with a control set (Azari et al. [6]) to isolate clinically relevant markers.

1.3 Expected Contributions

The main contribution of this dissertation is the development of a computational framework for the classification of BC subtypes based on miRNAs expression and patient clinical data. This framework will integrate and compare different ML and DL approaches (still underexplored for this decease) applied to a problem of high biological and statistical complexity.

In addition to the classification process, this framework will include a statistical analysis component aimed at validating the predictions made in order to give robustness to the decision made by the model. This robustness is particularly relevant in a clinical setting, where transparency and reliability of predictions are essential for possible future translation into medical practice.

Throughout the work, a critical and comparative analysis of the approaches explored will be promoted, focusing on their applicability to complex and heterogeneous biomedical data. It is thus hoped to contribute to the development of more robust, explainable computational solutions adapted to the reality of biological systems, reinforcing the potential of miRNAs as relevant molecular markers in the stratification of BC patients.

1.4 Document Organization

2

Background and Related Work

2.1 Biology

The modern understanding of how genetic information is stored, interpreted, and regulated in cells is based on a fundamentalprinciple known as the Central Dogma of Molecular Biology. This concept, first formulated in Pray [28] and Watson and Crick [33], describes the unidirectional flow of genetic information in cells: from DNA to Ribonucleic Acid (RNA) and from there to protein synthesis. According to this model, genes encoded in DNA are transcribed into messenger RNA (or mRNA), which in turn is translated into proteins—the functional molecules responsible for most essential biological processes. This dogma has served as the basis for much of the research in molecular biology and biotechnology.

However, in recent decades, it has become clear that this flow of information is regulated in a much more complex way than initially thought. In particular, it has been discovered that a substantial part of the genome is transcribed into non-coding RNA, i.e., RNA that does not give rise to proteins but plays fundamental regulatory roles. It is in this context that merge, small RNA molecules with central functions in the regulation of gene expression. Their discovery has broadened the classical view of the central dogma, introducing new layers of post-transcriptional control that decisively influence normal and pathological biological phenomena.

DNA & RNA - The Genetic Code

At the molecular level, the genetic information of all living organisms is encoded in a molecule called deoxyribonucleic acid (DNA). DNA consists of two complementary strands arranged in a double helix structure, with each strand consisting of a sequence of nucleotides. These nucleotides are composed of a sugar-phosphate structure and one of four nitrogenous bases: adenine (A), cytosine (C), guanine (G), and thymine (T) Sunrayce Biology Authors [31]. When in the helix structure, these bases can only be linked to their corresponding base: adenine can only be linked to thymine and cytosine to guanine, and it is in the sequence of bases that the instructions necessary for the synthesis of all the proteins that govern cell structure and function are encoded.

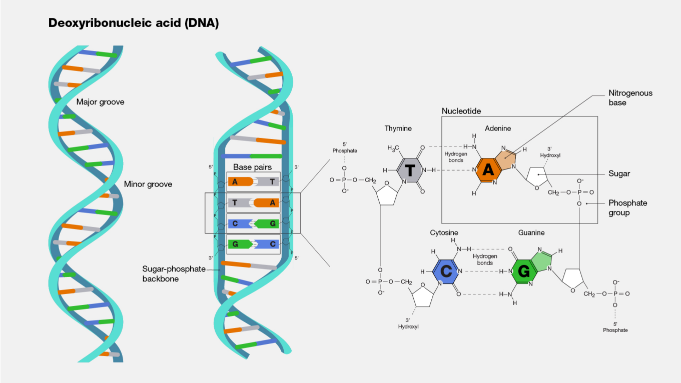


Figure 2.1: Structure of the DNA double helix

The functional units of DNA are called genes, which are discrete sequences that contain the instructions for producing proteins. However, DNA itself cannot participate directly in protein synthesis. Instead, a process called transcription is used to copy the information from a gene to a RNA molecule Alberts et al. [2]. Unlike DNA, RNA is single-stranded and uses uracil (U) instead of thymine as one of its bases.

Among the various types of RNA, the best known is messenger RNA (mRNA), which serves as an intermediary between genes and proteins. During transcription, an mRNA molecule is synthesized as a complementary copy of a gene, and this mRNA carries the genetic message from the DNA in the nucleus to the ribosomes in the cytoplasm, where protein synthesis occurs. This process, known as translation, is where the mRNA sequence is read in triplets (called codons), each of which corresponds to a specific amino acid Alberts et al. [3].

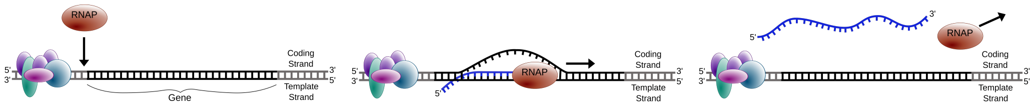


Figure 2.2: Illustration of the transcription mechanism: (a) initiation, (b) elongation, and (c) termination

The set of rules by which the nucleotide sequence in messenger RNA is translated into a sequence of amino acids is known as the genetic code. This code is composed of triplets of nucleotides, called codons, where each codon specifies one of the twenty standard amino acids used in protein synthesis Novozhilov and Koonin [24].

The genetic code is described as redundant but unambiguous. Redundancy means that most amino acids are encoded by more than one codon—for example, leucine is specified by six different codons—which provides a certain degree of robustness to the system. At the same time, the code is unambiguous because each codon corresponds to only one amino acid; that is, a given codon does not encode multiple amino acids Sunrayce Biology Authors [31].

Another fundamental characteristic of the genetic code is its universality. With very few exceptions, the same codons specify the same amino acids in virtually all living organisms, from bacteria to humans. This evolutionary conservation has been fundamental in enabling the development of many molecular biology tools and biotechnological applications Koonin and Novozhilov [18].

Although the focus of molecular biology for decades has been on the coding sequence of the genome—that is, the genes that give rise to proteins—it is now known that a large part of the human genome is transcribed into RNA that does not code for proteins. These non-coding RNA (ncRNA) molecules play crucial regulatory roles in controlling gene expression. One of the most studied groups within this class are microRNAs (miRNAs), which appear to be central elements in the fine-tuning of the genetic regulation process.

MicroRNAs - The Regulators of Gene Expression

MicroRNAs (miRNAs) are small non-coding RNA molecules, approximately 20 to 25 nucleotides in length, that play a key role in regulating gene expression at the post-transcriptional level Gulyaeva and Kushlinskiy [12], Lee, Feinbaum, and Ambros [19], and Wightman, Ha, and Ruvkun [34]. Instead of encoding proteins, miRNAs act by controlling the production of proteins from genes.

In simple terms, miRNAs function as molecular switches that bind to messenger RNA (mRNA) molecules, blocking their translation into protein or promoting their degradation. This mechanism depends on the degree of complementarity between the miRNA sequence and that of the target mRNA:

- When there is high complementarity, the mRNA tends to be degraded.
- When complementarity is partial, the miRNA generally acts by inhibiting translation without destroying the mRNA Calaf et al. [11].

The action of miRNAs occurs mainly in the untranslated 3' region (3'UTR) of mRNA and is mediated by protein complexes such as RISC (RNA-induced silencing complex), which facilitates this interaction Gulyaeva and Kushlinskiy [12]. This regulation is highly efficient: a single miRNA can control dozens to hundreds of different genes, and it is estimated that more than 60% of human coding genes are targeted for regulation by miRNAs Calaf et al. [11].

Due to this broad regulatory capacity, miRNAs play a central role in multiple cellular processes such as proliferation, differentiation, apoptosis, and stress response. Consequently, changes in miRNA expression profiles are associated with several diseases, including cancer, neurodegenerative and cardiovascular diseases. In an oncological context, miRNAs can act as oncogenes (promoting tumor growth) or as tumor suppressors, depending on the biological context and cell type Gulyaeva and Kushlinskiy [12].

Due to their specificity, stability, and direct involvement in relevant molecular mechanisms, miRNAs have been extensively investigated as promising biomarkers for diagnosis, prognosis, and subtype stratification in various diseases—including cancer.

Cancer - A Complex Disease

Cancer is a disease characterized by the uncontrolled proliferation of transformed cells, which can invade neighboring tissues and spread to other parts of the body through processes such as metastasis. This definition, based on that of the NCI, has recently been expanded to recognize the role of natural selection in the evolution of cancer: it is a cellular system that continuously evolves, adapting to internal and external pressures to ensure its survival Brown et al. [10] and National Cancer Institute [23].

Under normal conditions, the body's cells divide only when necessary, die when damaged or obsolete, and are replaced by new ones. However, in cancer, this biological balance is disrupted: abnormal cells gain the ability to multiply independently of the body's signals and to resist programmed cell death (apoptosis). These transformed cells become autonomous units that not only ignore normal growth controls but also interact with the tumor microenvironment to promote their own survival, using angiogenesis, immune evasion, and other adaptive mechanisms Brown et al. [10] and National Cancer Institute [23].

The result is a heterogeneous cell population, subject to natural selection within the human body. Cells that acquire adaptive advantages (e.g., higher proliferation rate, drug resistance, or migration ability) tend to prevail, making cancer a constantly evolving disease Brown et al. [10].

Although cancer can arise in virtually any tissue, not all cellular changes are malignant. There are precancerous conditions, such as hyperplasia or dysplasia, which represent an increase in the number of cells or changes in their morphology, but which do not yet invade surrounding tissues.

Progression to true cancer involves the acquisition of invasive and metastatic capacity—properties that distinguish malignant tumors from benign ones. This process can be silent for years, until more severe symptoms arise, often related to the invasion of vital organs.

Breast Cancer & its Subtypes

Breast cancer is the most commonly diagnosed cancer in women worldwide and is one of the leading causes of cancer death in developed and developing countries Hong and Xu [15] and Romanowicz, Smolarz, and Nowak [29]. It is estimated that one in eight women will be diagnosed with this disease during their lifetime, although it can also affect men—albeit with a much lower incidence Romanowicz, Smolarz, and Nowak [29].

Most breast tumors originate in the epithelial cells of the ducts or lobules of the breast, which acquire malignant properties after the accumulation of genetic and epigenetic changes.

These events alter the normal control of cell proliferation, differentiation, and apoptosis, allowing for unregulated tumor growth Polyak [26].

The development of the disease is associated with a set of well-established risk factors, which include:

- Age and family history of the disease;
- Hereditary genetic mutations, especially in the *BRCA1* and *BRCA2* genes;
- Prolonged exposure to endogenous or exogenous hormones (e.g., early menarche, late menopause, hormone therapy);
- Environmental and behavioral factors, such as obesity, physical inactivity, alcohol consumption, and a diet rich in saturated fats Adamo et al. [1] and Romanowicz, Smolarz, and Nowak [29].

From a molecular and clinical point of view, breast cancer is highly heterogeneous. Each tumor may have unique combinations of genetic alterations, signaling pathways, and gene expression profiles, which are reflected in different clinical behaviors, degrees of aggressiveness, and response to treatment Howlader et al. [16] and Polyak [26].

Early detection is crucial for prognosis. When diagnosed in its early stages, breast cancer has survival rates of over 90%. However, in more advanced stages, especially when metastases appear, controlling the disease becomes substantially more difficult and the therapeutic goal shifts from curative to palliative Adamo et al. [1] and Hong and Xu [15].

The therapeutic approach is typically multimodal, combining surgery, radiotherapy, chemotherapy, hormone therapy, and targeted or biological therapies, depending on the characteristics of the tumor and the patient's general condition. The most significant advance in the last decade has been the transition from a uniform model to a personalized treatment approach, tailored to the molecular subtype and individual risk Romanowicz, Smolarz, and Nowak [29].

In addition, it has been recognized that breast tumors are not static entities. Due to phenomena of intra-tumor heterogeneity and clonal evolution, tumors adapt to the selective pressure of treatments, often leading to the development of therapeutic resistance and disease progression Polyak [26].

Given the molecular complexity and clinical diversity of breast tumors, it is now well established that breast cancer is not a single disease but rather a collection of biologically distinct entities that arise from a common anatomical site. This heterogeneity is reflected in major differences in tumor progression, metastatic behavior, response to therapy, and long-term prognosis Adamo et al. [1] and Prat et al. [27].

To better capture this complexity and inform clinical decision-making, researchers have developed a molecular classification system that subdivides breast tumors into intrinsic subtypes. These subtypes are defined based on the expression status of three key biomarkers—estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2)—as well as proliferation indices (e.g., Ki-67) and gene expression patterns Perou et al. [25] and Prat et al. [27]. This classification underpins modern precision oncology approaches and has profound implications for therapy and prognosis.

The four main intrinsic subtypes are:

- Luminal A
- Luminal B
- HER2-enriched
- Basal-like, which substantially overlaps with Triple-Negative Breast Cancer (TNBC)

Each subtype exhibits a distinct molecular landscape, clinical behavior, and response to treatment:

Luminal A
Characterized by ER+/PR+, HER2– status and low proliferation (Ki-67 low). Common in older women, with a favorable prognosis. Highly responsive to endocrine therapy and typically does not require chemotherapy Adamo et al. [1] and Howlader et al. [16].

Luminal B
Also ER-positive, but with higher proliferation, lower PR, and possible HER2 positivity. More aggressive and worse prognosis than Luminal A. Often treated with hormone therapy, chemotherapy, and anti-HER2 agents if applicable Hong and Xu [15] and Prat et al. [27].

HER2-enriched
Defined by HER2 overexpression, ER– and PR–. Previously poor prognosis improved significantly with HER2-targeted therapies. Still associated with high-grade histology and early recurrence Adamo et al. [1] and Prat et al. [27].

Basal-like / TNBC
Triple-negative (ER–, PR–, HER2–) and most aggressive. Associated with younger patients, early metastasis, and poor survival. Chemotherapy remains primary treatment; targeted options like PARP inhibitors and immunotherapy are emerging for selected cases Mahalingam, Vagia, and Cristofanilli [21].

Clinical Implications and Intra-Tumor Complexity
Large-scale studies confirm survival and recurrence differences across subtypes:

- Luminal A: highest 5-year survival, lowest recurrence;
- Luminal B: intermediate survival, benefits more from chemotherapy;
- HER2-enriched: high early recurrence, improved with targeted therapy;
- TNBC: lowest survival, high early recurrence Howlader et al. [16] and Prat et al. [27].

Recent evidence, including single-cell sequencing, suggests multiple subtypes can coexist within the same tumor—a phenomenon called intra-tumor heterogeneity Polyak [26] and Yeo and Guan [35]. This complexity contributes to therapeutic resistance and disease progression.

3

Preliminary Work and Work Plan

4

Work Plan

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A

Appendix 1 Covers Showcase

B

Appendix 2 Lorem Ipsum

I

Annex 1 Lorem Ipsum