Survival analysis of multiple myeloma and B-cell lymphoma patients: predicting risk and survival curves with graph neural networks (SurvGraph)

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MOTIVATION

Multiple Myeloma (MM) and Diffuse Large B-cell Lymphoma (DLBCL) are cancers of the bone marrow and the lymphatic system characterized by the clonal proliferation of plasma cells and lymphocytes respectively. Diagnosis and follow-up of MM and DLBCL patients involve analyzing full-body 3-D Positron Emission Tomography (PET) images. For both conditions, PET images are characterised by multiple lesions (depicted as dark pixels in Fig. 1.)
Towards assisting the analysis and interpretation of nuclear physicians, there has been an increased interest

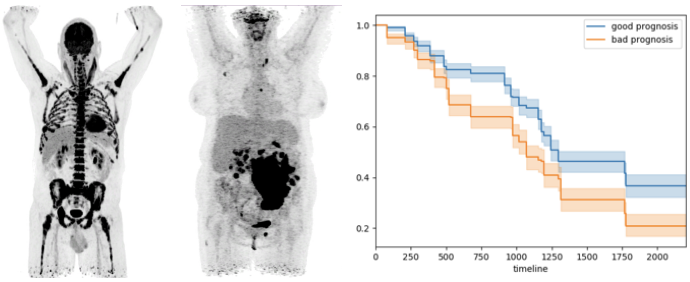

Figure 1: PET volumes from mutiple myeloma (**left**) and DLBCL (**middle**) patients. Kaplan Meier curve representing the progression free survival probability of two groups of MM patients over time (**right**).

in automatically extracting quantitative information (radiomics features) from PET images and combining them with machine learning methods [1]. The targeted predictions of interest include the outcome of a patient, its evolution profile, or his/her response to a given treatment. Such time-to-event predictions have been commonly addressed with survival analysis techniques.
Survival analysis covers a set of approaches modeling the time it takes for an event of interest to occur. In medicine, survival analysis is used for instance to determine the impact a variable has on the overall survival of a patient, the probability of survival at a given time, or the difference in survival between groups of patients. Classical survival analysis relies on describing with a feature vector the relevant information of a patient and applying statistical approaches, such as Kaplan Meier (KM) curves (Fig. 1-right) or Cox regression [2].
In the context of survival analysis from PET images, current advances focus on CNNs whose input are either a single lesion ([3], [4]), or full volumes [5]. Here, we propose to do survival analysis from multiple lesions and multi-modal data taking advantage of recent GNN models.

OBJECTIVES AND RESEARCH QUESTIONS

The clinical objective of the project will be identifying high-risk patients in MM from recent clinical studies (e.g. CASSIOPET) and the survival analysis of DLBCL patients relying a large national database (GAINED). Towards this goal, the PhD candidate will adapt and design new Graph Neural Network (GNN) models that learn from the databases to make predictions about the risk and survival of an individual or a group of patients. In particular, the project will address the following research questions:

i) How to model the spatial **relations within a patient**, e.g. between multiple lesions in a PET volume?

ii) How to incorporate multimodal phenotypic (non imaging) and clinical data into the learning framework? How can we model the existing **relations between patients**?

iii) How to define survival analysis tasks as a **graph learning problem**?

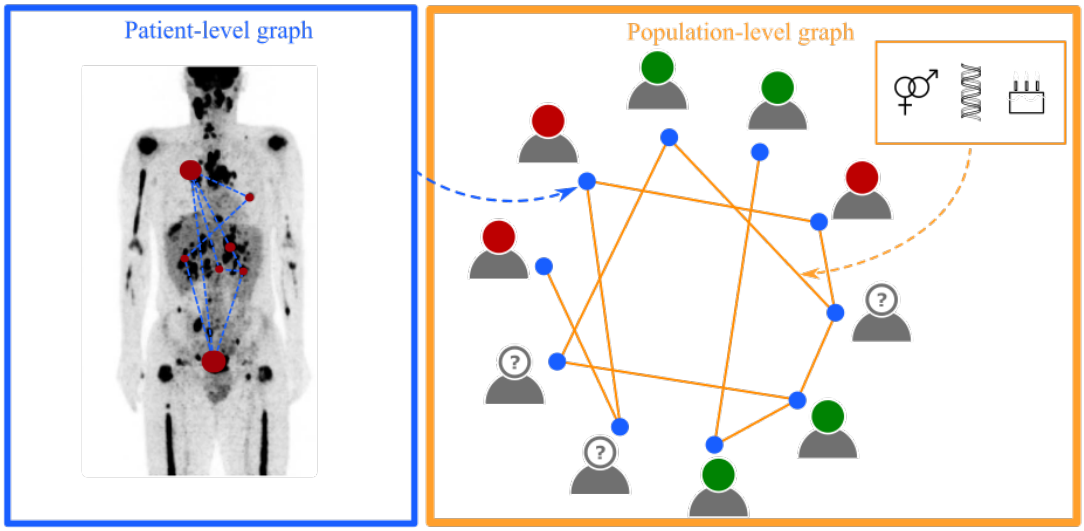

Figure 2: Examples of graphs constructed on both patient-level and population-level. On the patient level, the graph is made of a set of nodes representing the different lesions and connections denoting spatial spread and radiomics features. On the population level, the nodes are patients and connections embody the phenotypic and clinical variables.

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