APOLLO 11 will build a strong and long-lasting Italian lung cancer network formed by 48 care and research centres, creating a nation-wide database of real world data and a virtual multilevel biobank to perform translational research, located and managed directly in-house by each network member. This strategy will avoid the scattering of data, i.e. the fact that, when held by individual institutions without an effective sharing system between them, the single data sets lack significance and thus remain difficult to use well, and their analysis is often inconclusive. APOLLO 11 represents a high-impact translational research joint effort with at its core the creed of "unity is strength". Indeed, the multilevel structure above is designed to maximize and optimize every member's contribution to the biobank and the database, independently from their size or the technical equipment at their disposal.

In this three-year pilot, APOLLO 11 has two main goals:

The first is to set up the consortium by activating at least 20 of the 48 centres in total as contributors to the database, and by activating at least 10 local biobanks capable of collecting samples (tumor tissue, blood, stool and urine) according to shared, appropriately annotated, procedures. The second objective is to develop a "software" biomarker that can predict IO's efficacy and select patients more accurately than the current standard-of-care biomarker (PD-L1). This will help us in finding answers to a key scientific question for a NSCLC patients treated with IO: how can we better predict, accurately and in a personalized way, which tumours will best respond to what specific therapy?

We will collect real world (demographic, histologic, PD-L1, molecular, treatment and outcomes information, etc.), radiomic and retrospective multiomic data from approximately 1200 patients (1000 retrospectively and 200 prospectively) across all activated centres. To this database we will apply artificial intelligence/machine/deep learning (AI/DL/ML) methodologies which are able to integrate and merge these data from very different sources, analyse them, and from this analysis develop algorithms able to predict IO's efficacy in patients with NSCLC. In addition, in a first planned sub-study we will perform a single cell RNA sequencing analysis (scRNA) on the PBMCs of a group of about 40 patients. The biological insights from this analysis will then be validated in 120 further patients in order to investigate the PBMCs' role as an IO response predictor.

The Explainable trustworthy AI (XAI) method we will implement will be a true "black box" for IO, in other words an instrument to improve the current clinical and biological insights, to provide NSCLC patients with better tailored therapies, reducing risks and improving their quality of life.