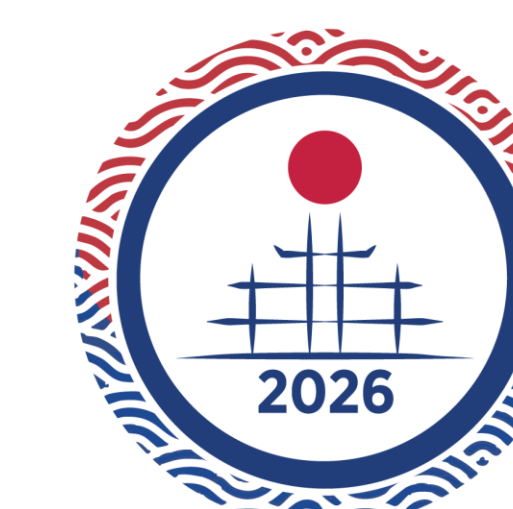
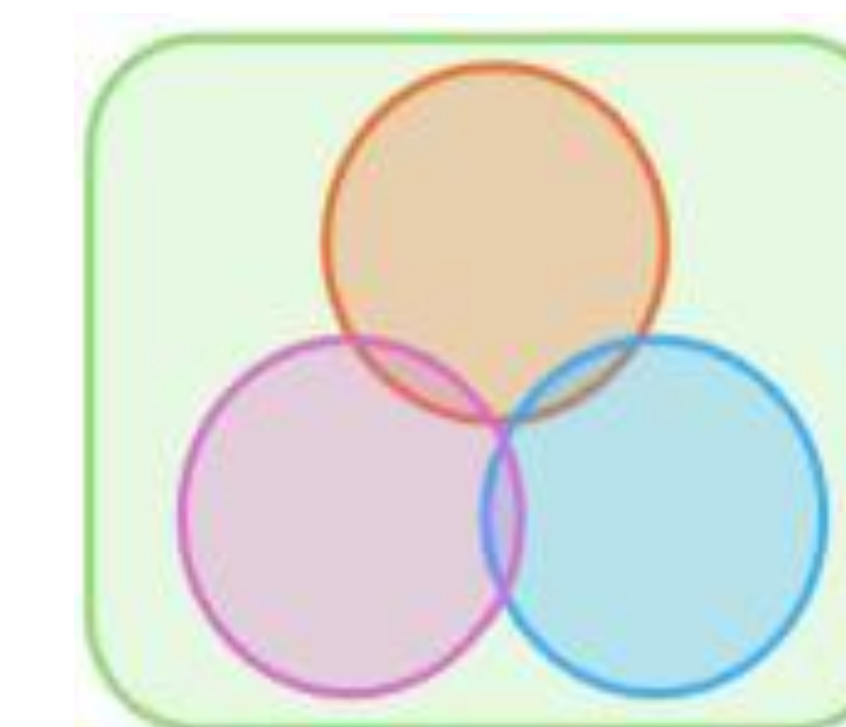


INGVER study Cross-sectoral integration and personalization of care of patients with NSCLC

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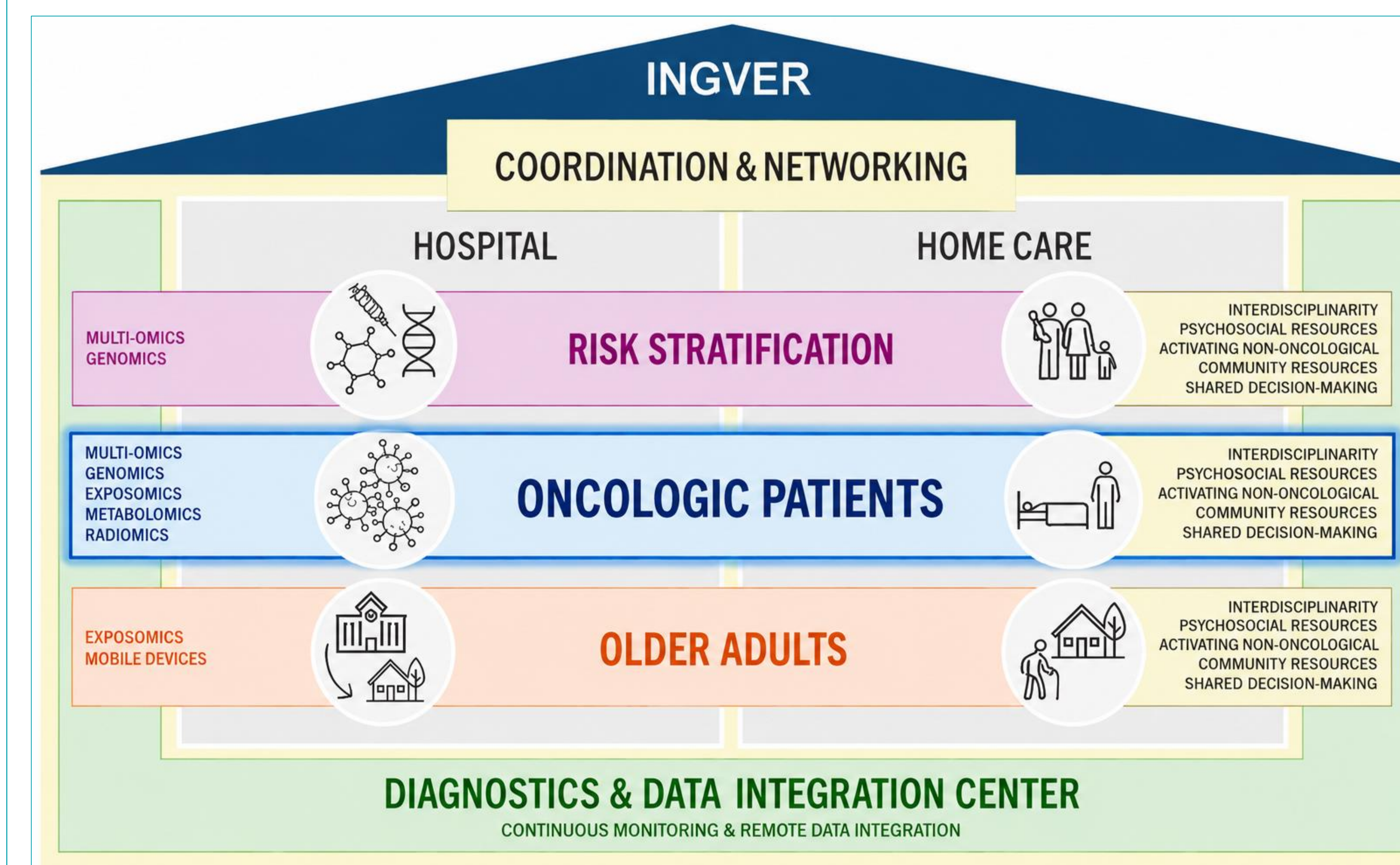
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INTRODUCTION

Cancer burden will considerably increase in the next years. The cancer centres at the Universitätsmedizin Oldenburg (UMO) are the largest in the Northwest Metropolitan Region of Germany and treat between 80 and 100% of diagnosed cases of lung cancer. The INGVER project supported by the BMFTR aims to improve efficiency of tumor board decisions, promote cross-sectoral integration and personalize treatment for this vulnerable cancer group. NSCLC pts are bad shedders for circulating tumor DNA. Therefore, studies to monitor NSCLC have been hampered by only a minority of NSCLC IB-III being positive prior to start of therapy. With an extremely sensitive tumor-informed method we try to overcome this limitation in NSCLC. Also, we will systematically check pts not progressing after 1 year of checkpoint inhibitors (CPI) for the presence of MRD to tackle the question of continuing vs. stopping CPI treatment. Similar question will be addressed as well in other malignant cohorts. In addition, tumor predisposition genes will be not only studied in these cohorts by short reads but also by long reads. This enables genetic alterations to potentially being detected that are missed by conventional short reads. The third key focus of the INGVER project are phenotyping analyses in patients with NSCLC-OMD (oligometastatic disease), to investigating metastasis patterns in CTCs (circulating tumor cells). This involves examining the expression of markers associated with homing receptors for different tissues.

FIGURE 1: INGVER-STUDY: A cross sectional care plan for the vulnerable groups



MATERIAL AND METHODS

Highly sensitive sequencing techniques for detecting ctDNA in the blood enable the early detection of potential MRD, which can persist even after seemingly successful treatment. For this purpose, we use a highly sensitive, tumor-specific MRD assay that measures the amount of tumor DNA in the blood. To develop the test, whole-genome sequencing (WGS) is performed on both the tumor DNA and the blood DNA. Therefore, we prospectively include 25 NSCLC pts in stages IIA–IIB who receive induction therapy and 25 NSCLC pts' stage IV who have not shown disease progression after at least 1 year of treatment with a CPI. Using long-read sequencing, 40 pts with NSCLC who have a family history of the disease and no evidence of a pathogenic germline mutation will be studied. In OMD pts, blood samples are tested for CTCs and, using flow cytometric analysis, for markers that include homing receptors for various organs. The correlation incidence of ctDNA positivity before start of treatment as well as the monitoring capacity of the sensitive method and the risk of recurrence will be demonstrated. The outcome parameters for pts after at least 1 year of CPI therapy are the detectability of ctDNA and the correlation between ctDNA results and outcome PFS and OS. The primary outcome in the OMD group is the detection of CTCs in peripheral blood and the correlation of the antigen expression pattern with the recurrence pattern (PFS) and the recurrence pattern (i.e., organ involvement). For survival analysis we'll use Log-Rank tests and hazard ratios. We are currently recruiting patients and hope to present our findings at the next WCLC meeting.