Glioma is one of the most aggressive and fatal brain tumors, mainly due to recurrence after treatment. Current diagnostics rely on imaging techniques such as computed tomography and magnetic resonance imaging, which may be unable to distinguish between tumor recurrence and postoperative changes due to technical limitations. Therefore, it is necessary to develop a method that will enable early diagnosis of recurrence.

The use of metabolomic, lipidomic, and proteomic tools enables comprehensive monitoring of biochemical and molecular changes associated with the development and recurrence of glioma. Metabolomics is a science that measures small molecules (metabolites), lipidomics - fatty compounds (lipids), and proteomics focuses on the analysis of proteins. These fields provide valuable information about the state of the body, taking into account pathological conditions, genetic and environmental factors, diet, the impact of treatment, and lifestyle. Combining metabolomic and lipidomic results with proteomic data increases the ability to interpret the changes observed as a result of the disease. Proteins, in particular enzymes and transporters, are often compounds that drive metabolic changes. This comprehensive approach enables the identification of compounds that differentiate patients at each stage of tumor progression. Therefore, the aim of this project is to identify metabolomic and proteomic changes in biological samples of patients with primary and recurrent glioma, enabling the development of models that predict glioma recurrence and estimate the time of recurrence using machine learning algorithms.

The research hypotheses assume that:

(1) glioma recurrence is preceded by metabolomic, lipidomic, and proteomic changes detectable by mass spectrometry,
(2) by integrating omic data obtained for plasma samples collected during the initial diagnosis of glioma, follow-up visits, and recurrence, it is possible to identify molecular features that distinguish different stages of disease progression,
(3) monitoring of multifactorial signatures enables the estimation of the probability of recurrence and the determination of the approximate time of recurrence.

The research tasks will include:

(1) non-targeted metabolomic and lipidomic analysis of plasma and tissues,
(2) targeted metabolomic and proteomic analysis of plasma,
(3) statistical analysis and modeling using machine learning algorithms.

The proposed project will enable the development of a model predicting the recurrence of glioma along with the time of its occurrence. A minimally invasive method based on plasma analysis may contribute to supporting patient diagnosis, which will significantly accelerate the implementation of an appropriate treatment strategy and thus positively impact their health. In turn, combining metabolomic and proteomic results will contribute to understanding the molecular changes occurring in glioma, enabling the development of new therapeutic targets and the monitoring of treatment outcomes.