52% to 68% of patients identify the cause of the disease. It is worth noting that among these patients, over 80% have undergone many tests before but have not been diagnosed (Khudari et al., 2025). Metabolomics can provide more comprehensive biochemical information, which is helpful in explaining those unexplained genetic variations, thereby reducing reliance on a single testing method.

7.2 Precise classification of patients and guidance for individualized treatment

Combining genetic data with metabolic data can lead to more accurate patient classification and enable the formulation of more suitable treatment plans. In many neuro-metabolic diseases, whole exome sequencing combined with detailed symptom analysis not only detects metabolic abnormalities but also provides references for treatment, such as adjusting diet, supplementing coenzymes, or using specific small molecule drugs. A study on neurodevelopmental disorders found that 44% of patients who received molecular diagnostic results later attempted targeted treatment, indicating that this classification method is gradually being applied in actual treatment (Mohammed et al., 2025). For diseases like leukodystrophy, enzyme replacement therapy and gene therapy need to be initiated as early as possible, so the timing of molecular diagnosis is crucial. Additionally, integrating various data can also help us classify diseases more precisely, such as differentiating between typical and mild types based on metabolic characteristics and providing references for medication timing and dosage.

7.3 Improving prognosis assessment and long-term management

The integration of genetic and metabolic data has also had a positive impact on prognosis evaluation and long-term follow-up. In children with neuro-metabolic diseases, molecular diagnosis not only guides current treatment but also changes the prognosis assessment and prevention strategies for 74%-83% of cases, including genetic counseling and family planning (Khudari et al., 2025). For rare cases that have not yet been diagnosed, regular re-analysis of genomic data can also continuously improve the diagnosis rate-with the continuous discovery of new gene-disease relationships and the integration of standardized phenotypic data sharing platforms, approximately 18% of patients can eventually receive a clear diagnosis. This indicates that dynamic updates of clinical and molecular information are valuable for prognosis management. For some slowly-progressing genetic diseases, researchers are attempting to use imaging, blood or skin-derived biomarkers as alternative indicators to capture disease changes in a shorter period of time, making clinical trials more feasible. Once validated metabolic markers are combined with genetic risk information, they can be used for dynamic monitoring of disease activity, warning of complications, and guiding adjustments to treatment plans. It can be said that the integration of genetic testing, metabolic analysis, and data technology is driving the diagnosis and treatment of neuro-metabolic diseases from a single diagnosis to comprehensive and precise management throughout the process.

8 Challenges and Future Perspectives

In the fields of neurometabolism and rare diseases, integrating genomic data and metabolomic data has many practical challenges in actual operation. The data obtained from different technical platforms often do not match, and due to differences in sample batches and inconsistent analysis methods, it is difficult to repeat and verify the results. The current common practice is to analyze each type of data separately before combining them. This approach is prone to subjective judgments and affects the accuracy of the conclusions. Some large-scale collaborative projects have also found that differences in sample sources and clinical information can cause difficulties in subsequent data integration. In the future, it is necessary to establish unified data standards, build shareable databases (such as OmicsDI, MetaboLights, etc.), and rely on cloud computing to efficiently integrate genomic, metabolic, imaging, and clinical data. If these foundations are not laid first, multi-omics analysis will be difficult to truly become a tool that can be used in clinical practice.

The large-scale sharing of data also brings about privacy and ethical issues. Everyone's genetic information is unique. Even if personal information such as names is concealed, it is still possible to identify the corresponding person through these data. The main concerns are how to obtain informed consent, how long the data can be stored, and whether there will be discrimination when applying for insurance or finding a job. Additionally, how to fairly distribute benefits in different regions is also a challenge. Cooperation between developed countries and regions with limited resources requires more reasonable approaches. Although there are currently encryption