

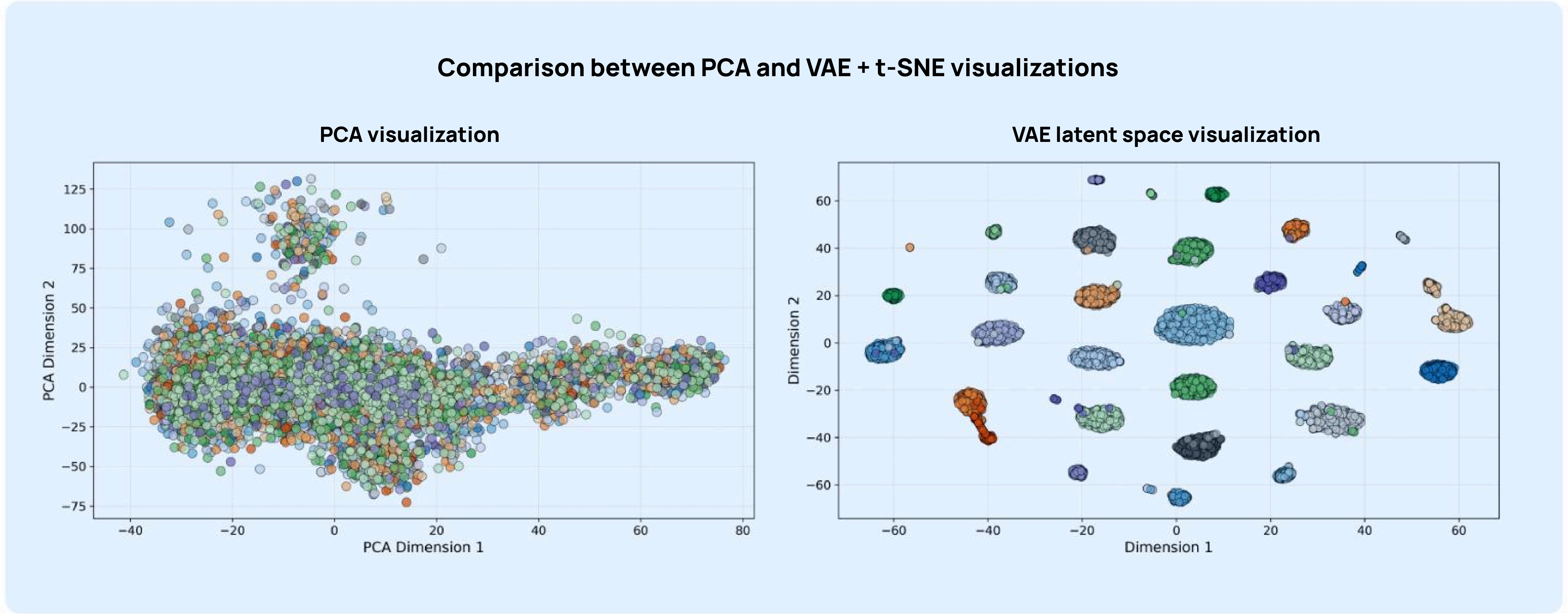
# White-label multi-omics cancer data analysis pipeline

- Our Multi-omics solution helps reduce complex data patterns to interpretable features to enable precise molecular classification of cancer subtypes and biomarker discovery.


Due to the advanced Variational Autoencoder (VAE) technology, it analyzes high-dimensional gene expression and DNA methylation data with unprecedented accuracy.

## Problems addressed

CHALLENGE	HOW WE SOLVE IT
High dimensional gene expression data	Dimensionality reduction via Variational Autoencoder (VAE) simplifies analysis while preserving biologically relevant features.
Complex data preprocessing requirements	Automated preprocessing including Y chromosome removal, zero-expression exon filtering, and high-missing-value feature elimination.
Limited accuracy in traditional methods	Deep learning ensemble models with optimized inference achieve 96% accuracy in classifying 33 distinct tumor types and normal samples.
Resource-intensive computation	Optimized architecture ensures rapid processing and scalability.




## User benefits



**Accelerated analysis workflows**

Significantly reduces computational requirements and analysis time for complex genomic datasets.




**Precision in clinical applications**

Exceptional tumor classification accuracy enables more precise diagnostics and informed treatment decisions.



**Deep biological insights**

Identify critical gene expression and DNA methylation markers for targeted therapies through interpretable VAE latent space.



**Extensible platform**

Compatible with additional genomic data types and complementary tools like NVIDIA Parabricks to enhance analytical capabilities.

## Implementation options

**Direct integration**

Pre-trained models and pipeline components available for deployment within the current infrastructure. This option provides a foundation for immediate use.

**Pipeline adaptation**

Modification of the existing pipeline to align with particular data types, research parameters, and analytical requirements. Offers a balance between speed and customization.

**Fully tailored development**

Ground-up development addressing specialized needs with optimized performance for unique research contexts. Provides maximum flexibility and control.

## Related services

**1 Genomics**

Disease gene and mutation identification for drug target prioritization.

**2 Transcriptomics**

Differential gene expression analysis for disease pathway and therapeutic target discovery.

**3 Proteomics**

Large-scale protein characterization for target validation and interaction mapping.

**4 Metabolomics**

Metabolic flux and small molecule quantification for biomarker and toxicity risk assessment.

**5 Multi-omics**

Integrated analysis of genomic, transcriptomic, and proteomic data for a holistic understanding of disease mechanisms and target identification.

## Get started

Contact us today for a demonstration or consultation on how our Multi-omics solution can accelerate your cancer research and clinical applications.

[ [info@voka.io](mailto:info@voka.io) ]