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Single-cell multi-omics data integration powered by PCA-like autoencoders



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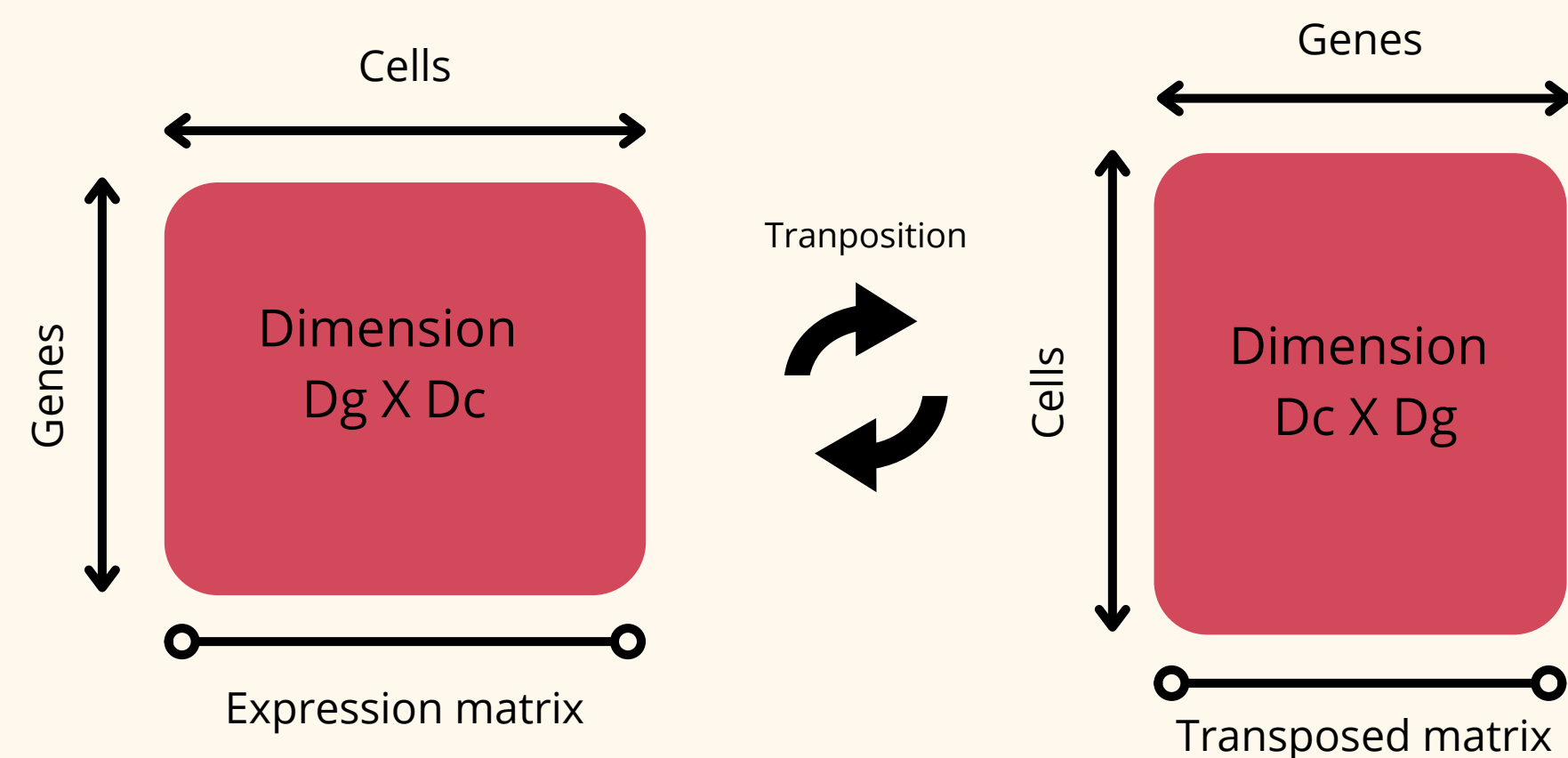


Introduction

Single-cell (sc) technologies combined with high-throughput sequencing are revolutionizing various omics fields. Each type of omics provides complementary cellular information, but **integrating** these data types remains only partially solved. While integrating data from the same omics or multiple types derived from the same cells is routine, **the current challenge is integrating data from different omics** that do not originate from the same cell population.

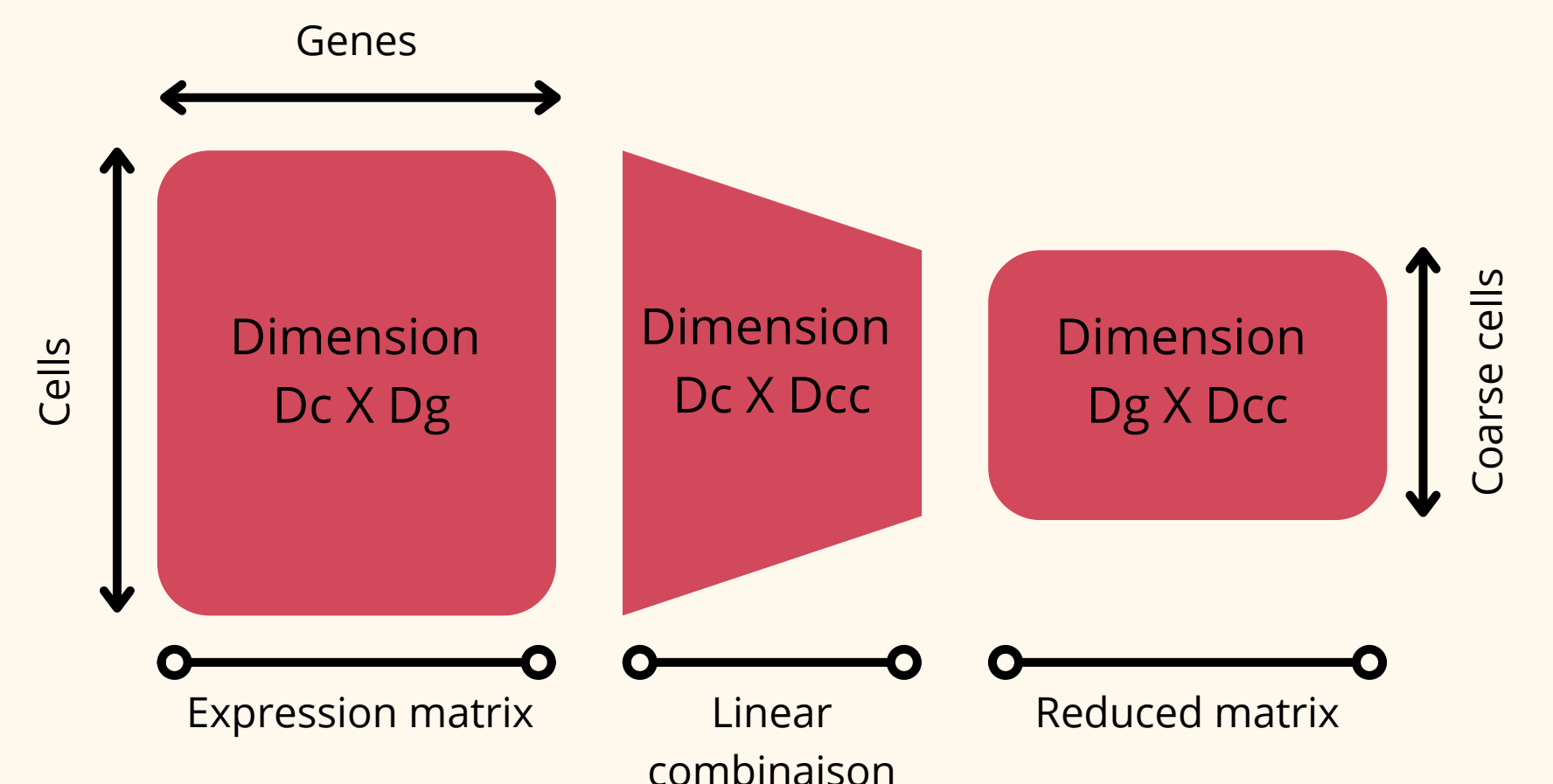
here I present the pipeline based on PCAAE [2] **autoencoder** to learn **gene representation** and integrate scRNA-seq data for multi-omics dataset integration.

1. Matrix transposition



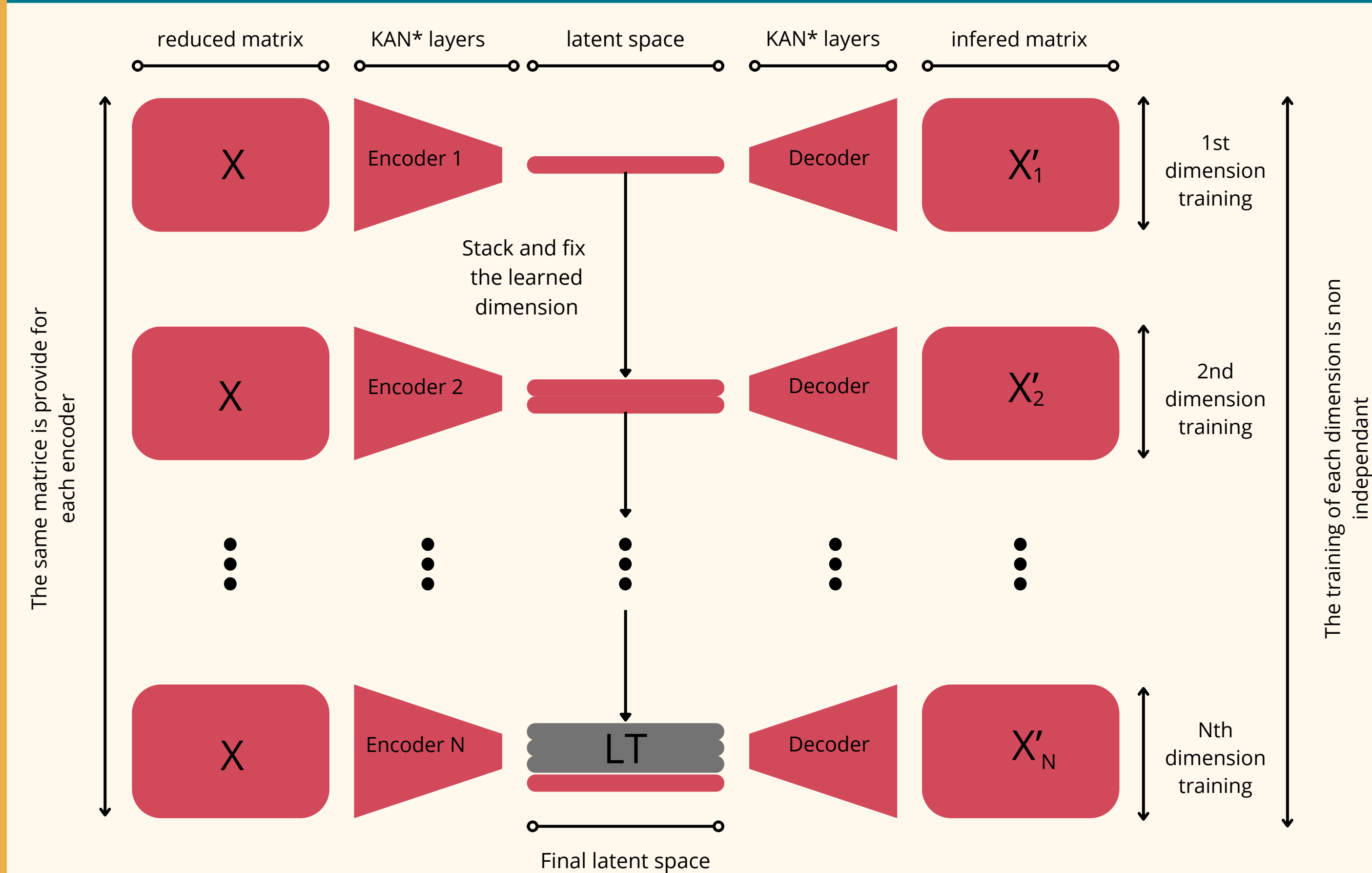
To focus on gene analysis, we transpose the expression matrix so that the observations are now genes and the features are cells.

2. Cells aggregation to coarse cells



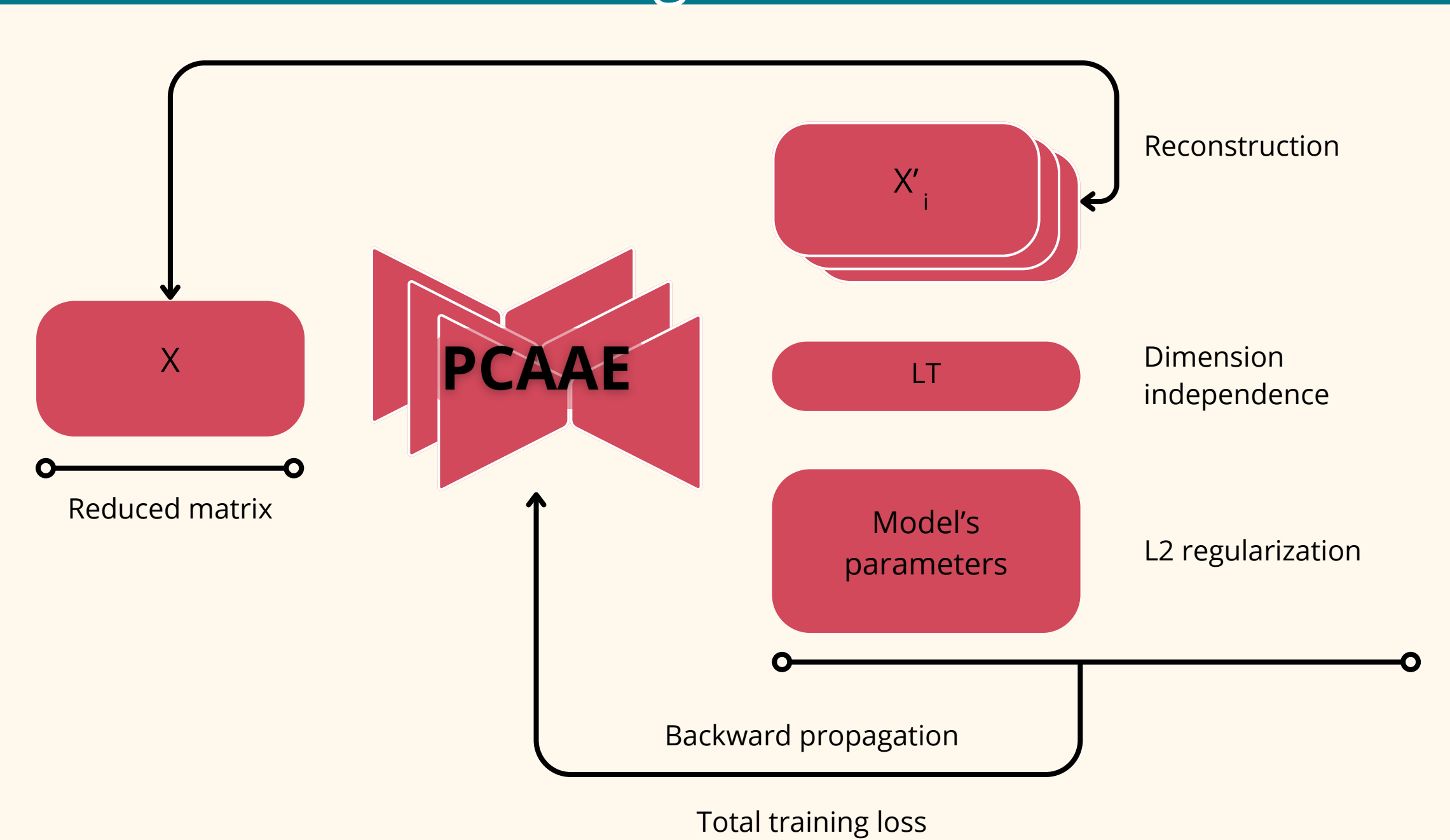
To **limit the number of features encoded** by the model, we perform dimensionality reduction by creating linear combinations of cells.

3. PCAAE auto-encoder architecture



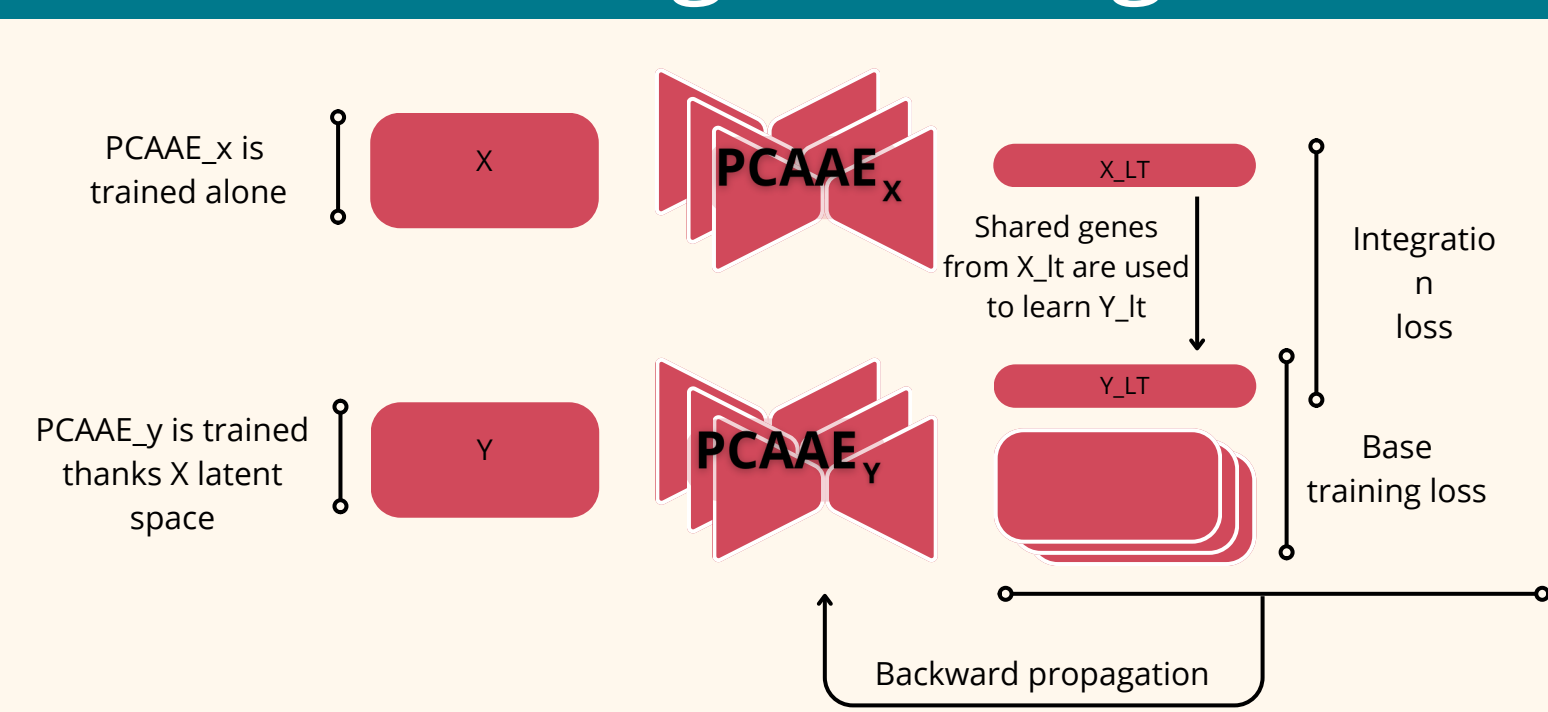
The autoencoder model consists of **N encoders, one for each dimension** in the latent space, and a **single decoder**. Each encoder-decoder pair is **trained sequentially**. Kolmogorov-Arnold Networks (KANs) [3] are used for encoder and decoder as **promising alternatives of Multi-Layer Perceptrons (MLPs)**.

4. PCAAE model training



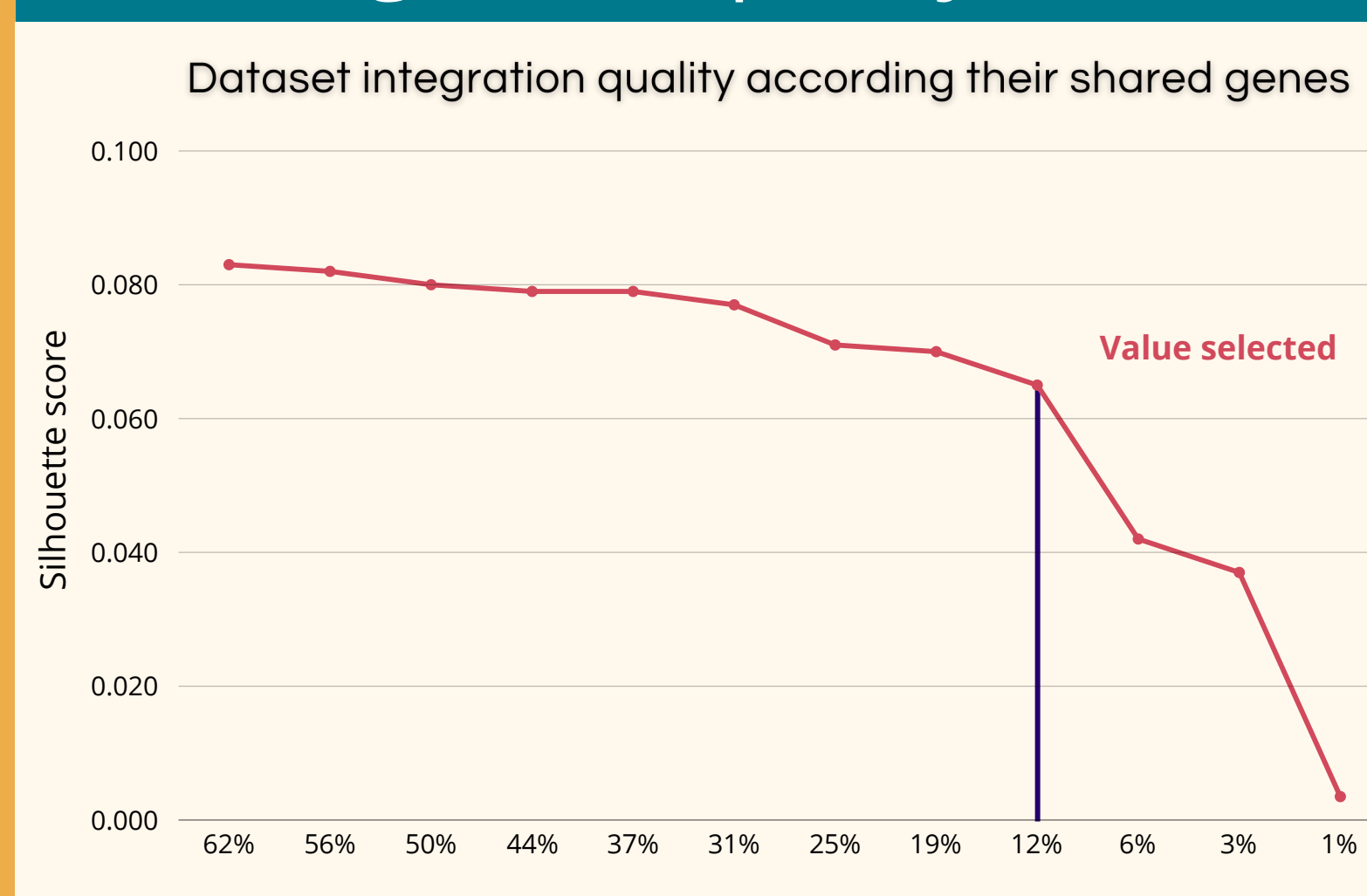
The loss function of the model comprises three terms. The mean squared error (MSE) **facilitates the extraction and compression of data**. The MSE between the covariance matrix of the latent space and the identity matrix **ensures independent dimensions in the latent space**. Finally, L2 regularization is applied to enhance the model's learning process.

5. PCAAE training for integration



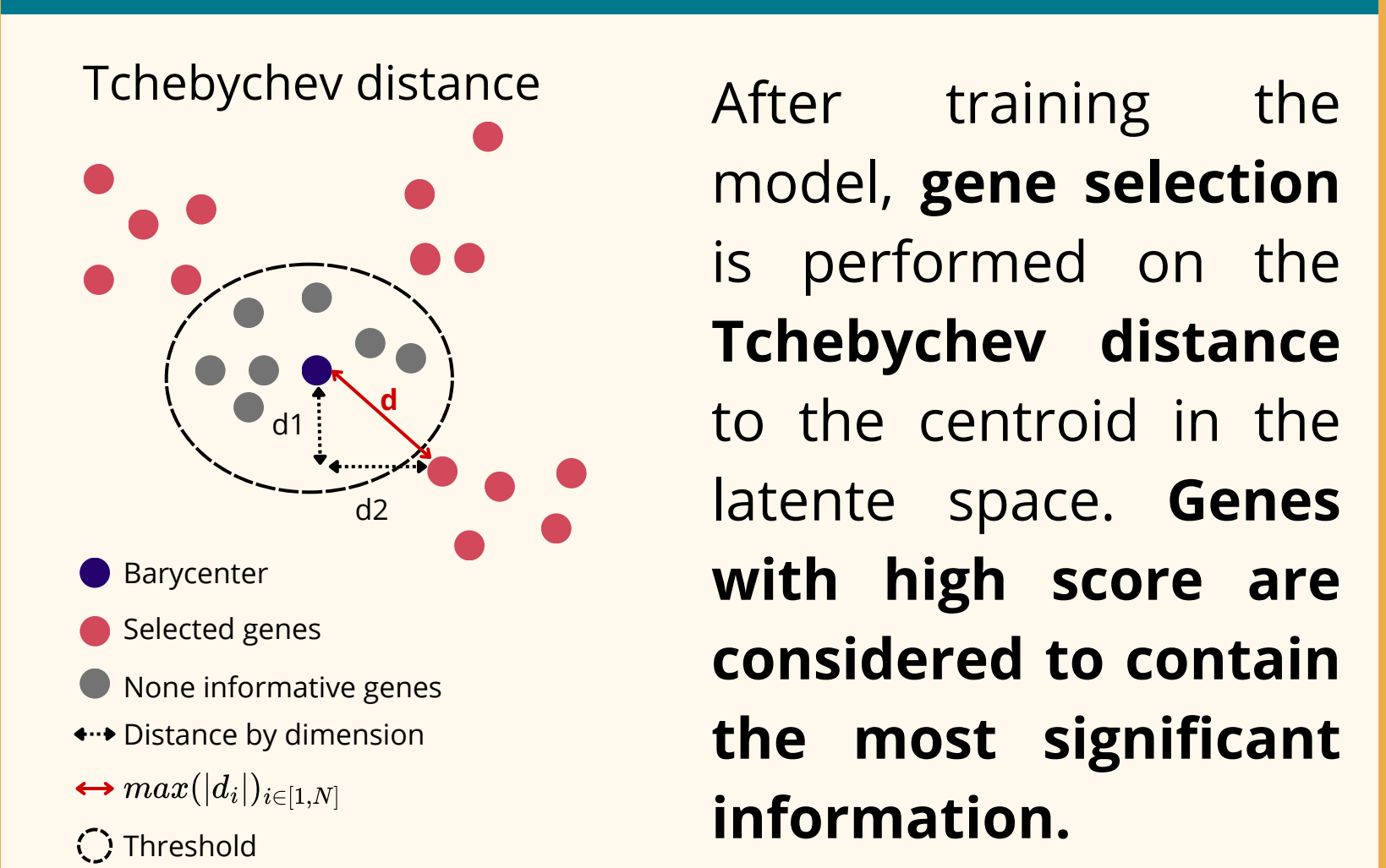
When integrating datasets from the same omics, **the latent space of one dataset is used as a reference to train another**. This adds a metric to the model's total loss.

6. Integration quality

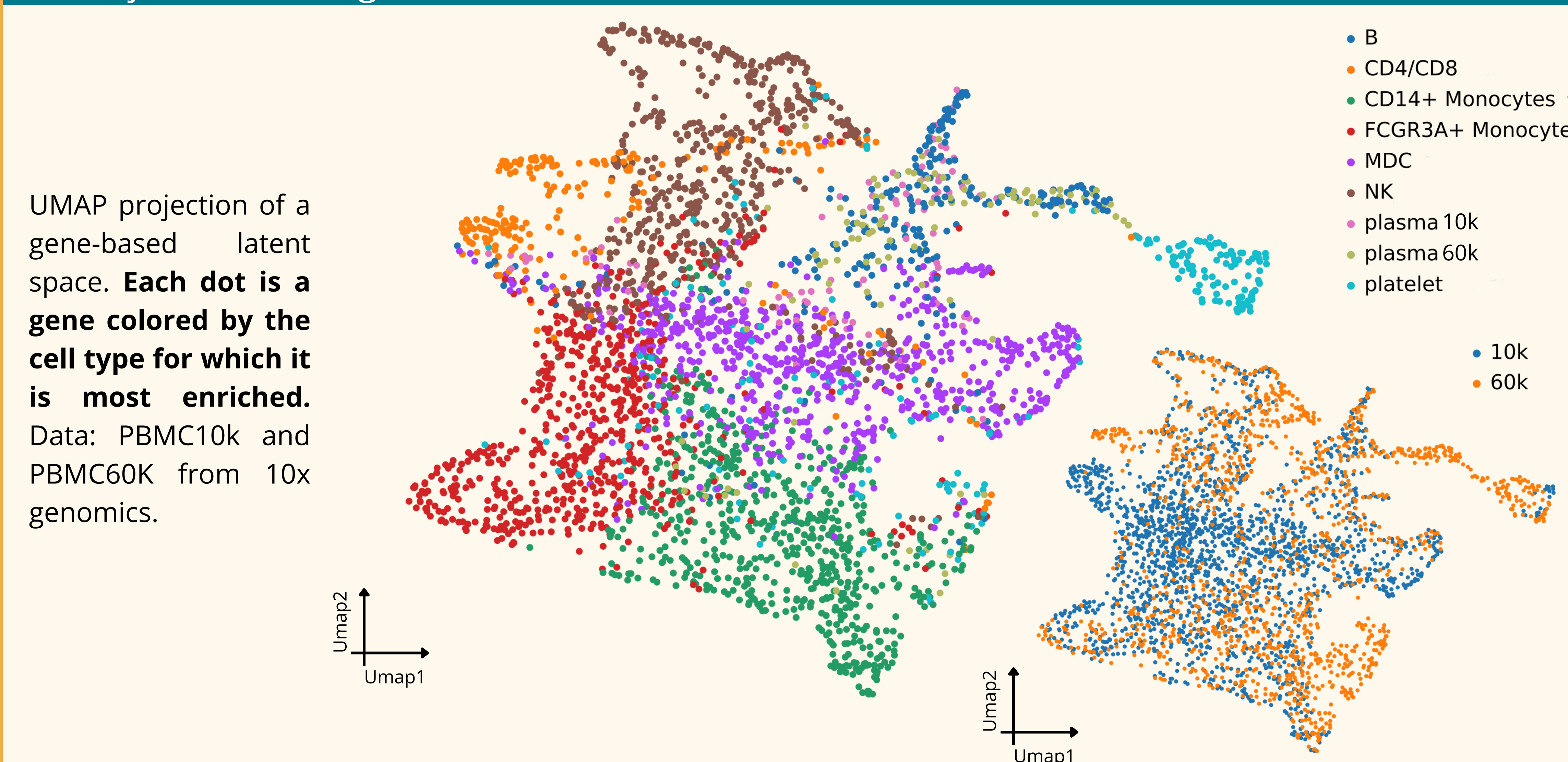


The quality of integration **depends on the percentage of shared genes** used during training. A threshold of 12% was used to demonstrate the quality of the results with the **minimal number of genes**.

7. Genes selection



8. Projection of integrated Genes



- First results demonstrate an **effective integration** of two scRNAseq datasets, with only 12% of genes used as a link.
- We observe that within the green cluster corresponding to CD14+ monocytes, **genes from both datasets are evenly mixed**
- It indicates that **genes represented are clustered according to their function**, rather than their dataset of origin. Encouraged by this first result
- We are now extending our method to integrate RNA and other omics data (e.g. ATAC).

1. Ghazanfar, S., Guibentif, C., & Marioni, J. C. (2024). Stabilized mosaic single-cell data integration using unshared features. Nat. Biotechnol., 42, 284–292. doi: 10.1038/s41587-023-01766-z

2. C.-H. Pham, S. Ladjal, and A. Newson, PCAAE: Principal Component Analysis Autoencoder for organising the latent space of generative networks, arXiv, (2020).

3. Liu, Ziming, et al. "KAN: Kolmogorov-Arnold Networks." arXiv, 30 Apr. 2024. doi:10.48550/arXiv.2404.19756.

