OF MULTIMODAL VARIATIONAL AUTO-ENCODERS IN COMBINING ASSESSMENT INFORMATION FROM BIOLOGICAL DATA TYPES IN CANCER CELLS

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- 1. Background
- Personalised treatment for cancer benefits from integrating modalities
- Correlation with clinical outcome and retrieval is difficult and costly
- Multimodal Variational Auto-Encoders (MVAE) can find a common latent representation of multiple modalities
- Potentially bring deeper understanding of cell relations
- **Predict** modalities for less intensive data gathering

 $\bigcirc \bigcirc \bigcirc$ 2. Research Question

HOW WELL ARE TRAINED MVAE MODELS ABLE TO PREDICT OR RECONSTRUCT MODALITIES IN CANCER CELLS?



3.1 Methods

GCN

DNAme

3000 Features

Comparison based approach of two MVAE Models

- \rightarrow Mixture-of-Experts¹ and Product-of-Experts² • Based on reconstruction loss to MOFA+, a linear method for modality integration
- Based on their efficiency in predicting modalities based on another modality using two MVAE models

RNA-seq



- RNA Sequencing
- Gene Copy Number
- DNA Methylation

Real patient data:

3000 Features 3000 Features >> 8,418 samples from 33 cancer types



4.1 Reconstruction and Prediction Loss





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- THCA UMAP of the latent space (Z) of each model, coloured by cancer type. UCEC Density of clusters indicates local structure -> good grouping of cancer types

 $\sum_{\rm UVM}$ Spread of clusters indicates global structure -> distinction between cancer types

• UMAP indicates Product-of-Experts is learning representation of cancer types • Mixture-of-Experts is **not** making any distinction between types

[2] M. Wu and N. D. Goodman. "Multimodal generative models for scalable weakly-supervised learning." CoRR, vol. abs/1802.05335, 2018