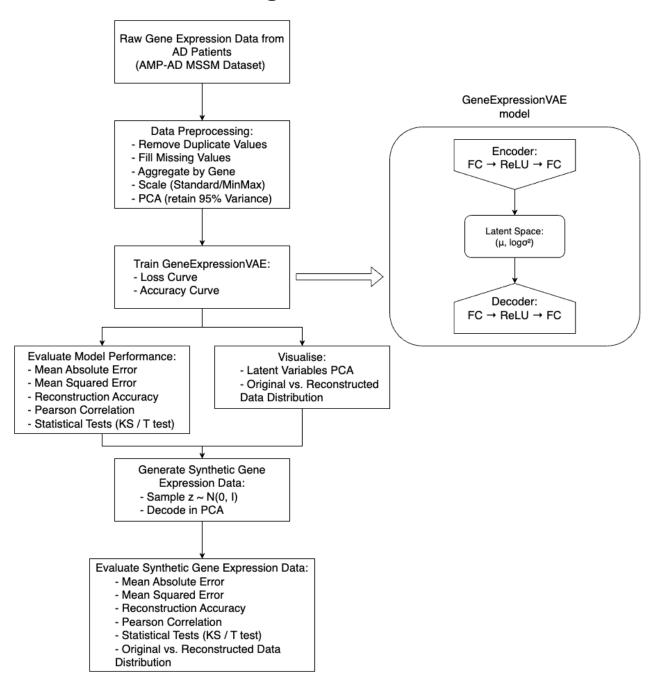
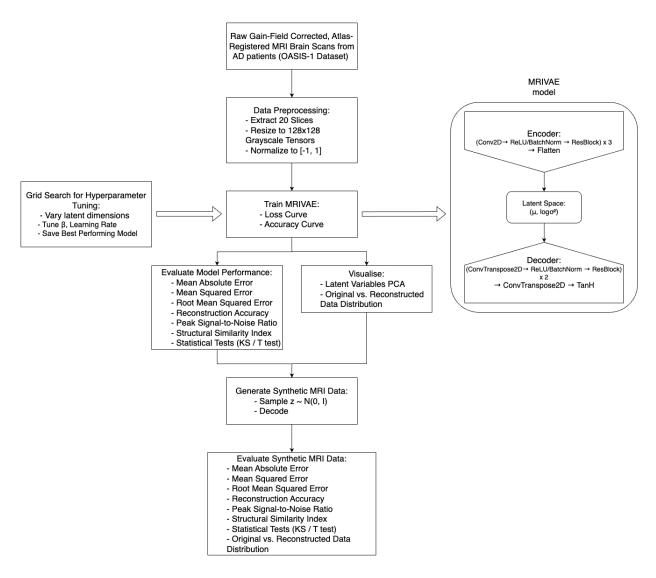
adVAE: Alzheimer's Data Variational Autoencoder Design Documents



Model Architecture - GeneExpressionVAE Pipeline



Model Architecture - MRIVAE Pipeline

Functional Description

adVAE aims to:

- 1. Aid Alzheimer's research by creating high-quality multimodal synthetic data (gene expression, EEG, MRI)
- 2. Easily integrate with existing biomedical workflows

User Interface

Command line interface (CLI)

Functionality

- 1. Preprocess input data used to train the VAE
- 2. Latent space representation of various data modalities
- Generation of synthetic data using latent space variables

Task Prioritization

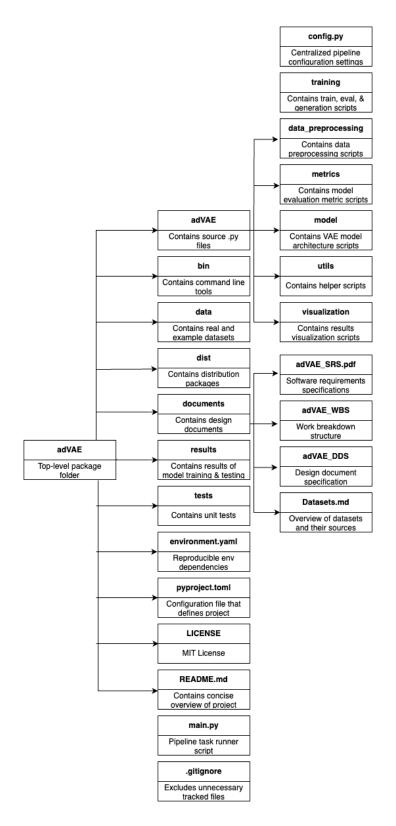
- 1. Identify example data (gene expression, EEG and MRI)
- 2. Create VAE model architecture for one modality (gene expression)
- 3. Train the model using the example gene expression dataset
- 4. Perform latent space optimization
- Validate the results by calculating KL loss and reconstruction error of generated dataset
- 6. Extend the model to include other modalities
- 7. Train, validate, and test the model using the bulk data

Goals and Milestones

- 1. Finish all design documentation
- 2. Set up GitHub repository
- 3. Create modules
- 4. Start implementing code
- 5. Create model for one modality
- 6. Extend model for other modalities
- 7. Peer review
- 8. Refine model and update design documentation

Solutions

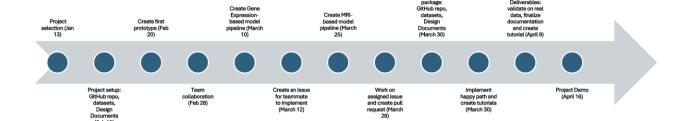
- 1. Tensorize all input data
- 2. Create separate modules/classes for handling different data modalities
- 3. Validate by calculating KL loss and reconstruction loss



Module Structure

```
[adVAE]
LICENSE
     README.md
[adVAE]
             __init__.py
config.py
             [data_preprocessing]
                    __init__.py
[gene_expression]
__init__.py
dataset.py
modified_preprocess.py
                    preprocess.py
misc_utils.py
                    [mri]
                           __init__.py
dataset.py
                           preprocess.py
             [metrics]
            __init__.py
performance.py
vae_loss.py
[models]
                    __init__.py
gene_expression_vae.py
                     mri_vae.py
             [training]
                    aining]
__init__.py
evaluate_gene_expression.py
evaluate_mri.py
evaluate_synthetic_gene_expression.py
evaluate_synthetic_mri.py
generate_synthetic_mri.py
train_gene_expression.py
train_mri.py
                    train_mri.py
             [utils]
                    __init__.py
data_loader.py
                    generator.py
                    utils.py
             [visualization]
                    __init__.py
plot_utils.py
                    visualize_gene_expression.py
visualize_mri.py
      [bin]
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             adVAE-0.1.0-py3-none-any.whl
advae-0.1.0.tar.gz
      [documents]
             Datasets.md
             adVAE_DDS.pdf
adVAE_SRS.pdf
adVAE_WBS.pdf
      environment.yaml
     main.py
pyproject.toml
[tests]
             __init__.py
test_dataloader.py
             test_datasets.py
             test_evaluate.py
             test_generator.py
test_metrics.py
             test_models.py
test_preprocess.py
             test_training.py
test_visualization.py
      [tutorials]
             example_dataset_tutorial.ipynb
real_dataset_tutorial.ipynb
```

Module Structure 2



Project Timeline