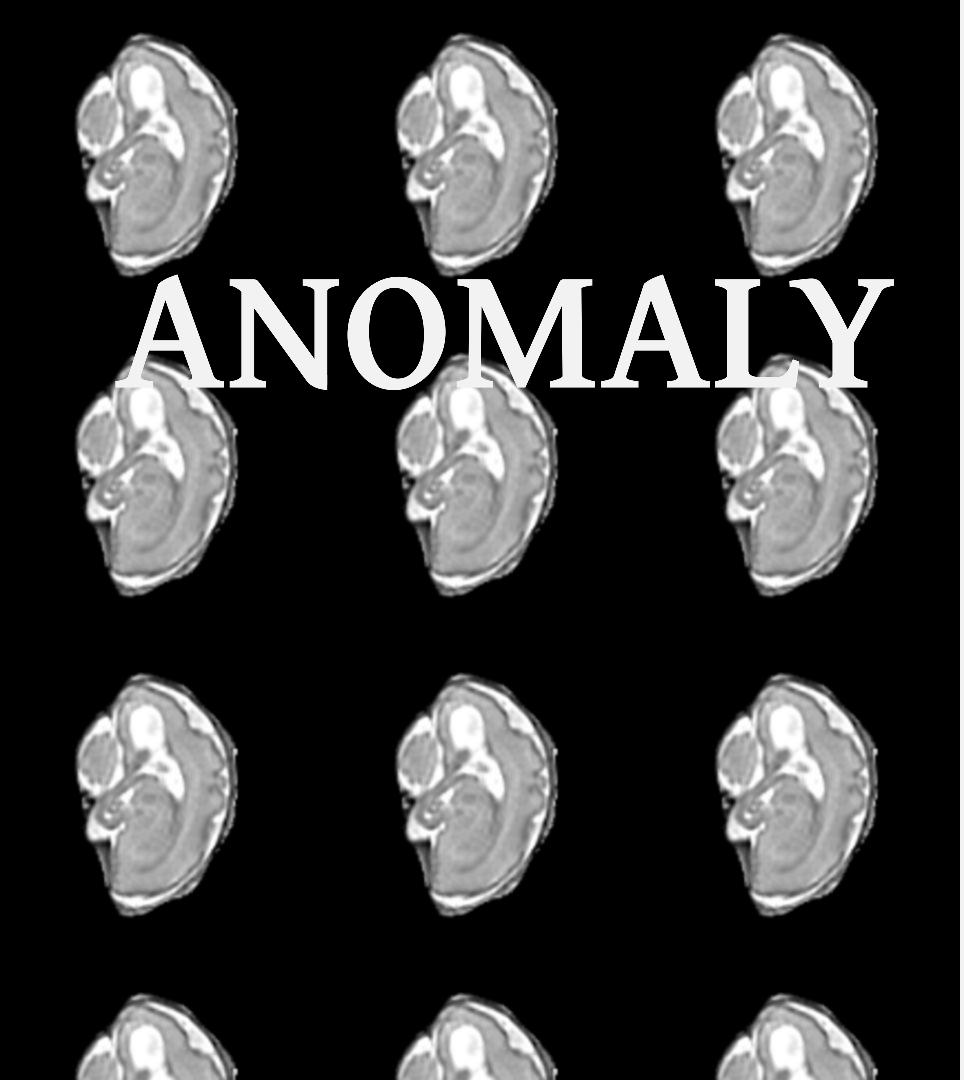
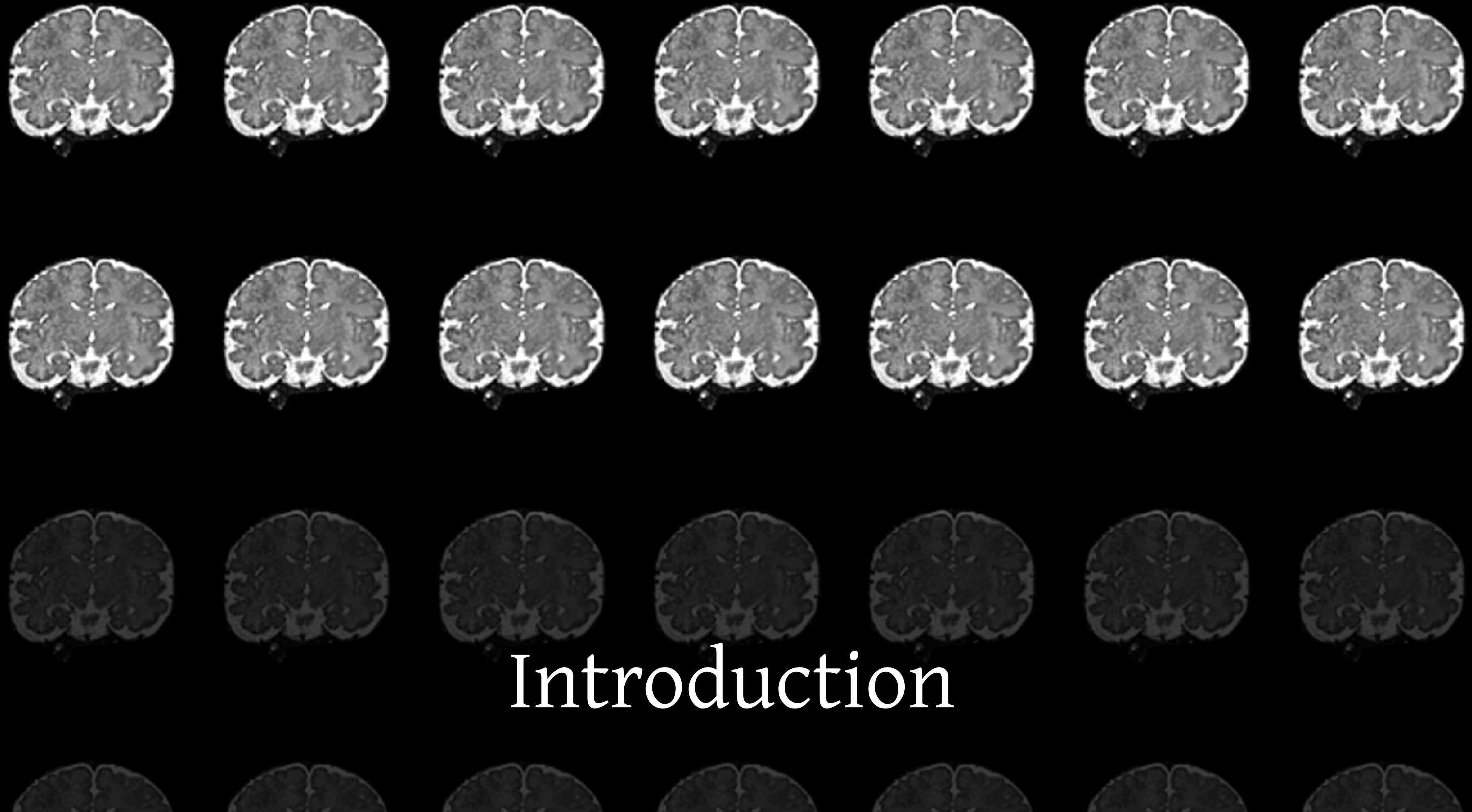


*Unsupervised learning for*

# ANOMALY DETECTION

*in fetal MRI*

HARVARD
MEDICAL SCHOOL



# Introduction

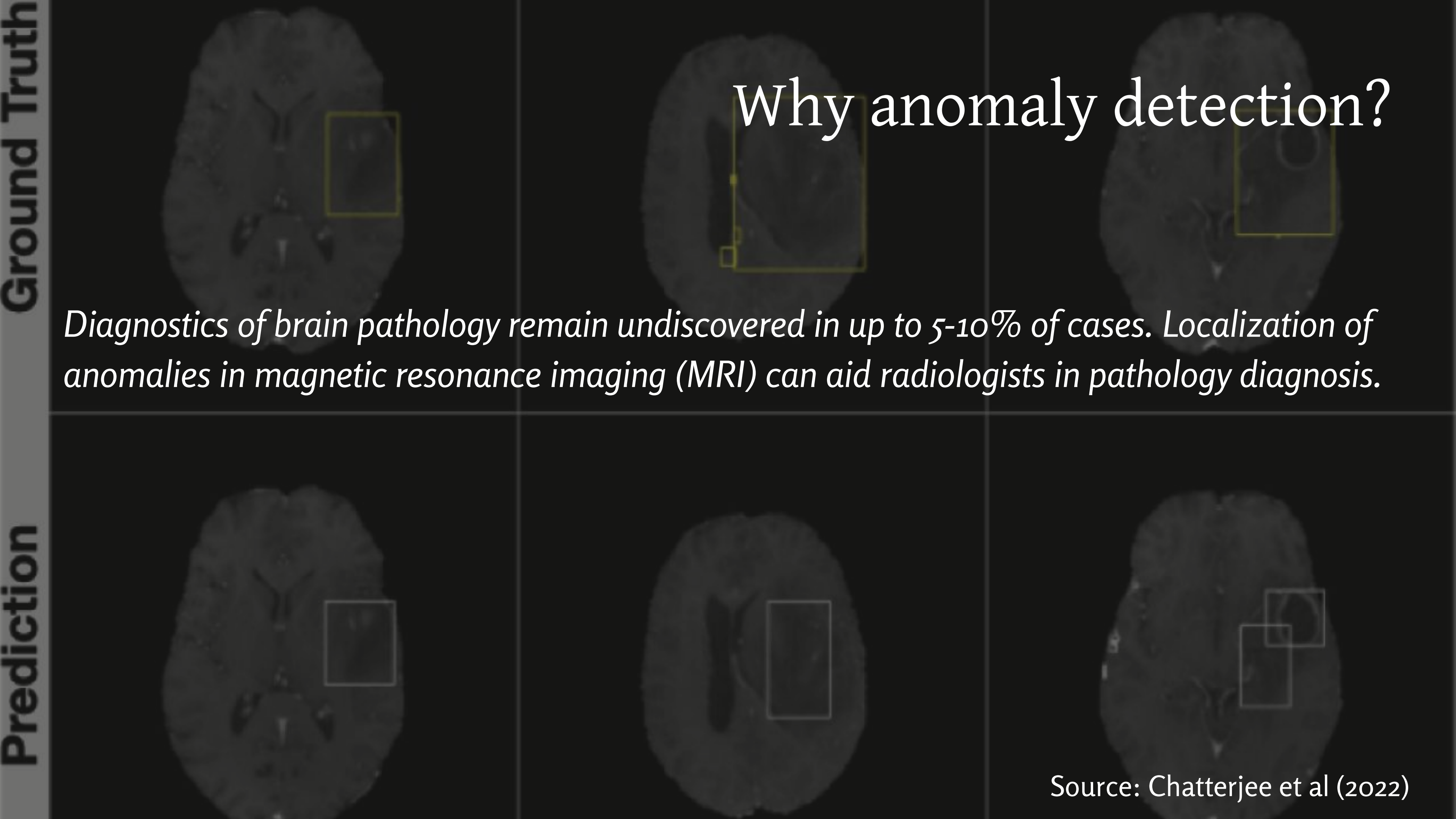
# What is anomaly detection?

*"Anomaly detection (AD) aims at finding unexpected or rare events in data streams, commonly referred to as* ***anomalous events****"*

*Identify relevant indicators of diseases and differentiating them from those of typical healthy tissue characteristics*

Source: Schneider & Xhafa (2022)
Source: Chatterjee et al (2022)

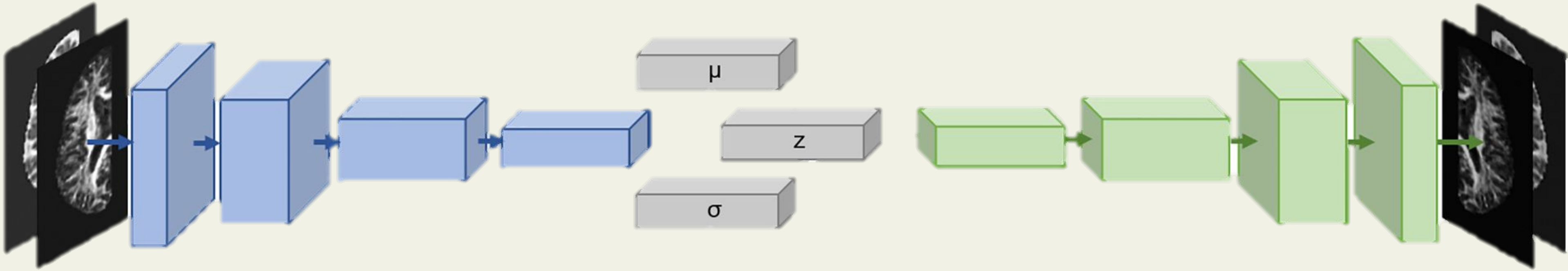
# Why anomaly detection?




*Diagnostics of brain pathology remain undiscovered in up to 5-10% of cases. Localization of anomalies in magnetic resonance imaging (MRI) can aid radiologists in pathology diagnosis.*

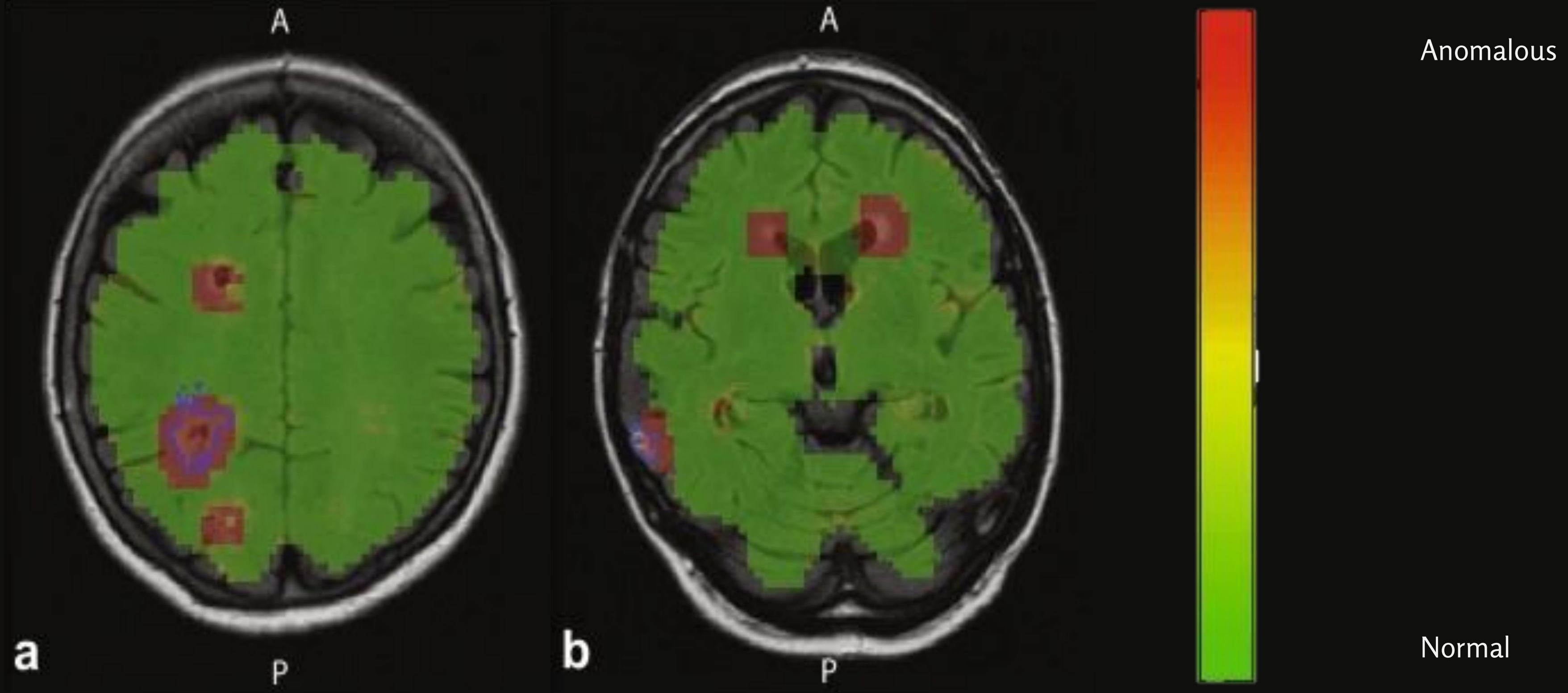
Source: Chatterjee et al (2022)

# What are unsupervised learning models?




Source: Muñoz-Ramírez et al (2022)

# Anomaly detection can be achieved through unsupervised learning methods.




Source: van Hespen et al (2021)

# Previous work

## Subtle anomaly detection: Application to brain MRI analysis of de novo Parkinsonian patients,

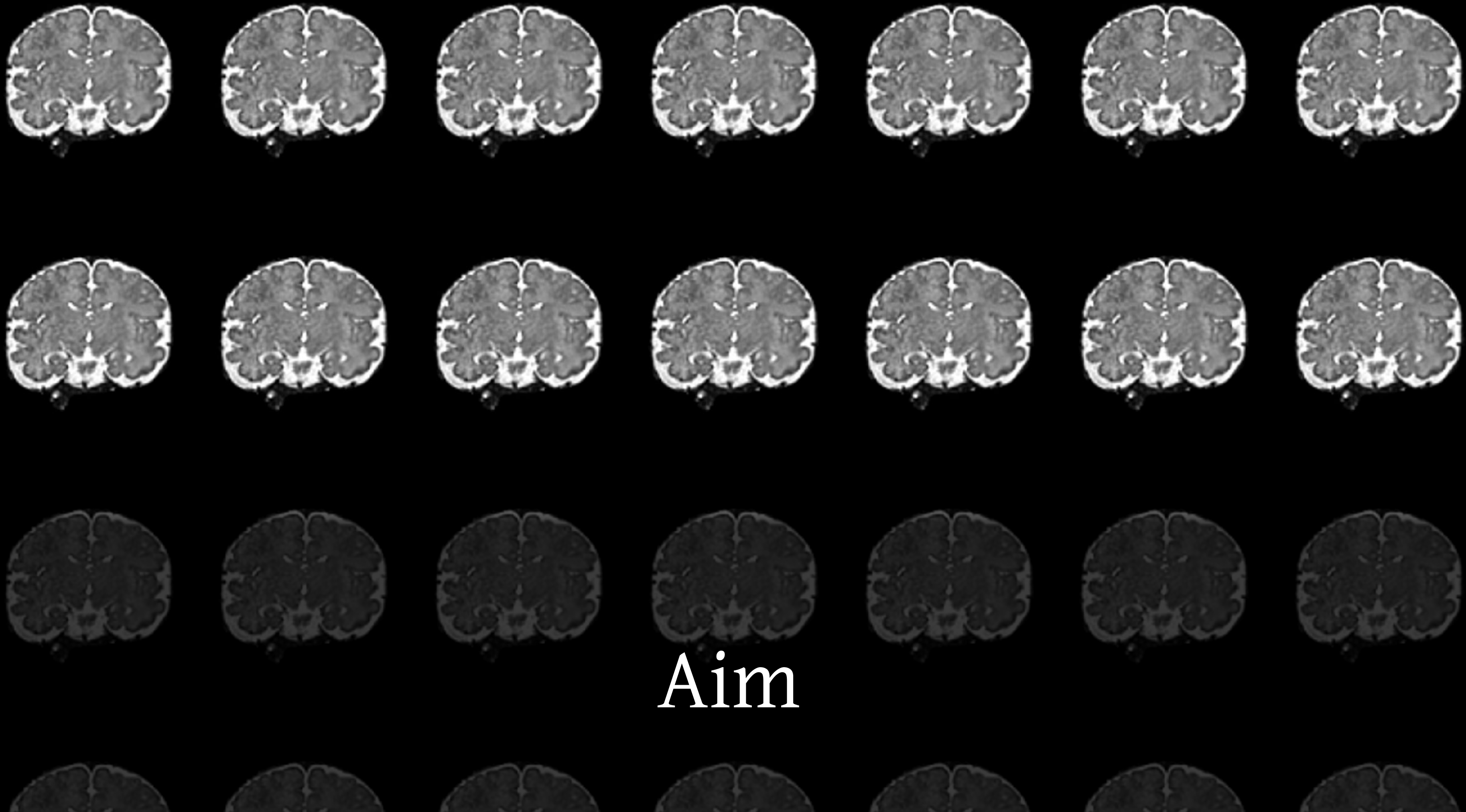
Muñoz-Ramirez et al (2021)
Implements Variational Auto-Encoder (VAE) model to detect brain MRI anomalies, validated with Parkinsonian patients.

## StRegA: Unsupervised anomaly detection in brain MRIs using a compact context-encoding variational autoencoder

Chatterjee et al (2022)
Implements a VAE model to detect brain tumors. Adds binarization methods and morphological openings to reduce false positives.

## Reversing the Abnormal: Pseudo-Healthy Generative Networks for Anomaly Detection

Bercea et al (2023)
Proposes a refinement model after a base reconstruction through an in-painting model to reduce false positives.



# Aim

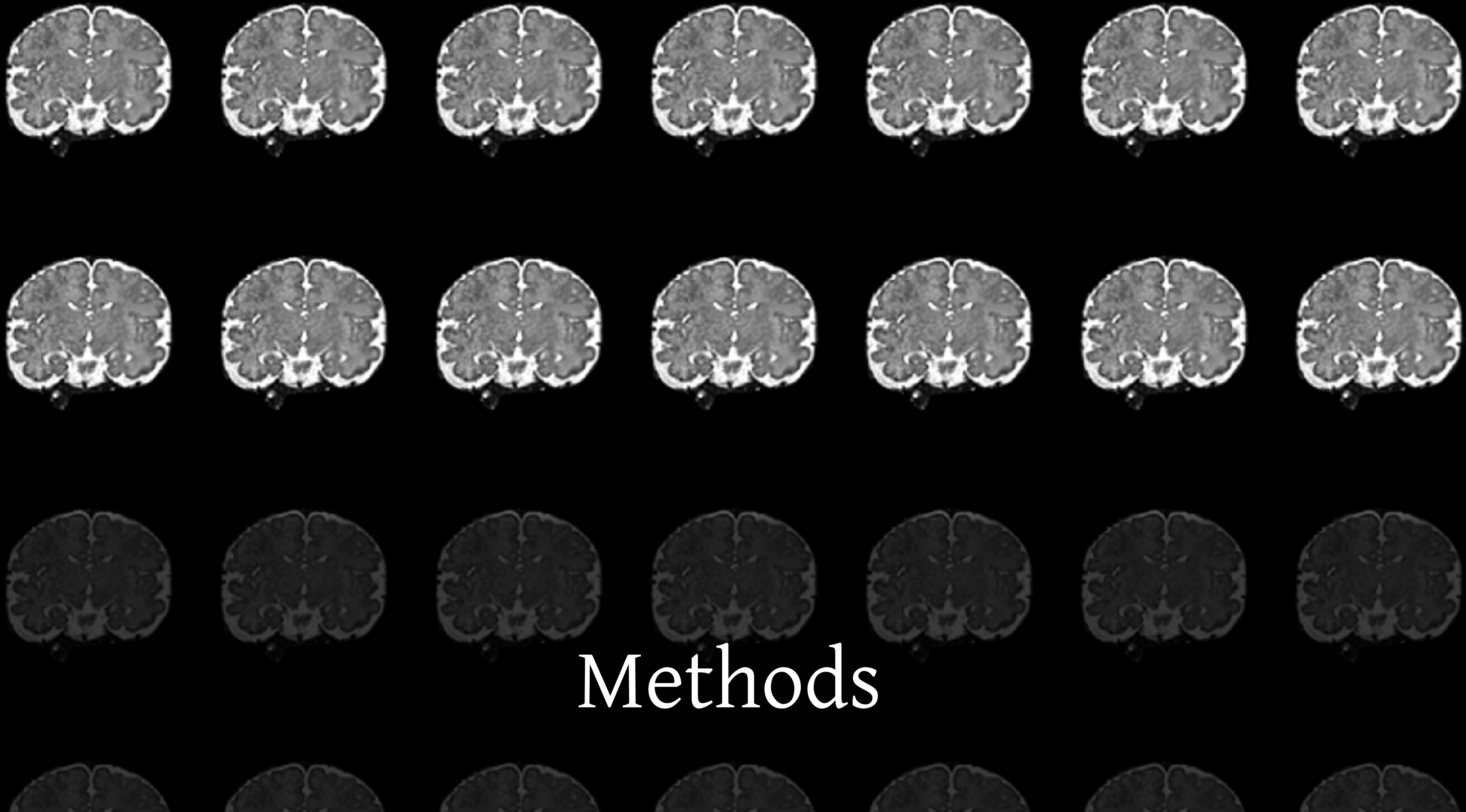
# Aim

Augment accuracy of the AD process

- Improve general detection performance of anomalies in fetal brain

Be able to detect not only developmental delays, but also developmental ones

- Detect true-positive anomalies by reflecting the temporal variation due to neurodevelopment during gestation



# Methods

# Datasets

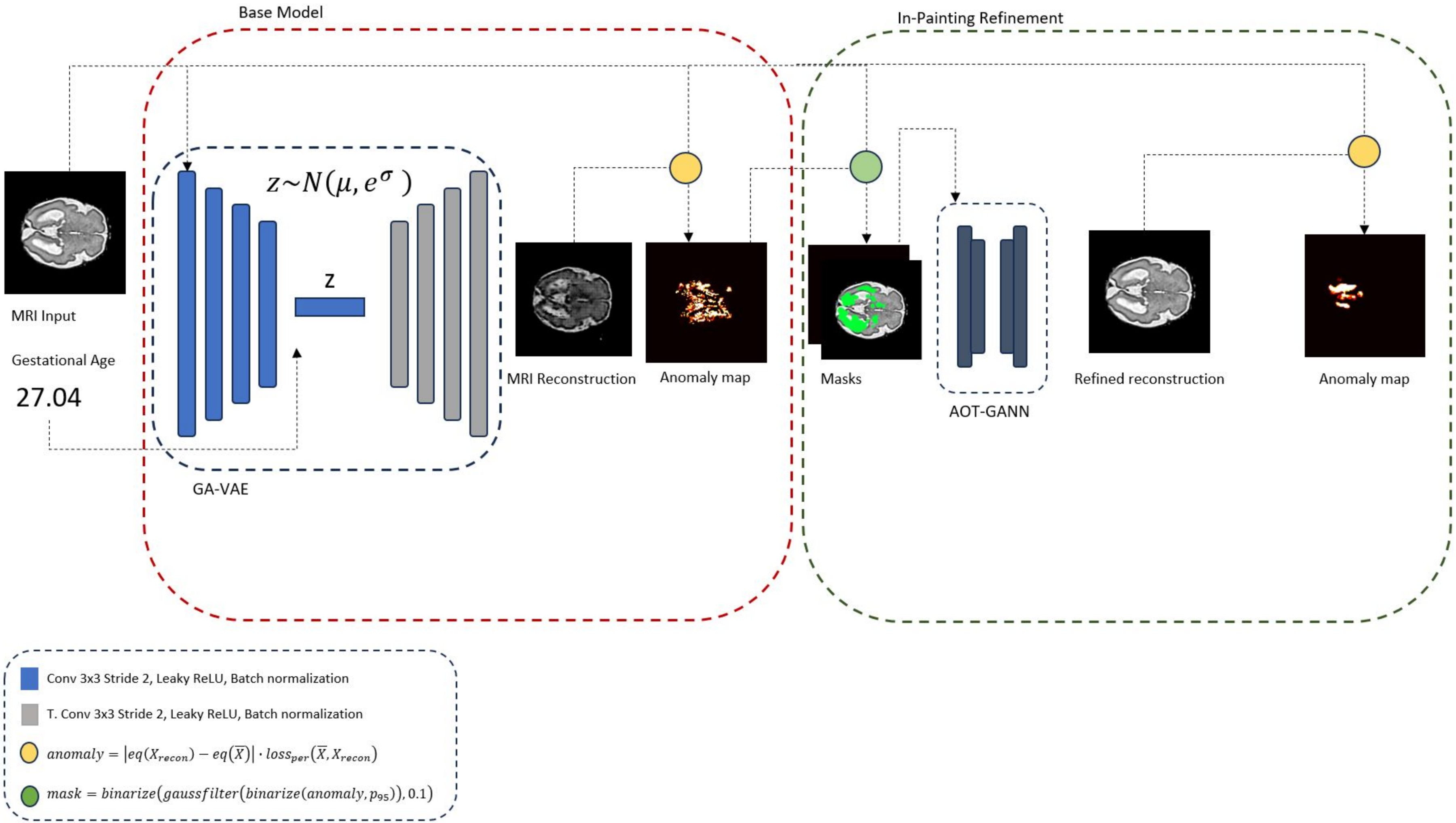
MRI data was extracted from the CHD, Placenta, TMC, VGH and BCH datasets.

## Typically Developing (TD) Subjects

A total of 227 subjects. 181 used for training and 46 for testing.

## Ventriculomegaly (VM) Subjects

A total of 69 subjects.

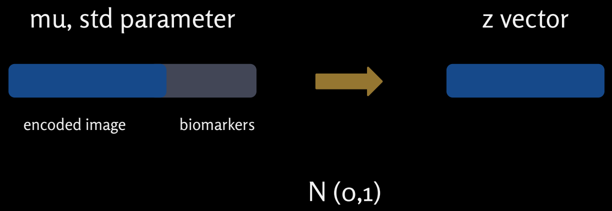

Base Model
In-Painting Refinement
$z \sim N(\mu, e^{\sigma})$
z
MRI Input
Gestational Age
27.04
GA-VAE
MRI Reconstruction
Anomaly map
Masks
AOT-GANN
Refined reconstruction
Anomaly map
Conv 3x3 Stride 2, Leaky ReLU, Batch normalization
T. Conv 3x3 Stride 2, Leaky ReLU, Batch normalization
$anomaly = |eq(X_{recon}) - eq(\overline{X})| \cdot loss_{per}(\overline{X}, X_{recon})$
$mask = binarize(gaussfilter(binarize(anomaly, p_{95})), 0.1)$

# Providing significant novelty for fetal MRI: gestational age (GA) as input

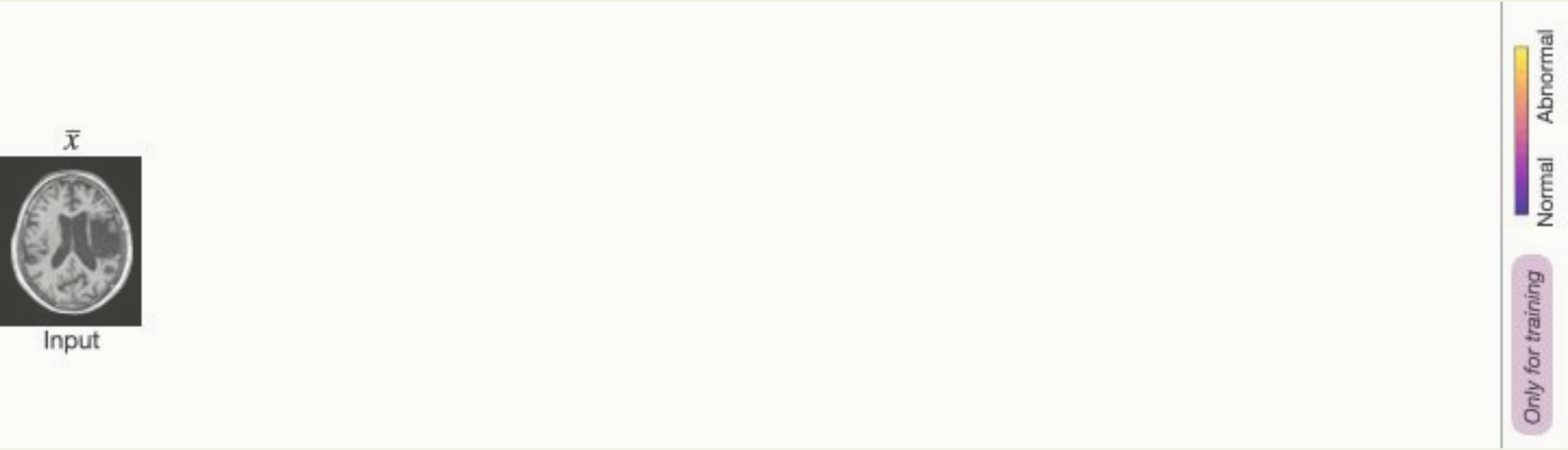
Developmental context

Recognition of developmental delays as anomalies

Concatenation method



# Refining reconstruction through in-painting model




Source: Bercea et al (2022)

# Training of VAE and AOT-GAN models are done separately

VAE

L2 loss only.

No adversarial training

AOT-GAN

Combination of L1, perceptual, and style losses

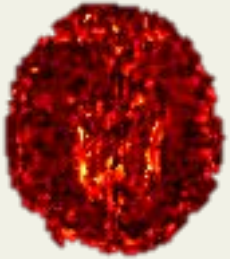
Adversarial training

# How do we define anomaly?

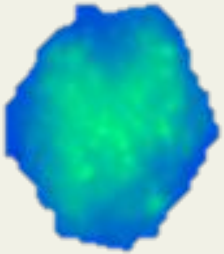
Input

Reconstruction

Mean Squared Error (MSE)



Mean Absolute Error (MAE)

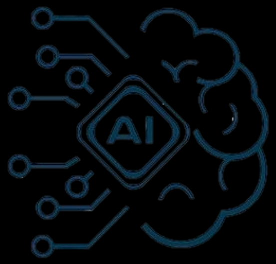


Saliency

$$anomaly = \left|eq(X_{rec}) - eq(\bar{X})\right| \cdot loss_{per}(\bar{X}, X_{rec})$$

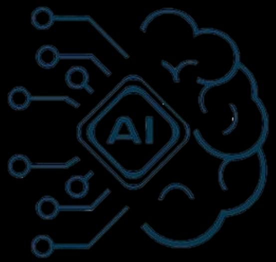
Anomaly Metric

# Our current models



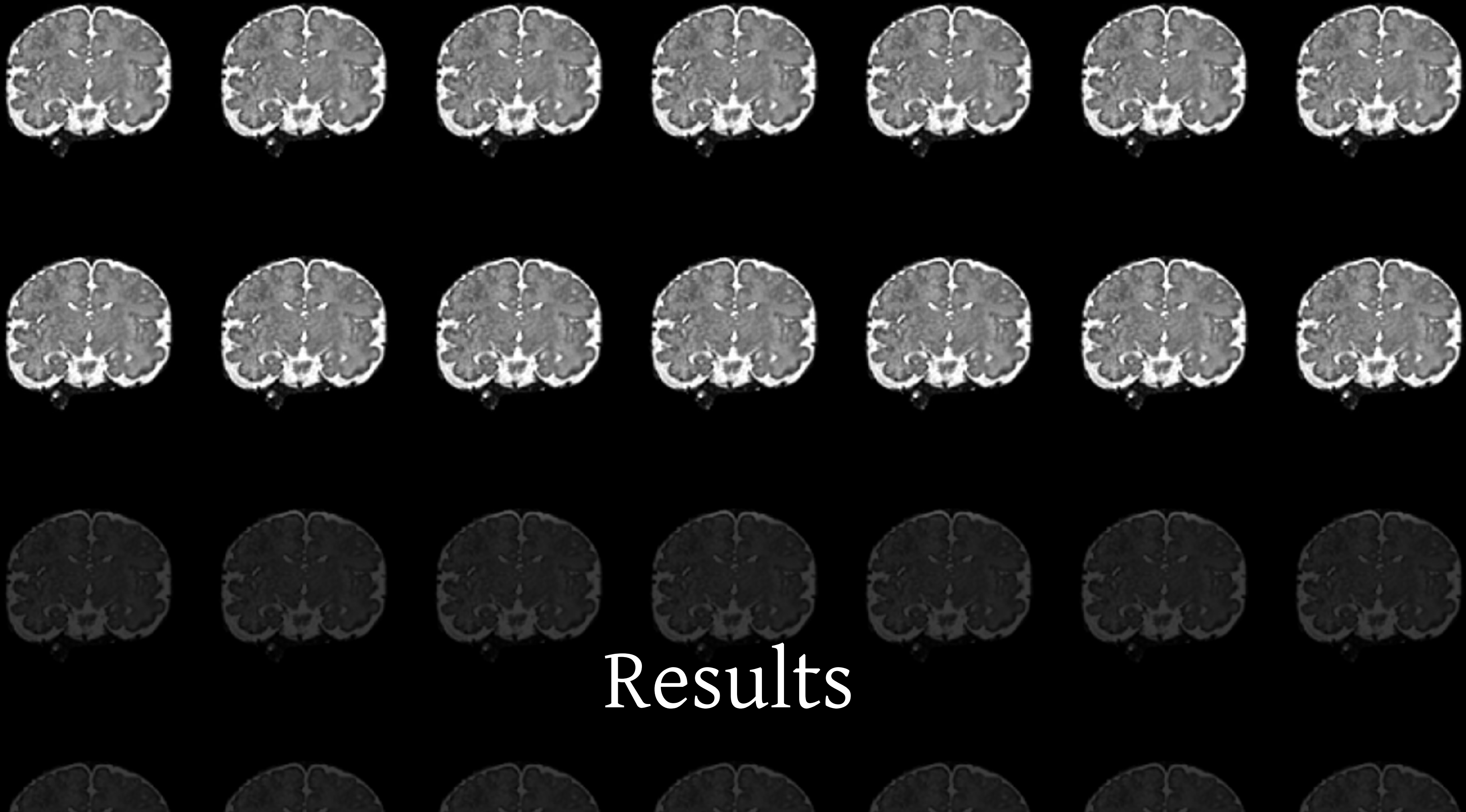
**Sapi** *(Quechua: Root)*

Trained for 2000 epochs. Pre-trained from a previous VAE model, it does not take GA as input. Trained with 151 subjects.



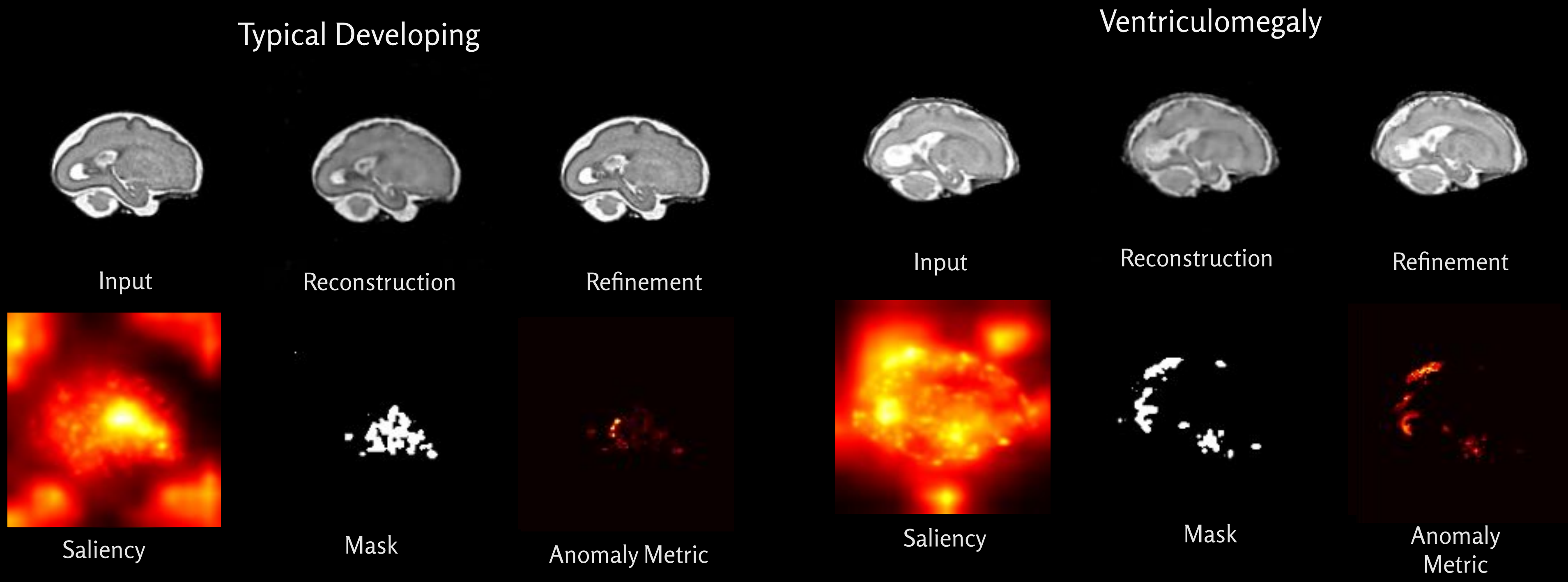
**Miraywa** *(Quechua: Fertility)*

Trained for 2000 epochs. Pre-trained from the Sapi model, it takes GA as input through concatenation. Trained with 227 subjects.

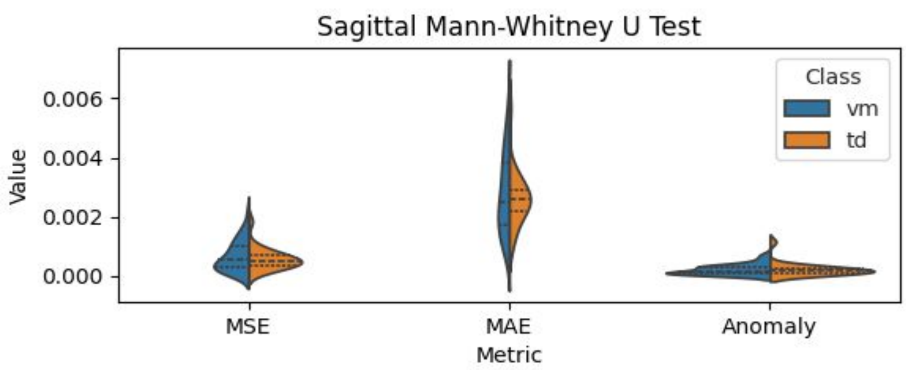


# Results

# Sagittal View



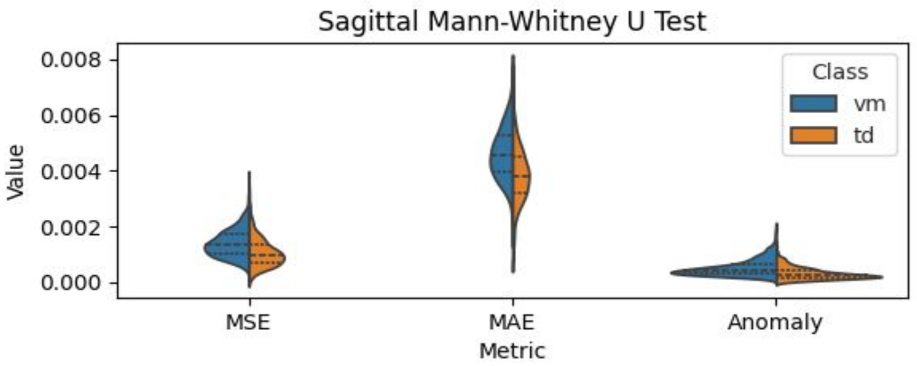
## Sapi




### P-Values

| | |
|---|---|
| MAE | 0.8535 |
| MSE | 0.9037 |
| Anomaly | 0.8635 |

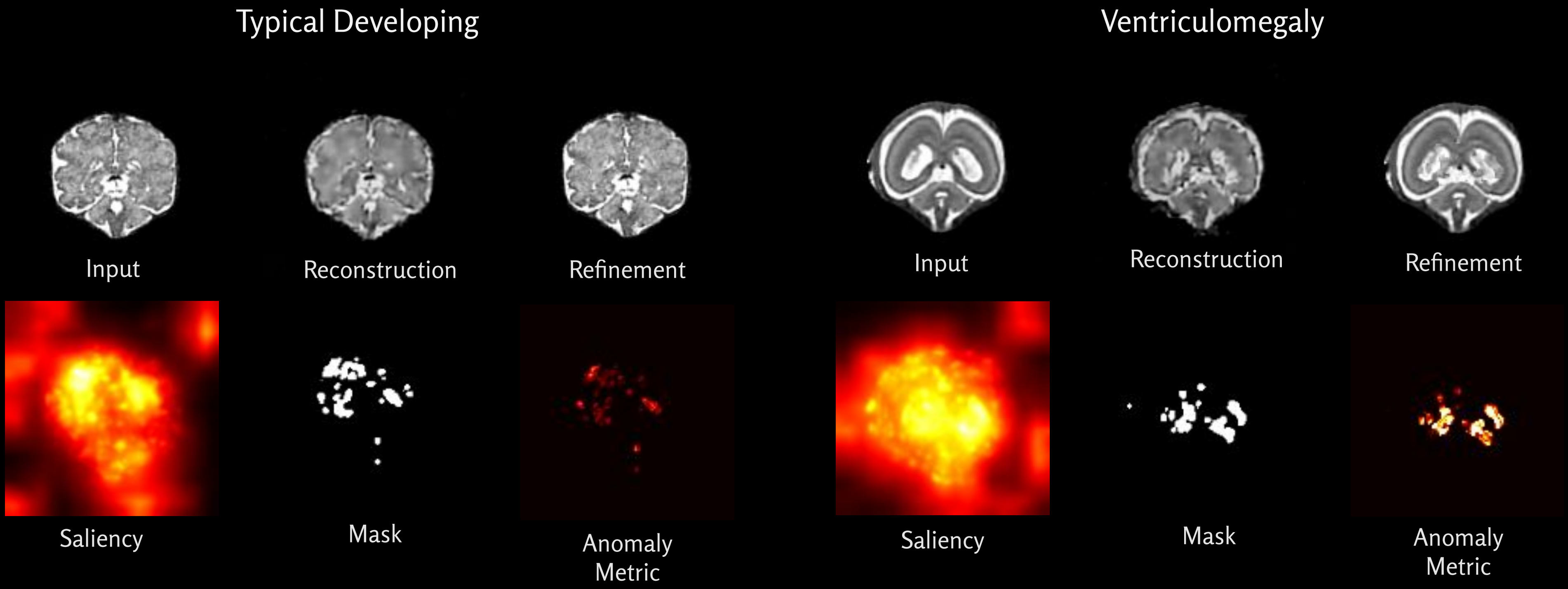
## Miraywa




### P-Values

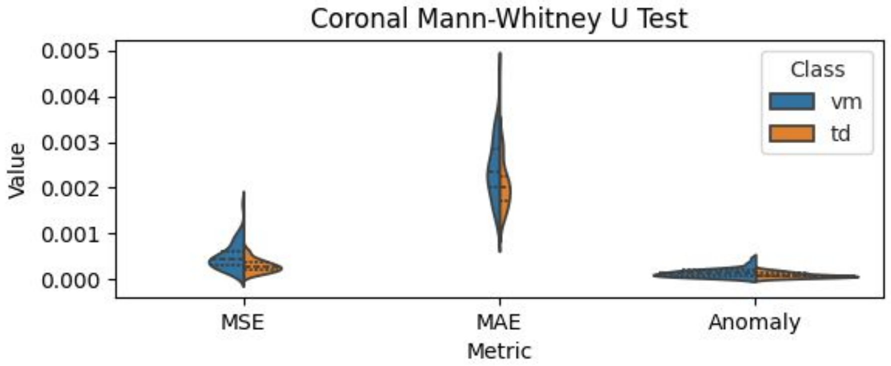
| | |
|---|---|
| MAE | **0.005** |
| MSE | **0.007** |
| Anomaly | **0.0002** |

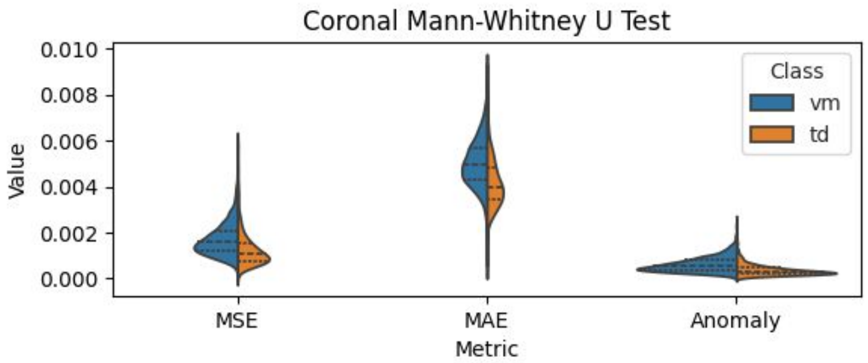
# Coronal View



## Sapi

## Miraywa



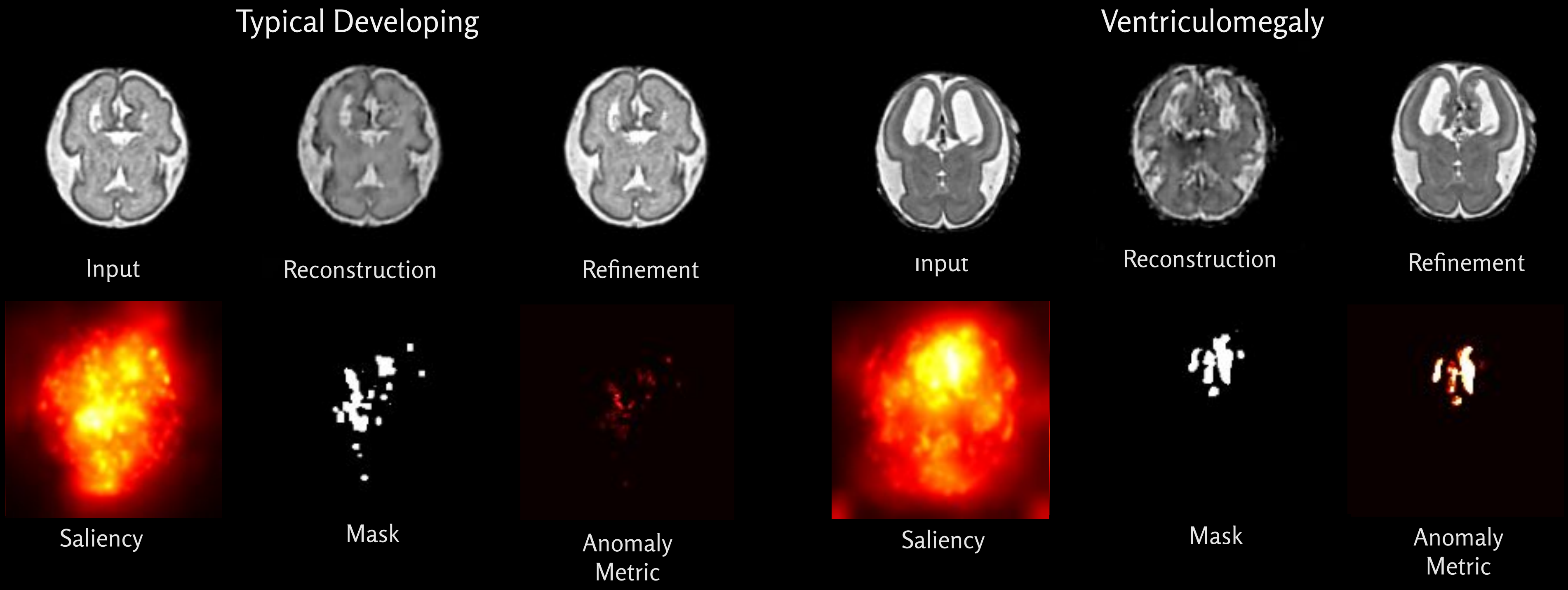

### P-Values

| | |
|---|---|
| MAE | 0.001 |
| MSE | 0.01377 |
| Anomaly | 0.01329 |

### P-Values

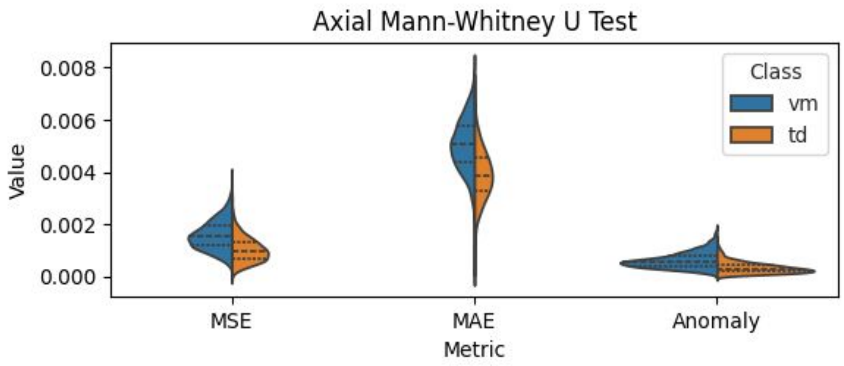
| | |
|---|---|
| MAE | $p < 10^{-5}$ |
| MSE | $p < 10^{-6}$ |
| Anomaly | $p < 10^{-7}$ |

# Axial View



Typical Developing
Ventriculomegaly
Input
Reconstruction
Refinement
Input
Reconstruction
Refinement
Saliency
Mask
Anomaly Metric
Saliency
Mask
Anomaly Metric

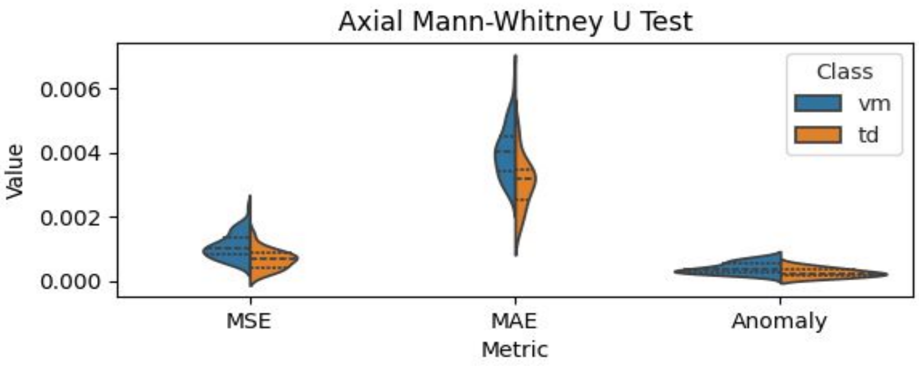
## Sapi




### P-Values

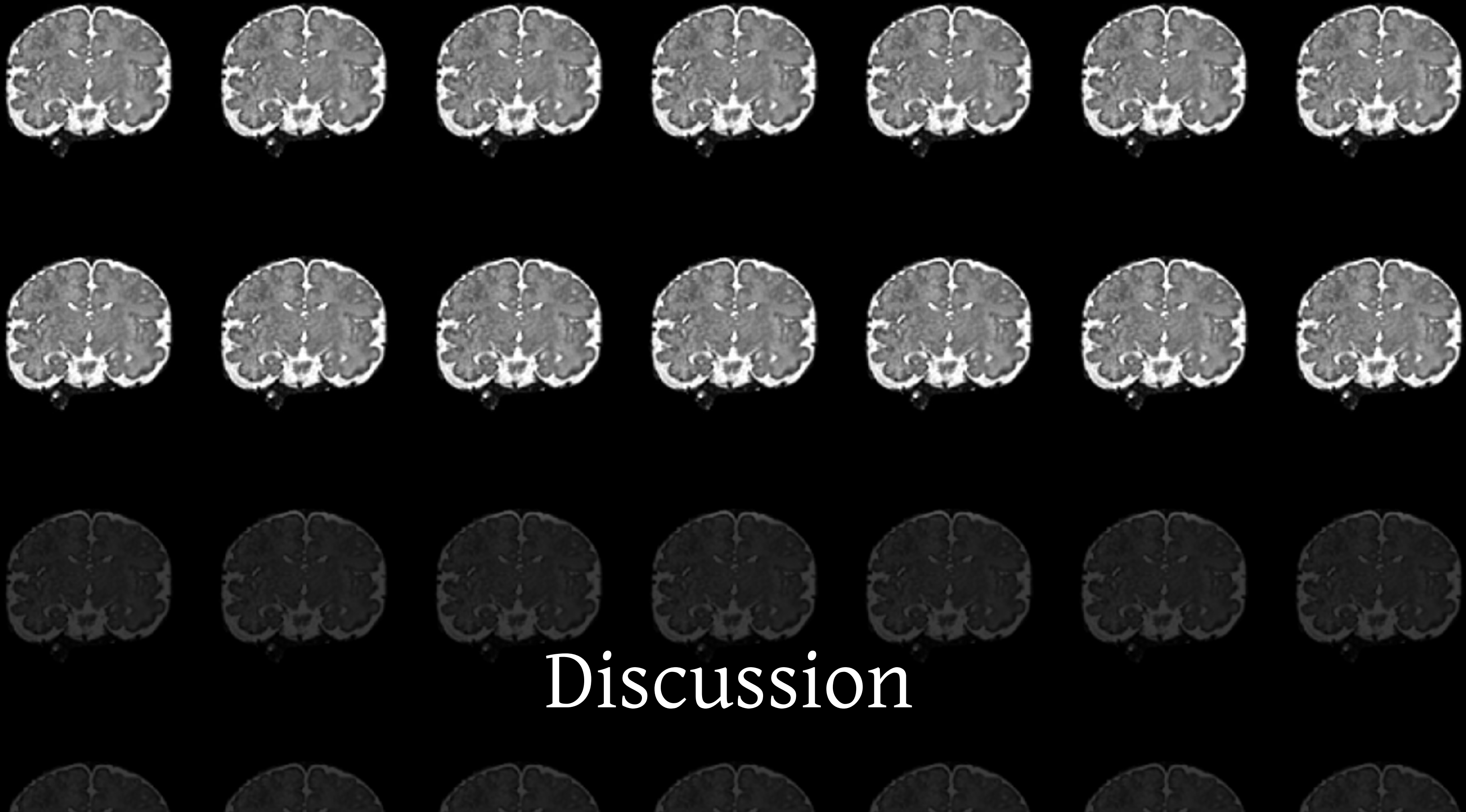
| | |
|---|---|
| MAE | $p < 10^{-5}$ |
| MSE | $p < 10^{-5}$ |
| Anomaly | 0.001 |

## Miraywa




### P-Values

| | |
|---|---|
| MAE | $\boldsymbol{p < 10^{-7}}$ |
| MSE | $\boldsymbol{p < 10^{-7}}$ |
| Anomaly | $\boldsymbol{p < 10^{-7}}$ |



# Discussion

# Limitations

## Comparing models is difficult due to the difference in datasets

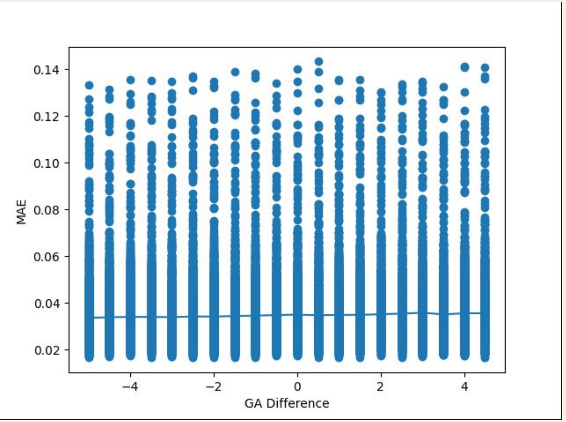
Due to the number of subject difference, it is difficult to determine if improvements are due to the dataset size or the difference in the model itself.

## GA Model presents low sensitivity to GA

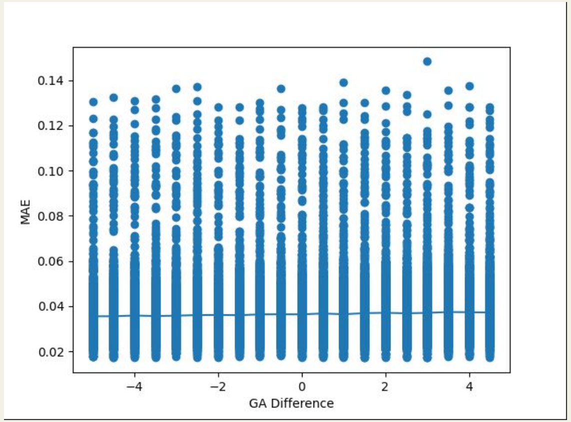
When running tests on the effects of the GA value to the errors between reconstruction and input, there is no notable influence of GA in the model.

# Miraywa presented low sensitivity to GA.

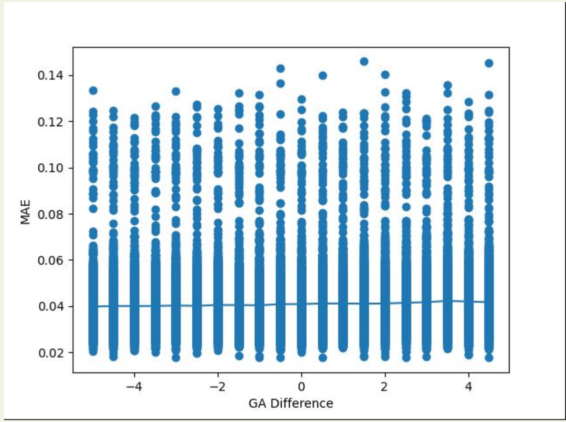
Sagittal




Coronal




Axial



# Future work

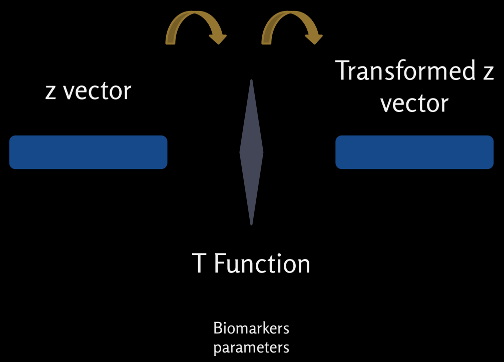
## Retrain Sapi model for better model comparison

Train a non-GA model with current dataset size to properly evaluate the effect of new model

## Using a new method for GA integration

Applying a parametrization method, instead of concatenation, might lead to GA holding more influence in reconstruction

Parametrization method



# Thank you.

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