Towards prediction of pseudo-normal SPECT image data using variational autoencoder

Kateřina Dudášová[1]
Ph.D. Candidate

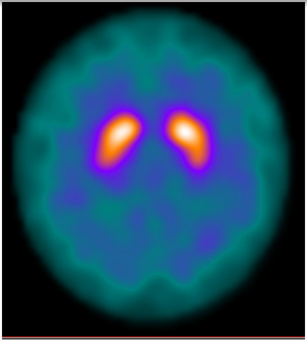
Jiří Trnka, PhD.[1,2]
supervisor

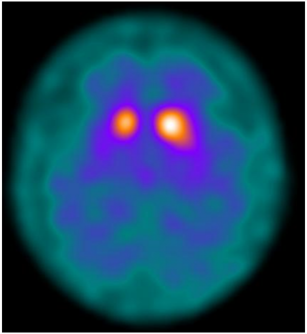
[1]Faculty of Nuclear Sciences and Physical Engineering, CTU in Prague, Czech Republic
[2]The General Teaching Hospital in Prague, Czech Republic

katerina.dudasova@fjfi.cvut.cz

Dudasova K, Trnka J. Towards prediction of pseudo-normal SPECT image data using variational autoencoder. Nucl Med Rev Cent East Eur. 2025;28(0):9-17. doi: 10.5603/nmr.101316. PMID: 40103394.

Diagnostics of Parkinson's disease





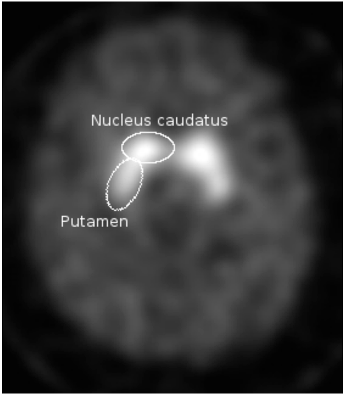
Dopamine Transporter binding in nigrostriatal pathway

^{123}I-ioflupane

Current clinical evaluation

Quantification of Striatal binding ratio

$$C_{gang} = \frac{\overline{N_{gang}} - \overline{N_{bcg}}}{\overline{N_{bcg}}} \qquad (1)$$



Key role in clinical outcome:

Extensive age-related **database** of individuals with **normal** uptake in basal ganglia ← **FBP** reconstructed SPECT

Key idea

Key idea

Generate **individual** normal image.

How?

Generative network

How?

Generative network → Variational Autoencoder

How?

Generative network → Variational Autoencoder

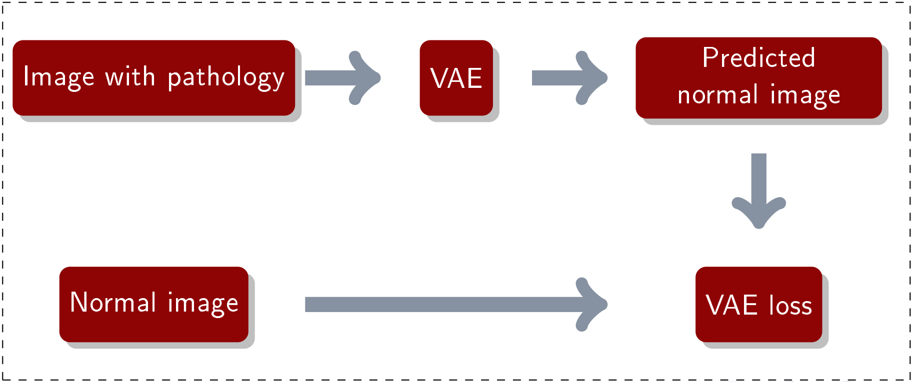
Restoration Task

Damaged image → VAE → Predicted original image → CVAE loss

Original image → CVAE loss

How?

Clinical Task



Creating a Dataset

45 MRI
segmented masks

basal ganglia

background brain

Creating a Dataset

45 MRI segmented masks → BG Degradation

controlled by PBR, CBR, SLR

basal ganglia

background brain

Creating a Dataset

45 MRI segmented masks → **BG Degradation** → **Sinogram**

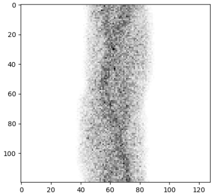
basal ganglia

background brain

BG Degradation: controlled by PBR, CBR, SLR

1. Poisson's variation
2. forward Radon

Sinogram: +Gaussian blur



Creating a Dataset

45 MRI segmented masks

BG Degradation

controlled by PBR, CBR, SLR

1. Poisson's variation
2. forward Radon

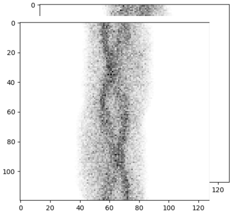
Sinogram

+Gaussian blur

basal ganglia

background brain

No degradation



Creating a Dataset

45 MRI segmented masks → BG Degradation → Sinogram

BG Degradation

controlled by PBR, CBR, SLR

No degradation

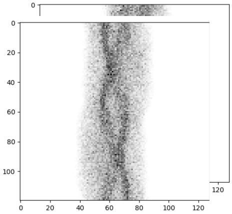
1. Poisson's variation
2. forward Radon

Sinogram

+Gaussian blur

basal ganglia

background brain



Validation dataset

- 36 MRI
- *10 (PBR,CBR,SRL)
- **360**

Creating a Dataset

45 MRI segmented masks → **BG Degradation** → **Sinogram**

45 MRI segmented masks → **No degradation** → **Sinogram**

basal ganglia

background brain

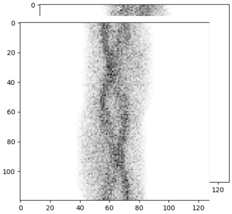
BG Degradation

controlled by PBR, CBR, SLR

1. Poisson's variation
2. forward Radon

Sinogram

+Gaussian blur



No degradation

Validation dataset

- 36 MRI
- *10 (PBR,CBR,SRL)
- **360**

Training dataset

- 36 MRI
- *17 (PBR,CBR,SRL)
- **612**

Creating a Dataset

45 MRI segmented masks → BG Degradation → Sinogram

BG Degradation: controlled by PBR, CBR, SLR

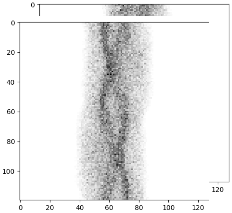
1. Poisson's variation
2. forward Radon

Sinogram: +Gaussian blur

45 MRI segmented masks → No degradation → Sinogram

basal ganglia

background brain



Validation dataset

- 36 MRI
- *10 (PBR,CBR,SRL)
- **360**

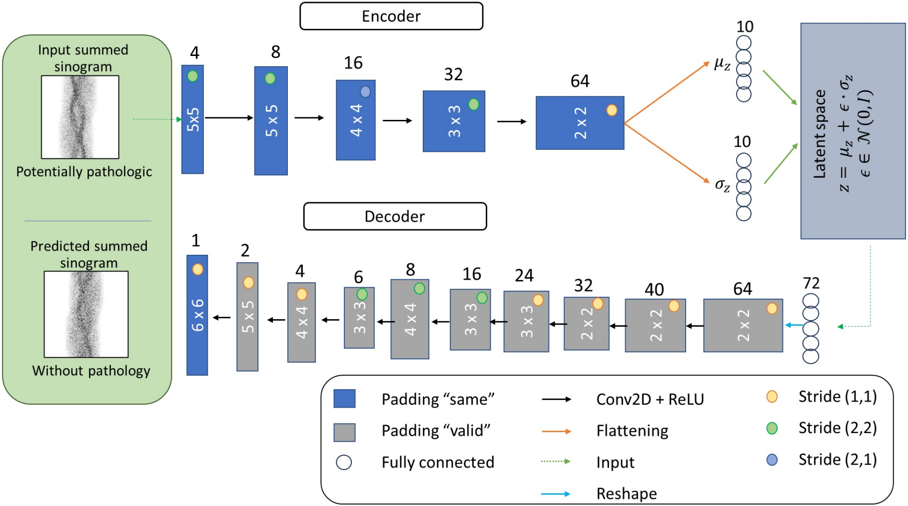
Training dataset

- 36 MRI
- *17 (PBR,CBR,SRL)
- **612**

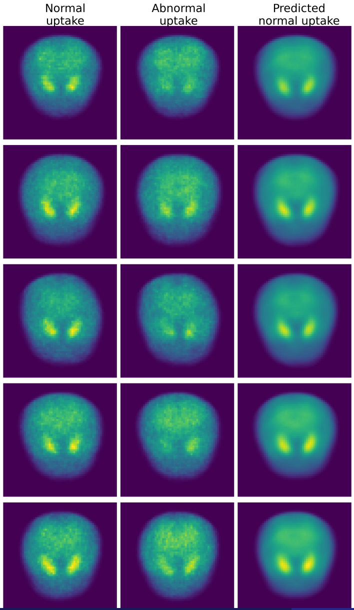
Testing dataset

- 9 MRI
- *17 (PBR,CBR,SRL)
- **153**

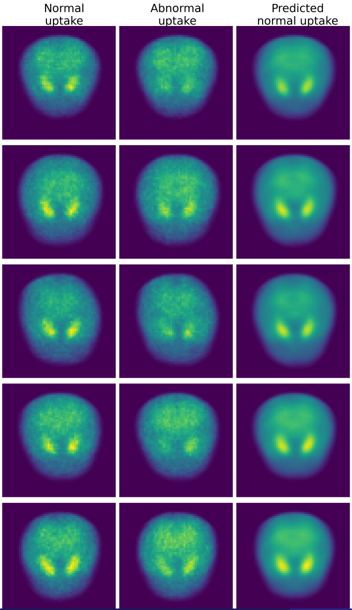
VAE architecture

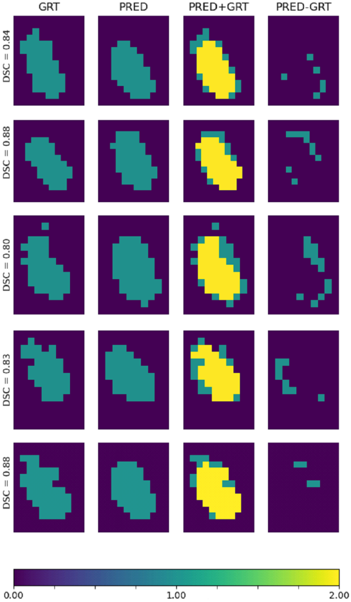


VAE predictions



VAE predictions

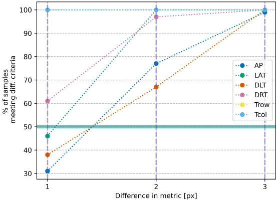


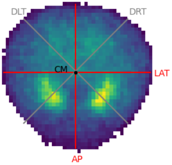


Performance evaluation

Anatomy Shape Precision (ASP)

Dimensions [px]:
AP, LAT
DLT = diagonal-left-top
DRT = diagonal-right-top
CM = center of mass (Trow, Tcol)

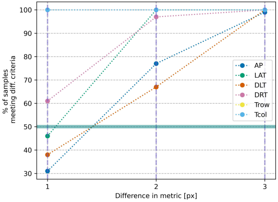


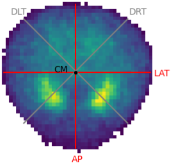


Performance evaluation

Anatomy Shape Precision (ASP)

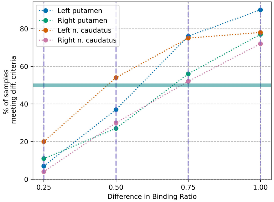
Dimensions [px]:
AP, LAT
DLT = diagonal-left-top
DRT = diagonal-right-top
CM = center of mass (Trow, Tcol)





Basal Ganglia (BG) uptake correspondence

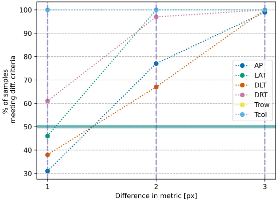
binding ratio match
assessed by Regression Conv NN

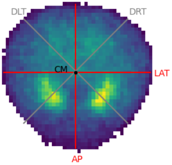


Performance evaluation

Anatomy Shape Precision (ASP)

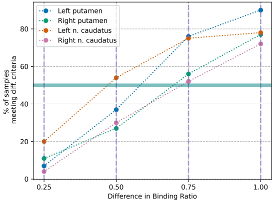
Dimensions [px]:
AP, LAT
DLT = diagonal-left-top
DRT = diagonal-right-top
CM = center of mass (Trow, Tcol)





Basal Ganglia (BG) uptake correspondence

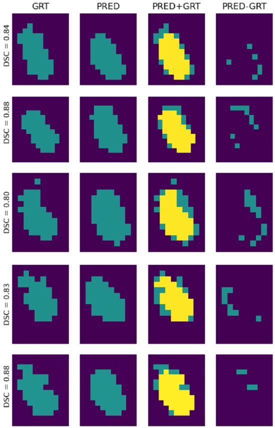
binding ratio match
assessed by Regression Conv NN



Dice Similarity Coefficient (DSC)

of segmented BG

	Mean±std	Min	Max
Left BG	78±8 %	62 %	90 %
Right BG	82±5 %	69 %	93 %



Discussion

Performance evaluation

Anatomy Shape Precision:	<3 pixels	satisfying
Dice Similarity Coefficient:	mean 78 %	satisfying
Binding ratio:	52 % <0.75	promising

Discussion

Performance evaluation

Anatomy Shape Precision:	<3 pixels	satisfying
Dice Similarity Coefficient:	mean 78 %	satisfying
Binding ratio:	52 % <0.75	promising

Limitations of the study

- 45 real brain MRI
- synthetic data (mathematical data generator vs. Monte Carlo)
- predicted images - blurred → False Positive Result
- **validation on real clinical data**

Application

- Virtual harmonization technique for multi-center studies in NM
- Generation of synthetic normal database

Summary

Original motivation

→**Individualize** the clinical evaluation by avoiding database of normals

Summary

Original motivation

→**Individualize** the clinical evaluation by avoiding database of normals

How?

→By comparing an **actual** image with an **expected** image of **normal** finding

Summary

Original motivation

→**Individualize** the clinical evaluation by avoiding database of normals

How?

→By comparing an **actual** image with an **expected** image of **normal** finding

Realistic applications

- Virtual harmonization technique
- Synthetic normal databases

Summary

Original motivation

→**Individualize** the clinical evaluation by avoiding database of normals

How?

→By comparing an **actual** image with an **expected** image of **normal** finding

Realistic applications

- Virtual harmonization technique
- Synthetic normal databases

Is it feasible?

YES. . .

Thank you for your attention!