

Student Intern Presentation (Neurolm Lab)

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Overview

- 1 Fetal MRI
- 2 Fetal dMRI
- 3 qMRI CHD Classification
- 4 High-resolution Subplate
- 5 FeTA Challenge @ MICCAI 2024
- 6 Acknowledgements

Section 1

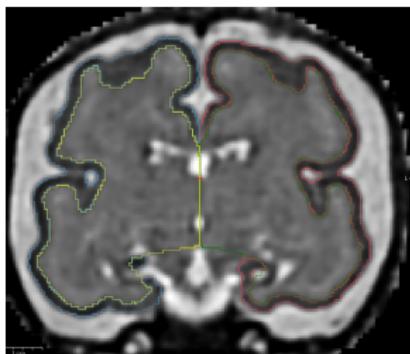
Fetal MRI

Manual MRI segmentation correction

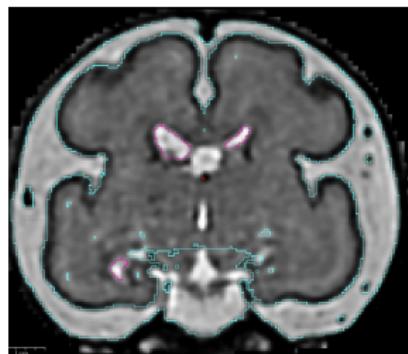
| Dataset | n | Year |
|-------------------------|-----------|------|
| Placenta/CHD | 20 | '23 |
| dHCP | 31 | '23 |
| High-res CP | 15+2 | '23 |
| VM | 30+10 | '23 |
| CSF | 19 | '24 |
| Ventricle | 19 | '24 |
| High-res SP | 63 | '24 |
| Coordinated high-res SP | (68) | '24 |
| | 209 (277) | |

Examples

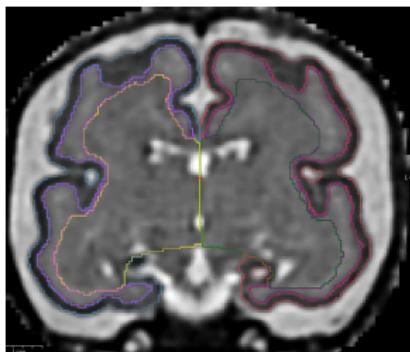
Cortical Plate



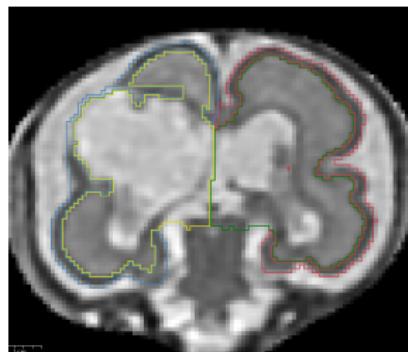
CSF & Ventricle



Subplate



Ventriculomegaly

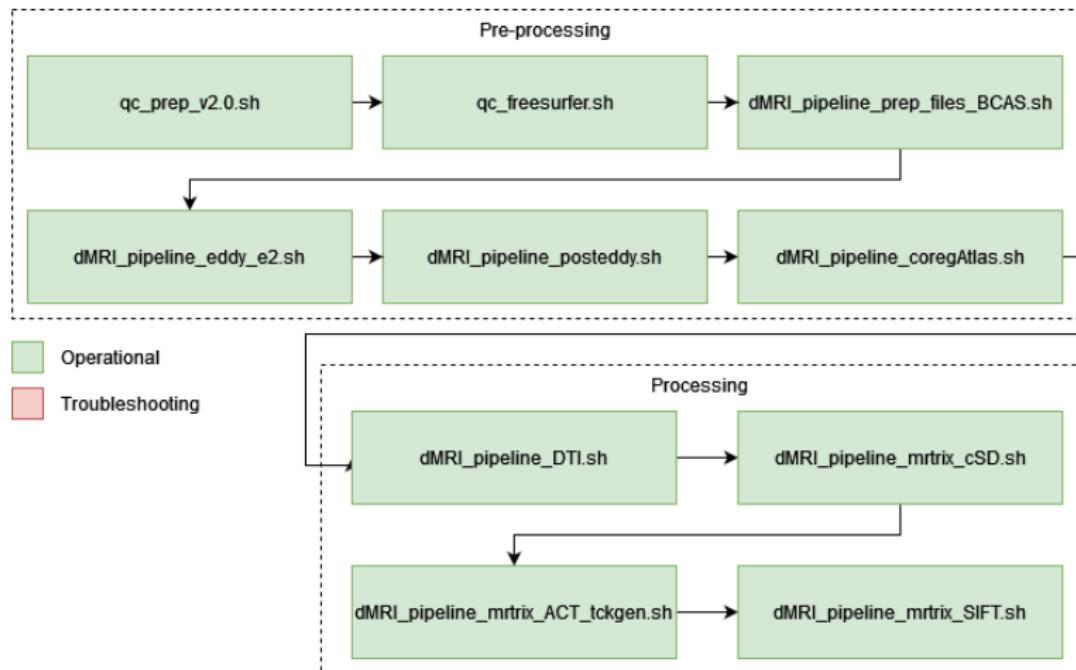


Section 2

Fetal dMRI

In collaboration with Alejandra Pérez Yañez (BSc)
Supervised by Kiho Im (PhD)

Flow diagram



- Ran Ai Wern Chung (PhD) pipeline for adult dMRI.
- Consolidated requirements in a single *conda* environment
(/MRI_processing/fetal_dMRI/dMRI_env) activated by dMRI_pkg.

Manual



FNNDSC
Fetal-Neuro Imaging
Developmental Science Center



Boston
Children's
Hospital



HARVARD
MEDICAL SCHOOL

DWI adults pipeline

Alejandra Perez Yanez
Milton Osiel Candela Leal

SCRIPT USAGES – AIWERN CHUNG
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Documented inputs and outputs of Chung's pipeline in a 56-slides presentation.
(github.com/miltoncandela/miltoncandela.github.io/fetaldmri_pipeline.pdf)

Issues on fetal dMRI

The DTI pipeline need further testing in fetal dMRI data due to:

- bvals and bvecs being different in:
 - Range: [0, 1000, 2000, 3000] in adults, [0, 500] in fetus
 - Size: 60 in adults, 12 in fetus
- Fetal DWI being noiser.



Figure: BRAIN



Figure: TRACEW

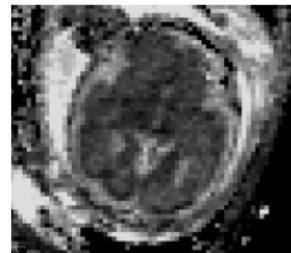
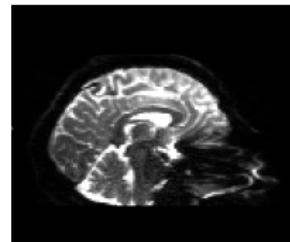


Figure: ADC



Figure: FA



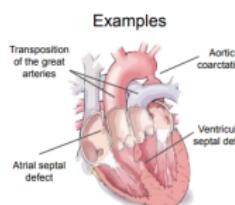
Section 3

qMRI CHD Classification

In collaboration with Samantha A. Esparza Esparza (BSc)
Supervised by Sungmin You (PhD)

Introduction

Congenital Heart Disease (CHD)



- Reduced oxygen supply
- Altered blood flow dynamics [1]
- Neuroinflammation

Early detection relevance

Enhanced Prenatal Counseling

Potential for discovery of **unique biomarkers**
indicative of CHD impact on fetal brain

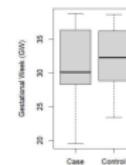
[1] Khalil et al., *Ultrasound Obstet Gynecol.*, 2016

[2] Im., *Advances in Magnetic Resonance Technology and Applications.*, 2021

Non-linear Combined qMRI Features Generation and Selection

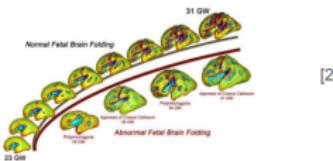
Cohort composed of:

- 96 CHD MRI (mean = 31.38 weeks, sd = 4.80)
- 62 TD MRI (mean = 32.38 weeks, sd = 4.17)



Age-adjusted qMRI features

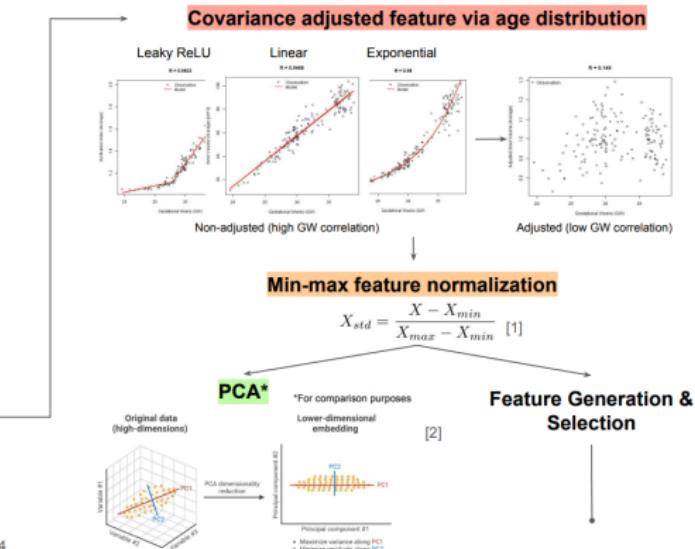
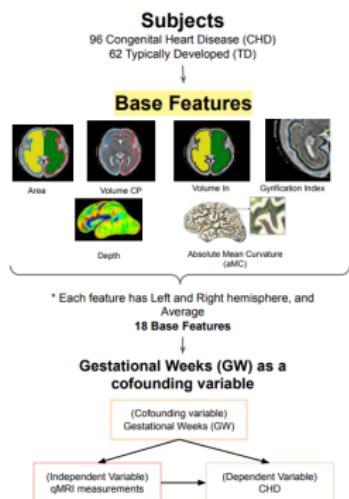
As Gestational Weeks (GW) is a confounding variable in fetal MRI



Presented by Samantha last week.

Symposium slides: miltoncandela.github.io/chd_slides.pdf

Data pre-processing



[1] Candela-Leal et al., *Appl. Sci.*, 2022

[2] Blanco-Rios and Candela-Leal et al., *Front. Hum. Neurosci.*, 2024

Data processing



[1] Aguilar-Herrera et al., *ML-DT Edu. Innovation Workshop*, 2021

[2] Ramírez-Moreno et al., *Int. J. Environ. Res. Public Health*, 2021

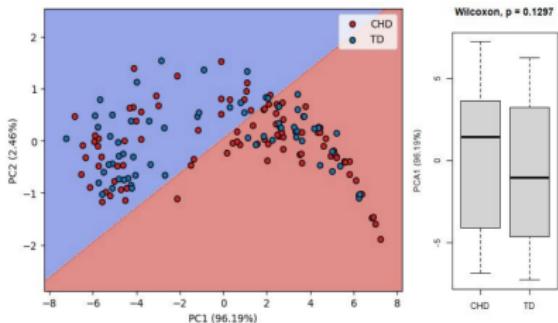
[3] Olivas-Martínez et al., *ML-DT Edu. Innovation Workshop*, 2021

[4] Candela-Leal et al., *IEOM-NA VI*, 2021

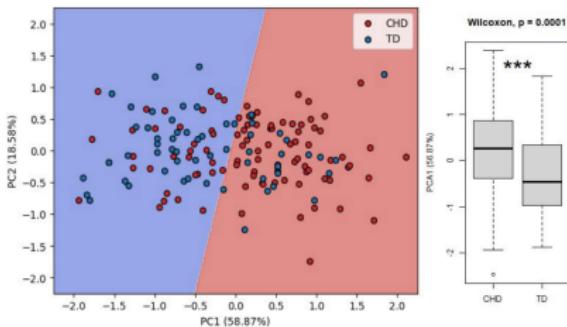
[5] Shon et al., *Int. J. Environ. Res. Public Health*, 2018

Better differentiation at PCA components

Base features

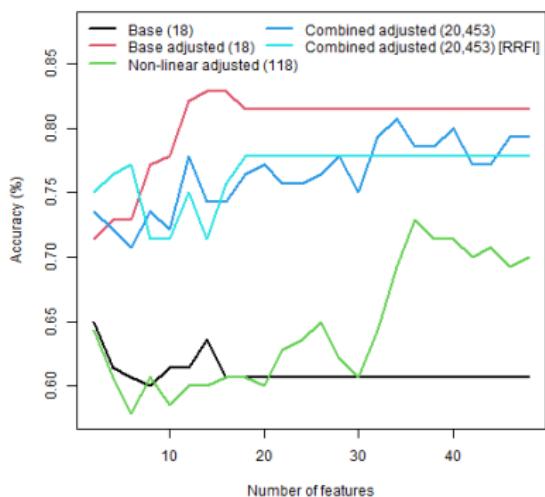


Adjusted features

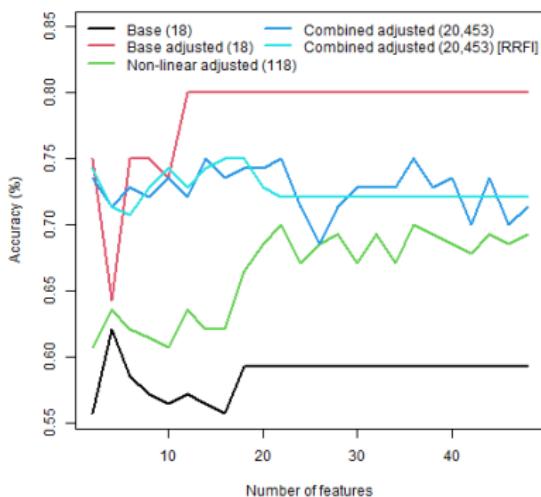


Increase in model's performance

kNN ($k = 3$)



DT

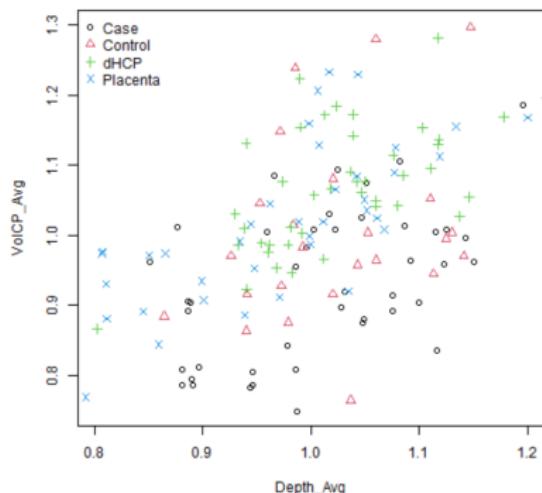
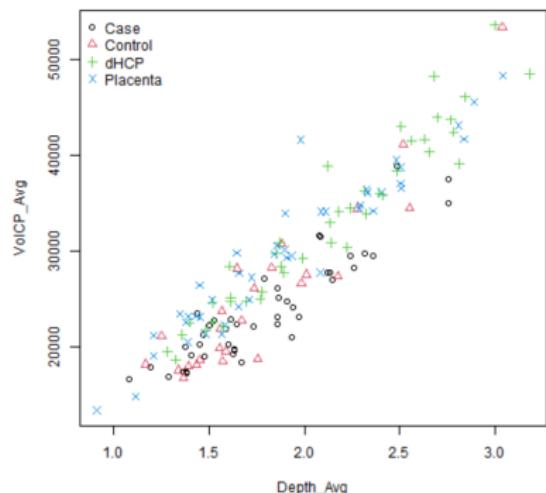


Adjusted features:

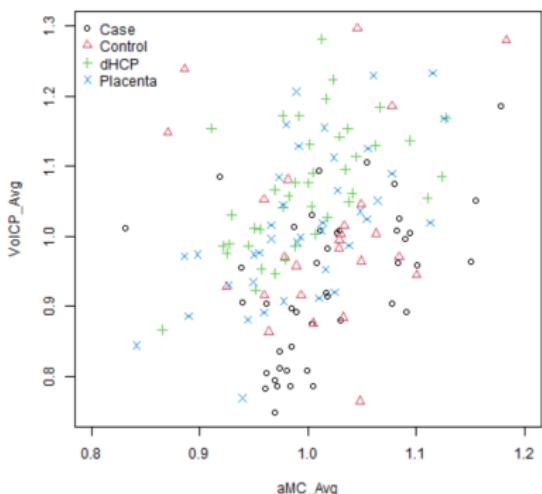
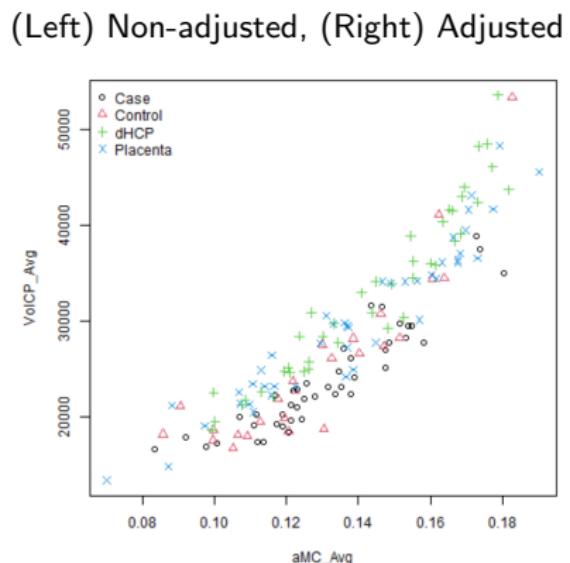
- Significantly outperformed non-adjusted features (+20% accuracy).
- Greatly outperformed combined adjusted features (+5% accuracy).

Adjusting only the right features (VolCP, Depth)

(Left) Non-adjusted, (Right) Adjusted

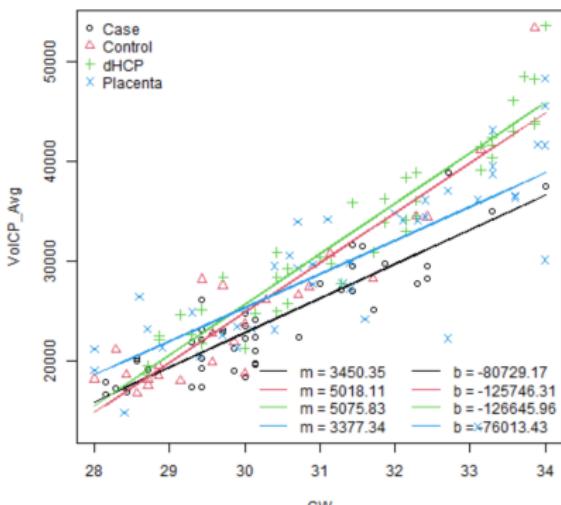
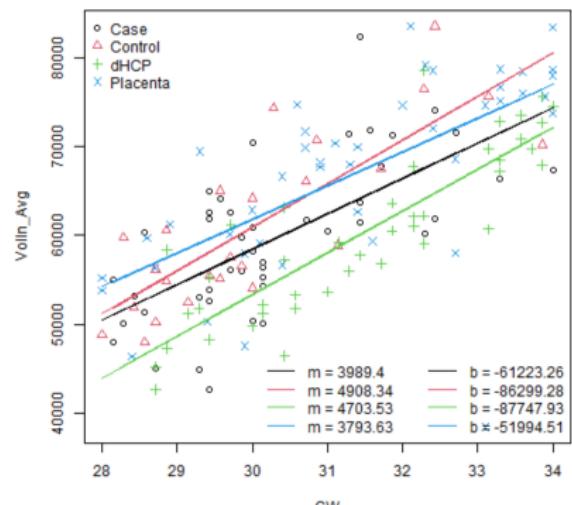


Adjusting only the right features (VolCP, aMC)



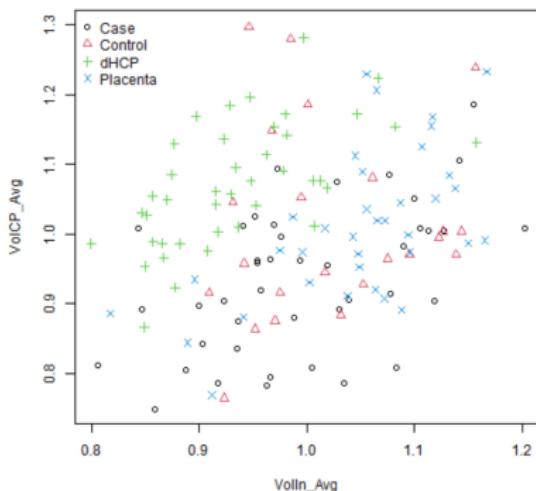
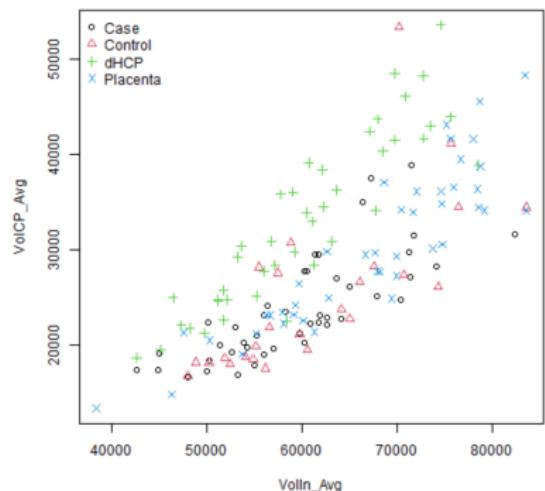
Which features shouldn't be adjusted?

Volln: Different b across datasets.



Clusterized behavior when adjusting Volln

(Left) Non-adjusted, (Right) Adjusted



Section 4

High-resolution Subplate

Supervised by HyukJin Yun (PhD)

Overview

Subplate (SP) in fetal brain is a **transitory** compartment^{1,2} that lasts until 31 weeks of gestational age (GA)^{3,4}, and it is critical for **brain development**⁵, **cortical circuitry** and **structure**^{2,6}.

Objective

- **Upsample** and **auto-smooth** existing low-resolution (0.86 mm) SP dataset ($n=82$) to high-resolution (0.5 mm), via IRTK and **Gaussian Smoothing**
- **Train** a high-resolution **U-Net model** for **automatic** SP, cortical plate (CP), and inner part (IP) **segmentation**

Benefits

- More **detailed delineation** of brain tissues such as the SP, CP, and IP
- More accurate SP **volume & thickness**

¹Serati et al., *Neuroscience*, 2019

²Kostovic et al., *Int. J. Dev. Neurosci.*, 2010

³Vasung et al., *Cereb. Cortex*, 2020

⁴Rados et al., *Eur. J. Radiol.*, 2006

⁵Allendoerfer and Shatz, *Annu. Rev. Neurosci.*, 1994

⁶Luhmann et al., *Front. Neural Circuits*, 2016

Procedure

First

- ① De-anonymize SP data ($n=51$) [BCH_XXXX_s1]
- ② Search for their native files in Placenta, Normative, CHD, and TMC folders
- ③ Make a reconstruction in 0.5 mm using NeSVoR
- ④ Upsample, align, and apply BGS to the SP data
- ⑤ Train pre-initial model ($n=40$) by proposing the usage of transfer-learning on the high-res CP model ($n=114$)

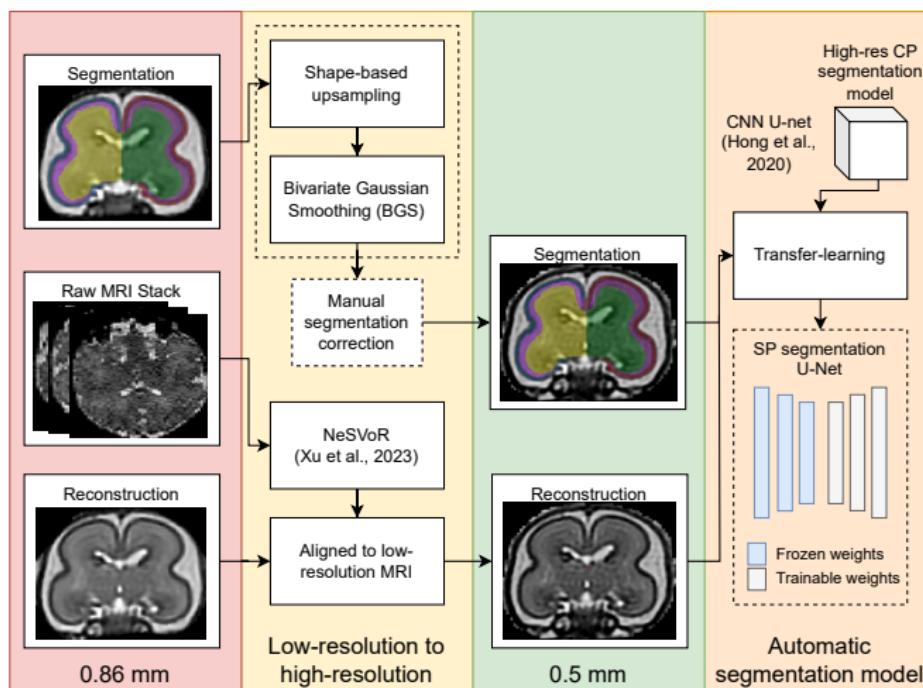
Then

- ① Predict and correct the segmentation of low-quality subjects ($n=9$)
- ② Train transfer-learning initial model ($n=49$), and predict on misaligned ($n=14$) and high-res CP data ($n=71$) to distribute to other interns

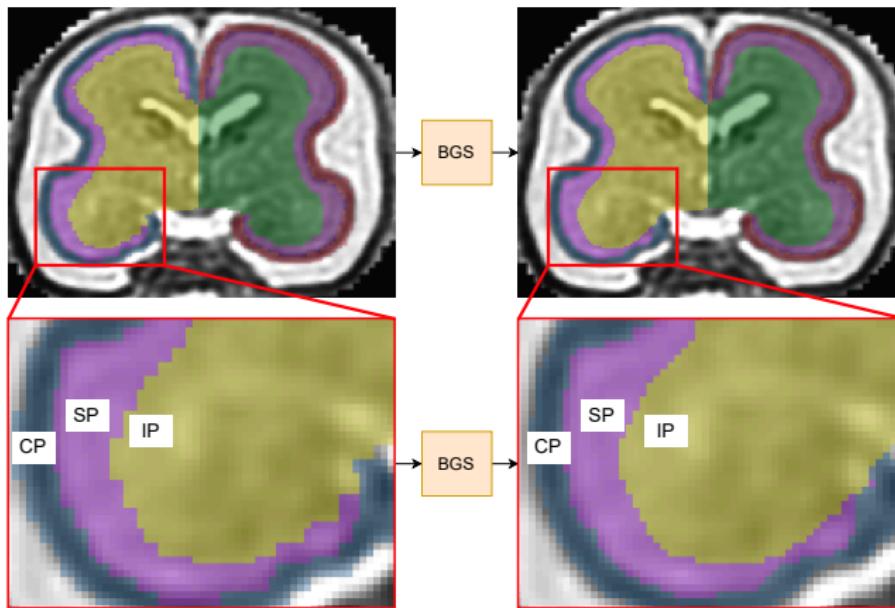
Finally

- ① Correct misaligned ($n=14$) while supervising interns' manual corrections
- ② Train final model ($n=120$) and test on a multi-site hold-out dataset

Flow diagram



Bivariate Gaussian Smoothing (BGS)



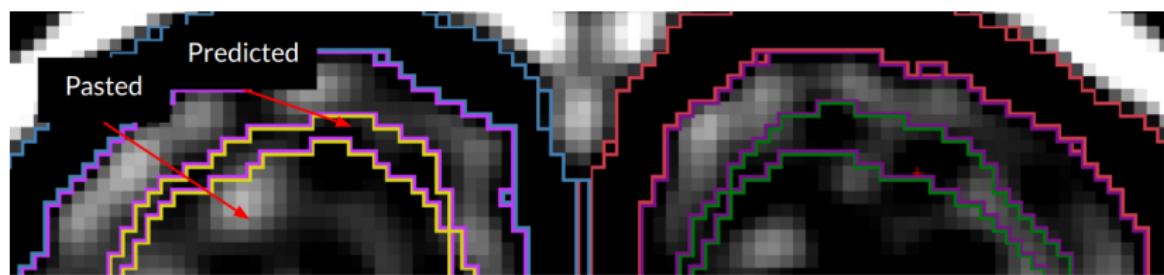
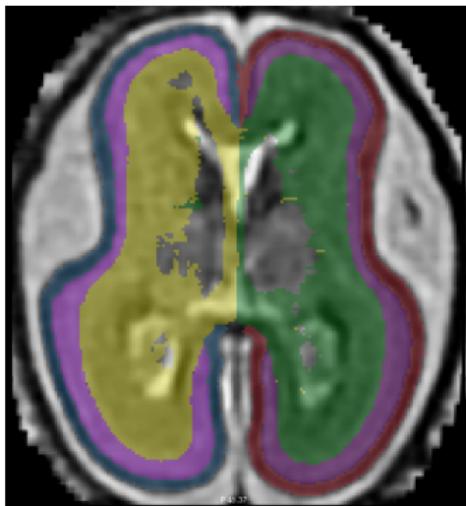
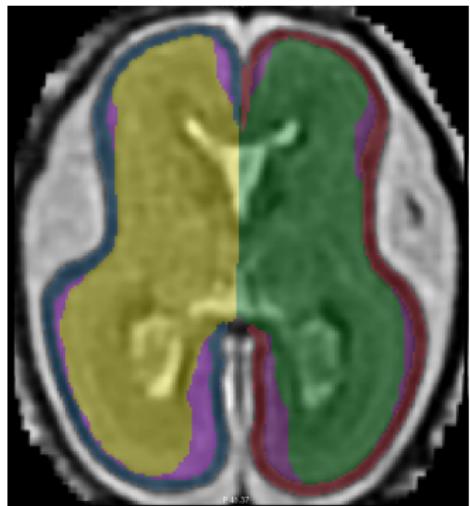
Univariate GS for IP mask (**dilatation**)

$$G(x, y, \sigma)_{ip} = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (1)$$

Univariate GS for -IP mask (**erosion**)

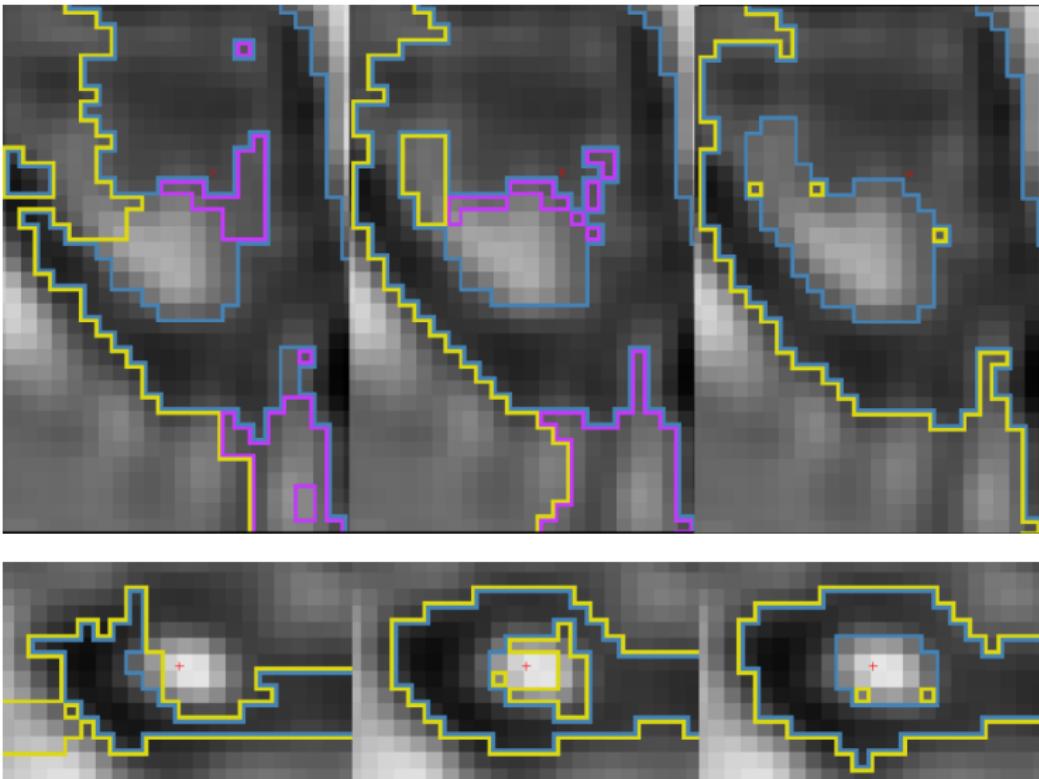
$$G(x, y, \tau)_{-ip} = \frac{1}{2\pi\tau^2} e^{-\frac{x^2+y^2}{2\tau^2}} \quad (2)$$

Misaligned & bad quality data prediction (n=40)

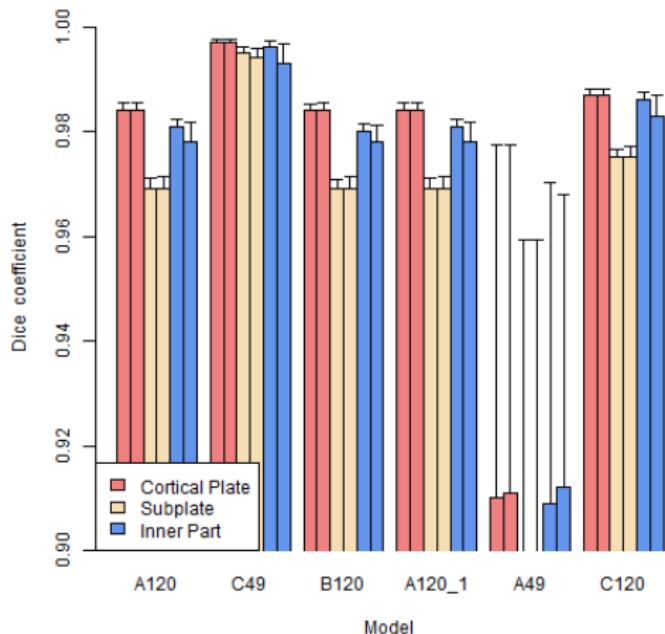


Better initial segmentation when using transfer-learning

No transfer-learning (n=40), transfer-learning (n=40), CP model (n=114)



Model's performance on multi-site testing dataset (n=14)



- A: No transfer-learning
- B: Without low-quality subjects
- C: Encoder & decoder pre-trained

C models (transfer-learning) outperformed A & B (no transfer-learning) at SP labels

Transfer-learning still having benefit in CSF areas

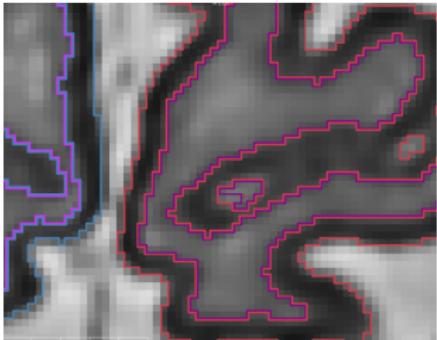
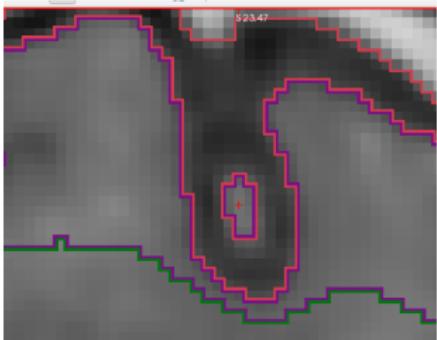


Figure: A120

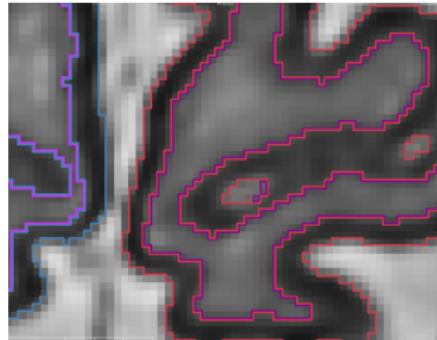
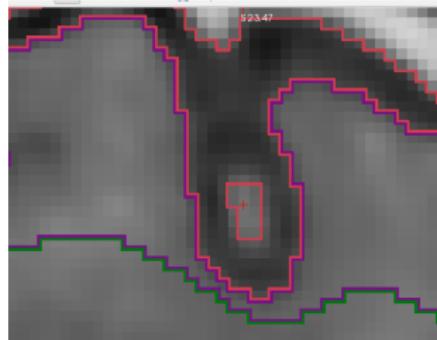
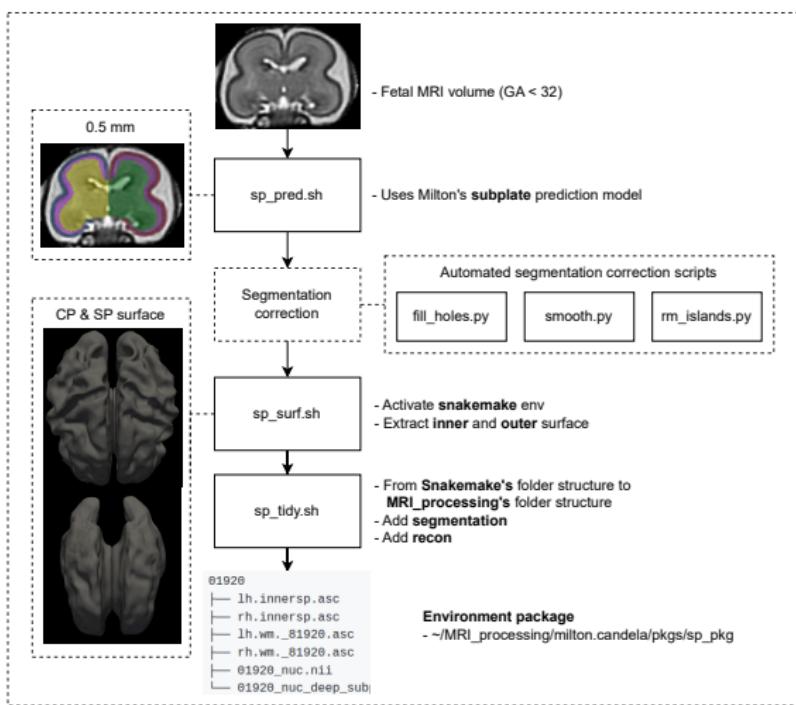


Figure: C49

Automatic subplate segmentation prediction and surface extraction



Subplate surface extraction

Surfaces look similar, but high-resolution SP thickness should be more accurate.

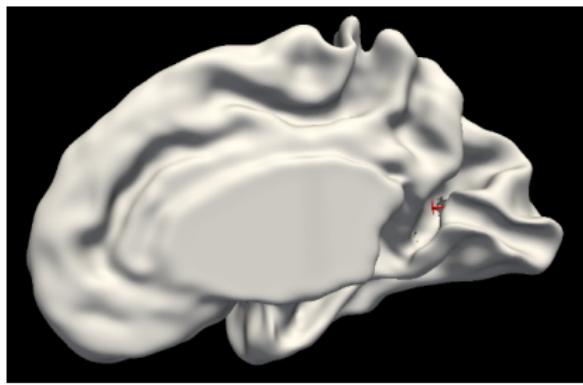


Figure: Low-resolution (0.86 mm)

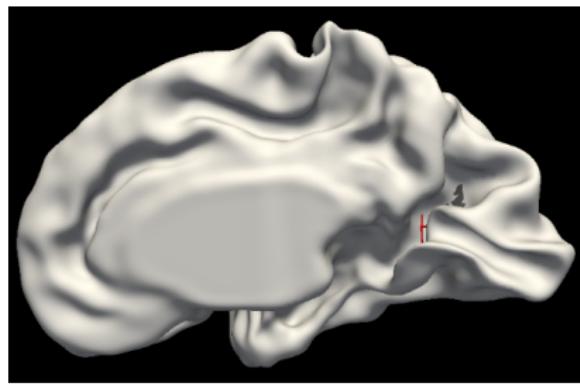


Figure: High-resolution (0.5 mm)

Section 5

FeTA Challenge @ MICCAI 2024

In collaboration with Andrea Gonová (PhD)
Supervised by Sungmin You (PhD)

Overview



I did tissue segmentation while Andrea did biometry measurements.
Segmentation consisted in creating a model that predicted 7 labels:

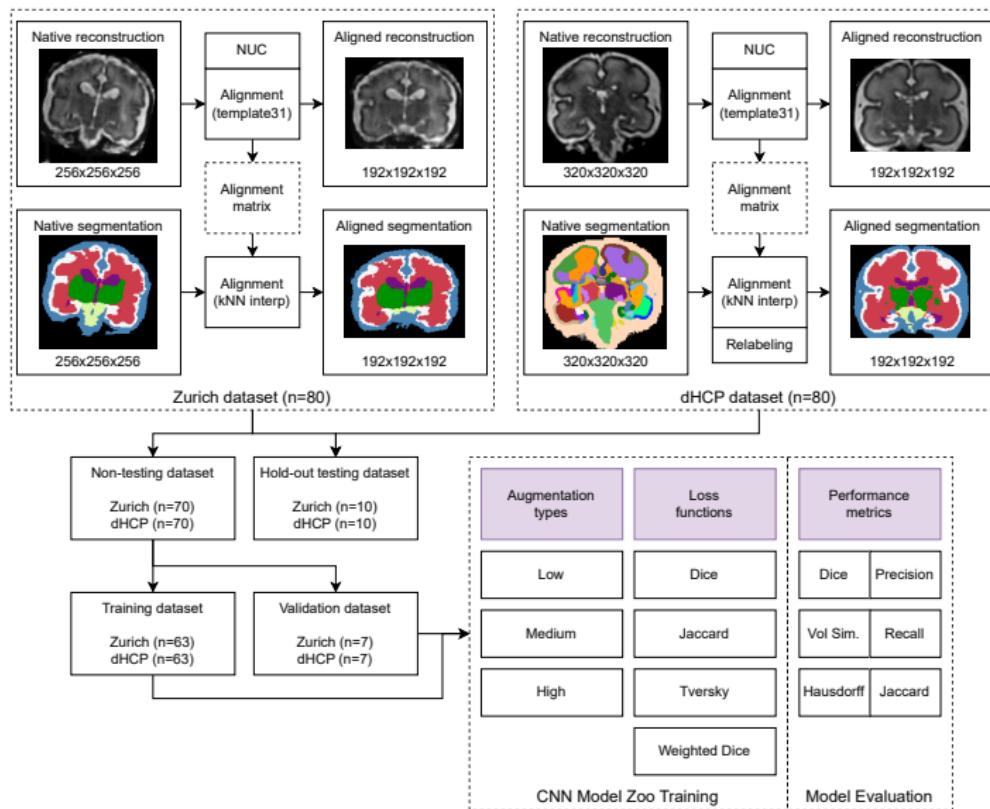
- ① External Cerebrospinal Fluid
- ② Grey Matter
- ③ White Matter
- ④ Ventricles
- ⑤ Cerebellum
- ⑥ Deep Grey Matter
- ⑦ Brainstem

Main issue



Testing dataset is composed of multi-site unseen data.

Flow diagram



Fetal MRI data augmentation

| Augmentation | Low | Medium | High |
|--------------------|------------|-------------------|-------------------|
| rotation_range | 15 | 30 | 30 |
| width_shift_range | 0.1 | 0.2 | 0.2 |
| height_shift_range | 0.1 | 0.2 | 0.2 |
| vertical_flip | True | True | True |
| horizontal_flip | True | True | True |
| zoom_range | 0.1 | 0.2 | 0.3 |
| brightness_range | [0.8, 1.2] | [0.7, 1.3] | [0.6, 1.4] |
| gaussian_noise* | [0, 0.1] | [0, 0.2] | [0, 0.3] |
| gaussian_blur* | 1 | 2 | 3 |

* not in Tensorflow's *ImageDataGenerator*

Adding the right amount of augmentation

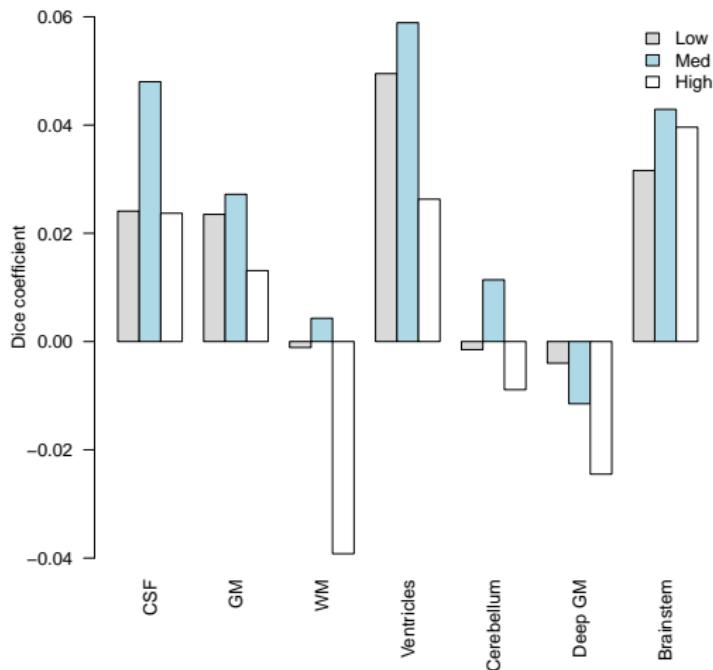


Figure: Dice difference when including augmentation at testing Zurich dataset (n=10)

- Med increased CSF, GM, ventricles, and brainstem differentiation.
- High augmentation saturated the model, making it incapable of learning.

Loss functions

Dice

$$1 - \frac{2|A \cap B|}{|A| + |B|} \quad (3)$$

Jaccard

$$1 - \frac{|A \cap B|}{|A \cup B|} \quad (4)$$

Tversky

$$1 - \frac{|A \cap B|}{|A \cap B| + \alpha|A \setminus B| + (1 - \alpha)|B \setminus A|} \quad (5)$$

Weighted Dice

$$1 - \frac{2 \sum_{i=1}^n w_i \cdot (A_i \cap B_i)}{\sum_{i=1}^n w_i \cdot (A_i + B_i)} \quad (6)$$

Where w_i is the label i inverse:

- Volume
- Posterior performance

W were softmaxed, based on:

$$\sigma(W)_k = \frac{e^{\frac{w_k}{\gamma}}}{\sum_{j=1}^K e^{\frac{w_j}{\gamma}}} \quad (7)$$

Where a high γ would lead to a more uniform distribution (low weight effect).

Performance metrics

Challenge-specific

Dice

$$DSC(A, B) = \frac{2|A \cap B|}{|A| + |B|} \quad (8)$$

Volume Similarity

$$VS(V_1, V_2) = 1 - \frac{|V_1 - V_2|}{V_1 + V_2} \quad (9)$$

Hausdorff Distance

$$d_H(A, B) = \max\{\sup_{a \in A} d(a, B), \sup_{b \in B} d(A, b)\} \quad (10)$$

Other

Jaccard

$$J(A, B) = \frac{|A \cap B|}{|A \cup B|} \quad (11)$$

Precision

$$P(TP, FP) = \frac{TP}{TP + FP} \quad (12)$$

Recall

$$R(TP, FN) = \frac{TP}{TP + FN} \quad (13)$$

Loss functions' performance

All 2D CNN models trained using a single 90:10 random split with axial view data, 150 epochs, medium augmentation, and no callbacks.

Performance measured on a hold-out stratified dataset (anomaly and GW).

| Loss function | Dice | Vol S. | Hausd | Jacc. | Precis. | Recall | Rank |
|-----------------------|---------------|---------------|---------------|---------------|---------------|---------------|------------|
| hybrid | 0.7614 | 0.8980 | 6.7119 | 0.6479 | 0.7711 | 0.7929 | 3 |
| whyb ($\gamma=5$) | 0.6700 | 0.8223 | 6.7405 | 0.5347 | 0.7478 | 0.6619 | 7.16 |
| whyb ($\gamma=10$) | 0.7355 | 0.8765 | 7.3656 | 0.6136 | 0.7695 | 0.7458 | 6.83 |
| whyb ($\gamma=15$) | 0.7548 | 0.8912 | 7.8590 | 0.6317 | 0.7727 | 0.7704 | 5.16 |
| thyb ($\alpha=0.7$) | 0.7662 | 0.8896 | 7.1658 | 0.6437 | 0.7586 | 0.7997 | 3.66 |
| jhyb | 0.7503 | 0.8842 | 7.2448 | 0.6308 | 0.7794 | 0.7591 | 5.33 |
| whyb (Jacc.) | 0.7662 | 0.9067 | 7.4884 | 0.6512 | 0.7747 | 0.7853 | 2.66 |
| whyb (Dice) | 0.7654 | 0.8999 | 7.1133 | 0.6483 | 0.7847 | 0.7771 | 2.5 |

- ❶ whyb (Jacc.) with the highest **Dice** and **Vol S.**, but a low **Hausd**
- ❷ whyb (Dice) overall superior performance than hybrid
- ❸ Or should we stick to the naïve hybrid loss?

Naïve hybrid loss' output was more stable

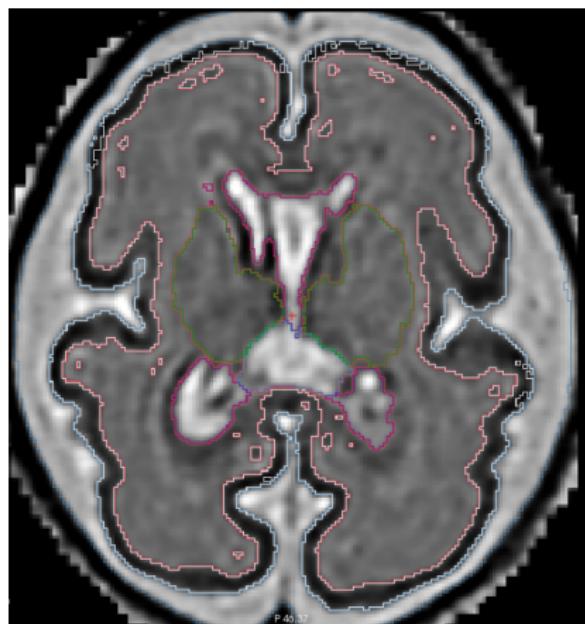


Figure: hyb

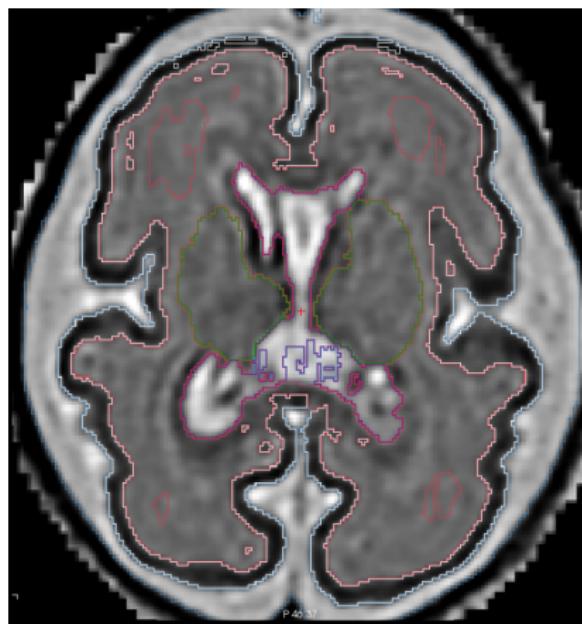


Figure: whyb

Internal dataset validation (hold-out test, Zurich)

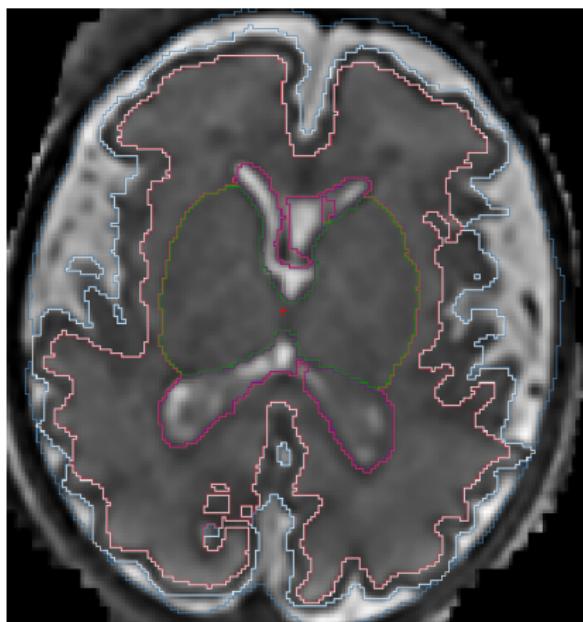


Figure: Ground truth

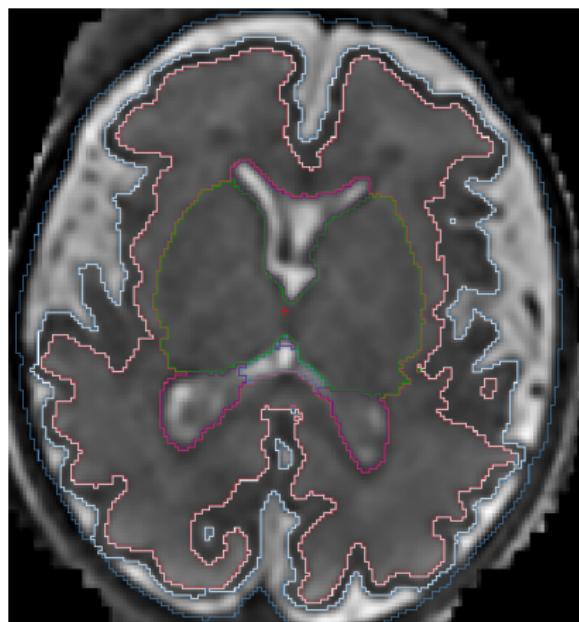


Figure: Model's prediction

External dataset validation (HBCD, TMC)

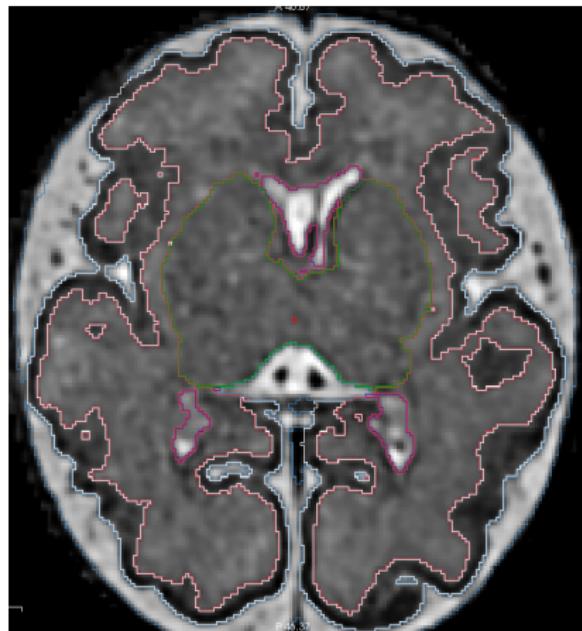


Figure: 100_005_1, GW = 31.14



Figure: BM47, GW = 24.71

External dataset validation (Placenta, CHD)

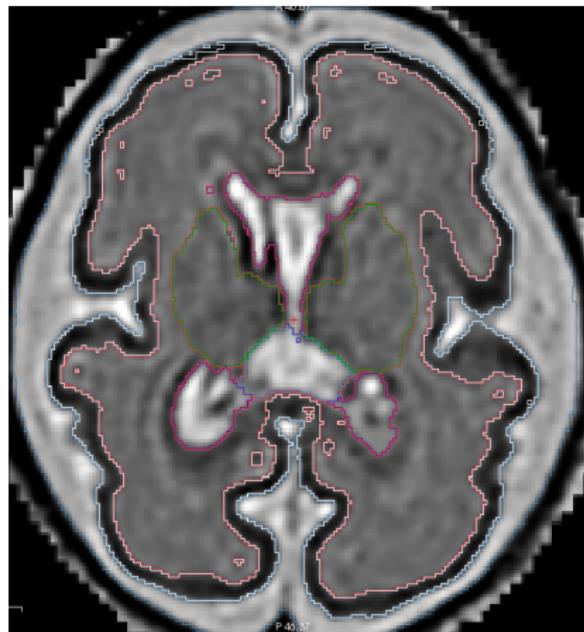


Figure: 5437941, GW = 29.7

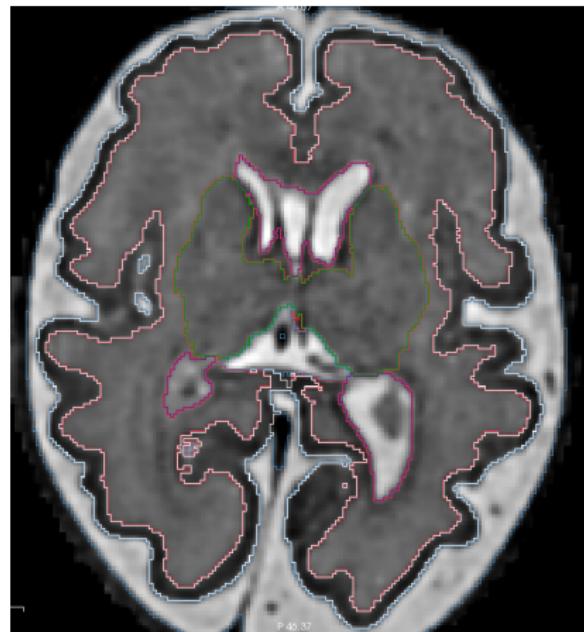


Figure: FCB147, GW = 30.7

Difference when including augmentation in BCH data

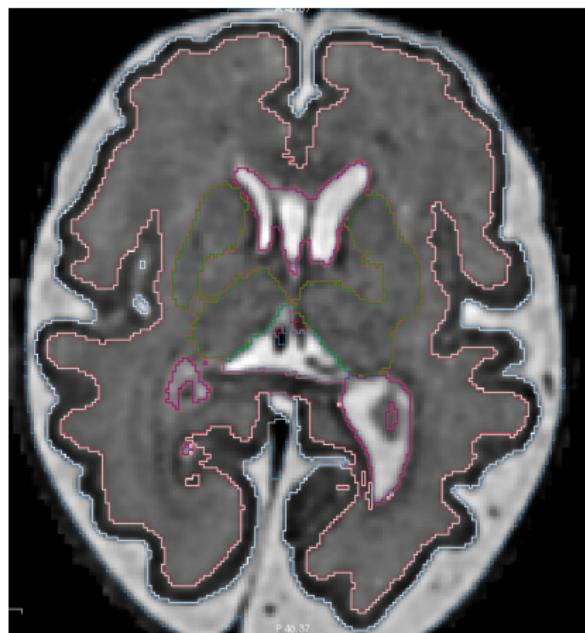


Figure: No augmentation

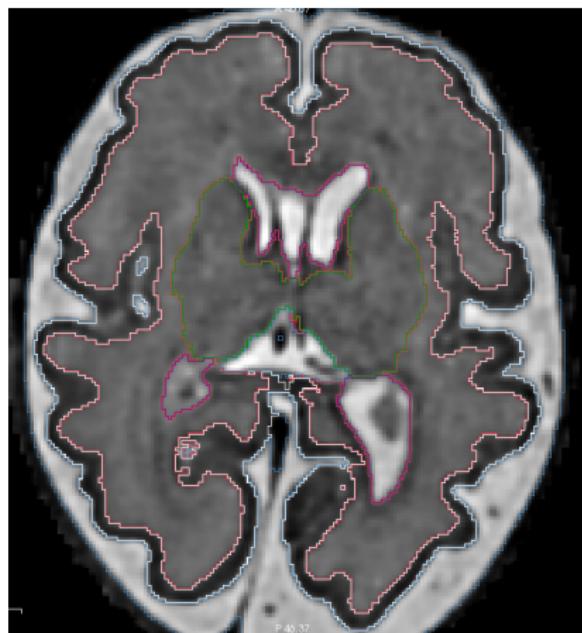


Figure: Medium augmentation

Thank you!



Thank you!

Center Director: P. Ellen Grant

Principal investigator: Kiho Im

Supervising instructors/post-docs:

Andrea Gonová, Sungmin You, Ai Wern Chung, HyukJin Yun

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