BIGR Open Lab Day 2026

Student Projects

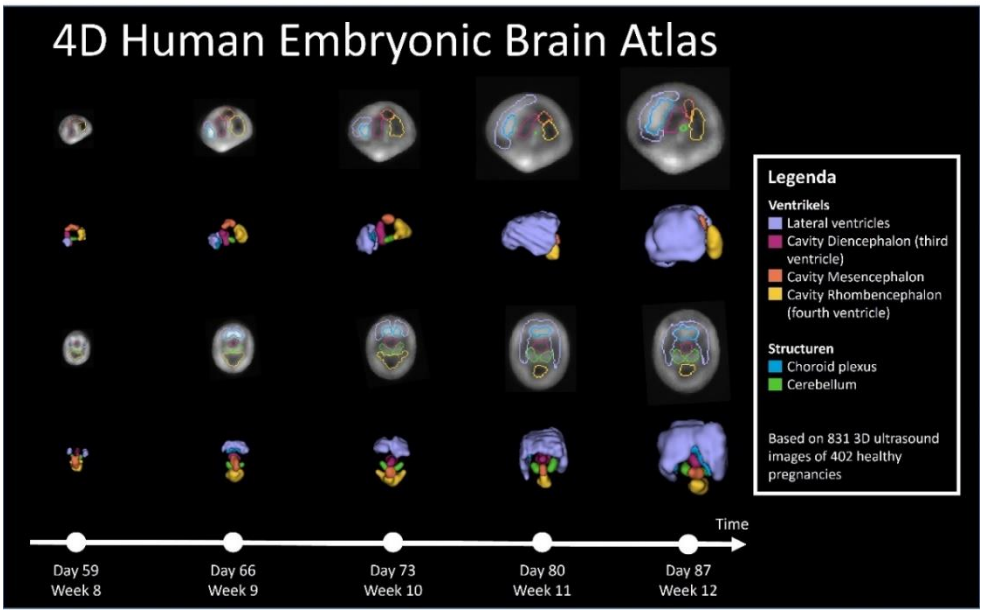
Contents

A Novel Prenatal–Postnatal Brain Atlas for Modeling Developmental Trajectories and Neurodevelopmental Outcomes

Research Line: Applied Medical Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Project description
Brain development from prenatal to postnatal stages involves rapid morphological changes and high inter-subject variability, posing challenges for quantitative analysis. In this project, you will develop components of the first prenatal–postnatal brain atlas using large-scale 2D and 3D ultrasound datasets (>3000 scans). Building on the inhouse developed 4D Human Embryonic Brain Atlas, you will apply advanced image registration and machine learning techniques to construct a continuous spatiotemporal model of brain development. A key aspect is the integration of patient-specific covariates (e.g., clinical and demographic factors) into the modeling framework, enabling differentiation between typical development and condition-specific deviations. You will analyze subject-specific growth trajectories and explore their association with postnatal neurodevelopmental outcomes, contributing to improved early detection of atypical brain development.

Interested?
Are you: an enthusiastic student with a clear interest in medical image analysis; looking for a master thesis or an internship between 6 – 9 months (shorter can be discussed); up for this challenge; having experience with programming (preferably Python)? Interested in early human development?



Interested in this project?

Supervisor(s): Wietske Bastiaansen, collaboration with the departments of Obstetrics and Gynecology and Neonatology.
Email: w.bastiaansen@erasmusmc.nl

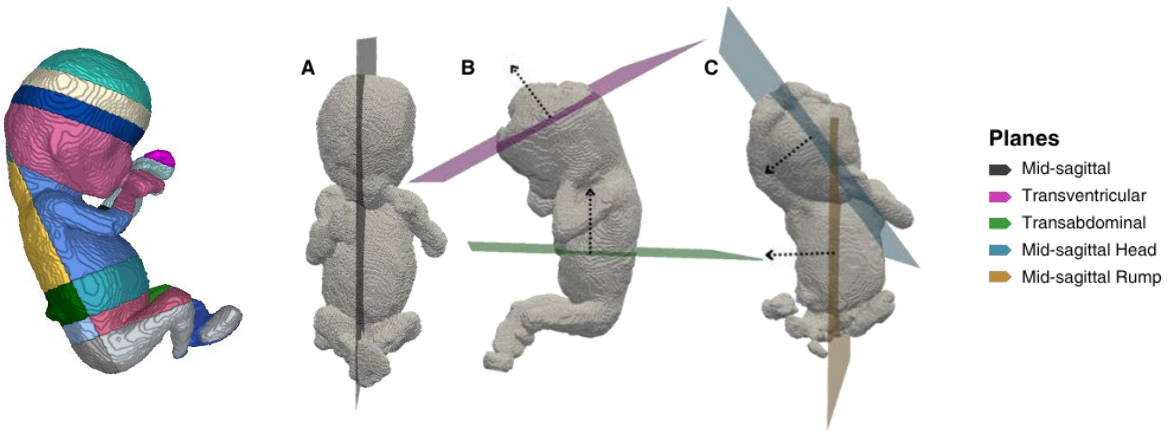
Automatic Fetal Posture Estimation from 3D Ultrasound

Research Line: Applied Medical Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Project description
First-trimester ultrasound imaging is challenged by fetal motion, variable posture, and incomplete anatomical visibility, limiting the effectiveness of 3D reconstruction and analysis. In this project, you will develop methods for automatic fetal posture estimation from 3D ultrasound data to support downstream image acquisition and reconstruction. Using existing datasets with posture annotations and derived measures (e.g., angles between anatomical planes), you will explore clustering and machine learning approaches to define meaningful posture representations. You will design and evaluate a posture estimation model and validate it on newly acquired time-series data. This work contributes to improved handling of motion and variability in early pregnancy imaging and supports first trimester anomaly screening.

Interested?
Are you: an enthusiastic student with a clear interest in medical image analysis; looking for a master thesis or an internship between 6 – 9 months (shorter can be discussed); up for this challenge; having experience with programming (preferably Python)? Interested in early human development?

A visit to the clinic is part of this project.



Interested in this project?

Supervisor(s):

Dr. Ir. Wietske Bastiaansen, Anne Akerboom (MD/PhD candidate), collaboration with the departments of Obstetrics and Gynecology and GE Healthcare within the FAST-AI project (https://www.kansrijkestart-ppp.nl/fast-ai/).

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Early sex prediction of the human embryo using deep learning

Research Line: Applied Medical Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Project description
In clinical practice, sex of the developing embryo is not determined during the first trimester. Besides the fact that most parents want to know the sex, research has shown that there are developmental differences between boys and girls early in pregnancy, which are currently neglected[1]. The most well-known method to determine sex during the first trimester is using the orientation of the genital tubercle in the mid-sagittal plane, see **Figure 1**. This proves to be accurate in about 70 - 85% of the cases[2]. The orientation of the genital tubercle is inspected manually using 3D ultrasound. We hypothesize that a deep learning-based approach can be of help in this case since it can automatically extract complex image-based features of the entire embryo. These features could contain information and patterns, which may be more informative than a visual inspection of the genital tubercle.

Interested?
Are you: an enthusiastic student with a clear interest in medical image analysis; looking for a master thesis or an internship between 6 – 9 months (shorter can be discussed); up for this challenge; having experience with programming (preferably Python)? Interested in early human development?

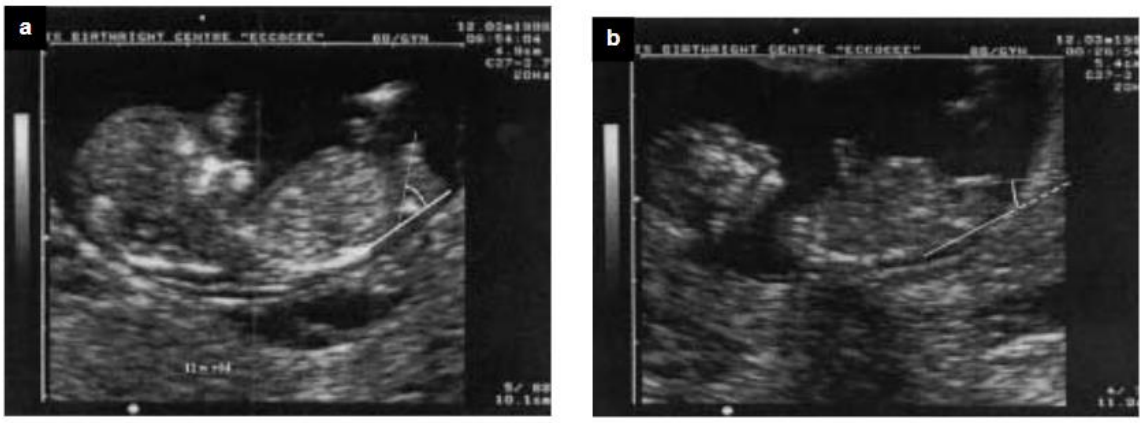

Figure 1 (a) Male fetus with acute angle of the penis shown. (b) Female fetus with converging angle of the clitoris shown

A visit to the clinic is part of this project.

[1]De Zegher, F., Devlieger, H., & Eeckels, R. (1999). Fetal growth: boys before girls. Hormone research, 51(5), 258-259.
[2]Efrat, Z., Akinfenwa, O. O., & Nicolaides, K. H. (1999). First-trimester determination of fetal gender by ultrasound. Ultrasound in Obstetrics and Gynecology, 13(5), 305-307.

Interested in this project?

Supervisor(s): Wietske Bastiaansen, collaboration with the Periconception Epidemiology group of the department of Obstetrics and Gynecology.
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Non-Invasive MRI-Based Glioma Genotyping and Grading Using Deep Learning

Research Line: Applied Medical Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

Glioma is the most common malignant primary brain tumor. Pre-operative, non-invasive prediction of molecular subtype and tumor grade can positively impact treatment planning, surgical strategy, and prognosis estimation. Previous work has shown that a multi-task U-Net can successfully segment glioma on MRI, while simultaneously predicting molecular markers such as IDH mutation, 1p/19q codeletion, and tumor grade (Figure 1) [1].

In this project, we will investigate more recent, state-of-the-art network architectures, such as transformer-based models or medical foundation models, to improve performance, robustness and generalization. A large dataset of over 3,000 patients will be available for this.

Interested?

Are you a motivated master student with strong Python skills and experience in deep learning (PyTorch / MONAI)? Are you excited about cutting-edge AI applied to clinically relevant problems? Are you looking for a 6-9 month master thesis or internship (shorted can be discussed)? Then this project might be an excellent fit for you!

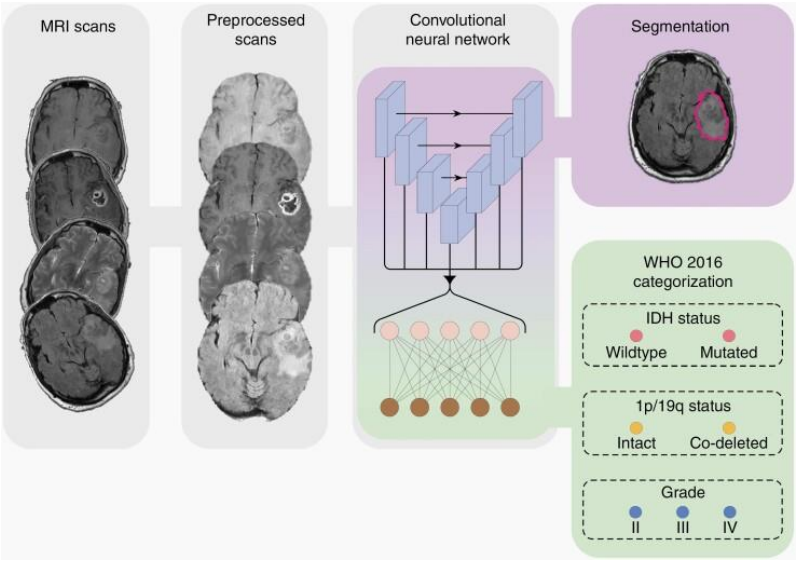

Figure 1: Multi-task deep learning framework for simultaneous glioma segmentation and molecular subtype prediction, from van der Voort et al. (2023).

[1] van der Voort SR et al (2023) Combined molecular subtyping, grading, and segmentation of glioma using multi-task deep learning. *Neuro-oncology*, *25*(2), 279-289

Interested in this project?

Supervisor(s): Gonzalo Mosquera Rojas, Juancito van Leeuwen, Stefan Klein, Marion Smits
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j.c.c.vanleeuwen@erasmusmc.nl

Towards precise Glioma subtyping with hierarchical Deep Learning

Research Line: Applied Medical Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

Glioma is the most common malignant primary brain tumor. Pre-operative, non-invasive prediction of molecular subtype and tumor grade can positively impact treatment planning, surgical strategy, and prognosis estimation. Previous work has shown that a multi-task U-Net can successfully segment glioma on MRI, while simultaneously predicting molecular markers such as IDH mutation, 1p/19q codeletion, and tumor grade [1].

Nonetheless, current efforts have been directed to separately predicting the tumor features instead of the final tumor subtype, i.e., oligodendroglioma, astrocytoma and glioblastoma multiforme. Such a prediction would make AI tools more appealing for clinicians to use, as many of the treatment decisions are tied to specific subtype which goes in line with the international standards defined by the WHO [2]. An example on how relationships between different molecular features can help determine final tumor type are depicted in Figure 1.
In this project, we will explore hierarchical Deep Learning to learn from such relationships and perform the final tumor subtype directly. We hypothesize that such a strategy would lead to better results and a more interpretable model. We have recently collected a dataset with rich information from such features to facilitate the training procedure.

Interested?

Are you a motivated master student with strong Python skills and sufficient experience in deep learning (PyTorch / MONAI)? Are you excited about cutting-edge AI applied to clinically relevant problems? Then this project might be an excellent fit for you!

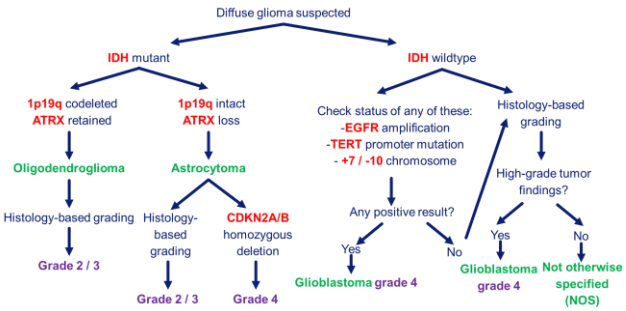

Figure 1. Glioma subtyping workflow

[1] van der Voort SR et al (2023) Combined molecular subtyping, grading, and segmentation of glioma using multi-task deep learning. *Neuro-oncology*, *25*(2), 279-289
[2] Louis, David N., et al. "The 2021 WHO classification of tumors of the central nervous system: a summary." *Neuro-oncology* 23.8 (2021): 1231-1251.


Interested in this project?

Supervisor(s): Gonzalo Mosquera Rojas, Juancito van Leeuwen, Stefan Klein, Marion Smits
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Lung vessel segmentation on chest CTs.

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Bachelor or Master Project
Approx. duration: To be discussed

Goal
Create a deep learning model capable of segmenting the lung artery vessels from contrast-enhanced computed tomography images.

Background
This project is part of a larger project researching the detection of blood cloths in the lung (pulmonary embolisms). These cloths can be relatively small; therefore, incorporating additional information from the computed tomography (CT) image could enhance detection accuracy. In particular the pulmonary arteries, the vessels going from the hart to the lung tissue, are of interest as the blood cloths only appear inside those vessels within the lung.

What you can expect
You will be developing, training, and validating your own deep learning model for segmenting the pulmonary arteries. A basic model is available to get started, which you can further research and develop to improve the detection of embolisms by providing the segmentation or other vessel related information to the embolism detection model. For this project two labeled publicly available dataset are available for training and validation of your model. A third unlabeled dataset is provided to test the generalizability of your approach.

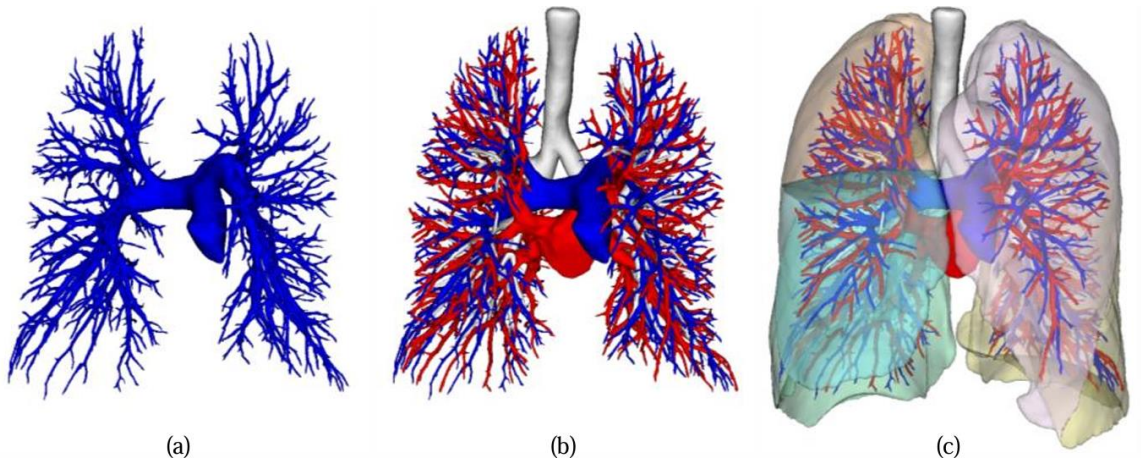

Fig. 1. Complex pulmonary artery topology structures: (a) the pulmonary arteries (blue); (b) the pulmonary arteries and pulmonary veins (red) are intertwined, while the pulmonary airways (grey) increasing the complex; (c) the pulmonary arteries, pulmonary veins and pulmonary airways with lungs (shade) (1).

1. Luo, G., Wang, K., Liu, J., Li, S., Liang, X., Li, X., ... & Gao, X. (2023). Efficient automatic segmentation for multi-level pulmonary arteries: The parse challenge. *arXiv preprint arXiv:2304.03708*.

Interested in this project?

Supervisor(s): Erik Kemper, Martijn Starmans, Frans Vos
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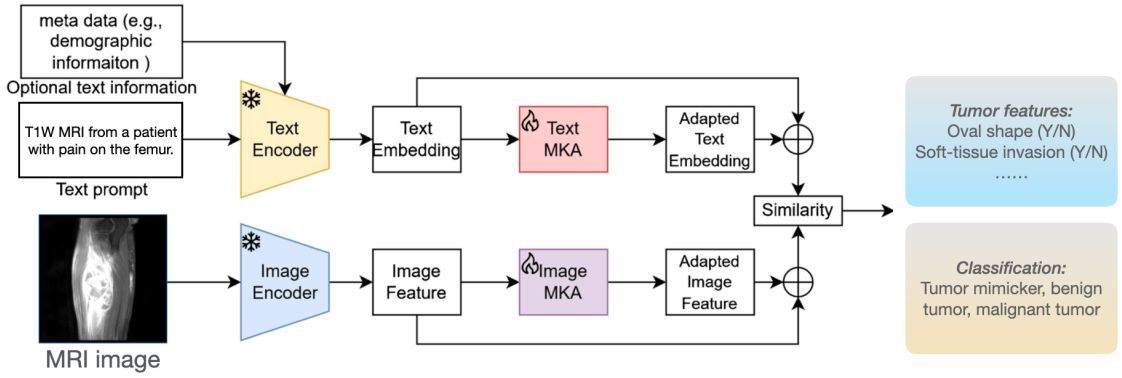
Classifying bone tumor and its mimicker via vison-language foundation model adaption

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Master Project
Approx. duration: 6 to 9 months

Background:
Bone tumors (BTs) are rare but the 3rd leading cause of cancer death in under-20s. Malignant vs. benign vs. tumor mimicker differentiation is critical: malignant require timely treatment, benign cases need monitoring and mimickers do no need any treatment. Current triage relies on expert radiologists, leading to over-referral of benign patients to expert centers and unnecessary biopsies. An automated tool would help non-expert hospitals triage effectively.
Vision-language foundation (VLM) model, trained on hundreds of millions of image-text pairs using a contrastive learning, aligns visual and textual representations within a shared semantic embedding space. Owing to its strong transferability and zero-shot generalization, vision-language foundation model is suited for data-efficient adaptation in medical tasks. Given the rarity and heterogeneity of BTs, VLM may serve as a optimal solution.

Research question:
Can a fine-tuned vision-language model, integrating routine MRI images and radiological reports, accurately classify benign BTs, malignant BTs, and tumor mimickers (or predict specific tumor features)? The consitancy of VLMs also warrants attention. We aim to explore improving the consistency of VLMs by integrating domain knowledge (e.g., via a customized loss function).

What you can expect:
You will implement a pipeline in training and validating vision-language model using routine clinical data (MRI + radiological reports).



Example of implementation adapted from He, Xingxin, et al. "Accessible cartilage tumor malignancy prediction via vision-language foundation model adaptation." *Skeletal Radiology* (2026): 1-13.

Interested in this project?

Supervisor(s): Xinyi Wan, Martijn Starmans
Email: x.wan@erasmusmc.nl

Shortcut learning for AI-based liver lesion diagnosis on MRI

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

Within the Liver Artificial Intelligence (LAI) Consortium, we are collecting MRI and clinical data from patients with solid-appearing liver lesions. This data is collected in ten centers across Europe, the US, and Australia (figure) and is very diverse in terms of lesion phenotypes, patient characteristics, and MRI characteristics. Because of these variations in the dataset, there is a risk of bias when training an AI-model for liver lesion diagnosis.

It is quite common for medical imaging datasets to contain spurious correlations: correlations in the training data that are predictive of the target label but are not causally related to the underlying task. AI-models have been shown to exploit these correlations, which is known as shortcut learning. This is very undesirable because it would mean that the AI-model bases the diagnosis on non-clinically relevant imaging features, such as image acquisition artefacts, instead of clinically relevant imaging features, such as the ones a radiologist would use.

As part of trustworthy AI-model development, we want to detect and quantify potential spurious correlations, or shortcuts, in our dataset and want to assess to what extent an AI-model picks up on these shortcuts. Furthermore, we want to explore methods to mitigate this undesirable behavior, such as pre-training a model on public datasets.

During this project you will:

- Investigate the potential shortcuts in the dataset
- Evaluate the extent to which an AI-model exploits these shortcuts
- Develop strategies to mitigate shortcut learning

Interested in this project?

Supervisor(s): Ruben Niemantsverdriet, Rick Bortsov
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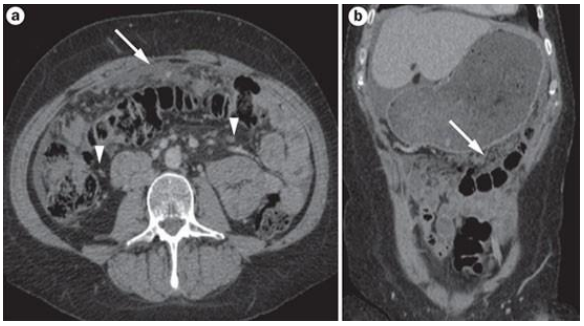
Detection of metastases on CT for Ovarian Carcinoma to prevent unnecessary surgery

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Bachelor or Master Project
Approx. duration: To be discussed

Background
Standard care for ovarian cancer often involves surgical resection. Despite preoperative examination, during surgery, the disease may turn out to be too extensive to continue. Our aim is to prevent such "open-close" procedures, as these are highly invasive for the patient without any benefit, while also costing precious time for alternative treatment. As the metastases may be subtle, these are difficult to detect on CT scans. However, retrospective inspection after surgery revealed that in several cases the metastases appear to have been visible. We therefore hypothesize that a deep learning based model should be able to aid radiologists in assessing the disease extent.



Goal
The goal of this project is to develop a deep learning model for the detection of ovarian cancer metastases on CT scans. Specific emphasis will be placed on the clinical value of the model: not all metastases have too be perfectly segmented, but specific design choices have to be made to optimize the value for surgery success prediction.

What you can expect
During the project, you will: 1) Work with the clinicians to determine the optimal design for a clinically valuable model; 2) Expand the data collection with additional patients from the PlaComOv trial; 3) Work with the clinicians on annotating the tumors; and 4) Develop and evaluate an AI model for segmenting the ovarian cancer metastases.

1. Nieuwenhuyzen-de Boer et al. (2023) Unresectable Ovarian Cancer Requires a Structured Plan of Action: A Prospective Cohort Study.
2. De Grauw et al. (2025) The ULS23 challenge: A baseline model and benchmark dataset for 3D universal lesion segmentation in computed tomography

Interested in this project?

Supervisor(s): Martijn Starmans, Lawrencia Dsana (Gynaecologist), Gatske Nieuwenhuyzen – de Boer (Gynaecologist)
Email: m.starmans@erasmusmc.nl

Development of a Model Context Protocol (MCP) layer to use AI Agents in medical imaging data management and discovery

Research Line: Biomedical Imaging Research Infrastructure
Project type: Bachelor or Master Project
Approx. duration: 6 to 9 months

Background Medical imaging research repositories commonly rely on XNAT [1] to store and organize imaging datasets and associated metadata**.** The amounts of data sometimes make it daunting to interpret the data. An AI agent based on Large Language Models (LLMs) can help answer meaningful questions about the data on an XNAT server and perform curation basic tasks.

However, before AI agents can interact with XNAT, XNAT's functionality must first be exposed through a standardized tool interface. XNAT offers a REST-API for programmatic access to the database. To make it easier for python users we created the XNATpy [2] package. But there is currently no mechanism that exposes XNAT/XNATpy in a manner directly consumable by AI agents. One emerging approach is the Model Context Protocol (MCP) [3,4].

Proposed Solution In this project, we propose to create a MCP layer for XNAT/XNATpy to communicate with an AI agent. To validate functionality, a test agent should be used to answer questions about the data on XNAT the user has access to and help with simple data management tasks.

Objectives

- Create an MCP for XNAT/XNATpy
- Test and validate MCP functionality by connecting to a simple AI agent.
- Enable the AI agent to perform simple data management tasks on the user's behalf.

Who are we looking for? We are looking for a student who enjoys working with modern technology and is not afraid of getting his/her hands dirty with programming. In the project you will have the freedom to design and implement the MCP and AI agents by yourself with supervision from experienced research software engineers. You are a student in a computer science or AI related fields and are in the final stages of your Bachelors or Masters.

References

https://xnat.org/
https://gitlab.com/radiology/infrastructure/xnatpy
https://www.anthropic.com/news/model-context-protocol
https://modelcontextprotocol.io/docs/getting-started/intro

Interested in this project?

Supervisor(s): Mahlet Birhanu, Hakim Achterberg

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Synthetic OCT-A Data for Automatic Retinal Segmentation

Research Line: Eye Image Analysis Group Rotterdam
Project type: Master Project
Approx. duration: 6 to 9 months

Background

Optical coherence tomography angiography (OCT-A) is a non-invasive imaging modality that acquires high-resolution volumes of the retinal vasculature. Biomarkers derived from these images, such as vascular properties, support the diagnosis and monitoring of both ophthalmic and systemic diseases.

Problem

The extraction of vascular biomarkers in retinal OCT-A data typically requires accurate vessel segmentation. However, manual annotation of microvasculature is unreliable and time-consuming. Therefore, current automatic segmentation methods are limited by the scarcity of large, high-quality datasets with detailed vessel annotations.

Proposed solution

This project aims to explore the use of generative models to produce synthetic OCT-A images along with corresponding vascular segmentations. These synthetic datasets will be used to augment existing training data, evaluating the impact of using synthetic data on automatic segmentation in real-world datasets (Figure 1).

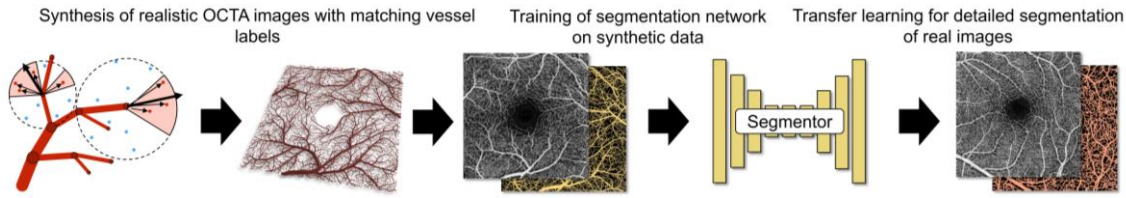

Figure 2. Pipeline for generating realistic synthetic OCT-A images and using them to train a U-Net model for blood vessel segmentation [1].

Objectives

- Benchmark open-source methods [1] for synthetic OCT-A data generation.
- Assess the realism and clinical relevance of the generated images and segmentations.
- Investigate the impact of synthetic data on the performance of existing vessel segmentation models.
- Validate the approach in real-world scenarios using public and in-house datasets.

Who are we looking for?

A student with an interest in medical imaging, preferably with experience with machine-learning models using Python, PyTorch, etc.

Related work

[1] Kreitner, L., Paetzold, J. C., Rauch, N., Chen, C., Hagag, A. M., Fayed, A. E., Sivaprasad, S., Rausch, S., Weichsel, J., Menze, B. H., Harders, M., Knier, B., Rueckert, D., & Menten, M. J. (2024). Synthetic Optical Coherence Tomography Angiographs for Detailed Retinal Vessel Segmentation

Interested in this project?

Supervisor(s): Adriana Falcão Neves, Danilo Andrade de Jesus, Luisa Sánchez Brea
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Tranfer Learning – Retinal macrovasculature from Fundus to OCT-A images

Research Line: Eye Image Analysis Group Rotterdam
Project type: Master Project
Approx. duration: 6 to 9 months

Background

Optical coherence tomography angiography (OCT-A) is a non-invasive imaging modality that acquires high-resolution volumetric images of the retinal vasculature. Biomarkers derived from these images support the diagnosis and monitoring of both ophthalmic and systemic diseases.

Problem

The extraction of macrovasculature-related biomarkers (e.g., tortuosity, length) requires accurate segmentation of those structures. However, performing this task manually is time consuming.

Proposed solution

This project aims to explore multi-modal registration methods to align paired OCT-A and color fundus images, along with their corresponding macrovasculature segmentations, and biomarkers computation methods (Figure 1).

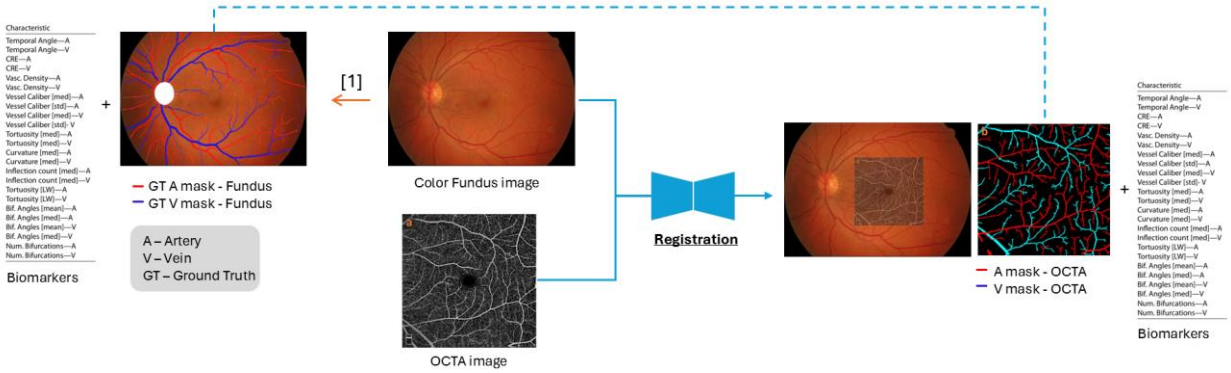


Figure 3. Pipeline for generating macrovasculature segmentations and correspondent biomarkers in OCTA, by transferring spatial information from fundus image.

Objectives

- Benchmark an open-source method [1] for macrovasculature segmentation and biomarkers computation in fundus images.
- Investigate image registration methods for aligning OCT-A and fundus image datasets.
- Transfer macrovasculature segmentation and biomarkers from fundus to aligned OCTA.

Who are we looking for?

A student with an interest in medical imaging, with experience with deep-learning models, Python.

Related work

[1] Jose Vargas Quiros, Bart Liefers, Karin A. van Garderen, Jeroen P. Vermeulen, Caroline Klaver; VascX Models: Deep Ensembles for Retinal Vascular Analysis From Color Fundus Images. *Trans. Vis. Sci. Tech.* 2025;14(7):19. https://doi.org/10.1167/tvst.14.7.19.

Interested in this project?

Supervisor(s): Adriana Falcão Neves, Danilo Andrade de Jesus, Luisa Sánchez Brea
Email: a.falcaoneves@erasmusmc.nl

Seeing the invisible – Optic Hollo Segmentation in OCT-A

Research Line: Eye Image Analysis Group Rotterdam
Project type: Master Project
Approx. duration: 6 to 9 months

Background

Optical coherence tomography angiography (OCT-A) is a non-invasive imaging modality that acquires high-resolution volumetric images of the retinal vasculature. Biomarkers derived from these images support the diagnosis and monitoring of both ophthalmic and systemic diseases.

Problem

The retinal vasculature growths in the shape of tree branches, from the optic hollow towards the macula. Because of the curved shape of the optic hollow, the appearance of microvasculature on the OCT-A data is altered. Therefore, the extraction of biomarkers requires accurate segmentation of the optic hollow boundaries (i.e., optic disc and optic cup). The optic hollow is not fully visible in OCT-A images, but it can be traced in other retinal imaging modalities, such as fundus.

Proposed solution

This project aims to explore 2D deformable multi-modal registration methods to align OCT-A and color fundus images, along with their corresponding segmentations. The aligned masks will then be used to train a model for segmenting the optic hollow using OCT-A images alone (Figure 1).

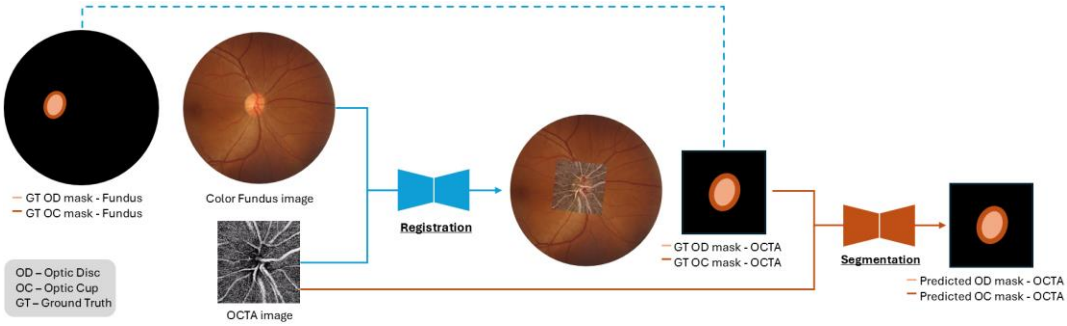


Figure 4. Pipeline for Optic Hollo (i.e., OD and OC) segmentation from OCT-A, by transferring spatial information from fundus image.

Objectives

- Benchmark an open-source method [1] for optic hollow segmentation in fundus images.
- Investigate image registration methods for aligning OCT-A and fundus image datasets.
- Develop a baseline model for optic hollow segmentation in OCT-A.
- Validate the proposed pipeline in real-world scenarios using public and in-house datasets.

Who are we looking for?

A student with an interest in medical imaging, with experience with deep-learning models.

Related work

[1] Scott Kinder,et al.; Optic Cup and Disc Segmentation of Fundus Images Using Artificial Intelligence Externally Validated With Optical Coherence Tomography Measurements. *Trans. Vis. Sci. Tech.* 2025;14(6):30. https://doi.org/10.1167/tvst.14.6.30.

Interested in this project?

Supervisor(s): Adriana Falcão Neves, Danilo Andrade de Jesus, Luisa Sánchez Brea
Email: a.falcaoneves@erasmusmc.nl

Augmented reality guided surgery

Research Line: Image guided in interventions and therapy
Project type: Bachelor or Master Project
Approx. duration: To be discussed

Project description

Augmented reality (AR) allows the visualization of virtual objects in the real world. It can help surgeons during their intervention by providing an overlay of the preoperative data directly on the patient. With head-mounted displays AR, surgeons do not need to switch attention between the patient and a 2D display, as is the case for conventional navigation systems.

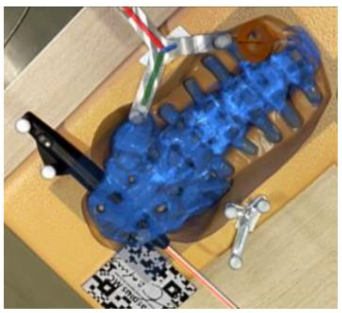
The HoloLens for example is equipped with a number of sensors and cameras, making it suitable for stand-alone navigation. It can track reference markers in the operative field that allows for tracking the patient and surgical instruments. The virtual overlay can be registered with the patient with multiple approaches such as point-based, surface or depth-based registration.

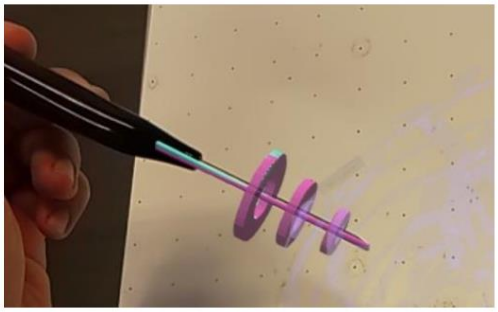
In our group, we investigate the different tracking and registration approaches for aligning the preoperative data with the patient. Furthermore, we also look at how to optimally visualize the virtual models and navigation data for optimum perception.

We have multiple projects that can fit BSc and MSc thesis projects. We offer more technical projects that focus on improving the current navigation frameworks we have in our lab, as well as technical-clinical projects that focus on validating the systems for the target surgical applications. The projects can be adjusted based on the interest of the students as well as background.

Example of possible projects:

- Reflective spheres tracking for HoloLens stand-alone navigation (Master).
- AR navigation for Zygomatic implant (Bachelor/Masters).
- Multi-marker detection & recognition using the Magic Leap 2 (Master).
- Instrument guidance & visualization in augmented reality-based intervention (Endoscopic/Headset).





Interested in this project?

Supervisor(s): Mohamed Benmahdjoub, Jiaqi Tang

Email: m.benmahdjoub@erasmusmc.nl, j.tang@erasmusmc.nl

Towards automated surgery planning for periacetabular osteotomy

Research Line: Musculoskeletal Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Background
Residual hip dysplasia (DDH) is characterized by insufficient acetabular coverage of the femoral head, resulting in abnormal joint loading and early-onset osteoarthritis. Periacetabular osteotomy (PAO) is a surgical intervention in young patients, in which the acetabulum is reoriented to improve femoral head coverage and restore more physiological joint mechanics. Surgical outcome is dependent on the degree and direction of acetabular correction. Currently, planning relies on 2D radiographic measures and expert judgement, which introduces variability and may not capture the full 3D complexity of the deformity. Our group has been developing and validating quantitative 3D morphology measures on MRI and CT data from PAO patients. The next step is to translate these validated metrics into a computational surgery planning framework that can automatically identify an optimal correction

Aim
The aim of this project is to develop a computational tool that uses 3D acetabular coverage measures to automatically optimize the acetabular reorientation for PAO surgery, with the goal of supporting and standardizing pre-operative planning in patients with residual DDH.

Objectives
- Review the literature on computational PAO planning
- Implement a simulation framework that models virtual acetabular reorientation and computes resulting 3D coverage metrics
- Develop an optimization strategy (e.g. learning-based) to identify the correction that best achieves target coverage within bounds
- Validate planned corrections against actual surgical outcomes in the existing patient cohort

Student profile
This project is ideal for a technically oriented student with programming experience (preferably Python) who:
- Has a background in Biomedical Engineering, Medical Informatics, Computer Science, or a related field
- Has completed a course in image processing or medical image analysis
- Is interested in orthopaedics, 3D geometric processing and 3D image analysis


Interested in this project?

Supervisor(s): Mirthe Kamphuis, Jukka Hirvasniemi, Jaap Tolk
Email: m.kamphuis@erasmusmc.nl

Anomaly detection for knee osteoarthritis using deep learning on MRI

Research Line: Musculoskeletal Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Background
Osteoarthritis (OA) is among the most prevalent musculoskeletal disorders worldwide, with the knee being the most affected joint. MRI enables detailed assessment of OA-related structural changes, including cartilage loss, bone marrow lesions, and meniscal damage, as captured by the validated MRI Osteoarthritis Knee Score (MOAKS). However, the manual scoring process is time-consuming and subject to inter-rater variability, motivating the development of automated, data-driven approaches.

Aim
The aim of this project is to develop and validate a deep learning framework for anomaly detection in knee MRI, with the goal of identifying deviations from normal anatomy that correspond to MOAKS-defined OA features. The student will explore whether models trained on normal knee MRI can flag pathological findings in an unsupervised or semi-supervised manner, extending existing pipelines from hip to knee.

Objectives
- Conduct a literature review of anomaly detection methods applied to musculoskeletal MRI
- Build a preprocessing and data pipeline for the knee OA MRI dataset
- Adapt and retrain existing hip MRI deep learning models for the knee domain
- Investigate anomaly detection approaches (e.g. autoencoders, normalizing flows, or contrastive methods) for identifying MOAKS-relevant pathology
- Evaluate model performance using MOAKS scores as a reference standard

Student profile
This project is ideal for a technically oriented student with programming experience (preferably Python) who:
- Has a background in Biomedical Engineering, Medical Informatics, Computer Science, or a related field
- Has completed a course in image processing or medical image analysis
- Is interested in musculoskeletal imaging and clinical applications of machine learning

Interested in this project?

Supervisor(s): Mirthe Kamphuis, Jukka Hirvasniemi, Jaap Tolk
Email: m.kamphuis@erasmusmc.nl

Longitudinal radiomic signatures of hip morphology in adolescents with DDH

Research Line: Musculoskeletal Image Analysis
Project type: Master Project
Approx. duration: 6 to 9 months

Background
Developmental dysplasia of the hip (DDH) is a spectrum of hip morphological abnormalities that, if undetected or inadequately treated during childhood and adolescence, can lead to early-onset osteoarthritis. The Generation R cohort, which is a population-based prospective cohort study from fetal life until young adulthood, provides a unique opportunity to study these mechanisms in a young adult population. Further radiomics, the extraction of high-dimensional quantitative features from medical images, has shown potential for capturing subtle texture information beyond what is visible to the naked eye. We have previously performed radiomic analysis at a single timepoint of the Generation R study. However, it remains unknown whether radiomic features evolve in a characteristic pattern over time, and whether such temporal trajectories are associated with specific hip morphology.

Aim
The aim of this project is to extend our existing single-timepoint radiomics framework to a longitudinal setting, characterizing how radiomic signatures of hip MRI change across multiple timepoints in children, and identifying whether distinct temporal patterns are associated with morphological features.

Objectives
- Build on the existing single-timepoint radiomic pipeline to handle multi-timepoint MRI data
- Assess the reproducibility and stability of radiomic features across timepoints
- Extract and harmonize radiomic features across the longitudinal dataset
- Apply statistical and machine learning methods (e.g. mixed-effects models, clustering, or trajectory analysis) to identify characteristic radiomic trajectories
- Correlate identified signatures with quantitative hip morphology measures (e.g. acetabular coverage)

Student profile
This project is ideal for a technically oriented student with programming experience (preferably Python) who:
- Has a background in Biomedical Engineering, Medical Informatics, Computer Science, or a related field
- Has completed a course in image processing or medical image analysis
- Is interested in musculoskeletal imaging and clinical translation of quantitative methods

Interested in this project?

Supervisor(s): Mirthe Kamphuis, Jukka Hirvasniemi, Jaap Tolk
Email: m.kamphuis@erasmusmc.nl

Cognition-Brain decoupling in the Rotterdam study

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

In the context of neurodegeneration, structural MRI is used to assess how an individual deviates in volumetric brain changes from what is expected given their age and sex. With aging, atrophy occurs naturally. With neurodegeneration, this process accelerates. Normative models have been developed to quantify these deviations at the individual level. In most studies, however, these models have characterized only the brain, and the relationship with cognition has been examined post-hoc. As a result, the direct comparison between an individual's brain and their cognition cannot be made within a single model.

This question is particularly relevant in clinical practice. A general practitioner or geriatrician requesting brain MRI in a patient with cognitive complaints essentially wants to know whether the scan can explain the complaints. One approach is to directly predict cognition from brain MRI. However, this is challenging for several reasons. First, cognitive tests are designed to detect pathology rather than to measure cognition continuously. Second, the brain-cognition relationship is weak in the cognitively healthy range, where most patients with mild complaints reside. Another approach is to investigate whether brain and cognition are consistent with each other at the individual level, that is, whether they are coupled or decoupled.

The aim of this project is to develop a method that quantifies brain-cognition decoupling at the individual level in a population-based cohort. We will implement a supervised variational autoencoder (VAE) [1] trained on cognitively healthy participants of the Rotterdam Study, using a combined loss function consisting of a reconstruction loss on the MRI scan, a variational (KL) loss on the latent space, and a supervised loss predicting cognitive domain scores from the latent representation. The model is conditioned on age, sex, and education. The hypothesis is that this combined objective yields an individual-level readout, the residual between observed and predicted cognition, that captures brain-cognition decoupling.

Who are we looking for? A student with an interest in neuroimage analysis and deep learning. Preferably with moderate to good python skills. A clinical program can be set up.

[1] Nemali, A., et al. "Smas: Structural MRI-based AD Score using Bayesian supervised VAE." *Computers in biology and medicine* 196 (2025): 110829.

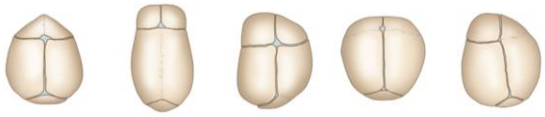
Interested in this project?

Supervisor(s): Sterre de Jonge, Esther Bron, Eline Vinke
Email: s.dejonge@erasmusmc.nl

Evaluation and Optimization of MRI-Based Brain Segmentation in Craniosynostosis

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 6 to 9 months

Project description
Craniosynostosis is a rare congenital disorder in which one or more skull sutures close prematurely, causing skull and facial deformations. Its prevalence in the Netherlands is about 0.9 per 10,000 live births and appears to be increasing. Although early surgical correction is performed within the first year of life, studies show an increased risk of behavioral and neurocognitive problems in several subtypes of craniosynostosis.



The Dutch Craniofacial Center aims to better understand the disease process and its consequences, particularly relating to visual, behavioral and neurocognitive functioning. In collaboration with BIGR (Biomedical Imaging Group Rotterdam), we use advanced MRI techniques to study brain structure and function, including high-resolution structural MRI (T1/T2), arterial spin labelling (ASL) for perfusion, and diffusion tensor imaging (DTI) for microstructural integrity.

A variety of standardized tools are available for analyzing these MRI scans. However, standard neuroimaging pipelines are typically designed for normally shaped brains and often fail in craniosynostosis patients due to severe anatomical deformation and low gray-white matter contrast in young children. In particular, (infant) FreeSurfer is widely used for brain segmentation but frequently underperforms, leading to substantial scan exclusion. This highlights the need to explore, evaluate, and potentially improve existing segmentation tools.

Objectives

- Evaluate performance of FreeSurfer 6.0.0 versus FreeSurfer 8.1.0
- Assess FreeSurfer performance with improved skull-stripping methods
- Compare FreeSurfer outputs with alternative segmentation approaches (e.g. FastSurfer, VINNA4Neonates, BIBSnet, SynthSeg, more t.b.d.)
- Develop or test automated quality control measures for segmentation outputs
- Optionally: explore or contribute to improved segmentation methods tailored to paediatric craniosynostosis patients

Candidate profile A student with an interest in neuroimage analysis, deep learning, and Python programming, preferably with a course in (medical) imaging processing. A clinical experience program is possible, both within radiology and plastic surgery.

Interested in this project?

Supervisor(s): Diede Wijnbergen, Esther Bron and Irene Mathijssen
Email: d.wijnbergen@erasmusmc.nl

Deep learning for etiologic diagnosis of dementia: multimodal data integration and missing data

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

Dementia can be caused by different etiologies, including Alzheimer's disease, frontotemporal dementia, Lewy body dementia and vascular dementia. Uncovering the underlying etiology is important for suitable patient care but remains difficult due to disease heterogeneity and overlap. The diagnostic process is inherently multidisciplinary, involving a range of diagnostic tests including brain MRI, neuropsychological testing, and blood plasma and/or cerebrospinal fluid analysis.

AI has potential to provide data-driven support by integrating these multimodal data to predict the most probable etiology. Specifically, deep learning models are suitable as these can extract fine-grained features from imaging data. However, the development of multimodal diagnostic models is complicated by two factors. First, imaging data and non-imaging data are often integrated by concatenating the non-imaging data to the feature vector. However, there may be better ways of performing this data integration, resulting in improved model performance, e.g. through cross-attention. Second, input data is often missing not at random, i.e. which diagnostic test a patient receives correlates to their final diagnosis. Not accounting for this might result in models that learn short-cuts in the data and do not make a meaningful prediction.

This student project focuses on addressing these two challenges in the context of etiologic dementia diagnosis. More specifically, the student will:

1. Develop a multimodal deep learning model for etiologic dementia diagnosis of Alzheimer's disease and frontotemporal dementia;
2. Explore different methods for multimodal data integration;
3. Explore different methods to account for data that is missing not at random, mainly focusing on brain MRI and neuropsychological tests.

Interested in this project?

Supervisor(s): Kaouther Mouheb and Myrthe van Haaften
Email: k.mouheb@erasmusmc.nl;
m.f.vanhaaften@erasmusmc.nl

Linking Cerebral Blood Flow With Small Vessel Markers at 7T using Machie

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 6 to 9 months

Project description

For the CHIME consortium, we are interested in cerebral blood flow (CBF) changes that occur in small vessel disease. Using Arterial Spin Labeling (ASL), which is a specific MRI sequence, it is possible to non-invasively measure CBF without a contrast agent. With 7T BOLD scans, it is possible to measure small vessel function due to the high quality of these scans. Unfortunately, these excellent quality scanners and scans are not widely available. Using machine learning, which will be likely deep learning, we aim to find patterns of CBF changes that relate to alterations in small vessel function, as assessed with 7T scans.

This project will make use of data from the Rotterdam Study, which is a large population-based cohort of ageing adults. A subset of these participants (n=200) where invited to undergo the 7T MRI scan. With this population, we are not looking into a specific disease, but general, healthy aging.

I am looking for a master student with interest in machine learning or deep learning, for which a specific master's program is not required it. It is for me much more important that you work on a subject that is interesting to you. In my research, I love to think out-of-the box and come up with creative solutions, and I would like to encourage this to you also in this internship

Interested in this project?

Supervisor(s): ir. Jordi Boons
Email: j.boons@erasmusmc.nl

LLM-based Data Extraction from Free Text for a European Craniosynostosis Registry

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 3 to 6 months

Project description
Craniosynostosis is a rare congenital disorder in which one or more skull sutures close prematurely, causing skull and facial deformations. As the prevalence of craniosynostosis is low, approximately 0.9 per 10,000 live births in the Netherlands, international collaboration is essential to collect sufficient data for research. Across Europe, clinical data on craniosynostosis patients are collected within the registry of the European Reference Network (ERN) Cranio. However, a large proportion of clinically relevant information is stored in unstructured free-text formats within electronic health records, limiting its usability for research and large-scale analysis.

To improve data accessibility and harmonization, this project aims to explore the use of natural language processing (NLP) and large language models (LLMs) for extracting structured clinical variables from free-text reports. These variables may include diagnosis subtype, surgical interventions, imaging findings, and neurodevelopmental outcomes.

The project is embedded within a European collaboration coordinated through ERN Cranio, aiming to improve data quality and completeness across craniofacial registries. Using modern NLP and LLM techniques, this work supports automated extraction of clinical information from routine documentation, reducing manual data entry and enabling large-scale multicentre research.

Objectives

- Develop and evaluate LLM-based methods for extracting structured clinical variables from free-text clinical notes (e.g. LLM Extractinator)
- Compare LLM performance with traditional NLP approaches (e.g. rule-based or classical machine learning methods)
- Assess accuracy, completeness, and robustness of extracted data against manually curated reference datasets
- Explore prompt engineering strategies and/or fine-tuning approaches for domain-specific improvement
- Optionally: design a prototype pipeline for semi-automated registry data curation

Candidate profile A student with an interest in machine learning, natural language processing, large language models, and Python programming. A clinical experience program is possible, both within radiology and plastic surgery.

Interested in this project?

Supervisor(s): Diede Wijnbergen, Esther Bron and Irene Mathijssen
Email: d.wijnbergen@erasmusmc.nl

Longitudinal brain aging patterns in the Rotterdam Study

Research Line: Neuroimage Analysis & Machine Learning
Project type: Master Project
Approx. duration: 6 to 9 months

Project description.

The Rotterdam Study, established in 1989, is a population-based cohort to investigate causes and consequences of age-related diseases. All residents aged over 45 years are invited for extensive examination. Since 2005, a 1.5 Tesla MRI scanner has been operational at the research center, resulting in brain scans in over 6,000 participants with up to 4 scans per participant (>18,000 scans). This has produced a rich longitudinal dataset to study how the brain changes over time in relation to aging and neurodegeneration.

To use this dataset for longitudinal analysis, the data first need to be harmonized to address a hardware update of the MRI scanner in 2020. This update, which included a replacement of the receiver coil, changed the scanner's signal reception across different brain regions. Comparisons of scans from the same individuals before and after the update show notable differences in brain measurements. The first part of the project will therefore focus on implementing and validating a harmonization strategy to remove these scanner-related effects.

The central aim of this project is to characterize trajectories of brain aging using longitudinal structural MRI and cognitive biomarkers, identifying individuals who deviate from a normal aging trajectory. To this end, we will apply latent class mixed models [1], which jointly model multiple longitudinal biomarkers as expressions of an underlying aging process and identify subgroups of individuals who follow different trajectories, that is different rates, of brain aging over time. To assess the biological and clinical relevance of these subgroups, we will examine associations with genetic risk factors and risk of dementia.

Objectives:

- Contribute to the processing of longitudinal structural MRI data using FreeSurfer or FastSurfer to derive imaging biomarkers
- Implement and validate ComBat harmonization to remove scanner-related effects while preserving biological variation
- Model longitudinal brain aging trajectories using latent class mixed models to identify subgroups with different aging patterns
- Examine the biological and clinical relevance of identified subgroups by assessing associations with genetic risk factors and risk of dementia

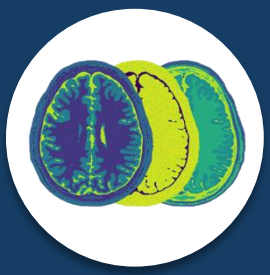
Who are we looking for? A student with an interest in neuroimage analysis and affinity with epidemiology. A clinical experience program is possible.

[1] Li, Dan, et al. "Bayesian latent time joint mixed-effects model of progression in the Alzheimer's Disease Neuroimaging Initiative." *Alzheimer's & Dementia: Diagnosis, Assessment & Disease Monitoring* 10.1 (2018): 657-668.

Interested in this project?

Supervisor(s): Sterre de Jonge, Esther Bron, Eline Vinke
Email: s.dejonge@erasmusmc.nl

Towards Clinical Translation of Quantitative MRI



Research Line: Quantitative MR reconstruction
Project type: Master Project
Approx. duration: 6 (with possible extension)

Background: Quantitative MRI (qMRI) aims to measure objective tissue properties (e.g., T1, T2, PD) and therefore provides richer and more reproducible information than conventional MRI. However, qMRI remains challenging to deploy in clinical practice due to long acquisition times and practical limitations.

We have developed a deep-learning method that is able to generate high-quality qMRI by combining a rapid lower quality qMRI scan with clinically acquired images. This shows promising results, but the evaluation was performed on a small set of images. We can use your help to extend this towards the real application with an already acquired large set of MRI scans.

Aim: The student will retrain and validate the deep-learning model using a large set of data from healthy volunteers, with the goal of moving qMRI closer to clinical acceptance.

Approach: During this project, the student will:

- Learn about qMRI, MR physics and current deep-learning models
- Retrain and adapt the existing model to real data
- Validate model performance
- Improve the quality of synthesized images from qMRI
- Develop tools for visualization and interaction with synthetic images

Funding: Partial financial support is available for this MSc project.

Project Opportunities:

- Opportunity to contribute to ongoing research with publication potential depending on project outcomes
- Access to real clinical MRI data and mentorship from experts at Erasmus MC
- Hands-on involvement in MRI data acquisition, including participation in scanner sessions when applicable

Requirements:

- MSc student in biomedical engineering, electrical engineering, computer science, physics, or a related technical field
- Interest in medical image analysis and machine learning
- Experience with Python and PyTorch
- Understanding of MRI physics fundamentals
- Availability for ~6 months and ability to work on-site in Rotterdam
- EU residency

Interested in this project?

Supervisor(s): Alireza Samadifardheris, Dirk H.J. Poot, Stefan Klein, Juan A. Hernandez-Tamames
Email: a.samadifardheris@erasmusmc.nl

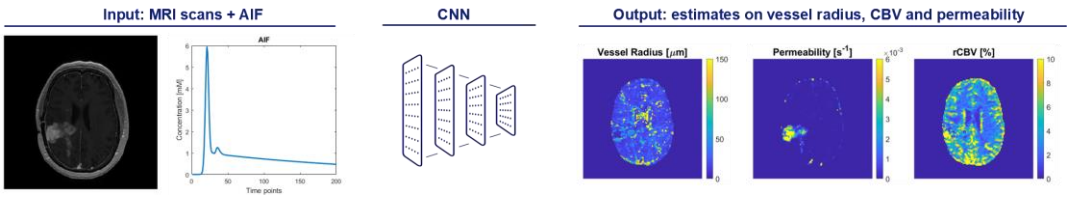
Developing a convolutional neural network for efficient MR fingerprint

Research Line: Quantitative MR reconstruction
Project type: Master Project
Approx. duration: 6 to 9 months

Background
Glioma is a primary brain tumor with a high morbidity and mortality. For optimal treatment, knowledge on the type and grade is necessary. Currently, this is determined through tissue analysis, for which a surgery is needed. Instead, we want to diagnose gliomas non-invasively using MRI. As the vasculature is related to the type and grade, we will use perfusion MRI, which provides information about the vasculature in the brain.

Project goal
In Dynamic Susceptibility Contrast (DSC) MRI, a bolus of contrast agent is injected, after which its passage through the brain is recorded. The shape of the bolus passage gives us information about the vasculature. By using a technique called MR Fingerprinting, we can obtain quantitative estimates on parameters such as vessel radius, cerebral blood volume (CBV) and permeability of the vasculature. Traditionally, MRF is done by simulating a dictionary of MR signals and matching the measured signal to the most similar signal in this dictionary. However, this approach is time-consuming, introduces discretization errors and is not easily adapted to patient-specific conditions (such as the arterial input function (AIF)). Therefore, we want to train a convolutional neural network that can obtain accurate estimates of the vascular parameters for different input AIFs.

Methods
We have a dataset with DSC scans from glioma patients and a dictionary of simulated MR signals using different AIFs. Furthermore, we have already trained a multilayer perceptron (MLP) that can estimate the vascular parameters for each voxel individually. Nevertheless, this does not take advantage of the spatial information available in such a scan (e.g. gray vs. white matter, arteries vs. veins, etc.). Therefore, we want to train a convolutional neural network (CNN) to estimate vascular parameters from the DSC scan and AIF. The performance can then be compared to the MLP to investigate to what extent the additional spatial context improves the performance.



Interested?
Are you a motivated master student with experience in Python and an interest in medical imaging, and looking to start your thesis project from the end of 2025? Let us know!

Interested in this project?

Supervisor(s): Karen van der Werff, Dirk Poot, Frans Vos
Email: k.vanderwerff@erasmusmc.nl

Investigating the glioma vasculature using MRI and the discrepancies in DSC / ASL

Research Line: Quantitative MR reconstruction
Project type: Master Project
Approx. duration: 6 to 9 months

Background
A glioma is a primary brain tumor with a high morbidity and mortality. For optimal treatment, knowledge on the type and grade of the glioma is necessary. Currently, this is determined through tissue analysis, for which a surgery is needed. Instead, we want to be able to diagnose gliomas non-invasively using MRI. As the glioma vasculature is related to the type and grade, we will use perfusion MRI, which provides information about the vasculature in the brain.

Project goal
Perfusion MRI can be performed using either Dynamic Susceptibility Contrast (DSC) or Arterial Spin Labelling (ASL). In DSC-MRI, a bolus of contrast agent is injected, after which its passage through the brain is recorded. The shape of the bolus passage gives us information about the vasculature. In ASL, no contrast agent is injected; the blood itself is used as the contrast agent instead. While these two techniques seem to provide similar information in healthy brain tissue, the information we obtain within glioma seems to contradict each other. That means we can do some interesting analyses! Where do these differences come from? Can we learn something new about the glioma vasculature? Or should we interpret the MR signals differently?

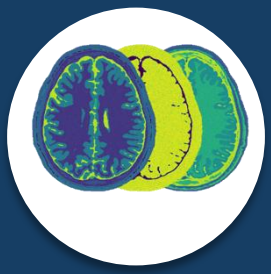
Methods
We have a dataset available which includes both DSC and ASL scans from a cohort of glioma patients. Of course, the first step is to process the data. For example, leakage correction should be applied on the DSC data and image segmentation should be applied to obtain the different tumor regions in each patient. Then, we can look for patterns in perfusion across these different regions. For instance, an approach is to train a variational autoencoder and analyze the latent space to disentangle patient-specific and scan-specific information.

Interested?
Are you a motivated master student with experience in Python and an interest in medical imaging? And are you looking to start your master thesis project from the end of 2025? Let us know!

Interested in this project?

Supervisor(s): Karen van der Werff, Dirk Poot, Frans Vos
Email: k.vanderwerff@erasmusmc.nl

Streamline DCE processing

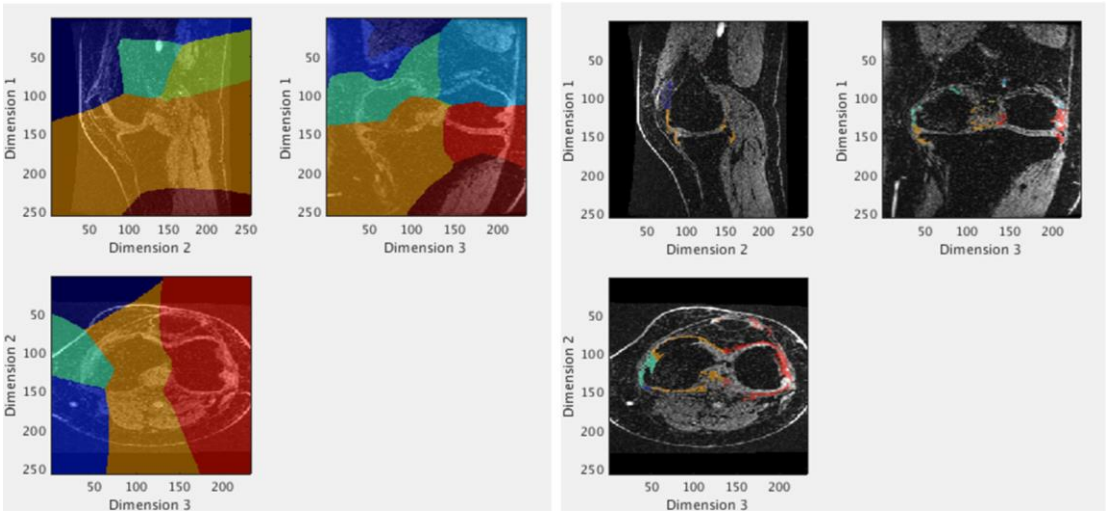


Research Line: Quantitative MR reconstruction
Project type: Bachelor or Master Project
Approx. duration: 3 to 6 months

Project description

For many projects we acquire dynamic contrast enhanced (DCE) image series. These allow investigating various disease processes. A strength of this method is that we can model how the contrast agent enters and leaves the tissue and hence recover pharmacokinetic parameters of the tissue and hence study the perfusion of the tissue. To do this we have developed various state of the art tools over the past years; providing high quality analysis. These tools are MATLAB based. However, integration of these methods into a package that clinical researchers use as well as to support further integration of AI into these methods would require a python version.

We are looking for someone that would like to enhance the usability of our methods in an internship or MSc project. This project will have a focus on software design and integration. Within the project there will be collaboration with clinical researchers and with the developers.



Subregion analysis of the perfusion; attributing perfusion changes to feeding arteries.

Interested in this project?

Supervisor(s): D. Poot
Email: d.poot@erasmusmc.nl