BIGR Open Lab Day 2025

Student Projects

Contents

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?

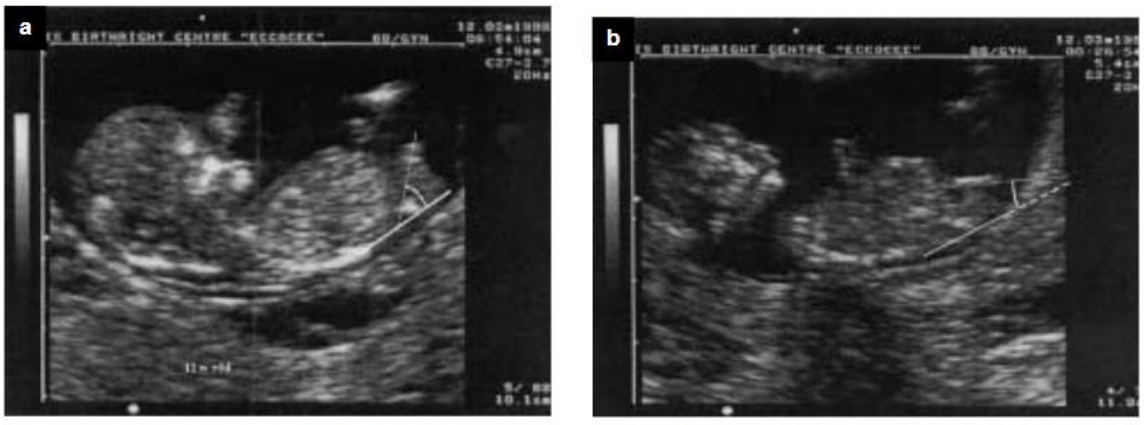

Figure 1 (a) Male fetus with acute angle of the penis shown. (b) Female fetus with converging angle of the clitoris shown

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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Enhancing glioma genotype and grade prediction using multi-modal MRI and AI

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

Project description

Glioma is the most common primary brain tumor and outcomes are dismal. Non-invasive prediction of genotype and grade prior to surgery can guide personalized treatment strategies and improve prognosis. Prior work has shown that AI models using structural MRI (T1w, T1w post-contrast, T2w, FLAIR) can successfully segment tumors and predict molecular markers like IDH mutation, 1p/19q codeletion, and grade [1].

In this project, we will investigate the added value of advanced MRI modalities for improving predictive performance, specifically using relative cerebral blood volume (rCBV) maps from perfusion MRI and apparent diffusion coefficient (ADC) maps from diffusion MRI (**Figure 1**). These modalities offer complementary physiological information about tumor vascularity and cellularity, which could enhance model accuracy [2].

Interested?

Are you an enthusiastic student with experience in Python (and preferably deep learning) and interested in medical image analysis? Are you looking for a 9–12 month thesis (shorter can be discussed), starting end of 2025/start of 2026? Then this project might be for you.

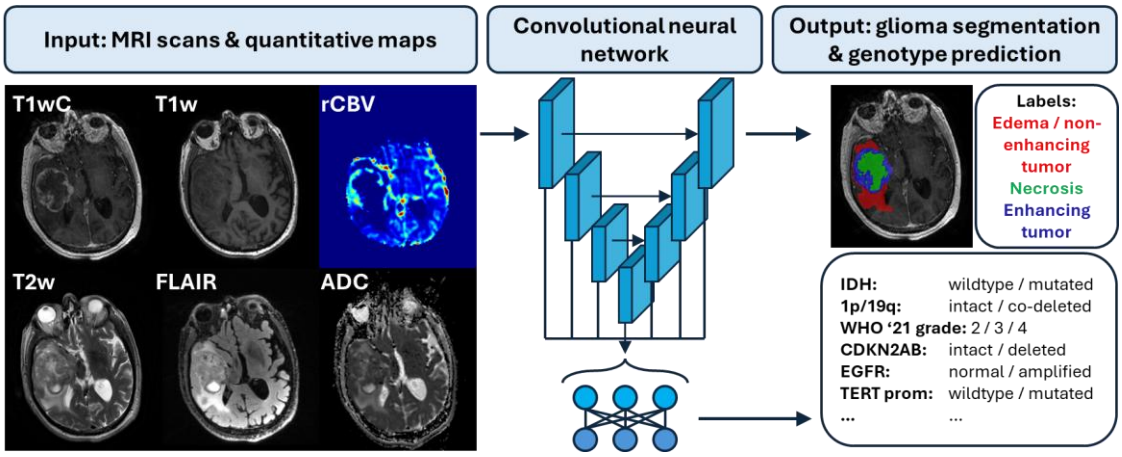

Figure 1: Overview of the method. A multitask U-Net will be trained to segment gliomas into three subregions and predict genotype and grade from structural MRI quantitative maps.

[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] Pruis IJ et al (2022) Noninvasive differentiation of molecular subtypes of adult nonenhancing glioma using MRI perfusion and diffusion parameters. *Neuro-oncology advances, 4*(1), vdac023

Interested in this project?

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Explainable Carnegie Staging of the Human Embryo using Artificial Intelligence

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

Project description: The Carnegie staging system provides a standardized framework for assessing both normal and abnormal morphological development during the embryonic period. The Carnegie stages define 23 distinct steps that chronologically outline embryonic development from conception to the start of the fetal stage, indicating that all major organ systems are formed. Examples of these stages are illustrated in Figure 1. We have developed a deep learning model that can accurately predict the Carnegie stage of an embryo, given a 3D ultrasound image [1]. Currently, the model gives no insight into which features were used to determine the stage. The aim of this project is to explore explainable deep learning methods or design novel features that explicitly assess developmental features such as neck curvature, limb position and brain ventricles in order to bring more insight into the models decision making.

Project ideal for: Are you a technical student with programming experience (preferably Python) who: is interested in medical image analysis and early human development, wants to learn more about deep learning and feature engineering and is eager to apply learned algorithms in the field of prenatal image analysis? ***A visit to the clinic is part of this project.***

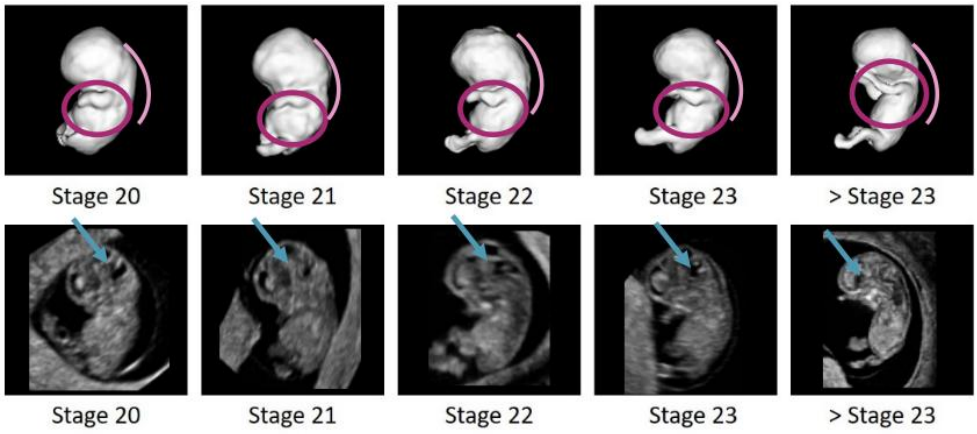

Figure 1. Examples of stages 20 – 23 and >23 showing the fetal stage. Top row shows 3D rendering highlighting limb and neck differences. Bottom row shows 2D slices highlighting brain development.

[1] Niemantsverdriet, R., Bastiaansen, W., Vos, F., Steegers-Theunissen, R. P., Klein, S., & Rousian, M. (2024). Artificial intelligence for automated Carnegie staging of the human embryo in three-dimensional ultrasound: The Rotterdam periconception cohort. Ultrasound in obstetrics & gynecology: the official journal of the International Society of Ultrasound in Obstetrics and Gynecology, 64(S1), 61-62

Interested in this project?

Supervisor(s): Nikolai Herrmann and Wietske Bastiaansen, in collaboration with the Periconception Epidemiology group of the Department of Obstetrics and Gynecology **Email:** n.herrmann@erasmusmc.nl , w.bastiaansen@erasmusmc.nl

The influence of maternal BMI on brain development in the second and third trimester

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

Project description

Brain growth and morphological development during pregnancy is of crucial importance for current and future health of the developing embryo and fetus. To address this, we created the 4D Human Embryonic Brain Atlas[1], which describes growth and development during the first trimester. Recently, the Fetal Brain Atlas was published[2], which covers the second and third trimester. Using the 4D Human Embryonic Brain Atlas, we studied the influence of maternal BMI (see **Figure 1**) and other important factors such as age, smoking and alcohol usage, on brain development. The aim of this project is to explore whether the Fetal Brain Atlas could be used in a similar fashion. Using groupwise image registration techniques, the deformation between the ultrasound images and the atlas can be determined, which in turn can be analyzed. A large dataset containing second and third trimester 3D brain ultrasound images is available.

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?

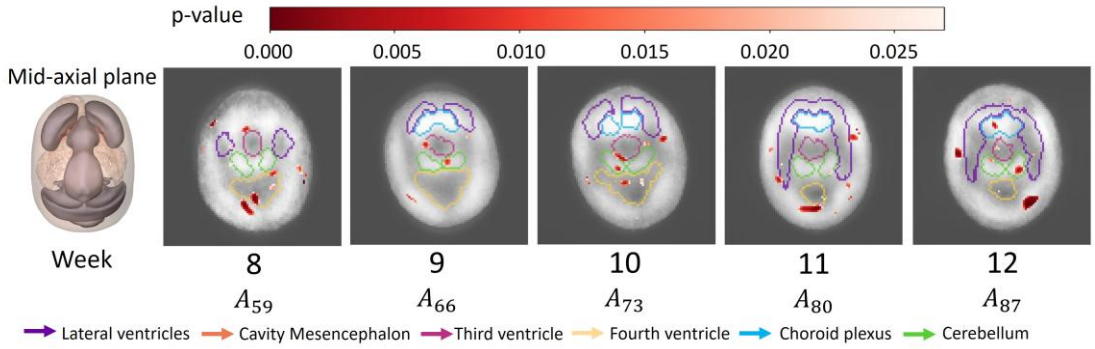

Figure 1: Important brain structures are outlined, in red the voxels are marked that significantly differ between the normal maternal and high maternal BMI group.

A visit to the clinic is part of this project.

[1]Bastiaansen, W. et al (2025). The 4D Human Embryonic Brain Atlas: spatiotemporal atlas generation for rapid anatomical changes using first-trimester ultrasound from the Rotterdam Periconceptional Cohort. arXiv preprint arXiv:2503.07177.
[2]Namburete, Ana IL, et al. "Normative spatiotemporal fetal brain maturation with satisfactory development at 2 years." *Nature* 623.7985 (2023): 106-114.

Interested in this project?

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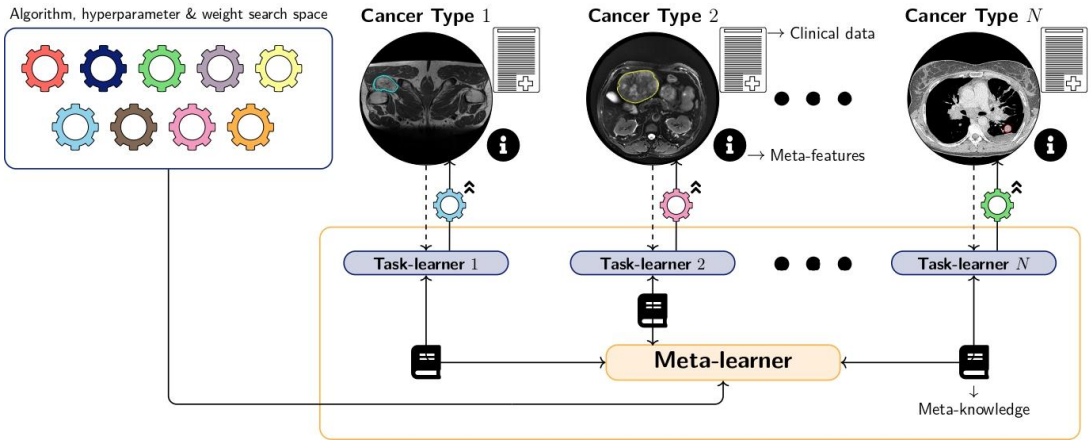
Automated Deep Learning for Soft-Tissue Tumor Classification Using Meta-Learning and AutoML

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

Background AI models in medical imaging are usually developed from scratch using disease-specific datasets. While this works for common diseases, it poses a major bottleneck for rare cancers like soft-tissue tumors (STTs), where labelled data is scarce. Unlike humans, who can learn new concepts from just a few examples by drawing on prior experience, current AI systems require large amounts of task-specific data due to how they are trained. This project addresses that limitation by combining meta-learning and automated machine learning (AutoML) to enable knowledge transfer across clinical and reducing reliance on large datasets.

Aim The aim of this project is to develop a novel methodology that integrates automated machine learning and meta-learning for medical image classification. Instead of trial-and-error model design, we will automate model selection and tuning using prior experience on related tasks and datasets. By learning from previous clinical applications, the system will be able to generalize across different diseases and imaging modalities, particularly in the context of rare cancers where data is limited. The project will involve designing model search strategies, incorporating knowledge transfer mechanisms, and evaluating the approach on real-world clinical datasets. Note that this project is quite technical.



Hutter, F., Kotthoff, L., & Vanschoren, J. (Eds.). (2019). *Automated machine learning: Methods, systems, challenges*. Springer.

Hospedales, T., Antoniou, A., Micaelli, P., & Storkey, A. (2021). Meta-learning in neural networks: A survey. *IEEE transactions on pattern analysis and machine intelligence*, *44*(9), 5149-5169.

Interested in this project?

Supervisor(s): Natalia Oviedo Acosta, Martijn Starmans, Stefan Klein
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Application development of right ventricle dysfunction measurement on chest CTs

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Bachelor or Master Project
Approx. duration: 3 to 6 months

Project description

An important risk factor for high-risk pulmonary embolisms is right ventricle dysfunction. Patients that have pulmonary embolisms and a right ventricle dysfunction are more likely to have an obstructive shock that can lead to death. Pulmonary embolisms can increase the resistance in the vessels such that the right ventricle is unable to provide enough pressure for adequate blood flow leading to shock. When pulmonary embolisms are detected in a patient, it is important to classify the patients risk of death from the embolisms. This is done using the following scoring (1):

Early mortality risk		Indicators of risk			
		Haemodynamic instability[a]	Clinical parameters of PE severity and/or comorbidity: PESI class III–V or sPESI ≥1	RV dysfunction on TTE or CTPA[b]	Elevated cardiac troponin levels[c]
High		+	(+)[d]	+	(+)
Intermediate	Intermediate–high	-	+[e]	+	+
	Intermediate–low	-	+[e]	One (or none) positive	
Low		-	-	-	Assesment optional; if assessed, negative

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Easy, fast and accurate evaluation of the right ventricle (RV) is thus important for an adequate response to patients with pulmonary embolisms. RV dysfunction can be determined on CT imaging by measurement of the ratio between the RV compared to the left ventricle (LV). Automation of this measurement already exist and have been shown to help decision making by treating physicians for patients with pulmonary embolisms (2).This project is part of a larger project on the automatic evaluation of incidental pulmonary embolisms for which risk stratification such as this can be extremely helpful. Although, automated methods and other related works exist (e.g., LV segmentation on MRI, general heart segmentation on CT), non of these is a publicly available, well validated method that can be adopted for our clinical need. The aim of this project is to unite and improve upon existing work to build a clinically deployable AI tool for quantifying RL/LV volume ratio used for patients mortality risk classification from pulmonary embolisms.

In this internship will you be combing, improving and validating multiple methods into a complete pipeline for quantifying the RV/LV volume ratio based on CT imaging. You will be validating you pipeline's robustness as part of the integration to clinical practice. A weakly labeled public and EMC database of CT imaging are available for testing.

(1) Stavros V Konstantinides, et al., ESC Scientific Document Group, 2019 ESC Guidelines for the diagnosis and management of acute pulmonary embolism developed in collaboration with the European Respiratory Society (ERS). European Heart Journal, Volume 41, Issue 4, 21 January 2020, Pages 543–603, https://doi.org/10.1093/eurheartj/ehz405

(2) Foley, R.W. et al. Automated calculation of the right ventricle to left ventricle ratio on CT for the risk stratification of patients with acute pulmonary embolism. Eur Radiol 31, 6013–6020 (2021). https://doi.org/10.1007/s00330-020-07605-y

Interested in this project?

Supervisor(s): Erik Kemper, Martijn Starmans, Frans Vos
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Benchmarking AutoML and Meta-Learning on Medical Image Classification

Research Line: Artificial Intelligence for Integrated Diagnostics (AIID)
Project type: Master Project
Approx. duration: 4 – 9 months

Background Medical image classification has advanced rapidly due to the availability of large pretrained models and foundation models. However, most model development workflows in medical imaging are still highly customized and dataset-specific, making it difficult to compare methods or reproduce results. This lack of standardization is especially limiting for techniques like automated machine learning (AutoML) and meta-learning, which aim to generalize across tasks and reduce manual effort. While generic AutoML benchmarks exist for natural images or tabular data, there is no established benchmark tailored to the unique characteristics of medical image data particularly in oncology. Creating such a benchmark would enable fair, systematic evaluation of AutoML and meta-learning approaches.

Aim This project aims to build a comprehensive and extensible benchmark for evaluating AutoML and meta-learning methods in medical image classification, with a particular emphasis on oncological tasks. It involves curating a diverse collection of publicly available medical imaging datasets, prioritizing cancer-related classification problems across modalities such as CT and MRI. In parallel, a portfolio of pretrained and foundation models—including resources such as SAM-Med3D [1], MONAI Model Zoo, and others—will be collected and structured into a unified, reusable model hub. Based on these components, the benchmark will support the systematic evaluation of AutoML and meta-learning frameworks, including methods like Quick-Tune [2] and DEHB [3]. Evaluations will focus on metrics such as classification accuracy, cross-dataset generalization, and computational efficiency. Note that this project is quite technical.

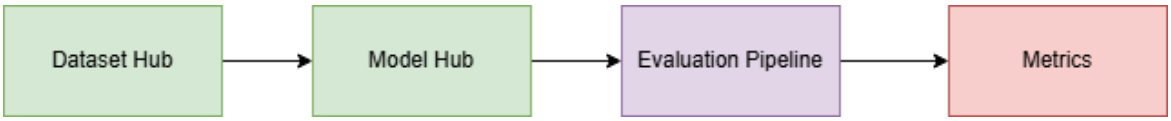

Figure 1: Overview of the proposed benchmarking framework for evaluating AutoML and meta-learning methods in medical image classification.

References

[1] Wang, S., Zhu, C., Lu, M. Y., Qian, Z., Chen, R. J., & Mahmood, F. (2023). *SAM-Med3D: Segment Anything in 3D Images with Med3D Adapter*. arXiv preprint arXiv:2308.16184.

[2] Arango, S. P., Ferreira, F., Kadra, A., Hutter, F., & Grabocka, J. (2023). Quick-tune: Quickly learning which pretrained model to finetune and how. *arXiv preprint arXiv:2306.03828*.

[3] Awad, N., Doerr, F., Müller, S., Benjamins, C., & Hutter, F. (2021). *DEHB: Evolutionary Hyperband for Scalable, Robust and Efficient Hyperparameter Optimization*. In *Proceedings of the 25th International Conference on Artificial Intelligence and Statistics (AISTATS)*, PMLR 130: 1344–1352.

Interested in this project?

Supervisor(s): Natalia Oviedo Acosta, Martijn Starmans, Stefan Klein
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Dynamic Preprocessing Pipeline for Soft Tissue Tumor Classification

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

Background In medical imaging, preprocessing steps like normalization, resampling, and cropping are often applied using fixed heuristics. While standard, these static methods can limit performance in complex settings such as soft tissue tumors (STTs), where anatomical variation and acquisition inconsistencies are common. nnU-Net [1] has shown that task-specific, well-chosen preprocessing can strongly influence performance by adapting settings to the dataset characteristics. Building on this idea, and inspired by OBELISK-Net [2], which integrates preprocessing within the network as a learnable module, this project explores a dynamic alternative: making preprocessing fully differentiable and trainable alongside the model.

Aim The aim of this project is to build an adaptive preprocessing pipeline for medical imaging with a focus on STTs. Instead of using fixed rules for intensity normalization, voxel spacing resampling, or spatial cropping, the project will implement these steps as learnable layers in a deep neural network. These layers will be differentiable and trained end-to-end with the downstream model, allowing them to discover the most effective image transformations in a data-driven, task-specific way. The proposed pipeline will be compared with conventional preprocessing strategies and evaluated on public medical imaging datasets, especially for rare cancers such as STTs. Note that this project is quite technical.

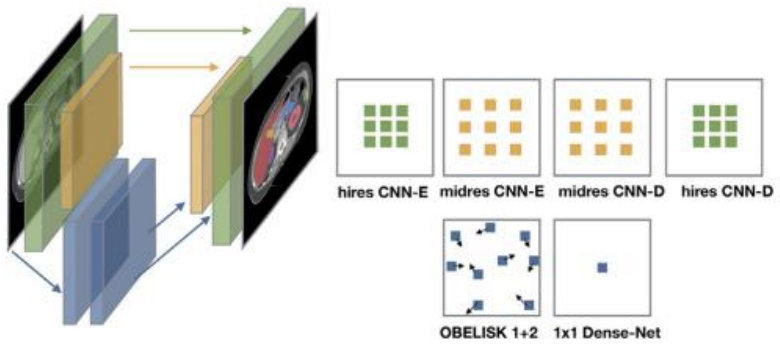

Figure 1: Overview of OBELISK-Net, which replaces standard dense convolutional layers with sparse, deformable sampling operations that learn optimal spatial locations for feature extraction.

References

[1] Isensee, F., Jaeger, P.F., Full, P.M., Vollmuth, P., Maier-Hein, K.H.: nnU-Net: A self-configuring method for deep learning-based biomedical image segmentation. Nature Methods 18, 203–211 (2021)

[2] Heinrich, M. P., Oktay, O., & Bouteldja, N. (2019). OBELISK-Net: Fewer layers to solve 3D multi-organ segmentation with sparse deformable convolutions. Medical image analysis, 54, 1-9.

Interested in this project?

Supervisor(s): Natalia Oviedo Acosta, Martijn Starmans, Stefan Klein
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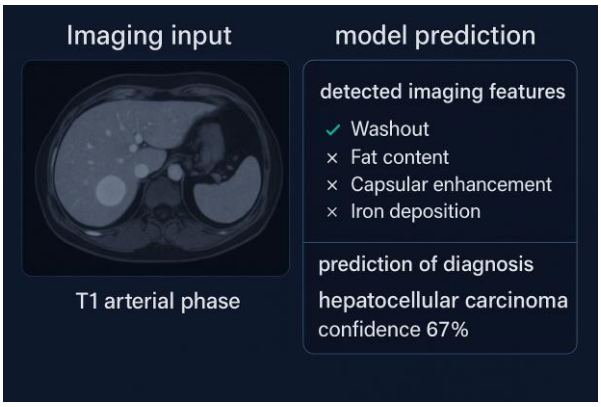
From Image to Insight: Can Vision Language Models see like Radiologists?

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

Project Description

Diagnosing liver lesions using multiparametric MRI requires detecting complex, often subtle features - such as washout, fat content, capsular enhancement, and iron deposition - However, these features can be subtle and challenging to detect, often requiring the expertise of experienced radiologists, which limits the scalability of supervised AI approaches.

With the rise of vision-language models (VLMs) like GPT-4V and DeepSeek-VL, a key question is whether such models can reliably identify and describe these features across diverse MRI sequences. This project explores the diagnostic potential of VLMs as assistive tools, with a particular focus on benchmarking their ability to "see" and reason over relevant imaging features in comparison to expert radiologist interpretations and pathology-confirmed diagnoses.



The primary goal is to systematically evaluate how well these models extract and describe clinically meaningful features from annotated MRI data, and to what extent their predictions aligns with real-world diagnostic outcomes. Depending on results and interest, the project may also explore fine-tuning existing models to improve domain-specific performance, or - if performance proves reliable - developing a lightweight graphical interface to make these models more accessible and interpretable in a clinical context. This research is part of the Liver Artificial Intelligene - Consortium, a collaborative initiative focused on advancing AI models in liver imaging, bringing together interdisciplinary expertise to unlock new diagnostic possibilities.

Interested in this project?

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Exploring the genetic basis of hand-facial morphology associations

Research Line: Computational Population Biology
Project type: Master Project
Approx. duration: 6 to 9 months

Research question:
To explore the association between hand skeleton (e.g., length of the finger) and facial morphology (e.g., width of the nose), and link it with genetics

Data sets:
Sevearl thousands hand skeleton X-ray images (at 9 and 13 years), 3D facial mesh images (at 9 and 13 years) and whole-genome SNP-based genotype data for each subject, from the Generation R Study. Sevearl thousands hand skeleton X-ray images (age > 50), 3D facial mesh images (age > 50) and whole-genome SNP-based genotype data for each subject, from the Rotterdam Study.

Datailed Tasks:
1. Develop a pipeline to automatically derive measurements (e.g, length of the finger) from x-ray hand skeleton image
2. Derive measurements from the facial mesh image. This part was done already.
3. Perform analysis to calculate the connection between hand measurements and facial measurements.
4. Explain the identified connections with genetics

Requirements:
Preferred background in statistics, genetics, epidemiology, computer science, biomedical engineering. Experience with machine/deep learning and image processing is a plus.

References:
1. Genome-wide association study identifies nine novel loci for 2D:4D finger ratio, a putative retrospective biomarker of testosterone exposure in utero. *Hum Mol Genet.* 2018
2. Novel genetic loci affecting facial shape variation in humans. *elife. 2019*
3. Automatic measuring of finger joint space width on hand radiograph using deep learning and conventional computer vision methods. *Biomedical Signal Processing and Control. 2023*

Interested in joining our research group?

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Analysis of photoreceptor density in patients using an automatic segmentation tool

Research Line: Eye Image Analysis Group Rotterdam
Project type: Bachelor or Master Project
Approx. duration: 3 to 6 months

Project description

Adaptive Optics (AO) is a technique that enables super-resolution imaging by correcting aberrations in the light pathway during acquisition. In ophthalmology, it can be used to visualize retinal structures, such as photoreceptors and capillary vessels, on a microscopic level. On a previous project, we developed in-house software for the location and analysis of cones (photoreceptors in charge of color vision) in images acquired with the rtx1 AO retinal camera (Figure 1). This software has been validated in healthy subjects, but we would like to extend its applicability further, to patients that show healthy-looking cell mosaics (e.g., initial stages of a disease or unaffected regions). In the context of the AO-Vision project, we have acquired a dataset of >150 patients of different inherited retinal dystrophies (IRDs), a family of diseases that damage the cells.

The goal of this project is to select the images that are measurable from the IRD patient set (the regions that have sufficient quality and have not been severely damaged by the disease), analyze them using the automatic analysis tool, review and correct the model output if needed, and refine the algorithm so that it can be applied to track the subtle changes due to disease progression.

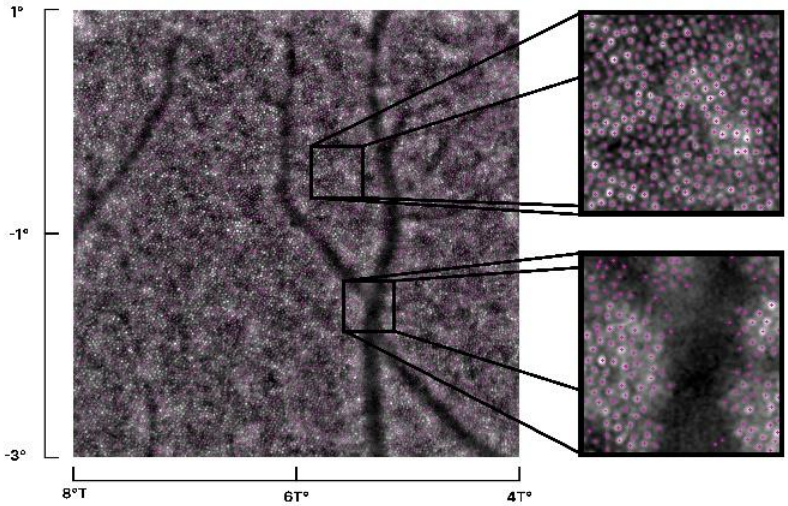

Figure 1. Example of automatic cone detection in an AO image.

Interested in this project?

Supervisor(s): Danilo Andrade de Jesus, Luisa Sánchez Brea
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Automatic segmentation and analysis of vasculature in optical coherence tomography angiography of the retina

Research Line: Eye Image Analysis Group Rotterdam
Project type: Master Project
Approx. duration: 4 to 9 months

Project description
Optical coherence tomography angiography (OCTA) is an imaging modality computed from the differences of several optical coherence tomography (OCT) scans taken at the exact same location. These differences are mainly due to the blood flowing through the vessels and, hence, OCTA depicts in great detail the vasculature, as long as there is blood flowing through it. In ophthalmology, OCTA has been used to assess and monitor different diseases with known vascular components, such as diabetes and glaucoma. However, OCTA images have a series of associated challenges, namely they are very difficult to interpret visually and prone to acquisition artifacts. Furthermore, the few objective parameters that are used in clinics are provided by the device manufacturers through closed and private software, which makes these markers obscure and not widely applicable through different datasets. Thus, there is a need for objective and open quantification tools.

The goal of this project is to segment the vasculature in OCTA images of the retina, and to compute features relevant to monitor disease progression in different use cases. There is a variety of both public and in-house datasets available for this project, which is a collaboration with the Faculty of Medicine of Porto University.

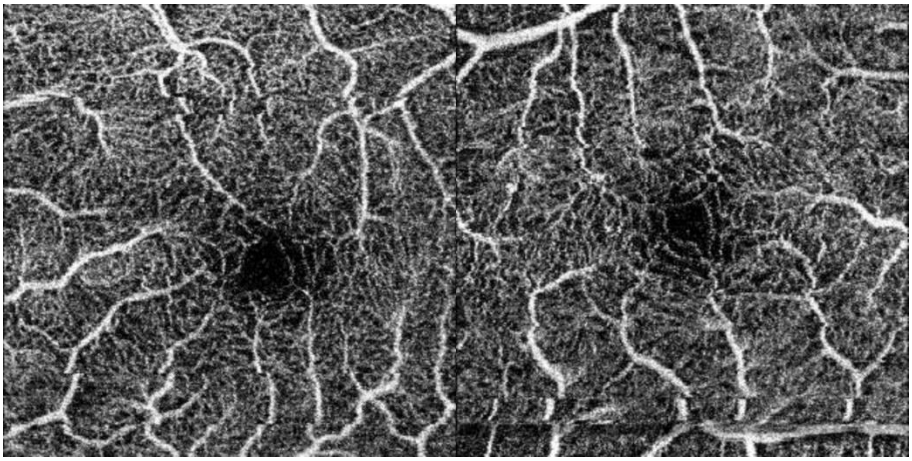

Figure 1. OCTA images (superficial vascular plexus slab) of representative quality, including some motion artifacts – observable where the vessels are not “continuous”, such as in the bottom half of the images.

Interested in this project?

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Fovea localization in high-resolution retinal images

Research Line: Eye Image Analysis Group Rotterdam
Project type: Master Project
Approx. duration: 4 to 9 months

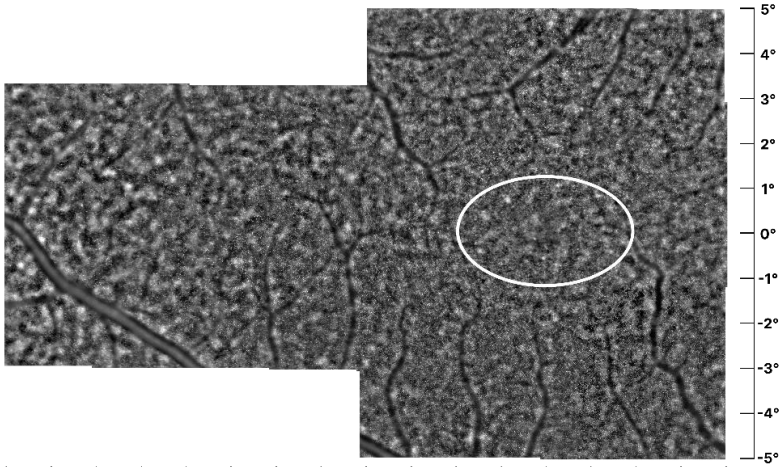
Project description

Adaptive Optics (AO) is a technique that enables super-resolution imaging by correcting optical aberrations during image acquisition. In ophthalmology, AO allows for the visualization of retinal structures—such as photoreceptors and capillary vessels—at a microscopic level.

The human retina has the highest concentration of cone photoreceptors in the fovea, the central region of the retina. The imaging device used in this project, the rtx1 AO retinal camera, captures images with a resolution of 1500 × 1500 pixels, covering approximately 1.2 mm × 1.2 mm in real-world dimensions. However, due to the extremely high density and small size of cones in a healthy fovea, this resolution is insufficient to resolve individual cells in this region. As a result, applying automatic measurement tools across the entire image yields artificially low cone density values in the fovea.

To address this, we aim to exclude the central foveal region from quantitative analyses. The acquisition device currently provides an initial estimate of the fovea center, which tends to be accurate in healthy individuals but less reliable in patients—particularly those with poor fixation.

The goal of this project is to develop and validate an algorithm that automatically detects the fovea center and delineates the surrounding region where individual cells cannot be distinguished (marked by the white circle in Figure 1).



Interested in this project?

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Email: d.andradedejesus@erasmusmc.nl , m.sanchezbrea@erasmusmc.nl

Augmented Reality guided surgery

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

Project description
The Microsoft HoloLens is a head mounted display (HMD) device that 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, without the need to switch attention between the patient and a 2D display, as is the case for conventional navigation systems.

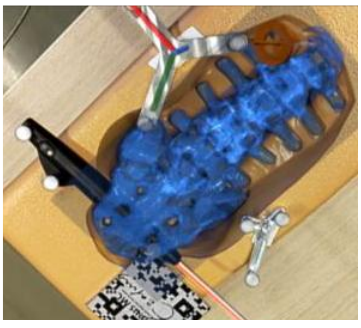
The HoloLens is equipped with a number of sensors and cameras, making it suitable for stand-alone navigation. It can track reference markers in the operative field that allows for tracking the patient and surgical instruments. The virtual overlay can be registered with the patient with multiple approaches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

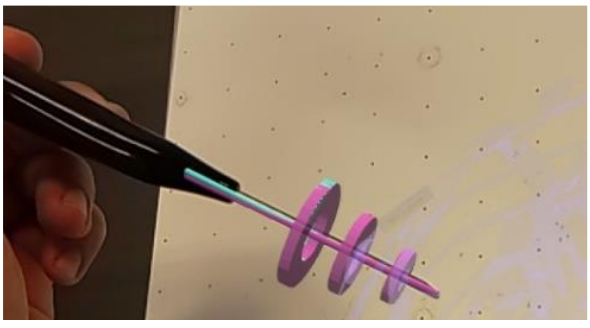
In our group, we investigate the different tracking and registration approaches for aligning the preoperative data with the patient. Furthermore, we also look at how to optimally visualize the virtual models and navigation data for optimum perception.

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
- Dynamic visualization of virtual extension in needle insertion
- Feasibility of AR navigation in Zygomatic implant





Interested in this project?

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Deep Learning in Acute Ischemic Stroke

Research Line: Image guidance in interventions and therapy
Project type: Master Project
Approx. duration: 6 to 9 months

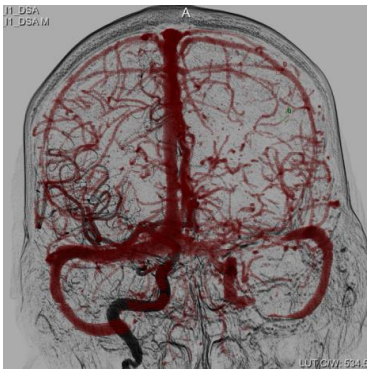
Project description
Acute ischemic stroke (AIS) is one of the leading causes of death and disability in the Western world. In this disease, a thrombus is blocking one of the intracranial arteries, depriving the distal brain tissue of oxygen and essential nutrients.

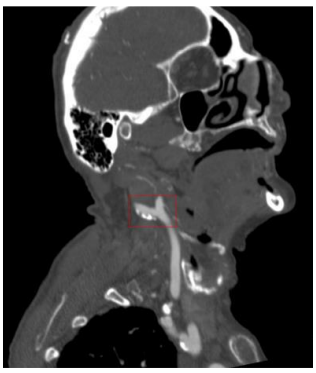
In recent years, mechanical thrombectomy has shown great promise as a novel treatment for AIS. In this procedure, a guidewire-catheter system is advanced through the arteries from the groin to the brain. Using the guiding catheter, a stent-retriever is positioned inside the thrombus. The stent retriever is pulled back, hopefully taking the thrombus with it. The entire procedure is performed under fluoroscopic guidance ("real-time X-ray imaging").

Along the entire stroke care pathway, myriad patient data are generated, but they are relatively unused. At the IGIT group and the ICAI Stroke Lab, we want to unlock the potential of the collected stroke data, harnessing the power of AI. This MSc thesis will contribute to this overarching goal by improving the automated analysis of stroke imaging.

The project has a flexible definition, and we have multiple suitable ideas. One interesting direction is the detection of vessel occlusions on fluoroscopy imaging using Deep Learning. Another idea is automated roadmapping using the preprocedural images to facilitate catheter guidance. Please feel free to contact me to discuss potential projects!

This project is a collaboration between IGIT and the ICAI Stroke Lab, and the prospective student will be embedded in both groups.





Interested in this project?

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Automated lesion detection in PET/MR imaging of lymph nodes

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

Background: Head and neck cancers can metastasize to locoregional lymph nodes. The presence of lymph node metastases significantly impacts prognosis and treatment options. To stage the disease, patients undergo a PET-scan with the racioactive tracer 18F-FDG combined with diagnostic CT or MRI. While PET-scans have a high negative predictive value, there are many false positives for cervical lymph nodes. Uptake of 18F-FDG is not only present in the primary tumor and lymph node metastases, but also in reactive lymph nodes, which can be numerous in the head-and-neck area, especially in winter when many patients have a cold. Accutely identifying metastastic lymph nodes is crucial. When a lymph node is PET-positive, patients will undergo additional ultrasound examinations with fine-needle aspiration, after which a pathologist examines the punctate. Not only is this an extra burden for the patient, but it also increases costs and delays the start of treatment. Our objective is to improve accuracy for lymph node metastases detection on PET-MRI, reducing the need for invasive additional procedures. To achieve this, we will use a large existing PET-MRI dataset to build an automated pipeline to aid the identification of lymph nodes. The project allows a wide range of methods to be pursued, like algorithmic and deep learning based methods.

Aim: The specific aims of this project are 1.) to build and train algorithmic and/or deep learning models (e.g. convolutional neural networks for identification of inflammation related lesions on PET/MRI scans and 2.) to evaluate the performance of the networks with real patient scans. Beyond the specific application and project, our goal is to establish a modular, well documented and transferable pipeline for later synthetic medical imaging projects. The project will build on our previous efforts and results developed for a different anatomy and pathology.

Methods: This project will use data from healthy PET/MRI scans collected from our patient database and PET/MRI scans from patients participating in our pain project. The algorithmic track will follow the human (expert reader) workflow, automate and improve its accuracy. The deap learning track will use training data from real and synthetic images. The model will be evaluated on the patient dataset.

References:

[1] Guedj D et al. FDG PET-CT for the Detection of Occult Nodal Metastases in Head and Neck Cancer: A Systematic Review and Meta-Analysis. Cancers. 2024. [2] Hoang JK et al. Evaluation of Cervical Lymph Nodes in Head and Neck Cancer with CT and MRI: Tips, Traps, and a Systematic Approach. Am J Roentgenol. 2013. [3] Sobek, J. MedYOLO: A Medical Image Object Detection Framework. arXiv preprint arXiv:2312.07729, 2023. [4] Isensee et al. nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation. Nature methods, 2021. [5] Ma et al. Segment anything in medical images. Nat Comm. 2024.


Interested in this project?

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AI-based assessment of hip disorders

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

Background: Hip dysplasia is diagnosed based on symptoms, physical examination, and 2D plain radiographs. One significant limitation of 2D imaging is that it is a summation of a 3D structure. Therefore, it can only provide limited information about the 3D anatomy of the hip joint and some important details may be missed. 3D measurements extracted from MRI and CT may provide more detailed information about the severity of the hip disorders. Imaging biomarkers from MRI and CT may therefore enhance our understanding of the biomechanics and pathophysiology of hip dysplasia. 3D imaging data have potential to improve the accuracy of dysplasia grading, monitor disease progression, and evaluate the effectiveness of treatments. Furthermore, 3D imaging facilitates personalized treatment planning, which can lead to better clinical outcomes and potentially reduce the long-term burden of hip-related disorders.

Aim: The aim of this project is to extract 3D hip morphology measures from MRI scans from clinical patient populations to assess the relationship of the measures to symptoms and severity of the hip dysplasia. Another aim is to translate the measurement pipeline to CT scans. Agreement between MRI and CT based measures will be assessed.

Methods: We will analyze clinical patient cohorts available at the Department of Orthopedics of Erasmus MC. The cohorts include patients undergoing to peri-acetabular osteotomy (pre-operative MRI and CT available allowing comparison of the measurements between modalities), and patients with slipped capital femoral epiphysis and with neuromuscular hip migration. To extract the 3D measurements from CT scans, a deep learning (nnU-Net or foundation models) method for automated segmentation of femur and acetabulum bones will be developed. For MRI, the generalizability of the current nnU-Net model will be explored.

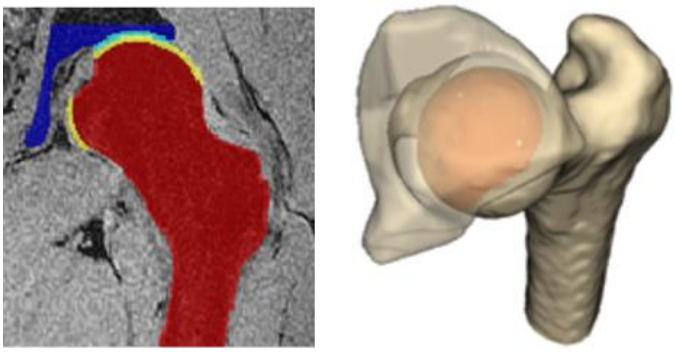

Figure 1. Automatically segmented hip MRI and 3D visualization of the femur coverage (unpublished work).

Interested in this project?

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Quantitative and artefact-free PET/MR imaging in heterogeneous anatomies and near-metal

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

Background: Quantitative PET/MRI faces several difficulties in anatomical regions with heterogeneity of magnetic susceptibility. Heterogeneity of magnetic susceptibility causes imaging artefacts in MRI. The attenuation correction in PET image reconstructions relies on MRI, hence these artefacts hinder quantitative PET imaging. Such inhomogeneity occurs naturally in the thorax (lung), head and neck (air cavities), abdominal, and pelvic regions. The situation is further aggravated in presence of metal implants. Segmentation and model-based attenuation correction methods have been proposed in the past. These promise accurate accounting for all tissue types and implants. The advancement and availability of deep learning (DL) methods give a new momentum to these methods and promise improvements of attenuation correction maps and the accuracy the estimation of tracer uptake. In our recent efforts we implemented DL-based segmentation methods for producing attenuation correction maps in the pelvic region. There are several methods becoming available (TotalSegmentator, Segment Anything, Nvidia MAISI) in a rapid pace which can be integrated in our current workflow or allow to a redesign for higher accuracy.

Aim: The current project aims for further improving the accuracy of attenuation correction maps with the utilization of DL methods from reduced information space (segmentation space or latent space representation instead of imaging space). Furthermore, the possibility to produce metal-artefact-free MR images based on information gained from PET images will be explored. This could present a breakthrough in the age-old problem of metal-artefacts in MRI. The mutual benefit of simultaneous PET and MR imaging presents a unique opportunity.

Methods: This project will use data from several sources: PET/MRI scans collected from our patient databases, from our partner institute UW Madison, and open access imaging databases. A model will be built to fully exploit the availability of simultaneously acquired PET and MR images. Various DL architectures will be trained and validated on PET/MRI scans. There is a set of underlying applied mathematics problems: reduced representation of images, shared information in images acquired by different physical measurements, separation of features, e.g., intensity and shape.

References:

[1] Renisch et al., Validation of model-based pelvis bone segmentation from MR images for PET/MR attenuation correction. Proceedings of SPIE 2012. [2] Wallstén et al., Improved PET/MRI attenuation correction in the pelvic region using a statistical decomposition method on T2-weighted images. EJNMMI Phys. 2020. [3] Krokos et al. A review of PET attenuation correction methods for PET-MR. EJNMMI Phys 2023. [4] Hasan et al., Evaluation of Deep Learning–Based Approaches to Segment Bowel Air Pockets and Generate Pelvic Attenuation Maps from CAIPIRINHA-Accelerated Dixon MR Images, Journal of Nuclear Medicine 2022. [5] Ma et al. Segment anything in medical images. Nat Comm. 2024. [6] Nvidia MAISI: https://catalog.ngc.nvidia.com/orgs/nvidia/teams/monaitoolkit/models/monai_maisi_ct_generative

Interested in this project?

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Automatic Segmentation Quality Check for Correct Biomarker Extraction

Research Line: Musculoskeletal Image Analysis
Project type: Bachelor or Master Project
Approx. duration: 1 to 3 months

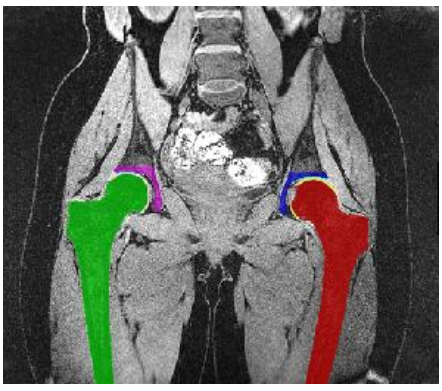
Project description

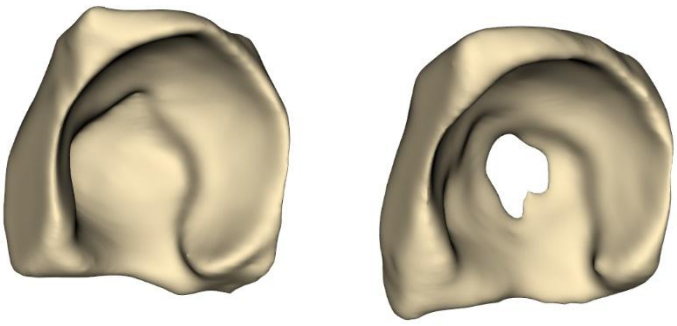
Hip disorders, particularly hip osteoarthritis (OA), are a growing global health concern, characterized by reduced quality of life and significant healthcare costs. Hip dysplasia is the strongest risk factor for developing hip OA. Accurate assessment of hip morphology is critical for early detection and intervention, yet current 2D imaging methods fail to capture the complex 3D structure of the hip. Recent advancements have facilitated the derivation of 3D biomarkers from MRI segmentations, but deficiencies in segmentation, such as errors in the acetabular cup, impact the reliability of these derived biomarkers.

Project Objective
The goal of this internship is to develop a method that can automatically detect (and correct) deficiencies in 3D hip segmentations, for accurate biomarker extraction. Machine learning for classification could be used as a framework for automated quality assessment of segmentation results.

Scope of Work

- Analyze common segmentation deficiencies in an existing dataset, with a focus on acetabular cup defects.
- Design and implement an algorithm for automated detection of deficiencies.
- Develop and validate a correction method to refine segmentation results.
- Evaluate the impact of the refined segmentation on extracted biomarkers.





Interested in this project?

Supervisor(s): Mirthe Kamphuis, Jukka Hirvasniemi
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Synthetic population for automated lesion detection in PET/MR imaging

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

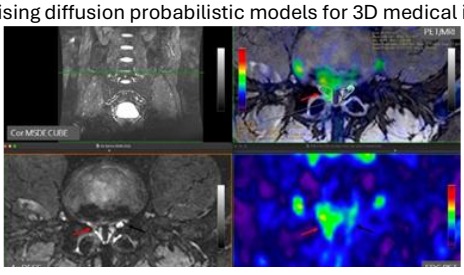
Background: The diagnosis of chronic painful conditions with unknown causes is a challenging task. Functional imaging techniques may help identify pain generators by providing functional information in addition to anatomical information. Metabolic activity can be identified with Positron Emission Tomography (PET) and the tracer 18F-FDG to detect and quantify inflammation. A prospective research project is being conducted currently at Erasmus MC - one of the first studies in the world - with the application of 18F-FDG PET/MRI in patients with chronic pain. This project aims to build an artificial intelligence (AI)-based application to aid the identification of inflammation-related lesions on 18F-FDG PET/MR images. Application of Deep Learning methods in nuclear medicine imaging is hindered by the scaricity of imaging data – in comparison with other radiological imaging fields. Beyond the general obstacles (privacy and consent to use personal data for research), nuclear medicine suffers from the disadvantage of using ionizing radiation. Our previous efforts delivered promising initial results in using synthetic data. Our goal is to extend our methods in size and quality of synthetic data and also investigate transferability to other anatomies and pathologies.

Aim: The specific aims of this project are 1.) create synthetic population serving as training data set; 2.) to build and train deep learning models (e.g. convolutional neural networks) for identification of inflammation related lesions on PET/MRI scans and 3.) to evaluate the performance of the networks with real patient scans. Beyond the specific application and project, our goal is to establish a modular, well documented and transferable pipeline for later synthetic medical imaging projects.

Methods: This project will use data from several sources: PET/MRI scans collected from our patient database and PET/MRI scans from patients participating in our pain project, similar scans from our partner institute University of Wisconsin in Madison and also open access imaging databases from diverse imaging modalities. Different methods (PCA, registration, diffusion models) to generate synthetic data will be tested. A model will be built and trained with synthetic dataset and evaluated on the patient dataset. Various deep learning architectures will be trained and validated on PET/MRI scans.

References:

[1] Isensee et al. nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation. Nature methods, 2021. [2] Khader et al. Denoising diffusion probabilistic models for 3D medical image generation. Sci Rep 2023.



Interested in this project?

Supervisor(s): Jukka Hirvasniemi, Gyula Kotek, Rianne van der Heijden, Edwin Oei
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Etiological Dementia Diagnosis with Disease Progression and Subtype Modeling

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

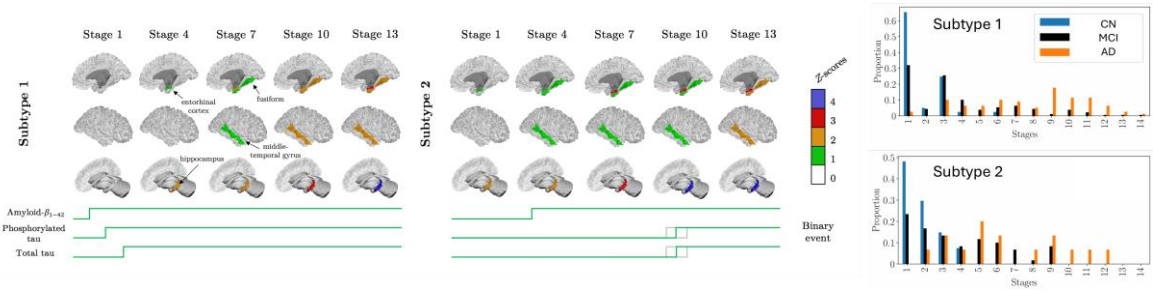
Project description

Dementia affects over 55 million people worldwide and is a leading cause of disability in the elderly. It is an umbrella term that covers wide a range of neurodegenerative disorders, including Alzheimer's disease (AD), frontotemporal dementia (FTD), Lewy body dementia (LBD), and vascular dementia. During the diagnostic process, MRI scans are commonly used to assess atrophy patterns, vascular pathology, and to exclude other causes of cognitive decline. However, reaching an etiological diagnosis can be difficult due to disease heterogeneity and the presence of mixed pathology.

This project aims to improve our understanding of imaging patterns across different memory clinic populations, representing a diverse population of dementia subtypes. To achieve this, we propose to implement Subtype and Stage Inference (SuStaIn) [1], an unsupervised method that models disease progression and identifies distinct subtypes from cross-sectional biomarker data. It simultaneously accounts for temporal heterogeneity (i.e., differences in disease stage) as well as phenotypic heterogeneity (i.e., distinct subtypes with characteristic progression patterns). SuStaIn has successfully been applied to various domains, including the AD-population. An example of our project is shown in Fig 1.

The objective is to apply SuStaIn to biomarker data from multiple memory clinic cohorts—specifically ACE (n=383) and OASIS-4 (n=357), with the possibility of including additional datasets—and to interpret the resulting subtypes and progression patterns by evaluating associated demographics, etiological diagnoses, and cognitive performance.

We are looking for a master student with proficient Python skills and an interest in unsupervised machine learning and neurodegenerative disorders.



[1] Young, Alexandra L., et al. "Uncovering the heterogeneity and temporal complexity of neurodegenerative diseases with Subtype and Stage Inference." Nature communications 9.1 (2018): 4273.

Interested in this project?

Supervisor(s): Sterre de Jonge, Myrthe van Haaften, Eline Vinke, Esther Bron
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Harmonizing Imaging Data in the Rotterdam Scan Study Before and After Scanner Update

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

Background. The Rotterdam Study, established in 1989, is a population-based cohort located in the neighborhood Ommoord in Rotterdam. This study is designed 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 (T1, FLAIR, PD, DWI) in over 6,000 participants with up to 4 scans per participant (over 18,000 scans in total). This has produced a rich dataset for studying neurodegenerative disorders.

Problem statement. In 2020, the MRI scanner underwent a hardware update, including a replacement of the receiver coil. This modification 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. To enable longitudinal analysis, it is essential to ensure that the derived imaging biomarkers are robust and not influenced by scanner-related changes.

Proposed solution. Several harmonization strategies exist to address scanner-related variability in imaging data. A common feature-based method is ComBat [1]. Harmonization based on the raw images can be achieved by (generative) deep learning approaches [2].

Objectives

- Implement a feature-based harmonization technique
- Optional: Explore an image-based approach and compare with feature-based technique
- Evaluate harmonization using matched data acquired before and after the scanner update and using small replication samples (individuals scanned in close succession)
- Apply the harmonized data to answer a clinically relevant research question focused on longitudinal evaluation in 6,000 participants from the Rotterdam Study

Who are we looking for? A student with an interest in neuroimage analysis and epidemiology. Preferably with course in imaging processing, e.g., Biomedical Engineering track Medical Physics or Technical Medicine track Imaging & Intervention. A clinical program can be set up.

References

[1] Beer, Joanne C., et al. "Longitudinal ComBat: A method for harmonizing longitudinal multi-scanner imaging data." *Neuroimage* 220 (2020): 117129.
[2] Hu, Fengling, et al. "Image harmonization: A review of statistical and deep learning methods for removing batch effects and evaluation metrics for effective harmonization." *NeuroImage* 274 (2023): 120125.

Interested in this project?

Supervisor(s): Sterre de Jonge, Julia Neitzel, Esther Bron, Eline Vinke
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Synthetic MRI Generation for Non-Alzheimer's Dementias Using Generative AI

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

Background and Motivation:

Dementia affects over 55 million people worldwide and is a leading cause of disability in the elderly. Among its subtypes, Alzheimer's Disease (AD) is the most common, but several other forms, such as frontotemporal dementia (FTD), Lewy body dementia (LBD), and vascular dementia, also contribute significantly to the burden. Differentiating between these types is clinically challenging, especially based on imaging, due to overlapping patterns of brain atrophy and variability across patients. Artificial intelligence (AI) has shown promise in aiding dementia diagnosis through analysis of brain MRIs. However, most existing AI models are trained predominantly on AD datasets, which are relatively abundant. In contrast, data for non-AD dementias is scarce, limiting model performance and generalizability.

Problem Statement:

There is a critical need for large, diverse datasets representing non-AD dementias to train robust diagnostic AI models. Traditional data augmentation methods are insufficient to address this gap.

Proposed Solution:

Generative AI, particularly diffusion models, offers a novel avenue for synthesizing realistic medical images. These models have recently achieved state-of-the-art results in generating high-fidelity images in various domains, including medical imaging. This project proposes to explore the use of diffusion models to generate synthetic brain MRIs representing non-AD dementias, with the aim of augmenting existing datasets. Beyond data augmentation, the project will also explore how generative models themselves might support diagnostic tasks.

Objectives:

- Train and evaluate diffusion-based generative models on limited datasets of non-AD dementia MRIs.
- Assess the realism, diversity, and clinical relevance of the synthesized images.
- Investigate the impact of synthetic data on the diagnostic performance of AI models.
- Explore the use of generative models in direct diagnostic applications, such as generating class-representative images or detecting deviations from normative patterns.

Interested in this project?

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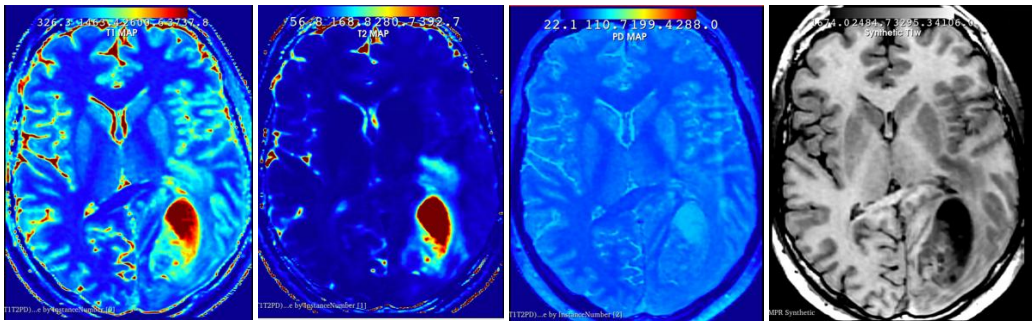
Toward Gadolinium-Free MRI: Synthesis of Contrast-Enhanced Images for Glioma

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



BACKGROUND

Gliomas are the most common type of primary brain tumors in adults. Standard assessment with magnetic resonance imaging (MRI) includes T1-weighted images before and after the injection of gadolinium-based contrast agents (GBCAs). The contrast agent has the ability to reveal impairment in the blood-brain-barrier (BBB), associated with aggressive tumor behavior. This procedure has two downsides:

1) While GBCAs are generally deemed safe, up to 2.4% of patients suffer from adverse reactions and a lower rate from severe complications.
2) Usage of weighted images as opposed to quantitative diagnostic methods.

Multiparametric maps, specifically, longitudinal relaxation time (T1), transversal relaxation time (T2), and proton density (PD), represent intrinsic tissue properties and preliminary evidence indicate that they are modified when there is BBB damage; even without using GBCAs. However, currently maps are not commonly acquired.

OBJECTIVES

As a first part of this project, the student will investigate an AI method able to predict multiparametric maps from conventional weighted images. While these images are not acquired for quantification of tissue properties their contrasts are due to them. For this we have in-house images as well as public data of patients diagnosed with glioblastoma.

Secondly, the aim is to synthesize contrast enhanced scans from the mutliparametric maps. Thorough statistical analysis and interpretation of predicted and acquired contrast enhanced images will provide more information on brain tumors and BBB breakdown, and their relation to the pre-contrast administration tissue properties T1 and T2.
If successful this may lead to reduced contrast agent use, reducing costs while benefiting patients and environment.

Interested in this project?

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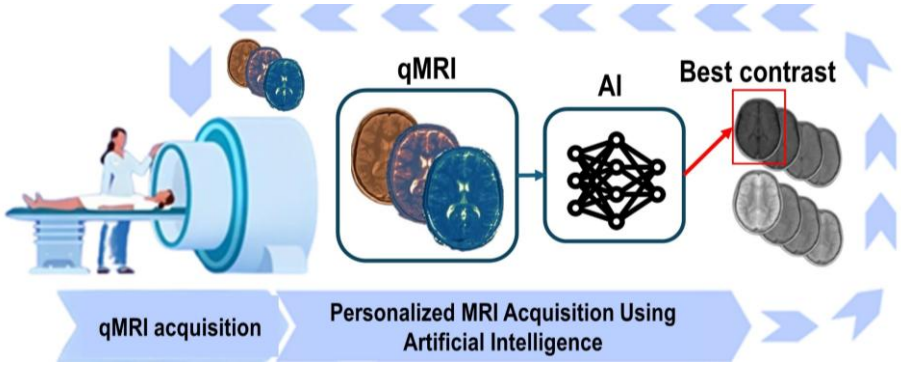
Towards AI-driven Online MRI Sequence Optimization for Precision Medicine

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

Background: Magnetic Resonance Imaging (MRI) is essential in diagnostic radiology, providing detailed, non-invasive views of tissue structure. However, conventional MRI protocols are typically standardized and not tailored to individual patients. With the increasing availability of quantitative MRI (qMRI), with voxel-wise maps of intrinsic tissue parameters (e.g. T1, T2, PD), it is now possible to move toward patient-specific imaging. These tissue parameters enable synthesis of contrast-weighted images, opening the door to adaptive, personalized AI-driven MRI protocols that are optimized in real time.

Aim and Impact: The aim is to develop an AI-based algorithm that uses qMRI of a patient to synthesize diagnostic-quality contrast images and/or recommend personalized acquisition settings for subsequent scans. This approach seeks to enhance diagnostic precision, reduce scan time, and enable efficient, patient-specific imaging without redundant acquisitions.



Project strategy: The project will begin with a literature review covering MR physics, quantitative MRI (qMRI) principles, and existing approaches to sequence optimization. A neural network model will then be developed to explore the contrast space and identify acquisition settings that best fulfill diagnostic objectives. Implementation will be carried out in Python using libraries such as PyTorch. To ensure clinical relevance and reliability, the method will be validated with expert input.

Project designed for: a motivated master student interested in MR physics, medical image analysis, and AI seeking a 6-9 month master's thesis starting Aug/Sept 2025. Experience with Python and some familiarity with deep learning (preferably PyTorch) is expected.

Interested in this project?

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