Fetal Brain Tissue Annotation and Segmentation Challenge: Structured description of the challenge design

CHALLENGE ORGANIZATION

Title

Use the title to convey the essential information on the challenge mission.

Fetal Brain Tissue Annotation and Segmentation Challenge

Challenge acronym

Preferable, provide a short acronym of the challenge (if any).

FeTA

Challenge abstract

Provide a summary of the challenge purpose. This should include a general introduction in the topic from both a biomedical as well as from a technical point of view and clearly state the envisioned technical and/or biomedical impact of the challenge.

Congenital disorders are one of the leading causes of infant mortality worldwide [1]. Recently, in-utero MRI of the fetal brain has started to emerge as a valuable tool for investigating the neurological development of fetuses with congenital disorders in order to aid in prenatal planning. Moreover, fetal MRI is a powerful tool to portray the complex neurodevelopmental events during human gestation, which remain to be completely characterized. Automated segmentation and quantification of the highly complex and rapidly changing brain morphology prior to birth in MRI data would improve the diagnostic process, as manual segmentation is both time consuming and subject to human error and inter-rater variability. It is clinically relevant to analyse information such as the shape or volume of the developing brain structures, as many congenital disorders cause subtle changes to these tissue compartments [2]–[5]. Existing growth data is mainly based on normally developing brains [6]–[8], and growth data for many pathologies and congenital disorders is lacking. The automatic segmentation of the developing human brain would be a first step in performing such an analysis.

From a technical standpoint, there are many challenges that an automatic segmentation method of the fetal brain would need to overcome. The physiology and structures of the human brain are constantly growing and developing throughout gestation. In addition, the quality of the images can be poor due to fetal and maternal movement and imaging artefacts [9]. The boundary between tissues is often unclear due to partial volume effects. Furthermore, structures in a pathological fetal brain can have a different morphology than those in a non-pathological brain. This can make it challenging for an automatic method to recognize what the structures are. The field of fetal MRI has so far been understudied due to challenges in imaging and due to the lack of public, curated, and annotated ground truth data.

The FeTA challenge is an important step in the development of reliable, valid, and reproducible methods of analyzing high resolution reconstructed MR images of the developing fetal brain from gestational week 21-33. Such new algorithms will have the potential to better understand the underlying causes of congenital disorders and ultimately to guide the development of antenatal/postnatal guidelines and clinical risk stratification tools for

early interventions, treatments, and care management decisions.

Challenge keywords

List the primary keywords that characterize the challenge.

Segmentation, Fetal Brain MRI, Multi-class, Congenital Disorders, Super-resolution reconstructions

Year

The challenge will take place in ...

2021

FURTHER INFORMATION FOR MICCAI ORGANIZERS

Workshop

If the challenge is part of a workshop, please indicate the workshop.

PerInatal, Preterm and Paediatric Image analysis workshop (PIPPI) - https://pippiworkshop.github.io/

Duration

How long does the challenge take?

Half day.

Expected number of participants

Please explain the basis of your estimate (e.g. numbers from previous challenges) and/or provide a list of potential participants and indicate if they have already confirmed their willingness to contribute.

We expect 15-30 submissions. Together with invited speakers and organizers, we expect a total number of 30-50 participants.

Publication and future plans

Please indicate if you plan to coordinate a publication of the challenge results.

We plan to coordinate a publication of the challenge results after the challenge, targeting publication at IEEE: TMI or NeuroImage. All teams who submitted before the deadline and presented their results at MICCAI 2021 will be included in the paper. Each team is allowed three co-authors in this paper.

Space and hardware requirements

Organizers of on-site challenges must provide a fair computing environment for all participants. For instance, algorithms should run on the same computing platform provided to all.

This challenge will be online, and only talks will be given on-site. We would need a seminar room with projector and screen, and a microphone on the day of the challenge.

TASK: Fetal Brain Tissue Segmentation

SUMMARY

Abstract

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Congenital disorders are one of the leading causes of infant mortality worldwide [1]. Recently, in-utero MRI of the fetal brain has started to emerge as a valuable tool for investigating the neurological development of fetuses with congenital disorders in order to aid in prenatal planning. Moreover, fetal MRI is a powerful tool to portray the complex neurodevelopmental events during human gestation, which remain to be completely characterized. Automated segmentation and quantification of the highly complex and rapidly changing brain morphology prior to birth in MRI data would improve the diagnostic process, as manual segmentation is both time consuming and subject to human error and inter-rater variability. It is clinically relevant to analyse information such as the shape or volume of the developing brain structures, as many congenital disorders cause subtle changes to these tissue compartments [2]–[5]. Existing growth data is mainly based on normally developing brains [6]–[8], and growth data for many pathologies and congenital disorders is lacking. The automatic segmentation of the developing human brain would be a first step in performing such an analysis.

From a technical standpoint, there are many challenges that an automatic segmentation method of the fetal brain would need to overcome. The physiology and structures of the human brain are constantly growing and developing throughout gestation. In addition, the quality of the images can be poor due to fetal and maternal movement and imaging artefacts [9]. The boundary between tissues is often unclear due to partial volume effects. Furthermore, structures in a pathological fetal brain can have a different morphology than those in a non-pathological brain. This can make it challenging for an automatic method to recognize what the structures are. The field of fetal MRI has so far been understudied due to challenges in imaging and due to the lack of public, curated, and annotated ground truth data.

The FeTA challenge is an important step in the development of reliable, valid, and reproducible methods of analyzing high resolution reconstructed MR images of the developing fetal brain from gestational week 21-33. Such new algorithms will have the potential to better understand the underlying causes of congenital disorders and ultimately to guide the development of antenatal/postnatal guidelines and clinical risk stratification tools for early interventions, treatments, and care management decisions.

Keywords

List the primary keywords that characterize the task.

Segmentation, Fetal Brain MRI, Multi-class, Congenital Disorders, Super-resolution reconstructions

ORGANIZATION

Organizers

a) Provide information on the organizing team (names and affiliations).

Kelly Payette (Center for MR Research, University Children's Hospital Zurich; Neuroscience Center Zurich, University of Zurich)
Priscille de Dumast (Department of Diagnostic and Interventional Radiology, Lausanne University Hospital and

University of Lausanne; Medical Image Laboratory Analysis, Centre d'Imagerie BioMédicale, University of Lausanne)
Andras Jakab (Center for MR Research, University Children's Hospital Zurich; Neuroscience Center Zurich, University of Zurich)
Meritxell Bach Cuadra (Department of Diagnostic and Interventional Radiology, Lausanne University Hospital and University of Lausanne; Medical Image Laboratory Analysis, Centre d'Imagerie BioMédicale, University of Lausanne)
Lana Vasung (Division of Newborn Medicine, Boston Children's Hospital, Harvard Medical School; Fetal-Neonatal Neuroimaging & Developmental Science Center)
Roxane Licandro (Computer Vision Lab, TUWien; Computational Imaging Research Lab, Medical University of Vienna)
Bjoern Menze, (Department of Quantitative Biomedicine, University of Zurich)
Hongwei Li (Department of Quantitative Biomedicine, University of Zurich)

b) Provide information on the primary contact person.

Kelly Payette (kelly.payette@kispi.uzh.ch)

Life cycle type

Define the intended submission cycle of the challenge. Include information on whether/how the challenge will be continued after the challenge has taken place.Not every challenge closes after the submission deadline (one-time event). Sometimes it is possible to submit results after the deadline (open call) or the challenge is repeated with some modifications (repeated event).

Examples:

- One-time event with fixed conference submission deadline
- Open call (challenge opens for new submissions after conference deadline)
- Repeated event with annual fixed conference submission deadline

Open call challenge.

Challenge venue and platform

a) Report the event (e.g. conference) that is associated with the challenge (if any).

MICCAI.

b) Report the platform (e.g. grand-challenge.org) used to run the challenge.

Grand-challenge.org

c) Provide the URL for the challenge website (if any).

Not available yet

Participation policies

a) Define the allowed user interaction of the algorithms assessed (e.g. only (semi-) automatic methods allowed).

Fully automatic.

b) Define the policy on the usage of training data. The data used to train algorithms may, for example, be restricted to the data provided by the challenge or to publicly available data including (open) pre-trained nets.

Publicly available data is allowed.

c) Define the participation policy for members of the organizers' institutes. For example, members of the organizers' institutes may participate in the challenge but are not eligible for awards.

May participate but not eligible for awards and not listed in leaderboard.

d) Define the award policy. In particular, provide details with respect to challenge prizes.

The top three ranking methods will be publicly named and awarded certificates and a small gift, such as chocolates.

e) Define the policy for result announcement.

Examples:

- Top 3 performing methods will be announced publicly.
- Participating teams can choose whether the performance results will be made public.

The results will be announced publicly at the MICCAI 2021 challenge session, and will be posted on the challenge website. The teams with the top 10 algorithms will be informed earlier so they can prepare a presentation for the challenge session. The top 3-5 teams will be asked to prepare a 7-10 minute presentation, and the remaining 5-7 teams will be asked to prepare a short ‘speed round’ presentation of 2 minutes.

f) Define the publication policy. In particular, provide details on ...

- ... who of the participating teams/the participating teams’ members qualifies as author
- ... whether the participating teams may publish their own results separately, and (if so)
- ... whether an embargo time is defined (so that challenge organizers can publish a challenge paper first).

Three authors per team who contributed to the design of the algorithm will be named co-author in the final challenge paper. Every participant can publish their algorithms and results independently after the challenge, but we request they cite the summary paper, and the data publication paper (currently under review). The results and our corresponding evaluation of all participating teams will be made publicly available on the challenge website after the conference session.

Submission method

a) Describe the method used for result submission. Preferably, provide a link to the submission instructions.

Examples:

- Docker container on the Synapse platform. Link to submission instructions: <URL>
- Algorithm output was sent to organizers via e-mail. Submission instructions were sent by e-mail.

Participants will create a Docker container with their algorithm, and provide this to the challenge organizers. Once the website is up, it will contain instructions on how to containerize the algorithms, and the organizers will provide support to the participants when requested. The organizers will run the Docker container on the test data set using publicly available evaluation code. The organizers will inform the participants if the Docker container fails to run, and allow the participants to provide a fix.

b) Provide information on the possibility for participating teams to evaluate their algorithms before submitting final results. For example, many challenges allow submission of multiple results, and only the last run is officially counted to compute challenge results.

No multiple submission will be allowed. The evaluation will be performed on the submitted Docker containers at the organizer's institute. Resubmissions are only allowed in cases of technical errors with the Docker.

Challenge schedule

Provide a timetable for the challenge. Preferably, this should include

- the release date(s) of the training cases (if any)
- the registration date/period
- the release date(s) of the test cases and validation cases (if any)
- the submission date(s)
- associated workshop days (if any)
- the release date(s) of the results

Training Data Release: April, 2021
Registration: Will be announced once the challenge is accepted
Docker Submission Deadline: 2 months before the challenge session
Top 10 teams informed: 2 weeks before the challenge, so they can prepare a presentation
Complete results will be announced at the challenge session

Ethics approval

Indicate whether ethics approval is necessary for the data. If yes, provide details on the ethics approval, preferably institutional review board, location, date and number of the ethics approval (if applicable). Add the URL or a reference to the document of the ethics approval (if available).

Mothers of the healthy fetuses participating in the BrainDNIU study were prospectively informed about the inclusion in the FeTA dataset by members of the research team and gave written consent for their participation. Mothers of all other fetuses included in the current work were scanned as part of their routine clinical care and gave informed written consent for the re-use of their data for research purposes. The ethical committee of the Canton of Zurich, Switzerland approved the prospective and retrospective studies that collected and analyzed the MRI data (Decision numbers: 2017-00885, 2016-01019, 2017-00167), and a waiver for an ethical approval was acquired for the release of an anonymous dataset for non-medical research purposes.

Data usage agreement

Clarify how the data can be used and distributed by the teams that participate in the challenge and by others during and after the challenge. This should include the explicit listing of the license applied.

Examples:

- CC BY (Attribution)
- CC BY-SA (Attribution-ShareAlike)
- CC BY-ND (Attribution-NoDerivs)
- CC BY-NC (Attribution-NonCommercial)
- CC BY-NC-SA (Attribution-NonCommercial-ShareAlike)
- CC BY-NC-ND (Attribution-NonCommercial-NoDerivs)

CC BY NC.

Code availability

a) Provide information on the accessibility of the organizers' evaluation software (e.g. code to produce rankings). Preferably, provide a link to the code and add information on the supported platforms.

Evaluation code will be available on the challenge website

b) In an analogous manner, provide information on the accessibility of the participating teams' code.

For participating teams who give permission, the Docker containers will be made publically available. We will encourage participating teams to make their code public.

Conflicts of interest

Provide information related to conflicts of interest. In particular provide information related to sponsoring/funding of the challenge. Also, state explicitly who had/will have access to the test case labels and when.

No sponsoring/funding is planned.
Only the organizers will have access to the test labels.

MISSION OF THE CHALLENGE

Field(s) of application

State the main field(s) of application that the participating algorithms target.

Examples:

- Diagnosis
- Education
- Intervention assistance
- Intervention follow-up
- Intervention planning
- Prognosis
- Research
- Screening
- Training
- Cross-phase

Decision support, Diagnosis, Research.

Task category(ies)

State the task category(ies).

Examples:

- Classification
- Detection
- Localization
- Modeling
- Prediction
- Reconstruction
- Registration
- Retrieval
- Segmentation
- Tracking

Segmentation.

Cohorts

We distinguish between the target cohort and the challenge cohort. For example, a challenge could be designed around the task of medical instrument tracking in robotic kidney surgery. While the challenge could be based on ex vivo data obtained from a laparoscopic training environment with porcine organs (challenge cohort), the final biomedical application (i.e. robotic kidney surgery) would be targeted on real patients with certain characteristics defined by inclusion criteria such as restrictions regarding sex or age (target cohort).

a) Describe the target cohort, i.e. the subjects/objects from whom/which the data would be acquired in the final biomedical application.

The target cohort would be pregnant mothers who, after a screening ultrasound, have been clinically referred a fetal MRI.

b) Describe the challenge cohort, i.e. the subject(s)/object(s) from whom/which the challenge data was acquired.

In the challenge, a clinically acquired dataset will be used representing the target cohort. Fetal MRI brain scans that were acquired clinically, and reconstructed using a super-resolution method.
There are two subgroups in the dataset:

1. Fetuses with normal neurodevelopment
2. Fetuses with pathological neurodevelopment

Imaging modality(ies)

Specify the imaging technique(s) applied in the challenge.

Magnetic Resonance Imaging: Several T2-weighted single shot Fast Spin Echo (ssFSE) images were acquired for each subject in all three planes (with at least one image in each of the axial, sagittal, coronal planes) with resolution 0.5mm x 0.5mm x 3mm, and were combined together to reconstruct into a single high resolution volume of 0.5mm x 0.5mm x 0.5mm using [10]–[12].

Context information

Provide additional information given along with the images. The information may correspond …

a) … directly to the image data (e.g. tumor volume).

Voxel-level segmentations of the fetal brain:
0 – Background
1 – External Cerebrospinal Fluid
2 – Grey Matter
3 – White Matter
4 – Ventricles
5 – Cerebellum
6 – Deep Grey Matter
7 – Brainstem

b) … to the patient in general (e.g. sex, medical history).

Gestational age (GA) in weeks
Pathological or Neurotypical brain

Target entity(ies)

a) Describe the data origin, i.e. the region(s)/part(s) of subject(s)/object(s) from whom/which the image data would be acquired in the final biomedical application (e.g. brain shown in computed tomography (CT) data, abdomen shown in laparoscopic video data, operating room shown in video data, thorax shown in fluoroscopy video). If necessary, differentiate between target and challenge cohort.

Fetal MRI Brain Scan.

b) Describe the algorithm target, i.e. the structure(s)/subject(s)/object(s)/component(s) that the participating algorithms have been designed to focus on (e.g. tumor in the brain, tip of a medical instrument, nurse in an operating theater, catheter in a fluoroscopy scan). If necessary, differentiate between target and challenge cohort.

Individual structures within the fetal brain (external cerebrospinal fluid, grey matter, white matter, ventricles, brain stem, cerebellum, deep grey matter)

Assessment aim(s)

Identify the property(ies) of the algorithms to be optimized to perform well in the challenge. If multiple properties are assessed, prioritize them (if appropriate). The properties should then be reflected in the metrics applied (see below, parameter metric(s)), and the priorities should be reflected in the ranking when combining multiple metrics that assess different properties.

- Example 1: Find highly accurate liver segmentation algorithm for CT images.
- Example 2: Find lung tumor detection algorithm with high sensitivity and specificity for mammography images.

Corresponding metrics are listed below (parameter metric(s)).

Precision, Accuracy.

DATA SETS

Data source(s)

a) Specify the device(s) used to acquire the challenge data. This includes details on the device(s) used to acquire the imaging data (e.g. manufacturer) as well as information on additional devices used for performance assessment (e.g. tracking system used in a surgical setting).

1.5T and 3T clinical GE whole-body scanner (Signa Discovery MR450 and MR750) were used to acquire the data, either using an 8-channel cardiac coil or body coil.

b) Describe relevant details on the imaging process/data acquisition for each acquisition device (e.g. image acquisition protocol(s)).

T2-weighted SSFSE sequences were acquired with an in-plane resolution of 0.5mmx0.5mm and a slice thickness of 3 to 5mm. The sequence parameters were the following: TR: 2000-3500 ms, TE: 120 ms (minimum), flip angle: 90°, sampling percentage 55%. Field of view (200-240 mm) and image matrix (1.5T: 256x224; 3T: 320x224) were adjusted depending on the gestational age (GA) and size of the fetus. Imaging plane was oriented relative to the fetal brain and axial, coronal and sagittal images were acquired.

c) Specify the center(s)/institute(s) in which the data was acquired and/or the data providing platform/source (e.g. previous challenge). If this information is not provided (e.g. for anonymization reasons), specify why.

The data was acquired at the University Children’s Hospital Zurich in Zurich, Switzerland.

d) Describe relevant characteristics (e.g. level of expertise) of the subjects (e.g. surgeon)/objects (e.g. robot) involved in the data acquisition process (if any).

Trained radiographers acquired the data using clinically defined protocols.

Training and test case characteristics

a) State what is meant by one case in this challenge. A case encompasses all data that is processed to produce one result that is compared to the corresponding reference result (i.e. the desired algorithm output).

Examples:

- Training and test cases both represent a CT image of a human brain. Training cases have a weak annotation (tumor present or not and tumor volume (if any)) while the test cases are annotated with the tumor contour (if any).
- A case refers to all information that is available for one particular patient in a specific study. This information always includes the image information as specified in data source(s) (see above) and may include context information (see above). Both training and test cases are annotated with survival (binary) 5 years after (first) image was taken.

Each case consists of a 3D super-resolution reconstruction of a fetal brain (256x256x256 voxels). Training cases have an annotated label map corresponding to 7 different brain tissue types. The label maps are not provided for the test cases. Each case will have a corresponding gestational age in weeks, as well as a label if it is a neurotypical fetal brain or a spina bifida fetal brain.
Test cases do not have the label map.

b) State the total number of training, validation and test cases.

Training/Validation cases: 70 3D volumes
Test cases: 30 3D volumes
Participants can choose to treat the images in 2D, in which case there are 70*256=17920 training/validation images, and 30*256=7680 test images

c) Explain why a total number of cases and the specific proportion of training, validation and test cases was chosen.

This is the number of volumes that has been manually annotated at this point. We aim to expand the dataset, potentially by the time the challenge is made public.
Existing studies have shown that case numbers such as what we are providing are sufficient to train U-Nets to segment the fetal brain from maternal tissue, as well as the fetal brain into different tissue classes [13], [14]. In addition, fetal MRI case numbers per hospital can be fairly small, making it a challenge for many hospitals to create such a uniform in-house single-center dataset. There are only a few of centers worldwide where fetal MRI case numbers are in the range of a few hundred per year. For comparison, in our hospital, 11.9 fetal MRI scans have been done per month over the past two years, while other university hospitals in Switzerland reported performing on average 2-3 fetal MRI scans, including neuro sequences per month. This renders the collection of data challenging and makes our data unique.
Our dataset is the first publicly released fetal brain dataset consisting of manually annotated volumes with multiple classes, making this a unique dataset.
Finally, the distribution of GAs and number of pathologic subjects is proportional between the test and training data

We are not providing an explicit validation set, it is up to each team to decide on their own based on the data given.

d) Mention further important characteristics of the training, validation and test cases (e.g. class distribution in classification tasks chosen according to real-world distribution vs. equal class distribution) and justify the choice.

In the training and test set, fetal brains with a variety of pathologies of varying severities will be included (such as spina bifida and ventriculomegaly), as well as fetal brains with normal neurodevelopment. There will be more pathological fetal brains included than normal, as in a clinical setting it is more common to see pathological brains. In addition, then main goal is the segmentation of fetal brains with congenital disorders for further analysis. In both of the training and test sets, a range of gestational ages (21-33 weeks) is included. The split/distribution of pathologies and gestational ages will be equal between the training and test sets. The fetal brain undergoes a large variety of changes throughout gestation such as brain volume increase, gyrification, neuronal migration, and synaptogenesis. As a result the tissue contrast, especially between the grey matter and white matter is changing throughout all gestation, adding more complexity to the segmentation. The tissues becomes either more distinguishable (such as between the deep grey matter and white matter) or less (such as between the white matter and grey matter) throughout gestation. Therefore we aim to include as equal case numbers as possible for each gestational week.

Annotation characteristics

a) Describe the method for determining the reference annotation, i.e. the desired algorithm output. Provide the information separately for the training, validation and test cases if necessary. Possible methods include manual image annotation, in silico ground truth generation and annotation by automatic methods.

If human annotation was involved, state the number of annotators.

Each label was created separately, with the annotator segmenting every second to every third slice for each label in the axial plane, except for the cerebellum and the brainstem/spinal cord, which were segmented in the sagittal plane. The final label map was created by post-processing these sparse annotations to create a single fully segmented fetal brain for each subject. For interpolating the sparsely annotated label maps, we used the Python implementation of the ITK nD Morphological Contour Interpolation algorithm, enforcing interpolation along the plane the given structure was annotated. After post-processing, each fetal brain was reviewed by an expert and small corrections were made either on the original annotations or the reconstructed full fetal brain annotation. See Section 23b) for more details.

b) Provide the instructions given to the annotators (if any) prior to the annotation. This may include description of a training phase with the software. Provide the information separately for the training, validation and test cases if necessary. Preferably, provide a link to the annotation protocol.

The annotation protocol can be found within the dataset in the documentation folder (FetalAnnotationGuideline.pdf):
http://neuroimaging.ch/sites/default/files/FetalAnnotationGuideline.pdf

c) Provide details on the subject(s)/algorithm(s) that annotated the cases (e.g. information on level of expertise such as number of years of professional experience, medically-trained or not). Provide the information separately for the training, validation and test cases if necessary.

Individuals with experience in segmenting medical images completed this task. The annotators were either radiographers with experience in MRI segmentation, or resident physicians with 5 to 10 years of experience in MRI.

d) Describe the method(s) used to merge multiple annotations for one case (if any). Provide the information separately for the training, validation and test cases if necessary.

N/A

Data pre-processing method(s)

Describe the method(s) used for pre-processing the raw training data before it is provided to the participating teams. Provide the information separately for the training, validation and test cases if necessary.

For each subject, we manually reviewed the acquired fetal brain images for quality in order to compile a stack of images. Each stack consisted of at least one brain scan in each orientation, with more scans included when available. The number of scans in each stack ranged between 3 and 13. Every image in the stack was then reoriented to a standard plane and a mask was created of the fetal brain using a semi-automated atlas-based custom MeVisLab (MeVis Medical Solutions AG, Bremen, Germany) module [10], [11]. An SR reconstruction algorithm was then applied to each subject's stack of images and brain masks, creating a 3D SR volume of brain morphology [10], [12], [15] with an isotropic resolution of 0.5mm*0.5mm*0.5mm. Each image was histogram-matched using Slicer [16], and zero-padded to be 256x256x256 voxels.

Sources of error

a) Describe the most relevant possible error sources related to the image annotation. If possible, estimate the magnitude (range) of these errors, using inter-and intra-annotator variability, for example. Provide the information separately for the training, validation and test cases, if necessary.

Sources of error in the image annotation depend mostly on the quality of the super-resolution reconstruction of the fetal brain. However, even the best quality reconstructions may contain annotator error. Errors can originate from:

- poor judgement of anatomical borders between certain developing brain structures, such as the cortical plate and subcortical white matter
- suboptimal image quality after reconstruction
- Annotations were made mainly in the axial plane, leading to some 'noisy' labels when looking at the coronal and sagittal planes

An investigation on the inter-rater variability was performed with 3 annotators annotating 9 volumes, with high and medium quality reconstructions having a Dice score of 0.84±0.09 between the three raters, and low quality reconstructions having a Dice score of 0.53±0.24 between raters, averaged across all labels.

b) In an analogous manner, describe and quantify other relevant sources of error.

None

ASSESSMENT METHODS

Metric(s)

a) Define the metric(s) to assess a property of an algorithm. These metrics should reflect the desired algorithm properties described in assessment aim(s) (see above). State which metric(s) were used to compute the ranking(s) (if any).

- Example 1: Dice Similarity Coefficient (DSC)
- Example 2: Area under curve (AUC)

The metrics used to compute the rankings will be the Dice Similarity Coefficient (DSC), The Volume Similarity (VS), and the 95th percentile Hausdorff coefficient (HD95), based on [17].
In addition, intracranial volume will be calculated, but not used in the rankings. Intracranial volume will be determined by adding all labels together.

b) Justify why the metric(s) was/were chosen, preferably with reference to the biomedical application.

As the task is a segmentation task, the DSC was chosen, as it is the most popular segmentation metric. However, we would like not just an overlap metric, but we are also interested in the shape and volume, therefore we will include the HD95 (shape), and VS (volume), and the final ranking will take all three metrics into account.

Ranking method(s)

a) Describe the method used to compute a performance rank for all submitted algorithms based on the generated metric results on the test cases. Typically the text will describe how results obtained per case and metric are aggregated to arrive at a final score/ranking.

In order to evaluate and compare the ability of each algorithm to segment the fetal brain, a final score incorporating the three metrics (DSC, HD95, VS) will be determined. All three metrics will be calculated for each label within each of the corresponding predicted label maps of the fetal brain volumes in the testing set. The mean and standard deviation of each label will be calculated, and the participating algorithms will be ranked from low to high (HD95), where the lowest score receives the highest scoring rank (best), and from high to low (DSC, VS), where the highest value will receive highest scoring rank (best). For each label, the three rankings were added together, and the algorithm with the highest ranking was ranked first. A ranking based on the average value of each metric across all labels will also be calculated.

In addition, the algorithms will be evaluated in the categories 'Non Pathological cases' and 'Pathological cases', as well as 'Excellent Quality', 'Good Quality' and 'Poor Quality', with the identical ranking scheme for each category.

b) Describe the method(s) used to manage submissions with missing results on test cases.

The only possibility for missing data would be if an algorithm does not find any of one particular label in the final label map, or if the entire label map is empty. If there are missing results, the worst possible value will be used. For example, if a label does not exist in the label map, it will receive a DSC and VS of 0, and the HD95 will be double the max value of the other algorithms submitted (to ensure it is ranked last for that sub-ranking).

c) Justify why the described ranking scheme(s) was/were used.

This ranking system was developed in order to take three different metric types equally into account. We also wanted to determine not just average ranking, but see if algorithms performed better in when the image was high quality vs low quality, as well as how well they perform on the pathological vs the neurotypical brains.

Statistical analyses

a) Provide details for the statistical methods used in the scope of the challenge analysis. This may include

- description of the missing data handling,
- details about the assessment of variability of rankings,
- description of any method used to assess whether the data met the assumptions, required for the particular statistical approach, or
- indication of any software product that was used for all data analysis methods.

The description of missing data handling can be found in Section 27.
The mean and standard deviation of each method will be calculated using both an average of all labels as well as individually, using the ranking method as described above.
Additional statistical analysis will be performed in the challenge paper.

b) Justify why the described statistical method(s) was/were used.

See Section 27

Further analyses

Present further analyses to be performed (if applicable), e.g. related to

- combining algorithms via ensembling,
- inter-algorithm variability,
- common problems/biases of the submitted methods, or
- ranking variability.

Inter-algorithm variability may be analyzed in the final paper, as well as an in-depth analysis as to why some algorithms performed better than others (potential problems/biases that may be present).

In addition, we plan to analyse the performance of the algorithms based on gestational age. The structure of the fetal brain changes greatly throughout development, especially in the cortex where there is increased cortical complexity, cortical specification (blurring of white matter and grey matter border) and partial volumes (blurring of white matter/grey matter border because of narrow gyri). Our preliminary work indicates that in the age period 29-33GW, the thickness of the grey matter remains relatively similar (~1.6-2mm) compared to the previous period (21-28 GW), and ongoing regional and areal specification of the grey matter (driven by neuronal growth, dendritic arborization and ingrowth of axons) leads to loosening of the white matter/grey matter border. In addition, partial volume effects caused by tall and narrow gyri result in poor grey matter/white matter border visibility in certain regions. Because of this, the random error in segmentation of the grey matter between 29-33 GW might be increased. We plan to split our cohort into two age groups (21-28 weeks, and 29-33 weeks), and will analyse the submitted algorithms within these two groups to see if gestational age impacts the success of a segmentation algorithm. We plan on analyzing the same subgroups of the age separated cohorts using the same metrics as in the main ranking, as well as using the additional categories 'Non Pathological cases', 'Pathological cases', 'Excellent Quality', 'Good Quality' and 'Poor Quality'. This analysis will be separate from the main ranking.

ADDITIONAL POINTS

References

Please include any reference important for the challenge design, for example publications on the data, the annotation process or the chosen metrics as well as DOIs referring to data or code.

[1] "WHO | Causes of child mortality," WHO. http://www.who.int/gho/child_health/mortality/causes/en/ (accessed Jun. 07, 2020).
[2] G. Egaña-Ugrinovic, M. Sanz-Cortes, F. Figueras, N. Bargalló, and E. Gratacós, "Differences in cortical development assessed by fetal MRI in late-onset intrauterine growth restriction," Am. J. Obstet. Gynecol., vol. 209, no. 2, pp. 126.e1-126.e8, Aug. 2013, doi: 10.1016/j.ajog.2013.04.008.
[3] A. Zugazaga Cortazar, C. Martín Martinez, C. Duran Feliubadalo, M. R. Bella Cueto, and L. Serra, "Magnetic resonance imaging in the prenatal diagnosis of neural tube defects," Insights Imaging, vol. 4, no. 2, pp. 225–237, Mar. 2013, doi: 10.1007/s13244-013-0223-2.

[4] C. Clouchoux et al., “Delayed Cortical Development in Fetuses with Complex Congenital Heart Disease,” Cereb. Cortex, vol. 23, no. 12, pp. 2932–2943, Dec. 2013, doi: 10.1093/cercor/bhs281.

[5] C. K. Rollins et al., “Regional Brain Growth Trajectories in Fetuses with Congenital Heart Disease,” Ann. Neurol., no. n/a, doi: https://doi.org/10.1002/ana.25940.

[6] D. Prayer et al., “MRI of normal fetal brain development,” Eur. J. Radiol., vol. 57, no. 2, pp. 199–216, Feb. 2006, doi: 10.1016/j.ejrad.2005.11.020.

[7] D. A. Jarvis, C. R. Finney, and P. D. Griffiths, “Normative volume measurements of the fetal intra-cranial compartments using 3D volume in utero MR imaging,” Eur. Radiol., vol. 29, no. 7, pp. 3488–3495, Jul. 2019, doi: 10.1007/s00330-018-5938-5.

[8] V. Kyriakopoulou et al., “Normative biometry of the fetal brain using magnetic resonance imaging,” Brain Struct. Funct., vol. 222, no. 5, pp. 2295–2307, 2017, doi: 10.1007/s00429-016-1342-6.

[9] P de Dumast, P Deman, M Khawam, T Yu, S Tourbier, P Hagmann, P Maeder, JP Thiran, R Meuli, V Dunet, M Koob, M Bach Cuadra, “Translating fetal brain magnetic resonance image super-resolution into the clinical environment [abstract],” Marseille, Feb. 2020, vol. 05.

[10] S. Tourbier, X. Bresson, P. Hagmann, J.-P. Thiran, R. Meuli, and M. B. Cuadra, “An efficient total variation algorithm for super-resolution in fetal brain MRI with adaptive regularization,” NeuroImage, vol. 118, pp. 584–597, Sep. 2015, doi: 10.1016/j.neuroimage.2015.06.018.

[11] Pierre Deman, Sebastien Tourbier, Reto Meuli, and Meritxell Bach Cuadra, meribach/mevislabFetalMRI: MEVISLAB MIAL Super-Resolution Reconstruction of Fetal Brain MRI v1.0. Zenodo, 2020.

[12] M. Kuklisova-Murgasova, G. Quaghebeur, M. A. Rutherford, J. V. Hajnal, and J. A. Schnabel, “Reconstruction of fetal brain MRI with intensity matching and complete outlier removal,” Med. Image Anal., vol. 16, no. 8, pp. 1550–1564, Dec. 2012, doi: 10.1016/j.media.2012.07.004.

[13] N. Khalili et al., “Automatic brain tissue segmentation in fetal MRI using convolutional neural networks,” Magn. Reson. Imaging, Jun. 2019, doi: 10.1016/j.mri.2019.05.020.

[14] S. S. M. Salehi et al., “Real-time automatic fetal brain extraction in fetal MRI by deep learning,” in 2018 IEEE 15th International Symposium on Biomedical Imaging (ISBI 2018), Apr. 2018, pp. 720–724, doi: 10.1109/ISBI.2018.8363675.

[15] S. Tourbier, X. Bresson, P. Hagmann, R. Meuli, and M. Bach Cuadra, sebastientourbier/mialsuperresolutiontoolkit: MIAL Super-Resolution Toolkit v1.0. Zenodo, 2019.

[16] R. Kikinis, S. D. Pieper, and K. G. Vosburgh, “3D Slicer: A Platform for Subject-Specific Image Analysis, Visualization, and Clinical Support,” in Intraoperative Imaging and Image-Guided Therapy, Springer, New York, NY, 2014, pp. 277–289.

[17] A. A. Taha and A. Hanbury, “Metrics for evaluating 3D medical image segmentation: analysis, selection, and tool,” BMC Med. Imaging, vol. 15, Aug. 2015, doi: 10.1186/s12880-015-0068-x.

Further comments

Further comments from the organizers.

No