# MMIV Activities
# Scientific Report 2020

**Statement of authorship**

This document is a collection of research activities performed at the Mohn Medical Imaging and Visualization center of Bergen's Haukeland University Hospital. As such the rights of all written word and images lies with the respective authors. Contact them before you use the content in any way publicly or privately.

**Contact information**

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# 1. Highlights

# Highlights of 2020

A summary of the research activities of 2020

The COVID-19 outbreak at the beginning of 2020 allowed all researchers of MMIV to focus on research efforts of disease prevention and characterization of patient data affected by the outbreak. The MMIV clinical response team created tools and procedures to manage the data capture of COVID-19 cases for image and assessment instruments. This included simple measures such as adjusting the radiology workflow at MMIV to allow all radiologists working at MMIV to occupy separate rooms limiting the potential effects of an outbreak.

In 2020 we have received new funding for a project on workflow-related machine learning from the Norwegian Research Council. The project is headed by Hauke Bartsch, Alexander Lundervold, Ingfrid Haldorsen, Arvid Lundervold, Erlend Hodneland, and Erling Andersen. The primary objective of this project is to construct a robust, working prototype that receive a DICOM study pushed from the PACS system, setup and run it through deep learning-based image processing methods, and format and return the resulting information, segmentation mask, derived reports, and quantitative measures back into the PACS. The system will also facilitate the evaluation and further training of the deep learning model based on feedback from the user by storing such modifications as annotations in the PACS. The prototype workflow will be assessed by experienced radiologists from the relevant clinical domains. Secondary objective is to prove that our approach is generalizable. This objective is three-fold: the approach should generalize to other computational medical imaging methods, different medical applications, and provide a clear path to embed our product in production-level, widely used PACS and image reading systems.

**Summary**

Tags: COVID-19, NRF projects
Date: 2020-04-01

# 2. Events

**Hauke Bartsch, Dr. rer. nat.**

# The very basics of web-programming - without any gaps

A workshop of the without-any-gaps series of MMIV

No prior programing skills are required to participate in this class but, bring a laptop and actively participate. After this class you can create a single page web applications for your machine learning and visualization projects that run on all major web-browsers and have an interface that people are familiar with. Programming concepts are explained in class and step by step we will enhance our example application with interactive components.

Any web-application consists of two components, the web-server that provides the database and the client application component that is executed in the users browser. All programming logic is executed on the client application programmed in JavaScript - a programming language designed for the web.

The minimal server component is programmed in our class in PHP, a simple programming language for the server that implements for example authentication (not covered in this class).
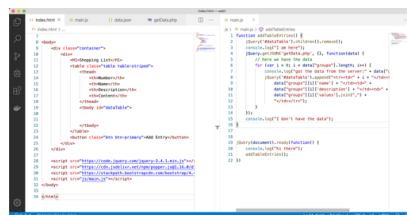


Figure 2.1: The concept of a single page web-application allows us to provide visualizations for the web.

We will focus our efforts on the client side programming and explain how events trigger actions that result in an update of the interface which creates reactive web experience for the user. The capabilities of styling the website using cascading style sheets (CSS) will allow us to generate custom interface components for special needs. For a basic styling framework we will use Bootstrap (v4). This library extends the HTML code describing the interface by an easy to understand grid-based layout that adapts to the size of the screen. Our applications will therefore adjust to large screens as well as cell-phones.

## Summary

Tags: Programming, Web, Education, Workshop
Date: 2020-01-13
Location: MMIV
Audience: World

**Hauke Bartsch, Dr. rer. nat.**

# The very basics of R-programming - without any gaps

A workshop of the without-any-gaps series of MMIV

No prior programming experience is required and everyone is welcome to our class, but bring a laptop. We start with an overview of tasks related to data imports and quality checks, cover basic visualization using ggplot2 and the simplest of regression models suitable as a baseline classification for your machine learning projects. Due to the complexity of the statistical models we will focus in this class on the data management part which starts any analysis task in the R-programming language.

R is especially suited as a programming language supporting data management tasks as well as basic and advanced statistical analysis tasks. With high-quality graphic generating packages all components of a scientific paper for bio-science can be created using R. In class we will use RStudio an integrated development environment that provides a convenient MATLAB-like interface for our class. The notebook feature is similar to python-notebooks and combines explanatory text, programming code and output generated by R.



Figure 2.2: R language class for everyone.

Together with the RStudio environment the CRAN package store is a useful repository of many advanced packages that integrate with R. We will use the TableOne package to explain how R can be extended with CRAN software. In the last part of the workshop we will look at ggplot as a language for specifying graphics in R.

In a future workshop we will focus on the basic statistical packages for linear models up to the use of generalized additive mixed models (gamm4, mgcv). Such packages provide the tools for many life-science analysis tasks.

**Summary**

Tags: Programming, Education, Workshop
Date: 2020-02-24
Location: MMIV
Audience: World

# Seminar series October 2019

MR & I – Magnetic resonance imaging from different viewpoints within the MMIV

The seminar talks of Mohn Medical Imaging and Visualization center are organized by a committee composed of graduate student, PhD students and post-docs. The format of the seminars is that of an open forum for 4 talks per day of 20min each about work in progress research topics across all of the MMIV projects. Each seminar day combines research of all projects at MMIV and each talk ends with a short discussion and feedback for the presented work. The seminar day concludes with a social get-together at MMIV with waffles and coffee.

Especially the more informal format of the seminar invite lively discussions that bridge the projects and presenters usually leave with many helpful suggestions for future research and potential collaborations.

The multi-project format of the seminars provide a valuable revenue to foster inter-group relationships at MMIV.

**Summary**

Tags: Education, Seminars
Date: 2019-10-01
Location: MMIV
Audience: MMIV

**Noeska Smit**



# Memento: Localized Time-Warping for Spatio-Temporal Selection in fMRI data

Seminar talk provided at the MMIV

This talk was presented by Noeska Smit of the MMIV. It is titled "Memento: Localized Time-Warping

for Spatio-Temporal Selection in fMRI data".

She introduced her talk with: *Interaction techniques for temporal data are often focused on affecting the spatial aspects of the data, for instance through the use of transfer functions, camera navigation, or clipping planes. However, the temporal aspect of the data interaction is often neglected. The temporal component is either visualized as individual time steps, an animation, or a static summary* *over the temporal domain. We propose a novel technique that allows users to interactively specify areas of interest in the spatio-temporal domain. By employing a time-warp function, we are able to slow down time, freeze time, or even travel back in time, around spatio-temporal events of interest. The combination of such a (pre-defined) time-warp function and brushing directly in the data to select regions of interest allows for a detailed review of temporally* *and spatially localized events, while maintaining an overview of the global spatio-temporal data. In this talk, I will demonstrate an application of this technique to functional MRI (fMRI) data in particular.*

**Summary**

Tags: Education, Seminars
Date: 2020-01-01
Location: MMIV
Audience: MMIV

**Njål Lura**



# MRI-assessed tumor size parameters predict mortality in uterine cervical cancer

Seminar talk provided at the MMIV

This talk was presented by Njål Lura of MMIV. It is titled "MRI-assessed tumor size parameters predict mortality in uterine cervical cancer".

He introduced his talk with: *Uterine cervical cancer represents a major threat to female health worldwide; it is the fourth most common female cancer and one of the leading causes of cancer-related* *death in low-income countries. Important limitations in cervical cancer treatment are due to: 1) insufficient diagnostic tools with which to identify high-risk disease and 2) insufficient diagnostic tools with which to guide more individualized treatment. This project aims to address these limitations by focusing on the value of preoperative advanced imaging to provide functional and morphological* *tumor characteristics relevant for treatment and prognosis in uterine cervical cancer.*

**Summary**

Tags: Education, Seminars
Date: 2020-01-01
Location: MMIV
Audience: MMIV

**Saruar Alam**



# Analyzing atlas-based MRI features on Alzheimer's disease detection

Seminar talk provided at the MMIV

This talk was presented by Saruar Alam of MMIV. It is titled "MRI-assessed tumor size parameters predict mortality in uterine cervical cancer".

He introduced his talk with: *Alzheimer's disease (AD) can be distinguished using the features obtained from Magnetic resonance imaging (MRI), and a supervised classifier. Multi-atlas-based-likelihood fusion (MALF) algorithms extract the volumes features of subcortical regions of interest (ROI). The correlation among these ROI features from different brain regions may provide additional valuable information. Subsequently, these ROI-correlative features may affect the classification performance of a supervised classifier. We have classified AD and Mild Cognitive Impairment from cognitively normal subjects using these features and a Support Vector Machine classifier. This article investigates the difference in classification performance between the ROI and ROI-correlative features. Our work also reports the ranks of ROI and ROI-correlative regions. We have observed marginal differences in classification performance and ranking of the most effective regions.*

**Summary**

Tags: Education, Seminars
Date: 2020-01-01
Location: MMIV
Audience: MMIV

**Rune Eikeland**
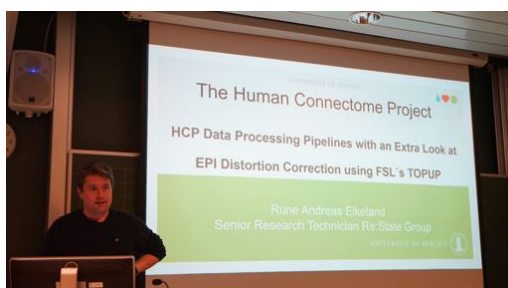
# The Human Connectome Project data processing pipeline and data visualization toolbox

Seminar talk provided at the MMIV

This talk was presented by Rune Eikeland of MMIV. It is titled "The Human Connectome Project data processing pipeline and data visualization toolbox".

He introduced his talk with: *The Human Connectome Project (HCP) is a five-year project sponsored by sixteen components of the National Institutes of Health, split between two consortia of research institutions. The project was launched in July 2009 as the first of three Grand Challenges of the NIH's*

*Blueprint for Neuroscience Research.*

*The goal of the Human Connectome Project is to build a "network map" (connectome) that will shed light on the anatomical and functional connectivity within the healthy human brain, as well as to produce a body of data that will facilitate research into brain disorders such as dyslexia, autism, Alzheimer's disease, and schizophrenia.*

*The data, processing and visualization tools are freely available*

*for the HCP and Rune will present them in this talk with an in-depth focus on EPI data pre-processing to reduce susceptibility and motion artefacts with FSL's eddy tool (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/eddy).*

**Summary**

Tags: Education, Seminars
Date: 2020-01-01
Location: MMIV
Audience: MMIV



# Seminar series September 2019

From mouse to man – Spatial and temporal medical imaging in different species and development phases

The seminar talks of Mohn Medical Imaging and Visualization center are organized by a committee composed of graduate student, PhD students and post-docs. The format of the seminars is that of an open forum for 4 talks per day of 20min each about work in progress research topics across all of the MMIV projects. Each seminar day combines research of all projects at MMIV and each

talk ends with a short discussion and feedback for the presented work. The seminar day concludes with a social get-together at MMIV with waffles and coffee.

Especially the more informal format of the seminar invite lively discussions that bridge the projects and presenters usually leave with many helpful suggestions for future research and potential collaborations.

The multi-project format of the seminars provide a valuable revenue to foster inter-group relationships at MMIV.

**Summary**

Tags: Education, Seminars
Date: 2019-09-01
Location: MMIV
Audience: MMIV

**Heidi Espedal**
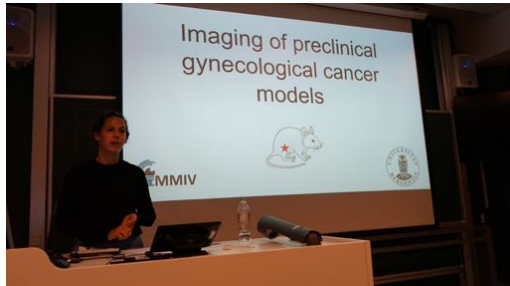


# Imaging of preclinical gynecologic cancer models

Seminar talk provided at the MMIV

This talk was presented by Heidi Espedal of MMIV. It is titled "Imaging of preclinical gynecologic cancer models". She is a post-doctoral fellow working at the molecular imaging center (MIC) of Haukeland University Hospital.

She introduced her talk with: *Endometrial cancer is the most common type of cancer of the female reproductive tract. Although prognosis is generally good for patients with low-grade and early-stage diseases, the outcomes for high-grade and metastatic/recurrent cases remain poor, since traditional therapy have limited effects. No targeted agents have been approved so far, although several new drugs have been tested without striking results in clinical trials. Patient-derived tumor xenograft (PDX) mouse models represent useful tools for preclinical evaluation of new therapies and biomarker identification. Preclinical imaging by PET-CT and MRI during disease progression enables visualization and quantification of functional tumor characteristics, which may serve as imaging biomarkers guiding targeted therapies. The primary objective for this presentation is to give an introduction of current and novel preclinical imaging methods relevant for endometrial cancer mouse models.*

**Summary**

Tags: Education, Seminars
Date: 2020-09-01
Location: MMIV
Audience: MMIV

**Eric Mörth**

# The Vitruvian Baby: Interactive reformation of 3D ultrasound data to a T-pose

Seminar talk provided at the MMIV

This talk was presented by Eric Mörth of MMIV. It is titled "The Vitruvian Baby: Interactive reformation of 3D ultrasound data to a T-pose". Eric is a PhD candidate for multi-modal medical visualization under the supervision of Noeska Smit (MMIV).

He introduced his talk with: *Three-dimensional (3D) ultrasound imaging and visualization is often used in medical diagnostics, especially in prenatal screening. Screening the development of the fetus is important to assess possible complications early*

*on. Performing the analysis in a 3D view would enable the viewer to better discriminate between artefacts and representative information. Additionally making data comparable between different investigations and patients is a goal in medical imaging techniques and is often achieved by standardization.*

*"The Vitruvian Baby" incorporates a complete pipeline for standardized measuring in fetal 3D ultrasound. The input of the method is a 3D ultrasound screening of a fetus and the output is the*

*fetus in a standardized T-pose. In this pose, taking measurements is easier and comparison of different fetuses is possible. In addition to the transformation of the 3D ultrasound data, we create an abstract representation of the fetus based on accurate measurements.*

**Summary**

Tags: Education, Seminars
Date: 2020-09-01
Location: MMIV
Audience: MMIV

**Hauke Bartsch**
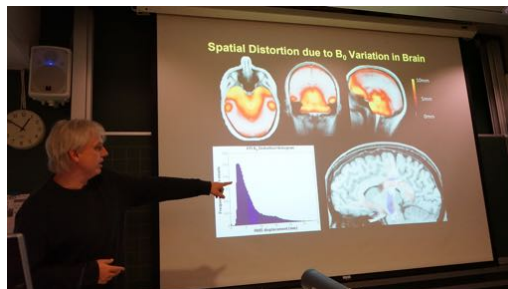
# The Brain Imaging Data of the ABCD Study – an Introduction into Protocols and Tasks

Seminar talk provided at the MMIV

This talk was presented by Hauke Bartsch of MMIV. It is titled "The Brain Imaging Data of the ABCD Study – an Introduction into Protocols and Tasks". Hauke is a researcher at the MMIV.

The ABCD study is recruiting and following the brain development and health of over 10,000 9-10 year olds through adolescence. The

imaging component of the study was developed by the ABCD Data Analysis and Informatics Center (DAIC) and the ABCD Imaging Acquisition Workgroup. Imaging methods and assessments were selected, optimized and harmonized across all 21 sites to measure brain structure and function relevant to adolescent development and

addiction. This article provides an overview of the imaging procedures of the ABCD study, the basis for their selection and preliminary quality assurance and results that provide evidence for the feasibility and age-appropriateness of procedures and generalizability of findings to the existent literature.

He introduced his talk with:

The Adolescent Brain Cognitive Development (ABCD) Study is the largest long-term study of brain development and child health in the United States. The ABCD Research Consortium have invited 11,878 children ages 9-10 to join the study. Researchers will track their biological and behavioral development through adolescence into young adulthood.

Using cutting-edge technology, scientists will determine how childhood experiences (such as sports, video-games, social media, unhealthy sleep patterns, and smoking) interact with each other and with a child's changing biology to affect brain development and social, behavioral, academic, health, and other outcomes.

As part of a research agreement,

MMIV will obtain access to the raw data that includes an extensive MRI protocol as well as behavioral and environmental data.

**Summary**

Tags: Education, Seminars
Date: 2020-09-01
Location: MMIV
Audience: MMIV

**Sathiesh Kaliyugarasan**



# Artificial intelligence in image diagnostics – transfer learning and active learning for efficient use of data and radiologist's expertise

Seminar talk provided at the MMIV

This talk was presented by Sathiesh Kaliyugarasan of MMIV. It is titled "Artificial intelligence in image diagnostics – transfer learning and active learning for efficient use of data and radiologist's expertise". Sathiesh is a PhD candidate at the MMIV.

He introduced his talk with: A common stumbling block for supervised learning methods based on deep neural networks is the large

number of labeled examples required for training. This is particularly troublesome when trying to use deep learning methods for segmentation in 3D medical image data. As creating labeled data for medical images is often a time-consuming, difficult and unreliable process, the amount of training data available is in general very small. To mitigate this problem we are looking into using

design methodologies such as transfer learning and active learning for efficient use of data and radiologist's expertise.

**Summary**

Tags: Education, Seminars
Date: 2020-09-01
Location: MMIV
Audience: MMIV

# 3. Dissertations

**Summary**

Tags:
Date:

**EXPLORER**

## 4. Software

ⓒ heat_equation.cxx > ⓒ main(int, char * [])

```cpp
171    command.AddField("outdir", "Output directory", MetaComman
172
173    command.SetOption("Temperatures", "t", false,
174                      "Specify the temperature per label as <
175                      "N the number of label and temperature
176                      "4 0 0.0 1 100.0". A label that is not
177                      "assumed to be variable and used for th
178    command.SetOptionLongTag("Temperatures", "temperature-Lab
179    command.AddOptionField("Temperatures", "temperature", Met
180
181    command.SetOption("Iterations", "i", false,
182                      "Specify the number of iterations (defa
183                      "Large number of iterations like 2000 (
184                      "monitored using the change value print
185
186    command.AddOptionField("Iterations", "iterations", MetaCo
187
188    // supersample the input (2 means 4 times more voxel)
189    command.SetOption("SuperSample", "s", false,
190                      "Specify the number up-sampling steps u
191                      "the resolution).");
192    command.AddOptionField("SuperSample", "supersample", Meta
193
194    // quantize the output temperature
195    command.SetOption("Quantize", "q", false, "Quantize the o
196    command.AddOptionField("Quantize", "quantize", MetaComman
197
198    command.SetOption("UnitNormalVector", "n", false,
199                      "Export the unit normal vector and the
200                      "(exported gradient field is the tangen
201
202    command.SetOption(
203      "InitField", "c", false,
204      "Initialize the temperature field with this volume. T
205      "of small to large volumes is created where each stag
206    command.AddOptionField("InitField", "initfield", MetaComm
207
208    command.SetOption("VectorFileFormat", "f", false,
209                      "Specify the file format for the vector
210    command.AddOptionField("VectorFileFormat", "vectorfilefor
211
212    if (!command.Parse(argc, argv)) {
213      return 1;
214    }
215
216    std::string input = command.GetValueAsString("infile");
217    std::string outdir = command.GetValueAsString("outdir");
218    // fprintf(stdout, "input: \"%s\"\n", input.c_str());
219    // fprintf(stdout, "outdir: \"%s\"\n", outdir.c_str());
```

**Hauke Bartsch, Dr. rer. nat.**
https://github.com/mmiv-center/LungSegmentation.git

# Geodesic distances in white matter

Curvilinear coordinates in human white matter

This module creates curvilinear coordinates from volumetric label fields. It simulates the heat equation and exports the temperature (potential) field and the gradient of the potential field (tangent unit vector). The gradient field represents the directions of geodesic lines connecting the fixed temperature regions.

This module can be used to compute the shorted path between points of the ventricles and points of the white/gray matter border using structural information (white matter) only. It can also be used to sample the white matter at a given distance perpendicular to the gray/white matter border.



Figure 4.1: A repository for software.

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.
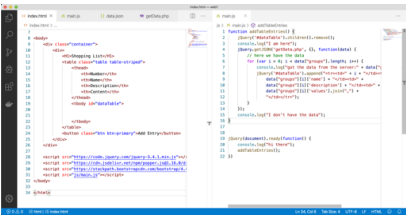
Summary

Tags: Programming, Software
Date: 2020-01-13

**Hauke Bartsch, Dr. rer. nat.**
https://github.com/mmiv-center/gen-id.git

# Research PACS component Gen-ID

Generate random participant ID's from regular expressions

This repository provides

access to program developed at MMIV that creates random participant identifiers based on a regular expression pattern. This feature allows research projects to use short participant identifiers that do not repeat and that blind the study to the order of enrollment. The generated participant identifiers remain concise and recognizable as belonging to the study. The software is part of the Research PACS at MMIV that provides a safe technical solution to perform medical data collection and data analysis.
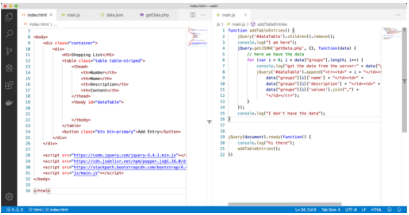


Figure 4.2: A repository for software.

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.

**Summary**

Tags: Programming, Software
Date: 2020-03-10

**Hauke Bartsch, Dr. rer. nat.**
https://github.com/mmiv-center/LungSegmentation.git

# LungSegmentation package

Create lung-segmentation fields from spiral CT

This repository provides access to programs developed at MMIV for lung segmentation of spiral CT images. This program is using a series of labelling and morphological operations to extract the Lung volume intensity image from chest CT scans. It was tested with the data from the LIDC-IDRI (Lung Image Database Consortium) project and depends on ITK/cmake.

After the initial step of extracting the intensities of the lungs and airways the algorithm attempts to separate the two lungs and the airways.
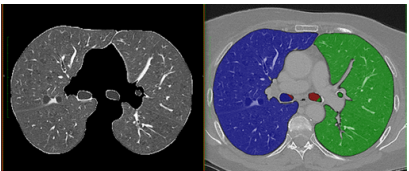


Figure 4.3: Lung segmentation into airwairs (red), left (green) and red (blue) lung.

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.

**Summary**

Tags: Programming, Software
Date: 2020-03-10

**Hauke Bartsch, Dr. rer. nat.**
https://github.com/mmiv-center/RewritePixel.git

# Sanitize DICOM image data

Machine learning algorithms for the removal of burned in image information

This repository provides access to programs developed at MMIV for the removal of burned in pixel information in secondary capture DICOM images.

Sharing medical images is most often straight forward as the DICOM format provides a globally agreed on file format for all reconstructed 2D, 3D, and 4D data generated by medical equipment. Special care has to be taken if DICOM data is generated as part of data analysis workflows. Such 'secondary-capture' DICOM images can contain burned in text information that might contain participant identifying information such as names. Before such data can be shared as part of research projects at Haukeland University Hospital the burned in image information needs to be removed. Previous approaches

This project uses the tesseract optical character recognition machine learning engine to identify text that is burned into DICOM images. For each text fragment (usually a word) a square black frame is written into the DICOM pixel information. The resulting DICOM file should be inspected - hopefully it is free of participant identifying information.

Warning: This program does not try to anonymize DICOM tags. Please check out the https://github.com/mmiv-center/DICOMAnonymizer project for a fast tag anonymizer.

Warning: There is no information yet on false/positive detection rates, verify the output by hand!

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.

**Summary**

Tags: Programming, Software
Date: 2020-03-10

**Hauke Bartsch, Dr. rer. nat.**
https://github.com/mmiv-center/DICOMAnonymizer.git

# DICOM-Anonymizer

Fast-anonymization engine for DICOM meta-data

This repository provides access to programs developed at MMIV for the removal of participant identifying information in meta-data tags of DICOM files.

This source code demonstrates how to anonymize DICOM files based on the DICOM PS 3.15 AnnexE. I provide a Dockerfile that can be used to build the executable and to run anonymizations. Entries such as uid entries are replaced with hash values. This ensures that partial runs of a studies DICOM files can be merged afterwards. This project is written in C++ using the gdcm library and multiple threads to accelerate processing.

**Warning**: The operation performed by this tool is a 'soft' de-identification. Instead of a white list of allowed tags the tool keeps a list of tags known to frequently contain personal identifying information (PII) and replaces only those. On the command line you specify a patient identifier (PatientID/PatientName). Only if you do not keep a mapping of the new and the old identifier this is considered an anonymization. If such a list exists the operation performed is a de-identification (permits a later re-identification).

I suggest to review files generated by this tool for additional PII information that might be present in text fields.

For a more flexible anonymizer please see the CTP DICOM Anonymizer project.

## Unique features

- fast de-identification (multi-threaded, C++)
- de-identifies data inside sequences instead of deleting them so overlays survive the procedure

## Limitations

This tool has been written to work as an importer for a (vendor neutral) PACS system. In such a setup data de-identified from the same participant is expected to align with previous data for the same participant and study if the same participant ID and name is used. This is achieved by using study instance uids that are hashed. Series that comes later should therefore match at the study level. It is not possible to recover the original patient ID, patient name and study/series/image instance UIDs from the de-identified fields as no tracking information is stored in the DICOM files. But, identical input data will result in the same hashes. This can be seen as an implicit coupling list - a price we have to pay to be able to use the tool in our research PACS during the data capture stage of a project.

The used SHA256 algorithm for hashing per project is very fast to compute. This will allow an attacker to create many random tries for a brute-force attack. At the worst case this would allow the attacker to recover the original study/series/image instance UIDs. PatientID and PatientName tags are set manually and are therefore not exposed to such an attack.

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.

### Summary

Tags: Programming, Software
Date: 2020-03-10

**Hauke Bartsch, Dr. rer. nat.**

https://github.com/mmiv-center/LesionProject.git

# Identifying Lesions in brain MRI

A software provided by MMIV

This repository provides access to programs developed at MMIV for the detection of brain lesions.

After detecting lesions in-painting can be used to synthetically create a version of the raw data were lesions are masked with assumed intensity values similar to the neighboring voxel in the data. Such synthetic data can be used for algorithms that are sensitive to the lesions otherwise - such as FreeSurfer.

The provided algorithm performs a region growing of initially 2 voxel to create a lesion border. This border might be affected by partial volume effect. Afterwards another 2 voxel morphological grow operation defines a region of background voxel used for the interpolation of the lesion and the lesion border voxel intensities.

For lesions that are close to the border of white matter the interpolation might not be correct as it would blur intensities from different tissue types across the lesion volume. Instead it might be more appropriate to limit the intensities for interpolation to the voxel of a single material. For these pusposes you can provide an additional mask argument - limiting the sample points for the interpolation to the white matter material only.

In order to quantify the location of a lesion relative to the cortical surface an approach can be used that calculates curvilinear (geodesic) distances between two labels, the ventricles located in the center of the brain and the cortical gray to white matter surface. This approach mimics the general direction of the path neurons travel during cortex development.

Please visit the https://github.com/mmiv-center/Heat project that implements such a method.

We share such source code to support similar research efforts internationally. The open-source nature of this research allows national and international researchers to test and verify our solutions, provide essential feedback and suggestions for improvement supporting advances in medical data handling.

### Summary

Tags: Programming, Software
Date: 2020-03-10

# 5. Research Projects

Hauke Bartsch,
Ingfrid Haldorsen,
Alexander Lundervold,
Arvid Lundervold,
Erlend Hodneland,
Erling Andersen

# Workflow-integrated machine learning

New funding 2020: Innovation Project for the Public Sector

Recent years have seen exciting applications of machine learning in medical data analysis, from radiology and dermatology to electronic health records and drug discovery. This has led to great interest and enormous expectations from the medical profession. However, it is still early days for the evaluation and integration of artificial intelligence and machine learning-derived information in clinical practice. This proposal addresses one of the crucial missing elements required for implementation and integration in clinical radiology: an innovative, direct integration of computational imaging methods with picture archive and communication systems (PACS). To ensure the usefulness of our innovation, we will apply it to two of the most important health challenges in modern society: cancers in women (uterus) and men (prostate).

Modern machine learning algorithms integrated deep into clinical workflows can have immense impact by offering more personalized treatments and predictions of outcome for a wide variety of conditions. By producing accurate measurements, predictions and pre-processing in close to real-time, machine learning methods make it feasible to do advanced image and data-processing in the clinical setting, potentially lessening workload, empowering physicians, and reducing interobserver variability. If machine learning is able to show convincing results in the clinic this could potentially open the avenue for innovations based on other advanced computational methods that have the potential to improve our understanding and predict health and disease, facilitating a stronger clinical presence for the broader field of computational medicine, an area that holds great promise for the future of medicine.

Primary objective: construct a robust, working prototype that receive a DICOM study pushed from the PACS system, setup and run it through deep learning-based image processing methods, and format and return the resulting information, segmentation mask, derived reports, and quantitative measures back into the PACS. The system will also facilitate the evaluation and further training of the deep learning model based on feedback from the user by storing such modifications as annotations in the PACS. The prototype workflow will be assessed by experienced radiologists from the relevant clinical domains. Secondary objective: prove that our approach is generalizable. This objective is three-fold: the approach should generalize to other computational medical imaging methods, different medical applications, and provide a clear path to embed our product in production-level, widely used PACS and image reading systems.
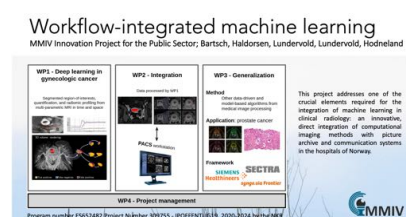


Figure 5.1: A new project supported by the Norwegian research council.

**Summary**

Tags: Project, NFR
Date: 2020-02-02

**Leif Oltedal,**
**Ute Kessler,**
**Jan Haavik**

# Brain changes induced by electroconvulsive therapy (ECT)

Understanding treatment mechanisms and predictors of clinical response

Electroconvulsive therapy (ECT) is a procedure, done under general anesthesia, in which electric currents are passed through the brain, intentionally causing a brief seizure. Although ECT has remained the most effective acute treatment for major depressive episodes for nearly 80 years, how it works and why it is effective is not well known. Only a small proportion of patients with treatment resistant depression are offered ECT, and typically 60-80% experience a good response ($> 50\%$ symptom reduction).

Several neuroimaging studies of ECT have demonstrated volume increases of brain areas after treatment. The most consistent finding has been volume increase of the hippocampus. However, a link between the treatment induced brain changes and clinical improvement has not been established.

This project explores how ECT changes the brain, and if the structural (or functional) changes that are seen can explain the effect (or side-effects) of the treatment.



Figure 5.2: The Global ECT MRI Research Collaboration.

An important reason for our knowledge gap is that single studies have limited samples and lack statistical power to reach firm conclusions. The Global ECT-MRI Research Collaboration was founded with a belief that collaboration and mega-analysis of combined data will lead to new knowledge that can be generalized across individual research sites.



Figure 5.3: The researchers at the global ECT MRI meeting 2019.

In May 2019 the group arranged a gathering to discuss how to combine the neuropsychological analyses with data in the study. At the seminar, Åsa Hammar (neuropsychologist and professor), Maria Semkovska (neuropsychologist and experienced researcher in the ECT field), Olga Therese Ousdal (PhD), Hauke Bartsch (director of informatics, image analyst IV), Ole Johan Evjenth Sørhaug (medical student), and Shawn McClintoch (neuropsychologist (via Skype)) presented ongoing projects, preliminary analyses, earlier research, and future recommendations. The gathering was a good day for discussions and new ideas.

**Summary**

Tags: Project
Date: 2020-02-02

**Karsten Specht**

# When Default Is Not Default

Re:State Research Group

When Default Is Not Default project is part of Karsten Specht's newly formed Re:State research group at the Institute of Biological and Medical Psychology, University of Bergen.



Figure 5.4: The Re:State research group.

This project addresses a very timely and highly important question of cognitive and clinical neuroscience studies: What factors influence the reliability of neuroimaging studies? What are the sources of individual variability? Which constraining factors may help predicting the outcome of a certain therapy?

Recent studies have estimated the reproducibility of psychological studies to be 39

The overall objectives of this project are to (i) improve our understanding of the neurophysiological mechanism of the BOLD signal and its sources of variability, to (ii) extend current methods on effective and functional connectivity measures (Connectoms), to (iii) find a solution to the replication crisis by developing new Bayesian, topology-based, and machine-learning based analysis methods as alternative approaches to today's analysis strategies, and to (iv) induce a paradigm shift from the current focus on an easy to measure but susceptible BOLD signal to the underlying, but (partly) hidden neuronal states that are presumably more stable and reliable.

The project aims to generate new insights into the neurophysiological mechanisms of the BOLD signal, its variability, dependency on endogenous and exogenous parameter, and reliability, and it will advance the research field of basic and clinical neuroimaging by providing new analysis strategies.

**Collaborating Partners**

National Partners: Assoc. Prof. Morten Brun, Dept. of Mathematics, University of Bergen Prof. Gaute Einevoll, Faculty of Science and Technology, Norwegian University of Life Sciences

International partners: Prof. Karl Friston, Wellcome Trust Centre for Neuroimaging, University College London

Prof. Viktor Jirsa, CNRS and Institut de Neurosciences des Systèmes, Aix-Marseille University.

Prof. Vince Daniel Calhoun, Mind Research Network and University of New Mexico

**PhD Candidates**

We are happy to announce that we start the year 2020 with two new PhD candidates in the Re:State group: Tania Martínez Montero and Vetle Hushagen. We wish them welcome and best of luck in their endeavors.

**Summary**

Tags: Project
Date: 2020-02-02

**Ingfrid Haldorsen**

# Precision imaging in gynecologic cancer

The search for biomarkers in cancer research

Gynecologic cancers have characteristic structural and functional imaging features reflected in clinical phenotypes, and these imaging biomarkers highlight pathogenic mechanisms potentially targetable by novel treatments. The challenge is now to integrate these imaging biomarkers into clinically relevant treatment algorithms by identifying molecular targets for treatment based on imaging biomarker profiles. Our multidisciplinary research team with competency in computer science, visualization and machine learning algorithms, diagnostic radiology, clinical gynecology, preclinical models and molecular biology/genetics will join efforts to pursue these challenges as one of the funded projects within Centre for Medical Imaging and Visualization in Bergen.
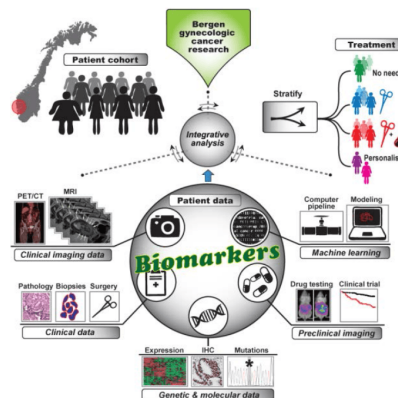


Figure 5.5: Biomarker research.

Molecular and imaging biomarkers in gynecologic cancer will be studied in patients and in preclinical gynecologic cancer models (Figure). Potential imaging biomarkers will be identified using machine learning algorithms applied to multiparametric and functional magnetic resonance imaging (MRI) and positron emission tomography/computed tomography (PET/CT) from patients and in mouse models during therapy. Furthermore, the molecular and genetic alterations in the tumors as well as clinical phenotype and survival will be studied in relation to the corresponding imaging biomarker profile using integrative analyses. This research initiative provides a unique platform for identifying promising molecular targets for treatment and their corresponding imaging biomarker profiles. Studying imaging biomarkers in mice during targeted therapy will also facilitate the integration of imaging biomarker guided treatment algorithms and imaging guided monitoring of treatment response in gynecologic cancer. This project has the potential to improve patient care by enabling individualized and targeted treatment in gynecologic cancer patients.

**Summary**

Tags: Project
Date: 2020-02-02

**Hauke Bartsch**

# A project title

Building a better future

**Research focus**
**Projects**
**Important results**
**Future plans**
**Current challenges in the field**
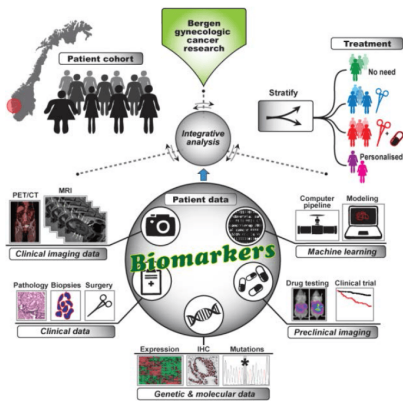**Focus in the comming years**

Summary

Tags: Project, Education, Public
Date: 2020-02-02

Figure 5.6: Figure caption.

# 6. Publications