

Zoom 210115

Optimize and verify a dynamic capture method and distance compensation for high dynamic/long range 3D-datacapture with custom time offlight camera – **Lovisa Stenlund** -
<https://umu.zoom.us/j/68316035249>

Performing measurements on an athlete's movements can be a powerful tool for his or her athletic development. In this thesis a custom 3D camera is used to track movements by making position measurements continuously over time. The measurements are made using a 3D camera based on the technique continuous wave time of flight (CW ToF), which relates the phase shift between light emitted from the camera to the light reflected back from the camera's field of view (FoV). The phase shift can thereafter be related to the image depth and provide a third dimension to the camera image. The depth measurements accuracy is though limited by systematic errors originating in the working principle of the camera. One important systematic error is the so called nonlinear error, which the camera have to be calibrated for. The goal of this project is to create a lookup-table (LoT) for the nonlinear error with 1mm precision and determine a realisable way of calibrating new cameras. Previous work have resulted in a calibration for the nonlinear error over a limited distance range. For many tests concerning athletic performance a larger distance range is though sought after. For a larger distance range the camera sensor brightness becomes a problem, as too much light makes the sensor saturated and too little light gives bad depth determination. To generate a calibration over the full range it has been suggested that the image brightness should be regulated. The image brightness can be influenced by changing the time during which light is emitted towards the scene. CW ToF uses several measurements at each distance to determine the image depth, and the total time it takes to determine the depth is referred to as the camera's duty cycle. By using different DCs the nonlinear error could be compensated for over the whole distance range. Some minor improvements were made to the way the actual measurements were carried out, but the main part of the project consisted of ways to simplify and reduce the measurements necessary to generate an accurate calibration for the nonlinear error. Using different amount of data to interpolate over the full distance range, as well as interpolating over part of the range and using a quadratic fit to extrapolate the data, the calibration could be recreated with different success rates. The result and recommended way of making the calibration of the nonlinear error for new cameras was to make measurements over the whole distance range, using step size 5mm. For calibrations using this strategy the nonlinear error could be calibrated within 2cm accuracy, which was deemed reasonable. By determine the distance ranges where each DC provided an accurate result the calibration for each DC only had to be determined over that range.

Temporal Multivariate Distribution Analysis of Cell Shape Descriptors – **Amanda Krantz** -

<https://umu.zoom.us/j/65110355976?pwd=YXdkYkpFU1cwYVExTOlTUERyV1dvUT09>

In early drug discovery and the study of the effects of new chemical compounds on cancer cells, the change in cell shape over time provides vital information about cell health. Live-cell image analysis systems can be used by researchers to extract cell-shape describing parameters of individual cells during exposure to new drugs. Multivariate statistical analysis is then applied to understand cell morphology and the correlation between various cell shape descriptors. Principal component analysis integrated with histogram distribution analysis is a method to compress and summarize important cellular data features without loss of information about the individual cell shapes. A workflow for this kind of analysis is being developed at Sartorius and aims to aid in the biological interpretation of different experimental results. However, methods for exploring the time dimension in the experiments are not yet fully explored, and a temporal view of the data would increase understanding of the cell morphology metrics. In this study, we implement the workflow to a data set generated from the microscope IncuCyte and investigates a possible continuation of time-series analysis on the data. The results demonstrate how we can use principal component analysis in two steps together with histogram distributions of different experimental conditions to study cell shapes over time. Scores and loadings from the analysis are used as new observations representing the original data, and the evolution of score-value can be backtracked to cell morphology metrics changing in time. The results show a comprehensive way of studying how cells from all experimental conditions relate to each other during the course of an experiment.

Machine learning for wavelets to enhance PET reconstruction – **Markus Argus**

In the field of Nuclear Medicine, positron emission tomography (PET) plays an important role as one of the most common diagnostic tools in the area of medical imaging. This technique uses a radioactive substance that releases a positron that soon annihilates with an electron and the result is the creation of two photons emitted at a 180-degree angle to each other. The sensors in the PET scan can detect these photons, the information gathered by the sensors gets stored in a sinogram that can be reconstructed into PET images. However, various physical degradation factors occur when the data is recorded, which leads to a low signal-to-noise ratio. This makes the quality of the PET images less than optimal. The proposed method for solving this problem is to use a machine learning approach to find a sparse representation of the sinograms. To accomplish this a sparse autoencoder was trained on wavelet decompositions of sinograms simulated from medical images in order to learn underlying structures. The trained model was able to find sparse representations of the input sinograms in the wavelet domain. Although the sparse autoencoder managed to learn the basic structures of the sinograms, it struggled with the more complex details. Compared to a conventional denoising method the sparse autoencoder did not manage to produce as good of a result in terms of the reconstructed PET image quality.

Cell Localization with Deep Learning – Fredrik Rolén

Object localization is a computer vision task that refers to identify one or more objects and draw their boundaries. In recent years deep learning, as a subfield of artificial intelligence (AI) have revolutionized computer vision and made it possible to solve more complex problems. Cell localization of cell cultivation with AI helps the biopharma industry to speed up the process of analyzing big data and makes it possible for new applications. Sartorius product IncuCyte® have a combined cell incubator with automated microscopic imaging and can collect big data very fast. There is now a strong need to find methods that help improve cell localization to keep up with the amount of data that is collected. This thesis investigates how methods in a unimodal and multimodal approach of deep learning affect the performance of cell localization. Two unimodal data sources will be used, Phase and Seed images. Phase images are more or less a photo of the cell cultivation, and Seed images are extracted from a unique technique developed by Sartorius. Information from Seed images will be fused with Phase images, in a multimodal approach, with the goal to make the artificial neural network (ANN) better in analyzing photos of cell cultivation. In this thesis, six methods are developed and performance tested with Panoptic-DeepLab (P-D), a predefined convolutional neural network (CNN) for object localization. Methods: (1) using Phase images only, (2) using concatenated Phase and Seed images, (3) using Phase images with an extended backbone to P-D, (4 - 6) three fusion techniques of the features from Phase and Seed images with an extended backbone to P-D. The three fusion techniques are concatenation, multiplication, and summation. The extended backbone to P-D in method (3) is a block of two convolutional layers. Method (4 - 6) is similar to (3) but with two blocks in parallel, one for Phase image and one for Seed images. In the experiment five different filter combinations ($f(4,16)$, $f(4,32)$, $f(8,32)$, $f(16,64)$, $f(16,96)$) is used in the two convolutional layers. In total, 22 test is made, one each for method (1 - 2), and five each for method (3 - 6) due to five filter combinations. The performance results for P-D was calculated as a percentage relative error, with method (1) as a reference value. Method (3) increases the P-D performance with 0.74% for $f(16,96)$, and 0.42% for $f(16,64)$. Method (4) increases the P-D performance with 0.25% with $f(16,96)$. Method (6) increases the P-D performance with 0.01% with $f(16,96)$. All other tests decreased the P-D performance relative to method (1). The experiment shows that a unimodal approach with only Phase images and an extended backbone of more convolutional layers improves P-D's performance by up to 0.74%. A multimodal approach with Seed images does not reach the same improvements as unimodal. The best fusion technique is method (4) with concatenation.

Simulated cerebrospinal fluid motion due to pulsatile arterial flow— **Jesper Hägglund** -
<https://umu.zoom.us/j/68027316272>

All organs including the brain needs a way to get rid of extracellular proteins, for the brain this is the glymphatic system. The glymphatic system works by exchanging proteins from interstitial fluids to cerebrospinal fluids. The extracellular proteins are then removed through the cerebrospinal fluid drains. The glymphatic system is believed to be driven by arterial pulsatility, cerebrospinal fluid production and respiration. In this paper we investigate how well COMSOL Multiphysics linear elastic model can replicate experiments in a deforming microchannel and a pulsatile flow in a common carotid artery to see if it is a good fit for future simulations. We show that COMSOL can simulate a deforming microchannel within the correct order of magnitude. In the case of common carotid artery we get a displacement along the arterial wall at around 6%. This displacement was found to not drive the cerebrospinal fluid, but help with exchanging of fluids between the cerebrospinal and interstitial fluids. The results overall shows that COMSOL Multiphysics linearly elastic model is not the ideal for modelling of non-linearly elastic solids, such as soft polydimethylsiloxane and artery walls. The long term aim is to simulate a part of the glymphatic system this paper is anticipated to be a starting point to reach this goal. For example using the same geometries a non-linear elastic model could be tested. Furthermore the model could be made smaller and changed to simulate a penetrating artery in the brain instead of the common carotid artery

Optimizing numerical modelling of quantum computing hardware – **Yasir Al-Latifi** -
<https://umu.zoom.us/j/62445630044?pwd=Z0pmKzNHVUtWNURtekhMN1hjaEdUZz09>

Quantum computers are being developed to solve certain problems faster than classical computers. They consist of quantum bits (qubits) instead of classical bits. These qubits can utilize quantum effects. At Chalmers University of Technology, researchers have already built a quantum chip consisting of two qubits and are trying to build systems with more qubits. To assist in that process, they make numerical simulations of the quantum systems on regular computers. The problem is that the Hilbert space of the system grows exponentially with the number of qubits. This requires the simulations to be as efficient as possible, by using certain approximations, while still giving accurate enough results. The aim of this project is to compare several approximations used for the simulations, to see how accurate they are and how fast they run on a classical computer. This was done by modeling a system consisting of two fixed-frequency superconducting transmon qubits that operate as anharmonic quantum oscillators. These are coupled to a variable-frequency qubit which allows the two qubits to exchange energy when necessary by changing its frequency, and in that way obtain quantum gates. The two qubits are also both connected to readout resonators that allow for their state to be observed. The approximations tested are: using three, four, or five energy levels when simulating the anharmonic oscillators, seeing how the rotating-wave approximation (RWA) affects the system, and finding out how large of an impact it is to include the readout resonators in the system. These cases were tested by implementing the iSWAP and CZ gates on the system. The simulations were all made using the Python library QuTiP. The results show that in order to obtain adequate results, one should simulate using at least one energy level higher than the maximum energy level required by the gate being simulated. For larger systems, the RWA will make a large difference in simulation times, even though it does not give as accurate results, but for most usage cases, they are accurate enough. When using the RWA, the number of levels used does not seem to affect the results significantly and one could therefore use the lowest possible energy levels that can simulate the system.

Design, modelling construction of a pump system for optimal outflow of wastewater – **Olle Stenlund**
- <https://umu.zoom.us/j/65831969994?pwd=WUcrYnYzWGVuVnFYcnhnR1F0K04vQT09>

In today's world, industries are becoming more and more aware over how they utilize water in their production process. In many cases is this contaminated wastewater released back into the water supply untreated, which can cause several negative side effects to the ecosystem. If humanity is striving to achieve a sustainable environment, changes have to be made. One way of purifying wastewater is by utilizing rotating bed reactors, where a impeller is filled with catalyst pellets that absorb the pollutants is lowered into the contaminated fluid. The inertia forces caused by the spinning forces the contaminated water to go through the packed bed, purifying it in the process. This project utilizes one of these rotating bed reactors. The task at hand is to develop a container around this impeller that will provide as fast an outflow as possible, using only the pumping capability of the impeller, i.e no external pump is allowed. This container should be designed, constructed and tested. Alongside this design and construction a CFD simulation of the container was made to help analyze the flow velocities and forces occurring inside. As the flow caused by the impeller displaces the fluid in a radial direction, the design chosen was akin to a custom made centrifugal pump. The container was constructed using plastic and wood with an outlet nozzle made of metal. Experiments of the pump capability of the container gave it an outflow of around 2.5 liters/second when the impeller was spinning at 300RPM. The developed CFD simulations gave a higher flow rate but overall helped shed light on the internal forces happening inside the container during high RPM testing. This design shows promise and there is room for further development.

Efficient graph embeddings with community detection – **Felix Djuphammar** -
<https://umu.zoom.us/j/9495037348>

For quite some time, companies in general have been becoming better at collecting data surrounding their business. In more recent years, the growing data sets have become increasingly difficult to extract valuable information from. Understanding what the available data tells us is crucial for making justified decisions in everything from marketing to product development. A common tool to interpret data sets is intuitive visualization. By visually observing how data points relate to each other it is much easier to understand the data as a whole, but this comes with limitations. Data is rarely collected in a way that simply allows for a direct 2D or 3D visualization. To solve this, techniques in dimensional reduction are often applied to enable a 2D visual representation of the relation between two higher dimensional data points actually are. Current implementations of dimensional reduction use the raw data set as starting point. This is not perfectly suited nor fully optimized for the task at hand, where an existing network is already created. By creating a new implementation of dimensional reduction that uses the complete network as an input it is far more simple to control and modularize the pipeline as well as improving performance. Furthermore, there exists a trade-off between performance and accuracy. Methods that give precise and satisfying results generally scale very poorly when applied to large scale networks. The purpose of this thesis is to derive a mathematical approximation of an existing method with improved scaling properties and write a program that accepts a predefined network as input. The program shall then be able to generate a layout structure for the network using the derived method. Using community detection a method of lower order was derived and implemented. The scaling of the algorithm was improved from a best case order of N^2 to $N^{1.5}$. This improvement is very significant for very large networks.

