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Good morning everyone. Today I'll be presenting my master thesis work in Medical Photonics, focusing on developing analysis techniques for dynamic MRI of the knee. This was done at the UKJ, in the Werner Kaiser MRT Forschungszentrum, as you can see from the picture. Let me begin by explaining why this work matters..."

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*'Problems with the knee are fairly common, especially as people get older. For example, knee osteoarthritis affects approximately **10% of men and 13% of women aged 60 and older.***

When the knee is afflicted by disorders like osteoarthritis or ACL deficiency, its kinematics—the way the knee moves—are altered. These alterations change the loading patterns on the joint, creating a vicious cycle: abnormal forces lead to tissue damage, which in turn accelerates disease progression.

Therefore, understanding knee kinematics is crucial for developing effective interventions to break this cycle and improve patient outcomes.

So, you can think of knee kinematics as the study of knee motion involving these three primary bones: the femur, tibia, and patella, along with supporting structures like ligaments and tendons. In studying knee kinematics, researchers typically focus on either patellofemoral kinematics—how the kneecap moves relative to the thigh bone—or tibiofemoral kinematics—how the shin bone moves relative to the thigh bone.

For this project, I focused on tibiofemoral kinematics, which we'll explore in more detail.

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When it comes to tibiofemoral kinematics, it is understood that the tibia has 6 degrees of freedom. Three translations and three rotations. A combination of these movements occur when we do daily activities like, walking, climbing stairs, jumping, etc

There are different methods to study these movements. For example, Motion capture systems with skin-mounted sensors. Or fluoroscopy imaging using real time x-rays. Both of these methods will have their pros and cons, but what we are concerned with is using magnetic resonance imaging, in particular dynamic MRI for capturing the knee motion.

So, today, i want to share how we set everything up that enabled us to capture the knee in motion using mri, which is not a standard approach by any means.

Then, i will spend a bit of time on how i tackled the main aim of my thesis, which was to track the tibia and femur throughout the motion cycle from the images that we obtain

Afterwards, I will show a group analysis of the kinematic parameters obtained after tracking

Lastly, I will share my interpretation of the results, along with the future potential.

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To begin, lets talk about how we can capture the knee in motion using mri. Now, normally, we want to avoid movement in the scanner as much as possible, because of motion artificats. But, since we want to do the opposite, we utilize a custom made device for this.

The device serves many purposes, b

-> first, it allows us to perform repeated active flexion-extension exercise inside the scanner in a consistent manner. Just imagine performing such an exercise without any device, it would be impossible to keep your leg in the same plane. And this consistent is key because of the next major reason for using the device:

-> second, this device allows us to sync the motion of the knee with the mri data, which enables the retrospective reconstruction of CINE images.

-> finally, we can also add load on the device, so movement with external load can also be analysed.

-> so, lets see how we set the volunteers in the device: they lie supine on the scanning table and their legs are attached in two places, one on the thigh, and one near the ankle. Using velcro.

-> on the distal end, we can add weights, and on the fulcrum here, we have a fibre optic sensor attached, which records the angle very precisely and in real time. The data is fed to a computer outside the scanner.

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-> Once they are in the scanner, the scan starts, and they hear a metronome. They move the leg according to this beat, the timing was set to 60 bpm. 1-2-3-4 you go up and 1-2-3-4 you come back down.

-> they do this for 160 for each scan. Once with weights and once without weights. ..
Now, you might wonder - how do we actually create images from all these repeated motions? This brings us to what we call CINE reconstruction, which is crucial for capturing knee motion using MRI."

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-> "In MRI, we collect our data in not in the spatial domain, but in the frequency domain, or k-space. As the knee moves we are continuously acquiring one k-space after another. So, one k-space contains information of the knee at various angles. But trying to directly use any one of the k-spaces will not work.

The Solution is clever> The magic happens in the reconstruction. Using the angle information from the rotary encoder, we can retrospectively sort and combine the k-space data from similar knee angles across multiple cycles. For example, when we want to reconstruct an image of the knee at 30 degrees, we identify all the k-space data acquired when the knee was at that angle across roughly 100 different cycles and combine them to form a complete k-space for that specific angle.

This process repeats for each angle throughout the motion cycle, allowing us to reconstruct clear images at multiple knee positions. Let me show you what this actually looks like..

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Here we see what this process produces for a single frame. On the left is our fully sampled k-space data for one specific angle of knee flexion. The brightness represents the signal intensity at different spatial frequencies. To convert this frequency information into an actual image, we perform what's called a 2D inverse Fast Fourier Transform, or IFFT. The result, shown on the right, is our reconstructed image of the knee at that particular angle.

This same process is repeated for each angle throughout the motion cycle, which brings us to our next slide..."

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Here we see the complete sequence of reconstructed frames showing the knee throughout its range of motion. While getting to this point was already a interesting, it

was just the starting point for my thesis work. The real challenge lay ahead: how do we actually extract meaningful kinematic information from these images?

To study knee kinematics, we need to track the tibia and femur bones precisely through every frame of motion. The traditional approach would be manual segmentation - drawing around each bone in every single frame. But this presents two major problems: First, it's extremely time-consuming. With dozens of frames per motion cycle, manual segmentation could take hours for just one dataset. Second, and perhaps more critically, manual segmentation tends to be inconsistent. Human operators inevitably introduce variations that can make the resulting motion appear jittery or unrealistic.

So, my main thesis objective was to develop an automated method for tracking these bones - one that would be both faster and more consistent than manual segmentation. The first step in this process was to apply edge detection to identify the bone boundaries, which I'll show you next.

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I used the canny algorithm of edge detection. The point is to isolate the inner boundary of the cortical bone of the tibia and the femur. This method works by smoothing the image and then computing gradients at each pixel to identify edges.

On the right, you can see how different value of gaussian blur affects the appearance of edges, and on the left you can see how the different combination of low and high threshold play a role. The double thresholding is what we refer to thresholding by hystereses which classifies pixels into weak edges, strong edges or non edges.

The idea here is that we can't use arbitrary values for this, so all sorts of combination had to be checked. However, once I was happy with the combination, I did not have to do it again for other datasets because of the same acquisition parameters, inter subject variability was minimal.

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Here, we can see what the edge detection output looks like. At this point, we need to refine these detected edges. Since there are multiple edges in the image that we don't need, a few additional processing steps were taken: first, removing small objects to eliminate noise, and then applying skeletonization, which thins all edges down to a single-pixel width.

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Even after these refinements, our target boundary isn't completely isolated because several other consistent, long edges remain, notably the outer boundary, which usually comes in tandem with the inner boundary. Rather than trying to remove these extra edges, I took a different approach: using connected component labeling to assign different labels to each distinct edge, allowing us to simply select the labels we need.

The key parameter here was choosing the right structuring element. Structuring elements are essentially small matrices of true/false values that scan across the image - when they encounter a foreground pixel, they determine whether neighboring pixels belong to the same connected component.

Here's where it gets interesting: instead of treating each frame separately, I considered the entire stack of 2D images as one 3D volume and used a fully-connected $3 \times 3 \times 3$ matrix as the structuring element. This turned out to be crucial because it maintained consistent labeling across frames. When I tried using just a 2D structuring element, while it could isolate edges within a single frame, the labels would change unpredictably between frames

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Now that we've isolated the inner boundary of the bones, what we actually have is a list of pixel coordinates for each frame where these edges are detected. Our goal is to compute the transformation between these coordinate sets as the bone moves from frame to frame.

Let me illustrate this with an example. Here we have Set R, which is our edge from the first frame, and Set Q from a later frame where the tibia has moved slightly. The question is: how do we determine the transformation that maps one set to the other?

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Well, it turns out we can't work directly with these raw coordinate sets. There are several fundamental issues that make this challenging:

First, there's a lack of correspondence - we don't know which point in Set R corresponds to which point in Set Q. Second, the order of points matters for tracking movement, but our edge detection gives us unordered sets. Third, we have inconsistent sampling - some parts of the edge have more points than others. And finally, we often end up with an unequal number of points between frames.

All these issues make it impossible to directly compute the transformation between frames. We need a way to create a more structured representation of these edges, which I'll show you next.

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To address the issues we just discussed, I developed a three-step process. Let's start with Set R on the left, and I'll show you how we transform it into Set P with well-organized reference points.

First, we need to sort the points in a consistent way. For this, I use anatomical landmarks as starting points - for the tibia, we begin at the most distal and posterior point, while for the femur, we start at the most proximal and posterior point. From there, we use a nearest neighbor approach to create an ordered path along the edge

Once sorted, I use cubic spline interpolation to fit a smooth, continuous curve through these points. This gives us a mathematical representation of the edge that we can sample from. The spline is parameterized by the cumulative distance along the curve, which allows us to place points at precise intervals.

Finally, for the downsampling step, we calculate the total length of the curve and divide it into equal intervals. I found that 80 points gave us the right balance between accuracy and computational efficiency. These new points, shown here in orange, are placed at these equal intervals along the spline curve.

As you can see, we now have a set of uniformly spaced, ordered points that faithfully represent the bone's edge - much better suited for computing transformations between frames."

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Now that we have our well-ordered Set P, finding the transformation becomes much simpler. Let me show you the mathematics behind this transformation in the next slides..

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Let me explain how we find the transformation between frames. First, we make a key assumption - bones are rigid bodies, meaning they don't deform during motion. This

simplifies our problem significantly because any rigid transformation can be described by just three parameters: one rotation angle ϕ and two translations Δx and Δy .

As you can see in this equation, any point (x,y) in Set P can be transformed using these three parameters. Our goal is to find the optimal values that give us perfect alignment with Set Q.

To find these parameters, we need a way to measure how well our sets align. To quantify this misalignment, I used the sum of distances between each point in the set P after transformation to the nearest point in setQ. Larger the sum larger is the misalignment.

The goal then is to find the rotation and translation values that make this sum as small as possible, which would mean we've found the transformation that best aligns our sets.

I've written this as a cost function, shown here in the equation. It takes our transformation parameters as input and outputs this sum of distances. Our goal is to minimize this function.

Let me show you in the next slide how we actually perform this minimization...

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To achieve this alignment, I used the Nelder-Mead simplex algorithm, which is an optimization method that efficiently minimizes our cost function.

The process works frame by frame, using each transformed frame as a reference for the next. We start with an initial guess of zero for all parameters, and the algorithm iteratively adjusts them until it finds the optimal values, or reaches our specified tolerance threshold.

Let's look at the result of our optimization. Here you can see three things overlaid: the original Set Q in white, our initial Set P, and in green, Set P' - which is Set P after applying our optimal transformation. You can see how well Set P' aligns with Set Q, validating our approach.

The beauty of this approach is that once we have these transformation parameters, we can apply them to any shape we draw on the bone in our first frame. This shape will automatically be transformed correctly across all frames of the motion cycle.

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Here, you can see the result - our segmentation correctly follows the bones throughout the motion cycle. So we've achieved the first goal of my thesis: successfully tracking these bones automatically.

Now comes our second challenge - extracting meaningful kinematic parameters from these segmented bones."

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For our kinematic analysis, I focused on two key measurements across all five datasets, comparing loaded versus unloaded conditions. On the right, you can see the long axes we calculated for both bones, using principal component analysis - these let us measure the angle between the femur and tibia throughout the motion cycle.

On the left, we tracked two anatomical landmarks: one at the most distal point of the femur, and one on the tibial plateau. By measuring the distance between these points, we can quantify how the bones move relative to each other.

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Here are our results, the first thing to note is that because different subjects had different number of frames, the time axis has been normalized from -100% to 100% flexion to allow comparison across datasets with different ranges of motion. I binned the data in 10% intervals and averaged across all five datasets. So instead of seeing number of frames on the x axis, we have percent of flexion.

-> Looking at the angle measurements [pointing to left graph], we see both loaded and unloaded conditions follow similar patterns, with the angle decreasing during extension and increasing during flexion. No significant difference was found in any of the bins.

-> The pattern is quite similar for the distance case, where the distance between the bones decrease as one extends the leg, however, there is a sig dif between loaded and unloaded for the f0 to 10% flexion range

What's particularly intriguing about these results is that we only found significant differences in the 0-10% flexion range - right when the knee begins to flex from full extension. This timing coincides with the Screw Home Mechanism (SHM), where the tibia naturally rotates externally relative to the femur to lock the knee at full extension.

Our measurement method assumes purely sagittal plane motion, but during early flexion, the tibia must rotate internally to "unlock" the knee. External loading is known to amplify this rotational movement. Therefore, the differences we're detecting in our distance measurements likely reflect this enhanced tibial rotation under load.

This finding has clinical relevance, as altered SHM function has been observed in osteoarthritis patients. Understanding how loading affects this mechanism could provide new insights for early detection of knee problems.

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Let me conclude this talk by summarizing what I achieved during my thesis. The primary challenge was to develop an efficient method for analyzing dynamic knee MRI data. As you can see from this workflow, I created a semi-automated pipeline that tracks the tibia and femur throughout the motion cycle. This eliminates the need for time-consuming manual segmentation while maintaining accuracy.

Using this pipeline, we were able to extract and analyze kinematic parameters, revealing interesting insights about knee mechanics under load, particularly during terminal extension. While these findings are promising, they also open up new possibilities. With more healthy volunteers, we could establish normative trends for clinical reference. Additionally, since the patella shows well-defined edges in our images, this same methodology could be extended to study patellofemoral kinematics.

Thank you for your attention. I'm happy to take any questions.