



## MRI-based assessment of hip joint translations

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### ABSTRACT

To better understand movement limitations and, to some extent, the pathogenesis of osteoarthritis, it is important to quantitatively measure femoroacetabular translations to assess if any joint subluxation occurs. In this paper, we aim at measuring hip joint displacements from magnetic resonance images (MRI) based on a surface registration technique. Because this measurement is related to the location of the hip joint center (HJC), we investigate and compare different HJC estimation approaches based on patient-specific 3D bone models. We estimate the HJC based on a simulated circumduction while minimizing inter-articular distance changes. Measurements of femoroacetabular translations during low amplitude abductions (80 samples) and extreme flexions (60 samples) in female professional dancers, which is a population potentially exposed to femoroacetabular impingements, do not show any significant subluxation.

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### 1. Introduction

Hip subluxation is a possible cause of pain and degenerative disorders in subjects undergoing repetitive and extreme movements of the joint, such as athletes and dancers. Femoroacetabular impingements (FAI) are obvious in maximal flexion (Yamamura et al., 2007) and explain superior labral lesions regularly observed in clinics (Pfirrmann et al., 2006). A current hypothesis is that FAI may lead to osteoarthritis (Klaue et al., 1991; Ganz et al., 2003). To better understand movement limitations and, to some extent, the pathogenesis of osteoarthritis, it is important to quantitatively measure femoroacetabular translations to assess if any joint subluxation occurs. In most biomechanical studies, the hip joint is considered as a ball and socket joint, meaning that no shift is allowed (perfect joint). However, it has been reported that both the femur and the pelvis are not strictly spherical (Menschik, 1997), which would result in joint translations during normal movement. It would be particularly interesting to know the influence of joint incongruity on joint translations and labral deformations. The objective of this study is

to test the hypothesis that the HJC remains fixed even in extreme ranges of motion for healthy subjects. We measure hip joint translations from magnetic resonance images (MRI) by registering 3D bone models to the images. Measurement of femoroacetabular translations relies on an accurate HJC location. Therefore, we investigate different predictive and functional approaches for hip joint center computation and compare them during both low amplitude and extreme movements.

In the literature, two main approaches have been presented to estimate the hip joint center:

- The predictive (static) approach (Bell et al., 1990; Kirkwood et al., 1999) estimates the HJC as a relative position of anatomical landmarks.
- The functional (dynamic) approach estimates the HJC from recorded optical motion capture data (Cappozzo, 1984; Camomilla et al., 2006; Siston and Delp, 2006; Piazza et al., 2001; Chang and Pollard, 2007) or from simulated movements (Kang et al., 2002).

It has been reported that the functional approach is more accurate since it accounts for joint dynamics (Wu et al., 2002). In Siston and Delp (2006), the functional method is tested with a known HJC (phantom), and a smallest error of  $2.2 \pm 0.2$  mm is reported (circumduction motion pattern). In Kang et al. (2002), a hip joint 3D model is used. An initial HJC is placed manually. The proposed algorithm adjusts it by testing points around the initial guess until no bone-to-bone collision occurs during low

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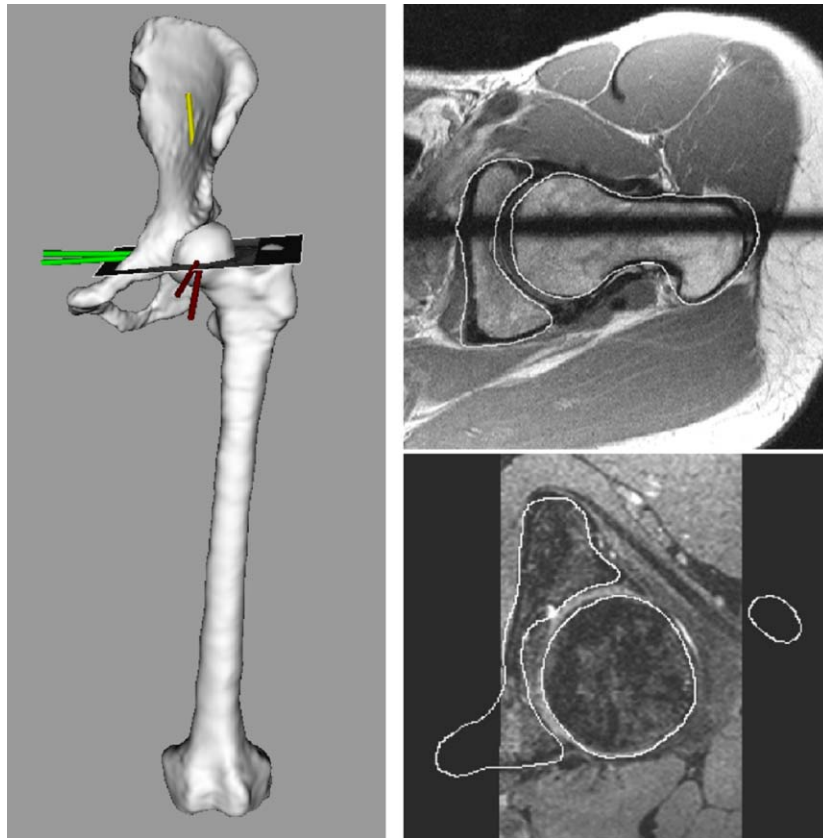


Fig. 1. Bone (31,874 vertices) surfaces extracted from MRI and two sample cutting planes (radial and TrueFISP sequences) with superimposed models (in white).

amplitude circumduction. The algorithm was not validated (motion was only simulated). On a standard PC (Pentium IV 3.4 GHz), it turns to heavy computation (several hours) for an accurate estimate and the manual initialization is a source of error.

The acquisition of a circumduction motion pattern with a reasonable number of samples is problematic with MRI due to tight acquisition time constraints. Instead, our approach estimates the HJC based on 3D models reconstructed in a reference neutral posture. We propose a predictive approach based on a least-squares sphere fit to bone surface and a fast functional approach that minimizes interarticular distance changes. 3D bone models are registered to extract joint poses in additional data sets. Joint translations are measured with reference to the previously estimated hip joint center. We present two case studies on normal subjects where 80 low-amplitude abductions and 60 extreme flexions (splits) are analyzed. The later study deals with on a potentially FAI-exposed population (30 female professional dancers).

## 2. Methods

### 2.1. 3D reconstruction and motion tracking

As opposed to the neurology and cardiology application domains, musculoskeletal research has not yet taken the full benefit of the recent advances in medical imaging and image processing (Blemker et al., 2007). This is mainly due to the complexity of the musculoskeletal system: it exhibits a large number of interdependent organs, difficult to delineate in images, undergoing large deformations and with a large inter-patient variability. However, we have recently shown that the musculoskeletal system could be quasi-automatically segmented from MRI with an acceptable accuracy and with the ability to interactively correct the alignment (Gilles et al., 2004, 2006). Our framework is based on discrete 3D deformable surfaces that delineate bone and soft-tissue (muscles, ligaments,

cartilages, skin and labrum) boundaries in images. The idea is to register template surfaces to MRI data by maximizing the image gradient on the surface and the similarity with a prior appearance model. The process is regularized through geometric and topological constraints (i.e. shape memory, smoothness and non-penetration). Patient-specific bone geometry is obtained by non-rigid registration. Subsequently, a rigid registration process is applied to extract joint pose in multiple MRI volumes.

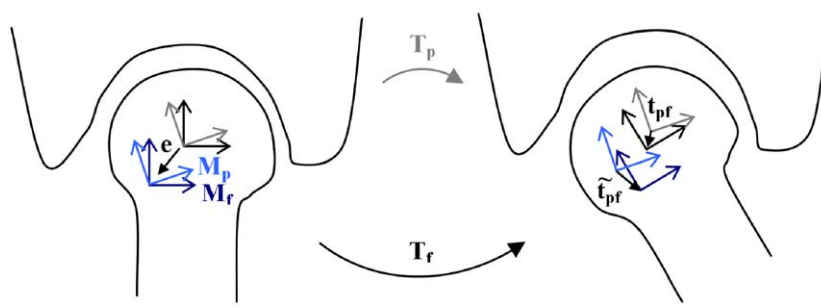
A typical reconstruction of the bones of both hips takes 2 min, with an accuracy of 1.5 mm (average distance between automatic and interactive segmentation). The accuracy is higher in the articular region because three overlapping MRI stacks are combined to improve the registration (see Fig. 1). Anatomical correspondences across models are known. Therefore, anatomical landmarks and regions of interest (e.g. femoral head, acetabulum) can be automatically wrapped from preselected points/regions in the generic reference model. Anatomical landmarks are used to construct bone coordinate systems (Wu et al., 2002). Bone motion tracking takes 2 min on a standard PC. We estimate the accuracy of our tracking algorithm using the data set where bones have been reconstructed and by applying a known rigid transform to each bone. The accuracy, calculated as the difference between the original position and the one after registration, is, for each bone, 0.5 mm in terms of translation and 0.05° in terms of rotation.

### 2.2. Hip joint center computation

We consider that the hip joint center (HJC) is the less moving point during motion and assume that the joint translation is null in the neutral posture. Let  $\mathbf{e}$  be the translation error when estimating the HJC and  $\mathbf{M}_p = [\mathbf{C}_p, \mathbf{C} + \mathbf{e}]$  (resp.  $\mathbf{M}_f = [\mathbf{C}_f, \mathbf{C} + \mathbf{e}]$ ) be the coordinate system of the pelvis (resp. femur) in the neutral position ( $\mathbf{C}_p$  and  $\mathbf{C}_f$  are  $3 \times 3$  rotation matrices and  $\mathbf{C}$  is a translation vector). Let  $\mathbf{T}_p = [\mathbf{R}_p, \mathbf{t}_p]$  (resp.  $\mathbf{T}_f = [\mathbf{R}_f, \mathbf{t}_f]$ ) be a rigid transformation applied to the pelvis (resp. femur) as shown in Fig. 2 ( $\mathbf{R}_p$  and  $\mathbf{R}_f$  denote rotations while  $\mathbf{t}_p$  and  $\mathbf{t}_f$  denote translations). The hip joint transform is given by the matrix  $\mathbf{T}_{pf} = \mathbf{M}_p^{-1} \mathbf{T}_p^{-1} \mathbf{T}_f \mathbf{M}_f = [\mathbf{R}_{pf}, \mathbf{t}_{pf} + \mathbf{C}_p^{-1} (\mathbf{R}_p^{-1} \mathbf{R}_f - \mathbf{I}) \mathbf{e}]$  ( $\mathbf{R}_{pf}$  represents joint rotations and  $\mathbf{t}_{pf}$  joint translations). This matrix can be converted to the three standard joint angles and shifts according to Grood and Suntay (1983).

#### 2.2.1. Initialization

We first locate the HJC as the center of the sphere that optimally approximates the femoral head or the acetabulum (predictive approach). We also consider the



**Fig. 2.** Influence of the HJC estimation error  $\mathbf{e}$  on joint translation measurement. The left figure shows the neutral posture with no translation between the pelvis ( $\mathbf{M}_p$ ) and the femur ( $\mathbf{M}_f$ ) coordinate systems. After joint motion (the pelvis and femur are transformed by  $\mathbf{T}_p$  and  $\mathbf{T}_f$ ), the measured joint translation  $\tilde{\mathbf{t}}_{pf}$  and the true joint translation  $\mathbf{t}_{pf}$  are different.

fitting of two spheres of identical center. The least-squares fitting of a sphere to a set of  $N$  points  $\mathbf{P}_i$ , is given by the minimization of  $\sum_{i<N} (\|\mathbf{P}_i\mathbf{C}\| - r)^2$  where  $\mathbf{C}$  is the HJC and  $r$  the radius of the sphere. Following Schneider and Eberly (2003), we set the function derivatives with regards to  $\mathbf{C}$  and  $r$  and obtain the following iterative process that quickly converges:

$$r_j = \frac{1}{N} \sum_i \|\mathbf{P}_i\mathbf{C}_j\|$$

$$\mathbf{C}_{j+1} = \mathbf{C}_0 + \frac{r_j}{N} \sum_i \frac{\mathbf{P}_i\mathbf{C}_j}{\|\mathbf{P}_i\mathbf{C}_j\|}$$

with:

$$\mathbf{C}_0 = \frac{1}{N} \sum_i \mathbf{P}_i$$

Using acetabulum points and femoral head points do not lead to the same results (about 2 mm difference) due to an inhomogeneous inter-articular distance in the models. By extending the above method with two spheres centered on the same point, we assume a constant inter-articular distance (perfect ball and socket). Let  $\mathbf{P}_i$ ,  $i < N$  be the acetabulum points and  $\mathbf{Q}_i$ ,  $i < M$  the femoral head points. The fitting process is given by

$$r1_j = \frac{1}{N} \sum_{i<N} \|\mathbf{P}_i\mathbf{C}_j\|$$

$$r2_j = \frac{1}{M} \sum_{i<M} \|\mathbf{Q}_i\mathbf{C}_j\|$$

$$\mathbf{C}_{j+1} = \mathbf{C}_0 + \frac{1}{N+M} \left( r1_j \sum_{i<N} \frac{\mathbf{P}_i\mathbf{C}_j}{\|\mathbf{P}_i\mathbf{C}_j\|} + r2_j \sum_{i<M} \frac{\mathbf{Q}_i\mathbf{C}_j}{\|\mathbf{Q}_i\mathbf{C}_j\|} \right)$$

With

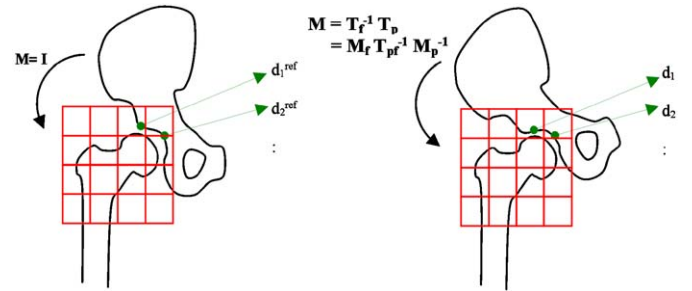
$$\mathbf{C}_0 = \frac{1}{N+M} \left( \sum_{i<N} \mathbf{P}_i + \sum_{i<M} \mathbf{Q}_i \right)$$

**2.2.2. Functional approach**

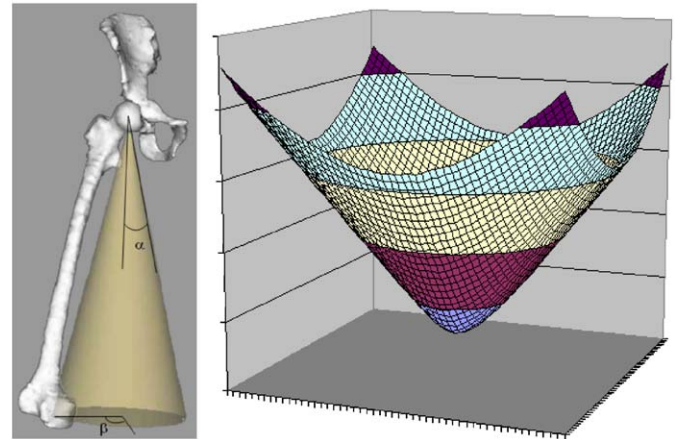
Given the initialized hip joint center and anatomical landmarks, we define the femur and pelvis coordinate systems (homogeneous rigid matrices  $\mathbf{M}_f$  and  $\mathbf{M}_p$ ) following the ISB recommendations in Grood and Suntay (1983) and Wu et al. (2002). To locally analyze the distance between the two bones, we pre-compute a distance map in a volume of voxel size  $1 \times 1 \times 1$  mm constructed in the reference frame around the femoral head. Each voxel intensity represents the signed distance to the femur surface. We can check the distance between any pelvis vertex  $\mathbf{P}_i$  and the femur by taking the distance value in the distance map at the position  $\mathbf{M} \cdot \mathbf{P}_i = \mathbf{T}_f^{-1} \cdot \mathbf{T}_p \cdot \mathbf{P}_i = \mathbf{M}_f \cdot \mathbf{T}_{pf}^{-1} \cdot \mathbf{M}_p^{-1} \cdot \mathbf{P}_i$  using trilinear interpolation (see Fig. 3). To simulate femoro-acetabular movements, we enforce a certain reference inter-articular distance at each acetabulum point  $i$ . We investigate two types of distance: (a) a constant value for all vertices: the radius difference between the two initialization spheres  $d_i^{ref} = r2 - r1$ ,  $\forall i < M$ ; (b) the initial distances in the neutral acquisition posture (see Fig. 3). For a given joint transform, we minimize the distances  $|d_i - d_i^{ref}|$  in an iterative process through multiple pelvis infinitesimal displacements. At each iteration, the rigid transform matrix  $\mathbf{M}$  is translated by

$$\mathbf{t} = \frac{\epsilon}{M} \sum_{i<M} (d_i - d_i^{ref}) \mathbf{M}_R \cdot \mathbf{n}_i$$

where  $\mathbf{n}_i$  is the normal of the pelvis at  $i$  (in the acquisition frame),  $\mathbf{M}_R$  is the rotational part of  $\mathbf{M}$  and  $\epsilon$  a parameter that weight the translation (set to 0.2). The



**Fig. 3.** Left: Reference inter-articular distance in the acquisition posture. Right: Inter-articular distance for a given joint transform.



**Fig. 4.** Left: Hip circumduction motion pattern. Right: Joint center displacement function in X–Y directions within a 5 mm distance. Other directions give similar results.

process typically converges in 300 iterations ( $\|\mathbf{t}\| < 1 \mu\text{m}$ ) for a total translation  $< 3$  mm. The total computation time is 1.5 s for 723 acetabulum points.

The algorithm presented above can optimize any joint transform in terms of shifts to seek reference inter-articular distances. To estimate the HJC, we propose to apply it for multiple joint angles and subsequently determine the less moving point from the sequence of optimized transforms. In Siston and Delp (2006) and Kang et al. (2002), it has been shown that a circumduction motion pattern is the better trajectory to estimate the HJC because all types of rotations are involved. A circumduction motion pattern is a conical movement characterized by two parameters: the elevation  $\alpha$  (set to  $20^\circ$ ) and the angle  $0 \leq \beta < 2\pi$  (see Fig. 4). Given the set of joint transforms  $\mathbf{M}_i$ ,  $i < n$  corresponding to a circumduction where translations have been optimized as previously described, we find the point of the pelvis frame that moves the less in the femur frame (the HJC estimate  $\hat{\mathbf{C}}$ ) through the minimization of the joint center displacement function:  $\hat{\mathbf{C}} = \text{argmin}(\sum_{i<n} \|\mathbf{M}_i - \mathbf{I}\| \cdot \mathbf{C})$ . Applying the AMOEBA minimization technique, the global minimum is quickly found because the initial HJC is already a good guess and because the function to minimize is convex (see Fig. 4). The computational

**Table 1**  
Summary of the MRI protocol.

Sequence	TR (ms)	TE (ms)	FOV (cm)	Matrix	FA (°)	Resolution
Low-res. axial 3D T1 (VIBE)	4.15	1.69	35	256 × 256 × 150	10	1.37 mm × 1.37 mm × 5 mm
High-res. sagittal 3D T2* (TrueFISP)	10.57	4.63	20	384 × 384 × 112	28	0.52 mm × 0.52 mm × 0.6 mm
Radial 2D intermediate weighted TSE	2180	13	16	384 × 384 × 18	180	0.41 mm × 0.41 mm × 10°

time for the whole hip joint center calculation process is 45 s (the number of transforms  $n$  is set to 30).

### 3. Results

#### 3.1. MRI acquisition

The MRI modality is chosen in order to analyze both bones and soft-tissues non-invasively. All acquisitions were performed on a 1.5T Siemens system and the imaging protocol was defined and optimized with reference to the limitations of our segmentation method (Section 2.1). This study has been approved by the local ethics committee (University Hospital of Geneva) and subjects gave informed consent to the work. Because of acquisition time restrictions, high resolution imaging of the complete bones was not applicable. Therefore, a fast (but low-resolution) protocol consisting in two axial 3D series (acquisition time: 3 min) was used to acquire the complete femurs and pelvises (required to place standard anatomical axis). A high resolution sequence centered on joints with isometric voxels (acquisition time: 4 min per hip) and a radial acquisition (6 min per hip) were run to improve details of the joints. In a second step, kinematic data was acquired using the same protocol except that the radial acquisition was skipped to reduce acquisition time. Kinematic data consisted in static acquisitions of the subject in various postures (i.e. low amplitude abduction or split). The overall acquisition time including both hips remained below 1 h. A surface coil and a fixation device were used to reduce noise and patient shifts between MRI series, and no contrast agent was injected. Imaging parameters are given in Table 1.

#### 3.2. Analysis of low amplitude abductions

In a first step, 12 healthy subjects in the lying position were analyzed. After a scan in the neutral posture, the joint was successively stepped in abduction using a MRI-compatible positioning device. In the 80 available measures, joint angles always remained relatively small ( $<30^\circ$ ). The resulting hip translation measurements were all in the order of magnitude of the tracking accuracy ( $\sim 0.5$  mm), meaning that the ball-and-socket assumption is valid in this case (i.e. pure rotation). The tested HJC computation methods were equivalent because there was almost no motion in the region of estimated hip joint centers.

#### 3.3. Analysis of splits

In a second study, we analyzed 30 professional dancers (60 hips) performing splits in the MRI tube. We compared the different HJC computation methods by studying hip joint translations. We considered the three predictive methods based on sphere fitting (femoral head, acetabulum or double sphere) and the two functional methods based on the less moving point during circumduction (use of constant or reference neutral inter-articular distance). We made the hypothesis that the HJC position estimation error  $\mathbf{e}$  is a Gaussian random vector with zero mean.

**Table 2**  
Hip joint angles in the split position.

Angles	Min (°)	Mean ± Std. Dev.	Max (°)
Flexion	109	133 ± 10	158.5
Abduction	17	32 ± 7	49
Internal rotation	-14.5	17.5 ± 13	41.5
Overall rotation	108	131 ± 8	148.5

**Table 3**  
Observed hip joint displacements during extreme flexions for different hip joint center estimation methods.

Methods	Min (mm)	Mean ± Std. Dev.	Max (mm)
Acetabulum sphere	0.34	2.76 ± 1.82	8.25
Femoral head sphere	0.57	2.12 ± 0.79	4.10
Double sphere	0.51	2.15 ± 0.91	5.03
Constant distance	0.60	3.21 ± 1.88	9.22
Reference distance	0.63	2.05 ± 0.74	3.56

Therefore, we approximated the average translation  $\|\mathbf{t}_{pf}\|$  over all subjects by the mean measured displacement  $\|\mathbf{t}_{pf} + \mathbf{C}\mathbf{S}_p^{-1}(\mathbf{R}_p^{-1}\mathbf{R}_f - \mathbf{I})\mathbf{e}\|$ . Tables 2 and 3 summarize the joint angles and translations obtained from the 60 splits.

### 4. Conclusion

Joint angles were fairly independent from the position of the HJC calculated with our methods (differences  $<0.5^\circ$ ), because a little variation of it does not influence axis direction. These angles showed low standard deviations, suggesting that movements were repeated almost identically across subjects. The ranges of motion from the two sides were well correlated (0.84). The internal rotation showed the highest variability (although almost all individuals performed an internal rotation). It has a morphological interpretation: the trochanter, that is the limiting structure, is not necessarily oriented like the knee (taken as the reference axis for computing int./ext. rotation). We think that this angular variability explains the rotation angle variability. The best hip joint center computation method was the dynamic functional method that enforces inter-articular distances from a neutral posture (measured HJC translations of  $2.05 \pm 0.74$  mm). Increasing the number of transforms  $n$  or the resolution of the distance map did not improve the results. Because standard deviations of the real displacements and the errors cumulate, we assume that the best estimation method is the one presenting the smallest standard deviation in the measured translation. Applied to a circumduction motion, the resulting hip joint center was a better guess than the one obtained with the predictive methods. However, the difference was not large and, surprisingly, the use of one sphere fit to the femoral head was better than two spheres. We believe that this is due to errors in the reconstruction of the

acetabulum (more difficult to segment than the femoral head). For the 60 hips that have been analyzed in the split position, hip joint center translations were all below 4 mm (average of 2 mm). We did not observe any privileged direction of hip joint translations. We conclude that there was no significant joint subluxation (no hinge-like motion pattern).

The next step will be to test severe cases with clear non-spherical cam types of joints and pincer cases. We believe that the presented methodology is suitable to assess the potential correlation between large joint translations and the pathological state of the articulation.

### Conflict of interest statement

There is no conflict of interest related to this work.

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