

Supplemental Material

BIGE : Biomechanics-informed GenAI for Exercise Science

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1. Data processing

1.1. Temporal Segmentation

Each sample in our reference dataset consists of an athlete performing an exercise multiple times (3–4 repetitions per sample). To process this data, we temporally segment individual motion iterations from the original recordings. The start and end frames for each motion segment are identified using the angular velocity of the joints.

Figure 1 illustrates this process, showing the angular velocity of various joints (in degrees per second) over time for an athlete performing squats. The red points in the bottom plot in Figure 1 indicate the timestamps where each squat iteration ends. For squats specifically, we used the maximum angular velocity of the *left and right knee flexion* to determine the start and end points of each motion. The closest matching time points from both knees were combined to ensure accurate segmentation.

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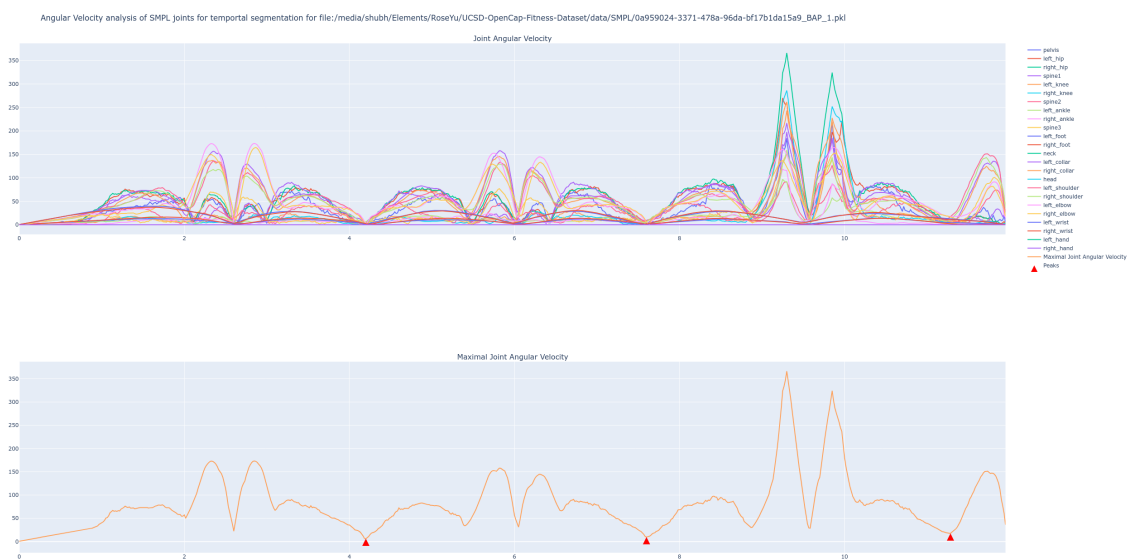


Figure 1: The top plot in the image shows the angular velocity for each joint (in deg/s) at each time step for an athlete doing squats. The red markers in the bottom plot indicate the time step at which the activity ends.

from the original recordings. The start and end frames for each motion segment are identified using the angular velocity of the joints.

Figure 1 illustrates this process, showing the angular velocity of various joints (in degrees per second) over time for an athlete performing squats. The red points arrows in the bottom plot of Figure 1 indicate the change points and the timestamps where each squat iteration ends. The motion was captured at 60 fps.

To automatically detect the start-stop cycle of each squat, first we apply savgol filter [Luo et al. \(2005\)](#) with a window length of 21 frames or (0.35 secs) with an order of 3 to smoothen the data. Next, to determine the candidates for the start and end points of each motion, we identify the valleys in the maximum angular velocity of the *left and right knee flexion*. We choose only from the bottom 10% percent and allow a distance of 6 frames or (0.1 seconds) between the candidates. Then for all best of 3 combinations of start and stop pairs, we perform cubic interpolation to normalize the segmented motion to 101 timesteps. Lastly, we choose the 3 pairs with the least standard deviation. We also penalize combinations with an average length greater than 2 seconds.

1.2. Muscle Simulation Setup

OpenCap [Uhrich et al. \(2022\)](#) can estimate dynamics using muscle-driven tracking simulations of joint kinematics. The tracking simulations are formulated as optimal control problems that aim to identify muscle excitations that minimize a cost function subject to constraints describing muscle and skeletal dynamics. The cost function J (Equation 1) includes squared terms for muscle activations (a) and excitations of the ideal torque motors at the lumbar, shoulder, and elbow joints (e_{tm}). It also includes tracking terms (squared differences between simulated and reference data), namely tracking of experimental joint positions (q), joint velocities (\dot{q}), and joint accelerations (\ddot{q}):

The musculoskeletal model is driven by 80 muscles actuating the lower-limb coordinates and 13 ideal torque motors actuating the lumbar, shoulder, and elbow coordinates. Ground reaction forces (i.e., external forces) are modeled through six-foot-ground contact spheres attached to the foot

segments of the model. Raasch’s model is used to describe muscle excitation-activation coupling and a Hill-type muscle model is used to describe muscle-tendon dynamics and the dependence of muscle force on muscle fiber length and velocity. Skeletal motion is modeled with Newtonian rigid body dynamics and smooth approximations of compliant Hunt-Crossley foot-ground contacts.

$$\begin{aligned}
 J = & w_1 \int_{t_0}^{t_f} \sum_{i=1}^{N_m} a_i^2(t) dt + w_2 \int_{t_0}^{t_f} \sum_{j=1}^{N_{tm}} e_{tm,j}^2(t) dt \\
 & + w_3 \int_{t_0}^{t_f} \|\mathbf{q}(t) - \mathbf{q}_{ref}(t)\|^2 dt + w_4 \int_{t_0}^{t_f} \|\dot{\mathbf{q}}(t) - \dot{\mathbf{q}}_{ref}(t)\|^2 dt \\
 & + w_5 \int_{t_0}^{t_f} \|\ddot{\mathbf{q}}(t) - \ddot{\mathbf{q}}_{ref}(t)\|^2 dt
 \end{aligned} \tag{1}$$

where t_0 and t_f are the initial and final times, w_i with $i = 1, \dots, 5$ are weights, t is time, N_m is the number of muscles, and N_{tm} is the number of torque motors. Experimental joint positions, velocities, and accelerations are low-pass filtered using fourth-order, zero-lag Butterworth filters (default cutoff frequencies are 12 Hz for gait trials and 30 Hz for non-gait trials). Each cost term is scaled with empirically determined weights. A penalty function is appended to the cost function with the remaining control variables to avoid singular arcs. Note that the optimal control problem formulation can be tailored to the activity of interest to incorporate activity-based knowledge by, for instance, adjusting the cost function, constraints, and filter settings. The optimal control problems are formulated in Python with CasADi (v3.5), using direct collocation and implicit formulations of the muscle and skeletal dynamics. Algorithmic differentiation is used to compute derivatives. IPOPT is used to solve the resulting nonlinear programming problems with a convergence tolerance of 1×10^{-3} (all other settings are kept at default).

2. Surrogate model

To predict muscle activations efficiently, we developed a surrogate model inspired by the approach in [Werling et al. \(2023\)](#), using a 3-layer transformer architecture with 3 attention heads per layer. The model captures temporal dependencies in the input motion data while approximating the muscle activation outputs generated by physics-based simulations.

The ground-truth data for training the surrogate model was generated by processing the reference dataset through the OpenCap muscle simulation pipeline, as detailed in Section 1.2. The input to the model consists of joint kinematics from the reference dataset with dimensions 196×33 (196 time-steps, 33 degrees of freedom), and the output comprises the corresponding muscle activations with dimensions 196×80 (196 time-steps, 80 muscle-tendon actuators). The model’s internal feature dimension was set to 128 to balance expressiveness and computational efficiency.

The surrogate model was trained with a dropout rate of 0.1 to prevent overfitting and an initial learning rate of 0.0002. The training was performed for 1000 epochs using the Adam optimizer [Joo et al. \(2018\)](#) with a batch size of 128. The learning rate was reduced by a factor of 0.5 whenever the validation loss plateaued for 10 consecutive epochs. The training loss was computed as the L1-smooth loss between the predicted and ground-truth muscle activations. Additionally, gradient clipping with a maximum norm of 1.0 was applied to stabilize training, and weight decay of 10^{-5} was used to regularize the model parameters.

Table 1 reports the performance of the trained surrogate model in predicting muscle activations for squat motions. Metrics include R^2 scores and root mean squared error (RMSE) for key muscles of interest. These results demonstrate the surrogate model’s accuracy in approximating the outputs of computationally expensive simulations.

Metrics	R2	RMSE
Soleus (Left)	0.639	0.117
Soleus (Right)	0.614	0.119
Vastus Intermedius (Left)	0.665	0.068
Vastus Intermedius (Right)	0.676	0.063
Vastus Lateralis (Left)	0.873	0.112
Vastus Lateralis (Right)	0.799	0.134
Vastus Medialis (Left)	0.727	0.089
Vastus Medialis (Right)	0.679	0.092

Table 1: Metrics for Surrogate

3. Experiment Details

3.1. Baselines

For comparison with BIGE, samples were generated from MDM Tevet et al. (2022) and T2M-GPT Zhang et al. (2023) by prompting them to create suitable squatting motion. Using NimblePhysics¹ (Werling et al. (2021)) the generated motion was retargeted to the joint kinematics format of Lai et al. (2017) musculoskeletal model.

Prompting: For both models, the phrase "person doing squats with hands behind head" worked best and led to the most accurate motion. Pre-trained models were used for both baselines to generate 20 samples for 'squat' motion.

Inverse Kinematics: Using individual athlete information (height, bone scale, etc), inverse kinematics was applied to convert the data from HumanML3D (Guo et al. (2022)) format \mathcal{H} into joint kinematics format K .

MDM and T2M-GPT utilize the joint representation proposed in Guo et al. (2022) where the pose at each instant is represented as a 263-dimensional pose vector composed of various components: $\mathbf{p} = [\mathbf{r}_r, \mathbf{r}_l, \mathbf{r}_y, \mathbf{r}_i, \mathbf{r}_o, \mathbf{v}_l, \mathbf{f}_c]$. For N samples with T time-steps, $\mathbf{r}_r \in \mathbb{R}^{T \times N \times 1}$ represents the root rotation velocity, $\mathbf{r}_l \in \mathbb{R}^{T \times N \times 2}$ is the root linear velocity, $\mathbf{r}_y \in \mathbb{R}^{T \times N \times 1}$ is the y-coordinate of the root, $\mathbf{r}_i \in \mathbb{R}^{T \times N \times (J-1) \times 3}$ is the translation of the remaining $J - 1$ joints (with respect to the root joint), $\mathbf{r}_o \in \mathbb{R}^{T \times N \times (J-1) \times 6}$ is the rotation data for the remaining $J - 1$ joints, $\mathbf{v}_l \in \mathbb{R}^{T \times N \times J \times 3}$ is the local velocity for all J joints, and $\mathbf{f}_c \in \mathbb{R}^{T \times N \times 4}$ is the foot contact information. Here $J = 22$ represents the first 22 joints of SMPL (Loper et al. (2015)).

The root joint is initialized at the origin. At time-step t , first using r_r , the orientation of root joint is calculated as:

$$R^t = [\cos(\sum_{i=0}^t r_{r,0}^i), 0, \cos(\sum_{i=0}^t r_{r,1}^i), 0]^T$$

1. <https://nimblephysics.org/docs/markers-and-joint-centers.html#converting-motion-between-skeleton-types>

The location of the root joint is obtained by cumulating the translation of root joint $\mathcal{H}_{root}^t = \mathcal{H}_{root}^t + R^t - 1 \cdot r_i^t$. The location of the remaining j joints, is calculated as $\mathcal{H}_j^t = R^t \cdot r_{i,j}^t$. To obtain joint kinematics K^t , we use inverse kinematics (IK) procedure in NimblePhysics using \mathcal{H} as markers until the difference in error rate converges to less than 10^{-4} .

3.2. Hyperparameters

Table 2 the hyperparameters used in the training. During guidance, we perform a cold start using only the proximity loss for the first 500 iterations and then gradually introduce all the guidance parameters α mentioned in Table 3. Again at the end of the last 500 iterations, we only apply the proximity loss.

Argument	Value	Description
total-iterations	300000	Total iterations for training
batch-size	128	Batch-size for training
learning-rate	0.0002	Initial learning rate for training
lr-scheduler	50000	Modify learning rate after every 50000 steps
gamma	0.05	Factor to modify learning rate
loss-commitment	0.02	Commitment loss of VQVAE
loss-penetration	0.05	Penetration loss of VQVAE
embedding-dimension	512	Dimension of the embedding space of VQVAE
nb-codes	512	Number of notebook vectors for VQVAE

Table 2: Hyperparameters for VQVAE training

Argument	Value	Description
total-iterations	3000	Total iterations for guidance
batch-size	20	Number of samples to generate
β	0.01	Proximity regularizer
α_{tilt}	0.5	Guidance parameter to reduce pelvis tilt.
α_{asymm}	1	Guidance parameter to reduce asymmetry
α_{ω}	0.5	Hyperparameter for foot regularizer
α_{vCOM}	50	Guidance parameter to reduce pelvis jitteriness
α_{aCOM}	100	Guidance parameter to reduce pelvis acceleration
α_{slide}	0.1	Guidance parameter to reduce foot sliding
α_{MAC}	1	Guidance parameter for muscle activation constrain

Table 3: Hyperparameters for guidance

3.3. Qualitative Comparison

We provide a frame-by-frame comparison of BIGE, MDM, and VQVAE over a single squat cycle in Figure 2. The motions generated by MDM and VQVAE fail to achieve sufficient depth in the squat and exhibit unnatural artifacts during the cycle. In contrast, BIGE produces motions closely aligned with the reference data and free of such artifacts. The biomechanical constraints enforced in BIGE enable the model to perform deep, natural squats throughout the cycle.

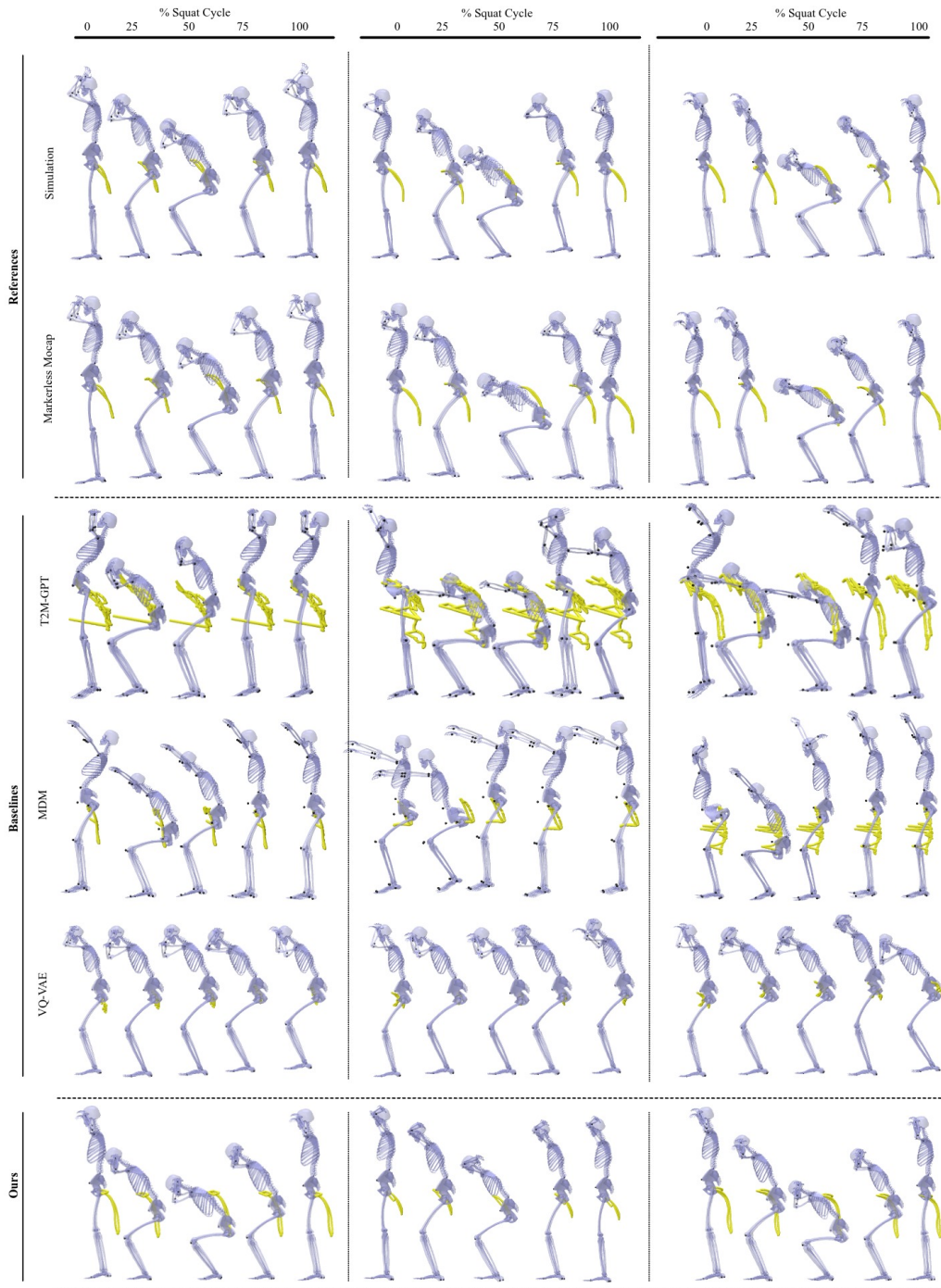


Figure 2: **Qualitative Results:** Comparison of generated samples of BIGE with references and baselines. The yellow curve represents the movement of the hip joint over the entire squat cycle. BIGE generates a more natural squat motion compared to MDM and T2M-GPT.

4. Computation Cost

Our experiments were conducted using a local cluster equipped with 8 Nvidia RTX 2080 Ti GPUs, each with 12GB of memory, an Intel Xeon processor, and 128GB of RAM. This setup enabled efficient training and inference for all components of our pipeline.

To train the VQ-VAE, we utilized DeepSpeed [Rasley et al. \(2020\)](#) to distribute the workload across all 8 GPUs, allowing for larger batch sizes and faster convergence. The VQ-VAE model required approximately 24 hours to train. The surrogate model, on the other hand, was lightweight and trained in just 30 minutes on a single GPU.

For inference, generating motion sequences with a batch size of 64 took approximately 3 seconds on a single GPU, demonstrating the computational efficiency of our approach. GPU memory utilization peaked at 10GB per GPU during training, while inference tasks required significantly less memory, making the framework practical for real-time or batch applications.

While training the VQ-VAE remains resource-intensive due to the size of the latent space and motion data, the use of DeepSpeed and distributed training substantially reduced the computational burden. Future optimizations, such as model pruning and more efficient architectures, could further enhance scalability and reduce training costs.

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