## **BIGE: Biomechanics-informed GenAI for Exercise Science**

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#### **Problem**

How to guide generative models to generate biomechanically accurate human motion?

#### **Our Results**

*We propose a novel framework, BIGE, that combines bio-mechanically meaningful scoring metrics with generative modeling. To achieve this, we:*

- develop and validate crucial physiological scoring metrics for injury avoidance and rehabilitation. Our scores incorporate observable and hidden biomechanical constraints, ensuring the clinical relevance of generated motions.
- integrate a differentiable surrogate model for muscle activation to reverse optimize the latent space of the generative model:
- enable the retrieval of physiologically valid motions through targeted search;
- demonstrates superior performance in generating diverse, physically plausible motions while maintaining high fidelity to clinician-defined objectives compared to existing approaches.
- We open source the code for simulation, data, and models at: Code: <https://github.com/Rose-STL-Lab/BIGE>

*t,*peak\_timestep*,*pelvis\_tilt\_index  $\sum_{ii}$  $j_l$ , $j_r$ ∈leg joints $(\hat{K}$ left −  $\hat{K}$ <sub>right</sub> $)^2$ 

 $\theta \in K^{\mathrm{angles}} ( \hat{K}_{t,\theta} - \hat{K}_{t,\theta} )^2$  $\sum_{t=1}^{T-1} (\hat{K}_{t+1}^{trans} - \hat{K}_{t}^{trans})^2$  is the

 $\sum_{t=2}^{T-1} (\nabla^2 \hat{K}^{trans})^2$  $T^{-1}_{t=1}$  (**p**<sub>lowest,*t*+1</sub> – **p**<sub>lowest,*t*</sub>)<sup>2</sup>

 $ax(x - high, low - x, 0)$ 

#### **Score-Guided Generative Model**



BIGE leverages score-guided optimization to refine latent representations in generative models, enforcing biomechanical constraints to produce high-quality human motion sequences.

### **Biomechanical Constraints**

Our framework allows clinicians to impose multiple biomechanical constraints and criteria on the generated motion, ensuring adherence to physiologically meaningful properties. These constraints can target various aspects of the motion, including joint kinematics, joint center dynamics, and muscle activations.

> We extend our gratitude to The Wu Tsai Human Performance Alliance for their invaluable support and resources. Their dedication to advancing human performance through interdisciplinary research has been instrumental to our project.



**Table:** Summary of loss constraints. The final objective is formulated as a weighted sum of the individual constraints.

### **Score calculation**



Latent variables (sampled randomly) are decoded using the VQ-VAE decoder to generate joint kinematics. Next, hierarchical transformations are applied to the biomechanical model, to compute joint centers and a surrogate model to predict muscle activations. Finally, clinician-defined constraints are imposed on the derived variables.

#### **Qualitative Comparison**



Comparison of squat motion sequences generated by MDM [\[1\]](#page-0-0) and BIGE against reference data from OpenCap [\[2\]](#page-0-1). The yellow trajectory traces hip joint movement throughout the complete squat cycle. BIGE produces biomechanically accurate squats that closely match the reference, while MDM exhibits unrealistic pelvic tilt (highlighted in red), resulting in less natural movement.

#### **Acknowledgments**

#### **Quantitative Comparison**



**Table:** Performance evaluation on guidance metrics. The right arrow  $(\rightarrow)$  indicates that the values should be close to the Reference data. Down arrow (↓) means a value closer to 0 is better. BIGE effectively adheres to clinician-accepted constraints, highlighting its efficacy in producing physiologically meaningful motion



#### **Muscle activation guidance**

Our guidance strategy leads to a more physiologically accurate squat motion as evidenced by the increased depth of the squat as muscle activation increases. The samples are ordered by the peak muscle activation. The red and green lines at 50% squat cycle represent the depth of the squat.

#### **References**

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