Predict Hip and Knee Kinematics During Stationary Cycling via Machine Learning Regression and Deep Learning Models

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Introduction:

- Lower limb kinematics in activities like cycling are vital for performance enhancement and injury prevention.
- Traditional marker-based motion capture systems have limitations like lab environment, time consuming, cost, human error and complexity in capturing some movements.
- Introduce a novel approach using Neural Networks (NN) and Convolutional Neural Network (CNN) to predict lower limb joint angles during cycling tasks.

Methods:

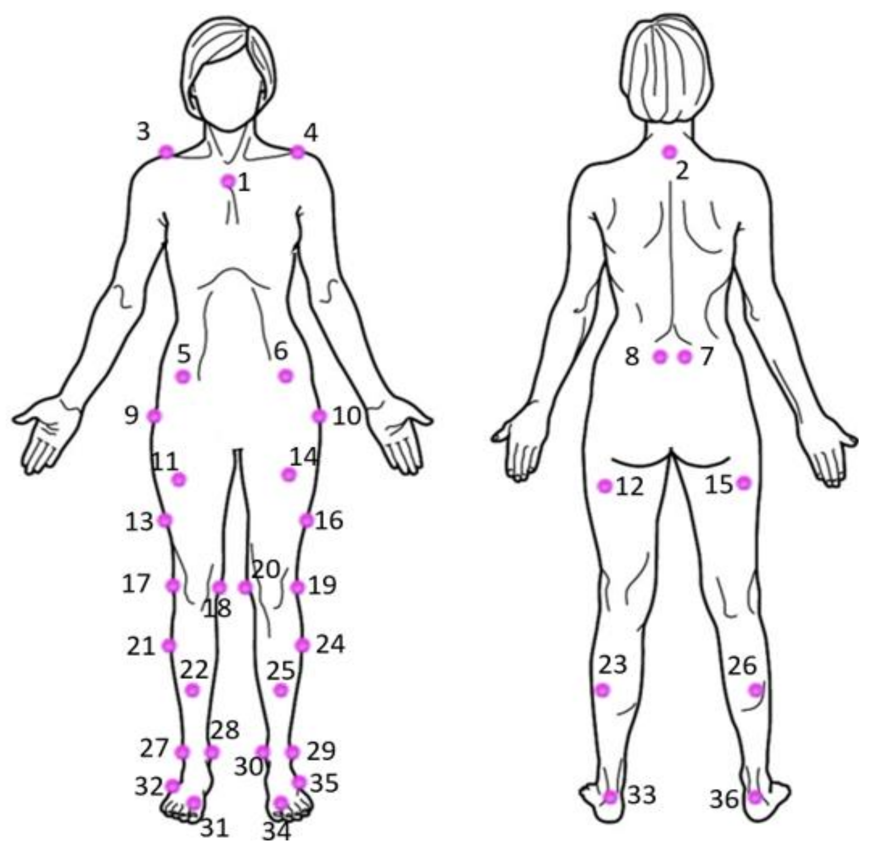


Fig. 1 Markers Placement

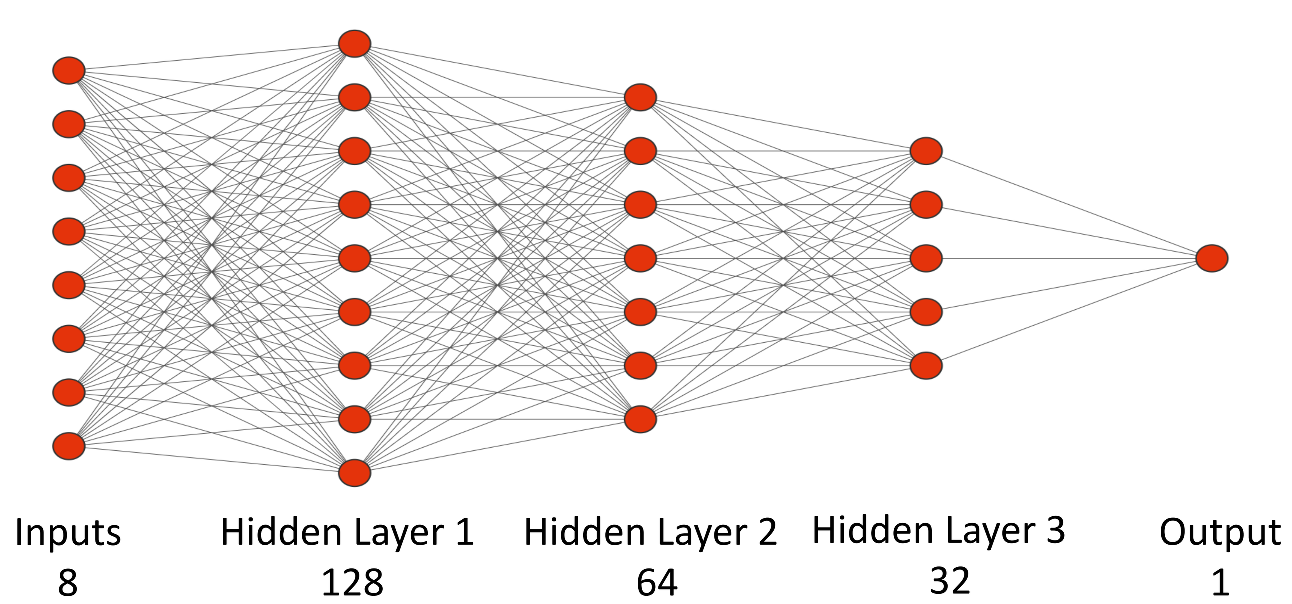
Collect 36 marker trajectories from 10 health participants.

Calculate joint kinematics via OpenSim

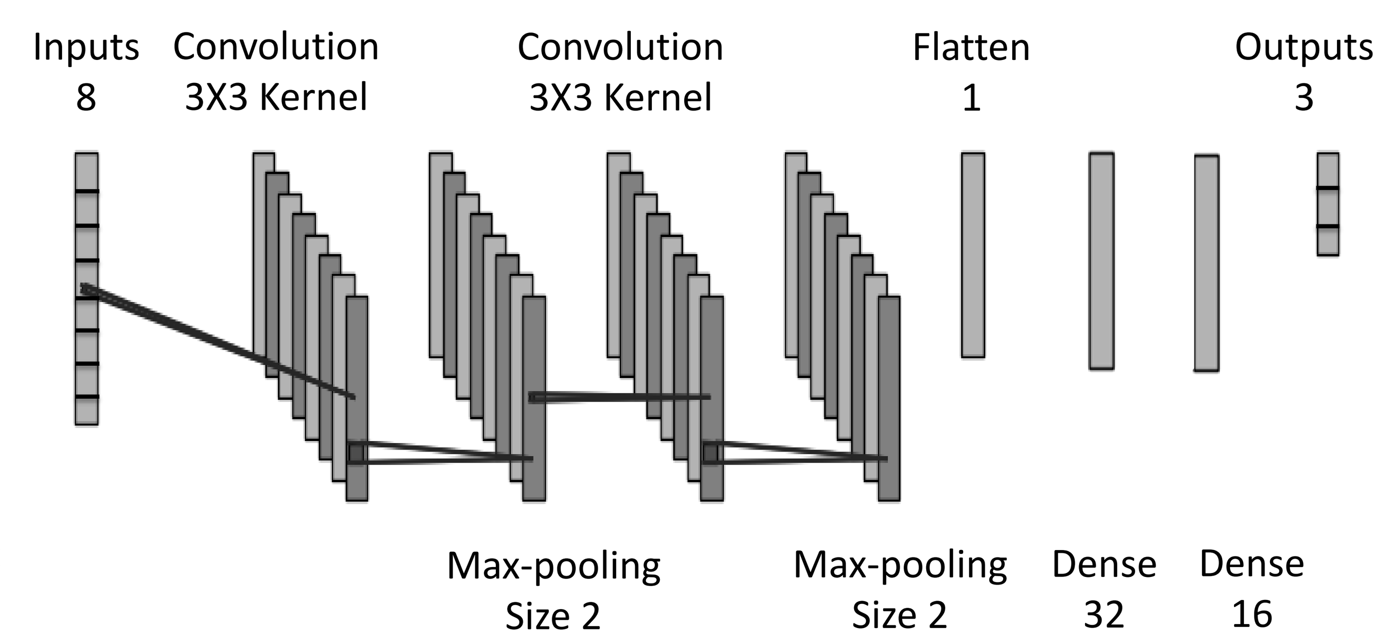
Using Pedal coordinates (x,y,z), time (percentage of task), duration of cycles, position of saddle, weight and height of partisipants

Learning Models and Prediction of Targets

❑ NN Model for Knee Kinematics



❑ CNN Model for Hip Kinematics



Results

❑ Knee flexion/extension angle:

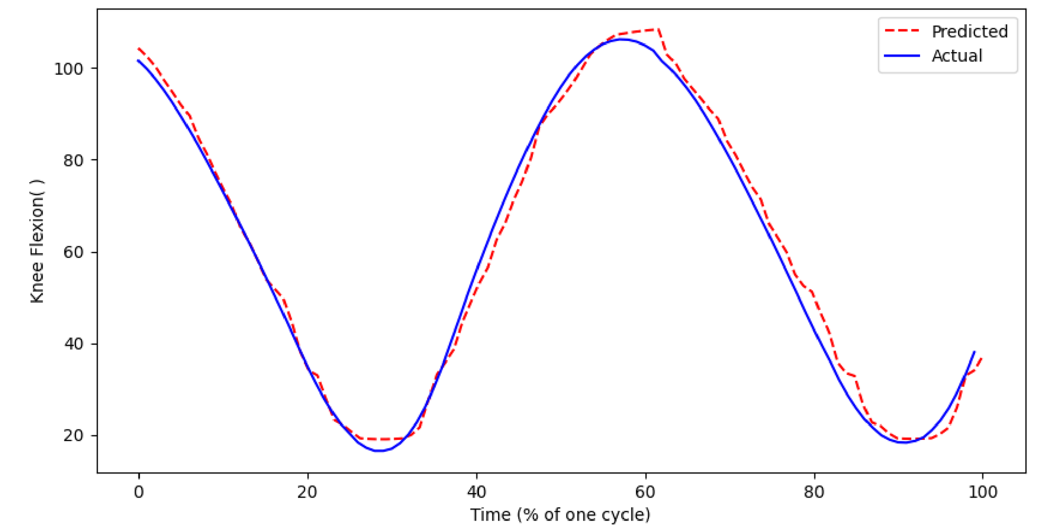


Fig. 2 Comparison between knee joint angle derived from OpenSim (Blue Solid Line) and predicted model from Neural Network Model (Red Dashed Line)

- The ranges of motion for hip flexion, adduction, and rotation were 60, 20, and 15 degrees.

	RMSE	R^2
Knee Flexion(NN)	2.12±0.71	0.99±0.12
Hip Flexion(CNN)	2.98±0.61	0.97±0.06
Hip Rotation (CNN)	1.73±0.49	0.89±0.15
Hip Adduction (CNN)	1.51±0.46	0.91±0.11

Table 1. RMSE and R2 values across hip joint angles predicted by the ML model and compared with those calculated from the OpenSim through inverse kinematics (ground truth).

❑ Hip flexion/extension angle:

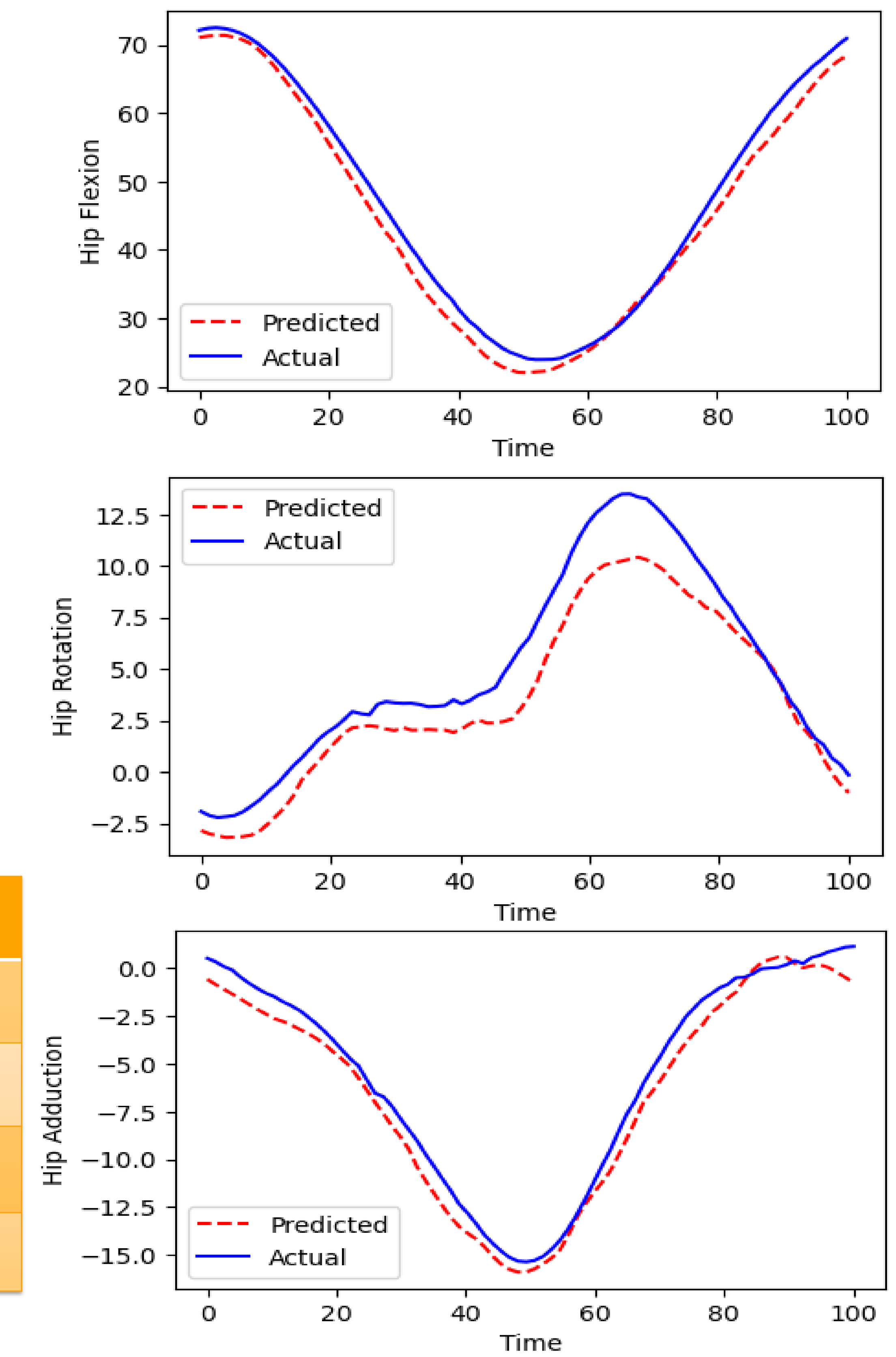


Fig. 3 Joint angles predictions by CNN model (Red Dashed Line) compared to joint angles derived from OpenSim IK tool (Blue Solid Line) across one cycle for Hip Flexion (a), Hip Rotation (b), and Hip Adduction (c) angles.

Conclusion

- Good prediction of joints kinematics
- No more limitation to Lab environment making kinematics analyses more accessible
- Less challenges comparing to traditional methods
- Robust performance of ML and DL in varied biomedical studies

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