A bipedal musculoskeletal model of the guinea fowl (Numida meleagris) to analyze muscle forces

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Summary

Here, we present a musculoskeletal model of the guinea fowl (*Numida meleagris*) suitable for analyses of muscle forces in dynamic movement. Validated with various experimental data (i.e., muscle force, lengths, and activations), this model provides a fundamental test-bed to elucidate the underlying mechanisms of locomotor agility.

Introduction

Muscles are the only actuators in our movements, yet experimental assessment of muscle forces and lengths during movement are limited to a few muscles due to feasibility of experiments. Computational musculoskeletal models and simulation offer a unique opportunity to estimate muscle states (i.e., length, force, activation) during movement. Here, we further developed an existing muscle model of the guinea fowl (*Numida meleagris*), a common animal model to study agile locomotion, to enable physiologically plausible simulations of the coordinated action of all muscles in dynamic movements. We used the model for inverse analyses of joint torques and muscle forces. and evaluated model outcomes based on experimental data.

Methods

We remodeled the existing one-legged muscle model of the guinea fowl [1] to a bipedal model, including all major muscles of the limb, resulting in 48 actuators per limb. We decreased the number of via points and wrapping surfaces to increase computational efficiency, while remaining as true as possible to anatomical reality. We estimated tendon slack lengths by optimizing for efficiency (minimizing activation squared) across a range of motions. This was crucial as tendon slack lengths determine the muscle's operating range but cannot be directly measured experimentally. We performed an inverse kinematic analysis followed by an inverse dynamic analysis based on marker trajectories and ground reaction forces [2,3]. We estimated muscle-tendon lengths and moment arms from kinematics using the model [4]. Inverse dynamic moments, muscle-tendon lengths and moment arms were input to dynamic optimization to estimate tendon slack lengths as well as the muscle states (activations, fiber lengths, and muscle forces).

Results and Discussion

Our model results in physiologically plausible estimates of inverse dynamics torques and muscle forces (Figure 1). Qualitatively we confirmed parameters with experimental data. The developed dynamic model can also be used for

predictive simulations that generate a movement pattern based on the model without relying on experimental data. Currently we are using such predictive simulations to explore the relative contribution of muscle mechanics and sensory feedback to agile locomotion.

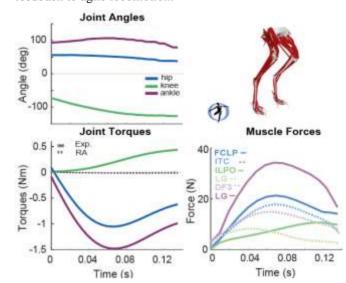


Figure 1: Joint angles and torques (experimental (Exp) and reserve actuators (RA) of the model), and a selection of muscle forces of muscles acting on hip (blue), knee (green), and ankle (purple) joint, during the stance phase while running.

Conclusions

The model we present captures inverse kinematics and dynamics, as well as muscle dynamics of walking and running guinea fowl, therefore it will be a useful tool to further explore the muscle dynamics of the major leg muscles during walking and other locomotor tasks. We will use predictive simulation methods to explore the causal relationship between muscle properties and movement, especially during agile locomotor tasks.

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References

- [1] Cox et al. (2019). Int Org Biol 1, obz022
- [2] Schwaner et al. (2024). J Exp Biol 227 (15)
- [3] Kambic et al. (2014). *J Exp Biol* **217** (15)
- [4] De Groote et al. (2016). Ann Biom Eng 44 (10)

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