Robotic modeling of mobile ball-catching as a tool for understanding biological interceptive behavior

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Abstract: We support Webb's insights into the potential benefits of using robotic modeling to better understand biological behavior. We defend the major points put forward by Webb by presenting a specific case study in which robotic modeling of mobile ball catching has helped refine and clarify aspects of our understanding of biological interceptive behavior.

In this commentary, we support Webb's insights into the potential benefits and pitfalls of using robotic modeling to better understand biological behavior. We defend the major points put forward by Webb by presenting a specific case study in which robotic modeling of mobile ball catching has helped refine and clarify aspects of our understanding of biological interceptive behavior. We show

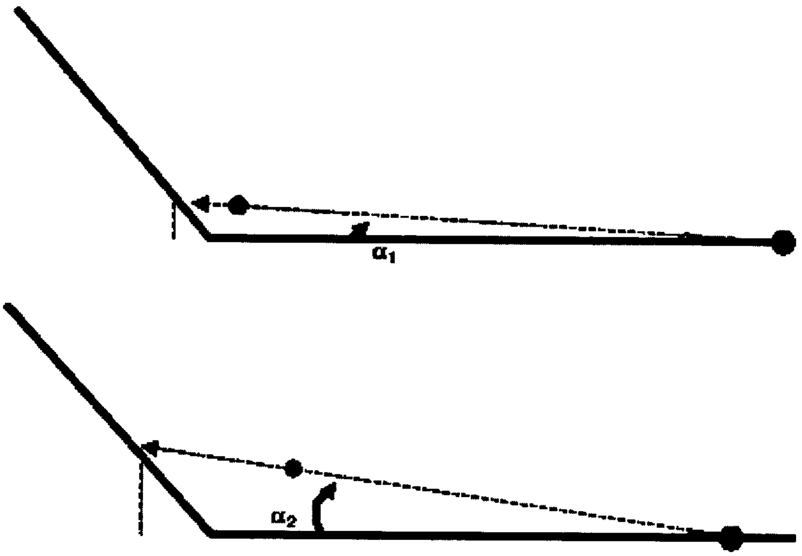

Figure 1 (Sugar & McBeath). The OAC Model. Shown is a side view of temporally successive images of a fielder (large dot) running up to catch an approaching fly ball (small dot). The fielder runs along a path that maintains a constant rate of increase in the vertical tangent angle of the ball, $\frac{d}{dt}\tan(\alpha)$. α is defined as the vertical optical angle of the ball from the perspective moving fielder. The optical change is equivalent to that produced by an imaginary elevator that rises at a constant speed along the tilted back-plane shown to the left.

how a robotic model designed to only use information that is perceptually available allows us to examine whether proposed perceptual heuristics can accurately account for biological interceptive behavior. A tunable robot also allows us to systematically control parameters such as thresholds, reaction lag time, and resolution to see if these accurately account for the patterns of variance observed in biological interception.

Recent perceptual models of how humans catch fly balls have been based largely on ecological principles that presume an ideal observer (and in much of the earlier work, on an ideal environment with no air-resistance or mechanical lag). Examples include the Optical Acceleration Cancellation (OAC) model introduced by Chapman (1968) and later refined by others (e.g., McLeod & Dienes 1996; Michaels & Oudejans 1992) and the Linear Optical Trajectory Model introduced by us (McBeath et al. 1995; 1996; Shaffer & McBeath 2002). Both of these approaches utilize control principles to guide the fielder to the correct destination by locomoting along a path that maintains constant movement of the image of the ball (Marken 1997). In the case of OAC, the vertical optical speed is maintained to be constant, while in the case of LOT, the optical trajectory is maintained to monotonically increase along a straight line (see Figs. 1 and 2). These models also treat the fielder as a point receptor, and assumed that ongoing calculations of optical angles from the perspective of the running fielder are recalibrated independent from the direction he is facing.

When we began trying to simulate biological interceptive behavior with a robotic model, we realized that important behavioral aspects were not clearly elucidated and defined in the previous perceptual models. In particular, we noted that there are two ways that the optical constancy of the trajectory of the ball can be encoded. One approach, which we refer to as "passive," is to keep the eye (or camera) stationary relative to the environmental reference frame, and control the position of the fielder to maintain constant optical ball movement across the stationary retina. A second approach, which we refer to as "active," is to move the eye relative to the environment. Here, the fielder or robot tracks the ball by moving the optics to keep them directed toward it, and then

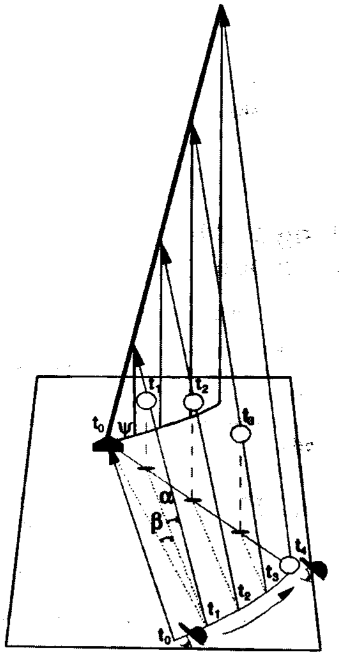

Figure 2 (Sugar & McBeath). The LOT Model. Shown is a bird's eye view of a fielder (hat) running along a path to intercept the ball (white dot) in successive temporal intervals (t_0-t_4). The fielder runs along a path that keeps the image of the ball moving along a monotonically rising Linear Optical Trajectory (LOT). Mathematically, a constant optical projection angle, Ψ, is maintained. The optical change is equivalent to that produced by an imaginary elevator that rises at a constant rate along the tilted line.

the position of the fielder is controlled to maintain constant movement of the eye (or camera) relative to the environment (McBeath et al. 2001; Sugar & McBeath 2001; Suluh et al. 2001).

From the perspective of the previous perceptual models and the assumption of an ideal observer, these two approaches are equivalent. But using the robotic simulation, we were able to demonstrate that the active approach is more robust against noise, and allows for a higher gain, so it is superior in a real world setting, with real mechanical and inertial constraints. This prompted us to confirm that biological fielders also appear to follow the active approach, and gave us insight as to why. Next we plan to systematically alter perceptual thresholds, lag, and gain parameters of the robotic model and verify that the variance in robotic fielding behavior matches that found in biological domains. The robotic platform has thus helped us to articulate and refine our biological model of interceptive behavior.

Our robotic simulation is an example that meets Webb's conditions for a useful scientific endeavor. It is relevant because it applies to real interceptive behavior in humans and animals (Collett & Land 1975; Jablonski 1998; Masters et al. 1985). It has the appropriate level, in that it models at the control parameter level just as do the perceptual interceptive models. It is generalizable in that it applies to all biological navigation that utilizes systematic control of optical variables. It has an appropriate level of abstraction, in that the complexity of the robotic and human perceptual models match well and account well for the variability of the running behavior during the interception task of catching a fly ball. It is structurally accurate, in that the design of the robotic model is a straightforward mapping from proposed biological control heuristics. It results in a good performance match with the types of running paths found with biological interception. And finally, the medium is the same as with biological interception, both are real-world, ball-catching tasks that utilize only information that is realistically available from the perspective of a moving organism.

In short, we designed and tested a robotic model of interceptive behavior and found that it meets Webb's validity test demands, and that it has added insight to our understanding of biological interceptive behavior by demanding a more refined and complete biological model to control an autonomous robot.

Soul searching and heart throbbing for biological modeling

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Abstract: Biological models are useful not only because they can simulate biological behaviors, but because they may shed light on the inner workings of complex biological structures and functions as deduced by top-down and/or bottom-up reasoning. Beyond the stylistic appeal of specific implementation methods, a model should be appraised according to its ability to bring out the underlying organizing and operating principles – which are truly the model's heart and soul.

In the target article, Webb proposes a set of useful criteria (or "dimensions") for assessing biological models. These criteria present a definitive lexis for "bottom-up" models that aim to simulate overall behavior based on the observed mechanisms at elemental levels. Another approach to modeling, which is alluded to in passing by Webb, is a "top-down" strategy that aims to infer the elemental processes from observed overall behavior. Although less well appreciated, top-down modeling is routinely practiced in hypothesis-driven investigations in the life sciences as well as the physical (Lightman 1992) and social sciences (Bradley & Schaefer 1998; Poon 1994).

Specifically, top-down models (Fig. 1) translate integrated phenomena into hypotheses about sub-level components and their interrelationships, often through the formulation of some overarching law or "theory." Because of their reliance on deductive reasoning, top-down models are necessarily controversial and could be met with skepticism, misunderstanding or outright indifference by others, particularly when the system is complex, the theory is abstract, and hard evidence is lacking. Nonetheless, such controversies may create an impetus for scientific inquiry into potentially revolutionary ideas which, if proven correct, could have far-reaching scientific implications in comparison to research approaches that target a specific reduced structure.

A masterpiece of top-down modeling comes from the legendary Mendelian theory of heredity, which laid the foundation of the genetics discipline. Like any avant-garde, however, the significance of this historic breakthrough was disregarded altogether by Mendel's peers, only to be resurrected with utmost reverence decades later when the cellular and molecular basis of the genetic code began to unfold.

By contrast, bottom-up models (Fig. 1) are grounded in experimental evidence of elemental structures and mechanisms, and their usefulness is determined by how well they match overall behaviors. This process of model building is well served by the conventional reductionist approach, which is an efficient strategy of systematically amassing discrete data. The feasibility of such a strategy is ultimately dictated by the advent of modern technology, namely, more powerful experimental tools afford further miniaturization, modularization, and proliferation of observations thereby laying the groundwork for model building at more elemental levels.

The bottom-up approach mistakenly presumes that the discovery of prime data, rather than modeling per se, is key to the understanding of biological mechanisms and behaviors. This oversimplification is not always true, however. Take, for example, the landmark discovery of the structure of DNA. Here, the reductionist's approach produced an impressive set of elemental data, and yet it was the ingenious modeling effort of Watson and Crick that ultimately fit all the pieces of the puzzle together, making sense of them. In most instances, both top-down and bottom-up approaches may be needed in order to solve a complex problem, and a model is fully validated only when bottom-up meets top-down (Lisberger & Nusbaum 2000; Poon 1992).

At another extreme, the recent mapping of the human genome has proved to mark just the beginning – rather than the end – of an odyssey to explain biological behavior from bottom up. This challenging task is hampered by its intrinsic combinatorial complexity which, in the absence of any unifying theories or models as guiding principles, may prove to be intractable in practice (XIII Oxford Conference, 2001). Could there be the equivalent of such grand deductive theories as law of gravity, relativity and evolution in the bioinformatics of genes and neurons?

That said, then how good are biological models – in particular bio-robotic models? In our view, a model should embody the key (observed or hypothesized) organizing and operating principles that relate top-level to bottom-level mechanisms – and vice versa – based on (observed or predicted) processes and behaviors at either or both ends as well as the intermediate levels. As such, the specific modalities and media for model implementation, such as bio-robotic or computer models, are secondary for the purpose of explaining biological behavior. The crux of a model is whether it captures (definitively or hypothetically) the fundamental working principles behind intricate biological structures and functions, which are truly the model's heart and soul. A model that only simulates the behavior without illuminating the underlying principles is nothing but a lifeless body.

This emphasis on principles over forms is consistent with that