

Subject: Thesis Defense: Erik Maki, MS Biology
Date: Tuesday, May 14, 2024 at 9:35:08 AM Eastern Daylight Time
From: SSB Faculty List on behalf of Diane St. Germain
To: SSB-FACULTY-LIST-L@LISTSERV.GMU.EDU

Thesis Defense Announcement
To: The George Mason University Community

Candidate: Erik Maki

Program: M.S. in Biology

Date: May 23, 2024

Time: 1:00 PM Eastern Time (US and Canada)

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Committee Chair: Dr. Ylenia Chiari
Committee Members: Dr. Daniel Hanley, Dr. Patrick Gillevet

Title: “Complexity in Animals’ Color Pattern: Estimating Sources of Non-Biological Variation in the Study of Color Pattern”

ABSTRACT:

Color pattern plays a crucial role in various aspects of an organism's biology, including camouflage, mating, and communication. Despite its significance, methods to capture, quantify, and study color pattern variation are often lacking, particularly for complex patterns that defy simple categorization. In this study, we examine existing methods for identifying and capturing animal color patterns and compare them with a new algorithm developed for this purpose. We also created codes to extract data from digital images and measure 19 different pattern

elements, aiming to capture the complexity of the color pattern of the Eastern box turtle. One key element we focused on was the symmetry of the pattern on the turtles' scutes, which is of interest in developmental and evolutionary studies. While much work on pattern symmetry relies on theoretical measures rather than empirical data due to quantification challenges, we aimed to address this gap. We chose the Eastern box turtle as our study species due to its accessibility for field photography, clear color pattern against a dark background, rigid shell structure, and lack of extensive pattern research. Our analysis included 55 individuals sampled from both the field and a museum. We evaluated various factors, such as the repeatability and accuracy of the pattern identification algorithm, image acquisition methods, lighting conditions, and animal shape, to understand their influence on pattern variation. It was crucial to account for these factors, as they contribute to non-biological variation and can affect data quality. We also incorporated a citizen science approach to assess color pattern complexity and determine which pattern elements best describe this complexity. Our findings suggest that the developed algorithm is robust and highly repeatable. Elements based on ratios, contrast, or coloration measures were more robust than those relying on the accuracy of the number of pattern objects. Additionally, angle influenced some variation, likely due to technical error. We observed some correlation between certain pattern elements and perceived complexity based on human interpretation of the color pattern. In conclusion, our study represents a significant advancement in the field by providing codes and a workflow for capturing and quantifying color pattern variation in organisms with complex patterns. It also helps differentiate between biological and technical variation in color patterns, improving our understanding of these intricate biological features.

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