様　式　Ｆ－１９－２

科学研究費助成事業　　研究成果報告書

令和　　元 年　　６ 月 ２０ 日現在

機関番号： ３８００５

研究種目： 国際共同研究加速基金（国際共同研究強化）

研究期間： 2016～2018

課題番号： １６ＫＫ０１７５

研究課題名（和文） Using machine vision to understand causes and consequences of collective behavior in a honey bee society（国際共同研究強化）

研究課題名（英文） Using machine vision to understand causes and consequences of collective behavior in a honey bee society(Fostering Joint International Research)

研究代表者

ミケェエヴ　アレクサンダー（Mikheyev, Alexander)

沖縄科学技術大学院大学・生態・進化学ユニット・准教授

研究者番号：９０６０１１６２

交付決定額（研究期間全体）：（直接経費）　　10,100,000円

渡航期間：　　17ヶ月

研究成果の概要（和文）：本研究の目的は、マシンビジョンを活用した社会性昆虫集団に属するミツバチの個体追跡であった。人は容易にミツバチの行動を識別できるが、何千もの個体を長期間観察する事は難しい。コンピューターはそれが可能だが、密集した環境で個体を識別するのは困難なタスクとなる。そこで、目印のない個体を追跡する計算手法を開発し、巣内の行動を数週間かけて観察。これまで社会性昆虫集団を乱すことなく最長継続観察を行った。主要プロジェクトのトレーニングデータは、人間との相互作用を通じて得られ、同じ技術的ツールキットを使い、ネット上での系統発生の可視化を行った。https://phylogeny.ioで研究成果を公開している。

研究成果の学術的意義や社会的意義
Understanding collective interactions between individuals requires advances in efficient tracking methods. Methods developed in the course of this grant allowed for tracking unmarked individuals and will improve the implementation of monitoring frameworks.

研究成果の概要（英文）：This project aimed to use machine vision to track individual honey bees in the social insect colony.While humans identify individual bees and their behavior easily, they don’t have time to look at thousands of individuals over months of observation. Computers can do that, but identifying individuals in a densely packed environment is a challenging computational task. Here we developed new computational approaches for the tracking of unmarked individuals in a densely packed hive and used this methodology to track hive behavior over the course of weeks, providing the longest continuous observation of an undisrupted social insect colony to date. Training data for the main project was acquired through interaction with human agents. While data were being passively acquired for the main project, we used the same technological toolkit to solve another scientific problem-the web-based visualization of phylogenetic. The results of this work are now publicly available at https://phylogeny.io

研究分野： ecology and evolution

キーワード： animal behavior　social insects　machine learning

１．研究開始当初の背景

Life on Earth has undergone several transitions in biocomplexity, from the formation of individual cells, to the origin of multicellular organisms, to the emergence of societies. Paralleling advances in the fields of cellular and developmental biology, the field of ‘sociogenomics’ aims to link the genetic and molecular basis of social function. A major challenge to this objective is the difficulty of accurately characterizing the behavior of all the individual in a complex society, preventing a complete understanding of how societies function. Social insects are an excellent model for exploring the interplay between the role of individual genes and social structure, because unlike those of humans, their societies can be experimentally altered, for instance, by changing gene expression patterns inside the individuals that make up a colony. Recent research has made progress in manipulating gene expression, and many candidate genes of social relevance have been identified in honey bees. However, because there are no accurate ways to track unmarked individuals, we know little about the effect these genes have in a social context.

２．研究の目的

The success of social insects depends on organization and cooperation of individuals that make up a colony. They act independently without coordination from a centralized command center, and the colony-level behavior emerges from millions of interactions between individual agents (the insects). The study of social insect behavior has been the object of human fascination since prehistoric times, and remains an active area of research to this day. Honey bees are among the best-studied of the social insects because of their agricultural importance, and are typically observed in through an observation hive, where their comb is positioned in between panes of glass, forcing bees into an approximately two-dimensional layer. Dense packing of bees in this environment makes them a challenging subject for computer-vision based tracking. In this project we aimed at identifying the positions of bees over long periods of time, and even attempting to track unmarked individuals for periods of time.

３．研究の方法

We generated extensive image data in which labeled examples were produced through a custom javascript interface with Amazon Mechanical Turk. This dataset contained over 375,000 labeled bee images sampled across 720 video frames at 2 FPS. This represented an extensive data set for the development and testing of tracking methods. This allowed us to develop an algorithms that can accurately identify the position and orientation of bees on the honey comb (Figure 1, Bozek et al 2018).

We also used these tools to try to reconstruct how colonies organize their‘manpower’in response to changing climactic conditions and food availability. Tracking the state of an unmanipulated hive around the clock over the course of weeks has never been done before, since it’s longer than the typical lifespan of an individual bee. As a result, previous studies needed to introduce new labeled individuals and potentially disrupt the functioning of a colony. We tracked five hives for at least two weeks each over the course of a field season, collecting data on the position of individual bees ever two minutes, as well as continuous data on the foraging activity at the entrance. The final data set contained 25,123 observations, each one containing a snapshot of the hive and all of the bees currently present there.

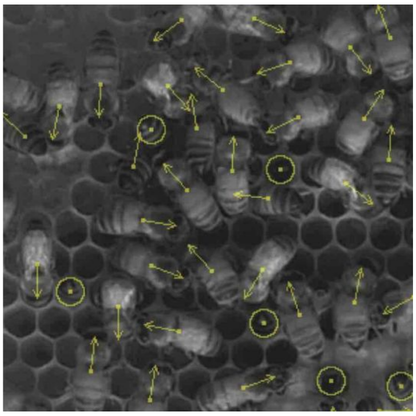

Figure 1.Automatic detection of unmarked honey bees inside an observation. Detected positions are given by arrows. Bees inside cells are shown by circles.

４．研究成果

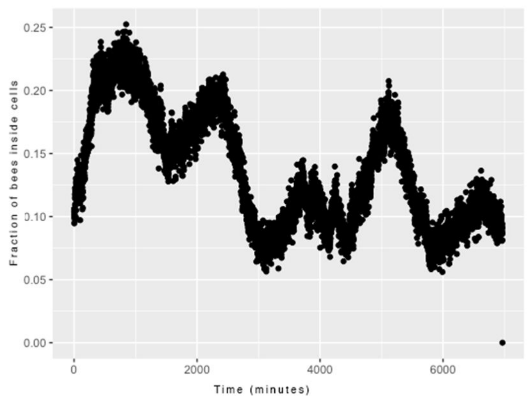

Figure 2. Bee locations over time

A) **Bee tracking.** We obtained accurate segmentation-based detection on individual bees, which rivaled humans’ performance of the same task. Specifically, we correctly detected 96% of individuals with a location error of ~ 7% of a typical body dimension, and orientation error of 12°. These results were an important step towards efficient image-based dense object tracking by allowing for the accurate determination of object location and orientation across time-series image data efficiently within one network architecture.

This technique was also applied to following short trajectories of unmarked bees. These trajectories can be joined across multiple frames allowing 46% of the trajectories to be followed 5 min recordings and over 71% of the tracks for at least 2 min, based on data from two different hived (Bozek et al 2018). We also applied the bee segmentation technique to monitoring unmanipulated hives for two weeks of more, tracking positions of every individual during that time. The data acquisition finished in December 2018, so the analyses are ongoing as of this report, but preliminary results show that data are able to capture key aspects of bee behavior, such as circadian activity over time (Figure 2).

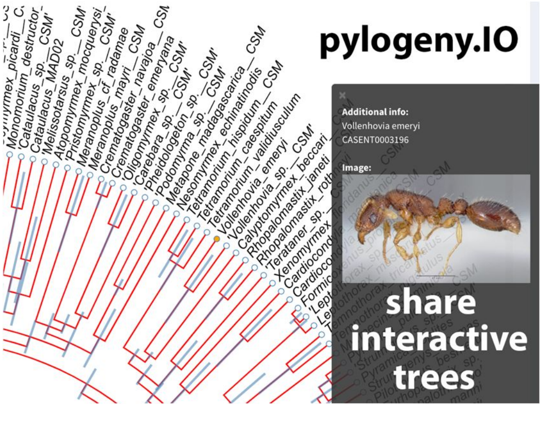

Figure 3. Phylogeny.IO

B) **Scientific visualization.** While the experiment was running we continued work on the javascript-based visualization and developed a tool for visualization of large phylogenetic trees and associated meta-data such as images. Traditional static publication formats make visualization, exploration, and sharing of massive phylogenetic trees difficult. A phylogenetic study often involves hundreds of taxa, and the resulting tree has to be split across multiple journal pages, or be shrunk onto one, which jeopardizes legibility. Furthermore, additional data layers, such as species-specific information or time calibrations are often displayed in separate figures, making the entire picture difficult for readers to grasp. Web-based technologies, such as the Data Driven Document (D3) JavaScript library, were created to overcome such challenges by allowing interactive displays of complex data sets. The new phylogeny.IO web server (https://phylogeny.io) overcomes this issue by allowing users to easily import, annotate, and share interactive phylogenetic trees. It allows a range of static (e.g. such as shapes and colors) and dynamic (e.g. pop-up text and images) annotations. Annotated trees can be saved on the server for subsequent modification or they may be shared as IFrame HTML objects, easily embeddable in any web page. The principal goal of phylogeny.IO is not to produce publication-ready figures, but rather to provide a simple and intuitive annotation interface that allows easy and rapid sharing of figures in blogs, lecture notes, press releases, etc.

５．主な発表論文等

(雑誌論文 3 件)

(1) Interactive web-based visualization and sharing of phylogenetic trees using phylogeny. IO
N Jovanovic, AS Mikheyev
Nucleic Acids Research, reviewed (2019) gkz356, https://doi.org/10.1093/nar/gkz356

(2) Pixel personality for dense object tracking in a 2D honeybee hive
K Bozek, L Hebert, AS Mikheyev, GJ Stephens
arXiv preprint (2018) arXiv:1812.11797

(3) Towards dense object tracking in a 2D honeybee hive
K Bozek, L Hebert, AS Mikheyev, GJ Stephens
Computer Vision and Pattern Recognition, reviewed, 2018 pp. 14185-4193

６．研究組織

(1)研究分担者

研究分担者氏名：

ローマ字氏名：

所属研究機関名：

部局名：

職名：

研究者番号（8 桁）：