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Methods

Simulating the socioecology of virtual primates using B3GET: a generalized behavioral modeling tool

Kristin N. Crouse[1], Clarence L. Lehman[1,2], Michael L. Wilson[1,2]

1 *Ecology, Evolution and Behavior, University of Minnesota, Saint Paul, Minnesota, USA*
2 *Institute on the Environment, University of Minnesota, 1954 Buford Avenue, Saint Paul, MN 55108, USA*
Corresponding author: Kristin N. Crouse (kncrouse@gmail.com)

Abstract

Understanding how individual behaviors scale up to population and ecosystem patterns remains a central challenge in ecology. Here, we introduce B3GET (Behavior, Ecology, Genetics, Evolution, and Tradeoffs), a generalized agent-based modeling framework that links individual stimulus–response rules to emergent ecological, evolutionary, and social dynamics. Stimuli include the observable traits of individuals, such as their sex, age, and fertility status, among other phenotypes and signals; responses include movement, body growth, and inclination to mate, eat, fight, and perform other behaviors. These rules are heritable and can mutate and recombine during sexual reproduction, resulting in the emergence of adaptive strategies and counterstrategies. We conducted 288 simulations totaling 370,199 individuals, divided equally among four emulated primate species: chimpanzees, geladas, hamadryas baboons, and olive baboons. We demonstrate that (1) B3GET can generate patchy and homogeneous virtual plant food environments; (2) virtual organisms can live and thrive in these habitats and persist for generations; (3) populations can evolve over generations; and (4) these virtual primate counterparts resembled the target species in terms of their dispersal patterns, mating strategies, and ranging behaviors. B3GET users can edit the starting files to create species-specific virtual organisms and collect simulation data for testing hypotheses. Because B3GET can emulate a broad range of animal species, it provides a promising approach for investigating broader questions in animal behavior and primate socioecology, both for research and education.

Key words: Agent-based modeling, animal behavior, behavioral ecology, individual-based modeling, primate societies, spatially explicit, stimulus-response rules, virtual evolution

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Introduction

Integrating biological theory and empirical observations across different ecological scales is essential as scientists grapple with ecosystem shifts driven by changes in climate (Steffen et al. 2015; Malhi et al. 2020), losses in biodiversity (Cardinale 2012), and environmental stresses (Freedman 2015; Jackson et al. 2021). Ecological modeling offers a structured framework for connecting processes across scales—integrating theory with empirical data, testing hypotheses, and generating predictions about ecological responses to change (Evans et al. 2013b). Individual-based models (also known as agent-based models) are particularly well-suited

to linking fine-grained, individual-level mechanisms with emergent patterns at population, community, and ecosystem levels (Grimm and Railsback 2005; Stillman et al. 2015). Despite the longstanding promise that individual-based modeling could unify ecological understanding across levels (Huston et al. 1988; Grimm et al. 2017), realizing this vision has proven difficult. This gap persists in part because classical demographic models operate at the population level and do not explicitly represent individual variation (Grimm et al. 2017), whereas mechanistic individual-level models become too complex to scale (Evans et al. 2013a).

As a result, ecologists have often built narrowly scoped individual-based models that limit complexity by focusing on a single species or research question (An et al. 2020). Such specialized models are often *ad hoc* solutions constructed for specific systems, guided by empirical observations and expert domain knowledge (Grimm et al. 2017). While specialized models provide clarity and precision tailored to specific questions (Edmonds et al. 2019), their inherent limitations restrict generalizability and adaptability to new contexts, reducing their contribution to broader theory (O'Sullivan et al. 2016; Lorscheid et al. 2019). Additionally, the proliferation of specialized models creates inefficiencies and redundancies in research efforts (An et al. 2020; Manson et al. 2020), prompting critiques such as the YAAWN syndrome: "Yet Another Agent-Based Model… Whatever… Nevermind…" (O'Sullivan et al. 2016).

To address these persistent challenges, we introduce B3GET, pronounced "bee'get" and standing for Behavior, Ecology, Genetics, Evolution, and Tradeoffs: an individual-based modeling framework designed to balance generality with mechanistic depth by simulating diverse and complex organisms and ecological processes. Drawing from behavioral ecology (Krebs and Davies 1993), evolutionary game theory (Maynard Smith 1982; McNamara and Leimar 2020), optimal foraging theory (MacArthur and Pianka 1966; Charnov 1976), life-history theory (Stearns 1989; Charnov and Berrigan 1993), resource competition (Brown and Orians 1970; Wrangham 1979), and artificial life (Gardner 1970; Ray 1994; Holland 1995), we designed B3GET to explore the complex interactions that shape social behavior, phenotypic variation, evolutionary dynamics, and other emergent biological patterns. As such, B3GET can function as a virtual "Petri dish" for *in silico* experiments, enabling controlled studies of behavioral evolution under varying ecological conditions.

B3GET simulations comprise a population of ANIMAL agents living on a landscape of PLANTS (Fig. 1; we distinguish simulated entities from their real-world counterparts using ALL CAPS, following Hogeweg's (1987) convention). User-defined controls set PLANT resource quality, spatial distribution, and seasonal cycles, driving the ecological pressures on ANIMALS. ANIMALS are equipped with heritable stimulus–response rules that guide their behaviors, including foraging, mating, fighting, helping, carrying, moving, and developing and maintaining their physiological state. These basic ANIMAL operations give rise to higher-level emergent patterns such as dispersal tendencies, mating strategies, infanticide frequency, degree of sexual dimorphism, home range distribution, intergroup tolerance, and more. ANIMALS must obtain energy from PLANTS, and behaviors incur nonzero energetic costs, enforcing realistic tradeoffs that shape how populations evolve their phenotypic traits and behavioral strategies. B3GET tracks gene-, individual-, group-, and population-level variables, enabling hypothesis testing across ecological levels.

In this study, we present B3GET as both a research and teaching tool for simulating diverse animal societies. The model is broadly reusable across species, ecological systems, and behavioral research questions. To showcase its core capabilities, we modify starting conditions and environmental parameters to demonstrate that a wide range of social and ecological outcomes can emerge. We provide concrete examples by modeling four distinct primate species: chimpanzees (*Pan troglodytes*), geladas (*Theropithecus gelada*), hamadryas baboons (*Papio hamadryas*), and olive baboons (*Papio anubis*). We focus on recreating species-typical behavioral patterns in terms of their sex-biased dispersal, mating strategies, and ranging behavior, which vary across these species.

We report results from 288 simulations in a full factorial design crossing four virtual primate species with 36 combinations of PLANT settings that regulate resource distribution. Each species × PLANT combination was simulated twice to assess stochastic variation among replicate runs. We assess model performance in four ways: (1) demonstrating that B3GET generates both patchy and homogeneous PLANT environments, (2) evaluating ANIMAL population persistence over generations, (3) analyzing evolutionary change in genotypes and phenotypes, and (4) showing that emergent ANIMAL behaviors reflect key behavioral traits observed in the four target species.

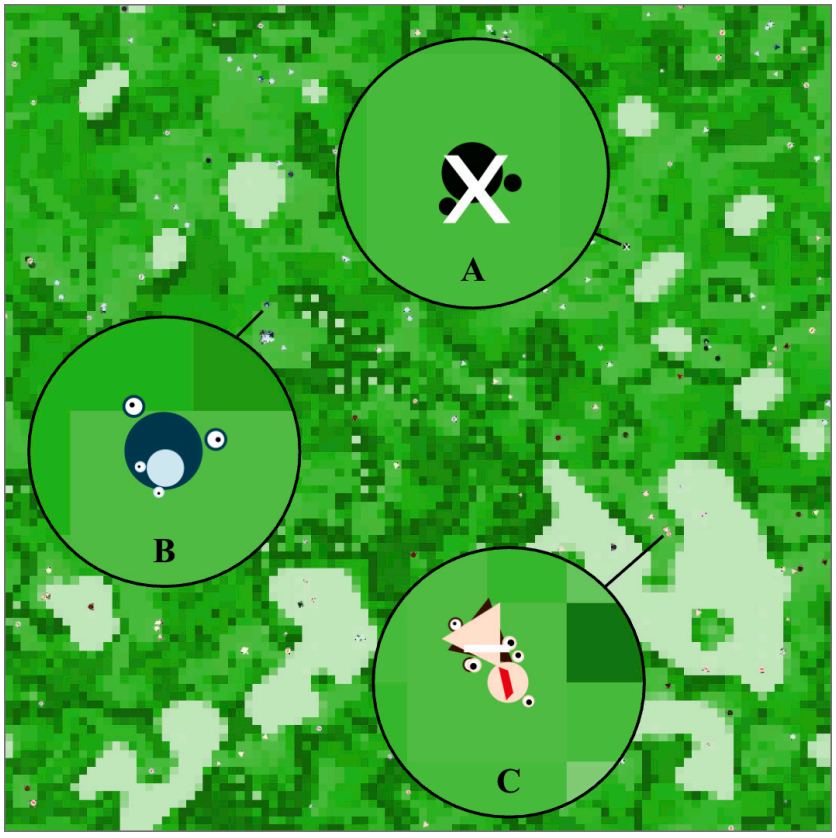

Figure 1. Screenshot of a B3GET simulation at timestep 10,000 (parameters: ***plant-annual-cycle*** = 1000, ***plant-daily-cycle*** = 10, ***plant-seasonality*** = 0.5, ***plant-quality*** = 5, ***plant-minimum-neighbors*** = 4, ***plant-maximum-neighbors*** = 6; population/genotype = CHIMPANZEES). ANIMALS are depicted as triangles (males) and circles (females), with size scaled to body.size, color indicating group.identity, and body.shade darkening with age. Inset circles provide magnified views of individual ANIMAL agents: **A.** An adult female that has died, indicated by the white "X" overlay; **B.** A mother (darker agent) carrying her infant daughter (lighter agent) on her back; **C.** A female with "cycling" fertility.status (i.e., sexual swelling), marked by a red line on her body, with two males fighting nearby, indicated by the white "–" symbol.

Methods

We designed B3GET as a hypothesis-testing tool to study how environmental pressures and energy limitations shape behavior, ecology, and evolution in virtual organisms. B3GET v1.2.0 is implemented in NetLogo 6.2.2 (Wilensky 1999), a freely available software program for creating and running agent-based models. We first developed B3GET at the University of Minnesota as a virtual laboratory tool for the course Primate Ecology and Social Behavior and refined it through multiple semesters of classroom use beginning in fall 2014. Students use B3GET to apply field observation methods to virtual PRIMATES, explore how plant ecology shapes behavior, and track predator–prey interactions. Crouse et al. (2019) used an earlier version, BEGET, to examine the evolution of stable breeding bonds by evolving diverse male strategies and comparing their reproductive success across simulations with female groups of varying sizes. This study supported the hypothesis that stable breeding bonds evolve in response to small female foraging parties (Lukas and Clutton-Brock 2013) rather than infanticide risk (Opie et al. 2013). We subsequently expanded B3GET to include spatially explicit PLANT dynamics, greater behavioral complexity, and improved usability through interface and file structure enhancements.

Here, we present results from 288 simulations with varying PLANT and ANIMAL settings. These simulations form part of a larger experiment we called BYTE, which includes additional runs under greatly altered conditions to evaluate B3GET's robustness. Because B3GET contains a large number of editable parameters, state variables, and behavioral rules, the main manuscript focuses only on those settings relevant to the present study. The BYTE Companion Guide (hereafter BYTE; Suppl. material 1), which contains the complete description of B3GET, ODD protocol (Grimm et al. 2020), user manual, BYTE experimental design details, dataset documentation, output summary analyses, and validation details. The validation material in BYTE—including runtime verification tests, multi-factor sensitivity checks, face validation using test populations, and detailed focal follows—builds on Crouse et al. (2022), which framed model validation as a series of comparisons among elements of the modeling cycle. A companion manuscript to the present study, currently in preparation, further develops this framework by organizing validation around explicit upstream-to-downstream relationships among model components, enabling more standardized evaluation at finer resolution.

Operations executed by ANIMALS are italicized (e.g., *mate-with*, *move-towards*), state variables are written with periods (e.g., life.stage, body.size), and user-defined parameters appear in ***bold italics*** (e.g., ***plant-seasonality***, ***plant-quality***).

Model design

The B3GET environment (Fig. 1) is a toroidal grid (i.e., individuals exiting one edge of the two-dimensional landscape re-enter from the opposite edge) with 10,000 PLANTS (100 × 100) and an initial population of ANIMALS defined via input files.

In modeling PLANT dynamics, we took inspiration from Conway's Game of Life (Gardner 1970), a model of cellular automata in which cell states change depending on the number of occupied neighboring cells. In B3GET, PLANTS represent a spatially explicit and dynamically changing resource base rather than specific plant species, with resource availability varying across both space and time. PLANTS grow best within a preferred neighborhood size and at specific times of the year (BYTE: Section 2.7.1, Suppl. material 1: fig. S2). The ***plant-minimum-neighbors*** and ***plant-maximum-neighbors*** settings (0–8 neighboring PLANTS) define the lower and upper bounds that promote growth, shaping clustered vs. even landscapes. Seasonal variation in resource availability is controlled by ***plant-seasonality*** (0–1: low to high), which determines the magnitude of annual fluctuations in PLANT growth, while ***plant-annual-cycle*** and ***plant-daily-cycle*** (timesteps per simulated year and day, respectively) determine the lengths of simulated annual and daily cycles. The maximum energy available per PLANT is defined by ***plant-quality*** (>0). Together, these environmental settings determine the foraging conditions experienced by ANIMALS throughout the simulation.

Each ANIMAL has a genotype composed of stimulus–response rules called genes that govern behavior and energy use (Fig. 2), with strategies subject to mutation and selection over generations (BYTE: Sections 2.3 and 2.7.2). Contingent on available energy, these rules determine which actions an individual performs and how much energy it allocates to them based on the observed states of nearby ANIMALS and PLANTS relative to its own internal state. The cumulative execution of these actions influences an individual's state variables (e.g., body.size, fertility.status, survival.chance), which together constitute its phenotype. Thus, genotypes influence phenotypes indirectly through their effects on behavior, while phenotypes ultimately determine survival and reproductive success. Simulations are initialized with ANIMAL starting states and genotype configurations specified in external input files, which can be modified to suit the intended purpose of each simulation experiment. Here, we outline the general ANIMAL state variables and actions (full ODD protocol in BYTE: Chapter 2), and in the following section, we describe the specific configurations used in this study (BYTE: Chapter 4).

B3GET operates in discrete timesteps, which represent abstract units of simulation time. Within a timestep, ANIMALS may perform multiple actions (e.g., foraging, mating, fighting, helping, or developmental investments), so a timestep is best interpreted as roughly comparable to one or several hours.

The fate of each ANIMAL depends on survival.chance, the probability from 0 to 1 of surviving to the next timestep. Although individuals begin life with survival.chance = 1.0, this value continuously declines according to ***deterioration-rate*** and must be maintained through energetic investment in the *survival-chance* action. The increase in survival.chance is proportional to the amount of energy allocated to this action, creating a tradeoff between survival and competing demands such as growth, reproduction, movement, and social behavior. Consequently, individuals that fail to acquire sufficient energy, or that invest too little in survival maintenance, may experience substantial reductions in survival.chance and die at any life stage.

All actions require sufficient energy.supply to enact; those with depleted energy are unable to act and may die of starvation. ANIMALS replenish energy

by *eating* PLANTS or other ANIMALS, with their bite.capacity setting the upper limit per feeding. ANIMALS may also invest energy to increase their bite.capacity. Thus, in general, an ANIMAL must weigh its needs to maintain its survival against all other activities, which may have immediate payoffs (e.g., *eating* to gain energy now) or delayed payoffs (e.g., growing bite.capacity to gain more energy later).

Operations such as *eating* require the interacting parties (e.g., ANIMAL and PLANT) to be in close proximity. To change locations, ANIMALS can perform movement operations such as *move-towards* to orient toward nearby objects and *go-forward* to move closer to them. ANIMALS decide which direction to move based on which objects they can detect in their environment. An ANIMAL's visual.range and visual.angle define its cone of perception, and its ability to see during the day or at night depends on the day.perception and night.perception attributes.

When two ANIMALS of opposite biological.sex meet, they may *mate-with* each other. Whether mating—or any other interaction—occurs is governed by a negotiation process. Each party may independently invest energy to initiate or inhibit the interaction, and the outcome depends on the relative contributions of the two parties. If mating occurs, the conception probability is the mean of both partners' conception.chance; the mother's litter.size sets the number of offspring.

New agents begin in the "gestatee" life.stage with minimal capabilities. Mothers and offspring use *supply-to* and *demand-from* interactions to transfer energy. Offspring use this energy to increase traits such as body.size, their own conception.chance, or visual.range to nonzero values. Life-stage transitions (e.g., to infant, juvenile, and adult) occur probabilistically (e.g., infancy.chance). Mothers likewise manage offspring development by investing in birthing.chance and weaning.chance with the actions *check-birthing* and *check-weaning*.

Mothers who conceive begin by holding their gestatees and later infants in their carried.items inventory. All carried.items stay with the carrying ANIMAL as it moves across the landscape, imposing locomotor costs on the carrier (BYTE: Section 2.7.2.3). A mother can *put-down* her offspring to remove it from her carried.items and force it to walk on its own. An infant may reverse this operation by *clinging-to* its mother, which has the effect of putting it back in the carried.items inventory. Likewise, an infant may *squirm-from* its mother, and the mother can *pick-up* her offspring.

Group dynamics are governed by shared group.identity, which can be updated during *join*, *leave*, *recruit*, and *expel* interactions. Within or between groups, ANIMALS can *attack* or *help* others, negatively or positively affecting the survival.chance of recipients. ANIMALS can assess their degree of relatedness to visible individuals based on inherited identity markers, with individuals having perceived relatedness ≥ 0.25 treated as kin (BYTE: Section 2.4.7).

During simulations, B3GET collects data using methods adapted from field studies in animal behavior and ecology (e.g., Altmann 1974; Amato et al. 2013), treating virtual agents as study subjects (Zurell et al. 2010). We recorded scan-sample states of groups every 2,000 timesteps (Amato et al. 2013) and measures of PLANT phenology every 10,000 timesteps (Tang et al. 2016). We also computed end-of-run summaries and logged complete life histories at death.

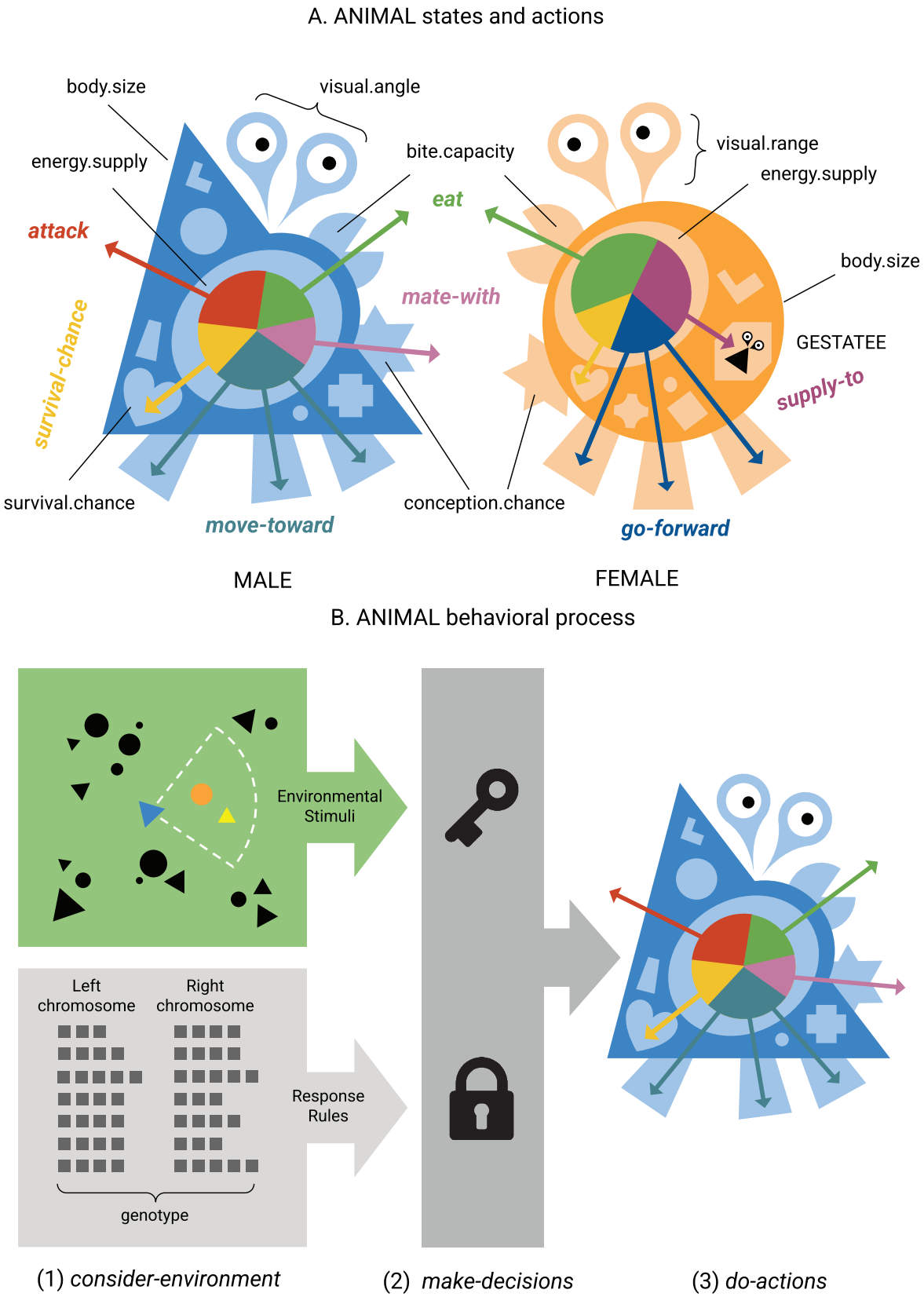

Figure 2. ANIMAL states, actions, and behavioral processes. **A.** Hypothetical ANIMAL agents, a blue male (left) and an orange female (right), shown with representative attributes (i.e., regular text and shapes), typical actions (italic text and arrows), and energy reserves (energy.supply) used to perform those actions (pie chart); **B.** Example timestep from the blue male's perspective: (1) detect objects in the environment; (2) map stimuli to genotype rules, unlocking responses to perform; and (3) execute those actions given sufficient energy.supply.

Simulation experiment

Our description above presents a general view of ANIMAL behaviors. However, small genotype edits can produce large societal differences. For this study, we constructed ANIMAL populations with differing genotypes to simulate four primate species: CHIMPANZEES, GELADAS, HAMADRYAS, and OLIVES, which we refer to collectively as PRIMATES. We chose these four species because they vary in patterns of sex-biased dispersal, mating systems, and ranging behavior—behavioral differences that we can capture with B3GET to demonstrate the capacity of the model to emulate a broad range of social behavior. Our objective was not to produce exact simulations of these species, but rather to determine whether a common modeling framework could reproduce the generalized social, ecological, and life-history patterns that distinguish them.

To construct PRIMATE genotypes, we built on Crouse et al. (2019) and refined them using field observations, expert consultation, and published empirical literature (BYTE: Section 4.2). Over many rounds of edits, we systematically modified the genotype text files and observed how these changes affected the emergent PRIMATE behaviors in the B3GET interface. This yielded 112 core genes governing general mammalian functions, including growth, maintenance, mating, gestation, and lactation. To ensure biologically meaningful group structure and selection pressures, all genotypes constrained mating to occur only between non-kin (perceived relatedness < 0.25), thereby preventing mating among parents and offspring, siblings, half-siblings, and other close relatives. In addition, each genotype included ~10 species-specific genes (CHIMPANZEES: 10; GELADAS: 11; HAMADRYAS: 9; OLIVES: 6; BYTE: Section 4.2). This iterative process became more efficient as we reused and adapted genes. For example, the dispersal genes we originally created for GELADA males were later repurposed for OLIVE males. As a result, the genotype development process improved over time: GELADAS took several months, CHIMPANZEES 1 month, HAMADRYAS 2 weeks, and OLIVES 1 week. Species-specific genes were fixed to maintain species identity, whereas core genes could mutate in energy values so that populations could fine-tune their energy-allocation strategies. We summarize below the starting conditions and intended behaviors for each species, as programmed into their genotype.

Each CHIMPANZEE simulation began with four groups of 11 adult males and 17 adult females, each occupying a separate quadrant of the landscape to reflect territorial communities (Wilson and Wrangham 2003). We programmed the CHIMPANZEE genotype with rules designed to recreate fission–fusion dynamics (Kummer 1968; Aureli et al. 2008), with preferences for male–male cohesion (Wrangham 1999) and female spacing influenced by feeding competition (Williams et al. 2002). CHIMPANZEES were the only PRIMATE genotype programmed with territoriality. PLANT cells retain information about which groups have occupied them most recently (BYTE: Section 2.7.3), allowing individuals to distinguish familiar areas from those primarily used by other groups and to avoid the latter. We included movement rules for adult males to patrol territory edges (Mitani 2009) and modified the default aggression rule so that CHIMPANZEE adult males reduce attacks on adult males who are both group members and close kin, allowing coalition formation (Wrangham

1999). Individuals are classified as kin when perceived relatedness ≥ 0.25. We also included female dispersal at the juvenile stage (Pusey 1980), along with red-signal development to simulate sexual swellings and facilitate immigration into new groups (Deschner and Boesch 2007).

Each GELADA simulation began with 16 evenly spaced groups of one adult male and five adult females. We programmed rules to recreate their multilevel society, in which reproductive units maintain stable spatial cohesion (Dunbar and Dunbar 1975; Erskine 2016) and tend to aggregate into larger herds and bands influenced by female kinship (Snyder-Mackler et al. 2012). We programmed females to leave their group if too many unrelated females were present (Tinsley Johnson et al. 2014), promoting group fission and the formation of smaller units (Le Roux et al. 2011). We programmed juvenile males to disperse from their natal group at the end of development (Beehner et al. 2009; Snyder Mackler et al. 2014), after which they could form bachelor groups with other solitary males (Kawai et al. 1983; Pappano et al. 2012). Solitary males maintained proximity to one another while avoiding aggression (Pappano et al. 2012), as modeled by reduced attack tendencies toward other solitary males. These males sought access to females through takeover attempts on reproductive units, joining groups with sufficient numbers of unrelated females (Dunbar and Dunbar 1975; Beehner and Bergman 2008). Meanwhile, resident males resisted by moving toward encroaching bachelors and attempting to prevent them from joining their groups.

Each HAMADRYAS simulation began with 16 groups of one adult male and three adult females, arranged into two spatial clusters of eight groups each. We programmed males to form reproductive units by forcibly recruiting females from other groups (Swedell et al. 2011). These actions could lead to conflicts between males, and if a male became too injured, he left his group and fled. We programmed unit cohesion to reflect male coercion (Kummer 1968; Swedell and Schreier 2009), with each agent moving toward other adult group members. Male–female bonds were maintained by rules preventing females from leaving their leader male (Kummer 1968; Abegglen 1984), provided he was alive. In contrast to female-philopatric species, females were not bonded to each other, and unit dissolution occurred if the leader male was removed (Swedell and Schreier 2009; Swedell et al. 2011). We programmed juvenile males to disperse from their natal units and seek proximity to related males in other groups, modeling kin-based male associations (Abegglen 1984; Phillips-Conroy et al. 1992) and multilevel aggregations (Schreier and Swedell 2009). Reproductive groups can also include additional "follower" males (Pines et al. 2011), modeled with a gene enabling leader males to recruit other males as well as females. We initially set the gene value to 0 (i.e., males did not recruit any followers) and allowed this gene to mutate over generations, enabling the emergence of follower males, should this strategy prove advantageous.

Each OLIVE simulation began with four groups of four adult males and 12 adult females, each clustered in a separate quadrant of the virtual environment. To recreate stable within-group cohesion (Harel et al. 2021), we programmed individuals to move toward other adults in their own group. We also modeled intergroup avoidance by programming OLIVES to move away from adults belonging to other groups, based on patterns documented in phenotypically and behaviorally similar species of yellow baboons (Markham et al. 2013). Males

dispersed during the juvenile stage and preferred joining new groups with unrelated females (Packer 1979). We also modeled secondary dispersals such that males were more likely to leave their current group if many females were close kin and more likely to stay if surrounded by unrelated females.

We seeded simulations with one of the four PRIMATES and set PLANT parameters to the values used during model development and genotype construction (***plant-quality*** = 4, ***plant-seasonality*** = 0.5, ***plant-annual-cycle*** = 1000, ***plant-daily-cycle*** = 10, and ***deterioration-rate*** = 0.1), ensuring a hospitable environment for PRIMATE persistence. We varied ***plant-minimum-neighbors*** (0–7) and ***plant-maximum-neighbors*** (1–8) at integer intervals. Each run lasted 100,000 timesteps (~5 adult lifespans). These 288 simulations (4 PRIMATES × 36 PLANT configurations × 2 replicates [Run A and Run B]) form this study's baseline. Although these four primate species occupy different habitats in nature, we exposed each genotype to the full range of simulated PLANT configurations, allowing us to assess which genotypes persisted or flourished under different habitat conditions.

We assessed model performance in four ways: (1) whether B3GET generated both patchy and homogeneous PLANT environments, (2) whether ANIMAL populations could persist across generations under some conditions, (3) whether genotypes and phenotypes could evolve over time, and (4) whether emergent ANIMAL behaviors reflected known dispersal patterns, mating strategies, and ranging behaviors of the target species.

To evaluate PLANT ecology, we recorded total PLANT energy abundance at regular intervals by summing the energy.supply values of all PLANTS in the simulation. We also quantified patchiness by dividing the landscape into 10 × 10-cell windows—approximating the maximum ANIMAL visual.range—and calculating the variance-to-mean ratio of PLANT energy abundance across these windows. We also captured aerial snapshots every 10,000 timesteps to visually track PLANT dynamics, with green color shading denoting energy.supply levels.

To assess ANIMAL persistence, we recorded population size every 250 timesteps through timestep 100,000 and tracked generational change by assigning each new offspring a generation.number one higher than its mother. A population was considered persistent if individuals were still present at timestep 100,000 and new generations continued to be produced. To assess ANIMAL evolution, we logged mean phenotype values (e.g., bite.capacity, gestation duration) and corresponding mean gene values by generation. We identified evolutionary change as population-level shifts in these values across generations. As a measure of reproductive success, we tallied lifetime conceptions per individual.

To evaluate how well emergent species-specific behavioral patterns were recreated, we assessed three behavioral axes: dispersal, mating, and home range fidelity. For dispersal, we tracked all individuals throughout life, recording their sex, whether they left their natal group, whether they joined a new group, and how often they transferred. For mating strategies, we tracked group demography over time and recorded the number of unique mating partners per individual of both sexes. To obtain detailed mating histories, B3GET randomly selected individuals as focal subjects, tracking every action and state from conception to death. We constructed "field notes" from these data (BYTE: Section 7.3), including when and with whom the individual mated. For ranging behavior,

we reviewed aerial snapshots taken at regular intervals and color-coded home ranges based on group identity. A group's home range is the set of PLANTS occupied by that group more frequently than by any other group in the recent past (BYTE: Section 2.7.3), reflecting accumulated and continually shifting familiar vs. unfamiliar areas. We quantified home range fidelity by counting how many individuals were inside vs. outside their own group's home range when the simulation concluded at timestep 100,000.

Results

We ran the 288 baseline simulations at the Minnesota Supercomputing Institute from 22 July 2021, 4:07 p.m. to 28 July 2021, 12:20 a.m. All simulations reached timestep 100,000 without crashing, producing 370,199 ANIMALS with complete life histories (conceived after the start and deceased before the end).

PLANT ecology

PLANT abundance and patchiness varied widely across simulations (BYTE: Section 6.1). Mean energy.supply per cell ranged from 0.7 to 3.3 (median = 1.2), while patchiness values ranged from 0.6 to 160 (median = 10). Higher values of ***plant-minimum-neighbors*** and ***plant-maximum-neighbors*** generated discrete PLANT energy patches (Fig. 3; BYTE: Section 6.3), whereas lower values for either parameter produced more homogeneous distributions. Unexpected maze-like PLANT patterns emerged when ***plant-maximum-neighbors*** was low (BYTE: Section 6.3). Temporal trends confirmed that these spatial differences persisted throughout the 100,000-timestep runs (Fig. 4). CHIMPANZEE home-range boundaries closely followed the spatial distribution of PLANT energy, and elevated PLANT energy frequently formed along those boundaries (Fig. 3).

ANIMAL persistence

Across the 288 baseline simulations, 204 populations (83.6%) persisted for the full 100,000 timesteps (Table 1). OLIVE populations showed the highest extinction rate (21 of 72 runs; 29.2%), followed by CHIMPANZEES (12.5%), GELADAS (8.3%), and HAMADRYAS (5.6%). HAMADRYAS populations increased in size on average (Table 1), whereas the other species maintained population sizes that fluctuated without collapsing over the duration of the simulation (Fig. 4). OLIVES lost nearly half their groups by the end of the simulations, whereas the other species retained group numbers close to their starting values. Consistent increases in mean generation number over time (Fig. 4) indicate sustained generational turnover in persisting populations, rather than persistence driven by long-lived individuals.

Time-series records for PLANT abundance (green), patchiness (blue), and ANIMAL population size (orange) show that population persistence was tightly linked to PLANT resource stability (Fig. 4; BYTE: Section 6.1). Populations declined or went extinct when mean PLANT abundance fell below ≈ 1.5 energy units per cell and patchiness exceeded ≈ 20. When abundance exceeded ≈ 2.0 and patchiness remained < 10, populations reached 150–250 individuals or more. All four species exhibited this relationship: stable, homogeneous land-

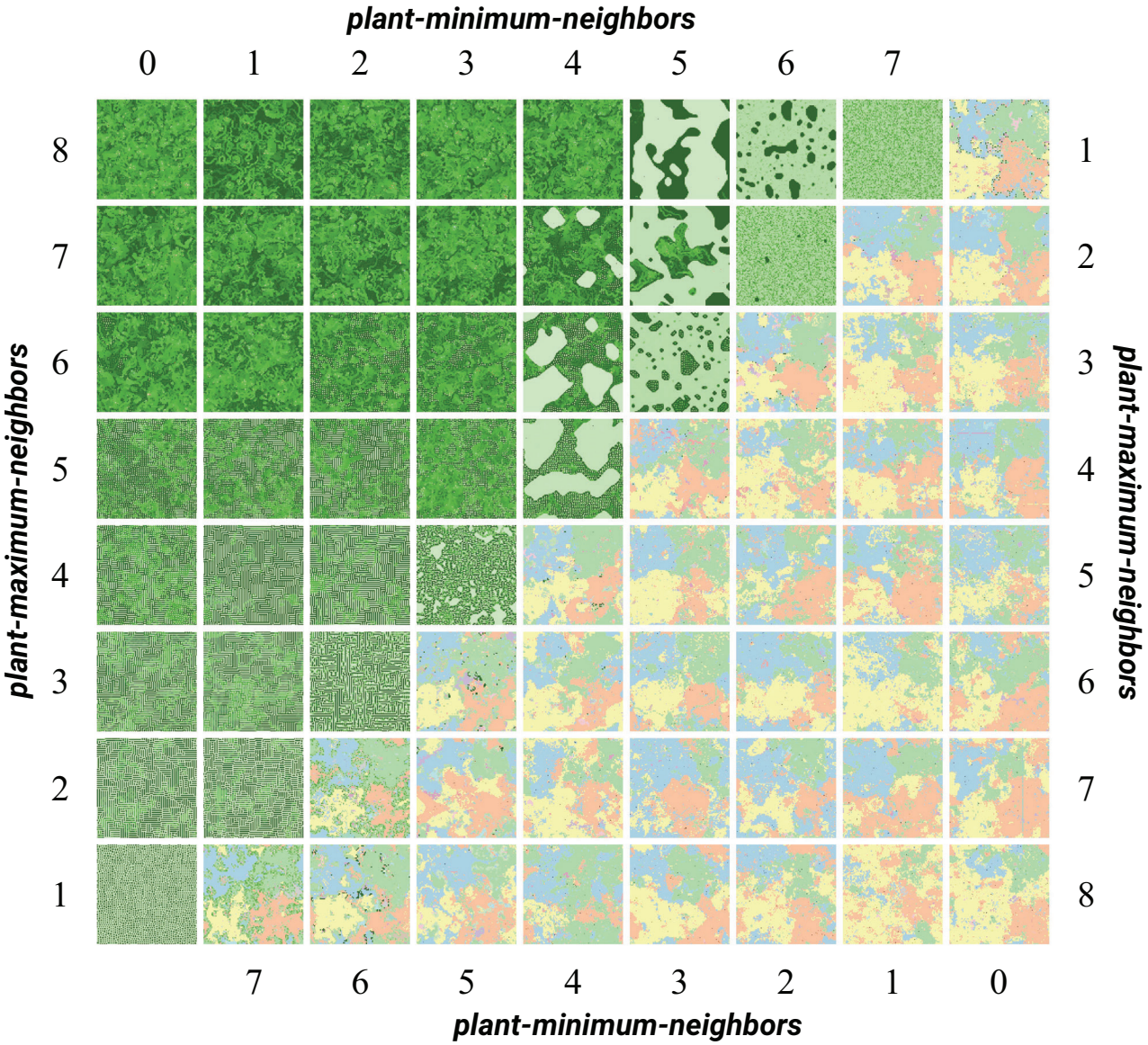

Figure 3. Spatial outcomes of PLANT ecology and CHIMPANZEE ranging behavior at timestep 100,000 for baseline simulations (Run A only). The matrix is symmetrical across the diagonal, with each simulation represented by two small panels that correspond to a distinct pair of ***plant-minimum-neighbors*** (*x*-axis, 0–7) and ***plant-maximum-neighbors*** (*y*-axis, 1–8) settings. Upper-left panels display PLANT energy distributions, with darker green indicating higher energy and lighter green indicating lower energy. Lower-right panels show color-coded home ranges of the four CHIMPANZEE communities (blue, green, yellow, and orange). See BYTE: Section 6.3 for all baseline PRIMATE spatial outcomes.

scapes supported sustained or expanding populations, whereas highly patchy environments coincided with collapse.

ANIMAL evolution

We illustrate evolutionary change using two arbitrarily chosen simulation case studies to demonstrate that B3GET can generate both evolutionary change and evolutionary stasis (Fig. 5). The first example focuses on a morphological trait (bite.capacity), and the second on a life-history trait (gestation duration). We defined “ancestral” and “descendant” individuals by dividing the sample at the median generation number within each simulation.

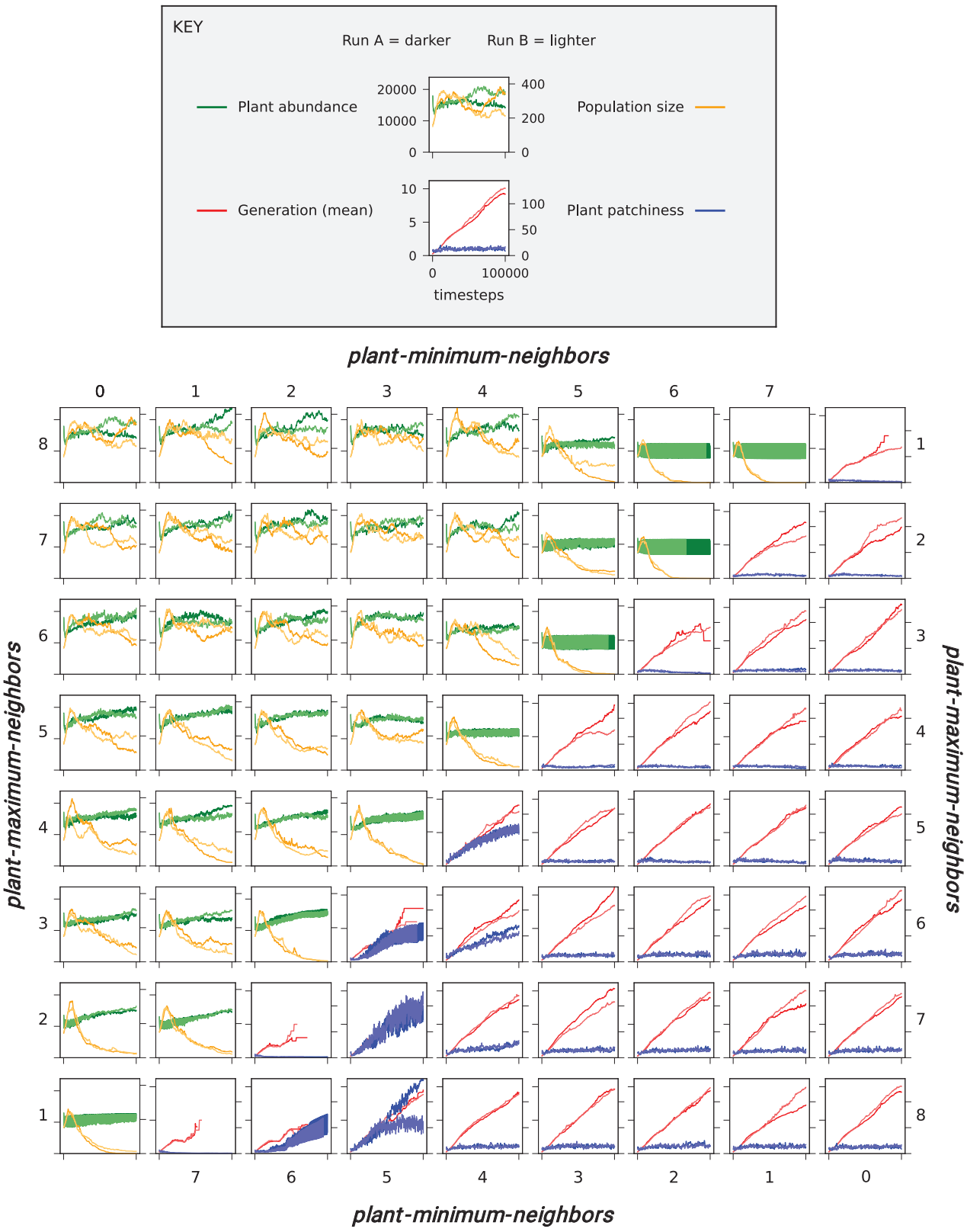

Figure 4. Temporal dynamics of PLANT ecology and populations across 100,000 timesteps in baseline CHIMPANZEE simulations. Each small panel presents data from two simulations (Run A, darker lines; Run B, lighter lines) with the same ***plant-minimum-neighbors*** (*x*-axis, 0–7) and ***plant-maximum-neighbors*** (*y*-axis, 1–8) settings. Lines show four tracked variables: PLANT abundance (green) and population size (orange) in panels above the diagonal, and PLANT patchiness (blue) and mean generation number (red) in panels below the diagonal. Axis scales vary among variables and are illustrated in the reference key at the top. See BYTE: Section 6.1 for all simulation outcomes.

Adult bite.capacity (simulation sAC47A)

All four PRIMATE genotypes include a single gene that grows bite.capacity each timestep during gestation. This gene was initialized at 0.001, meaning that both inherited chromosomes initially contributed 0.001 energy units per timestep toward increasing bite.capacity. In sAC47A, a CHIMPANZEE simulation, the population mean value of this gene rose gradually to 0.014 by timestep 100,000 (Fig. 5A(i)). At the phenotype level, adult bite.capacity increased between the "ancestral" (generation.number < 4) and "descendant" (generation.number > 4) subsets: 0.2384 ± 0.1598 vs. 0.3752 ± 0.3050 (mean ± SD), a statistically significant difference (t = 11.175, df = 1267.6, p < 0.0001, CI [0.1127752, 0.1608047]) (Fig. 5A(ii)). Reproductive outcomes for adult bite.capacity (binned to the nearest tenth) show that most conceptions were achieved by individuals with bite.capacity 0.2–0.5 (n = 3,727; 88%), with many of the remaining conceptions from individuals at bite.capacity = 1.0 (n = 407; 9.6%) (Fig. 5A(iii)).

Gestation duration (simulation sAG38A)

Gestation timing can be influenced by three genes present in all PRIMATE genotypes: a female gestatee development gene, a male gestatee development gene, and a maternal investment in birth gene. Each started at 0.0005, so mothers and gestatees initially invested equally in triggering birth. In sAG38A (Fig. 5B(i)), a GELADA simulation, the female gestatee gene remained relatively stable (0.00097 at timestep 100,000); the male gestatee gene was stable for most of the run and then declined late to 1.0E-4; the maternal gene dropped toward zero early (mean = −5.2E-4 at timestep 50,000) and remained near zero by the end (mean = 0.00015 at timestep 100,000). Thus, the male-gestatee and maternal genes evolved lower investment in triggering birth, tending to lengthen gestation. At the phenotype level, however, the distribution of gestation durations did not differ significantly between "ancestral" (generation.number < 3: 548.8613 ± 152.1546 timesteps) and "descendant" (generation.number > 3: 566.4499 ± 170.2555 timesteps) subsets (t = 1.5368, df = 697.77, p = 0.1248, CI [−4.882257, 40.059403]) (Fig. 5B(ii)). Reproductive outcomes for gestation duration (binned to the nearest hundred) were concentrated between 500 and 700 timesteps (n = 1,332; 66.6% of conceptions), with fewer conceptions as durations deviated from this range (Fig. 5B(iii)).

PRIMATE behavior

We evaluate how well B3GET reproduced species-specific behavioral patterns by comparing simulated PRIMATE populations to empirical observations along three behavioral axes: dispersal, mating, and home-range fidelity (Table 1). Together, these measures capture major differences in social organization among the study species. CHIMPANZEES exhibited female-biased dispersal and strong home-range fidelity. GELADAS and OLIVES both showed female philopatry and male dispersal, but GELADAS formed many small groups, whereas OLIVES formed fewer, larger groups. HAMADRYAS exhibited dispersal by both sexes and frequent female transfers between groups, driven by males recruiting them.

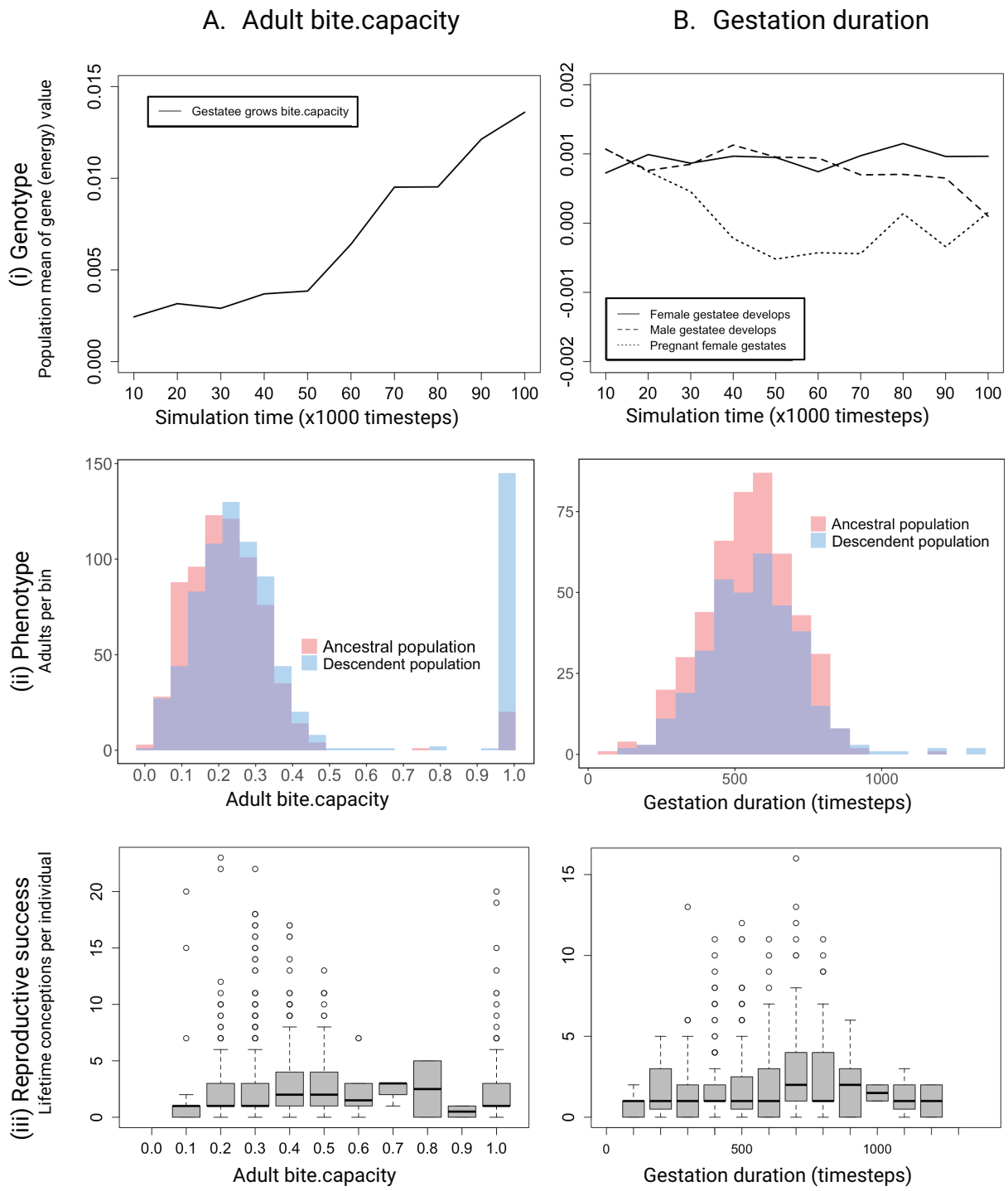

Figure 5. Evolution of selected traits in B3GET simulations. **A.** bite.capacity in simulation sAC47A; **B.** Gestation duration in sAG38A. (i) temporal change in the population mean of the gene(s) controlling each trait; (ii) trait distributions in the ancestral (earlier generations) and descendant (later generations) populations; (iii) reproductive outcomes of the trait measured as lifetime conceptions achieved per individual. In panels showing ancestral (red) and descendant (blue) distributions, purple regions indicate overlap between the two distributions.

CHIMPANZEES

Male CHIMPANZEES were strictly philopatric, while nearly all females (≈ 99.5%) dispersed from their natal groups upon reaching adulthood. However, dispersal success was variable: only approximately half of dispersing

females (48.0%) joined a new group, mirroring patterns observed at Gombe (Walker and Pusey 2020) and Ngogo (White et al. 2024), whereas 41.6% ultimately rejoined their natal group, and 10.4% never found another group before dying. Dispersal was costly; 56.7% of juvenile females that died did so after leaving their natal group but before joining a new one, suggesting mortality during transit. Qualitatively, these observations are consistent with the female-biased dispersal pattern characteristic of wild chimpanzees (Table 1).

CHIMPANZEE communities were the largest among the four PRIMATES (mean = 43.2 ± 26.2 individuals at timestep 100,000; Table 1), with group sizes reaching up to 149 individuals. Groups generally contained more adult males (21.6 ± 11.8) than adult females (9.5 ± 6.3), and both sexes averaged more than two unique mating partners. Simulated populations thus had a substantially more male-biased sex ratio than is observed in wild chimpanzees (median = 8.2 males, 14.4 females; N = 18 communities; Wilson et al. 2014).

CHIMPANZEES exhibited high range fidelity: 91.3% of individuals were observed within their home range at timestep 100,000 (Table 1). Focal follow data (BYTE: Section 7.3) confirm that individuals avoided crossing group boundaries, a pattern also visible in aerial views of the simulation showing distinct home ranges (Fig. 3). The home-range area varied from ≈ 500 to 6000 cells—over half the 10,000-cell landscape—and correlated strongly with group size (R^2 = 0.703).

GELADAS

Female GELADAS were largely philopatric, with 78.0% of adult females remaining in their natal group throughout life, consistent with the strong female philopatry reported in wild geladas (Table 1). Approximately one-fifth (22.0%) dispersed to form new groups consisting of themselves, one or more adult males that later joined, and their offspring. Female philopatry, combined with females forming new groups with their offspring, generated high within-group female relatedness (r = 0.38 ± 0.137).

Most adult males (84.3%) dispersed from their natal groups and successfully joined new ones upon reaching maturity, transferring a mean of ≈ 25 times (Table 1). Only 7.2% of adult males remained in their natal group, and that strategy was unfavorable—just 4.2% conceived offspring, compared to 86.3% among dispersing males, likely because natal groups consisted primarily of close female kin and thus offered few mating opportunities.

GELADA groups averaged 1.3 ± 1.2 adult males and 2.2 ± 1.5 adult females but ranged widely (0–16 males, 0–18 females). Approximately 41.7% of groups contained a single male, 33.3% included multiple males, and 25.0% lacked an adult male entirely. Although real gelada societies include leader and follower males, this distinction was not encoded separately here; nevertheless, focal observations revealed multiple sires within some groups.

At timestep 100,000, GELADA populations averaged 13.19 ± 8.53 groups (Table 1). Their low range fidelity (36.1% within home range) and aerial maps (BYTE: Section 6.3) indicate that groups lacked fixed boundaries and moved in loose, shifting clusters, consistent with the fluid, multilevel social organization characteristic of geladas.

HAMADRYAS

In HAMADRYAS, both sexes commonly dispersed from their natal group upon maturity, consistent with dispersal patterns reported for wild hamadryas baboons (Table 1). Among adult females, 92.6% left their natal groups to join a recruiting male. The few that stayed experienced major fitness costs—only 36.9% conceived offspring vs. 96.8% of transferred females—likely because natal groups included their fathers. Females changed groups frequently, residing in a median of 12 groups over their lifetimes (range 0–326).

Of adult males, 71.8% established new groups, 27.2% joined an existing group, and 0.9% rejoined their natal group. The initial HAMADRYAS genotype included a gene enabling adult males to recruit solitary males nearby. This gene began at zero energy allocation (inactive) but mutated to positive values in most runs: 67 of 72 simulations evolved follower males, confirmed by focal follow observations (BYTE: Section 7.3) and nonzero recruitment gene values by simulation end.

HAMADRYAS populations averaged 26.06 ± 13.32 groups comprising 1.3 ± 1.4 adult males and 1.1 ± 1.0 adult females (Table 1). The mean group size (3.5 individuals) was lower than the ≈ 5.5 observed in the wild (Schreier and Swedell 2012) but varied widely—from solitary pairs to groups exceeding 100 individuals. Groups typically persisted for shorter durations than the adult male's lifespan, expanding mid-tenure when several females were present. Focal follows revealed high female turnover, with some males mating with 10 or more partners over a lifetime.

Group composition was highly variable (up to 38 adult males and 19 adult females). More than half of all groups (53.5%) contained a single adult female, 23.7% contained multiple females, and 22.8% contained none. HAMADRYAS groups showed no spatial fidelity; they roamed freely and altered the surrounding vegetation more than any other PRIMATE (BYTE: Section 6.3). Simulations that produced patchy PLANT distributions for other species (e.g., sAC46A, sAG46A, and sAO46A) became more homogeneous under HAMADRYAS (e.g., sAH46A), suggesting that their higher population stability may have modulated the PLANT landscape.

OLIVES

In OLIVE populations, females were strictly philopatric and never dispersed, while all males dispersed upon adulthood, reproducing the sex-biased dispersal pattern characteristic of olive baboons (Table 1). Most (69.2%) dispersed males died before successfully joining a new group, likely contributing to their species' relatively low survival rates. Compared with GELADA males—84.3% of whom successfully transferred—only 27.7% of OLIVE males joined one of the three other groups in a simulation. Consequently, OLIVE groups tended toward female-biased, polygynous structures (mean = 2.0 ± 2.5 adult males; 7.9 ± 4.6 adult females per group).

A small fraction (3.7%) of OLIVE males returned to their natal group; these males achieved 83.1% of conceptions in their group vs. 88.6% among males that transferred elsewhere, indicating minimal fitness difference. As in GELADAS, female philopatry produced elevated within-group relatedness (r = 0.244 ± 0.085 among adult females vs. r = 0.139 ± 0.085 among adult males). OLIVE groups, comparable to GELADAS, HAMADRYAS, and their real-world counterparts, exhibited overlapping ranges rather than discrete boundaries (BYTE: Section 6.3).

Table 1. Measurements of simulated PRIMATE populations at timestep 100,000.

	CHIMPANZEES	GELADAS	HAMADRYAS	OLIVES
Persistence to timestep 100,000				
Total simulated individuals	123,354	86,119	121,362	39,364
Populations that persisted	63/72 (87.5%)	66/72 (91.6%)	68/72 (94.4%)	51/72 (70.8%)
Population size at timestep 0	112	96	64	64
Population size at timestep 100,000 (mean ± SD)	114 ± 94	86 ± 60	157 ± 77	55 ± 69
Generations transpired (mean ± SD)	8.79 ± 1.21	6.25 ± 0.66	8.23 ± 0.95	5.92 ± 1.57
Dispersal patterns*	Female dispersal; Male philopatry	Female philopatry; Male dispersal	Female dispersal; Male dispersal	Female philopatry; Male dispersal
Female lifetime group transfers (mean ± SD)	0.834 ± 0.536	0	3.40 ± 3.90	0
Male lifetime group transfers (mean ± SD)	0	25.7 ± 118	1.23 ± 9.44	1.28 ± 9.46
Mating strategies*	Polygynandrous	Polygynous	Polygynous	Polygynandrous
Group size at timestep 100,000 (mean ± SD)	43.2 ± 26.2	4.80 ± 3.60	3.50 ± 2.80	13.3 ± 9.90
Female lifetime unique mating partners (mean ± SD)	2.08 ± 2.19	1.38 ± 1.21	1.77 ± 1.73	1.35 ± 1.07
Male lifetime unique mating partners (mean ± SD)	2.08 ± 2.32	1.60 ± 1.84	2.11 ± 2.38	1.68 ± 3.22
Home range characteristics*	Territorial	Non-territorial	Non-territorial	Non-territorial
Number of groups at timestep 0	4	16	16	4
Number of groups at timestep 100,000 (mean ± SD)	3.15 ± 1.43	13.19 ± 8.53	26.1 ± 13.3	1.61 ± 1.49
Range fidelity (% within home range at timestep 100,000)	91.3%	40.0%	36.1%	44.8%
Spatial boundaries (visual assessment: see Fig. 3, BYTE: Section 6.3)	Strict boundaries	Overlap	Overlap	Overlap

Qualitative behavioral descriptors* (e.g., dispersal patterns, mating strategies, and home-range characteristics) represent *a priori* expectations based on empirical knowledge of each target species and are used here as reference categories for evaluating whether simulated populations reproduce those species-typical patterns.

Discussion

B3GET successfully reproduced key ecological, evolutionary, and behavioral patterns across biological scales. The model met all four evaluation goals: it generated both homogeneous and patchy PLANT environments, sustained realistic ANIMAL population dynamics over long timescales, produced measurable evolutionary change in heritable traits, and simulated species-typical dispersal, mating, and ranging behaviors across multiple primate species. These PRIMATES also experienced full life histories: beginning from a zero state and requiring energy to develop to adulthood, reproduce, and eventually die. Together, these results demonstrate that B3GET provides a general yet mechanistically detailed framework capable of modeling diverse animal taxa and linking individual decision rules to emergent behavioral and ecological patterns.

Key findings

The spatial ecology of PLANTS and the behavioral ecology of ANIMALS interacted to produce dynamic and biologically plausible virtual ecosystems. PLANT distributions ranged from homogeneous to patchy depending on plant-neighbor settings and often smoothed over time due to foraging pressure. This feedback between ANIMAL consumption and PLANT regrowth created dynamic resource landscapes that, in turn, shaped emergent space-use patterns, including

CHIMPANZEE home-range boundaries that followed PLANT energy contours. ANIMAL population persistence depended strongly on available PLANT energy, with many populations surviving to 100,000 timesteps, suggesting robust population stability under favorable ecological conditions.

Evolutionary change was commonly observed within B3GET populations. We focus here on two representative case studies to demonstrate, as a proof of concept, that the model can generate both evolutionary change and evolutionary stasis. Because the model does not impose an explicit global fitness function, differential survival and reproduction arose naturally from energetic and behavioral tradeoffs. In one CHIMPANZEE population (Fig. 5A), both genotype and phenotype data indicated directional selection for greater energy-intake capacity: mean adult bite.capacity increased steadily relative to the ancestral population, and the associated gene's energy investment evolved toward progressively higher values over time. This trend showed no sign of plateauing within the simulated timeframe, implying that continued selection would further increase bite.capacity. In contrast, gestation duration in another population remained stable (Fig. 5B), suggesting stabilizing selection. Although the gestatee's gestation gene remained constant, the maternal gene evolved toward zero early in the run, consistent with the expectation that mothers conserve energy for future offspring (Stearns 1989).

PRIMATES expressed expected social behaviors without any top-down enforcement, showing that B3GET's bottom-up, genotype-encoded rule structure can reliably generate complex emergent societies that reflect species-typical traits. Dispersal behaviors: CHIMPANZEE males were philopatric, while approximately half of females dispersed to neighboring communities; GELADA males transferred frequently, whereas females were largely philopatric; HAMADRYAS females dispersed to join recruiting males; and OLIVE males dispersed, while females remained in natal groups. Mating behaviors: CHIMPANZEES maintained promiscuous, large multi-male, multi-female communities; GELADAS maintained small, single-male and multi-male units through male acquisition of female groups; HAMADRYAS males formed small groups by recruiting females and sometimes male followers; and OLIVES sustained multi-male, multi-female groups with a male-biased reproductive skew. Ranging behaviors: CHIMPANZEE groups maintained distinct home ranges, whereas GELADA, HAMADRYAS, and OLIVE groups occupied overlapping or shifting ranges without fixed boundaries.

Using B3GET

We have demonstrated that B3GET can effectively simulate a broad range of primate societies with minor adjustments to PRIMATE genotypes and populations. Previous studies with agent-based models showed that simple rules can yield complex emergent behaviors (Te Boekhorst and Hogeweg 1994; Hemelrijk 1999). B3GET advances this tradition by providing a user-friendly "sandbox" model in which users can adjust environmental and behavioral parameters to generate indefinitely many new societies without requiring extensive programming experience. In classroom laboratories, student projects, and conference workshops, users with no coding background have successfully edited, saved, and reloaded population and genotype files to conduct new experiments.

Traditional animal agent-based models often struggle to integrate field measurements because relevant data are scarce, inconsistent, or collected using

incompatible protocols (Murphy 2025). In B3GET, new genotype and population files can be created using general qualitative knowledge of the target species, rather than empirical parameterization. By simulating multiple species or ecological regimes under standardized assumptions, researchers can compare relative outcomes—such as evolved trait values, group demography, or persistence—without forcing a literal one-to-one parameter match with noisy field data.

Although this study focused on primates, B3GET's population and genotype files can be readily adapted to represent other taxa. The model can also generate novel ANIMAL genotypes as populations evolve away from their initial set of rules, shifting toward configurations that better allocate energy under a given simulation's environmental pressures. The symbolic stimulus–response architecture offers a vast and largely unexplored behavioral space—on the order of more than 300 trillion possible ANIMAL behaviors when all potential mutations to genotype symbols are considered (Crouse 2021, p. 84).

B3GET's rich ecological context—encompassing energy landscapes, social organization, individual life histories, and intergenerational change—makes it a powerful framework for examining how environmental structure and behavioral adaptation interact. Its multilevel output system provides fine-grained data spanning genes, individuals, groups, populations, and environments, enabling integrative analyses of feedback across scales. Together, these features position B3GET as a robust and versatile platform for research and education in individual-based ecology.

Beyond its value as a theoretical research tool, B3GET provides a means to explore ecological and social scenarios that would be impractical, prohibitively expensive, or unethical to impose on real animal populations. For example, researchers can experimentally alter mortality rates, dispersal opportunities, resource distributions, social structures, or developmental processes and then observe how those changes propagate across ecological levels. Because B3GET simultaneously records measurements across these levels, it can help identify the mechanisms through which population declines, social instability, or other emergent outcomes arise. In this way, it complements empirical research and may help address conservation-relevant questions.

Limitations

Although B3GET is a powerful tool for theoretical exploration, several limitations warrant consideration. The current implementation uses abstract representations of ecological processes: PLANT growth is governed by internal rule-based dynamics and does not use phenology, climate inputs, or externally derived resource maps. Timesteps and energy units are non-dimensional and do not directly correspond to real-world measures. This abstraction enhances generality and allows comparisons across simulated systems, but it reduces realism for system-specific forecasting. Consequently, B3GET is presently best suited for theoretical investigations, hypothesis comparison, and mechanistic exploration rather than predictive modeling, although future iterations will aim to bridge this gap.

Another limitation concerns interpretation. B3GET can identify combinations of mechanisms capable of reproducing empirical or theoretically expected patterns, but successful reproduction of a pattern does not demonstrate that the underlying mechanisms are uniquely correct. Multiple behavioral or ecological

processes may generate similar outcomes, especially given the vast parameter space of B3GET. Consequently, B3GET should not be viewed as providing definitive proof of causation. We encourage users to build confidence in proposed mechanisms by explicitly evaluating alternative explanations and corroborating model predictions with independent data.

The model's scope and potential extend beyond what was captured in the present simulations. For this study, we turned off mutation for most gene loci to preserve interspecific distinctions, constraining within-species evolutionary dynamics. Populations often crashed in highly patchy environments, suggesting the need to adjust initialization parameters to permit persistence under these conditions. Some unexpected outcomes—such as lower persistence in OLIVES and highly male-biased sex ratios in CHIMPANZEES—likely reflect suboptimal energetic allocations. Further exploration of the simulation space will help identify parameter combinations that better sustain each virtual population and reveal additional model behavior.

Future directions

In future iterations, we intend to expand B3GET's ecological realism and evolutionary scope while strengthening its integration with empirical data.

We intend to simulate longer time horizons so that the system's internal feedbacks can unfold more fully. Preliminary time-series results reveal oscillatory resource–consumer dynamics between PLANTS and ANIMALS—patterns reminiscent of classical predator–prey interactions (Lotka 1925; Volterra 1926). For genes that we allowed to mutate, we observed both directional and stabilizing selection, although simulations lasted only a short time by evolutionary timescales: approximately 10 generations. To examine these processes in greater detail, we intend to conduct substantially longer simulations, enhanced by implementing B3GET performance optimizations that reduce runtime and enable extended evolutionary experiments.

We also intend to introduce new model features to enhance ecological realism. To represent environmental pressures more faithfully, we plan to include multiple PLANT species coexisting within the same landscape (e.g., Howard-Spink et al. 2025; Yoshihara et al. 2025) and enable ANIMALS to evolve distinct feeding efficiencies for each species—analogous to unique bite.capacity parameters for different food types. We further plan to expand spatial scale by linking multiple B3GET simulations running in parallel as adjacent environments, allowing regional metacommunity dynamics to emerge. At the behavioral level, we will expand the current stimulus–response design—which is static over an individual's lifetime—into a neural-network architecture that maps stimuli to responses and permits learning and plasticity. We will also increase mutation flexibility and introduce multiple ANIMAL species within shared environments to examine how these changes influence the emergence of ecological complexity and interspecific interactions.

Finally, we intend to extend B3GET from a theoretical platform toward applied ecological modeling. One possible approach would be to implement a calibration procedure that uses empirical data to construct genotype rules more efficiently than the current manual approach. Following Crouse et al. (2019), this calibration will impose additional fitness costs on individuals that deviate

from empirical target values—such as body.size dimorphism, number of mating partners, or group transfer count—thereby guiding simulated populations toward genotype configurations consistent with real-world systems.

Conclusion

B3GET provides a reusable framework for: (1) creating virtual analogues of living species to address species-specific questions; (2) investigating how populations evolve and vary in response to ecological pressures; (3) tracing complete evolutionary histories across indefinite timescales and generations; and (4) tracking individuals throughout their entire life histories, from conception to postmortem decay. The model is well suited for exploratory, explanatory, and hypothesis-driven research. By demonstrating realistic ecological pressures, evolutionary responsiveness, and species-specific behavioral emergence, B3GET establishes a reusable foundation for multiscale, multisystem ecological modeling. We anticipate that B3GET will serve as a useful tool for students, teachers, and researchers alike, offering a flexible platform for controlled, repeatable experiments in animal behavior, ecology, and evolution.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Artificial Intelligence (AI) use

The authors accept full responsibility for the content of the manuscript, including the disclosure of any use of AI.
Regarding the use of AI in the preparation of this manuscript, the authors declare the following: GPT.
Used for: Language, style and writing, Figures, tables and charts.
We used ChatGPT to assist with editing text and improving clarity in the manuscript and supplementary document. We verified all text and produced all scientific content, model design, simulations, analyses, and interpretations independently.

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Author contributions

Kristin Crouse: Conceptualization, Methodology, Software, Validation, Formal analysis, Investigation, Data Curation, Project administration, Writing – Original Draft, Writing – Review & Editing, Visualization; Michael Wilson: Conceptualization, Methodology, Supervision, Writing – Review & Editing, Validation; Clarence Lehman: Conceptualization, Methodology, Supervision, Writing – Review & Editing, Validation.

Author ORCIDs

K.N. Crouse https://orcid.org/0000-0002-4878-7477
C.L. Lehman https://orcid.org/0000-0002-1369-1205
M.L. Wilson https://orcid.org/0000-0003-3073-4518

Data availability

The BYTE dataset generated by B3GET is available on Dryad (https://doi.org/10.5061/dryad.d2547d8d4). Code availability: B3GET (v1.2.0) is available for download on CoMSES (https://doi.org/10.25937/3dfb-js17).

Supplementary material 1

BYTE Simulations of the B3GET Model

Authors: Kristin N. Crouse

Data type: pdf

Explanation note: BYTE Simulations of the B3GET Model: A Comprehensive Companion Guide.

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