LoversFlow v2: an individual-based evo-eco simulator on sexual dimorphism
– A challenge toward evolutionary aesthetics –

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Abstract: Studies on evolution of sexual dimorphism are including useful suggestions to understand more deeply not only the ecological diversity in the nature but also the gender diversity in the human society. Here we present the design of our individual-based evo-eco simulator targeting an evolutionary process on sexual appearance, preference, and dimorphism, including sex-influenced traits. The simulator can manage some thousands of individual agents in continuous 2D space for birth, roaming, mating, reproduction, separation, and death. It also has some auxiliary functions for monitoring and recording the evolutionary process for visualization and further statistical analysis. Accompanying with a detail of the mathematical model, some results are shown as example analysis concerning effects of distance bias and locality from view points of speciation and dimorphism. By expanding the complexity of appearance so as to include shape, texture, and the other features of subjects in the research on computational aesthetics, it will be able to contribute to seek the origin of beauty.

Keywords: evo-eco simulator, mating strategy, sexual dimorphism, sexual selection, sympatric speciation

1 INTRODUCTION

Mating is an important action that affects the evolutionary process of animals when they rely on sexual reproduction. It strongly relates love and sex of human life, that is one of the popular themes for a variety of artistic and entertainment activities in human culture. A lot of researches has been conducted in the field of evolutionary psychology [1] to investigate the cultural, racial, and gender differences of preferences related to sexual selection such as [2]. These works are mainly motivated from scientific curiosity for human nature in general, and some of them are focusing on the origin of aesthetics. Beauty itself is not always necessary to promote the reproductive success, but it is one of the effective strategies for an individual to win in the mating competition by attracting another individual of opposite sex as much as possible. This causes well-known phenomena called sexual selection where some type of morphological traits escalate even though they are obstacles for metabolic efficiency, such as tail feathers of male peacock. Human's aesthetics might be one of the side effect from sexual selection accompanying with an evaluation of scenery for exploration and migration to new habitats [3].

A number of research methods are possible and the combination of them are promising, such as a philosophical study to establish a framework of thought, a field work to investigate how real humans behave, a psychological experiments in a laboratory, and so on. This paper introduces our approach from the field of computer science, that is, a design and implementation of individual-based simulator on evolutionary ecology. This type of simulators have been developed for more than quarter a century in a context of artificial life research for a variety of research focuses, such as [4]. Our motivation is to investigate how the physical appearance and the psychological preference co-evolve together in an evolutionary ecological system with sexual selection. To focus on this purpose, we omitted some of the common features implemented in the similar systems, such as energy metabolism, morphology of the body shape, kinematic motion control, learning ability, and so on.

The following part of this paper describes the model overview, control and monitor of the process, tools for analysis, result examples, and future extension of the simulator.

2 MODEL OVERVIEW

This section describes an overview of simulation model on both an individual agent and the environment.

2.1 2D world

The agents' habitat is a square shape of two dimensional plane with continuous Cartesian coordinates. The characteristic of boundaries is selectable from the two choices, walls or torus. If the boundaries are fenced by walls, any agent cannot move beyond the boundary. Otherwise, the right edge is connected to the left, and the top edge is connected to the bottom. Each of agent has its own coordinate (x, y) and velocity (v_x, v_y). Agent's action is acceleration synthesized from a number of

forces as its selected action following the rules described in a later subsection 2.4. We also introduce "objects" placed in the world to test the evolutionary dynamics of object sexuality. An object is specified by the position and color. It assumed to have the similar size with the agent but does neither move nor die.

2.2 Genetics

Each agent has its own genome inherited from the parents. The hereditary traits encoded on a genome are 1. appearance, 2. preference, 3. love/hate threshold, 4. fickleness, 5. duration to love enough, 6. distance bias, 7. activeness to propose, 8. tolerance to accept the proposal, 9. abandonment, and 10. maximum speed of motion. In the current implementation, both appearance and preference are represented by a combination of features for each; color, aging, and plumpness. A color consists of three scalar components for red, green and blue. Each of the other traits is represented by a single scalar value. All of the scalar values in genome are floating point numbers within the range from 0 to 1. The trait of aging represents how much the age of agent affects the chronological change of appearance, that is, the agent looks older than the real age if the value is large. The trait of plumpness has a special effect for female. If a female agent is slender, its appearance largely changes to be plumper when it becomes pregnant.

It is possible to switch for each of the scalar values whether it is sex influenced or not, or is a constant fixed value or hereditary with mutation. In case of it is hereditary, it is allowed to specify the initial value distribution by the central value and the width of distribution. In the current implementation, the initial scalar values follow the uniform distribution. If it is indicated to be sex influenced, the genome includes double number of values to maintain the genes for male and female separately. Either part of them manifests on the phenotype and the other part is hidden, depending on the sex of the individual agent. In nature, most of the sexual organisms have a type of diploid chromosomes and sex chromosome determines the sex type of the phenotype. This model does not assume diploid but haploid for simplification.

Each scalar value is treated as a locus when it is inherited to an offspring. This means that it is not separated into parts in the crossover operation. In the process to organize a new genome for an offspring, the value of each locus in the genome is copied from the corresponding part of either father or mother. Then, it is modified by adding a small random value in the range $[-\mu, \mu]$ as mutation operation, where we call the value of μ "mutation width." In case the result value of mutation became out of range, it is forced to be revised to the nearest boundary value 0 or 1.

The functionalities of the ten traits are described in the later sections.

2.3 Sense, state and action

Each agent observes its surroundings to check the other agents, objects and walls within a circular area of constant radius named "view range" R_v. An agent decides its action by applying the rules to the internal state and the external state. The situation it observes composes the external state. The internal state includes 1. age, 2. appearance, 3. parents' IDs, 4. lover's ID, 5. love duration, and 6. pregnancy duration if it is female.

The aging appearance O_i of agent i is calculated as,

$$O_i = \frac{1}{1 + \omega_i - \omega_i \cdot y_{\max}/y_i}, \quad \omega_i = 1 - \frac{1}{o_i} \quad (1)$$

where o_i is the value in the gene, y_i is the real age of the agent i, and $y_{\max}$ is the maximum life span given as a simulation parameter. As roughly described in 2.2, o_i works to express how fast or slow the appearance changes. This equation was designed so that $O_i = 0$ when $y_i = 0$ and $O_i = 1$ when $y_i = y_{\max}$, and O_i for intermediate age looks older when $o_i > 0.5$ and younger when $o_i < 0.5$.

The plumpness P_i of female agent i's appearance is calculated as following when it is pregnant,

$$P_i = p_i + \frac{\phi_i}{10/12}(1 - p_i) \quad (2)$$

where p_i is the value in the gene, and ϕ_i is the pregnancy duration in year. $P_i = p_i$ if the agent is male or not pregnant.

We assume the motion of an agent is based on Newtonian mechanics represented by a linear second order differential equation with mass and friction. The limitation of the speed is also applied. The move action of agent i is to apply a force $\mathbf{F}_i$ calculated by the rules, of which detail is described in the next subsection 2.4. In the simulation software, the position and velocity of an agent are calculated using simple Euler method for each simulation step. It calculates the acceleration from force and mass; modifies the velocity by the acceleration and friction limiting it to the predefined maximum speed; and then modifies the position by the velocity.

The age of an agent increases step by step from zero to the highest age $y_{\max}$, 120 years for example. It is adjustable by a simulation parameter to assign how long time passes for each step. The age span is divided into three periods, child, adult, and elderly adult. The age of boundaries between the periods are adjustable by a simulation parameter, y_{adult} and y_{old}, such as 16 years to shift from childhood to adulthood, and 50 years to shift from adult to old one. Some of the rules to be applied to the agent have different effects depending on the age since an agent of middle period is treated to be marriageable. We assume the the boundary ages is fixed for all of agents, though it might be more realistic to assign different ranges depending on the agent's sex.

An agent may take other type of action than move, such as falling in love, proposing, accepting, bearing a child, and dying, as described in 2.5 and 2.6.

2.4 Mobility

An agent is always affected by repulsion forces from obstacles near from it, including other agents, objects, and walls, to avoid collision. The total repulsion force is calculated by a summation of all of forces caused by surroundings. Each force is inversely proportional to the square of distance from the agent to the obstacle.

If the agent is a child, it follows its mother m by adding an attraction force toward m to $\mathbf{F}_i$. If it reaches the adult age and is still younger than the elderly age, it is marriageable and seeks a candidate of its new partner. It may also hate other ones in case love/hate threshold θ_i is less than 1. As described in the former subsection 2.2, θ_i is an hereditary trait encoded on a gene. If it found the best candidate, it approaches the best one by adding an attraction force as similarly as the case toward the mother. The "best" one means the most attractive agent b_i for the agent i, that is:

$$b_i = \arg\max_{j\in\mathbf{N}_i} A_{ij} \qquad (3)$$

where $\mathbf{N}_i$ is the set of neighboring agents within the view range R_v, and attractiveness A_{ij} is measured by following equation:

$$A_{ij} = (1 - H_{ij})^{1-d_i} \cdot \left(1 - \frac{D_{ij}}{R_v}\right)^{d_i} \qquad (4)$$

where d_i is a hereditary trait, distance bias, H_{ij} is the difference between appearance of j and preference of i normalized into the range $[0, 1]$, and D_{ij} is the distance between the positions of these two agents. Because both appearance and preference are represented by vectors of five elements, RGB colors, aging, and plumpness, in the current implementation, we use Euclidean distance between them divided by $\sqrt{5}$ for H_{ij}, since each element is within the range $[0, 1]$. The value of d_i works as a degree of compromise. If d is 0, the best one is always the best look in all of the agents it observed. If d_i is 1, the agent does not care about the appearance but always choose the nearest agent.

If an agent i found another one j whose H_{ij} is lager than θ_i, it tends to escape from it by multiplying a coefficient E_{ij} to a repelling forces for collision avoidance, that is calculated as,

$$E_{ij} = \begin{cases} E_{\max}^{e_i} \dfrac{H_{ij} - \theta_i}{1 - \theta_i} + 1 & \text{if } H_{ij} > \theta_i \\ 1 & \text{otherwise} \end{cases} \qquad (5)$$

where e_i is a simulation parameter named "escape exponent," and $E_{\max}$ is a constant whose value is 10 in the current implementation. An agent who reached the oldest limit of marriageable age does not care about the preference anymore. Summarizing the physical mobility described above, the force $\mathbf{F}_i$

applied to agent i is defined as:

$$\mathbf{F}_i = -\alpha_w \frac{\mathbf{v}_{iw}}{D_{iw}^2} - \alpha_o \sum_{j\in\mathbf{N}_i} E_{ij} \frac{\mathbf{v}_{ij}}{D_{ij}^2} + C_i \qquad (6)$$

$$C_i = \begin{cases} \beta_m \mathbf{v}_{im} & \text{if agent } i \text{ is a child,} \\ \beta_b \mathbf{v}_{ib_i} & \text{if agent } i \text{ is at marriageable age,} \\ \beta_b \mathbf{v}_{il_i} & \text{otherwise} \end{cases} \qquad (7)$$

where D_{iw} and D_{ij} are the distances from the agent i to the nearest wall and to the other agent j respectively. $\mathbf{v}_{iw}, \mathbf{v}_{ij}, \mathbf{v}_{im}$, $\mathbf{v}_{ib_i}$ and $\mathbf{v}_{il_i}$ are unit vectors toward the targets; nearest wall, the other agent j, the mother m, the best candidate as a partner b_i, and the mutual lover l_i; respectively if exists. The value is a zero vector if the target is absent. The coefficients α_w, α_o, β_m, and β_b are specified as parameters of simulation in the current implementation.

The simulator has four scalar parameters as settings for allowance probabilities of homosexuality, object sexuality, inbreed, and age unconsciousness. If it prohibits homosexuality, an agent does not watch the agents of same sex to find a partner. If it prohibits object sexuality, an agent ignores objects to prevent from falling in love with an object. If it prohibits inbreed, an agent refers the parents' IDs before it measures the attractiveness in order to prevent from falling in love with its parents, brothers, sisters, and children. If an agent makes age-conscious choice, it does not approach or propose a child or an elderly because it is hopeless to be accepted. $\mathbf{N}_i$ in equation (3) is replaced with its appropriate subset in these cases.

2.5 Proposal and acceptance

An agent who found any candidates for its new partner may propose the best one among them. The probability of this action is proportional to the value of a hereditary trait, activeness a_i, in principle. Because a number of agents living in the world presented their proposals in the same simulation step, an agent may receive more than one proposals in a single step. An agent at marriageable age may accept one proposal presented by the most attractive proposer if it is tolerant enough. The tolerance t_i is also a hereditary trait that acts as the probability of acceptance. If the agent already has a mutual lover, the probability of the action, either proposal or acceptance, is affected by another hereditary trait, fickleness f_i, that is multiplied with a_i or t_i to calculate the probability of the action. An agent whose f_i is zero is faithful enough to keep the relation with the lover until one of them dies or the partner leaves because of unfaithfulness. In case agent A proposed agent B and A was also proposed by another agent C at same time, if both A and B accepted the proposals then the acceptance by B fails.

An optional feature to decide the best candidate is abandonment by memorizing a list of the identifiers who rejected a proposal from the agent. The agent gives up proposing a candidate whose identifier is in the list. The degree of abandonment

g_i is also a hereditary trait encoded in the gene of which value acts as the probability to make each element remain in the list. This means the agent tends to abandon the attractive agents once the proposal was rejected, when the value is high.

2.6 Sex, pregnancy, birth, and death

When two agents of different sexes start having a relation, they may wait for some steps to make their mutual love deep enough. Each agent has a hereditary traits l_i that indicates this duration, then the couple of agent i and agent j employs the longer value, $\max(l_i, l_j)$. After this duration passed, the female agent i may become pregnant in a probability P_{pi}, that is defined as:

$$P_{pi} = P_p^0 \cdot \frac{1}{1 + \gamma^{y_i - y_h}} \cdot \left(1 - \alpha_d \frac{W^2 |\mathbf{N}_i|}{\pi R_v^2 N_{\max}}\right) \quad (8)$$

where P_p^0 is the default rate used in spars area, γ is a constant, y_h is the age when pregnancy rate becomes a half, W is the length of a single edge of the world, $N_{\max}$ is the maximum number of agents in the world capacity, and α_d is a simulation parameter named "density bias." In the current settings,

$$
\begin{aligned}
y_h &= 0.265 \cdot y_{\text{adult}} + 0.735 \cdot y_{\text{old}} &(9) \\
\gamma &= 0.222 \cdot (y_{\text{old}} - y_h) &(10)
\end{aligned}
$$

referring to the statistical data of assisted reproductive technology in 2014 issued by Japanese Society of Obstetrics and Gynecology [5]. πR_v^2 is the area size of observable range from the agent, which is revised by eliminating the area beyond the walls when any part of walls is visible in the range. The multiplication factor at the right hand side in equation (8) is attached in order to prevent from population explosion. It is important to avoid massive memory consumption in order to guarantee the executability of the simulation. It is also reasonable to simulate the situation of resource shortage by such suppression of birth rate when the population is crowded. A new baby is born after ten months of pregnancy. The genome is organized as described in the subsection 2.2. The sex, male or female, is assigned in the ratio of 0.5137 : 0.4863 referring the real population statistics in Japan. The initial speed is zero and the position is randomly located at near place from the mother.

As a simulation parameter, the maximum life span of agents is specified to be 120 years for example. To simulate realistic situation somehow, we employ the population statistics issued by Japanese governmental organization [6] for assigning death rate for each age and sex. The ratio of male and female in the population is almost even although the male's birth rate is higher than female, because the male's death rates in any age is larger than female.

3 CONTROL AND MONITOR

A single simulation process starts with the initial random population scattered in the world. The scales of simulation for both
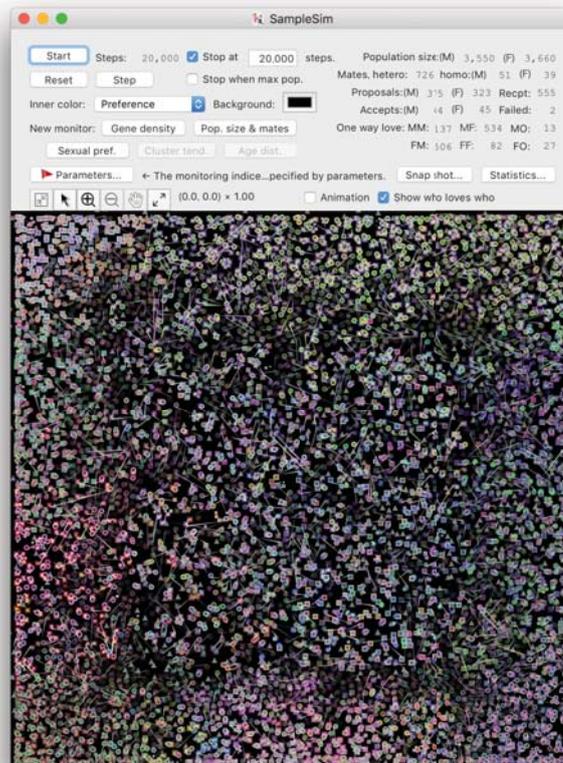

Figure 1: Main window of the simulator.

time and space are adjustable by the simulation parameters of "months per step" and "world size" W. The shape of agent is assumed to be a circle of fixed diameter 1. The maximum size of the population $N_{\max}$ is also adjustable, though the huge size, such as more than ten thousands agents, may damage the smooth run. It is also possible to restrict the place of initial population within a smaller square than whole of the world in order to adjust the initial density in a small population.

The user can start, stop, reset, and step the process by operating proper buttons on graphical user interface (GUI). It is also possible to set the number of steps to indicate when the process should automatically stop. The simulation software has an interface for another software typically written in AppleScript to be controlled and monitored. This interface is useful to examine a several times of processes for a variety of settings in order to compare the effects of parameters on the evolutionary processes to induce a statistically feasible consequence.

The following subsections describe other features of the simulator for control and monitor. Some of them are important to visualize what happens behind the evolutionary process.

3.1 Spacial distribution

Figure 1 shows an example view of the simulator's main window whose upper part contains a number of buttons to control the simulation process and texts to observe its progress. The lower part of the window is the view of the world where the agents are acting. A small square is a male agent, and a circle is a female. A smaller one is a child, and a darker one is an elderly agent. A triangle is an obstacle object. An agent is colored with the appearance in the outer part and the preference in the inner part for each. It is possible to replace the inner color to indicate the value of gene by user's operation using a popup menu. A line segment connecting two agents represents the relation of love. The long line segment with a sharp edge visible in figure 1 is so called one side love. The mutual lovers are usually positioned in a short distance each other, and they are displayed with two parallel line segments of round ends connecting them. The view of the world is arbitrarily changeable in the scale and the size by user's operation. Since the rendering process of the view consumes much of computational cost when it contains thousands or more objects, the user stops the animation but not the simulation process by operating a switch in the GUI panel in order to make the execution faster.

3.2 History of gene density distribution

Monitoring the history of the density for each gene is important to track the evolutionary process. The user can open arbitrary number of monitor windows to observe it for each gene. The density distribution over the population for each step is arranged along the vertical line, and it is horizontally extended along with the progress of simulation steps. The range of gene value $[0, 1]$ is divided into 100 spans to calculate the density by counting the number of individual agents for each value span. The density is displayed with the color to indicate the value in blue, green, yellow, red, and white corresponding from lower value to higher value.

The image is expanded as the simulation steps is progressing, by adding one vertical stripe at the right side of the image and the image data is rendered with scaling to adapt to the fixed rectangular area in the window. To reduce the computational costs of both time and space, the data of 100 spans for each step is combined with the next step so as to reduce the capacity of the data into half. The image is displayed as 100 horizontal lines at the first step, and is seen as if it is horizontally compressed as the step goes by.

3.3 Trends of statistical indexes

It is also helpful to observe the runtime changes of statistical indexes during the simulation process is progressing. The most common index in such type of simulation is the population size. If it grows more rapidly in a specific parameter settings than the others, it suggests that the settings provides more successful reproduction than the others. It also suggests that the parameter would be evolutionarily tuned toward that settings if the parameter values were encoded in genotype. Another interesting indexes are on the number and rate of couples from our motivation. Sexual dimorphism is promoted by co-evolution between appearance and preference, and it is revealed as increase of rate of heterosexual couples and decrease of homosexual couples if homosexuality is allowed as the simulation settings. Because the value of latter index is much smaller than the former, the vertical scale for these two types of indexes are independent. The ranges of vertical axis is displayed at the bottom of the window. The scale of both vertical and horizontal axes is automatically adjusted so as to display it in a fixed size of area.
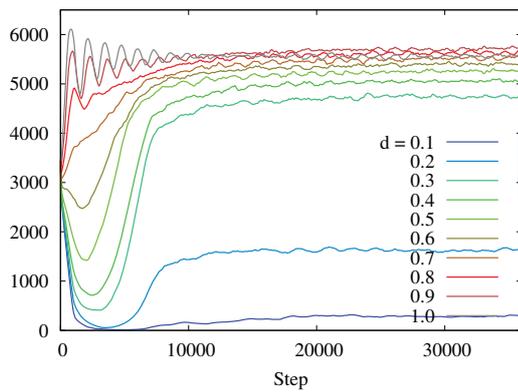
Other indexes for dimorphism from a view point of genes rather than the social phenomena is also helpful. The gene distance between male appearance and female appearance should represent how the dimorphism is clear. This index should be compared with the distance between appearance and preference of same sexes and opposite sexes. If the initial population has wide distribution of these colors, the all of these indexes are relatively long, and the distance between appearance and preference opposite sexes would be shortened through evolution. On the other hand, if the initial colors have narrow variation, appearance and preference of same sexes would be going separate. These indexes of gene distances are also possible to be monitored using another window.

As a research result of another model of sexual dimorphism suggested [7], it also promotes sympatric speciation. This means that the population does not always converge toward a single species but a diversity of the species might remain stable in a process of a large number of steps. To monitor such process of speciation, we introduced Hopkins statistic [8] that was proposed as an index of cluster tendency. This is a measure to show how the distribution is different from uniformly random case. Because it wastes much of computational cost if we use the gene values of all of individuals, the user is allowed to adjust the number of sample individuals, 500 for example, to estimate the index.
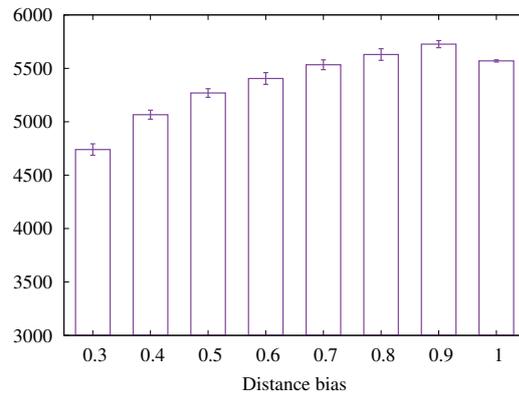
It is possible to work together with another software specialized for statistical analysis via output data from the simulator. All of the monitoring facilities described in 3.2 and 3.3 have functionalities to write the contents into files in CSV format.

4 EXPERIMENT EXAMPLE

As an extension of our preliminary experiment [9], we tried it again using this simulator to investigate more detail effects of distance bias in the evolutionary process. When a person selects a candidate to propose, he/she may compromise by choosing an acceptable neighbor than a beauty/handsome in the distance. Such compromise may helpful to organize as many couples as possible, but at the same time, it may be an obstacle for sexual dimorphism that promotes heterosexual mating. Under

Evolutionary processes of population size.   Average population size in final 2,560 steps.

Figure 2: Average population size over ten trials for different values of distance bias in case the appearance and preference are sex influenced.

the assumption that there is the optimal balance of the degree of compromise, we examined evolutionary processes with a variety of settings to investigate the effects of the distance bias, the parameter of compromise for each individual. Figure 2 shows the results of evolutionary process and the population sizes for different values of distance bias in the average values of ten runs for each settings. If the value is one, each individual always selects the nearest neighbor as the best candidate. As we predicted, both edges could not produce large population size, and 0.9 looks the best in this settings.

5   CONCLUDING REMARKS

It is clear that we cannot build a perfect model of human evolution because there are too many factors to be considered. We always have to solve the balance between simplification and explainability. It is easy to explain what happened in a simulation if it is based on a very simple model, but there is often a big gap with the reality, that is, it is difficult to provide a reliable explanation for the phenomena in the real world if the model is too simple. On the other hand, it becomes difficult to make an understandable explanation when the model is too complicated even if the gap is small.

In this version of the simulator, the appearance is represented by three dimensional vector corresponding to the color. By expanding the complexity of appearance so as to include shape, texture, and the other features of subjects in the research on computational aesthetics, it will be able to contribute to seek the origin of beauty.

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