

# Culture in oranzees

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cultural transmission | cultural evolution | cumulative culture | chimpanzees culture | individual-based models

Cumulative culture, the transmission and improvement of knowledge, technologies, and beliefs from individual to individual, and from one generation to the other, is key to explain the extraordinary ecological success of our species (1, 2). Which cognitive abilities underpin humans cumulative cultural capacities, and how these abilities affect the evolution of culture itself are among the most pressing question of evolutionary human science.

Many other species, besides humans, are able to use social cues to modify their behaviour. Various primates have shown to possess complex traditions that are socially transmitted (3–5). Differently from other primate species, however, humans have cumulative culture. While there are various definitions of cumulative culture (6), some of its characteristics are broadly accepted. Cumulative culture requires the accumulation of cultural traits (more cultural traits are present at time  $t$  than at time  $t-1$ ), their improvement (cultural traits at time  $t$  are more effective than traits at time  $t-1$ ), and ratcheting (the innovation of cultural traits at time  $t$  depends on the presence of other traits at time  $t-1$ ).

Not all human culture needs to be supported by faithful copying (7), but our cumulative culture depends on our ability to transmit and preserve accurately *new* information. Experiments have indeed shown that humans are capable of copying, and that routinely do it across cultures. More controversial is the claim that other species copy. Claims regarding the existence of animal cultures based on copying raise a puzzling question: if other species can and do copy, why did they not develop cumulative cultures? There are only two possible answer to this question. Either they do not copy, or copying does not automatically lead to cumulative culture.

Primatologists have claimed the existence of copying-based cultures from observations of wild populations. (3) examined the population-level distribution of behavioral traits in populations of chimpanzees across seven sites, and argued that this distribution proved the existence of different cultures in these populations. We developed an individual-based model to assess whether the patterns observed in the wild and described in (3) actually warrant to pinpoint copying as the underlying learning mechanism. We reproduced several details of the original study, including realistic demographic and spatial features, and effects of ecological availability and genetic predisposition, to investigate whether an equivalent distribution of behavioral traits could emerge in absence of any copying. While our simulated species, *oranzees*, can be influenced by social cues present in the environment (as widespread in the

animal kingdom), we did not model any copying.

Our results show that, under realistic values of the main parameters, we can reproduce the distribution of behavioral traits found in (3), without any copying required. In other words, as oranzees can and do show cultural patterns resembling wild ape patterns, this is proof that such patterns cannot be counted as evidence that copying must have taken place. This provides an answer to the puzzling question we presented above: copying is necessary and leads to cumulative culture, but ape cultures are not based on it.

## Materials and methods

We built an individual-based model that reproduces a world inhabited by six populations of “oranzees”, a hypothetical ape species. The model is space-explicit: the oranzees populations are located at relative positions analogous to the six chimpanzees sites in (3). This is important to determine the genetic predispositions and ecological availabilities associated to their possible behaviours (see below). Population sizes are also taken from the sites in (3). Following (8), we use data from (9), and we define population sizes as  $N = \{20; 42; 49; 76; 50; 95\}$ .

Oranzees are subject to an age-dependent birth/death process, broadly inspired by descriptions in (10). A time step  $t$  of the simulation represents a month in oranzees’ life. From when they are 25 years old ( $t = 300$ ), there is a 1% probability an oranzeer will die each month, or they die when they are 60 years old ( $t = 720$ ). The number of individuals in the population is fixed, so each time an oranzeer dies is replaced by a newborn.

A newborn oranzeer does not show any behaviour. Behaviours can be innovated at each time step. The process of innovation is influenced by: (i) the oranzees ‘state’, which depends on the behaviours an individual already possesses, (ii) the frequency of the behaviours already present in the population (“socially-mediated reinnovation”), and (iii) the genetic propensity and ecological availability locally associated to the behaviour. At the beginning of the simulations, the

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populations are randomly initialised with individuals between 0 and 25 years old.

**State.** In the oranzees world, 64 behaviours are possible. Behaviours are divided in two categories, namely 32 social and 32 food-related behaviours. These figures were chosen to resemble the behaviours considered in (3).

In the case of social behaviours, we assume four sub-categories, each with eight possible different behaviours, that serve the same goal. Oranzees' state is based on how many of the four goals are fulfilled. A goal is considered fulfilled if an oranzee has at least one behaviour out of the eight in the sub-category. An oranzee has a state value of 0.25 if, for example, it has at least one behaviour among the first eight behaviour, and none of the others, and a state value of 1 if there is at least one behaviour in each sub-category.  $p_{\text{social}}$ , the probability to innovate a social behaviour, is drawn from a normal distribution with mean equal to  $1 - \text{state}_{\text{social}}$ .

Food-related behaviours are analogously divided in sub-categories, with the differences that there is a variable number of behaviours in each sub-category, and that sub-categories are associated to two different 'nutrients',  $Y$  and  $Z$ . The idea is that individuals need to balance their nutritional intake, so that their optimal diet consist in a roughly equal number of food for one and the other nutrient. The state, for food-related behaviours, depends on the total amount of food ingested and on the balance between nutrients, and it is calculated as the sum of each sub-category fulfilled (as above, for this to happen there needs to be at least one behaviour present) minus the difference between the number of sub-categories providing nutrient  $Y$  and the number of sub-categories providing nutrient  $Z$ . We normalize the state between 0 and 1, and, as above  $p_{\text{food}}$  is then calculated as  $1 - \text{state}_{\text{food}}$ . (Further details in SI).

**Socially-mediated reinnovation.** At each time step, all oranzees have a probability of innovation for social and food-related behaviours calculated as described above. The specific behaviour an oranzee will innovate depends both on the frequency of the behaviours already present in the population, and on the ecological availability and genetic propensity associated to the behaviour. A further parameter of the model,  $S$ , controls the probability that each reinnovation is socially-mediated. When a reinnovation is socially-mediated, the probability of innovating each behaviour  $B_i$  is weighted by its proportional instances in the population, among the behaviours of the same category, so that common behaviours are more likely to be reinnovated.

When the reinnovation is not socially-mediated, the probability of innovating each behaviour is random. Only one behaviour per category can be innovated at each time step.

**Genetic propensity and ecological availability.** The behaviour selected in the previous step is then innovated or not according to its genetic propensity and, in case of food-related behaviours, ecological availability.

Genetic propensity is a probability  $p_g(0, 1)$ , assigned independently for each of the 64 behaviours. A parameter of the model,  $\alpha_g$ , determines the probability that the genetic propensity of each behaviour is equal for all the six populations or whether is different.

If it is equal,  $p_g$  is randomly drawn. If it is different, we assign the propensity using a geographical gradient. We choose a random point and calculate its distance to each population. Distances are then transformed to  $p_g$  by rescaling them between 0 and 1, so that for the farther site  $p_g = 0$  i.e. the associated behaviour will be impossible to express (see SI). Notice that  $\alpha_g = 0$  does not mean that there are no genetic influences on the behaviours, but that there are no differences between the populations with regard to this aspect.

Ecological availability is a probability  $p_e(0, 1)$  that represents the likelihood of finding a resource, or its nutritional value, in each site. Ecological availability is assigned only to food-related behaviours, and it is calculated in the same way of  $p_g$ , using the parameter  $\alpha_e$  to determine the probability of ecological availability being different in the six populations.

**Model's output.** We run simulation for  $t_{\text{max}} = 6000$  (corresponding to 500 years of oranzee-time). For each simulation, following (3), we classify each behaviour, in each population, as:

- *customary*: a behaviour observed in over 50% of individuals in at least one age class (see SI for how age classes are defined in our model).
- *habitual*: a behaviour observed in at least two individuals across the population.
- *present*: a behaviour observed in at least one individual across the population.
- *absent*: a behaviour not observed even once in the population.
- *ecological explanations* is a behaviour that is absent because of complete lacking of local ecological availability (i.e., in our model, associated to  $p_e = 0$ ).

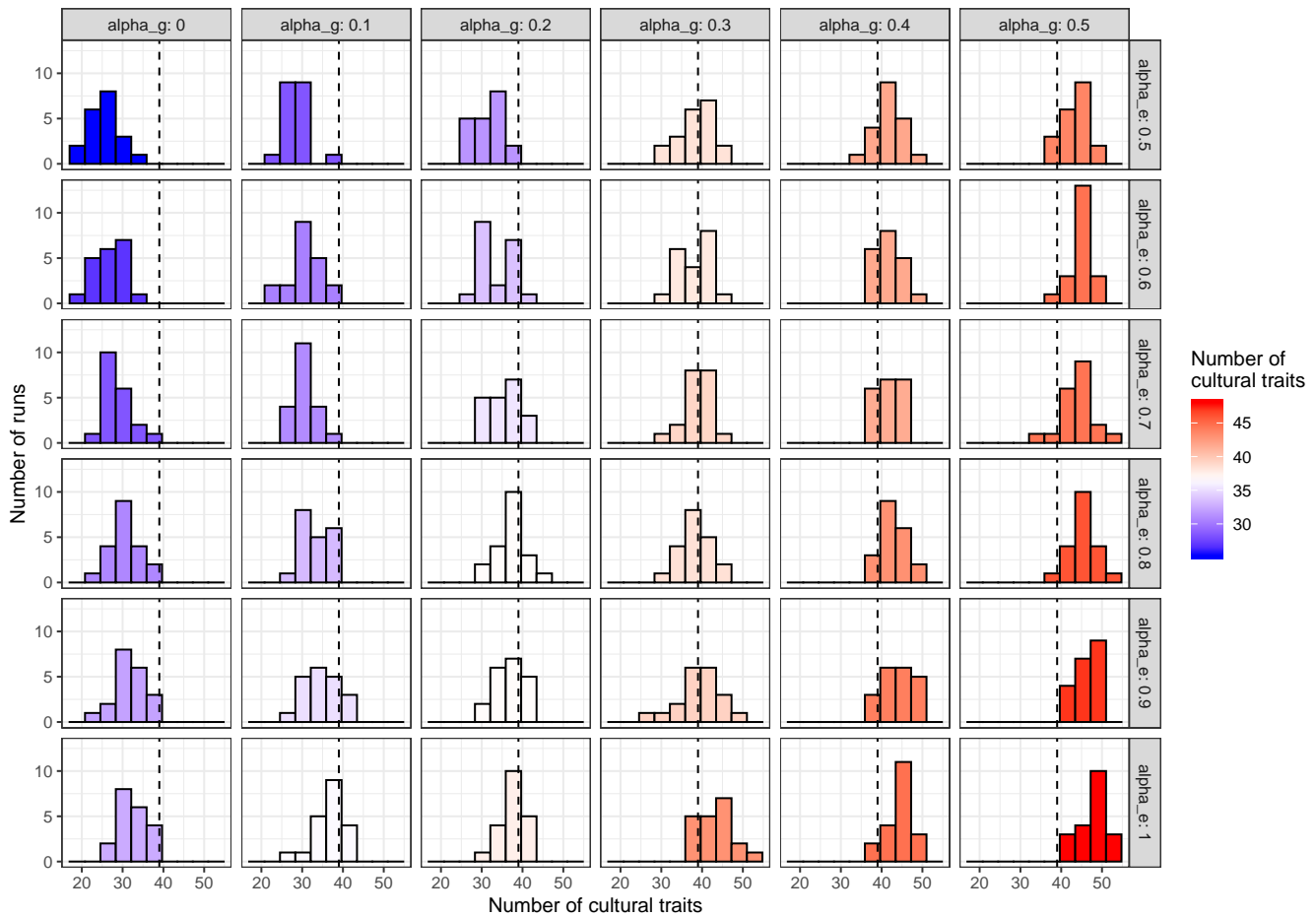
Notice the last category in (3) (*unknown*, i.e. "the behaviour has not been recorded, but this may be due to inadequacy of relevant observational opportunities") does not apply in our case.

Finally, we calculate the same "patterns" described in (3):

- $A$ : behaviour absent at no site.
- $B$ : behaviour not achieving habitual frequencies at any site.
- $C$ : behaviour for which any absence can be explained by local ecological factors.
- $D$ : behaviour customary or habitual at some sites yet absent at others, with no ecological explanation, i.e. the behaviours defined as "cultural".

## Results

We are particularly interested in the realistic parameter conditions of moderate to high environmental variability ( $\alpha_e = (0.5, 1)$ ) and zero to moderate genetic differences ( $\alpha_g = (0, 0.5)$ ). We run 20 simulations for each combination (for a total of 600 runs). For all, reinnovation is socially-mediated ( $S = 1$ ). The results show that various combinations



**Fig. 1.** Number of cultural traits in oranzees, when varying ecological and genetic diversity. Red colour indicates simulation runs that produced more than 38 cultural behaviours; blue colour indicates simulation runs that produces less than 38 cultural behaviours. For all simulations,  $S = 1$ ,  $\alpha_e$  and  $\alpha_g = 0$  as indicated in the plot.  $N = 20$  runs for each parameters combination.

of parameters produces a number of cultural behaviours (pattern *D*) consistent with the 38 found in (3), in absence of any explicit copying mechanism implemented (see Figure 1).

We also analyse the effect of the parameter  $S$  (proportion of socially-mediated reinnovations), in three conditions (see Figure 2): (a) no genetic differences and intermediate ecological differences (compare to the high-left angle of Figure 1, where with  $S = 1$  simulations produce less than 38 cultural behaviours), (b) good match with (3), and (c) intermediate genetic differences and high ecological differences (compare to the low-right angle of Figure 1, where with  $S = 1$  simulations produce more than 38 cultural behaviours). As expected, decreasing  $S$ , decreases the number of cultural behaviours. Conditions where, with  $S = 1$ , there were more than 38 cultural behaviours could still produce results analogous to (3), when not all reinnovations are socially mediated.

Our results show that our model not only easily reproduces the number of cultural behaviours (pattern *D*), but also the number of behaviours classified in the other three patterns (A,

B, C) in (3). Figure 3 show the four patterns produced in one of the conditions for which we have a good match for cultural behaviours ( $\alpha_e = 0.8$ ;  $\alpha_g = 0.2$ ,  $S = 1$ ).

Finally, we run 100 simulations for the same condition where we have a good match for cultural behaviours with (3) ( $\alpha_e = 0.8$ ;  $\alpha_g = 0.2$ ,  $S = 1$ ). In each simulation, we recorded, for each population, the number of behaviours (habitual + customary + present) that are also classified as cultural (see Figure 4). We find a small, but significant, correlation between population size and number of cultural traits ( $p < 0.00001$ ,  $\rho = 0.2$ ,  $N = 600$ ). In other words, our model reproduces the effect of cultural accumulation relative to population size found in real populations.

## Discussion

TO DO

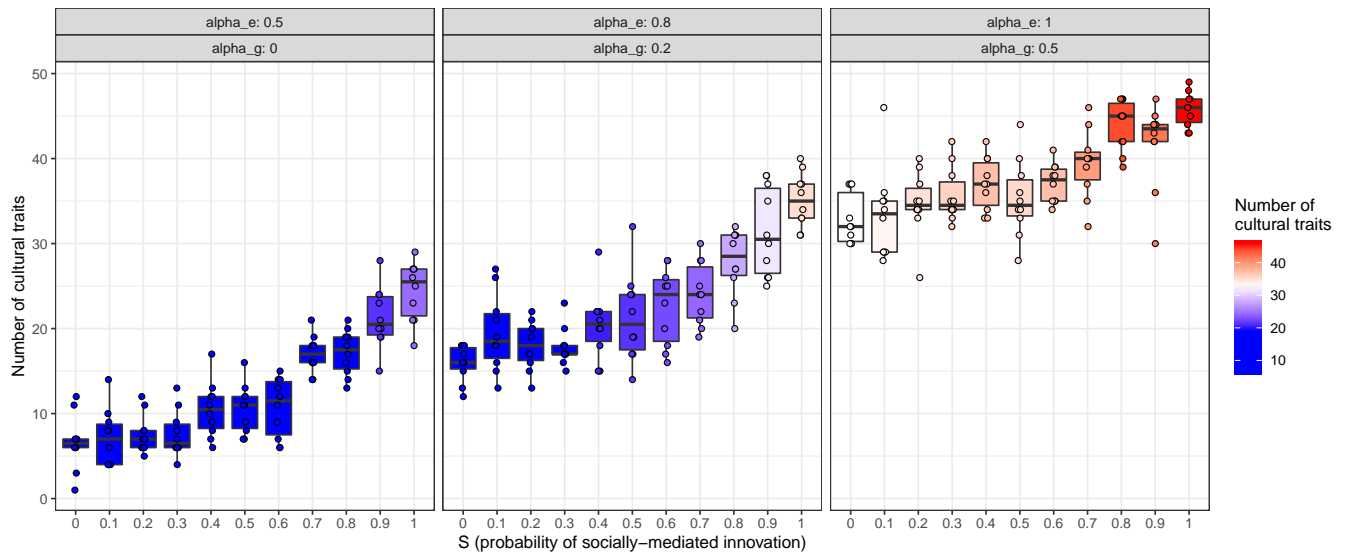
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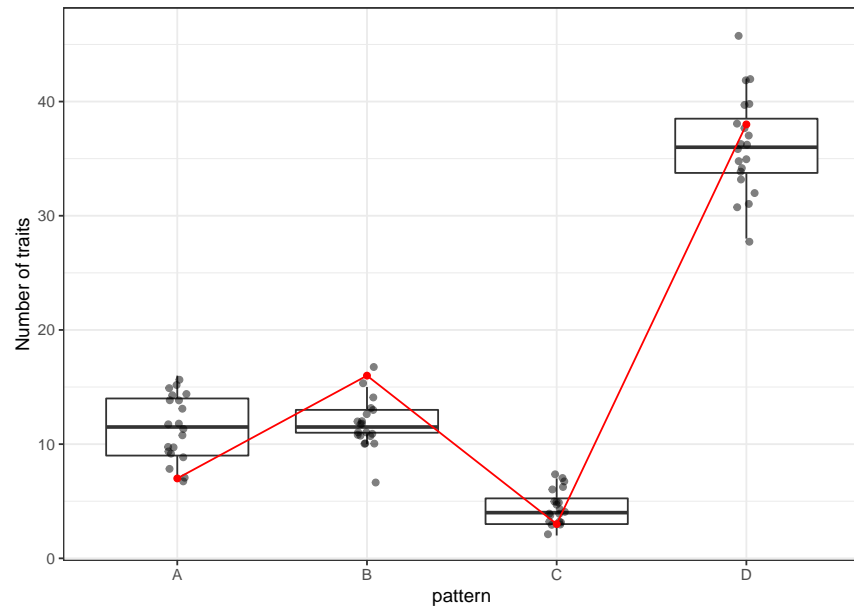
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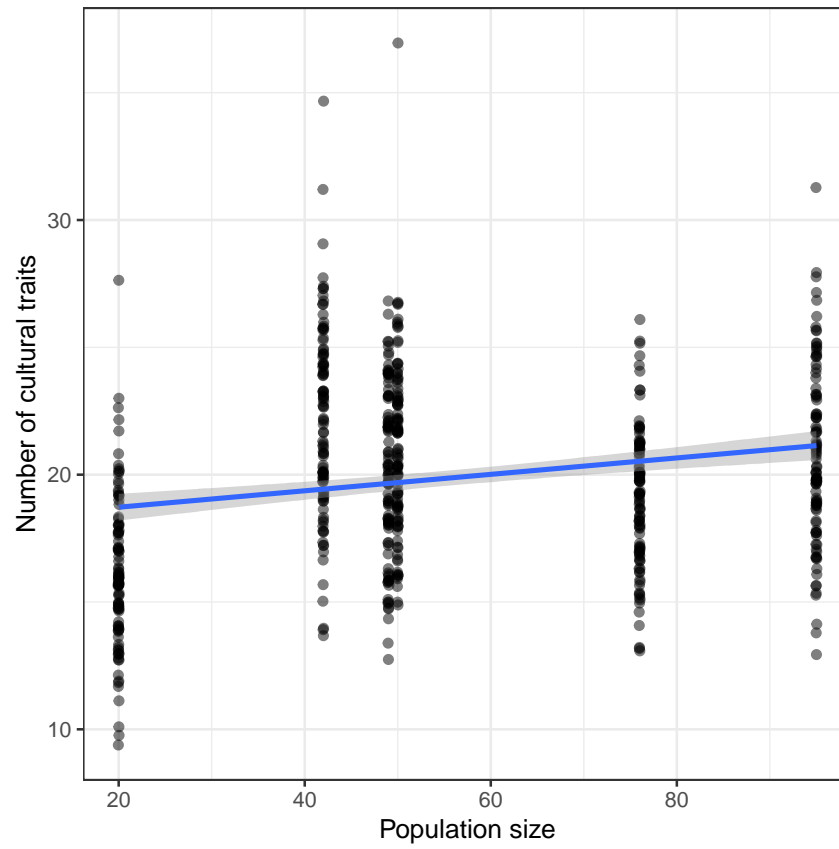
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**Fig. 2.** Cultural traits in oranzees, varying the probability of socially-mediated innovations. Red colour indicates simulation runs that produced more than 38 cultural behaviours; blue colour indicates simulation runs that produces less than 38 cultural behaviours.  $S$ ,  $\alpha_e$  and  $\alpha_g = 0$  as indicated in the plot.  $N = 10$  runs for each parameters combination.



**Fig. 3.** Number of behaviours for each of the four patterns (\*A\*, \*B\*, \*C\*, \*D\*) for the parameters  $\alpha_e = 0.8$ ;  $\alpha_g = 0.2$ ,  $S = 1$ . The red values are the values described for real chimpanzee populations.  $N = 20$  runs.



**Fig. 4.** Number of cultural behaviours for each population for the parameters  $\alpha_e = 0.8$ ;  $\alpha_g = 0.2$ ,  $S = 1$ . The blue line is a linear fit of the data.  $N = 100$  runs.