



Stochastic processes: the case of ancestor's trees and the inbreeding relationships

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Abstract:

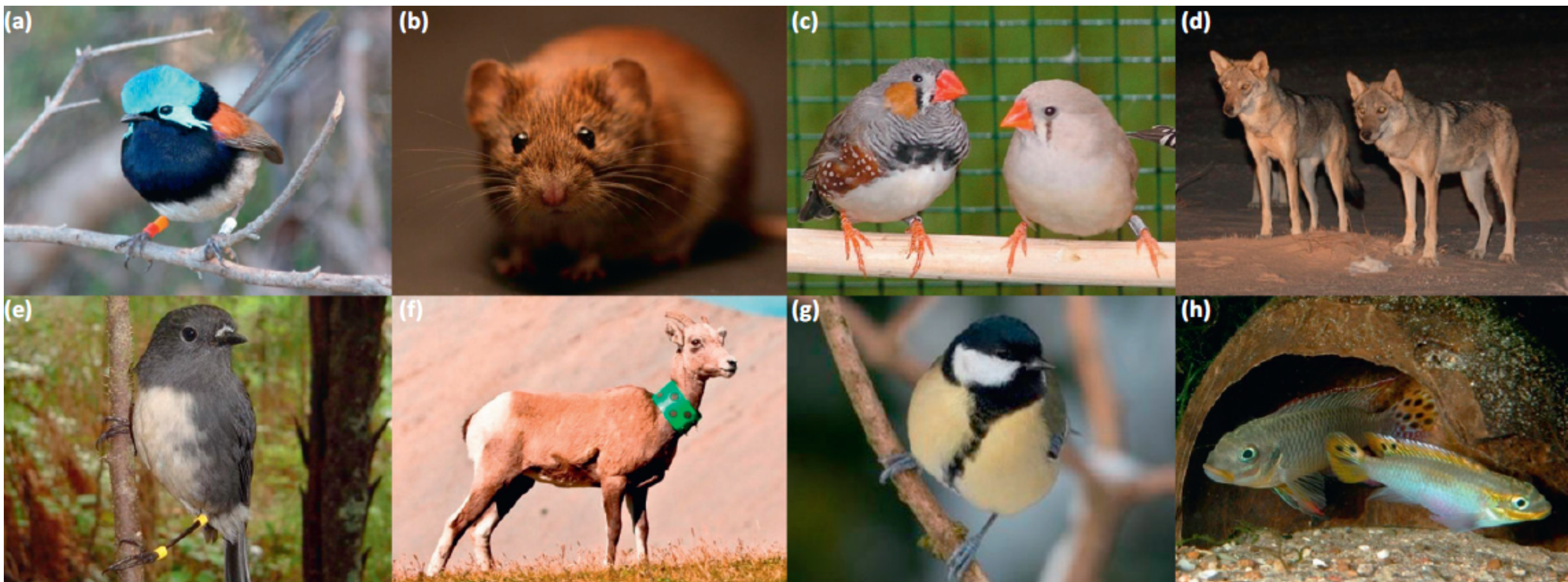
Based on our previews work [1], where we performed a simulation to reconstruct ancestor's trees for individuals of sexual reproduction, we count and studied all the different possible relationships between the ancestors in a tree. In our previous model we withdraw the links or kinship between the parents and studied how to produce the convergence of the tree. Now we built a graph to represent the tree and studied the properties of the graph. We also propose an analytical way to count all the possible trees that can be generated with a fix number of male and female ancestors.

Idea:

Consider a binary tree with N generations → remove A_k individuals from the tree at random → connect the remaining nodes so that each individual has a female and a male parent → Count how many different it is possible to generate.

A motivation to develop the model from wild animal populations

Studies of inbreeding strategy have reported inbreeding tolerance in different species. Recent studies have also found evidence of regular incest in wild mammals, even in social species where relatives are spatio-temporally clustered [2-6].



Inbreeding avoidance in: (a) red-winged fairy wrens *Malurus elegans*; (b) bank voles *Myodes glareolus*; (c) zebra finches *Taeniopygia guttata*; (d) grey wolves *Canis lupus*.

Inbreeding tolerance in: (e) New Zealand robins *Petroica australis*; (f) bighorn sheep *Ovis canadensis*; (g) great tits *Parus major*.

inbreeding preference in: (h) cichlid fish *Pelvicachromis taeniatus*.

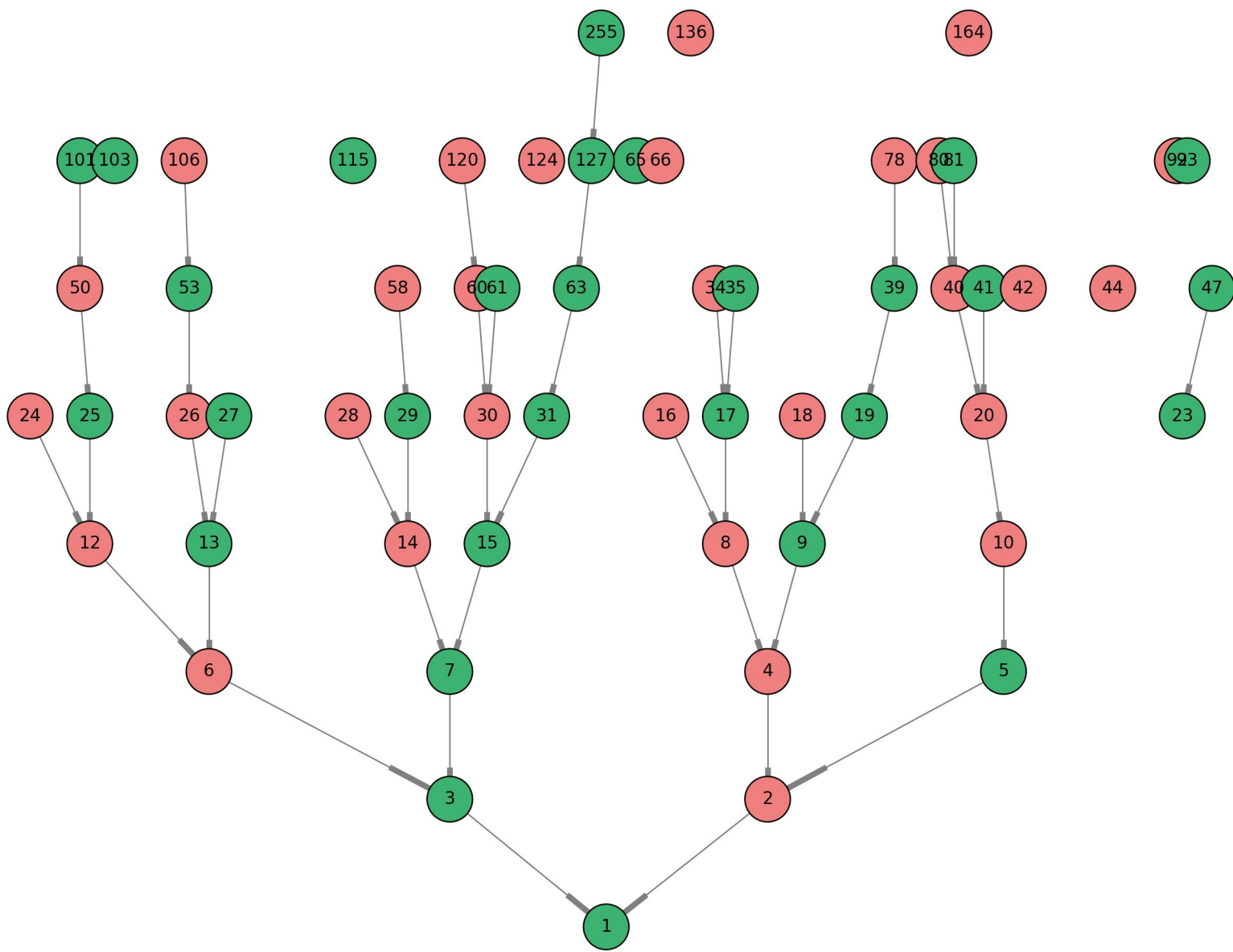
Building one tree of ancestors

- In each generation k the maximum number of possible ancestors is 2^{k+1} , where the generation number starts from k = 0 (parents generation).
- We used a recurrence algorithm combined with a random number generator for each generation.
- The ancestor's number in the k generation is used to constraint maximum ancestors number for the following generation k+1.
- The problem was a model based on Markov chains.

One of the many possible representation for the links between the ancestors

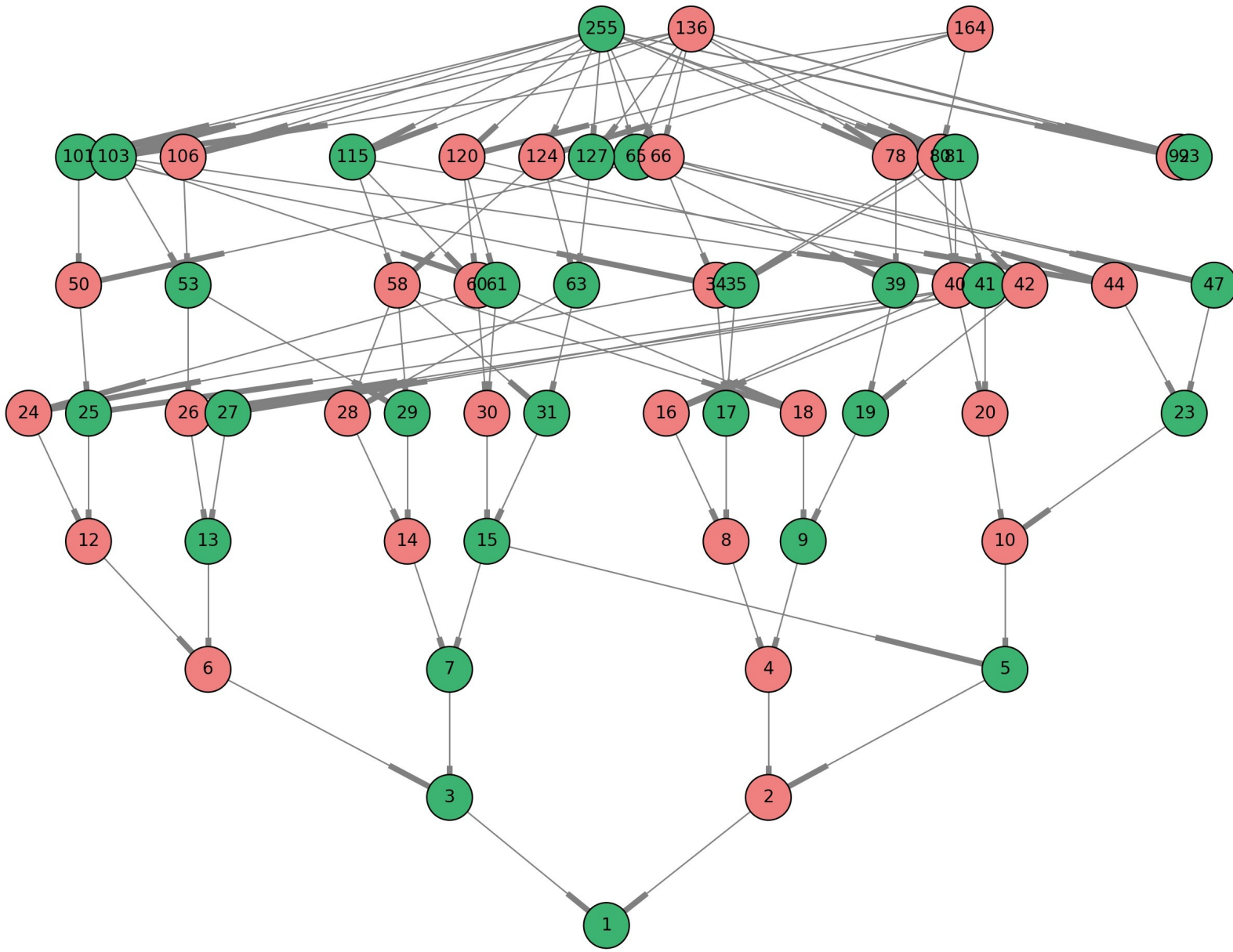
- From a labeled binary tree, we removed as many nodes as indicated for our simulation.
- C_k is the number of ancestors (male and female) in the k generation.
- The number of removed ancestors is: $A_k = 2^{(k+1)} - C_k$.
- A_k is the number of labels (or "parents" or "individuals") removed from the binary di-graph tree including male (M_k) and female (F_k).
- We keep close to the 50% the fraction of removed F_k and M_k

A binary random tree with subtracted ancestors



Adding the links between the ancestors

- We chose the remaining nodes (ancestors) at random to be the parents of the nodes (children) in the following generation.
- We considered the gender of the ancestor to complete for each node one parent of each gender.



How many different trees could you build?

- We used the constraints: $A_k = F_k + M_k$ $d_k + h_k = F_{k+1}$ $l_k + h_k = M_{k+1}$
- d_k , l_k and h_k is the number of individuals without mother, father and without any of them.

We obtain an analytical expression to count all the possible trees:

$$T^{Kmax} = \prod_{k=1}^{Kmax} (2^k - M_{k+1})^{M_{k+1}} (2^k - F_{k+1})^{F_{k+1}}$$

Further work

This work is currently under development. Some further steps are related to an statistical study of the graphs types produced by the algorithm and equation properties.

References

[1] M.Caruso, C. Jarne. Physical Review E 90, 022125 (2014) .[2] Jamieson, I.G. et al. (2009) .Behav. Ecol. 20, 575584 [3] Rioux-Paquette, E. et al. (2010) . Anim. Behav. 80, 865871. [4] Szulkin, M. et al. (2009) Anim. Ecol. 78, 778788.[5] Thunken, T. et al. (2007). Curr. Biol. 17, 225229. [6] Nichols HJ, Cant MA, Hoffman JI, Sanderson JL. 2014 Biol. Lett. 10: 20140898.