

On Species Evolution

Term paper 498Bio; Peter Fleck; 12/15/2001

An interesting subfield of theoretical biology consists in how species develop in their identity for a given distribution of resources, type of competition and set of copresent species, forming a self-organized system¹. Some impressions on this developing field[1, 2, 3, 4, 5, 7, 6, 9] together with the discussion of a recent preprint[8] shall be given in the following.

The two possible dynamical effects in the evolution of species are characteristics shifts[2, 4], i.e. a coherent change of the traits defining the species throughout its entire group, and sympatric speciation[3, 5, 7], i.e. the formation of subspecies from a common ancestor group². The scientific interest obviously lies in the question, under which circumstances and in which manner can and do these processes occur. The precise mathematical description of these systems is –as in every new field– still developing, some ingredients seem to be common however:

- choose a set of genotypic ('what's in the genes') or phenotypic ('what has actually come to life') traits, \mathbf{x} and ϕ resp. , according to which to identify the species at hand³;
- represent the entire population in your system as a number distribution $f(\mathbf{x}, \phi, t)$, where the time variable t can be either continuous or discrete, representing an generation index in the latter case⁴; and
- construct an "equation of motion" to obtain the distribution $f(\mathbf{x}, \phi, t)$ for the next generation (t discrete) or its change in continuous time.

This equation of evolution would in general integrate a product of f with itself, modelling sexual reproduction, over the space of characteristics, while

¹Species in this context are defined as a group of individuals that distinguish themselves from other beings through a set of common characteristics.

²We mainly have eukaryotes in mind, excluding the merger of species.

³Actual models however frequently limit themselves to a single "effective characteristic" or "characteristic of interest"

⁴The researcher may feel free to add (coarse grained) space variables into the genotypic traits ϕ .

further prefactors or terms in the equation represent the influences of available resources, competition, mating decisions, and death onto the evolution of the population distribution $f(\mathbf{x}, \phi, t)$.

Kral in his recent preprint[8] first stresses the geometrical aspect of this modelling by defining the vector space of characteristics as the direct product of the spaces of the traits of interest and introducing a measure

$$\langle f|g \rangle \equiv \int d^n \mathbf{x} \sqrt{f(\mathbf{x})g(\mathbf{x})} = 1 - \mu \quad (1)$$

between two species $f(\mathbf{x})$ and $g(\mathbf{x})$, thereby defining $f(\mathbf{x})$ to be "orthogonal to $g(\mathbf{x})$ with measure μ ". Note this definition being based on the genotype only. He proposes the equation of evolution

$$\frac{\partial f(\mathbf{x})}{\partial t} = \mathcal{R}(\phi, \mathbf{x}) \int \int d\mathbf{x}_I d\mathbf{x}_{II} \mathcal{S}(\mathbf{x}_I, \mathbf{x}_{II}) (f(\mathbf{x} - \mathbf{x}_I) f(\mathbf{x} + \mathbf{x}_{II}))^\alpha - \frac{f(\mathbf{x})}{\tau(\mathbf{x})} \quad (2)$$

with an effective resources function \mathcal{R} , a sexual function \mathcal{S} with second order mating in a power α , and an average lifetime τ . He then chooses \mathcal{S} to be gaussian in its variables and \mathcal{R} gaussian times a prefactor representing available resources under competition with other individuals.

The author investigates these equations computationally for a single effective trait x , various powers α and resources richnesses \mathcal{R}_0 (in \mathcal{R}), starting out with a gaussian population distribution $f(x)$ to represent a single species. He finds that

- sympatric speciation occurs only for $\alpha > 0.5$;
- the number of forming subspecies increases with the amount of available resources;
- competition creates subspecies while a lower average lifetime τ smoothens their distributions.

The author intends to thereby support the concept of "species orthogonalization", i.e. "a process in which species approach a state, where they share resources and habitats in the most effective way, fully stabilized in time"[8], that he wishes to introduce in the beginning of the paper. The measure he defines for this purpose is able to evaluate the degree of speciation between two populations, however, his concept of orthogonalization, apparently with

the idea of an effective "repulsion" of species in the characteristics space, might probably have been better supported by studying the response of a system with a number of existing species to the immigration of an additional one with comparable characteristics and competing for resources.

The speciation equation (2) he suggests is not directly being compared to previous work, leaving to the reader to discuss the quality of this approach. The system is obviously simplistic by considering a single trait, and neglects among many others predator-prey interactions, spatial distributions of species, the quantization of the population and possible time dependences of the external parameters.

The danger of modelling lies in constructing your approach from the outset in a manner that it will merely reproduce the desired results, a point that comes back to mind when comparing the resources profiles used in this paper and the population distributions thereby achieved. The formation of subspecies however does not explicitly seem to be incorporated into the approach taken by Kral, as no subspecies form in the case of scarce resources, so that this paper seems to form a genuine contribution to the field of species evolution.

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