

Population Genetics and Evolutionary Theory

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This note presents a rational argument for the claim that if population genetics is viewed as a part of the research program of evolutionary theory in biology, the current research program in population genetics is deeply flawed. It then points to a modified version of population genetics, which we may call categorial genetics as a better fit with evolutionary theory.

1. The Flaw

1.1 What this Note Seeks to Defend

The initial sentences in the entries on Population Genetics in *Wikipedia*, *Science Direct*, and *Stanford Encyclopedia of Philosophy* are:

- 1) *Wikipedia*: "Population genetics is a subfield of genetics that deals with genetic differences within and between populations, and is a part of evolutionary biology." (https://en.wikipedia.org/wiki/Population_genetics)
- 2) *Science Direct*: "Population genetics is the branch of genetics that explores the consequences of Mendelian inheritance at the level of populations, rather than families." (<https://www.sciencedirect.com/topics/neuroscience/population-genetics>)
- 3) *Stanford Encyclopedia of Philosophy*: "Population genetics is a field of biology that studies the genetic composition of biological populations, and the changes in genetic composition that result from the operation of various factors, including natural selection." (<https://plato.stanford.edu/entries/population-genetics/>)

In what follows, I attempt to show that

if

population genetics is taken to be

a part of evolutionary theory, as in statement (1),, and

a study of population, as in statement (2) and implied in statement (3), as

distinct from categories of organisms such as primate, mammal, vertebrate,

insect, worm, animal, plant, prokaryote, etc.,

then

the current research program of population genetics is deeply flawed.

1.2 The Concepts of Macro and Micro Evolution

To critically evaluate the argument that I am going to present, it is important to distinguish between macroevolution and microevolution.

I assume that

- 4) The terms primates, mammals, vertebrates, insects, ants, worms, birds, animals, plants, and prokaryotes denote different kinds of biological *taxa*,
- 5) *Species* is a specific form of taxa,
- 6) What are called *varieties* of species are sub-taxa of species, and
- 7) *Macroevolution* is the evolution of biological taxa.

As for the term microevolution, we make take it as either (8) or (9)

- 8) Microevolution is the study of *the change from one taxon to another*, i.e., it is the study of evolutionary changes (where speciation is an instance of evolutionary change)
- 9) Microevolution is the study of the evolution of *traits and trait values* (i.e., Mendelian traits and alleles)
- 10) Microevolution is the study of evolution of *biomolecules* (i.e., evolution at the molecular level)

In addition to the above, one may also study
the evolution of systems in organisms (e.g., the evolution of the respiratory system, circulatory system, reproductive system)
the evolution of organs (the evolution of the internal organs in animals, the evolution of the heart, evolution of the skull, ...)
the evolution of tissues (the evolution of the blood, the evolution of the bone material, ..)
the evolution of cells (e.g., the evolution of eukaryotic cells, the evolution of neurons, ...)

But the question whether these come under macro evolution or microevolution we will side step for now.

1.3 The Concepts of Sets, Populations, and Categories

My reasoning in support of the my claim of the flaw in the research program of population genetics is based on the conceptual distinction between populations and categories.

A set can be defined in terms of

- A) the intrinsic traits shared by the individual organisms, or
- B) some extrinsic or contextual feature.

For instance, the statements

- The set of organisms with compound eyes, and
- The set of organisms with bones

define the population in terms of shared traits. If we do this, the set constitutes a **category**. In contrast, the statements

- The set of organisms in the pond in my backyard
- The set of organisms in the village Choondal in Thrissur District in Kerala

do not yield a category. If we adopt this mode of defining, the set constitutes a **population**, not a category. It may be a population within a category, or a population composed of multiple categories.

Every noun in a language denotes a category. Thus, when use English words like stone, rock, river, stream, flower, leaf, leg, eye, child, adult, girl, boy, woman, man, doctor, teacher, table, chair, plant, creature, animal, butterfly, dog, cat, monkey, ... the concept denoted by those words are categories. The sentence "That dog is loves me" means "The X such that X is member of the category of dogs and I am pointing to X loves me." The sentence "Dogs are animals" means "The category of dogs is a subcategory of animals".

The concepts expressed by the vocabulary of natural languages (such as the words cited above) are not theoretical categories. They are not even academic categories. In contrast, words like canine, feline, and equidae are part of the academic vocabulary

of the life sciences. When these academic categories are used in a theory to explain and predict the phenomena we observe, they are categories of a scientific theory.

Whether it is the evolution of taxa (and varieties), evolution of the traits and trait values that distinguish taxa and varieties, or evolution of systems, organs, tissues and cells, *all forms of evolution involve the emergence novel categories.*

1.4. The Final Step of the Proof

Population genetics is not concerned with the emergence of novel categories resulting from novel traits or novel trait values. It is concerned only with the frequency distribution of trait values in a population. Unless this research program evolves into one that studies processes that lead to the emergence of novel biological categories, it has no power to shed light on evolution. As it exists, however, it does not seek to investigate the emergence of biological categories.

Hence, *the current research program of population genetics is deeply flawed.* (QED)

2. From Population Genetics to Categorical Genetics

2.1. The Need for Categorical Theories in Biology

Why bother with this proof? How does it lead to better research in the life sciences?

Here is why. The concept of population is located in statistics, which is a form of inductive reasoning to arrive at conclusions based on quantitative data, that is, data coded in numbers that are subject to arithmetic operations. The conceptualisation of biological taxa as categories (e.g., multi-cellulars, animals, vertebrates, mammals, and felines, lions, and Asiatic lions are categories of biological organisms) allows us to formulate statements such as:

The lions in the Thrissur zoo are members of the category of Asiatic lions

Asiatic lions are a sub-category of lions

Lions are a subcategory of felines

That path allows us to construct ***classificatory theories*** that make testable *predictions* based on the relations of ‘X is a member of category Y’ and ‘category Y is a subcategory of category Z’ (analogous to but more powerful than the set theoretic relations ‘X is a member of set Y’ and ‘Y is a subset of Z’). This advantage comes from the following principle that we may call the Principle of *Logical Inheritance*.

If X is a subcategory of Y, then all properties (trait values) of Y are properties of X.

For instance, from the statement that

Animals have digestive tracts.

and the sub-category relations that connect animals to Asiatic lions, we can deduce

Asiatic lions have digestive tracts.

Logical inheritance lends itself to choosing between alternative classifications on the basis of the standard criteria of correct predictions, generality, and simplicity.

[A detour. Notice that for such predictions, the labels that assign ***ranks*** to categories, namely, variety, species, family, order, class, phylum, kingdom, and domain are irrelevant. In fact, this is a spurious terminology that has no place in theoretical biology. It should have no place even in biology textbooks.]

2.2. The Desirability of Categorical Genetics

Given the formal concepts of **categories**, **category membership** and **sub-categories**, we may say that population genetics can evolve into categorical genetics if it seeks to investigate the genetic composition of categories in biology. This would involve not only categories of organisms, but also categories of organs, categories of tissues, categories of cells, and categories of biomolecules.

Naturally, that research program would also include the investigation the formal concepts of **units** and **subunits** (e.g., biomolecules, cells, tissues, organs, and organisms are biological units, while proteins, muscle cell, muscle tissue, and heart are categories of units.)

Going beyond changes in the frequency distribution of trait values within populations, such a theory would investigate the correspondences between units and categories (e.g., what are the proteins that distinguish, say, muscle cells and bone cells? What are the trait values that distinguish butterflies from dragon flies? Insects from worms? Felines from canines? Animals from Plants? Multi-cellulars from uni-cellulars? Eukaryotes from prokaryotes?)

I would like to invite graduate students to consider the possibility that the line of research outlined above can lead to powerful predictive explanatory theories in the life sciences. I am aware that this research program need not qualify for funding, but I would like to invite you to engage in research in categorical genetics outside of funding, perhaps even outside of institutionalised academia, at your own spare time, as a passion, not for a tertiary degree.

And I would like to invite the biology faculty in this group to critique what has been sketched above.