

Poster:

The Structure of Population Genetics



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In 1980 Richard Lewontin sketched out his view of a **split of population genetics in two** main “research traditions” (**Mendelian** and **biometrical** genetics), each of which based on a “theoretical structure” or “scheme”. For Lewontin, such two components had not been successfully brought together (1980, p. 59): they persisted as separated. Today population genetics is sometimes referred to as a homogeneous theoretical field, and when we evoke “population genetics equations” we often do not specify which theoretical structure within population genetics we are interested in. What did Lewontin mean? And, is it still the case?

Fisher (1918) showed that even with a small number of loci genetic variation approaches the normal distribution. With a greater number of genes the distribution of (geno)types is expected to approach normal distribution even better. And normal distribution is also typical of continuously varying phenotypic traits. If we assume Lewontin’s idea, **in Fisher’s work we find integration** (or, reduction, see Sarkar 2004) **but also separation**. On the one hand, indeed, Fisher demonstrated the compatibility between the two pre-existing theoretical structures. On the other hand, he legitimated the two in pursuing autonomous research strategies, each through equations that handled specific phenomena of inheritance and evolution, yielding continuity of variation and change in different ways.

I see two distinct ways by which from discrete genetic variation continuity is re-established: the Mendelian way finds continuity in frequency of alleles in the population; the biometrical way deals with the continuously varying heritable portion of phenotypic variation.

Today (Hartl & Clark 2007) there is a flourishing development of the part Lewontin called Mendelian genetics, while the biometrical part is largely unchanged. In 1980 Richard Lewontin was probably right: population genetics was split into two theoretical structures, the “Mendelian” and the “biometrical”. The former dealt with **gene frequencies**, the latter with **phenotype variation**. Today the Mendelian part appears much more developed, while the biometrical tradition didn’t go far from Francis Galton’s pioneering statistical, descriptive methods. However, **a better and better integration between the two traditions is under way**, thanks to theoretical and technological advances. **Yet, a clear separation remains** between the kinds of mathematics and phenomena: the integrative attempt of quantitative genetics raises “paradoxes [...] in contrasting evolution at the levels of the phenotype and of the DNA sequence” (Hartl & Clark 2007, p. xiv). **In conclusion, I think that much caution is still needed in referring to population genetics as a solid and fully integrated body of knowledge: it seems not, thus we should always specify what part we are referring to.**

References

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Picture credits

Lewontin: subversivethinking.blogspot.com

Graph and charts: Hartl & Clark (2007), published by Sinauer & Ass., pp. 13, 14, 97, 98, 389, 390 and cover.

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