Preface to the English Edition

The book was first published in Russian. The authors revised the text for the English edition. The little mistakes and inexactitudes of the Russian edition have been corrected. Table 5.1, 6_ϕ-configurations of the genetic element 5-Methylcytosine, which was abridged for the Russian edition, has now been represented completely in the English version.

The non-Abelian calibration field theory is the rapidly developing branch of modern theoretical physics, and this could be the basis of quantum genetics. The introduction of non-Abelian group of internal symmetry for the biological structure (e.g., SU(2) for DNA with the isotopic triplet of information nucleotides **T**, **C**, **U**) gives rise to a phenomenon of asymptotic independence of the complementary DNA pairs' interaction potential from Coulomb forces. It is conditioned by the operation of internal symmetry, which contains the transposition of scattering matrix of interacting physical structure. The Coulomb charge of these structures abrogates and the physical structures couple. Hypochromal effect of DNA is the consequence of pushing of the Coulomb field out to the DNA surface.

The concept of marked point is strongly associated with skewing while transforming of the physical structure within the Poincaré group. In this case, the marked point of terminator with the charge –1 is replacing one of the structure elements. The replaced element is interpreted as an 'observer'. Instead of this element its conformal copy is being introduced. Restoration of the initial structure can be carried out via replacement of the field 'ϕ' by its proper meaning. In other words, the number of elements in the structure increases by +1 and annihilation of the terminator takes place. In many cases, marked point is the part of a physical structure to which the internal symmetry transformation cannot be applied. That is why it can serve as a countable basis generator for the quantitative interpretation of the physical process.

The isotopic invariability of the information nucleotides **T**, **C**, **U** is the consequence of the fact, that only these three nucleotides have one 3, 4_ϕ – genetic code amino acid configuration:

$$\mathbf{T}: -A + D + H, -P + E + H + \phi.$$
$$\mathbf{U}: -V + E + H, -P + D + H + \phi.$$
$$\mathbf{C}: -V + Q + H, -P + N + H + \phi.$$

Among the other tRNA information nucleotides we should mention inosine (**I**), which has only one 5-genetic code amino acid configuration:

$$\mathbf{I}: -N - I - L + F + R$$

and does not have 3, 4_ϕ-configurations.

The doubled six-dimensional Riemann space forms as a result of SU(2) group stratification in the four-dimensional space and in the conformal field of genetic code SU(4) the group occupies two-dimensional subspace.

In avoidance of tangle the signature of real vector space V (p, q) of dimension $n = p + q$ we designate as p^+q^-, where p is the dimension of the positive definite subspace and q is dimension of negative definite subspace in space V. In quantum genetics any covering function of biological structure has the signature because the comparison of covering function with functions, which belong to separate parts of biological structure, gives an example of incomplete cover . Even rather complex organization of a living cell does not give complete covering functions [of separate units of a cell. In this case the negative part of the signature of covering function] determines that freedom, which is a source of development and transformation of cell structures.

The authors hope that this book will be of interest to geneticists, molecular biologists and physicists-theorists and would appreciate any comments and suggestions.

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