%\begin{abstract}

A proposal unifying four approaches to genetic code is discussed.

The first approach is introduced by myself and is geometric: genetic code
is interpreted as an imbedding of the aminoacid space to DNA space possessing a fiber bundle like structure with DNAs coding for a given
aminoacid forming a discrete fiber with a varying number of points. Also
Khrennikov has proposed an analogous approach based on the identification
of DNAs coding for a given aminoacid as an orbit a discrete flow defined by
iteration of a map of DNA space to itself.

Much later (2014) I have
introduced a variant of this scenario in which the fiber space structure is
by assigning aminoacids to the 20 vertices of icosahedron. This model
allows to understand the degeneracies of genetic code group theoretically.

Second approach starts from the 5-adic approach of Dragovich and Dragovich.
Codons are labelled by 5-adic integers n which have no non-vanishing
5-digits so that the n is in the range $[31,124]$. The number of primes
in the range $[31,124]$ is 20. This suggests the labelling of aminoacids by
these primes. This inspires an additional condition on the geometric code:
if possible, one of the integers n projected to p equals to $p(n)$.
This condition fails only for the primes 53,79,101,103 for which some of
5-digits vanishing in 5-ary expansion.

The third approach relies on the generalization of the basic idea of the
so called divisor code proposed by Khrennikov and Nilsson. The requirement
is that the number of factors for integer n labelling one of DNAs, call
it n_d coding for a given aminoacid is the total number of codons coding
for the aminoacid, its degeneracy. Therefore a given aminoacid labelled by
prime p with no non-vanishing 5-digits is coded   by DNAs

labelled by
p itself and by n_d. A group theoretic and physical interpretation for
the origin of the divisor code is proposed.

The fourth approach is a modification of the earlier 4-adic number theoretic thermodynamics approach of Pitk\"anen.

\begin{enumerate}

\item 5-adic thermodynamics involving a maximization of number theoretic
negentropy $N_p(n)=-S_p(n)>0$ (!) as a function of p-adic prime p labelling aminoacids assigns a unique prime to the codon. If no prime in
the range divides S_p, the codon is identified as a stopping codon.

\item The number theoretic thermodynamics is assigned with the partitions
P of the integer $n_{2)}$ determined by the first two letters of the
codon (16 integers belonging to the range $[6,24]$). The integer valued
number theoretic Hamiltonian $h(P)\in Z_{25}$ appearing in the Boltzmann
weight $5^{h(P)/T_5}$ is assumed to depend on the number r of summands
for the partition only. $h(r)$ is assumed to be tailored by evolution so
that it reproduces the code.

\item The effect of the third nucleotide is described in terms of 5-adic
temperature $T_5=1/n$, $n\in [0,24]$: the variation of T_5 explains the
existence of variants of genetic code and its temporal variation the observed context sensitivity of the codon-aminoacid correspondence for some
variants of the code. \end{enumerate}

A numerical calculation scanning over $N\sim 10^{30}$ candidates for $h(r)$
allows only 11 Hamiltonians and with single additional symmetry inspired
condition there are 2 solutions which differ only for 5 largest values of
r. Due to the limited computational resources available only 24 percent
of the available candidates have been scanned and the naive expectation is
that the total number of Hamiltonians is about about 45 unless one poses
additional conditions.

The problem of the number theoretic models is that they do not predict but
only reproduce. This is in sharp contrst to the model based on dark proton
sequences, which leads to a radically new vision about the evolution of
prebiotic life and to the vision about how immune system and genetic code
evolved and what is the meaning of the genetic code.

%\end{abstract}