%\begin{abstract}

The number of DNA triplets is 64. This inspires the idea that DNA sequence
could be interpreted as an expansion of an integer using 64 as the base.
Hence given DNA triplet would represent some integer in
\{0,1....,63\}
(sequences of I Ching symbols give a beautiful realization of these sequences).

The observation which puts bells ringing is that the number of primes
smaller than 64 is 18. Together with 0, and 1 this makes 20: the number of
amino-acids!

{\vm 1. Questions}\vm

The finding just described stimulates a whole series of questions.

Do amino-acids correspond to integers in the set $S=\{primes <64\}\cup\{0,1\}$. Does amino-acid sequence have an interpretation as a
representation as a sequence of integers consisting of 0, 1 and products of
primes $p=2,...,61$? Does the amino-acid representing 0 have an interpretation as kind of period separating from each other structural
units analogous to genes representing integers in the sequence so that we
would quite literally consists of sequences of integers? Do 0 and 1 have
some special biological properties, say the property of being biologically
inert both at the level of DNA and amino-acids?

Does genetic code mediate a map from integers 0,...,63 to set S such that
0 and 1 are mapped to 0 and 1? If so then three integers $2\leq n\leq 63$
must correspond to stopping sign codons rather than primes. What stopping
sign codon property means at the level of integers? How the map from integers 2,...,61 to the primes $p=2,...,61$ is determined?

\vm{\it 2. The chain of arguments leading to a number theoretical model for
the genetic code}\vm

The following chain of arguments induced to large part by concrete numerical experimentation leads to a model providing a partial answer to
many of these questions.

\begin{enumerate}

\item The partitions of any positive integer n can be interpreted in terms
of number theoretical many boson states. The partitions for which a given
integer appears at most once have interpretation in terms of fermion states. These states could be identified as bosonic and fermionic states of
Super Virasoro representation with given conformal weight n.

\item The generalization of Shannon entropy by replacing logarithms of
probabilities with the logarithms of p-adic norms of probabilities allows
to have systems with negative entropy and thus positive negentropy. The
natural requirement is that n corresponds to such prime $p\leq 61$ that
the negentropy assigned to n is maximal in some number theoretic thermodynamics. The resulting correspondence $n\rightarrow p(n)$ naturally
determined the genetic code.

\item One can assign to the bosonic and fermionic partitions a number
theoretic thermodynamics defined by a Hamiltonian. Purely bosonic and
fermionic thermodynamics are defined by corresponding partition functions
Z_B and Z_F whereas supersymmetric option is defined by the product
$Z_B\times Z_F$. Supersymmetric option turns out to be the most realistic
one.

\item The simplest option is that Hamiltonian depends only on the number r
of the integers in the partition. The dynamics would be in a well defined
sense local and would not depend on the sizes of summands at all. The
thermodynamical states would be degenerate with degeneracy factors given by
total numbers $d_I(n,r)$ of partitions of type $I=B,F$. The invariants
known as rank and crank define alternative candidates for the basic

building blocks of Hamiltonian.

\item Ordinary exponential thermodynamics based on, say $e^{-H/T}= q_0^{r-1}$, q_0 a rational number, produces typically unrealistic genetic codes for which most integers are mapped to small primes $p\leq 11$ and many primes are not coded at all. The idea that realistic code could result at some critical temperature fails also.

\item Quantum criticality and fractality of TGD Universe inspire the idea that the criticality is an inherent property of Hamiltonian rather than only thermodynamical state. Hence Hamiltonian can depend only weakly on the character of the partition so that all partitions contribute with almost equal weights to the partition function. Fractality is achieved if Boltzmann factors are given by $e^{-H/T}=(r+r_0)^{n_0}$ so that $H(r)=log(r+r_0)$ serves as Hamiltonian and n_0 corresponds to the inverse temperature. The super-symmetric variant of this Hamiltonian yields the most realistic candidates for the genetic code and there are good hopes that a number theoretically small perturbation not changing the divisors $p\leq 61$ of partition function but affecting the probabilities could give correct degeneracies.

Numerical experimentation suggests however that this might not be the case and that simple analytic form of Hamiltonian is too much to hope for. A simple argument however shows that $e^{-H/T}=f(r)$ could be in quantum critical case be deduced from the genetic code by fixing the 62 values of $f(r)$ so that the desired 62 correspondences $n\rightarrow p(n)$ result.
The idea about almost universality of the genetic code would be replaced with the idea that quantum criticality allows to engineer a genetic code maximizing the total negentropy associated with DNA triplet-amino-acid pair.

\item A natural guess is that the map of codons to integers is given as a small deformation of the map induced by the map of DNA codons to integers

induced
by the identification of nucleotides with 4-digits 0,1,2, 3 (this identification depends on whether first, second, or third nucleotide is in
question). This map predicts approximate $p(n)=p(n+1)$ symmetry having also
a number theoretical justification. One can deduce codon-integer and
amino-acid-prime correspondences and at (at least) two Boltzmann weight
distributions $f(n)$ consistent with the genetic code and Negentropy Maximization Principle (NMP) constrained by the degeneracies of the genetic code.
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