

DIARY JUNE 13 2021: OPTIMISM ABOUT FOUR-SPHERE DETERMINATION OF PRINCIPLES OF BIOLOGICAL CELLS

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1. ZULF'S LIFE HYPOTHESIS

Consider a single biological cell of a simple bacterium. Consider the problem of S4 Electromagnetism on Spinor Fields of a Four-Sphere that goes on for an infinite time. The problem is to determine if there must exist a single biological cell. If so we know that Four-Sphere Physics will tell us origin of life in the universe, and this is my hypothesis.

2. HUMAN GENETIC UNIQUENESS

Is it really true that every human being has unique genome? On one hand this is considered trivial knowledge of biology. On the other hand, what is the certainty that we have here? Is it possible in an infinite time environment to have identical genome for two human individuals? It would be nice to have certainty regarding this issue. If we ignore fundamental problems of science, where this absolute uniqueness of genome of human beings is just *assumed* and not known with absolute certainty, then this is an elementary issue in a sense but I don't like this situation unless there is deeper understanding of the issue. Watson and Crick only discovered double helix of genome in 1953 which is not long ago in scientific time span, so the understanding of science here is not as deep and certain as it could be. A second great question is the issue of possible actual genetic diversity for human beings in theory. This is a surprisingly difficult problem because there needs to be a fundamental understanding of the possible genetic sequences and this is not simply a power set or some other simple combinatorial formula because those sorts of things will produce nonsense easily. I'll give the sense of things that are no good. For example, 4^K with some fixed K of total length of genome is a useless answer because there is no sense in all sequences. An *intelligent* answer has to produce sequences that are human genome and not genomes of Frankenstein's fanciful monsters from the deformed creatures of the Underworld and so on.

3. GETTING DISTRIBUTIONS ON THE REAL LINE FOR GENOMES

We consider the interval $(0, 1)$ first in base 4 expansion. Then we consider genome of length K map to $(0, 1)$ using a map like $[A, C, T, G] \rightarrow [0, 1, 2, 3]$. Then we use the map

$$g : (0, 1) \rightarrow \mathbf{R}$$

given by $g(x) = \log(-\log(x))$.

Then we consider distributions produced from empirical genome distributions on $(0, 1)$ and push them forward by $g_*(\cdot)$.

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The end product is that we have reduced a vast complex messy situation of strings to distributions on \mathbf{R} . Then we can have sanity when considering distributions of genomes in a probabilistic sense. Picking from distributions on \mathbf{R} then correspond to picking genomes at random.

4. LOSSLESS REPRESENTATION OF HUMAN GENETIC VARIATION IN A EUCLIDEAN SPACE

The human genome is a complete set of nucleic acid sequences in 23 chromosomes and DNA in mitochondria. Somatic human cells have 6 billion base pairs and germ cells have 3 billion. All human genomes have the same sequence of 3 billion base pairs and human variation is due to possible differences in 3 *million* single nucleotide variants only. Therefore we can represent variation by just tracking the DNA at those locations.

Now double precision on 64 bit computers track 52 bits in the mantissa. Therefore full possible diversity of humans is represented in 4^{K_0} possibilities with $K_0 = 3 \times 10^6$. If we map these losslessly to double precision floating point in 64 bit computers, we can absorb 26 base pairs per real (floating point) numbers.

$$N_0 = 115385$$

Therefore human genetic variation can be represented in \mathbf{R}^{N_0} .

5. VARIATION DATA REFSNP

```
> available.SNPs()
'getOption("repos")' replaces Bioconductor
standard repositories, see '?repositories' for
details
```

```
replacement repositories:
CRAN: https://cran.rstudio.com/
```

```
[1] "SNPlocs.Hsapiens.dbSNP.20101109"
[2] "SNPlocs.Hsapiens.dbSNP.20120608"
[3] "SNPlocs.Hsapiens.dbSNP141.GRCh38"
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[12] "XtraSNPlocs.Hsapiens.dbSNP144.GRCh38"
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6. MISSING MEASUREMENTS BY INDIVIDUALS

The sort of measurements that people have done for snips (SNPS) for example in dbSNP are to note down the *possible values* at snip locations of the DNA. I have not seen measurements of all these jointly for a large sample N of individuals yet. That is what is interesting for human genetic individuality.

Here's an example of what can be obtained from public facilities on snip locations.

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##source=dbSNP
##track_name="Cited Variations, dbSNP b154 v2"
##sequence_region="NC_000014.9 1 107043718"
##INFO=<ID=RS,Number=1,Type=String,Description="dbSNP ID">
##INFO=<ID=Source,Number=1,Type=String,Description="Variation source">
#CHROM POS ID REF ALT QUAL FILTER INFO
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NC_000014.9 19941099 rs2792135 G A . . RS=rs2792135;Source=dbsnp
NC_000014.9 19944880 rs2635556 T C . . RS=rs2635556;Source=dbsnp
NC_000014.9 19958583 rs12891630 G A,T . . RS=rs12891630;Source=dbsnp
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NC_000014.9 20060162 rs1958716 A C,G,T . . RS=rs1958716;Source=dbsnp
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NC_000014.9    105706543   rs11621145 G A . . RS=rs11621145;Source=dbsnp
NC_000014.9    105721893   rs1134590 C T . . RS=rs1134590;Source=dbsnp
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NC_000014.9    105766769   rs34295723 G A . . RS=rs34295723;Source=dbsnp
NC_000014.9    105767411   rs12897751 G C . . RS=rs12897751;Source=dbsnp
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NC_000014.9    105769317   rs79545032 T C . . RS=rs79545032;Source=dbsnp
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NC_000014.9    105769806   rs74093865 G A,C . . RS=rs74093865;Source=dbsnp
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NC_000014.9    105782836   rs2725142 C A,G,T . . RS=rs2725142;Source=dbsnp
NC_000014.9    105786362   rs2753571 C A,G,T . . RS=rs2753571;Source=dbsnp
NC_000014.9    105855107   rs281865422 C T . . RS=rs281865422;Source=dbsnp
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NC_000014.9    106189185   rs1981496 A G,T . . RS=rs1981496;Source=dbsnp
NC_000014.9    106349484   rs61995642 C A,T . . RS=rs61995642;Source=dbsnp
NC_000014.9    106486643   rs34614900 T C . . RS=rs34614900;Source=dbsnp
NC_000014.9    106514189   rs9324088 G A . . RS=rs9324088;Source=dbsnp
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 NC_000014.9 106680856 rs1961901 G T . . RS=rs1961901;Source=dbsnp
 NC_000014.9 106684476 rs17113284 T C . . RS=rs17113284;Source=dbsnp
 NC_000014.9 106685105 rs1024350 C A,G,T . . RS=rs1024350;Source=dbsnp
 NC_000014.9 106686431 rs8005468 G A . . RS=rs8005468;Source=dbsnp
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 NC_000014.9 106771605 rs2007467 C T . . RS=rs2007467;Source=dbsnp
 NC_000014.9 106772332 rs2337406 C A,G,T . . RS=rs2337406;Source=dbsnp
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 NC_000014.9 106823737 rs17112078 A G . . RS=rs17112078;Source=dbsnp
 NC_000014.9 106825769 rs7140253 A G . . RS=rs7140253;Source=dbsnp
 NC_000014.9 106865837 rs885883 T C,G . . RS=rs885883;Source=dbsnp

This is a good start, but I would like to see some sort of chip measure all these snips and only these snip DNA for individuals for a large sample of individuals. I'd like to see this for a low price of \$0.2-\$0.5 for use across the world as soon as possible. I have many ideas of what we can do with the data.

REFERENCES

- [1] https://ftp.ncbi.nih.gov/snp/latest_release/JSON/JSON_README.txt