

# For Whom the Bell Tolls

Sergey Feranchuk

(self-employed; residence: Smolensk, Russia; e-mail: feranchuk@gmail.com)

January 16, 2021

*to my mother*

## Abstract

## 1 Introduction

Harmonic oscillator is a simplest mathematical model which can simulate periodic changes as a physical phenomenon. It is exactly solvable both in classical and in quantum physics. The simplest extension of harmonic oscillator model is to introduce a quadratic term to the linear equation of the model.

The changes in the surrounding nature are often distinguish from a harmonic periodicity. The marginal cases of unharmonicity are a chaotic noise and an abrupt crash. Attempts to manage these extreme cases by means of "traditional" science are knowingly wrong, although some empirical rules do observed in these processes.

Suitable for a minimally simple approach to systematically describe in some way the possible distortions of a periodicity is the model of harmonic oscillator with an introduced perturbation, like the unharmonic oscillator model mentioned above.

The problem in any crash is to be ready for it, and the prediction of crash is impossible. As in the cases of a phase transition, the mixing of large-scaled and local-scale factors occurs and is of importance in a transitional period. Anyway any clever decisions in a crisis time are always based on a rational reasoning even if this reasoning do not fit to a format of a "traditional" science which has been developed for another purposes.

As an attempt to rationally describe the risks which are accumulated in microbial communities at resent times, a wide and broad look is proposed here to a composition of some selected communities. The simple model of unharmonic oscillations can be of use to measure and clarify in some way an unharmonicity in the composition of the communities.

Recent advances in sequencing technologies lead to the "outbreak" in the microbiology. A wide classes and even kingdoms of poorly known living creatures become visible in the common and custom microbiological samples. The present research is focused on eukariotic part of the microbiomes for the purposes declared in it. Besides the kingdoms of animals, plants and fungi, it is presently extended to include much of another eukariotic species, mostly unicellular, hardly classified and poorly investigated. Some of them are supposed to be conservative

and neutral, some are highly adaptive and predator-oriented. The group of eukariotic divisions known as SAR ("*Strametopiles*", "*Alveolata*", "*Cercozoa*") was introduced to broadly join the species with the latter of the strategies. These divisions are considered separately and other unicellular divisions with mostly first of the strategies are joined together in the analysis provided below.

## 2 Methods

## 3 Results

## 4 Discussion

## Conclusions

## 5 References

1. Feranchuk, S., Belkova, N., et al., Evaluating the use of diversity indices to distinguish between microbial communities with different traits. Res. Microbiol., 2018
2. Feranchuk, I., Komarov, L., et al., Operator method in the problem of quantum unharmonic oscillator, Annals of Phys., 1995
3. Nottale, L., Scale relativity and fractal space-time: theory and applications, arxiv.org, 2008

Figure 1

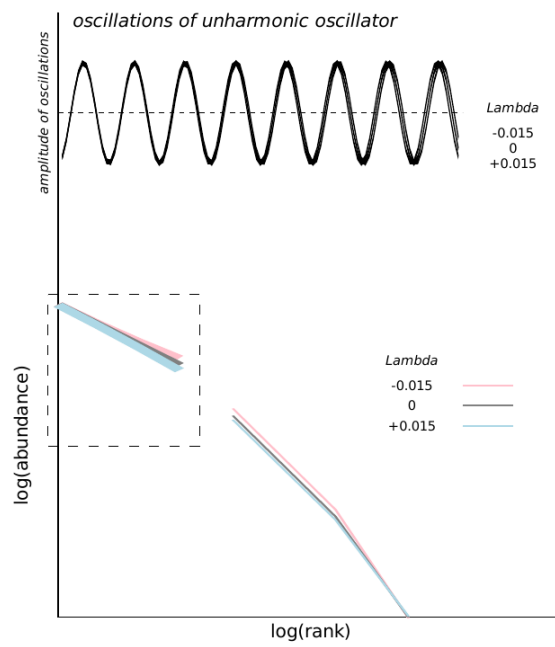
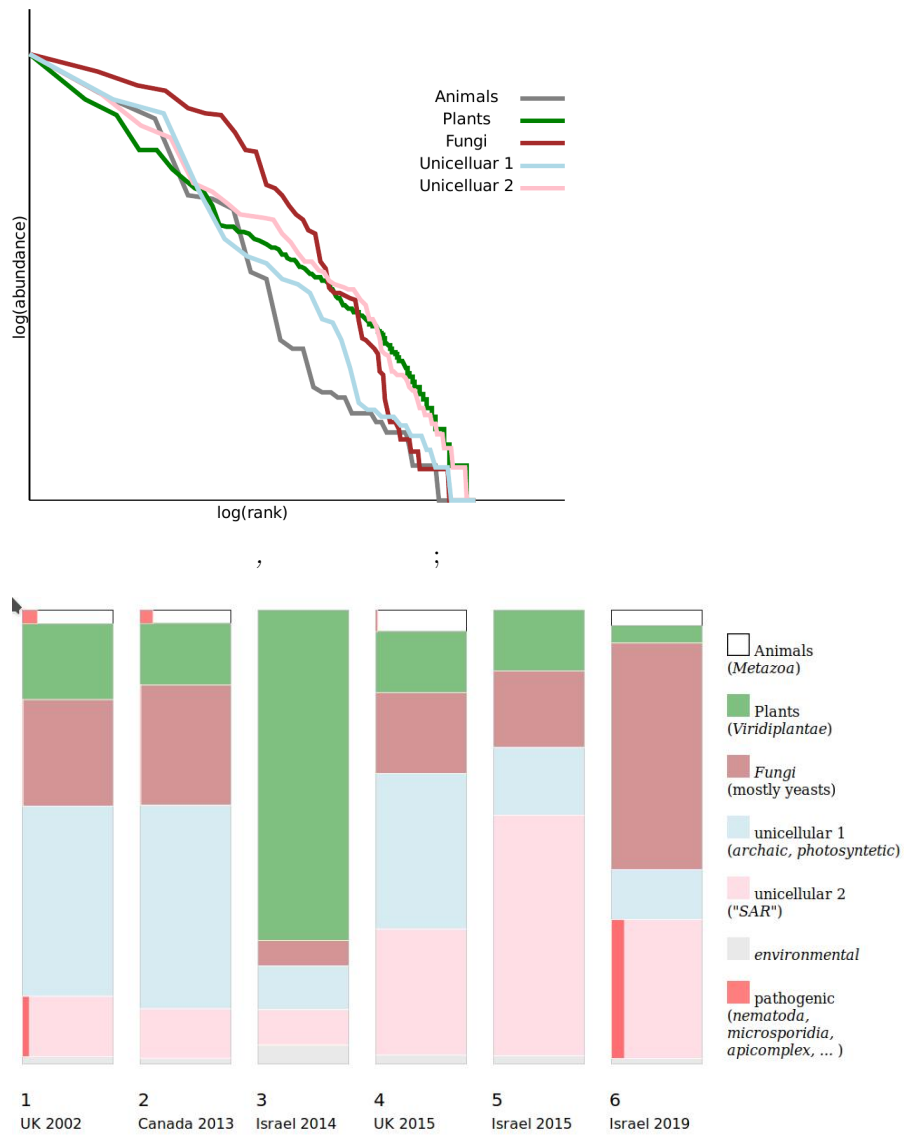


Figure 2



**Table 1**

	Sample ID	Bases	Reads	Location	Date	18S RRNAs
1	ERR981203	5.3G	10M	51.83N 0.21E	2002.06.23	1517(*)
2	SRR6030929	2.4G	6.1M	42.98N 81.24W	2013	125002(*)
3	ERR588716	8.2M	159K	Israel	2014 or earlier	848
4	ERR970400	4.2G	13M	51.61N 3.95E	2015.01.01	18747 (*)
5	SRR7642476	77M	128K	30.78N 34.76E	2015.08.20	4231
6	SRR12806764	48M	97K	31.86N 34.72E	2019.02.25	116666

**Table 2**

Animals	<i>Mollusca, Arthropoda</i>
Plants	<i>Chlorophyta, Streptophyta</i>
Fungi	95% - 100% <i>Saccharomycotina</i> (yeast)
Unicellular 1	<i>Euglenozoa, Rhodophyta, Haptophyta, Glaucophyta, Cryptophyta</i>
Unicellular 2	<i>Cercozoa, Strametopiles, Alveolata, Acanthamoeba</i>

**Table 3**

Taxonomy(*)	1	2	3	4	5	6
Acanthamoebidae Acanthamoeba	2	4		1		
Alveolata Apicomplexa	12			14		
Alveolata Ciliophora				2	9	1
Alveolata Haplosporida		4				5406
Cercozoa Cercomonadida		2				
Cercozoa Chlorarachniophyceae	4307	197	5	108	876	14637
Cryptophyta Cryptomonadaceae	91			9	389	382
Cryptophyta Teleaulax		2				
Diplomonadida Hexamitidae	19	5		2		
environmental samples	357	50	35	25	1206	1490
Euglenozoa Euglenida	407	84		46		1
Euglenozoa Kinetoplastida	2072	785	4	270	1206	5343
Fungi Ascomycota	3343	1044		347	11860	60992
Fungi Basidiomycota			48	3	4	
Fungi Chytridiomycota				1		
Fungi Microsporidia	1	12		3	2	12
Fungi Zygomycota	5	8			1	
Glaucocystophyceae Glaucocystales	77	56		12	2890	5020
Glaucocystophyceae Gloeochaetales	244	8	8	9	5042	1845
Granuloreticulosea Foraminifera	3					
Haptophyceae Isochrysidales	317	103	11	24	33	19
Haptophyceae unclassified Haptophyceae	17	2		1	32	24
Metazoa Acanthocephala						1
Metazoa Arthropoda	382	12		13	2424	627
Metazoa Chordata		2		5		
Metazoa Cnidaria						6
Metazoa Mollusca	475	91		22	8907	3641
Metazoa Myxozoa				8		2
Metazoa Nematoda		15				38
Metazoa Platyhelminthes	26					13
Metazoa Porifera					6	
Parabasalidea Trichomonadida	2			1		
Rhodophyta Bangiophyceae	2962	541	43	175	714	801
Rhodophyta Florideophyceae	232	227	16	88	148	110
stramenopiles Bacillariophyta	125	47	3	10	3091	312
stramenopiles Chrysophyceae	41	10	1	1	3	3
stramenopiles Olisthodiscus	379	29		17	28	78
stramenopiles Oomycetes		2				
stramenopiles Phaeophyceae	33	6			1	
stramenopiles Placididea	303	136	57	48	33139	17046
Viridiplantae Chlorophyta	1636	401	478	139	1563	2569
Viridiplantae Streptophyta	876	315	137	113	7886	4583

**Supplement A**

Unharmonic oscillator

### classical system:

```
awk '{ lambda=$1; x = 1; v = 0; dt = 0.01; s = ''; for ( i = 1; i < 5000; i++ ) { x = x + v * dt; v = v - x * ( 1 + lambda * x *
x ) * dt; if ( i % 50 == 0 ) { s = s ' ' ( i * dt ) ' ', ' x; }; }; print s }'
```

### C code:

```
void solve_cubic( double h, double g, double *e1 ) {
double d = atan2( sqrt( pow( h, 3 ) - g * g ), -g ) / 3.;
double c = sqrt( h ) * cos( c ); *e1 = 2 * c; }
int main( int argc, char **argv ) {
double lambda = atof( argv[1] ); double nmax = atoi( argv[2] ); double omega_n; int n;
for ( n = 0; n < nmax; n++ ) { solve_cubic( 1. / 3., -3. * lambda * ( 1. + 2. * n + 2. * n * n ) / ( 1. + 2. * n ), &omega_n );
printf( '%.2f ', ( 1. / 4. ) * ( 3. * omega_n + 1. / omega_n ) * ( n + 1. / 2 ) ); } }
```

### Reference database

```
cat ssu_jan03.tsv | bash -c 'while read line; do if [ "${line:0:4}" == "tax," ]; then if [ "${line:5:5}" == "Eukar" ]; then if
["$f" == "2" ]; then echo "$1" "${line:5}; i="echo $1 + 1 | bc`; f="1"; fi;fi; else if [ "$f" == "1" ]; then if [ "${line:5}"
!= "" ]; then echo "${line:5}; f="2"; fi; fi; fi; done; ' | awk '{ if ( $2 == "Eukaryota;" || ( p == "Eukaryota;" && length(
$0 ) > 100 ) ) { print $0 }; p = $2 }' | awk '{ if ( p != $2 ) { print $0 }; p = $2 }' >rrna_euk.fa
cat $sample | awk '{ print substr( $1, 1, length( $1 ) - 1 ) }' | bash -c 's="";c=0;while read line; do if [ "$line" != "$s"
]; then if [ "$s" != "" ]; then echo "'$s' : $c,"; fi; s=$line; c=1; else c="echo "$c+1" | bc`; fi; done;
sort $sample | bash -c 's="";c=0;while read line; do if [ "$line" != "$s" ]; then if [ "$s" != "" ]; then echo "'$s $c";
fi; s=$line; c=1; else c="echo "$c+1" | bc`; fi; done;' | awk '{ print $3 ' ' $(NF-1) ' ' ' $NF }' | sort - | bash -c 's="";b="";c=0;while
read line; do if [ "${line:0:5}" != "${s:0:5}" ]; then h="echo $s |awk '{print $1}'"; echo "'$h $b"; c=0; s=$line;
else n="echo $line | awk '{print $NF}'"; if [ $n -gt $c ]; then c=$n; b="echo $line | awk '{print $(NF-1) }';
fi; fi; done; h="echo $s |awk '{print $1}'"; echo "'$h $b"'
```

### Annotation of samples

```
head -n 4000000 $sample.fastq >t0.fastq
sortmerna --ref ssu.fa,ssu.idx --reads t0.fastq --aligned t1 --sam
cat t1.sam | awk ' print ">" $1 '
n' $10 ' > t2.fa
blastn -db ssu.db -query t2.fa -evalue 1e-2 -task blastn -max_target_seqs 1 -out t3.tsv -outfmt '6 sallseqid' out=test-$sample
mv $out.tsv t3.tsv
cat t3.tsv | while read line; do t="grep '>$line ' ssu.fa'; echo $t:1 >>$out.txt; done;
cat $out.txt | awk ' gsub(/[0-9]/, ''); gsub( ' ', ' ', ' '); print ' | sort >$out.csv
cat $out.csv | awk -F ' ', ' ' print $2 ' ' ' $3 ' | bash -c 's="";c=0;while read line; do if [ "$line" != "$s" ]; then if [ "$c"
!= "0" ]; then echo "'$s' : $c,"; fi; s=$line; c=1; else c="echo "$c+1" | bc`; fi; done; echo "'$s' : $c";';
```

### Rank-abundance charts

e.g, SAR:

```
grep -E 'Cerczoalstrametopiles|Alveolata|Acanthamoeba' test*.txt | sort | awk '{ print $1 }' | bash -c 's="";c=0;while read line;
do if [ "$line" != "$s" ]; then if [ "$s" != "" ]; then echo $c; fi; s=$line; c=1; else c="echo "$c+1" | bc`; fi; done; echo
$c' | sort -g | awk '{ s = $0 ' ' ' s } END { print s }' | awk '{ s = ''; for ( i=1; i <= NF; i++ ) { s = s ' ' log(i)/log(NF)
', ' log($i)/log($1) }; print s }'
```

### Rna-seq

#### rank-abundance

```
for ft in FAL MAL FCR MCR; do for cn in 28 29 30; do cat RNAseq_WT$ft.csv
| awk -F ' ', ' ' -v cn=$cn -v i=0 '{ if ( $cn > 0 && i > 0 ) print $cn; i = i + 1 }' |
sort -g -r | awk -v sname=" '$ft$cn' " 'BEGIN { print sname ":["; s = " "; i = 0
```



```

} { i = i + 1; if ( ( i % 20 ) == 0 ) { print s ", "; s = $1 } else { if ( i > 1 ) { s =
s ", " $1; } else { s = $1 } }; } END { print s "], " }' »rnaseq_distributions.txt;
done; done;
fractal dimension:
awkcmd='{ n1 = abs( $1 - $2 ) + abs( $2 - $3 ) + abs ( $3 - $4 ) + abs( $4
- $5 ) + abs( $5 - $6 ); n2 = 0.5 * ( abs( $1 - $3 ) + abs( $2 - $4 ) + abs( $3 -
$5 ) + abs( $4 - $6 ) ); n3 = 0.3333 * ( abs( $1 - $4 ) + abs( $2 - $5 ) + abs(
$3 - $6 ) ); l2 = log(2 ); l3 = log( 3 ); if ( n1 > 0 && n2 > 0 && n3 > 0 ) { y
= log( n1 ) + log( n2 ) + log( n3 ); b = ( 3 * ( log( n3 ) * l3 + log( n2 ) * l2 )
- y * 1.79 ) / 1.84; a = ( y - b * 1.79 ) / 3; d1 = log( n1 ) - a; d2 = log( n2 ) -
a - b * l2; d3 = log( n3 ) - a - b * l3; sumd = d1 * d1 + d2 * d2 + d3 * d3; if (
sumd < 0.01 ) { print abs(b) } } } function abs( v ) { if ( v > 0 ) { return v; }
else { return -v; } }'
fdim='awk "$awkcmd" | sort -g | head -n $median | tail -n 1'

```