Research Paper IV

Maxwell–Scretching, Scretching Quantum Chain, and Scretching Equations of Quantum Molecular Biology Analysis of Representative Microorganisms with Biological Classification

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Abstract

This paper extends the prior Scretching gene, mRNA, and viral analyses to a representative set of microorganisms across **Bacteria, Archaea, Fungi, Protists/Apicomplexa, and unicellular algae**. The selected organisms are *Escherichia coli* K-12 MG1655, *Staphylococcus aureus* N315, *Bacillus subtilis* 168, *Mycobacterium tuberculosis* H37Rv, *Pseudomonas aeruginosa* PAO1, *Halobacterium salinarum* NRC-1, *Saccharomyces cerevisiae* S288C, *Candida albicans* SC5314, *Plasmodium falciparum* 3D7, and *Chlamydomonas reinhardtii* CC-503.

The analysis applies the Maxwell–Scretching Chain, the Scretching Quantum Chain, and the Scretching Equations of Quantum Molecular Biology to genome-level GC content, deriving thermal, density, refractive-index, UV-absorbance, oscillator-strength, and fine-structure-scaled coefficients. The input page establishes the general basis that %GC correlates with melting temperature, buoyant density, and other DNA/RNA physicochemical properties. The present paper expands that principle across microbial classification categories.

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1. Biological Classification of Selected Microorganisms

The dataset includes microorganisms from several major biological groups. NCBI verifies *E. coli* as Taxonomy ID 562 and *P. falciparum* as Taxonomy ID 5833. NCBI also lists *Saccharomyces cerevisiae* as brewer's yeast in Saccharomycetaceae and provides reference genome data for *S. cerevisiae* S288C. NCBI identifies *Mycobacterium tuberculosis* as a high-GC Gram-positive bacterium in the family Mycobacteriaceae. NCBI identifies *Halobacterium salinarum* as an archaeal species in Halobacteriaceae.

Microorganism	Domain/group	Classification summary	Biological or medical role
Escherichia coli K-12 MG1655	Bacteria	Pseudomonadota; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae	Model gut bacterium; some strains are pathogenic
Staphylococcus aureus N315	Bacteria	Bacillota; Bacilli; Bacillales; Staphylococcaceae	Gram-positive pathogen; MRSA/VSSA clinical strain
Bacillus subtilis 168	Bacteria	Bacillota; Bacilli; Bacillales; Bacillaceae	Soil bacterium; spore-forming model organism
Mycobacterium tuberculosis H37Rv	Bacteria	Actinomycetota; Actinomycetia; Mycobacteriales; Mycobacteriaceae	Tuberculosis pathogen
Pseudomonas aeruginosa PAO1	Bacteria	Pseudomonadota; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae	Opportunistic pathogen
Halobacterium salinarum NRC-1	Archaea	Halobacteriota/Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae	Halophilic archaeon; extremophile
Saccharomyces cerevisiae S288C	Eukarya / Fungi	Ascomycota; Saccharomycetes; Saccharomycetaceae	Brewer's yeast; model eukaryote
Candida albicans SC5314	Eukarya / Fungi	Ascomycota; Saccharomycetes; Debaryomycetaceae	Opportunistic fungal pathogen
Plasmodium falciparum 3D7	Eukarya / Apicomplexa	Alveolata; Apicomplexa; Aconoidasida; Plasmodiidae	Malaria parasite
Chlamydomonas reinhardtii CC-503	Eukarya / Green alga	Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadaceae	Photosynthesis and cilia model organism

2. Genome Size and GC-Content Basis

NCBI reports *E. coli* K-12 MG1655 reference genome size near 4.6 Mb. *Staphylococcus aureus* N315 is reported as 2,814,816 bp, and another genome analysis reports 2.81 Mb with 32.8% G+C content. *Mycobacterium tuberculosis* H37Rv is reported as 4,411,532 bp. *Pseudomonas aeruginosa* PAO1 is reported as 6,264,404 bp, and published analyses place the *P. aeruginosa* genome at approximately 65–67% GC. *Halobacterium salinarum* type-strain chromosome data include 2,178,608 bp with 67.1% G+C content, and NCBI gives the NRC-1 assembly near 2.6 Mb. *Candida albicans* SC5314 is reported by NCBI to be approximately 14.3 Mb, and a genome

sequencing study reports an average GC content of 33.5%. *Chlamydomonas reinhardtii* has an approximately 111 Mb GC-rich genome with ~64% genome-wide GC content.

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3. Scretching Framework Equations

Let:

$$G_m = \%GC_{\text{microorganism}}$$

3.1 Microbial Thermal Equation

$$T_{m,m} = 69.3 + 0.41G_m$$

3.2 Microbial Buoyant-Density Equation

$$\rho_m = 1.660 + 0.00098G_m$$

3.3 JDCS Density–Temperature Bridge

$$\frac{d\rho_m}{dT_{m,m}} = \frac{0.00098}{0.41} = 0.002390243902$$
$$3\frac{d\rho_m}{dT_{m,m}} = 0.007170731707$$

3.4 Scretching Reduced Fine-Structure Coefficient

$$\beta_s = \frac{10.8601}{127.114} = 0.0854359079252$$
$$\alpha_s = \beta_s^2 = 0.0072992943630$$

3.5 Microorganism Scretching Coefficient

$$\Theta_m = \alpha_s\left(\frac{G_m}{100}\right)$$

This Θ_m is the proposed microorganism-level fine-structure-scaled coefficient.

3.6 Maxwell–Scretching UV Absorbance Approximation

$$\bar{\varepsilon}_{260,m} = 12080 - 25.9G_m$$
$$f_{\text{MS},m} = 4.32 \times 10^{-9}\bar{\varepsilon}_{260,m}(5000)$$
$$f_{\text{MS},m} = 0.260928 - 0.00055944G_m$$

3.7 JDCS Absorbance-Ratio Branch

$$R_{\mathrm{JDCS},m} = \frac{1.825 - \rho_m}{\beta_s}$$

3.8 Refractive-Index Branch

$$\eta_{D,m} = \frac{\rho_m + 13.4947}{10.8601}$$

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4. Verified Computational Table

Organism	Genome size Mb	%GC	T_m°C	ρ	Θ_m	ε_{260}	f_{MS}	R_{JDCS}	η_D
Escherichia coli K-12 MG1655	4.600	50.8	90.128	1.709784	0.003708	10764.28	0.232508	1.348566	1.400032
Staphylococcus aureus N315	2.810	32.8	82.748	1.692144	0.002394	11230.48	0.242578	1.555037	1.398407
Bacillus subtilis 168	4.210	43.5	87.135	1.702630	0.003175	10953.35	0.236592	1.432302	1.399373
Mycobacterium tuberculosis H37Rv	4.410	65.6	96.196	1.724288	0.004788	10381.04	0.224229	1.178802	1.401367
Pseudomonas aeruginosa PAO1	6.264	66.6	96.606	1.725268	0.004861	10355.06	0.223669	1.167331	1.401457
Halobacterium salinarum NRC-1	2.600	67.1	96.811	1.725758	0.004898	10342.11	0.223390	1.161596	1.401503
Saccharomyces cerevisiae S288C	12.100	38.3	85.003	1.697534	0.002796	11088.03	0.239501	1.491949	1.398904
Candida albicans SC5314	14.300	33.5	83.035	1.692830	0.002445	11212.35	0.242187	1.547008	1.398471
Plasmodium falciparum 3D7	23.300	19.4	77.254	1.679012	0.001416	11577.54	0.250075	1.708743	1.397198
Chlamydomonas reinhardtii CC-503	111.100	64.0	95.540	1.722720	0.004672	10422.40	0.225124	1.197155	1.401223

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5. Correlation and Regression Analysis

Because the Scretching observables are derived from $G_m = \%GC$, the theoretical regression structure is exact.

Regression pair	Derived equation	Direction
T_m vs. G_m	$T_m = 69.3 + 0.41G_m$	Positive
ρ vs. G_m	$\rho = 1.660 + 0.00098G_m$	Positive
Θ_m vs. G_m	$\Theta_m = 0.00007299294363G_m$	Positive
ε_{260} vs. G_m	$\varepsilon_{260} = 12080 - 25.9G_m$	Negative
f_{MS} vs. G_m	$f_{\mathrm{MS}} = 0.260928 - 0.00055944G_m$	Negative
R_{JDCS} vs. G_m	$R_{\mathrm{JDCS}} = (0.165 - 0.00098G_m)/\beta_s$	Negative
η_D vs. G_m	$\eta_D = (15.1547 + 0.00098G_m)/10.8601$	Positive

Thus:

$$G_m \uparrow \Rightarrow T_m \uparrow \Rightarrow \rho \uparrow \Rightarrow \eta_D \uparrow \Rightarrow \Theta_m \uparrow$$

but:

$$G_m \uparrow \Rightarrow \varepsilon_{260} \downarrow \Rightarrow f_{\mathrm{MS}} \downarrow \Rightarrow R_{\mathrm{JDCS}} \downarrow$$

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6. Ranking by Proposed Microorganism Scretching Coefficient

Rank	Microorganism	%GC	Θ_m
1	*Halobacterium salinarum* NRC-1	67.1	0.004898
2	*Pseudomonas aeruginosa* PAO1	66.6	0.004861
3	*Mycobacterium tuberculosis* H37Rv	65.6	0.004788
4	*Chlamydomonas reinhardtii* CC-503	64.0	0.004672
5	*Escherichia coli* K-12 MG1655	50.8	0.003708
6	*Bacillus subtilis* 168	43.5	0.003175
7	*Saccharomyces cerevisiae* S288C	38.3	0.002796
8	*Candida albicans* SC5314	33.5	0.002445
9	*Staphylococcus aureus* N315	32.8	0.002394
10	*Plasmodium falciparum* 3D7	19.4	0.001416

The ranking reflects genome GC content under the Scretching coefficient definition. It is not a direct clinical severity ranking. For example, *P. falciparum* has the lowest. Θ_m in this dataset because of its AT-rich genome, but it remains a major human pathogen.

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7. New Derived Microorganism Equations

Equation 1: Microorganism Fine-Structure Coefficient

$$\boxed{\Theta_m = 0.0072992943630\left(\frac{G_m}{100}\right)}$$

Equation 2: Microbial Thermal–Scretching Bridge

$$G_m = \frac{T_m - 69.3}{0.41}$$
$$\boxed{\Theta_m = 0.000178031570(T_m - 69.3)}$$

Equation 3: Microbial Density–Scretching Bridge

$$G_m = \frac{\rho - 1.660}{0.00098}$$
$$\boxed{\Theta_m = 0.07448259554(\rho - 1.660)}$$

Equation 4: Microbial Oscillator–Scretching Bridge

$$G_m = \frac{0.260928 - f_{\mathrm{MS}}}{0.00055944}$$
$$\boxed{\Theta_m = 0.130476880(0.260928 - f_{\mathrm{MS}})}$$

Equation 5: Classification-Weighted Microorganism Scretching Index

A classification-weighted coefficient may be written:

$$\boxed{\Omega_m = \Theta_m \Lambda_D \Lambda_C \Lambda_P \Lambda_E}$$

where:

Λ_D = domain factor
Λ_C = cellular organization factor
Λ_P = pathogenicity or biological role factor
Λ_E = ecological niche factor

This separates pure genome-composition physics from biological classification and phenotype.

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8. Interpretation by Classification Group

8.1 Bacteria

The bacterial organisms cover a wide GC range. *S. aureus* N315 is low-GC at approximately 32.8%, whereas *M. tuberculosis* H37Rv and *P. aeruginosa* PAO1 are high-GC bacterial genomes. This produces a large spread in T_m, ρ, and Θ_m. The high-GC bacterial group gives the strongest bacterial Scretching coefficients in this dataset.

8.2 Archaea

Halobacterium salinarum NRC-1 gives the highest $\Theta_m$in the present table because of its high GC content. This is consistent with its extremophile biology and genome composition, but the Scretching coefficient itself is a physicochemical descriptor, not a full explanation of halophily.

8.3 Fungi

The two fungal organisms differ biologically and medically: *S. cerevisiae* is a model yeast, while *C. albicans* is an opportunistic pathogen. Their GC contents are moderate-to-low relative to high-GC bacteria and archaea, giving lower. $\Theta_m$values.

8.4 Protist / Apicomplexan Parasite

P. falciparum has the lowest GC content and the lowest $\Theta_m$in the table. Its AT-rich genome strongly lowers the calculated. T_m, ρ, and fine-structure-scaled coefficient. BioNumbers lists *P. falciparum* GC content at 19.4%, referencing the *Nature* genome sequence report.

8.5 Unicellular Green Alga

Chlamydomonas reinhardtii is a unicellular green alga with an unusually GC-rich genome near 64%, giving one of the highest. $\Theta_m$values among eukaryotic microorganisms in this dataset.

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9. Conclusion

This paper extends the Maxwell–Scretching Chain, Scretching Quantum Chain, and Scretching Equations of Quantum Molecular Biology to a taxonomically diverse microorganism dataset. The analysis shows that microbial classification can be paired with genome GC content to form a structured Scretching table of T_m, ρ, ε_{260}, f_{MS}, R_{JDCS}, η_D, and Θ_m.

The primary result is:

$$\boxed{\Theta_m = \alpha_s \left(\frac{\%GC_m}{100}\right)}$$

where:

$$\alpha_s = 0.0072992943630$$

The highest coefficient in this dataset is assigned to *Halobacterium salinarum* NRC-1, followed by *Pseudomonas aeruginosa* PAO1 and *Mycobacterium tuberculosis* H37Rv. The lowest coefficient is assigned to *Plasmodium falciparum* 3D7 because of its AT-rich genome. The model provides a proposed physicochemical classification index and can be expanded to exact FASTA-derived genome calculations, species-level comparisons, strain-level pathogenicity analysis, antimicrobial target ranking, and optical/spectroscopic microbial identification.

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