Bioinformatyka 2

Wydział Biochemii, Biofizyki i Biotechnologii
Adrian Kania

OXFORD

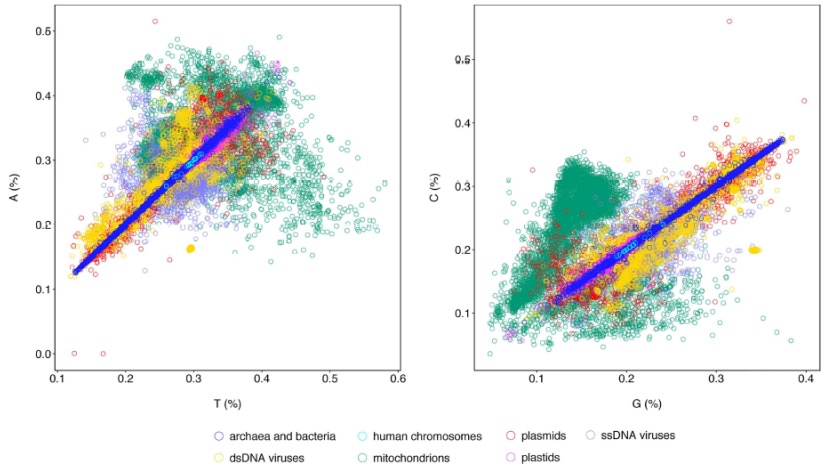# DNA sequence symmetries from randomness: the origin of the Chargaff's second parity rule

Piero Fariselli, Cristian Taccioli, Luca Pagani and Amos Maritan

Corresponding author: Piero Fariselli, Dipartimento di Scienze Biomediche, Università di Torino, Via Santena 19, Torino 10126, Italy. Tel.: +39 011 6705871;
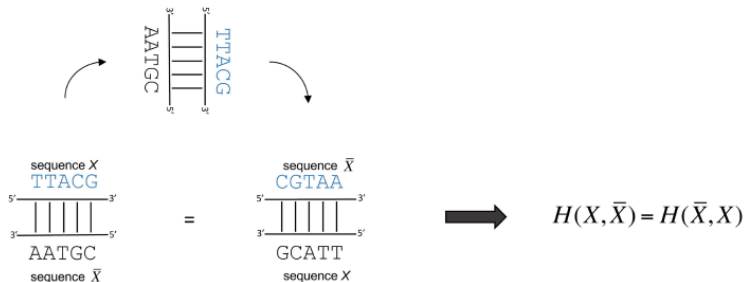E-mail: piero.fariselli@unito.it
Authors Piero Fariselli and Cristian Taccioli contributed equally to this work.
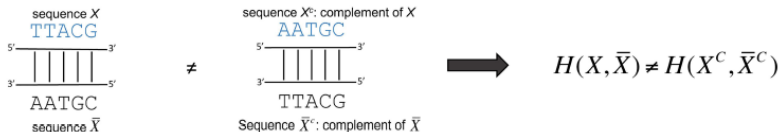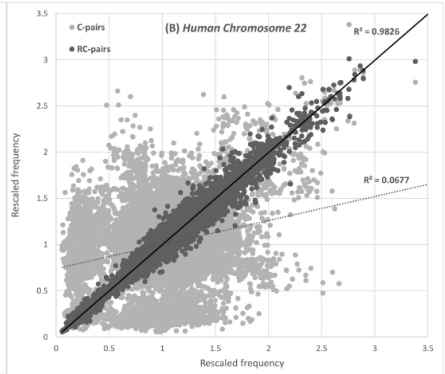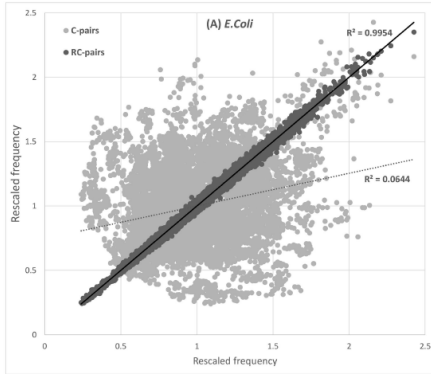
Drugie prawo Chargaffa

Drugie prawo Chargaffa

a

sequence X
TTACG
5'—————3'
|||||
3'—————5'
AATGC
sequence $\bar{X}$

$=$

sequence $\bar{X}$
CGTAA
5'—————3'
|||||
3'—————5'
GCATT
sequence X

$\longrightarrow$ $H(X, \bar{X}) = H(\bar{X}, X)$

b

sequence X
TTACG
5'—————3'
|||||
3'—————5'
AATGC
sequence $\bar{X}$

$\neq$

sequence X^c: complement of X
AATGC
5'—————3'
|||||
3'—————5'
TTACG
Sequence $\bar{X}^c$: complement of $\bar{X}$

$\longrightarrow$ $H(X, \bar{X}) \neq H(X^C, \bar{X}^C)$

Drugie prawo Chargaffa

ELSEVIER

Harnessing the information theory and chaos game representation for pattern searching among essential and non-essential genes in Bacteria

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ARTICLE INFO

ABSTRACT

Proteins encoded by genes are engaged in most of the processes within a cell. Typing a minimal set of genes required for survival is still a challenging task. Essential genes seem to be more conservative and are usually responsible for basic functions, for instance, genetic information flow or energy production. Despite persistent advances in experimental methods, computer predictions may constitute an important part of this investigation. Firstly, they may embrace a huge amount of data and provide some characteristic patterns. Furthermore, they enable scientists to build models for predicting essential genes which are not yet verified experimentally. Some papers indicate interesting dependencies within essential genes sequences using different computer models. In this paper, an author took a three-step analysis for a deeper understanding of the fundamentals of essential and non-essential genes. Beginning from a simple nucleotide composition and finishing at long-range correlations, presents some characteristic patterns that are expected to be developed in future studies.
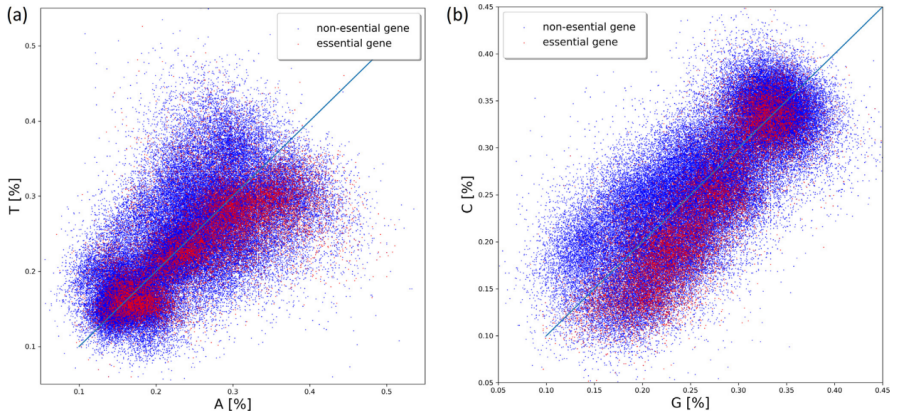
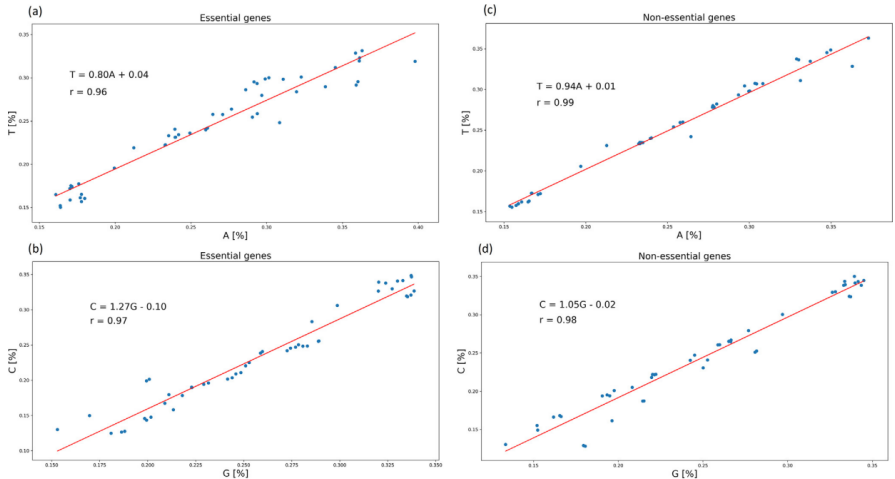**Fig. 3.** AT (a) and GC (b) dependence in essential and non-essential genes for all sequences.

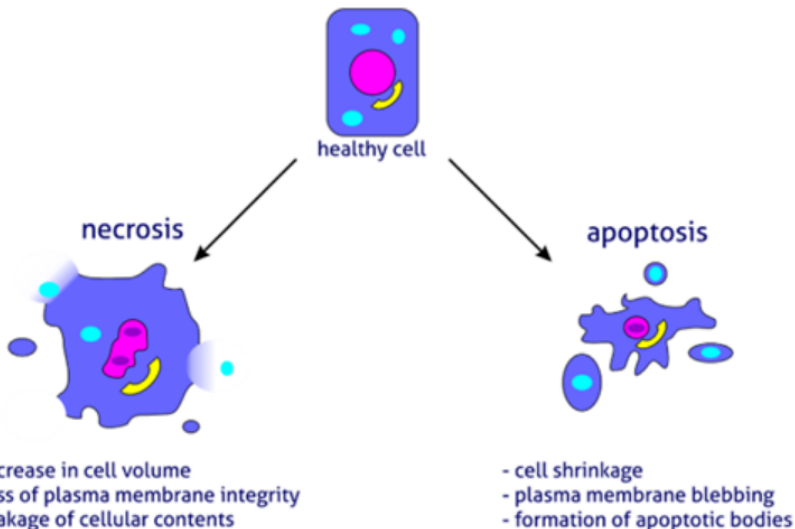**Fig. 4.** AT and GC dependence in essential (a-b) and non-essential (c-d) genes for all bacteria.

Apoptoza i nekroza

Novel Bioinformatics-Based Approach for Proteomic Biomarkers Prediction of Calpain-2 & Caspase-3 Protease Fragmentation: Application to βII-Spectrin Protein
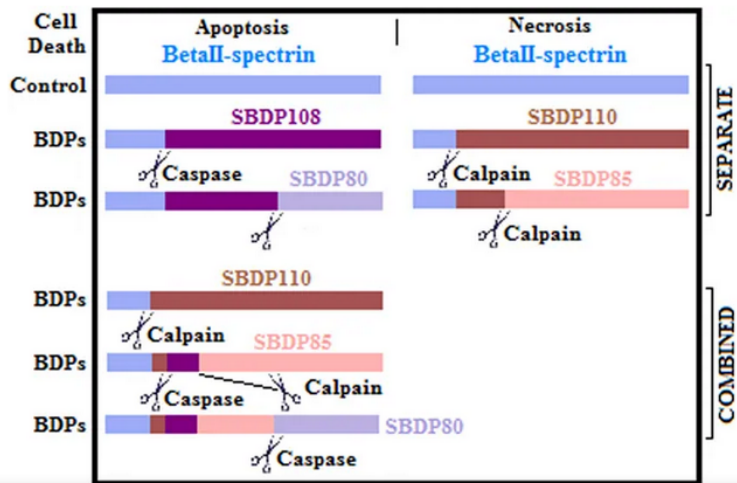
Atlal El-Assaad, Zaher Dawy ✉, Georges Nemer & Firas Kobeissy ✉

Apoptoza i nekroza

Figure 1: Schematic of necrosis and apoptosis cell death pathways.

Apoptoza i nekroza

	Calpain	Caspase
Protease Class	Cysteine Protease	Cysteine Protease
Preferred Cleavage Site (*)	AspxxAsp*x	(Leu, Val, Ile)x*x
Common Substrates	αII-spectrin 280 kDa	αII-spectrin 280 kDa
	βII-spectrin 260 kDa	βII-spectrin 260 kDa
Fragments Produced by	SBDP110 kDa	SBDP108 kDa
βII-spectrin	SBDP85 kDa	SBDP80 kDa
Cell Death Involvement	Most forms of necrosis	Most forms of apoptosis
	Some forms of apoptosis	

The table shows the different properties specific to calpain and caspase. Most importantly, it shows the consensus patterns at which each of the proteases cleaves. For caspase protease, the consensus pattern is DXXD and the cleavage site is right after this pattern (D is Aspartic Acid and X is any amino acid). Calpain, on the other hand, cleaves after the consensus patterns LX, VX, or IX, where L is Leucine, V is Valine, and I is Isoleucine.