

„NoStat” technologia naukowa dla statystyków

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22.10.2019

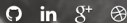
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Sebastian Zając

Physicist

Data Analyst

Programmer



<https://sebastianzajac.pl>

na początku było ... "Ekono co ? "

- 2002-2005 Licencjat - Modelowanie szeregów czasowych za pomocą procesów ARMA i ARIMA.
- 2005-2007 Mgr - Topologiczne i geometryczne metody w klasycznej i kwantowej teorii pola.

"NoStat"

chaos → statystyka → chaos deterministyczny

chaos liczbowy → teoria mnogości → teoria kategorii

chaos → statystyka → mechanika kwantowa → QFT

$$P_{\psi}(\phi) = |\langle \phi | \psi \rangle|^2.$$

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*basic solid state physics*

Volume 246, Issue 5
May 2009
Pages 1033-1037

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Original Paper

The method of the likelihood and the Fisher information in the construction of physical models

E.W. Piotrowski, J. Sładkowski, J. Syska , S. Zając

First published: 20 April 2009 | <https://doi.org/10.1002/pssb.200881566> | Cited by: 6

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Abstract

The subjects of the paper are the likelihood method (LM) and the expected Fisher information (FI) considered from the point of view of the construction of the physical models which originate in the statistical description of phenomena. The master equation

"The method of the likelihood and the Fisher information in the construction of physical models."

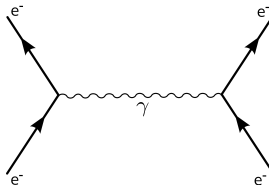
E. W. Piotrowski, J. Sładkowski, J. Syska, S.Z. Physica Status Solidi B vol. 246 no. 5 (5.2009).

Rozprawa doktorska

"Oscylacje akceleratorowych neutrin z uwzględnieniem ich niestandardowych oddziaływań" Prof. dr hab. Marek Zrałek.

„We can't solve problems by using the same kind of thinking we used when we created them.” (Albert Einstein)

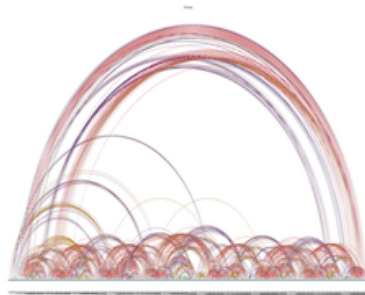
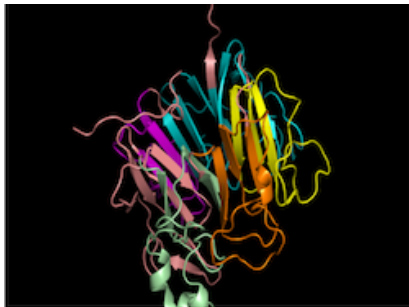
mass → charge → spin →	<div>~2.3 MeV/c² 2/3 1/2 u up</div>	<div>~1.275 GeV/c² 2/3 1/2 c charm</div>	<div>~173.07 GeV/c² 2/3 1/2 t top</div>	<div>0 0 1 g gluon</div>	<div>~126 GeV/c² H Higgs boson</div>
QUARKS	<div>~4.8 MeV/c² -1/3 1/2 d down</div>	<div>~95 MeV/c² -1/3 1/2 s strange</div>	<div>~4.18 GeV/c² -1/3 1/2 b bottom</div>	<div>0 0 1 γ photon</div>	
	<div>0.511 MeV/c² -1 1/2 e electron</div>	<div>105.7 MeV/c² -1 1/2 μ muon</div>	<div>1.777 GeV/c² -1 1/2 τ tau</div>	<div>91.2 GeV/c² 0 1 Z Z boson</div>	
LEPTONS	<div><2.2 eV/c² 0 1/2 ν_e electron neutrino</div>	<div><0.17 MeV/c² 0 1/2 ν_μ muon neutrino</div>	<div><15.5 MeV/c² 0 1/2 ν_τ tau neutrino</div>	<div>80.4 GeV/c² ±1 1 W W boson</div>	GAUGE BOSONS



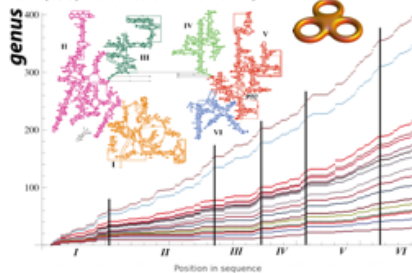
- Jak na podstawie modeli niestatystycznych wybrać, który model realizuje dane i które rozszerzenie jest istotne ?
- 7 publikacji dotyczących fizyki neutrin - oddziaływania i zastosowanie dyskretnych grup symetrii do mas i mieszania leptonów.
- udział w 2 grantach, prezentacje na 5 międzynarodowych konferencjach neutrinowych.



Poza Fizyką ale z fizykami na UW



1S72 (LSU, *Haloarcula Marismortui*)



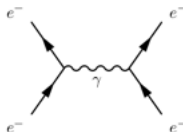
Gdzie znajdziesz diagramy chordowe ?

Physics



“Physics is like sex: sure, it may give some practical results, but that's not why we do it.”

— Richard Feynman



„Category Theory is like sex: it may give some practical results, but that's not why we do it. „ - Sebastian Zając

Server danych

<http://genus.fuw.pl>



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Article | [Open Access](#) | Published: 03 December 2018

Genus trace reveals the topological complexity and domain structure of biomolecules

Sebastian Zajac, Cody Geary, Ebbe Sloth Andersen, Paweł Dabrowski-Tumanski, Joanna I. Sulikowska & Piotr Sułkowski

Scientific Reports **8**, Article number: 17537 (2018) | [Download Citation](#)1014 Accesses | [7 Altmetric](#) | [Metrics](#) 30

Abstract

The structure of bonds in biomolecules, such as base pairs in RNA chains or native interactions in proteins, can be presented in the form of a chord diagram. A given biomolecule is then characterized by the genus of an auxiliary two-dimensional surface associated to such a diagram. In this work we introduce the notion of the genus trace, which describes dependence of genus on the choice of a subchain of a given backbone chain. We find that the genus trace encodes interesting physical and biological

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Genus for biomolecules

Paweł Rubach, Sebastian Zajac, Borys Jastrzebski, Joanna I Sulkowska,
Piotr Sułkowski 

Nucleic Acids Research, gkz845, <https://doi.org/10.1093/nar/gkz845>

Published: 04 October 2019 **Article history ▾**



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Abstract

The 'Genus for biomolecules' database (<http://genus.fuw.edu.pl>) collects information about topological structure and complexity of proteins and RNA chains, which is captured by the genus of a given chain and its subchains. For each biomolecule, this information is shown in the form of a genus trace plot, as well as a genus matrix diagram. We assemble such information for all and RNA structures deposited in the Protein Data Bank (PDB). This database presents also various statistics and extensive information about the biological

The category of chord diagrams

We fix three positive integers k , ℓ , and m and a multifunction

$$\varphi: \ell \times \ell \rightarrow m$$

The objects of $\mathfrak{C}_{k,\varphi}$ are structures of the form

$$\mathbb{S} = \langle S, <^S, \{B_i^S\}_{i < k}, \{N_i^S\}_{i < \ell}, \{E_i\}_{i < m} \rangle,$$

where:

- (D1) $\langle S, <^S \rangle$ is a finite linearly ordered set.
- (D2) $\{B_i^S\}_{i < k}$ and $\{N_i^S\}_{i < \ell}$ are partitions of S .
- (D3) $B_{i_0} < B_{i_1}$ whenever $i_0 < i_1 < k$.
- (D4) $\langle S, E_i \rangle$ is a graph for every $i < m$.
- (D5) $E_{i_0} \cap E_{i_1} = \emptyset$ whenever $i_0 \neq i_1$.
- (D6) If $x \in N_{i_0}$, $y \in N_{i_1}$ and $\langle x, y \rangle \in E_j$, then $j \in \varphi(i_0, i_1)$.

The sets B_i are called *backbones*, while the sets N_i are *types of nodes* and E_i are *types of edges*.

A $\mathfrak{C}_{k,\varphi}$ -morphism from \mathbb{S} to $\mathbb{T} = \langle T, <^T, \{B_i^T\}_{i < k}, \{N_i^T\}_{i < \ell}, \{E_i\}_{i < m} \rangle$ is a mapping $f: S \rightarrow T$ that preserves the linear orderings (that is, $x <^S y \implies f(x) <^T f(y)$) and satisfies for every $x, y \in S$:

$$(M1) \quad f(x) \in B_i^T \iff x \in B_i^S$$

$$(M2) \quad f(x) \in N_i^T \iff x \in N_i^S$$

$$(M3) \quad \langle f(x), f(y) \rangle \in E_i^T \iff \langle x, y \rangle \in E_i^S.$$

Informally, a $\mathfrak{C}_{k,\varphi}$ -arrow is a mapping that preserves the structure of \mathbb{S} , “adding” new vertices and new edges of various types.

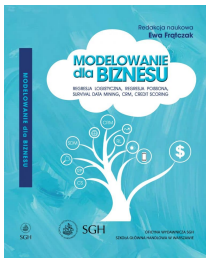
In the language of model theory, $\mathfrak{C}_{k,\varphi}$ -arrows are called *embeddings*.

It is clear that $\mathfrak{C}_{k,\varphi}$ forms a category.

- Nowy przedmiot dla studentów SGH - Analizy danych w czasie rzeczywistym.
- Twórca portalu do analiz plików JPK
- Współtwórca darmowej i płatnej wersji biblioteki w pythonie do automatycznego generowania modeli scoringowych - Advanced Scorecard Builder.
- Programowanie i przetwarzanie danych oraz statystyka w SAS.
- Badania statutowe - Metody doboru zmiennych z wykorzystaniem narzędziami machine i deep learning.

- 28.XI.2019 Konferencja - Analityka dla Biznesu
- 4.XII.2019 roku w Sali 2b w budynku C , odbędzie się promocja książki **Modelowanie dla biznesu**.

<https://businessintelligence.pl/pl/wizualizacja-wynikow-modelowania-z-qlik-sense/>





Wyjaśnienie

"NoSTAT" czytamy i tłumaczymy jako **Not Only Stat** !

Dziękuję za uwagę !