

學術論文抄錄—2005年發表

Energy-dependent point interactions in one dimension

F. A. B. Coutinho, Y. Nogami, L. Tomio and F. M. Toyama*

Journal of Physics A: Math. Gen., **38**, 4989-4998 (2005).

We consider a new type of point interaction in one-dimensional quantum mechanics. It is characterized by a boundary condition at the origin that involves the second and/or higher order derivatives of the wavefunction. The interaction is effectively energy dependent. It leads to a unitary S -matrix for the transmission-reflection problem. The energy dependence of the interaction can be chosen such that any given unitary S -matrix (or the transmission and reflection coefficients) can be reproduced at all energies. Generalization of the results to coupled-channel cases is discussed.

A time-dependent model for teleportation of a quantum state
of position and momentum

F. M. Toyama* and K. Saito

Canadian Journal of Physics **83**, 687-698 (2005).

We present a time-dependent model for teleportation of an unknown quantum state of position and momentum. With this model, we analyze a situation in which Bob (receiver) is ignorant of the Hamiltonian that describes the time-evolution of a post-measurement state generated at Bob's site. We illustrate that the time-evolution of the post-measurement state deteriorates the fidelity of the quantum teleportation. We also illustrate a special situation in which a two-mode input state is transformed into a one-mode state by the teleportation. In addition, we discuss an optimal situation in which a high teleportation probability and a high degree of teleportation fidelity can be achieved.

PT-invariant point interactions in one dimension

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Journal of Physics A: Math. Gen., **38** (2005) L519-L522.

By using Wu and Yu's pseudo-potential, we construct point interactions in one dimension that

are complex but conform to space-time reflection (*PT*) invariance. The resulting point interactions are equivalent to those obtained by Albeverio, Fei and Kurasov as self-adjoint extensions of the kinetic energy operator.

Enhancing PET images by means of Bates' blind deconvolution

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先端科学技術研究所所報第4号, 69-106 (2005).

Positron emission tomography (PET) is an innovative inspection method for early detection and treatment of cancer etc. The practical use of PET is rapidly advanced in recent years. However, the resolution of the PET images is yet to be improved for both purposes. There are two elements in improving the resolution of the PET images. One is the gamma-ray detection-system, and other is the image processing system. The purpose of this work is to examine whether or not the improvement of the resolution of the PET images can be achieved by image-restoration technique. For the purpose, we explore Bates' blind deconvolution that is regarded as an extended method of the one-dimensional signal conditioning with zero-values of signals. We developed some new technical tools for that study and show how they are useful. We present a PET image that we successfully enhanced by means of Bates' blind deconvolution.

Simulation Model of P2P Information Distribution based on Collaborative Filtering

Hidehiko OKADA*

Proceedings of the 11th International Conference
on Human-Computer Interaction, CD-ROM (2005)

Our goal is to develop a tool for evaluating ease of finding links from the viewpoint of webpage visual design. This paper describes our tool for measuring webpage visual features that will affect ease of finding links. We first describe our concept of webpage visual design evaluation method. It can be empirically said that the time spent for finding a link reflects the ease of finding the link: if a link is easy/difficult to find, the time for users to find the link will be short/long. Therefore, ease of finding links can be estimated by 1) analyzing how long users spend to find a link in a webpage with what visual features, and 2) modeling a function that estimates time to find

links from values of webpage/link visual features. The analysis is possible by user studies with various kinds of webpages, but it requires a tool for measuring webpage/link visual features that will affect ease of finding links. As such visual features, we describe 24 webpage attributes and 14 link attributes. We then describe our tool for measuring the 38 attribute values. Unlike tools in other researches, our tool can measure attribute values that cannot be measured by simply parsing HTML source files. Such attributes include the position and area of a link in a webpage. The essence of our method is to analyze webpage screens shown in Web browser windows by using a GUI accessibility function implemented in a GUI operating system. The accessibility function is usually applied to GUI screen readers for visually challenged users. By using the function, an application program can obtain property values of GUI widgets shown in the current screen (i. e., labels, positions and sizes) from the OS. We apply this function to our tool for measuring the attribute values not measurable by parsing sources.

Interaction Logging and Analysis Tool Estimating Expected Operations for Unexpected User Operations

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and Hideo SHIMAZU

Proceedings of the 11th International Conference
on Human-Computer Interaction, CD-ROM (2005)

This research aims to develop a model for evaluating effectiveness of a P2P network application by computer simulations. To evaluate effectiveness of an application system on a large-scale P2P network, a large number of nodes must participate in the evaluation, but obtaining the participation and cooperation of the large number of nodes in a short period of time is usually difficult. Instead of evaluating the system in the real world, it will be effective to pre-evaluate the system by developing a simulator. This paper describes a simulation model for P2P information distribution systems based on collaborative filtering. Collaborative filtering is a method for information recommendation and filtering that can discover information a user does not yet know but other users know. In the description, webpage bookmarks are the example of data to be distributed. This paper first describes a simple basic model and then further describes four model extensions for enabling simulations closer to an envisioned real-world system.

Tool for Measuring Webpage Visual Features

Hidehiko OKADA*, Toshiyuki ASAH and Izumi KOHNO

Proceedings of the 11th International Conference
on Human-Computer Interaction, CD-ROM (2005)

This paper proposes a method for logging and analyzing user interactions with GUI applications and webpages that can estimate expected operations for each unexpected user operation. Expected operations are those expected by UI designers for completing a task. The method judges whether a user operation is an expected one or not. If the operation is not an expected one, the method further checks whether any widget shown in the current screen (in which the user inputted the operation) is included in expected interaction sequences for the task. This check is achieved by analyzing what widgets are shown in the screen each time a user operation is inputted. For this widget analysis, our method utilizes GUI accessibility functions provided for developing GUI accessibility applications such as screen readers. We have developed a tool for the proposed method. Future work includes evaluation of the proposed method by applying the tool to actual usability evaluations.

A topological property of Lipschitz mappings

Kazuhiko FUKUI* and Taro NAKAMURA

Topology Appl., 148, 143-152 (2005)

We study a topological property of function spaces in the Lipschitz category and show that certain subspaces behave nice and that this holds in the smooth category. As a corollary, we show that the so-called “Inverse function theorem” holds in this category.

On the first homology of automorphism groups of manifolds with geometric structures

Kojun ABE and Kazuhiko FUKUI*

CEJM, 3(3), 516-528 (2005)

Herman and Thurston proved that the group of diffeomorphisms with compact support of a

smooth manifold M which are isotopic to the identity is a perfect group. We consider the case where M has a geometric structure. In this paper we shall survey on the recent results of the first homology of the diffeomorphism groups which preserve a smooth G -action or a foliated structure on M . We also work in Lipschitz category.

H_0 from an orientation-unbiased sample of Sunyaev-Zel'dovich and X-ray clusters

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Monthly Notices of the Royal Astronomical Society, 357, 518-526 (2005)

We have observed the Sunyaev-Zel'dovich (SZ) effect in a sample of five moderate-redshift clusters with the Ryle Telescope, and used them in conjunction with X-ray imaging and spectral data from ROSAT and ASCA to measure the Hubble constant. This sample was chosen with a strict X-ray flux limit using both the Bright Cluster Sample and the Northern ROSAT All-Sky Survey (RASS) cluster catalogues to be well above the surface brightness limit of the RASS, and hence to be unbiased with respect to the orientation of the cluster. This controls a major potential systematic effect in the SZ/X-ray method of measuring H_0 . Taking the weighted geometric mean of the results and including the main sources of error, namely the noise in the SZ measurement, the uncertainty in the X-ray temperatures and the unknown ellipticity and substructure of the clusters, we find $H_0 = 59_{-9}^{+10}$ (random) $_{-7}^{+8}$ (systematic) km/s/Mpc assuming a standard cold dark matter model with $\Omega_M = 1.0$, $\Omega_\Lambda = 0.0$ or $H_0 = 10_{-10}^{+11+9}$ km/s/Mpc if $\Omega_M = 0.3$, $\Omega_\Lambda = 0.7$.

ASCA and XMM-Newton observations of A2029

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Advances in Space Researches, 36, 752-756 (2005)

The X-ray data of A2029 obtained with XMM-Newton show no evidence of embedded AGN in the central region of this cluster, which was suggested from the analysis of restored ASCA image

data, although some hot spots are seen within or around the central cD galaxy. The absence of AGN at the center is consistent with the result of Chandra observations. Radial profiles of the iron abundance and the 2D (surface) temperature obtained from the XMM-Newton data are in good agreement with Chandra data as a whole.

Identification of earthquake epicenter from measurements of electromagnetic pulses in the Earth

Minoru Tsutsui*

Geophysical Research Letters, Vol. 32, No. 20, L20303 (2005. 10)

We have developed a system for finding arrival directions of electromagnetic (EM) pulses detected in the earth. The system detected an intense EM pulse just when an earthquake (M5.5) occurred. In the analysis of the detected EM pulse, we first derived its frequency dispersion characteristics. Using the data of the dispersion characteristics, we obtained frequency-dependent arrival directions of the EM pulse. Among them, an exact direction pointing toward the EM pulse source was determined. Finally, we could find the source location of the EM pulse from the estimation of its propagation distance as a waveguide mode, which has shown that the EM pulse source location was on the earthquake epicenter.

Words, Languages and Combinatorics

Masami Ito

Elseviers (Amsterdam), 131 pages (2004)

This book is a special issue of the journal "Theoretical Computer Science" (volume 324) devoted to the Third International Colloquium on Words, Languages and Combinatorics held in Kyoto in 2000.

Mathematical Foundation of Informatics

Do Long Van and Masami Ito

World Scientific (Singapore), 202 pages (2005)

This book is a proceedings volume of the First International Conference on Mathematical Foundation of Informatics held in Hanoi in 1999.

On regular languages determined by nondeterministic directable automata

Balazs Imreh and Masami Ito

Acta Cybernetica Vol. 17, 1-10 (2005)

In this paper, we introduce several results on nondeterministic directable automata and related regular languages.

Commutative closure of languages

Masami Ito

Automata and Formal Languages, Proceedings of the 11th International Conference, AFL 2005 (Institute of Informatics, University of Szeged, Hungary), 144-149 (2005)

In this paper, we provide a necessary and sufficient condition for the commutative closure of a special type of regular (context-free) language to be regular (context-free).

Deterministic and nondeterministic directable automata

Masami Ito

The Mathematical Foundation of Informatics
(World Scientific, Singapore), 71-83 (2005)

This paper is a survey article to introduce some results on deterministic and nondeterministic directable automata and their related languages.

2004年に京都を襲った台風の気象学的特性について

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京都産業大学総合学術研究所所報, 3, 93—102 (2005. 7).

2004年に日本に上陸した10個の台風のうち、京都に影響を与えた6号、16号、21号、23号の4個の台風について、気圧場の数値解析を行った。その結果を1955～94年に上陸した51個の顕著台風の解析結果 (Fujii, 1998) と比較したところ、上陸時の中心気圧低下量 (周辺気圧—中心気圧), Δp , の再現期間は5～13年に相当した。また、上陸時の最大風速半径は、21号を除いて、過去に上陸した同じ Δp の台風の値に比べて大きく、強さのわりにはスケールの大きい台風であった。一方、上陸後の Δp の減衰率は、23号を除いて、過去に上陸した同じ Δp の台風の値とほぼ同じであった。

Structural dynamics of cereal mitochondrial genomes as revealed by complete nucleotide sequencing of the wheat mitochondrial genome

Ogihara Y, Yamazaki Y, Murai K, Kanno A, Terachi T*, Shiina T, Miyashita N, Nasuda S, Nakamura C, Mori N, Takumi S, Murata M, Futo S, Tsunewaki K.

Nucleic Acids Research, 33-19, 6235-6250 (2005. 10)

The application of a new gene-based strategy for sequencing the wheat mitochondrial genome shows its structure to be a 452 528 bp circular molecule, and provides nucleotide-level evidence of intra-molecular recombination. Single, reciprocal and double recombinant products, and the nucleotide sequences of the repeats that mediate their formation have been identified. The genome has 55 genes with exons, including 35 protein-coding, 3 rRNA and 17 tRNA genes. Nucleotide sequences of seven wheat genes have been determined here for the first time. Nine genes have an exon-intron structure. Gene amplification responsible for the production of multicopy mitochondrial genes, in general, is species-specific, suggesting the recent origin of these genes. About 16, 17, 15, 3.0 and 0.2% of wheat mitochondrial DNA (mtDNA) may be of genic (including introns), open reading frame, repetitive sequence, chloroplast and retro-element origin, respectively. The gene order of the wheat mitochondrial gene map shows little synteny to the rice and maize maps, indicative that thorough gene shuffling occurred during speciation. Almost all unique mtDNA sequences of wheat, as compared with rice and maize mtDNAs, are redundant DNA. Features of the gene-based strategy are discussed, and a mechanistic model of mitochondrial gene amplification is proposed.

Variations in a hotspot region of chloroplast DNAs among common wheat and *Aegilops* revealed by nucleotide sequence analysis.

Guo CH, Terachi T*

Genes & Genetic Systems, 80-84, 277-285 (2005. 8)

The second largest *Bam*HI fragment (B2) of the chloroplast DNA in *Triticum* (wheat) and *Aegilops* contains a highly variable region (a hotspot), resulting in four types of B2 of different size, i. e. B2l (10.5kb), B2m (10.2kb), B2 (9.6kb) and B2s (9.4kb). In order to gain a better understanding of the molecular nature of the variations in length and explain unexpected identity among B2 of *Ae. ovata*, *Ae. speltoides* and common wheat (*T. aestivum*), the nucleotide sequence between a stop codon of *rbcL* and a *Hind*III site in *cemA* in the hotspot was determined for *Ae. ovata*, *Ae. speltoides*, *Ae. caudata* and *Ae. mutica*. The total number of nucleotides in the region was 2808, 2810, 3302, and 3594 bp, for *Ae. speltoides*, *Ae. ovata*, *Ae. caudata* and *Ae. mutica*, respectively, and the sequences were compared with the corresponding ones of *Ae. crassa* 4x, *T. aestivum* and *Ae. squarrosa*. Compared with the largest B2l fragment of *Ae. mutica*, a 791bp and a 793 bp deletion were found in *Ae. speltoides* and *Ae. ovata*, respectively, and the possible site of deletion in the two species is the same as that of *T. aestivum*. However, a deleted segment in *Ae. ovata* is 2 bp longer than that of *Ae. speltoides* (and *T. aestivum*), demonstrating that recurrent deletions had occurred in the chloroplast genomes of both species. Comparison of the sequences from *Ae. caudata* and *Ae. crassa* 4x with that of *Ae. mutica* revealed a 289 bp and a 61 bp deletion at the same site in *Ae. caudata* and *Ae. crassa* 4x, respectively. Sequence comparison using wild *Aegilops* plants showed that the large length variations in a hotspot are fixed to each species. A considerable number of polymorphisms are observed in a loop in the 3' of *rbcL*. The study reveals the relative importance of the large and small indels and minute inversions to account for variations in the chloroplast genomes among closely related species.

Cloning and structural analysis of wheat cDNAs encoding *Ndr* protein kinase homolog by data mining of the EST database KOMUGI

Imai T, Terachi T*

Breeding Science, 55-52, 207-212 (2005. 6)

In order to gain a better understanding of the nature of nuclear *dbf*-related (*Ndr*) protein

kinase homologs in monocots, three cDNA clones were isolated from common wheat (*Triticum aestivum*) by data mining of expressed sequence tag (EST) databases, and their primary structure was determined by reverse transcription-polymerase chain reaction (RT-PCR), 5'-rapid amplification of cDNA ends (RACE), and nucleotide sequencing. Deduced amino acid sequences of the cDNA clones contained all 12 highly conserved subdomains of the eukaryotic Ser/Thr protein kinase, including the ATP-binding site (in subdomain I-II) and the Ser/Thr protein kinase active-site (in subdomain VI). The sequences also contained an insert of 56 amino acids between subdomains VII and VIII, and three conserved Ser/Thr residues, being characteristic of the *Ndr* family of eukaryotic protein kinases. A sequence comparison among cDNAs from wheat and those from ancestral diploid species (*T. boeoticum*, *Aegilops speltoides* and *Ae. squarrosa*) revealed that at least three homeologous genes were expressed in hexaploid wheat. The results confirmed the usefulness of current EST databases including KOMUGI for gene cloning of wheat, since the use of specific primers designed with information about EST sequences has considerably facilitated the cloning of rare cDNAs such as *Ndr*.

Marker-based Selection as a Tool for Enhancing the Efficiency of Two Conventional Breeding Methods of Self-fertilizing Crop Plants, the Generation-accelerated Bulk Breeding and Doubled Haploid Breeding

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Breeding Science 55, 397-407 (2005. 12)

The effectiveness of marker-based selection (MBS) for enhancing the efficiency of two conventional breeding methods of self-fertilizing crop plants, i. e., generation-accelerated bulk breeding (GAB) and doubled haploid breeding (DHB), is evaluated. When incorporated into GAB, MBS is assumed to be applied in F_2 and F_3 generations based on DNA markers that are linked with desirable trait genes. The effectiveness of MBS is evaluated based on its contribution to increasing the probability of obtaining the desired genotype. Our calculations of the probability show that the effectiveness of MBS depends on the number of trait genes involved in the breeding objective as well as the number of available markers; MBS will produce a great increase in the probability when more than about 12 genes are involved in the breeding objective and markers are available for several or more of these trait genes. In such a case, MBS is useful even when as few as 100 plants are tested in F_2 and F_3 generations, compared to conventional GAB in which 2000 plants are grown for generation acceleration. The effectiveness of MBS increases in the presence of repulsion

linkage between desirable trait genes, whereas it decreases in the presence of coupling linkage. Although codominant markers are superior under most practically possible conditions, dominant markers (linked with desirable trait genes) could be superior when relatively few, roughly fewer than 12, genes are involved in the breeding objective and desirable trait genes are linked prevalently in the coupling phase. When MBS is based on more than several codominant markers, it is important to widen the range of the marker genotypes to be selected; not only the best but also the second and third best, partially heterozygous genotypes should be selected. Linkage between trait genes and markers needs not to be perfect; when many markers are available, the advantage of MBS is not lost even with a map distance as long as 10 cM. When desirable trait genes are linked prevalently in the repulsion phase, MBS could effectively be combined with DHB for eliminating unpromising doubled haploid genotypes prior to field test, or for selecting from an F₂ population, plants that should be treated for doubled haploidization.

「バイオリージョナリズムに基礎をおいた上賀茂社家町での環境学習の展開」

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京都産業大学総合学術研究所所報, 第3号, 59—72 (2005. 7)

本論文では, 上賀茂社家町ではじめた社家屋敷の見学会を地元による地元の子供たちへの環境学習として定着させるまでの地元との協働の過程と問題点, アンケート結果などについて検討し, 今後の地域との協働のための条件について実証的に考察した。

「線維芽細胞増殖因子レセプター1アイソフォームによる
細胞増殖および神経分化誘導とシグナル伝達」

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京都産業大学論集自然系列 (第34号) p177-209, 2005 March 発行

線維芽細胞増殖因子 (FGF) の作用は細胞特異的であり, FGF は線維芽細胞のみならず様々な細胞の増殖を促進し, 神経細胞においては分化を誘導し神経繊維を進展させる。標的細胞の FGF に対する感受性は FGF レセプター (FGFR) の発現に依存している。FGFR は4種類の異なる遺伝子が存在し, 選択的スプライシングによりさらに多くのアイソフォームを生じる。FGFR は細胞外に3個の免疫グロブリン様ドメイン (Ig) を持つチロシンキナーゼ型レセプターである。FGFR1 には Ig1 部位 (N 末端側の Ig) の欠損している FGFR1S と欠損していない FGFR1L が存在しているが, その機

能の違いは明らかにされていない。著者らは以前、FGFR1Sの細胞膜近傍領域に一アミノ酸変異のある変異体FGFR1Smをクローニングしている。そこで著者らはそれぞれを安定発現させたクローンを用いて、FGF刺激による細胞増殖能、分化能などの機能を解析した。その結果、IgIの選択的スプライシングにより生じるFGFR1LとFGFR1Sでは、FGF感受性が異なっていることを示した。さらにIgIの有無は細胞内シグナル伝達経路にも違いを生じさせ、FGFによる細胞増殖や分化誘導に異なる作用を及ぼすことを明らかにした。また、FGFR1Smの変異はFRS2チロシンリン酸化やその他のシグナル伝達経路の活性化を惹起し、その結果FGFR1SやFGFR1Lよりも強く神経細胞の分化と細胞増殖を促進することを明らかにした。

Cloning and Expression of A Brain-specific Putative UDP-GalNAc: Polypeptide N-Acetylgalactosaminyltransferase Gene

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Biological & Pharmaceutical Bulletin, 28, 429-433 (2005, 3)

We isolated a rat cDNA clone and its human orthologue by homology-based PCR from brain, which are most homologous to UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase 9. Nucleotide sequence analysis of these putative GalNAc-transferases (designated pt-GalNAc-T) showed that they contained structural features characteristics of the GalNAc-transferase family. It was also found that human pt-GalNAc-T was identical to the gene WBSCR17, which is reported to be in the critical region of the Williams-Beuren Syndrome, a neurodevelopmental disorder, and be predominantly expressed in brain and heart. In order to investigate the expression of pt-GalNAc-T in brain in more detail, we first examined the expression of human pt-GalNAc-T by Northern blot analysis and found the most abundant expression of 5.0-kb mRNA in cerebral cortex with the somewhat lesser amount in cerebellum. The expression of rat pt-GalNAc-T was investigated more extensively. Its brain-specific expression of 2.0-kb and 5.0-kb transcripts was demonstrated by Northern blot analysis. In situ hybridization in the adult brain revealed its high expression in cerebellum, hippocampus, thalamus, and cerebral cortex. Moreover, a high magnification analysis revealed that its expression was exclusively associated with neurons, but not with glial cells. Analysis of the rat embryos also demonstrated that rat pt-GalNAc-T was expressed in the nervous system, such as diencephalons, cerebellar primordium, and dorsal root ganglion. However, recombinant human pt-GalNAc-T, which was expressed in insect cells, did not glycosylate several peptides derived from mammalian mucins, suggesting that it may have strict substrate specificity. The brain-specific

expression of *pt*-GalNAc-T suggested its involvement in the brain development, through O-glycosylation of proteins in the neurons.

Free Energies of Macroionic Suspensions and the Equation of State for Osmotic Pressure

Ikuo S. Sogami, Martin V. Smalley and Tadatomi Shinohara

Progress of Theoretical Physics, Vol. 113, No. 2, p. 235 (2005)

A generating functional which, together with an extremal condition, results in the Poisson-Boltzmann equation and its boundary conditions for the average electric potential of a macroionic suspension is constructed within mean field theory. We demonstrate that the extremum of the generating functional is identical to the Helmholtz free energy of the system, which has an integral representation in terms of the average electric potential. From the Helmholtz free energy, the chemical potentials of small ions and the chemical potentials of the effective charge numbers of macroions are calculated, and, in the form of their sum, an integral representation of the Gibbs free energy of the system is derived. The difference between the two free energies leads to an equation of state for the osmotic pressure of the small ion gas in the environment of the macroionic suspension.

A Non-Semisimple Hidden Symmetry for Flavor Physics

Ikuo S. Sogami

Progress of Theoretical Physics, Vol. 114, No. 4, p. 873 (2005)

With linearly independent elements extracted from 3×3 unitary matrix representations $\text{Rep}(S_3)$ of the permutation group S_3 , a non-semisimple algebra A and its associated Lie group $G(A)$ are constructed for the purpose of describing flavor physics. While the group $G(A)$ is isomorphic to the $SU(2) \times U(1)$ group, the algebra A has a unique, elaborate structure. A flavor-mixing matrix that is completely different from that of the conventional theory is expressed in terms of four group parameters of the Lie group in an essentially unique way. Adjusting the values of the group parameters of the flavor-mixing matrix for quark sector allows us to account for experimental results to high precision. In order to describe the mass matrices leading to hierarchical mass spectra, a minimal extension of the algebra A is made by adding an additional element.