

学術論文抄録—2012 年発表

地殻岩盤での衝撃応力に伴って励起する電磁波パルスの確認に向けて

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早川正士（編）「地震予知研究の最前線」,
日本専門図書出版株式会社, 364–387 (2012.2)

地震前兆現象の最有力候補の一つとして、「岩盤同士の応力衝撃印加による圧電現象により電磁波パルスが放射される」との仮説を立て、その確認のための観測研究を始めた。この研究では、地上からの雑音を抑制し、地中からの電磁波を優先的に検出する目的で、地中に向けた深いボアホールを確保し、そこに電磁波センサーを挿入して地中起源の電磁波パルスを検出する事を目指している。これまでの試行錯誤の繰り返しによる地中での観測から、検出される電磁波パルスの詳細な振る舞いを明らかにできた。その結果として、検出される電磁波パルスの殆どは雷放電に起因しており、自然電磁波観測研究に重大な影響を及ぼすもう一つの要因である送電線からの人工電磁波パルスの性質をも明らかにし、地中での電磁波環境の様相を明確にした。これらで得られた知見を基に、更なる斬新なセンサーと検出信号の独特な解析処理法から成るシステムの開発を進めてきて、最近それを完成させる事ができた。これにより、本来の目的である「地中で励起される電磁波パルスの波源位置特定」に向けて、そのシステムによる試験観測を進めている。本論文では、研究開始から現在に至るまでの過程で遭遇した様々な問題点とその克服に向けた方策について紹介している。

EFFECTS OF SERUM PROTEINS ON *IN VITRO* MELAMINE-CYANURATE CRYSTAL FORMATION

Sarawut TAKSINOROS and Hideo MURATA*

The Journal of Veterinary Medical Science, 74-12, 1569–1573 (2012.12).

Melamine toxicity is recognized as a distinct form of renal failure due to occlusion of the renal tubules by the compound melamine and its deaminated derivative, cyanuric acid. The morphology of melamine-cyanurate crystals *in vivo* differs from that *in vitro*, being rounded in the former case but needle-like in the latter. The reasons for this difference in morphology between *in vivo* and *in vitro* crystals remain unknown. In the present study, we investigated the *in vitro* effects of several possible intra-renal factors, i.e., pH and serum and urinary proteins, on the morphology of melamine-cyanurate crystals in order to clarify what might be responsible for the formation of rounded urolites *in vivo*. We found that serum proteins, such as fetal bovine serum, bovine serum albumin and bovine gamma-globulin, can alter the morphology of melamine cyanurate, turning it into rounded crystals. The urinary protein beta-2-microglobulin had a less pronounced effect. The crystal morphology was unaffected by pH. Based on the present *in vitro* findings and known clinical data, we suggest a putative protein-related model for melamine-cyanurate formation in the kidney.

The necessary and sufficient condition for the group of leaf preserving diffeomorphisms to be simple

Kazuhiko FUKUI*

Jour. of Math. Soc. Japan, 64-1, 181–184 (2012)

Let F be a C^∞ -foliation on a compact C^∞ -manifold M . We consider the group of all leaf preserving C^∞ -diffeomorphisms of (M, F) which are isotopic to the identity through leaf preserving C^∞ -diffeomorphisms. Then we show that the group is simple if and only if all leaves of F are dense.

Commutator Length of Leaf Preserving Diffeomorphisms

Kazuhiko FUKUI*

Publ. Res. Inst. Math. Sci. Kyoto Univ., 48-3, 615-622 (2012)

We consider the group of leaf preserving C^∞ -diffeomorphisms for a C^∞ -foliation on a manifold which are isotopic to the identity through leaf preserving C^∞ -diffeomorphisms with compact support. Then we show that the group for a one-dimensional C^∞ -foliation F on the torus is uniformly perfect if and only if F has no compact leaves. Moreover we consider the group of leaf preserving C^∞ -diffeomorphisms for the product foliation on $S^1 \times S^n$ which are isotopic to the identity through leaf preserving C^∞ -diffeomorphisms. Here the product foliation has leaves of the form $\{pt\} \times S^n$. Then we show that the group is uniformly perfect for $n \geq 2$.

Fine genetic mapping of *RXopJ4*, a bacterial spot disease resistance locus from *Solanum pennellii* LA716

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Theoretical and Applied Genetics DOI 10.1007/s00122-012-2004-6 (2012. 11)

The *RXopJ4* resistance locus from the wild accession *Solanum pennellii* (Sp) LA716 confers resistance to bacterial spot disease of tomato (*S. lycopersicum*, Sl) caused by *Xanthomonas perforans* (Xp). *RXopJ4* resistance depends on recognition of the pathogen type III effector protein *XopJ4*. We used a collection of Sp introgression lines (ILs) to narrow the *RXopJ4* locus to a 4.2-Mb segment on the long arm of chromosome 6, encompassed by the ILs 6-2 and 6-2-2. We then adapted or developed a collection of 14 molecular markers to map on a segregating F_2 population from a cross between the susceptible parent Sl FL8000 and the resistant parent *RXopJ4* 8000 OC₇. In the F_2 population, a 190-kb segment between the

markers J350 and J352 cosegregated with resistance. This fine mapping will enable both the identification of candidate genes and the detection of resistant plants using cosegregating markers. The RXopJ4 resistance gene(s), in combination with other recently characterized genes and a quantitative trait locus (QTL) for bacterial spot disease resistance, will likely be an effective tool for the development of durable resistance in cultivated tomato.

A high-throughput method for Illumina RNA-seq library preparation

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Frontiers in Plant Genetics and Genomics 3, 1–10 (2012.8)

With the introduction of cost effective, rapid, and superior quality next generation sequencing techniques, gene expression analysis has become viable for labs conducting small projects as well as large-scale gene expression analysis experiments. However, the available protocols for construction of RNA-sequencing (RNA-Seq) libraries are expensive and/or difficult to scale for high-throughput applications. Also, most protocols require isolated total RNA as a starting point. We provide a cost-effective RNA-Seq library synthesis protocol that is fast, starts with tissue, and is high-throughput from tissue to synthesized library. We have also designed and report a set of 96 unique barcodes for library adapters that are amenable to high-throughput sequencing by a large combination of multiplexing strategies. Our developed protocol has more power to detect differentially expressed genes when compared to the standard Illumina protocol, probably owing to less technical variation amongst replicates. We also address the problem of gene-length biases affecting differential gene expression calls and demonstrate that such biases can be efficiently minimized during mRNA isolation for library preparation.

Mechanical regulation of auxin-mediated growth

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Current Biology 22, 1468–1476 (2012.8)

The phytohormone auxin is a primary regulator of growth and developmental pattern formation in plants. Auxin accumulates at specific sites (e.g., organ primordia) and induces localized growth within a tissue. Auxin also mediates developmental responses to intrinsic and external physical stimuli; however, exactly how mechanics influences auxin distribution is unknown. Here we show that mechanical strain can regulate auxin transport and accumulation in the tomato shoot apex, where new leaves emerge and rapidly grow. Modification of turgor pressure, application of external force, and artificial growth induction

collectively show that the amount and intracellular localization of the auxin efflux carrier PIN1 are sensitive to mechanical alterations. In general, the more strained the tissue was, the more PIN1 was present per cell and the higher the proportion localized to the plasma membrane. Modulation of the membrane properties alone was sufficient to explain most of the mechanical effects. Our experiments support the hypothesis that the plasma membrane acts as a sensor of tissue mechanics that translates the cell wall strain into cellular responses, such as the intracellular localization of membrane-embedded proteins. One implication of this fundamental mechanism is the mechanical enhancement of auxin-mediated growth in young organ primordia. We propose that growth-induced mechanical strain upregulates PIN1 function and auxin accumulation, thereby promoting further growth, in a robust positive feedback loop.

Interspecific RNAi of *STM* disrupts *Cuscuta pentagona* plant parasitism

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Plant Cell 24, 3153–3166 (2012.7)

Infection of crop species by parasitic plants is a major agricultural hindrance resulting in substantial crop losses worldwide. Parasitic plants establish vascular connections with the host plant via structures termed haustoria, which allow acquisition of water and nutrients, often to the detriment of the infected host. Despite the agricultural impact of parasitic plants, the molecular and developmental processes by which host/parasitic interactions are established are not well understood. Here, we examine the development and subsequent establishment of haustorial connections by the parasite dodder (*Cuscuta pentagona*) on tobacco (*Nicotiana tabacum*) plants. Formation of haustoria in dodder is accompanied by upregulation of dodder KNOTTED-like homeobox transcription factors, including SHOOT MERISTEMLESS-like (*STM*). We demonstrate interspecific silencing of a *STM* gene in dodder driven by a vascular-specific promoter in transgenic host plants and find that this silencing disrupts dodder growth. The reduced efficacy of dodder infection on *STM* RNA interference transgenics results from defects in haustorial connection, development, and establishment. Identification of transgene-specific small RNAs in the parasite, coupled with reduced parasite fecundity and increased growth of the infected host, demonstrates the efficacy of interspecific small RNA-mediated silencing of parasite genes. This technology has the potential to be an effective method of biological control of plant parasite infection.

Toward elucidation the mechanisms that regulate heterophylly

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Neelima Sinha and Seisuke Kimura*

Plant Morphology 24, 57–63 (2012.5)

The leaves of some plant species are able to change their morphology in response to environmental conditions. This phenomenon is termed heterophylly. Various aquatic plants exhibit drastic changes in leaf shape in response to submerged aquatic conditions. Heterophyllic variation ranges from mere modification of leaf width to drastic alteration in the outline of leaves and is interpreted as an adaptation to aquatic habitats. Although this phenomenon is widely observed among angiosperms, there is limited information on the regulation of heterophyllic switch in leaf development. Here, we have reviewed existing knowledge on leaf development and heterophylly and have introduced *Neobeckia aquatica* as an emerging model to elucidate the mechanisms underlying heterophylly.

A note on infinite divisibility of zeta distributions

Shingo Saito and Tatsushi Tanaka*

Applied Math. Sci. vol. 6, no. 30 (2012), 1455–1461

The Riemann zeta distribution, defined as the one whose characteristic function is the normalised Riemann zeta function, is an interesting example of an infinitely divisible distribution. The infinite divisibility of the distribution has been proved with recourse to the Euler product of the Riemann zeta function. In this paper, we look at multiple zeta-star function, which is a multi-dimensional generalisation of the Riemann zeta function and is believed to have no Euler product, and show that the corresponding distribution is not infinitely divisible.

The Bowman-Bradley theorem for multiple zeta-star values

Hiroki Kondo, Shingo Saito and Tatsushi Tanaka*

J. Number Theory 132 (2012), 1984–2002

The Bowman-Bradley theorem asserts that the multiple zeta values at the sequences obtained by inserting a fixed number of twos between $3, 1, \dots, 3, 1$ add up to a rational multiple of a power of π . We establish its counterpart for multiple zeta-star values by showing an identity in a non-commutative polynomial algebra introduced by Hoffman.

Method for Estimating Presence/Absence of Breadcrumb Trails in Webpages

H. Okada* and H. Kamishima

ICIC Express Letters, Vol. 6, Issue 12, pp. 3015–3020 (2012.12)

It is recommended for better web accessibility that a web page shows its “breadcrumb trail” in a website. In this paper, we propose a method for estimating presence/absence of breadcrumb trails in webpages. Our idea is to apply a data mining method for the estimation: the method mines a set of estimation rules from a set of webpage instances that include/do not include their breadcrumb trails. Several kinds of data mining methods can be applied in our method, including decision trees derived by C4.5. To evaluate the estimation accuracy, we have collected 560 webpage instances and applied our method to the instances. We measured the accuracy by the 10-fold cross validation. The mean accuracy was 71.1%, and the range was [60.7%, 82.1%].

Evolving RoboCup Soccer Player Formations by means of Particle Swarm Optimization

H. Okada*, A. Yamashita and T. Wada

International Journal of Science and Engineering Investigations (IJSEI), 10912–17,
Vol. 1, Issue 9, pp. 78–81 (2012.10)

Researchers have applied evolutionary algorithms to RoboCup Soccer players/teams and evaluate the effectiveness of the algorithm in evolving good players and teams, but further investigations are required to know more about the ability of the algorithms. We report our application of particle swarm optimization (PSO) to the evolution of RoboCup Soccer player formations: how well formations for various team performances (e.g., offensive, defensive, balanced) can be automatically obtained by means of PSO.

Comparison of Evolution Strategy, Genetic Algorithm and Their Hybrids on Evolving Autonomous Game Controller Agents

H. Okada*, J. Tokida and Y. Fujii

International Journal of Science and Engineering Investigations (IJSEI), 10612-02,
Vol. 1, Issue 6, pp. 11–16 (2012.07)

Researchers have been applying artificial/computational intelligence (AI/CI) methods to computer games. In this research field, further researches are required to compare AI/CI methods with respect

to each game application. In this paper, we report our experimental results on the comparison of two evolutionary algorithms (evolution strategy and genetic algorithm) and their hybrids, applied to evolving autonomous game controller agents. The games are the CIG2007 simulated car racing and the MarioAI 2009. In the application to the simulated car racing, premature convergence of solutions was observed in the case of ES, and GA outperformed ES in the last half of generations. Besides, a hybrid which uses GA first and ES next evolved the best solution among the whole solutions being generated. This result shows the ability of GA in globally searching promising areas in the early stage and the ability of ES in locally searching the focused area (fine-tuning solutions). On the contrary, in the application to the MarioAI, GA revealed its advantage in our experiment, whereas the expected ability of ES in exploiting (fine-tuning) solutions was not clearly observed. The blend crossover operator and the mutation operator of GA might contribute well to explore the vast search space.

ユーザビリティ定量化手法の構築 ～客観的評価のためのチェックリストと支援ツールの開発

池上 輝哉, 岡田 英彦*, 福住 伸一

ヒューマンインタフェース学会論文誌, Vol. 14, No. 1, pp. 101–110 (2012.02)

A research goal on usability evaluation methods is to achieve reliable usability “scoring”. Toward the goal, the authors have developed quantitative usability evaluation method that uses a usability checklist and a checking support tool. Our checklist consists of 114 checking items with more clearly and precisely defined checking steps and judgment criteria than existing checklists. Such clear and precise definitions enable checklist-based evaluations more reliable and less independent of differences among evaluators. Effectiveness of our checklist has been evaluated by experiments with novice evaluators. Besides, the authors have evaluated effectiveness of our checking support tool by an experiment. This article reports our evaluation method and support tool, and the method and results of the experiments.

GA with Fuzzy-valued Genotypes and its Application to Neuroevolution

H. Okada*, T. Matsuse and Tetsuya Wada

Asia Pacific Symposium of Intelligent and Evolutionary Systems (IES) 2012,
pp. 15–18 (2012.12)

In this paper, we propose an extension of genetic algorithm (GA) for evolving fuzzy-valued neural networks. In the proposed GA, values in the genotypes are not real numbers but fuzzy numbers. We apply our fuzzy GA (FGA) to the approximate modeling of fuzzy functions with fuzzy neural networks (FNNs). Experimental results showed that an FNN evolved by our FGA could well approximate a hidden test function, despite that the learning was not supervised.

Interval-valued Evolution Strategy for Evolving Neural Networks with Interval Weights and Biases

H. Okada*, T. Wada, A. Yamashita and T. Matsuse

Proc. of the 6th International Conference on Soft Computing and Intelligent Systems
and the 13th International Symposium on Advanced Intelligent Systems
(SCIS-ISIS 2012), pp. 2056–2060 (2012.11)

In this paper, we propose an extension of evolution strategy (ES) for evolving interval-valued neural networks. In the proposed ES, values in the genotypes are not real numbers but intervals. We apply our interval-valued ES (IES) to the approximate modeling of interval functions with interval-valued neural networks (INNs). Experimental results showed that INNs trained by our IES could well approximate a hidden test function, despite the fact that the learning was not supervised.

Fuzzy-valued Evolution Strategy for Evolving Neural Networks with Fuzzy Weights and Biases

H. Okada*, A. Yamashita, T. Matsuse and T. Wada

Proc. of the 6th International Conference on Soft Computing and Intelligent Systems
and the 13th International Symposium on Advanced Intelligent Systems
(SCIS-ISIS 2012), pp. 277–280 (2012.11)

In this paper, we propose an extension of evolution strategy (ES) for evolving fuzzy-valued neural networks (FNNs). In the proposed ES, values in the genotypes are not real numbers but fuzzy values. We apply our fuzzy-valued ES (FES) to the approximate modeling of fuzzy functions with FNNs. Experimental results showed that an FNN trained by our FES could approximate a hidden test function to a certain extent, despite that the learning was not supervised.

Proposal of Fuzzy Evolutionary Algorithms with Fuzzy Valued Genotypes

H. Okada*

Proc. of International Conference on Instrumentation, Control and Information
Technology (SICE Annual Conference 2012), pp. 1538–1541 (2012.08)

This paper proposes EAs that utilize fuzzy values directly as the genotype values. In the proposed method, each element in a genotype is a fuzzy value. The author extends EA operations for the fuzzy-

valued genotypes. Section 2 describes the extensions of EA operations including population initialization, fitness evaluation, and reproduction. The fitness evaluation methods are extended according to application problems, and the reproduction methods are extended according to EA variations.

Interval GA for Evolving Neural Networks with Interval Weights and Biases

H. Okada*, T. Matsuse, T. Wada and A. Yamashita

Proc. of International Conference on Instrumentation, Control and Information Technology (SICE Annual Conference 2012), pp. 1542–1545 (2012.08)

In this paper, we propose an extension of genetic algorithm for neuroevolution of interval-valued neural networks. In the proposed GA, values in the genotypes are not real numbers but intervals. We apply our interval-valued GA (IvGA) to the approximate modeling of interval functions with interval-valued neural networks. Experimental results showed that INNs trained by our IvGA approximated a test function to a certain extent, despite the fact that the learning was not supervised.

Association Analysis for Web Accessibility Problem on Topic Path

H. Okada* and M. Ogawa

Proc. of the 10th Asia Pacific Conference on Computer Human Interaction (APCHI 2012), Vol. 2, pp. 639–640 (2012.08)

We report our experimental result of mining association rules on web accessibility problems from 100 page instances with/without their topic paths. In the extracted rules, the four JIS guidelines, #5.3e, #5.9a, #5.1a and #5.4e, appeared more. Thus, pages which violate these guidelines are likely to lack their topic paths.

Evaluation of Evolution Strategy, Genetic Algorithm and Their Hybrid on Evolving Simulated Car Racing Controllers

H. Okada* and J. Tokida

World Academy of Science, Engineering and Technology, issue 65, pp. 1185–1188 (2012.05)

Researchers have been applying artificial/computational intelligence (AI/CI) methods to computer games. In this research field, further researches are required to compare AI/CI methods with respect to each game

application. In this paper, we report our experimental result on the comparison of three evolutionary algorithms ? evolution strategy, genetic algorithm, and their hybrid ?, applied to evolving controller agents for the CIG 2007 Simulated Car Racing competition. Our experimental result shows that, premature convergence of solutions was observed in the case of ES, and GA outperformed ES in the last half of generations. Besides, a hybrid which uses GA first and ES next evolved the best solution among the whole solutions being generated. This result shows the ability of GA in globally searching promising areas in the early stage and the ability of ES in locally searching the focused area (fine-tuning solutions).

Comparison of Evolutionary Algorithms and Their Hybrids Applied to MarioAI

H. Okada* and Y. Fujii

World Academy of Science, Engineering and Technology, issue 65, pp. 1189–1192
(2012.05)

Researchers have been applying artificial/computational intelligence (AI/CI) methods to computer games. In this research field, further researches are required to compare AI/CI methods with respect to each game application. In this paper, we report our experimental result on the comparison of evolution strategy, genetic algorithm and their hybrids, applied to evolving controller agents for MarioAI. GA revealed its advantage in our experiment, whereas the expected ability of ES in exploiting (fine-tuning) solutions was not clearly observed. The blend crossover operator and the mutation operator of GA might contribute well to explore the vast search space.

Modular organization of the mammalian Golgi apparatus

Nakamura N*, Wei J-H and Seemann J

Current Opinion in Cell Biology, 24, 467–474 (2012)

The Golgi apparatus is essential for post-translational modifications and sorting in the secretory pathway. In addition, it further performs a broad range of specialized functions. This functional diversity is achieved by combining basic morphological modules of cisternae into higher ordered structures. Linking cisternae into stacks that are further connected through tubules into a continuous Golgi ribbon, greatly increases Golgi efficiency and broadens its repertoire of functions. During cell division, the different modules of the Golgi are inherited by different mechanisms to maintain the functional and morphological composition of the Golgi.

HIV-1 Nef perturbs the function, structure, and signaling of the golgi through the Src kinase Hck

Hiyoshi M, Takahashi-Makise N, Yoshidomi Y, Chutiwitoonchai N, Chihara T, Okada M, Nakamura N*, Okada S and Suzu S *Journal of Cellular Physiology*, 227, 1090–1097 (2012)

The interaction between HIV-1 Nef and the Src kinase Hck in macrophages has been shown to accelerate the progression to AIDS. We previously showed that Nef disturbed the N-glycosylation/trafficking of Fms, a cytokine receptor essential for maintaining macrophages in an anti-inflammatory state, in an Hck-dependent manner. Here, we show the underlying molecular mechanism of this effect. Using various Hck isoforms and their mutants and Golgi-targeting Hck mutants, we confirmed that Hck activation at the Golgi causes the Nef-induced Fms N-glycosylation defect. Importantly, we found that both the co-expression of Nef and Hck and the expression of a Golgi-targeted active Hck mutant caused alterations in the distribution of GM130, a Golgi protein that was shown to be required for efficient protein glycosylation. Moreover, the activation of Hck at the Golgi caused strong serine phosphorylation of the GM130-interacting Golgi structural protein GRASP65, which is known to induce Golgi cisternal unstacking. Using pharmacological inhibitors, we also found that the activation of Hck at the Golgi followed by the activation of the MAP kinase ERK-GRASP65 cascade is involved in the Fms N-glycosylation defect. These results suggest that Nef perturbs the structure and signaling of the Golgi by activating Hck at the Golgi, and thereby, induces the N-glycosylation/trafficking defect of Fms, which is in line with the idea that Src family kinases are crucial Golgi regulators.

The ATPase activity of molecular chaperone HSP60 is inhibited by immunosuppressant mizoribine

Tanabe M, Ishida R, Izuhara F, Komatsuda A, Wakui H, Sawada K, Otaka M, Nakamura N* and Itoh H

American Journal of Molecular Biology, 2, 93–102 (2012)

The molecular chaperone HSP60 is a chaperonin homolog of GroEL. We had previously shown that the immunosuppressant mizoribine is bound directly to HSP60 and inhibited its chaperone activity. However, the inhibitory mechanisms of HSP60 by mizoribine have not yet been fully understood. In the present study, we investigated the influence of mizoribine on a folding cycle of HSP60 and co-chaperone HSP10. Our results showed that mizoribine inhibited the folding cycle of HSP60/HSP10. The ATPase activity of HSP60/HSP10 was decreased in the presence of mizoribine and the dissociation of HSP10 from HSP60 was also decreased by mizoribine. The same functions of GroEL and/or GroES were slightly affected by mizoribine. Based on our findings, we discuss the inhibitory mechanisms of HSP60 by mizoribine.

ゴルジ体に局在するタンパク質群

中村 暢宏*, 石田 竜一

生体の科学, 63, 408–411 (2012)

ゴルジ体は小胞体で新規合成された膜タンパク質や分泌タンパク質を受け取り, 糖鎖の付加やペプチド鎖の切断などの修飾を行い, さらにタンパク質の最終の品質管理を行ったのち, リソソームなどの細胞内オルガネラや形質膜へ向けて選別配送する重要な役割を担っている. 本稿では, 古典的な分泌タンパク質や膜タンパク質の加工にかかわるゴルジ体の酵素群について, 次にゴルジ体の構造や機能の調節にかかわる主要なタンパク質群について, さらに近年明らかになってきたゴルジ体で情報伝達に働くタンパク質について最後にゴルジ体への膜タンパク質局在化機構について概説したい.

One-dimensional point interaction with Griffiths' boundary conditions

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

Can. J. Phys. **90**, 383–389 (2012)

Griffiths proposed a pair of boundary conditions that define a point interaction in one-dimensional quantum mechanics. The conditions involve the n -th derivative of the wave function where n is a non-negative integer. We re-examine the interaction so defined and explicitly confirm that it is self-adjoint for any even value of n and for $n = 1$. The interaction is not self-adjoint for odd $n > 1$. We then propose a similar but different pair of boundary conditions with the n -th derivative of the wave function such that the ensuing point interaction is self-adjoint for any value of n .

Quantum search with certainty based on modified Grover algorithms: optimum choice of parameters

F.M. Toyama*, W. van Dijk, Y. Nogami

Quantum Information Processing, Published Online 30 October 2012:

DOI 10.1007/s11128-012-0498-0

In the original Grover algorithm, an exact or almost exact search such that the success probability is unity or infinitesimally close to unity is possible only for certain values of the fraction $\lambda = M/N$ where M is the number of marked items that are stored in an unsorted database of N items. There are various modified algorithms with an adjustable phase or phases such that an exact search can be done for any value of λ by means of a finite number of Grover-type operations. Among them, the algorithm proposed

by Long is the simplest in the sense that it has only one adjustable phase and that the phase can be obtained in a closed form. We show that other more general algorithms with additional phases are not more efficient than Long's version with a single phase.