Syst Synth Biol (2013) 7:161–173
DOI 10.1007/s11693-013-9109-3

RESEARCH ARTICLE

A model of epigenetic evolution based on theory of open quantum systems

Masanari Asano · Irina Basieva · Andrei Khrennikov · Masanori Ohya · Yoshiharu Tanaka · Ichiro Yamato

Received: 5 January 2013 / Revised: 18 May 2013 / Accepted: 6 June 2013 / Published online: 18 June 2013

Abstract We present a very general model of epigenetic evolution unifying (neo-)Darwinian and (neo-)Lamarckian viewpoints. The evolution is represented in the form of adaptive dynamics given by the quantum(-like) master equation. This equation describes development of the information state of epigenome under the pressure of an environment. We use the formalism of quantum mechanics in the purely operational framework. (Hence, our model has no direct relation to quantum physical processes inside a cell.) Thus our model is about probabilities for observations which can be done on epigenomes and it does not provide a detailed description of cellular processes. Usage of the operational approach provides a possibility to describe by one model all known types of cellular epigenetic inheritance.

Keywords Epigenetic markers · Quantum-like operational model · Cellular epigenetic evolution · Neo-Darwinism · Neo-Lamarckism · Open quantum systems

M. Asano · M. Ohya · Y. Tanaka
Department of Information Sciences, Tokyo University of Science, Yamasaki 2641, Noda-shi, Chiba 278-8510, Japan
e-mail: ohya@rs.noda.tus.ac.jp

I. Basieva · A. Khrennikov (✉)
International Center for Mathematical Modeling in Physics and Cognitive Sciences, Linnaeus University, 35195 Växjö, Sweden
e-mail: Andrei.Khrennikov@lnu.se

I. Yamato
Department of Biological Science and Technology, Tokyo University of Science, Yamasaki 2641, Noda-shi, Chiba 278-8510, Japan
e-mail: iyamato@rs.noda.tus.ac.jp

Introduction

During last years cell biologists are finding that non-genetic variation acquired during the life of an organism can sometimes be passed on to offspringa phenomenon known as *epigenetic inheritance*, see, e.g., Russell (2010). Recently several examples of adaptive mutations in eukaryotes by the *epigenetic mechanism* were reported, see Jablonka and Raz (2009) for a detailed review. By the influence of an environment, the epigenome structure including DNA methylation and histone modification may change during growth and such changes sometimes would be inherited by the progenitors. This is the adaptive mutation and a kind of *neo-Larmarkism* (Jablonka and Raz 2009). Everywhere below we shall use the term *epimutation*: a heritable change in gene expression that does not affect the actual base pair sequence of DNA. Four types of cellular epigenetic inheritance (CEI)[1] are recognized today: the CEI based on self-sustaining regulatory loops, the CEI based on three-dimensional templating, the chromatin-marking CEI, and the RNA-mediated CEI (Jablonka and Raz 2009). These types of CEI are realized in cells with the aid of very different mechanisms which structures are known only in general (many important details still have to be clarified). Nevertheless, all mentioned CEIs are parts of one universal phenomenon, namely, development of special adaptive features under the pressure of the environment and transmission of these features from a mother cell to the daughter cells. Therefore a perspective to create a universal model of CEI describing all its types in the common framework is very

[1] Cellular epigenetic inheritance is a narrower aspect of epigenetic inheritance as discussed in the broad sense. It refers to epigenetic transmission in sexual or asexual cell lineages, and the unit of this transmission is the cell.

attractive. Of course, such an activity does not contradict to continuation of intensive studies in cellular system biology aimed to creation of detailed models for each CEI and their interrelations. In this paper we present an operational model of CEI which is applicable to all its possible types (known and even yet unknown). Here the keyword is *adaptive dynamics*. Our aim is creation of an adaptive dynamical model of CEI. This model, although it does not describe concrete cellular mechanisms, can be interesting for cellular biology. It presents a general mathematical structure of CEI and it justifies the epigenetic mechanism from the viewpoint of theory of adaptive dynamical systems.

An important class of adaptive dynamical systems (Ohya 2008) can be described by the apparatus of theory of *open quantum systems*, see also Ohya and Volovich (2011). In this paper we use the quantum-like (QL) paradigm by which the formalism of QM can applied to describe measurements and information processes even outside of quantum physics, in particular, in biology (Khrennikov 2006; Accardi et al. 2008). In a series of papers (Basieva et al. 2011; Asano et al. 2012a, b) we elaborated a QL model of a cell processing information in accordance with the laws of quantum information theory, cf. also Wanke et al. (2009). By the QL paradigm (Khrennikov 2006; Accardi et al. 2008) complex biological systems can process information by violating laws of classical probability theory and, hence, classical information theory.[2] In particular, in Basieva et al. (2011) we demonstrated that one of the basic laws of classical probability theory, the law of total probability, is violated by well known experimental data, e.g., Inada et al. (1996), on functioning of the *lac*-operon in *E. coli* bacteria. This violation can be interpreted as an interference effect which is similar to interference of probabilities in the two slit experiment with photons.

We now apply the formalism of QM to describe evolution of *cell's epigenetic state*. The key point is encoding (mathematically) of this state by a normalized vector of complex Hilbert space (or more generally by a density operator). What are the reasons for usage of such representation in epigenetics and biology in general? We call our model *quantum-like* (QL) to distinguish it from really quantum models in cell biology: reducing cell's behavior to quantum particles inside a cell, e.g., Ogryzko (1997, 2008), McFadden and Al-Khalili (1999), McFadden (2000). Thus we do not motivate Hilbert space representation by quantum physics inside a cell. We use the operational viewpoint to the quantum formalism as a general theory of measurements. And it can be applied to any class of measurements having features similar to quantum ones. We discuss this question in detail in Sect. 2 where we present evidences from the biological papers on similarities between extraction of information from quantum and biological "realities."

The basis of the Hilbert state space is given by states corresponding to all possible epigenetic markers in a cell with the tensor product structure with respect to markers. This is the standard quantum information approach: encoding of information by qubit states without the direct relevance to physical representation. Our aim is to model the evolution of the epigenetic states of cells interacting with an environment by using QL-representation.[3] By theory of open quantum systems, dynamics of cell's epigenetic state is approximately described by *quantum master equation*, the Gorini-Kossakowski-Sudarshan-Lindblad (GKSL) equation, e.g., Ohya and Volovich (2011); often called simply "Lindblad equation". By our model in the process of evolution the epigenetic state becomes *entangled* with the environment. Hence, we shall consider the cell-trace dynamics of the dynamics of the compound system, cell unified with the environment. This trace dynamics is very complex and therefore one typically considers its Markovian approximation given by GKSL-equation.[4]

In our model at the beginning of interaction with an environment the (epigenetic) state of a cell is characterized by a *high degree of uncertainty about possible epigenetic changes* which can be generated via the coupling with an environment. This is a *pure quantum state*, superposition with respect to the basis states corresponding to epigenetic markers. The GKSL-equation describes the process of resolution of this state of uncertainty and approaching the complete matching with the environment. This process can be considered as *decoherence of cell's state* through interaction with an environment, cf. with *quantum Darwinism*, see Sect. 2. As the result, cell's epigenetic state loses its fundamentally quantum(-like) feature, superposition of a few alternatives, and the final situation[5] can be

[2] These biological systems can be macroscopic comparing with the space and time scales of quantum mechanics. We stress that a cell is a macroscopic system from the quantum-mechanical viewpoint.

[3] In the framework of cognitive science a similar problem was studied in our papers (Asano et al. 2010a, b, 2011a, b). See also, e.g., Khrennikov (2003, 2004, 2006), Busemeyer et al. (2006a, b, 2008), Cheon and Takahashi (2010), Conte et al. (2008, 2009), Takahashi and Cheon (2012) for other QL models in cognitive science and psychology.

[4] The same dynamical (GKSL-)equation describes not only epimutations (induced by the environment), but also the process of selection of these epimutations leading to forming of a stable phenotype. Our QL-model *unifies (neo-)Darwinism (Evolutionary Synthesis) and (neo-)Lamarkism*, but on the epigenetic level, cf. Jablonka and Raz (2009), see also Koonin and Wolf (2012) for unification of (neo-)Darwinism and (neo-)Lamarkism on the genetic level. This is a model of adaptive epimutations and "natural selection" in a single living cell. Such kind of natural selection is performed not on the cellular, but on the molecular level.

[5] Mathematically it is characterized by approaching a steady state solution of the quantum master equation.

described by classical probability theory, see Asano et al. (2010a, b, 2011a, b) for a similar cognitive model for decision making.

Our model is of a qualitative value, since we do not try to model epigenetic evolutions corresponding to concrete environments and cells. We proceed with phenomenological "Lindblad operators." Our aim is to describe mathematically general QL features of epigenetic evolution such as, e.g., contextuality (encoded in Lindblad operators), entanglement of epigenetic markers (it speeds up the evolution[6]), observer-dependence, non-Kolmogorovness (impossibility to embed the evolutionary pathways in a single probability space), evolutionary leaps combined with continuous evolution. We understand well that to find the concrete operators and the time scales of stabilization to steady states for special cellular populations is a problem of huge complexity. We point that a method of reconstruction of operators from experimental statistical data was approbated in Basieva et al. (2011), Asano et al. (2012a, b) for QL-modeling of functioning of the *lac*-operon in *E. coli* bacteria. Generalization to epigenetics is a subject of our further studies. One of the problems is the absence of experimental statistical data for a sufficiently reach class of experimental contexts for cell populations of the same type, cf. Inada et al. (1996).

Brief introduction to quantum formalism is presented in Appendix, Sect. 9.1.

Can one resort to quantum mechanics or analogies drawn from quantum mechanics, in the study of any biological phenomenon?

The aim of this section is to present concrete motivations for usage of the mathematical formalism of QM for the description of biological phenomena. On one hand, we shall show that recent studies in quantum foundations provide a totally new viewpoint to the quantum measurement problem; in particular, it can be possible to proceed without usage wave function collapse (collapse of the state vector). The latter (collapse) would be difficult to accept in the macroscopic biological framework. Thus a rather common claim that quantum(-like) models cannot be used in biology, since biosystems are macroscopic, is not justified. On the other hand, we discuss biological literature which reflects some special features of biological phenomena which match well with features of quantum phenomena. Although such biological publications do not rely directly on QM, they can serve to justify the application of the quantum formalism in biology, as a formalism representing some fundamental features of biological measurements.

Of course, the question in the title of the present section is very complicated. And we do not hope to convince everybody that the present situations in quantum foundations and in biology imply the answer "yes". However, this section can serve as the starting point of a possible debate on this question.

Quantum Darwinism

This is a physical theory explaining the emergence of the classical world from the quantum world as the result of the process of Darwinian-like natural selection in the space of quantum states. A stable pointer state is selected from many possible quantum states, see Kohout and Zurek (2006), Zurek (2009). Quantum Darwinism explains how the classical world emerges from the quantum world. It can be considered as a possible solution of the quantum measurement problem, one of the main interpretational problem for quantum theory. The essence of this problem is incompatibility of the continuous dynamics of an isolated quantum system which is mathematically described by the Schrödinger equation and the discontinuous "quantum jumps" due to measurements which are described by the von Neumann projection postulate. The pointer-state is approached via a *selection process* imposed on the quantum system through its continuous interactions with the environment. Such a selection process can be considered as *decoherence process* or classical representation of a quantum system with respect to a special basis, the basis of pointer states.

The quantum Darwinian interpretation of the process of measurement is extremely important for justification of our approach and more generally applications of the mathematical formalism of QM to macroscopic systems, physical as well as biological. It essentially demystifies the process of measurement; in particular, such an intriguing, but at the same ambiguous notion as state's collapse is completely eliminated from the description of the process. As a consequence, a continuous process of stabilization to a specially selected stable state takes the place of the temporal singularity of collapse. In our paper, we use precisely quantum Darwinian picture to present a QL model of the epigenetic evolution. Thus first Kohout and Zurek (2006), Zurek (2009) used a biological analogy (with Darwinian natural selection) to create an adequate model of quantum measurement. Then we, in fact,[7] used quantum Darwinism as an interpretation of QM which can be serve for elaboration of an adequate QL model of the biological evolution.

[6] Otherwise, i.e., by using selective (purely Darwinian) trials, it would be too slow to be finalized in one cellular generation.

[7] Unfortunately, we were totally unaware of the quantum Darwinian interpretation.

The whole is more than the sum of its parts

One of the main distinguishing features of the quantum description of composite systems is that in general the state of a compound system cannot be reconstructed from the states of its subsystems. This is the essence of quantum entanglement. Even if one knows dynamics of all subsystems the dynamics of the compound system is still unknown. Precisely, as Aristotle taught us, *the whole is more than the sum of its parts*. The later reference to Aristotle is the starting point of the paper of Huang (2012) in which the author pointed out that such a wholistic picture of cellular biological phenomena (appearance and interaction of diverse populations of cells in an organism) is not provided neither by molecular biology nor evolutionary biology and ecology. In particular, phenotypes cannot be reduced to genes and pathways. Other theories are demanded to describe properly complex biological systems. Huang (2012) did not appeal directly to QM. However, this study supports essentially usage of the quantum formalism (based on tensor products) to describe complex biological systems.

Contextuality and observer-dependence of quantum and biological phenomena

Contextuality is one of the most fundamental features of quantum phenomena. One of the fathers of QM, Niels Bohr, emphasized the role of context in quantum measurement, he taught us that the whole experimental arrangement has to to be taken into account. Contextuality of QM was formalized in Kochen-Specker theorem and recently it was confirmed experimentally in the framework of neutral interferometry (Bartosik et al. 2009). Quantum phenomena are irreducibly observer-dependent. The contributions of a measurement device and a quantum system to the result of quantum measurement cannot be separated. By the Copenhagen interpretation QM describes not *physical reality* as it is (ontic phenomena), but the results of measurements performed by *macroscopic measurement devices*. The presence of an observer separated from a system is the basis assumption of QM (except the many worlds interpretation). There is no observer-independent and noncontextual quantum reality.

Contextuality of biological phenomena and its observer-dependency were reported in many articles, see Banerji (2009) for a detailed review, a discussion and analysis of consequences for biocomplexity theory. The conclusion of this author about biological reality practically coincides with the Copenhagen viewpoint on quantum reality. There is no such a thing as observer-independent and noncontextual biological reality. This is really surprising since this work does not refer to quantum theory at all. Although Banerji (2009) derived a kind of bio-observable uncertainty relation, its derivation was performed in the classical framework; similar to uncertainty between time and energy representations in classical signal theory. Thus the intrinsic development of foundations of biology (biocomplexity theory) leads to the same viewpoint on reality as development of quantum foundations.

We also remark that contextuality of psychological and more generally cognitive phenomena was one of the main motivation for application of the quantum formalism in psychology and cognitive science (Busemeyer et al. 2008; Khrennikov 2010).

Dynamics of cell's epigenetic state in the process of interaction with an environment

In this section we shall present a formal description of dynamics of the epigenetic states of cells interacting with an environment. In Sect. 4 this scheme will be concreted. Denote the space of QL-states of cell's epigenome by the symbol H_{epi}. These states represent statistical information about possible observations on phenotype's changes. The space of QL-states of the environment is denoted by H_{env}. Since, finally, we shall be interested only in the dynamics of cell's epigenetic state, the degrees of freedom of the environment will be excluded from the direct consideration by tracing with respect to the space H_{env}. The state space of the compound system is the tensor product $H_{\text{epi}} \otimes H_{\text{env}}$.

Normalized vectors from a Hilbert state space are called *pure states*. However, some ensembles of systems (physical or biological) cannot be represented by pure states. They are described as *statistical mixtures of pure states* and mathematically represented by *density operators*, see Sect. "Appendix". In general the QL state of epigenomes of a biological population is represented by a density operator, ρ_{epi}.

Our proposal is to use the machinery of the theory of *open quantum systems* and to describe dynamics of the epigenetic QL-state by using the quantum master equation (the GKSL-equation). This equation can be used to describe transitions from states of uncertainty given by QL-superpositions to classical probability distributions. In the quantum Markovian approximation the dynamics of the state of a system interacting with an environment is described by the GKSL-equation[8]:

$$\gamma \frac{d\rho_{\text{epi}}}{dt}(t) = -i[\mathcal{H}, \rho_{\text{epi}}(t)] + \mathcal{W}\rho_{\text{epi}}(t), \rho_{\text{epi}}(0) = \rho^0_{\text{epi}}, \tag{1}$$

[8] Applicability of this equation to the description of dynamics of epigenome is discussed in Appendix, Sect. 9.2.

where $\mathcal{H}$ is a Hermitian operator determining the internal dynamics of epimutational changes in cells which are isolated from the environmental pressure ("cell's Hamiltonian") and the linear operator $\mathcal{W}$ describes the environmental pressure. Opposite to $\mathcal{H}$, in general the operator $\mathcal{W}$ has a complex mathematical structure. It has such a form that starting with a density operator ρ_C^0 we shall get density operators at all instances of time. For a moment, the concrete structure of $\mathcal{W}$ is not important for us; see, e.g., Ohya and Volovich (2011) and Sect. 9.3 for mathematical details. Biologically this operator is determined by the properties of the environment, including the initial state of the environment. Here γ is the time scale constant, it determines the temporal dimension of the epigenetic evolution.

For a very general class of GKSL-equations, the environmental operator $\mathcal{W}$ drives (in the limit $t \to \infty$) the epigenetic state of an ensemble of cells, $\rho_{\text{epi}}(t)$, to the *steady solution*: $\rho_{\text{epi}}(t) \to \rho_{\text{epi;st}}$. Typically the uncertainty (in the form of superposition) is eliminated from the asymptotic state $\rho_{\text{epi;st}}$, compare with quantum Darwinism.

In our QL-model the steady state is considered as the result of the epigenetic evolution in the environment (mathematically represented by the operator $\mathcal{W}$). The limiting probability distribution $\rho_{\text{epi;st}}$ describes the probability distribution of epimutations which took place in a cell population as a consequence of interaction with the environment. Internal uncertainty, to (epi)mutate or not mutate, was resolved and a stable *phenotype* was created.[9] An important feature of the GKSL-dynamics is that it can be represented as a combination of continuous drifts and and jumps. The later dynamical component can model *evolutionary jumps*, see Appendix, Sect. 9.3.

Dynamics of a single epimutation of the chromatin-marking type

In this section as well as in Sect. 5 we restrict consideration to epimutation of the chromatin-marking type. This special case has illustrative advantages: epimutations of this type can be directly coupled with physical carriers, genes to which DNA methylations and histone modifications can be coupled. Hence, in the same way as in quantum mechanics we can couple a quantum(-like) state with the corresponding physical system, the gene. Of course, our approach is applicable to all four types of epimutations which were discussed in Jablonka and Raz (2009), see introduction. We shall consider the general situation in Sect. 6.

Consider the concrete gene g in cell's genome. Suppose that this cell interacts with an environment such that some type of epigenetic mutation, say μ, in g can happen. This epimutation changes the level of expression of g.

By ignoring the presence of other genes and corresponding gene expressions we can model the μ-mutation by considering simply the two dimensional state space H_{epi} (qubit space). States of no mutation and mutation are represented by two orthogonal vectors $|0\rangle$ and $|1\rangle$. Hence, a (pure) QL-state can be represented as superposition

$$|\psi_{\text{epi}}\rangle = c_0|0\rangle + c_1|1\rangle, \tag{2}$$

where $c_0, c_1 \in \mathbf{C}, |c_0|^2 + |c_1|^2 = 1$.

Thus here *the basis of Hilbert state space is given by vectors representing possible epigenetic changes of the fixed type* μ.

As was remarked, the quantum master equation does not respect pure states, so sooner or later superposition (2) will be transferred into the statistical mixture given by a density matrix. We remark, see Sect. "Appendix", that in terms of density matrices the pure state (2) can written as

$$\rho_{\text{epi}} = \begin{pmatrix} |c_0|^2 & c_0\bar{c_1} \\ \bar{c_0}c_1 & |c_1|^2 \end{pmatrix}. \tag{3}$$

Thus nontrivial superposition is characterized by the presence of the nonzero off-diagonal terms. We remark that the absolute value of the off-diagonal terms is maximal and equals 1/2 for the uniform superposition $|\psi_{\text{epi}}\rangle = \frac{1}{\sqrt{2}}(|0\rangle + |1\rangle)$, representing the maximal uncertainty. The dynamics (1) suppresses the off-diagonal terms and, finally, a diagonal density matrix (steady state) arises,

$$\rho_{\text{st}} = \begin{pmatrix} \rho_{00;\text{st}} & 0 \\ 0 & \rho_{11;\text{st}} \end{pmatrix}. \tag{4}$$

Its elements $\rho_{00;\text{st}}$ and $\rho_{11;\text{st}}$ give probabilities of the events: no μ-epimutation and μ-epimutation. Thus in a large population of cells, say M cells, $M >> 1$, the number of, e.g., cells with mutation is given (approximately) by $N_m \approx \rho_{11;\text{st}} M$. The limiting QL-state (represented by the diagonal matrix (4) obtained the stability with respect to the influence of this (concrete) environment. We remark that mathematically a population needs infinite time to stabilize completely to the steady state. Therefore in reality one can expect fluctuations (of decreasing amplitude) on a finite interval of time.

We remark that under a special interrelation between operators $\mathcal{H}$ and $\mathcal{W}$ the stabilization is achieved with the state ρ_{st} such that $\rho_{11;\text{st}} >> \rho_{00;\text{st}}$ (or even $\rho_{11;\text{st}} = 1$,

[9] We, finally, remark that under natural restrictions a selection operator produces the same steady state for all possible initial states. Therefore the variety of internal epigenetic states produced the Schrödinger's dynamics before the environment started to play a crucial role is transformed in the same steady state, the fixed phenotype, see Appendix, Sect. 9.4 for mathematical details.

$\rho_{00;st} = 0$, Sect. 9.4.) In such a case the epimutation μ spreads to practically the whole population and, moreover, it will be inherited. Thus the quantum master equation is sufficiently general to represent (on the epigenetic level) the regime which is similar to one represented by *Fisher's equation* that was used to describe the spreading of biological populations. The main distinguishing feature of the epigenetic situation is that the epimutation spreads in a single generation of cells and then it is inherited by the next generation.

"Entanglement" of epimutations in genome

We start with construction of QL-representation of the information state of epigenome expressing CEI of the chromatin-marking type. Consider a cell with genome consisting of m genes $g_1, \ldots, g_m$. Let assign to each gene g all its possible epimutations (of the chromatin-marking type); we simply enumerate them by numbers[10]: $j_g = 1, \ldots, k_g$.

The state of all potential epimutations in the gene g is represented as superposition

$$|\psi_g\rangle = \sum_j c_{g;j}|j_g\rangle, \tag{5}$$

where $\sum_j |c_{g;j}|^2 = 1$.

What is the meaning of this superposition from the biological viewpoint? Can a gene really be in superposition of a few different epimutations?

Although our model is operational and in principle we are not interested in such questions, we make a comment to clarify the coupling of operational and biological descriptions of this situation. A cell by itself "knows its epigenome" at each instant of time; so it is well aware which epimutations took place up to this instant of time. However, biologist performing an experiment with cells does not know the situation inside an individual cell in such details. And superposition is related to uncertainty of *observer's information*.

If epimutations in different genes are independent from each other, then the QL-state of cell's epigenome is represented as the tensor product of states $|\psi_g\rangle$:

$$|\psi_{\text{epi}}\rangle = |\psi_{g_1}\rangle \otimes \cdots \otimes |\psi_{g_m}\rangle. \tag{6}$$

However, in living cells, most of the genes/proteins are correlated somehow forming a big network system. So one epimutation affects other genes usually. Hence, the assumption of independent epimutations is nonbiological. Therefore we have to consider more general states describing the consistent epimutations of all genes in the genome of a cell. These are so called *entangled states* which are widely used in quantum information theory:

$$|\psi_{\text{epi}}\rangle = \sum_{j_1 \ldots j_m} c_{j_1 \ldots j_m} |j_{g_1} \ldots j_{g_m}\rangle, \tag{7}$$

where $|j_{g_1} \ldots j_{g_m}\rangle$ is just the short notation for the tensor product of states of superpositions in various genes, $|j_{g_1} \ldots j_{g_m}\rangle \equiv |j_{g_1}\rangle \otimes \cdots \otimes |j_{g_m}\rangle$ and the sum of all squared coefficients is equal to 1.

We remark that the notion of *entanglement* is in the very heart of quantum mechanics. However, although it is widely used in quantum information, the understanding of the physical essence of entanglement is far from to be complete, see, e.g., Accardi et al. (2009) for debates. Nevertheless, in quantum community there is the complete consensus that entanglement implies *correlations*—in our epigenetic modeling these are correlations between epimutations in different genes.

The form of the tensor space representation (7) of potential epimutations in cell's genome implies that epimutation in one gene imply the consistent epimutations in other genes. If the state (7) is not factorized, then by acting, i.e., through change in the environment, to one gene, say g_1, and inducing, see Sect. 4, some epimutation in it, we can induce consistent epimutations in other genes. Entanglement is the main source of the speedup of quantum computers. However, we do not advertise a rather common viewpoint that biological quantum computing plays some role in genetics and brain's functioning. Quantum algorithms are based on *unitary dynamics* described by the Schrödinger's equation. In our opinion such dynamics cannot survive on the biological scales of space, time and temperature. In our QL-model a cell is an open QL-system; its dynamics is described by the quantum master equation; it is nonunitary. In our QL-model we also explore entanglement between various epigenetic markers to speed up the epigenetic evolution in a living cell. Otherwise, i.e., by using purely epi-Darwinian approach, we would be not able to explain the high speed of the epigenetic evolution. Evolution in the case of epimutations in a large number genes as the reaction to the environment would be too slow if epimutations inducing new levels of gene expressions would randomly and independently generated and then selected.

Let an environment acts to genes g_1, …, g_m. Suppose that, for, e.g. g_1, as an individual gene, some epimutation, say M_{g1} can be useful in this environment. However, this epimutation may disturb functioning of other genes in a negative way. Hence, epimutations $M_{g_1}, \ldots, M_{g_n}$ induced by the environment have to be consistent. How can they

[10] Depending on biological context, it is always possible to select a few epimutations of the main importance. Hence, the number k_g need not be very large. We state again that our model is operational. It need not be very detailed.

become consistent? Either via iterations, first the state of epimutations $(M_{g_1}, \ldots, M_{g_n})$ is created, but the cell "feels" disagreement between levels of genes expressions corresponding to these epimutations. New epimutations are induced by this inconsistency and so on. This process is similar to Darwinian natural selection and approaching of consistency in genes expressions would take too long period (for the time scale of one living cell). Our proposal is that dynamics are entangled and at one step all genes epimutate consistently. The state again that the main difference from quantum computing is using nonunitary evolution described by the quantum master equation, instead of the unitary (Schrödinger) evolution. Hence, we use entanglement, but without unitary evolution.

Our model based on QL-control by the environment of epigenetic evolution in combination with entanglement between epimutations in different genes matches very well with the epigenetic canalization model discussed by Sollars et al. (2003).[11]

In Sect. 3 we pointed that, although under the environment driven QL-dynamics superposition will be finally resolved and a steady state solution will be approached, the complete stabilization is possible only in the limit $t \to \infty$. Hence, for any finite interval of time, the total stabilization is impossible. This feature of our QL-model also matches well with observation of Sollars et al. (2003).[12]

[11] "In light of our data, we propose a refinement of the 1942 evolutionary 'canalization' model of Waddington to an 'epigenetic canalization' model. In the canalization model Waddington (1942), environmental stress induces a novel phenotype, and selection of existing genetic variation in subsequent generations allows fixation of the novel phenotype. According to Waddington, "by such a series of steps, then, it is possible that an adaptive response can be fixed without waiting for the occurrence of a mutation which, in the original genetic background, mimics the response well enough to enjoy a selective advantage" Waddington (1942). In our epigenetic canalization model, we propose that an environmental stress causes a reduction in Hsp90 levels and, through some unknown interaction with TrxG proteins, induces an immediate 'chromatin effect'. Our model allows an adaptive response to be 'fixed' epigenetically, and therefore obviates the need to wait for the selection of existing genetic variation. In other words, it predicts a more rapid evolutionary process than is required for selection of existing genetic variation."

[12] "Because of the inherent instability of epigenetic inheritance, fixation of an epigenetically-determined phenotype is probably less stable than fixation through a genetic selection mechanism. Waddington, for example, was unable to reduce the frequency of the crossveinless phenotype in negative selection experiments once the phenotype was fixed (Waddington 1953). In contrast, after only two or three generations of negative selection, we observed a complete reversion to wild-type frequency of ectopic outgrowth in our sensitized iso-KrIf-1 strain in the geldanamycin selection experiment (data not shown). Similarly, epigenetic traits such as color variegation or cold adaptation in plants are unstably inherited (Bender 2002; Kohler and Grossniklaus 2002). Therefore, a combination of both epigenetic and genetic mechanisms is probably required to explain the rapid changes in body plans that are observed in the fossil record (Gould and Eldredge 1993).

Adaptive dynamics in space of epigenetic markers

We now proceed by operating with epigenetic markers as information quantities, i.e., without to couple each of them with a special form of cellular material. We enumerate all possible epigenetic markers which are involved in the process of evolution under the pressure of some fixed environment, $j = 1, \ldots, n$. Each marker can be quantified by the classical random variable $\xi_j = 1$, if this marker is created and then inherited, and $\xi_j = 0$, in the opposite case. These are observables which can be measured in experiments. The space of all classical states of the epigenome consists of vectors corresponding to fixation of the values of all epigenetic markers: $\alpha = (\alpha_1, \ldots, \alpha_n$, where $\alpha_j = 0,1$. This classical state space consists of 2^n points. This space is the basis of the classical information description of the process of epigenetic evolution. However, we move to the quantum information description by assuming that classical states can form superpositions. To match with the Dirac ket-vector notation which is used in quantum physics, we denote the classical state α as $|\alpha\rangle$. Then QL state space of (possible) epigenetic mutations, H_{epi}, consists of superpositions of the form

$$|\psi\rangle = \sum_{\alpha} c_\alpha |\alpha\rangle,$$

where $\sum_\alpha |c_\alpha|^2 = 1$. This is the complex Hilbert space of the dimension 2^n. Now we repeat our previous considerations, see Sects. 4, 5, for epimutations of the chromatin-marking type. The QL adaptive dynamics described by the quantum master equation can be considered as mixture of neo-Darwinian, neo-Lamarckian, and Wrightean evolutions. This cocktail of stochasticity and determinism is consistently represented in the QL operational framework. The final steady state gives to experimenters the classical probability distribution of the inherited epigenetic markers.

As we have seen in Sect. 5, entanglement may play an important role in the speedup of the epigenetic evolution. Since epimutations of the chromatin-marking type can be coupled to physical carriers, it was easy to use the standard notion of entanglement (as entanglement of systems) in the epigenetic framework. In general epigenetic markers are merely information structures in a cell such as, e.g., self-sustaining regulatory loops. However, we are lucky, since recently a new general viewpoint on entanglement was elaborated in quantum information community. Entanglement can be considered not from the system viewpoint, but from the observer viewpoint. One considers a family of algebras of observables, say $\{\mathcal{A}_i\}$, on the total state space, in our case on H_{epi}. Under some restrictions on these algebras the state space can be represented as the tensor product of subspaces corresponding to these algebras. In our case we

consider algebras of observables corresponding to different epigenetic markers, corresponding subspaces are two dimensional qubit spaces, $H_{\text{epi}} = \otimes_{j=1}^{n} H_{j;\text{qubit}}$. Now we can use the notion of entanglement corresponding to this tensor product decomposition of the state space and repeat the speedup argument which was discussed in detail in Sect. 5.

Quantum operational unification of Darwinism, Lamarckism, and Wrightinism

Jablonka and Raz (2009) suggested that the different mechanisms of epigenetic inheritance should be understood and studied within a shared evolutionary framework that incorporates the developmental construction of heredity and that acknowledges the Lamarckian aspects of heredity and evolution. They criticized the purely neo-Darwinian approach to cellular evolution. Recently neo-Darwinism was criticized not only in the epigenetic framework, but even in the traditional framework of the genetic evolution. The present situation can be described as the following (Koonin and Wolf 2012):

> More generally, recent empirical and theoretical studies of Diverse processes of stochastic and deterministic change in genomes make it clear that evolution is not limited to the basic Darwinian scheme of random variation that is subject to selection. Evolution can be more adequately depicted as a continuum of processes from completely random ones,under the Wrightean modality defined by random variation and random fixation of changes via genetic drift; to the Darwinian modality with random changes fixed by the deterministic process of selection; to the Lamarckian mode in which both variation and fixation are deterministic.

All these processes of deterministic and stochastic changes (in the present paper we consider changes in epigenomes) are operationally encoded in quantum master equation. From our viewpoint it is very difficult (if possible at all) to distinguish contributions of the Darwinian, Lamarckian, and Wrightean components in cellular epigenetic evolution. Therefore it is natural to unify all them in one QL dynamics. Mathematically this dynamics is described by linear differential equation in the space of matrices; so this is *deterministic dynamics*. However, observational predictions based on this dynamics are *purely random*. As was already emphasized, the quantum master equation describes both random epimutations and selection under the pressure of an environment. Such a selection is adaptive. However, adaptivity is nondeterministic.

Concluding remarks

We explored the similarities between biological and quantum physical processes, such as, e.g., contextuality, non-Kolmogorovness, observer-dependence, nonreducibility of the state of a compound system to the states of its subsystems (entanglement), superposition of potentialities, environment driven evolution, biological and quantum Darwinisms, to model the epigenetic evolution in the quantum(-like) framework.

The basis states of the QL state space correspond to all possible epigenetic markers. Thus usage of QL representation provides a possibility to unify in one model the evolutions of all possible types of epigenetic markers having in general very different biological nature. The mathematical formalism of theory of open quantum systems describes the process of selection of special states (representing fixed phenotypes) from huge ensemble of potentially possible. Quantum superposition provides an adequate mathematical representation of uncertainty in possible results of evolution.[13] Entanglement represents the consistent evolution of all epigenetic markers. It is crucial to speed up the processes of evolution to finalize it in one cellular generation. Quantum master dynamics can be decomposed in combination of continuous shifts and discontinuous jumps. The continuous counterpart of the dynamics represents the Darwinian-type continuous evolution (on the molecular level in a cell). And quantum jumps can be used to describe mathematically evolutionary jumps (see appendix, Sect. 9.3, for mathematical details.). Further development of this approach will be directed to elaboration of techniques to reconstruct QL dynamical operators from statistical experimental data, cf. Asano et al. (2012b).

However, a more detailed experimental studies of epigenetic statistics are needed – in the form of some quantity

[13] We believe, the open system dynamics such that a pure state changes to a statistically mixed state is useful for descriptions of various phenomena in physics, biology, psychology and social science. How one should interpret a pure state in the model and distinguish it from a mixed state is a key point for understanding of our model. Any density matrix gives a statistical property of an event system, namely, it gives a representation of uncertainty behind a system. And we have two different senses seeing uncertainty. One is a sense to statistical uncertainty which can be identified with diversity. This is recognition that various existences have various functionalities different each other. It is an uncertainty given for a population: each of existences can be specified by each of functionalities. Another is the sense of "deep uncertainty" which is encoded in a pure state in the form of superposition. We interpret it as uncertainty given for various functionalities which are hold in "one existence" as "possibilities". In this sense, we cannot explain its existence by a specific functionality, rather, this existence can be specified by "diversity" itself. An open system dynamics may be interpreted as a description of transition between these two senses to uncertainty for a phenomenon.

specifying the correlation between gene expression and methylation and histone modification accumulated in a cell (the chromatin-marking CEI) or data on correlations for other types of CEI, e.g., the RNA-mediated CEI. We point to the following experimental complication. Typically in epigenetic studies experimenters expose some cellular population on the pressure of one fixed type of environmental factors, e.g. Sollars et al. (2003), fixed environmental context. However, even very good statistical sampling for just one context is not sufficient to construct QL operational representation. One has to collect statistical data for a few (at least two) incompatible environmental contexts. Here incompatibility means that contexts' influences on cells are not independent; exposing a cellular population on the pressure of two incompatible contexts would destroy intrinsic effects of each of them.[14] We hope that our QL model may stimulate such experimental studies in epigenetics.

Acknowledgments This paper was written under the support of the grant Quantum Bio-Informatics of Tokyo University of Science and the grant Mathematical Modeling of Complex Information Systems of Linnaeus University. Intensive discussions related to the last version of the paper took place during the visit of one of coauthors (A. Kh.) to Tokyo University of Science, February–March 2013. He would like to thank N. Watanabe for hospitality.

Appendix

Mathematical formalism of quantum mechanics: brief introduction

The mathematical formalism of quantum mechanics describes states of systems, observables and dynamics of states and observables. We assume that the reader knows about Hilbert spaces: linear complex spaces endowed with Hermitian, positively defined and nondegenerate forms—scalar products, the pair of vectors (ϕ, ψ) is mapped into the complex number denoted as $\langle\phi|\psi\rangle$ (Dirac's notation which is common in quantum information theory).

We are interested in complex vectors normalized by one, i.e., $\psi \in H$ (H being a Hilbert space) such that:

$$\|\psi\|^2 = \langle\psi|\psi\rangle = 1. \tag{8}$$

Such vectors encode so called *pure states* of quantum systems. The normalization by one is crucial for the probabilistic interpretation of pure states. Observables (e.g., the energy-observable or the position observable) are encoded by Hermitian operators.

The dynamics of pure states of isolated systems are described by the Schrödinger differential equation:

$$i\frac{d\psi}{dt}(t) = \mathcal{H}\psi(t), \psi(0) = \psi_0; \tag{9}$$

where the operator $\mathcal{H}$ is the generator of evolution, also called the 'Hamiltonian', the operator of energy.

We remark that each pure state ψ determines a Hermitian operator, the projector onto this state; $\rho \equiv |\psi\rangle\langle\psi|$ (the last symbol is simply the Dirac notation): $\rho\phi = \langle\phi|\psi\rangle\psi$. We recall the basic properties of ρ_ψ:

(a) it is positively defined, i.e., $\langle\phi|\rho|\phi\rangle \geq 0$ for any ϕ ;
(b) it is Hermitian;
(c) its trace (the sum of diagonal elements) equals to one.

The Schrödinger dynamics for pure states (vectors) can be rewritten as the dynamics for corresponding operators:

$$i\frac{d\rho}{dt}(t) = [\mathcal{H}, \rho(t)], \rho(0) = \rho_0; \tag{10}$$

where $[\mathcal{H}, \rho] = \mathcal{H}\rho - \rho\mathcal{H}$ is the commutator of operators.

Consider now a statistical mixture (in the classical sense) of a few projection operators ρ_i corresponding to pure states ψ_i with weights $p_i \geq 0$, $\sum p_i = 1$,

$$\rho = p_1\rho_1 + \cdots + p_n\rho_n. \tag{11}$$

Each operator of this form satisfies conditions (a)–(c) and vice versa. Denote the class of all operators with properties (a)–(c) by the symbol $D(H)$. This is the space of states of quantum systems. Its elements (called density operators) can be interpreted as statistical mixtures of pure states. In general a density operator can be represented in the form (11) in many ways. There is one special expansion corresponding to eigenvectors of ρ. The density operator corresponding to a pure state can be characterized in the following way: in the basis of eigenvectors, its matrix has only one nonzero element (equal to one), i.e., up to a permutation of eigenvectors:

$$\rho = \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix}; \tag{12}$$

where the blocks of zeros have the corresponding sizes. However, this takes place only in the basis of eigenvectors.

Consider, for example, the two dimensional Hilbert space H and fix some orthonormal basis in this space, $\{e_1,e_2\}$; take a pure state:

$$\psi = xe_1 + ye_2; \tag{13}$$

[14] A delicate point is that the initial QL states of cellular populations exposed on the pressures of each of contexts have to be identical. Such a biological experiment (in fact, a group of experiments) would mimic measurement of incompatible quantum observables for the same quantum state. This is the key point of our operator-reconstruction method. Thus a single population has to be cultivated under some special conditions (in quantum terminology—the preparation procedure). Then this population has to be divided into a few subpopulations which will be exposed on the environmental pressure of incompatible contexts. Finally, we remark that, of course, this division into subpopulations has to satisfy the fair sampling assumption.

where $|x|^2 + |y|^2 = 1$. The density matrix ρ corresponding to this pure state has the form:

$$\rho = \begin{pmatrix} |x|^2 & x\bar{y} \\ \bar{x}y & |y|^2 \end{pmatrix}. \quad (14)$$

On applicability of quantum master equation to description of dynamics of epigenome

The quantum Markovian dynamics (1) is derived under the requirement that the reaction of the environment to a system is negligibly small. This requirement is natural in modeling of the epigenetic evolution. We can assume that a cell cannot change essentially the structure of the environment. Another condition for derivation of the Eq. (1) is factorization of the initial state of the compound system: the cell in the combination with the environment. In the cell biological terms it means that before being under influence of the environment the population of cells and the environment were not correlated, i.e., previous evolution of cells was independent from this concrete environment.

This special form of the open quantum dynamics is derived under the assumption of Markovness. In the cell biological framework this assumption has the following form. A cell does not "remember" about a long chain of interactions with the environment; its state at the instant of time $t + \delta t$, $\psi_C(t + \delta t)$, where δt is very small (mathematically infinitely small) interval, is determined by its state at the instant of time t, $\psi_C(t)$, and not by the family of its states in previous instants of time, i.e., $\{\psi_C(s)\colon s < t\}$. This is the most questionable assumption. We cannot exclude the presence of long term memory effects in the epigenome of a cell interacting with an environment. As well as in physics, we treat the Markovian condition as an approximate condition, i.e., long term memory effects may be present in a cell, but they are sufficiently weak to justify the approximation in use.

Evolutionary jumps as quantum-like jumps

This section is more complicated mathematically than other sections. In principle, the reader can jump directly to the summary at the end of this section. To enlighten the structure of the GKSL-evolution, we have to discuss the form of the "environment-operator" $\mathcal{W}$ in (1). In the finite dimensional case it can be represented as the finite sum:

$$\mathcal{W}\rho = \sum_j \left(L_j \rho L_j^* - \frac{1}{2}\{L_j^* L_j, \rho\} \right), \quad (15)$$

where L_j are traceless operators (Lindblad operators) and $\{A, B\} = AB + BA$ denotes the anticommutator of two operators. Consider the dynamics driven by a single Lindblad operator L (Rooney et al. 2012); we set the time scaling $\gamma = 1$:

$$\frac{d\rho}{dt} = L\rho L^* - \frac{1}{2}\{L^* L, \rho\}. \quad (16)$$

(We also set $\mathcal{H} = 0$. We know that the corresponding $\mathcal{H}$-dynamics, the Schrödinger dynamics, is reduced to fluctuations. Now we are interested only in the impact of the environment).

Hence, for a very small interval of time δt, the state is changed as

$$\rho \to \rho - \frac{1}{2}\{L^* L, \rho\}\delta t + L\rho L^* \delta t + o(\delta t). \quad (17)$$

This expression can be written as

$$\rho \to V_0 \rho V_0^* + V_1 \rho V_1^*, \quad (18)$$

where V_1 is simply equal to $L\sqrt{\delta t}$ and $V_0 = I - \frac{1}{2}L^* L \delta t$.

Now consider the actions of these operators to a pure state $|\psi\rangle$. We remind that the corresponding density operator is the operator of the orthogonal projection to the state $|\psi\rangle$: $\rho_\psi = |\psi\rangle\langle\psi|$. The pure state vector is always normalized.

We start with the V_1-action. We first remark that $L|\psi\rangle\langle\psi|L^* = |L\psi\rangle\langle L\psi|$. Hence, under the V_1 action the original state $|\psi\rangle$ jumps to the state

$$\frac{1}{\||L\psi\rangle\|}|L\psi\rangle \quad (19)$$

(where the denominator is just the normalization constant) with the probability

$$P_{\text{jump}} = \||L\psi\rangle\|^2 \delta t = \langle\psi|L^* L|\psi\rangle \delta t. \quad (20)$$

We regard this action as a *jump*, since for $\delta t \to 0$ the output state does not approach the input state $|\psi\rangle$. The probability of no jump is given by $P_{\text{no jump}} = 1 - \langle\psi|L^* L|\psi\rangle\delta t$. However, the absence of a jump does not imply that the input state is preserved. The branch without jump evolves as $|\psi\rangle \to |\psi\rangle - \frac{1}{2}L^* L|\psi\rangle\delta t$ with the corresponding normalization. We call this branch the *drift-type evolution*, since the output state approaches the input state for $\delta t \to 0$.

Thus, in the QL-model the environment driven evolution can be considered as the branching process with *"evolutionary jumps"* ("quantum jumps")[15] and *continuous drift-evolution*. We shall study this problem in more details in Sect. 9.4 in which the simplest model of epigenetic mutation in a single gene will be considered.

The sum in representation (15) of the environment operator can contain a few terms. The number of terms can be very large, it grows as $N^2 - 1$, where N is the dimension

[15] Quantum jump (leap) is a jump of an electron from one quantum state to another within an atom. Quantum jumps were invented by Einstein who postulate that electrons in atom can absorb and emit electromagnetic energy only by discrete portions which were later called photons. Thus, opposite to classical systems, electron's energy cannot change continuously.

of the state space. In our model the dimension of the epigenetic state space grows as $N = 2^n$, where n is the number of epigenetic markers under consideration, Sects. 5, 6. Therefore the QL evolution is a combination of in general about 2^n quantum jumps to the states determined by the operators L_j and the corresponding drifts. This is a branching process of the great complexity. The epigenetic state jumps in different directions (determined by the environmental operators L_j), outputs of jumps form superpositions; if no L_j-jump occurs, the state deforms continuously, and these continuous deformations are superposed with superposition of jumps. At the next step, the state directions of jumps and drifts are randomly changed...

Although in this paper we restricted our quantum-like model to the description of the epigenetic evolution, it is clear that it can be extended to describe evolution of biological organisms in general. (We restricted the model to epigenetics, since here we can use a closer analogy with quantum mechanics and mimic behavior of a cell by behavior of a quantum particle. In general we have to take into account cell's death (annihilation in quantum terminology) and birth (creation). Mathematically such a model is more complicated.) The discussion on evolutionary jumps (leaps, saltations, transiliencies) was started by Galton (1894) who attacked Darwin's theory of evolution through small, incremental steps, see Gillham (2001) for the detailed historical presentation. This debate between Galton's and Darwin's adherents was later transformed into the well known debate between adherents of Mendelianism and biometricians. Since at the beginning Mendel's theory was in visible contradiction with Darwin's continuous evolution, Bateson (1894), one of the most prominent aliens of Galton, actively used Mendel's laws as supporting evolution by jumps. (Later it became clear that Mendel's approach also can be used to explain continuous changes a la Darwin.)

In our QL model we cannot escape consideration of evolutionary jumps, see (19). It is impossible to reduce the dynamics (18) to just its first component, the continuous drift$\rho \to V_{0\rho}V_0^*$. The law of conservation of probability would be violated. On the other hand, as was already pointed out, the absence of a jump does not imply the stationarity of the state. It has to drift continuously and permanently. Thus by the QL model of evolution of *"open biological systems"* evolutionary jumps ("saltations") are indivisibly coupled with continuous dfrits. The first one can be considered as the Galtonian component and the second one as the Darwinian component of evolution. Thus in the mathematical framework of theory of open quantum(-like) systems Galtonism is much closer to Darwinism than it can be imagined. Moreover, in our model Lamarckism is realized as the combination of Galtonism and Darwinism. (We stress that we model cellular evolution.)

Evolution to the same pure state

As was already pointed out, it is possible to construct QL dynamics such that *starting with any state the trajectory will stabilize to the same pure state* (see Asano et al. 2010b for cognitive applications), e.g., $\rho_{\rm st} = \pi_1 = |1\rangle\langle 1|$. Even if at the beginning only a few cells were (epi)mutated, finally, cells will mutate with the unit probability. By moving from a mixed state, e.g., from the state given by the diagonal matrix with equal elements, to the pure state $|1\rangle$,

$$\rho_0 = \begin{pmatrix} 1/2 & 0 \\ 0 & 1/2 \end{pmatrix} \to \rho_{\rm st} == \begin{pmatrix} 0 & 0 \\ 0 & 1 \end{pmatrix}, \tag{21}$$

the von Neumann (quantum) *entropy decreases*. We emphasize the role of environment in such an evolution.

Consider now the environment operator $\mathcal{W}$ based on a single Lindblad operator, see (15), acting in the one qubit space and having the form

$$L = \sqrt{p}|1\rangle\langle 0|, \tag{22}$$

i.e., $L|\psi\rangle = \sqrt{p}\langle 0|\psi\rangle|1\rangle$. Thus during a small time interval δt, each state $|\psi\rangle$ can jump only towards the same state $|1\rangle$, see (19). For the pure state $|\psi\rangle = c_0|0\rangle + c_1|1\rangle$, the probability of such a jump is equal to $P_{\rm jump} = p|c_0|^2\delta t$.[16]

In such a process all evolutionary jumps are oriented towards mutation (the concrete mutation under consideration); cell's state cannot jump back by eliminating this mutation. However, as we know from section 20, the evolution is not reduced to just jumps. There is also the continuous evolutionary drift which changes the probability of a jump.

We now consider the evolutionary drift encoded by the operator $V_0 = I - \frac{1}{2}L^*L = I - \frac{p}{2}\pi_1$, where $\pi_1 = |1\rangle\langle 1|$. The later operator is simply the orthogonal projector onto the state of mutation $|1\rangle$. For a pure state, this dynamics can be mathematically represented as dynamics of a vector ("non-normalized state")

$$\frac{d|\phi\rangle}{dt}(t) = -\frac{p}{2}\pi_1|\phi\rangle(t). \tag{23}$$

The solution of this linear differential equation is given by $|\phi\rangle(t) = e^{-pt/2}c_{00}|0\rangle + c_{10}|1\rangle$ and the corresponding QL state evolves as

$$|\psi\rangle(t) = \frac{e^{-pt/2}c_{00}|0\rangle + c_{10}|1\rangle}{\sqrt{e^{-pt}|c_{00}|^2 + |c_{10}|^2}}. \tag{24}$$

[16] As in Sect. 9.3, we proceed under the assumption that the time scale constant γ was set as $\gamma = 1$. If we take γ into account, then the formula for the jump-probability takes the form: $P_{\rm jump} = p|c_0|^2\frac{\delta t}{\gamma}$. Hence, the smallness of the jump duration is relative to the time scale of evolution.

Thus the pure no-mutation state $|0\rangle$ is stationary with respect to the continuous evolutionary drift. This state can always jump to the mutation state $|1\rangle$ and the probability rate of evolutionary jumps is constant, p.

If the input (pure) state differs from the pure no-mutation state, then it drifts towards the pure mutation state as given by (24) and the probability rate of sudden jumps to the pure mutation state $|1\rangle$ decreases as

$$P_{\text{jump}} = \frac{e^{-pt} p |c_{00}|^2 \delta t}{e^{-pt}|c_{00}|^2 + |c_{10}|^2}.$$

Thus the evolution corresponding to the very simple environment operator given by (22) has the complex branching structure combining evolutionary jumps with continuous drifts.

The evolution driven by the operator (22) is widely used in quantum physics. For example, it describes the *spontaneous emission* of a photon by an electron in the excited state $|1\rangle$, as the result this electron jumps to the ground state $|0\rangle$. We remark that by the conventional interpretation of quantum mechanics quantum randomness is *irreducible*, i.e., it is in principle impossible to find causal sources leading to a quantum jump. Quantum jumps are considered as an intrinsic feature of nature; this feature is not refinable. One may speculate that this quantum ideology can be extended to evolutionary jumps in biological evolution.

From the presented analysis it is clear that the Lindblad operator L, (22), can be easily reconstructed from the experimental data. It depends on a single real parameter p, and this parameter is nothing else than the rate of transition probability from the state $|0\rangle$, no mutation, to the state $|1\rangle$, mutation.

References

Accardi L, Khrennikov A, Ohya M (2008) The problem of quantum-like representation in economy, cognitive science, and genetics. In: Accardi L, Freudenberg W, Ohya M (eds) Quantum bio-informatics II: from quantum information to bio-informatics. WSP, Singapore, pp 1–8

Accardi L, Adenier G, Fuchs C A, Jaeger G, Khrennikov A, Larsson J-A, Stenholm S (eds) (2009) Foundations of probability and physics-5. In: Ser. conference proceedings 1101, American Institute of Physics, Melville, NY

Asano M, Ohya M, Khrennikov A (2010a) Quantum-like model for decision making process in two players game. Found Phys 41(3):538–548

Asano M, Ohya M, Tanaka Y, Khrennikov A, Basieva I (2010b) On application of Gorini-Kossakowski-Sudarshan-Lindblad equation in cognitive psychology. Open Syst Inf Dyn 17:1–15

Asano M, Basieva I, Khrennikov A, Ohya M, Yamato I (2011a) A general quantum information model for the contextual dependent systems breaking the classical probability law. ArXiv:1105.4769

Asano M, Ohya M, Tanaka Yu, Khrennikov A, Basieva I (2011b) Dynamics of entropy in quantum-like model of decision making. J Theor Biol 281:56–64

Asano M, Basieva I, Khrennikov A, Ohya M, Tanaka Yu, Yamato I (2012a) Quantum-like model for the adaptive dynamics of the genetic regulation of E. coli's metabolism of glucose/lactose. Syst Synth Biol 6:1–7

Asano M, Basieva I, Khrennikov A, Ohya M, Tanaka Yu, Yamato I (2012b) Quantum-like model of diauxie in *Escherichia coli*: operational description of precultivation effect. J Theor Biol 314:130–137

Bartosik H, Klepp J, Schmitzer C, Sponar S, Cabello A, Rauch H, Hasegawa Y (2009) Experimental test of quantum contextuality in neutron interferometry. Phys Rev Lett 103:040403

Basieva I, Khrennikov A, Ohya M, Yamato I (2011) Quantum-like interference effect in gene expression: glucose–lactose destructive interference. Syst Synth Biol 5:59–68

Bateson W (1894) Materials for the study of variation treated with especial regard to discontinuity in the origin of species. Macmillan, London

Bender J (2002) Plant epigenetics. Curr Biol 12:R412–R414

Banerji A (2009) Existence of biological uncertainty principle implies that we can never find 'THE' measure for biological complexity. arxiv.org/pdf/0902.0490v2.pdf

Busemeyer JR, Wang Z, Townsend JT (2006a) Quantum dynamics of human decision making. J Math Psychol 50:220–241

Busemeyer JR, Matthews M, Wang Z (2006b) A quantum information processing explanation of disjunction effects. In: Sun R, Myake N (eds) The 29th annual conference of the cognitive science society and the 5th international conference of cognitive science. Erlbaum, Mahwah, NJ, pp 131–135

Busemeyer JR, Santuy E, Lambert-Mogiliansky A (2008) Comparison of Markov and quantum models of decision making. In: Bruza P, Lawless W, van Rijsbergen K, Sofge DA, Coeke B, Clark S (eds) Quantum interaction-2. College Publications, London, pp 68–74

Cheon T and Takahashi T (2010) Interference and inequality in quantum decision theory. Phys Lett A 375:100–104

Conte E, Khrennikov A, Todarello O, Federici A, Zbilut JP (2008) A preliminary experimental verification on the possibility of Bell inequality violation in mental states. Neuroquantology 6:214–221

Conte E, Khrennikov A, Todarello O, Federici A, Zbilut JP (2009) Mental states follow quantum mechanics during perception and cognition of ambiguous figures. Open Syst Inf Dyn 16:1–17

Galton F (1894) Discontinuity in evolution. Mind (n.s.) 3:362–372

Gillham NW (2001) Evolution by jumps: Francis Galton and William Bateson and the mechanism of evolutionary change. Genetics 159:1383–1392

Gould SJ, Eldredge N (1993) Punctuated equilibrium comes of age. Nature 366:223–227

Inada T, Kimata K, Aiba H (1996) Mechanism responsible for glucose–lactose diauxie in *Escherichia coli* challenge to the cAMP model. Genes Cells 1:293–301

Huang S (2012) The molecular and mathematical basis of Waddington's epigenetic landscape: a framework for post-Darwinian biology? Bioessays 34:149–157

Jablonka E, Raz G (2009) Transgenerational epigenetic inheritance: prevalence, mechanisms, and implications for the study of heredity and evolution. Q Rev Biol 84:131–176

Khrennikov A (2003) Quantum-like formalism for cognitive measurements. Biosystems 70:211–233

Khrennikov A (2004) On quantum-like probabilistic structure of mental information. Open Syst Inf Dyn 11(3):267–275

Khrennikov A (2006) Quantum-like brain: interference of minds. BioSystems 84:225–241

Khrennikov A (2010) Ubiquitous quantum structure: from psychology to finance. Springer, Berlin

Kohler C, Grossniklaus U (2002) Epigenetics: the flowers that come in from the cold. Curr Biol 12:129–131

Kohout RB, Zurek WH (2006) Quantum Darwinism: entanglement, branches, and the emergent classicality of redundantly stored quantum information. Phys Rev A 73:062310

Koonin EV, Wolf YI (2012) Evolution of microbes and viruses: a paradigm shift in evolutionary biology? Front Cell Infect Microb 2:art. number 119

McFadden JJ, Al-Khalili JV (1999) A quantum mechanical model of adaptive mutation. Biosystems 50:203–211

McFadden J (2000) Quantum evolution. Harper Collins, London

Ogryzko VV (1997) A quantum-theoretical approach to the phenomenon of directed mutations in bacteria (hypothesis). Biosystems 43:83–95

Ogryzko VV (2008) On two quantum approaches to adaptive mutations in bacteria. arxiv.org/ftp/arxiv/papers/0805/0805.4316.pdf

Ohya M (2008) Adaptive dynamics and its applications to chaos and NPC problem. QP-PQ:Quantum Prob. White Noise Anal 21:186–216

Ohya M, Volovich I (2011) Mathematical foundations of quantum information and computation and its applications to nano- and bio-systems. Springer, Heidelberg

Rooney P, Bloch A, Rangan Ch (2012) Decoherence control and purification of two-dimensional quantum density matrices under Lindblad dissipation. arxiv.org/abs/1201.0399

Russell PJ (2010) "iGenetics". Pearson Benjamin Cummings, San Francisco

Sollars V, Lu X, Xiao L, Wang X, Garfinkel MD, Ruden DM (2003) Evidence for an epigenetic mechanism by which Hsp90 acts as a capacitor for morphological evolution. Nat Genet 33:70–74

Takahashi T, Cheon T (2012) A nonlinear neural population coding theory of quantum cognition and decision making. World J Neurosci 2:183–186

Waddington CH (1942) Canalization of development and the inheritance of acquired characters. Nature 150:563–565

Waddington CH (1953) Genetic assimilation of an acquired character. Evolution 7:118–126

Wanke D, Kilian J, Bloss U, Mangelsen E, Supper J, Harter K, Berendzen KW (2009) Integrating biological perspectives: a quantum leap for microarray expression analysis. Quantum bioinformatics. In: Accardi L, Freudenberg W, Ohya M (eds) quantum bio-informatics II: from quantum information to bio-informatics. WSP, Singapore, pp 327–336

Zurek WH (2009) Quantum Darwinism. Nat Phys 5:181–188