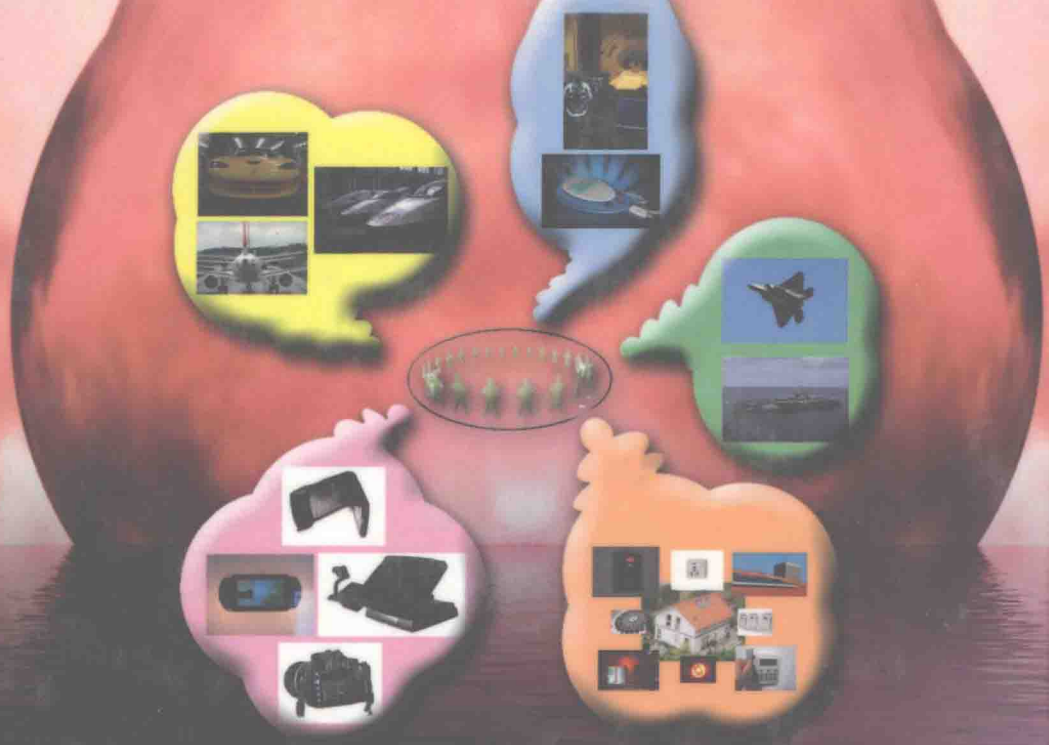

# Computer Science Research and the Internet

Jaclyn E. Morris
Editor

Computer Science, Technology and Applications

NOVA

# COMPUTER SCIENCE RESEARCH AND THE INTERNET

For permission to use material from this book please contact us:
Telephone 631-231-7269; Fax 631-231-8175
Web Site: http://www.novapublishers.com



**LIBRARY OF CONGRESS CATALOGING-IN-PUBLICATION DATA**

Computer science research and the internet / editors, Jaclyn E. Morris.
p. cm.
Includes index.
ISBN 978-1-61728-730-5 (hardcover)
1. Computer science--Research. 2. Internet. I. Morris, Jaclyn E.
QA76.27.C6735 2010
004--dc22

2010025442

*Published by Nova Science Publishers, Inc. † New York*

# COMPUTER SCIENCE, TECHNOLOGY AND APPLICATIONS

Additional books in this series can be found on Nova's website under the Series tab.

Additional E-books in this series can be found on Nova's website under the E-book tab.

COMPUTER SCIENCE, TECHNOLOGY AND APPLICATIONS

# COMPUTER SCIENCE RESEARCH AND THE INTERNET

JACLYN E. MORRIS
EDITOR


Nova Science Publishers, Inc.
*New York*

# PREFACE

This book presents leading-edge research from across the globe in the field of computer science research, technology, the internet and applications. Each contribution has been carefully selected for inclusion based on the significance of the research to this fast-moving and diverse field. Some topics included are virtual applications in ENT medicine and for teaching surgery; genome web-browsers as critical bioinformatics tools; Ethernet networks; routers and networks with near-zero buffers; and augmented reality systems using 3D fiducial markers.

In Chapter 1, prokaryotic (T4 phage) and eukaryotic (human) molecular genetic data demonstrating quantum information processing of coherent DNA states by transcriptase measurements (BioSystems 2009, 97, 73-89) are reviewed and possible contributions to quantum computing are suggested. Coherent states – within decoherence-free base pair sites – are introduced as consequences of interstrand hydrogen bond arrangement, *keto-amino* → *enol-imine*, where product protons are shared between two sets of indistinguishable electron lone-pairs, and thus, participate in coupled quantum oscillations at frequencies of ~ $10^{13}$ $s^{-1}$. This quantum mixing of proton energy states introduces stability enhancements of ~ 0.25 to 7 Kcal/mole. Transcriptase genetic specificity is determined by hydrogen bond components *contributing to* the formation of complementary hydrogen bonds which, in these cases, are variable due to coupled quantum oscillations of coherent enol-imine protons. The transcriptase deciphers and executes genetic specificity instructions by implementing measurements on superposition proton states at G'-C', *G-*C & *A-*T sites in an interval $\Delta t << 10^{-13}$ s. Transcriptase measurement on a coherent G' site can yield observable specification for 3 of the 4 quantum G' states where – just before transcriptase measurement – the ket for the two G' quantum protons is $|\psi> = \alpha|+ +> + \beta|+ -> + \gamma|- +> + \delta|- ->$. Data demonstrating entanglement between coherent protons and transcriptase components are identified. After initiation of transcriptase measurement, model calculations indicate proton decoherence time, $\tau_D$, satisfies the relation $\Delta t < \tau_D < 10^{-13}$ s. Decohered isomers participate in *accurate* Topal-Fresco replication to introduce base substitutions G' → T, G' → C, *C → T & *G → A, but coherent state *A-*T sites are evolutionarily deleted. Quantum uncertainty limits on amino protons drive the *keto-amino* → *enol-imine* arrangement. A 'rate constant' expression for introducing coherent states into duplex DNA is obtained. This allows an analytical expression for consequences of coherent states populating unstable $(CAG)_n$ repeats in human genomes. Measurements of $37^0$ C lifetimes of the metastable keto-amino DNA hydrogen bond indicate a range of ~ 3000 to 60000 yrs. These results imply that natural

selection at the quantum level has generated effective schemes (*a*) for introducing superposition proton states – at rates appropriate for DNA evolution – in decoherence-free subspaces and (*b*) for creating entanglement states that augment (*i*) transcriptase quantum processing and (*ii*) effective decoherence for complete (~100%) participation in Topal-Fresco replication of decohered isomers. In this scenario, the evolutionarily generated quantum information processing system has implemented coupled quantum proton oscillation in decoherence-free subspaces for 'low error' entangled qubits, which may provide insight into improved designs for room temperature quantum processing.

Chapter 2 discusses two applications which were developed to allow an instructor to guide and teach a medical student in a surgical training scenario. The most interesting feature of these applications is that both participants can simultaneously interact within the scene with haptic (force) feedback, allowing them to co-operatively touch and manipulate the virtual body organs. As well as this, the instructor can effectively grasp the student's hand and haptically guide it in a task within the scene. The first application was designed to teach the procedural aspects of a cholecystectomy (removal of the gall bladder), and incorporated several pliable body organs. The second application focused on temporal bone surgery, a procedure that involves drilling away part of the skull behind the ear to gain access to the middle and inner ear. Both applications allow instructor and student to be located in different places connected by the Internet. The first application was used for distance trials to determine the maximum geographical distance that was feasible between the two participants. Results showed that interaction between Australia and the USA was excellent and between Australia and Europe was adequate. The second application was used in a clinical trial with ear surgeons and their students. The results of these trials showed improved learning times over traditional methods. It was also discovered that there were unexpected benefits of having a networked system even when the two networked workstations were side-by-side.

A quantum algorithm is implemented using a quantum logic circuit that uses quantum mechanical phenomena to solve the problem. The quantum logic circuit is constructed with quantum gates using reversible logic synthesis techniques. Most of the quantum algorithms are binary algorithms. However, there are ample possibilities to develop multiple-valued quantum algorithms. The reasons are (i) multiple-valued quantum gates are realizable using existing quantum technologies, (ii) multiple-valued reversible logic synthesis is now possible, and (iii) multiple-valued quantum logic circuit is more compact and manageable than binary quantum logic circuit. The quaternary quantum logic circuit has additional advantage that qubits can be very easily encoded into quaternary qudits by grouping two qubits together. This advantage opens an avenue for using quaternary quantum logic circuit internally in binary quantum algorithms. Though there are other approaches of multiple-valued reversible/quantum logic circuit synthesis, the most promising and practical approach is to synthesize multiple-valued reversible/quantum logic circuit as Galois field sum of products (GFSOP) circuit. The advantage of this approach is that any multiple-valued non-reversible logic function with many input variables can be expressed as minimized GFSOP expression and the GFSOP expression can be realized as cascade of 1-qudit, M-S, Feynman, and Toffoli gates. Moreover, macro-level Feynman and Toffoli gates can be realized on the top of 1-qudit and M-S gates without using any ancilla input constant. In Chapter 3 the authors have developed effective method for synthesis of ternary and quaternary multiple-output logic functions as GFSOP circuit. For this purpose, the authors have introduced the concept of Galois filed (GF) with example of GF(3) and GF(4) and discussed the notion of GFSOP

expression. The authors have developed Galois field expansions (GFE) for ternary and quaternary cases and have proposed heuristic algorithm for GFSOP minimization by application of these GFEs. For synthesizing quantum logic circuits with lesser width, the authors have developed method of realizing macro-level ternary and quaternary Feynman and Toffoli gates on the top of 1-qudit and M-S gates without use of any ancilla input. Finally, the authors have proposed method for multiple-output GFSOP realization as cascade of 1-qudit, M-S, Feynman, and Toffoli gates, which minimizes both the gate count and the width of the synthesized quantum circuit. The authors have established effectiveness of the GFSOP minimization algorithm with sufficient experimental results. The very important feature of the proposed synthesis method is that the method inherently converts a non-reversible function into a reversible one for GFSOP based realization using quantum gates.

In the last decades quantum theory – a theory based on quantum mechanical principles – has appeared in space research. Quantum theory based communication offers answers for some of nowadays' technical questions in satellite communication. In the authors' point of view, the quantum computing algorithms can be used to affirm their free-space communication in the following four ways: open-air communication, earth-satellite communications, satellite broadcast and inter-satellite communication. Quantum cryptography – cryptography based on quantum theory principles – gives better solutions for communication problems e.g. key distribution than the classical cryptographic methods, which have been found to have vulnerabilities in wired and wireless systems as well. The long distance quantum communication technologies in the future will far exceed the processing capabilities of current silicon-based devices. In current network technology, in order to spread quantum cryptography, interfaces able to manage together the quantum and classical channel must be implemented. Currently, the quantum cryptographic key generation systems (QKD) have been realized in metro-area networks over couple of ten kilometers The QKD can be used in wired or wireless (free-space) environment as well. The free-space based QKD solutions can achieve megabit-per-sec data rate communication. Long-distance open-air and satellite quantum communication experiments have been demonstrated the feasibility of extending quantum channel from ground to satellite, and in between satellites in free-space. The satellite based single photon links already allow QKD on global scale. In Chapter 4 the authors introduce how the quantum principles will affect the world of space communication. The authors summarize the ideas from the past until present and show solutions to set up an efficient quantum channel for the quantum based satellite communication.

Recently, virtual reality systems have been presented for simulation of machining processes, aiming at the determination of specific machining parameters, such as the required fixtures and the machining environment, the cutting tool dynamics, the chip shape and volume, and the shape of the cutting tool.

A methodology is presented in Chapter 5 for the development of a virtual environment for 3 axis milling process simulation. The technological and research challenges involved in this methodology are described.

The operation of a new system developed by the authors for machining-process simulation in a virtual environment is presented. This system integrates a virtual reality environment with computational and graphical models for the simulation of three axis milling processes. A computational model has been developed for the visualization of the milling process in the virtual environment and graphical model has been developed for the calculation of quantitative data related to surface roughness of machined surfaces.

Chapter 6 presents a review of some of the most common virtual environments to the neural simulation and a technological approach to make feasible the visualization of the simulation of neuron birth, growth and death, at the neural tissue level. This is called Distributed Environment to Neural Simulation (DENS).

As discussed in Chapter 7, analysis of the architecture and organization of protein structures is a major challenge to better understand protein flexibility, folding, functions and interactions with their partners and to design new drugs.

Protein structures are often described as series of α-helices and β-sheets, or at a higher level as an arrangement of protein domains. Due to the lack of an intermediate vision which could give a good understanding and description of protein structure architecture, the authors have proposed a novel intermediate view, the Protein Units (PUs). They are novel level of protein structure description between secondary structures and domains. A PU is defined as a compact sub-region of the 3D structure corresponding to one sequence fragment, defined by a high number of intra-PU contacts and a low number of inter-PU contacts. The methodology to obtain PUs from the protein structures is named Protein Peeling (PP). For the algorithm, the protein structures are described as a succession of Cα. The distances between Cα are translated into contact probabilities using a logistic function. Protein Peeling only uses this contact probability matrix. An optimization procedure, based on the Matthews' coefficient correlation (MCC) between contacts probability sub matrices, defines optimal cutting points that separate the region examined into two or three PUs. The process is iterated until the compactness of the resulting PUs reaches a given limit. An index assesses the compactness quality and relative independence of each PU.

Protein Peeling is a tool to better understand and analyze the organization of protein structures. The authors have developed a dedicated bioinformatic web server: Protein Peeling 2 (PP2). Given the 3D coordinates of a protein, it proposes an automatic identification of protein units (PUs). The interface component consists of a web page (HTML) and common gateway interface (CGI). The user can set many parameters and upload a given structure in PDB file format to a perl core instance. This last component is a module that embeds all the information necessary for two others softwares (mainly coded in C to perform most of the computation tasks and R for the analysis). Results are given both textually and graphically using JMol applet and PyMol software. The server can be accessed from http://www.dsimb.inserm.fr/dsimb_tools/peeling/. Only one equivalent on line methodology is available.

With the increasing amount of data being produced by radiological imaging modalities such as Magnetic Resonance Imaging (MRI) and especially Multi Detector Computed Tomography (MDCT) with datasets ranging up to over 1000 individual slices of half a millimeter thickness the demand for other visualization methods than just paging through all these slices in a stack is also growing rapidly. Traditionally, the evaluation of such datasets would be performed on dedicated workstation, powerful enough to handle the large amounts of data at acceptable speed using more advanced visualization techniques such as maximum intensity projection (MIP), Multi Planar Reformation (MPR) and three-dimensional volume rendering (VR). Although the need certainly existed, the more widespread use of these advanced visualization techniques was hampered by the fact that these tools were expensive and only available at a limited number of locations in the hospital. However, higher availability of advanced visualization has nowadays grown into a requirement to keep up with the growing data production. To meet this requirement, server based strategies for advanced

visualization have found their way in to the clinical practice in radiology. In Chapter 8 the different levels of "thickness" of the server-client combinations will be covered as well as the current state-of-the-art both for the intranet of the hospital and for tele-medicine on the internet. Next implementation requirements will be covered that are obligatory to provide the conditions under which a server based advanced visualization system can strive within radiological practice. Besides this description of past and present the authors will also try to provide a view into the future and discuss where the server based advanced visualization could lead us.

Genome browsers are critical bioinformatics tools for biologists to visualize genome annotations and the other sequence features along a reference sequence. GBrowse is one of the most popular genome browsers used by the research community. However, its installation and configuration prove to be difficult for many biologists. The authors have developed a web server, WebGBrowse, which takes a user-supplied annotation file in GFF3 format, guides users through the configuration of the display of each genomic feature, and allows them to visualize the genome annotation information via the GBrowse software. Chapter 9 describes an upgraded WebGBrowse server, WebGBrowse 2.0, which provides users with a choice to display their genome annotation with different versions of the GBrowse software. The modular design of WebGBrowse 2.0 allows easy integration of future GBrowse upgrades. The authors have also developed a web-based GFF3 template generator to facilitate the preparation of the required annotation file in the correct format. The entire WebGBrowse 2.0 package is portable and can be freely downloaded and installed locally.

Virtual three-dimensional (3D) models of the individual human anatomy support the understanding in ENT (ear, nose, throat) medicine significantly. The interdisciplinary coactions of medicine and engineering enabled encompassing developments in reconstructing complex anatomies. Different fields of application can benefit from virtual models such as pre-surgery planning, medical education, and postoperative planning and patient information. To date, various visualization systems are available but according processes are not compatible and lead to time consuming efforts by veering away from medical needs. To overcome that limitations standardization is necessary to realize. Therefore, Chapter 10 intends to state the substantial needs of ENT medicine on virtual environments.

In Chapter 11 the authors analyze, through simulations, the performance of *Spanning Tree Protocol* (STP)-based Ethernet networks with ring and double ring topologies. In particular, the authors consider both the presence and the absence of *Virtual Local Area Networks* (VLANs), and they derive the optimized STP parameters which minimize the STP convergence time and maximize the network stability. Two possible techniques for STP internal timers management are evaluated. The presence of failures (either broken links or nodes) is also taken into account, in order to determine the proper STP parameters which guarantee connectivity recovery and convergence in all possible network scenarios. Some of the simulation results are also verified through an experimental testbed. Finally, the use of "transparent" switches is proposed as a solution to (i) accelerate the STP convergence, (ii) increase the reaction capability to failures, and (iii) overcome the limitations, imposed by the STP, on the maximum sustainable number of nodes. In particular, this approach allows to extend the number of nodes in the network, still guaranteeing the possibility of incorporating VLANs. In order to evaluate the impact of failures in a realistic network, the Open Shortest Path First (OSPF) protocol and the Hot Standby Router Protocol (HSRP) are introduced in an STP-based network. This analysis shows that the use of OSPF protocol and the HSRP does

not affect the STP performance, even if a longer delay is required in order to start the transmission of ping messages and a reduced reaction capability to node/link failures must be accounted for.

All routers have buffers to store packets during periods of congestion. However, as Internet link speeds reach hundreds of Gigabits-per-second and beyond, it is becoming increasingly difficult to equip high-speed routers with large buffers, especially as switching moves into the all-optical domain. In Chapter 12 the authors first trace the evolution in thinking over recent years on how much buffering is required at Internet routers, focusing specifically on the push towards smaller buffers, from Gigabyte down to Kilobyte sizes, making them amenable for all-optical realisation. The authors then highlight some of the implications of the move towards such small buffers, such as end-to-end performance for real-time and TCP traffic, the reaction of TCP to reduced buffer availability in the network, and the unexpected interactions between TCP and open-loop traffic. Finally, the authors propose mechanisms ranging from edge traffic conditioning to packet-level forward error correction within the network as means of overcoming the limitations posed by small buffers in the network, and speculate on the feasibility of a zero-buffer Internet core in the future.

Augmented reality (AR) often makes use of a 2D fiducial marker to render computer graphics onto a video frame so that the computer-generated object appears aligned with the scene. In Chapter 13 the authors extend this idea to 3D where real-world objects are used as fiducial markers and propose a distributed AR system that utilizes geographically located resources to meet high computing demand, enable sustained remote operations, and support collaborative efforts. Within the distributed AR system, the authors present technical solutions to several key modules in AR that form a linear computing pipeline. The authors generalize and formulate the pipeline network mapping as optimization problems under different mapping constraints and develop heuristic algorithms that maximize the frame rate to achieve smooth data flow. Extensive simulation-based results show that the proposed mapping heuristics outperform the existing methods.

Multi-Processors System on Chip (MPSoCs) and Massively Parallel Processors (MPPs) architectures are conceived to efficiently implement Thread Level Parallelism, a common characteristic of modern software applications targeted by embedded systems. Each core in a MPP environment is designed to execute a particular instructions flow, known as thread, in a completely self-sufficient manner, being able to communicate with the other cores in order to exchange shared data. The demand of parallelism in MPPs and MPSoCs entails the design of an efficient communication layer able to sustain it. This means that the interconnection medium has to be both scalable, to allow multiple accesses of the different cores to the shared resources, and optimized in terms of wiring. These are all native characteristics of Networks on Chip (NoCs).

In MPSoCs and MPPs, it is necessary to provide:

- quick resolution of the interdependencies among different threads, single scalar data or even vectors. Interdependencies are responsible of completion time delay because prevent a thread from completion when not resolved;
- load balancing support techniques to avoid hot spots and to efficiently exploit all the cores available on chip. When threads migration occurs, a regular and continuous traffic is generated, made up of long streams of data;
- management of end-to-end small control data.

Circuit Switching (CS) technique is the method by which a dedicated path, or circuit, is established prior the sending of the sensitive data. Circuit switched networks are suitable for guaranteed throughput applications, especially in case of real time communications.

In Packet Switching (PS) methodologies the intermediate routers are responsible for routing the individual packets through the network, neither following a predefined nor a reserved path. Packet switched networks are suitable for best-effort services or for soft-timing constrained communications. In Chapter 14 the authors will look at the possibility of combining CS and PS in order to support the heterogeneous traffic patterns coexisting in a MPP environment. Hybrid switching networks are designed to guarantee the benefits of both CS and PS consisting in a better usage of the available bandwidth and in a global increase of the overall throughput, at the price of a more complex hardware implementation. In this scope, the latest approaches in literature are presented, together with a particular NoC model able to provide dual-mode hybrid switching in a non-exclusive way, intended as the possibility of co-sharing the amount of available bandwidth between CS and PS communications.

# CONTENTS

In: Computer Science Research and the Internet
Editor: Jaclyn E. Morris, pp. 1-41

ISBN: 978-1-61728-730-5


*Chapter 1*

# EVOLUTIONARILY DESIGNED QUANTUM INFORMATION PROCESSING OF COHERENT STATES IN PROKARYOTIC AND EUKARYOTIC DNA SYSTEMS*

***W. Grant Cooper****
International Physics Health & Energy, Inc.,
Lubbock, Texas

## Abstract

Prokaryotic (T4 phage) and eukaryotic (human) molecular genetic data demonstrating quantum information processing of coherent DNA states by transcriptase measurements (BioSystems 2009, 97, 73-89) are reviewed and possible contributions to quantum computing are suggested. Coherent states – within decoherence-free base pair sites – are introduced as consequences of interstrand hydrogen bond arrangement, *keto-amino → enol-imine*, where product protons are shared between two sets of indistinguishable electron lone-pairs, and thus, participate in coupled quantum oscillations at frequencies of ~ $10^{13}$ $s^{-1}$. This quantum mixing of proton energy states introduces stability enhancements of ~ 0.25 to 7 Kcal/mole. Transcriptase genetic specificity is determined by hydrogen bond components *contributing to* the formation of complementary hydrogen bonds which, in these cases, are variable due to coupled quantum oscillations of coherent enol-imine protons. The transcriptase deciphers and executes genetic specificity instructions by implementing measurements on superposition proton states at G'-C', *G-*C & *A-*T sites in an interval $\Delta t << 10^{-13}$ s. Transcriptase measurement on a coherent G' site can yield observable specification for 3 of the 4 quantum G' states where – just before transcriptase measurement – the ket for the two G' quantum protons is $|\psi> = \alpha|++> + \beta|+-> + \gamma|-+> + \delta|-->$. Data demonstrating entanglement between coherent protons and transcriptase components are identified. After initiation of transcriptase measurement, model calculations indicate proton decoherence time, $\tau_D$, satisfies the relation $\Delta t < \tau_D < 10^{-13}$ s. Decohered isomers participate in *accurate* Topal-Fresco replication to introduce base substitutions G' → T, G' → C, *C → T & *G → A, but coherent state *A-*T sites are evolutionarily deleted. Quantum uncertainty limits on amino protons drive the *keto-amino → enol-imine* arrangement. A 'rate constant' expression for introducing coherent states into duplex DNA is obtained. This allows an analytical expression for consequences of coherent states

* E-mail address: cooperwg@sbcglobal.net.

populating unstable $(CAG)_n$ repeats in human genomes. Measurements of $37^0$ C lifetimes of the metastable keto-amino DNA hydrogen bond indicate a range of ~ 3000 to 60000 yrs. These results imply that natural selection at the quantum level has generated effective schemes (*a*) for introducing superposition proton states – at rates appropriate for DNA evolution – in decoherence-free subspaces and (*b*) for creating entanglement states that augment (*i*) transcriptase quantum processing and (*ii*) effective decoherence for complete (~100%) participation in Topal-Fresco replication of decohered isomers. In this scenario, the evolutionarily generated quantum information processing system has implemented coupled quantum proton oscillation in decoherence-free subspaces for 'low error' entangled qubits, which may provide insight into improved designs for room temperature quantum processing.

**Keywords:** Quantum information storage; Quantum information transfer; Coupled quantum oscillation; Decoherence-free subspaces; Transcriptase quantum processing; 'Stable' entanglement; Transcriptase-assisted decoherence; Coherent proton bonds; Quantum uncertainty limits; Quantum biology

# I. Introduction

Quantum information science (Vedral, 2007; Leon, J., Martin-Martinez, E., 2009; Appel et al., 2009) is an extremely active endeavor where current designs of quantum computers (e.g., Kim et al., 2009; Herskind et al., 2009; Roloff et al., 2009; Devitt et al., 2009) employ different quantum systems – electrons (Tsai et al., 2009), atoms (Gaetan et al., 2009), ions (Feng et al., 2009) and molecules (Mishima et al., 2009) – as single and multiple qubits (Fedichkin et al., 2009) that participate in entanglement (Goold et al., 2009) to implement quantum computing. This activity in quantum information science is motivated by the potential to exploit applications of quantum theory to significantly enhance the versatility of acquiring, transmitting and processing information, using a quantum mechanical basis for information codes (Nielson and Chuang, 2000; Rezakhani, et al., 2009). Consistent with the notion that quantum information science could benefit from direct evidence of quantum information processing by living cells (Vedral, 2003), this chapter reviews recent studies (Cooper, 2009a, b, 2010) and presents new evidence that genetic specificity information residing within time-dependent coherent states in duplex DNA is routinely measured and deciphered by transcriptase quantum processing. Although the initial assessments were on bacteriophage T4 DNA systems (Cooper, 1994), the introduction of coherent states and subsequent transcriptase quantum processing are also exhibited by human DNA systems (Sec. V). In an effort to connect molecular genetic observations of quantum information processing to concepts utilized in quantum computing, this chapter identifies (*a*) the quantum model for DNA instability, (*b*) the origin of coupled coherent states (e.g., Fedichkin et al., 2009) in decoherence-free subspaces (Bell et al., 2002; Oreshkov et al., 2008; Poccia et al., 2009; Mei et al., 2009) of duplex DNA and (*c*) the necessity of quantum coherence to explain molecular genetic observations, including (*i*) multiple genetic specificities exhibited by transcriptase measurements on coherent states within individual G' and *C genetic sites (see Figure 2 for notation) and (*ii*) entanglement between coherent protons and transcriptase components.

Genetic sites capable of exhibiting coherence, and thus transcriptase quantum processing, are time-dependent 'point' lesions in mammalian genomes (Hwang and Green, 2004; Beerenwinkel et al., 2007; Elango et al., 2008) and in bacteriophage T4 DNA (Kricker & Drake, 1990; Cooper, 1994, 2009a, b). The time-dependent molecular clock (Bromham and Penny, 2003) event, CpG → TpG, is the most frequent point mutation observed in the human genome and the rate is ~ 15-fold greater when cytosine is methylated (Elango et al., 2008). Since this form of time-dependent substitution, C → *C → T, is one of four related substitutions, i.e., also G' → T, G' → C & *G → A, exhibited by T4 phage DNA, this chapter and other studies (Cooper, 1994, 2009a, b) assume a general mechanism is responsible for time-dependent substitutions (hereafter, ***ts***) and time-dependent deletions (hereafter, ***td***) in all duplex DNA systems. Phage T4 DNA systems are particularly susceptible to an examination of ***ts*** and ***td*** since their origin and consequences of transcription and replication can be evaluated in terms of fine scale genetic mapping (Benzer, 1961), reversion analysis (Baltz et al., 1976) and strand analysis (Cooper, 1994, 2009b). The latter can specify the particular isomer of a complementary G'-C' or *G-*C pair responsible for a ***ts***. Consequently the two classes of time-dependent point lesion accumulated in extracellular T4 phage DNA (Ripley, 1988), G-C → G'-C' and G-C → *G-*C (Figs 1-2), can be assayed genetically at the resolution of an individual G', C', *G or *C isomer within a G'-C' or *G-*C genetic site (Benzer, 1961; Kricker and Drake, 1990). In an attempt to provide insight into "room temperature" quantum information processing, this chapter illustrates how evolutionarily designed coherent state genetic specificities are created, and subsequently – measured, deciphered and decohered – at biological temperatures by transcriptase quantum processing, which is the purpose of this (Figure 1a) article. The resulting quantum model of intrinsic DNA instability is consistent with observation (Cooper, 1994, 2009a, b) and quantum theory (Merzbacher, 1997; Zurek, 1991; Bell et al., 2002; Ghosh et al., 2003; Vedral, 2003; Chen et al., 2009).

The next section summarizes the quantum model for introducing time-dependent coherent states into duplex DNA and identifies the rationale for transcriptase quantum processing. The quantum system for transcriptase processing of two interacting two-level proton states on G' is outlined in Sec. III. Reactive proton states within duplex DNA are treated in Sec. IV. Quantum uncertainty limits on $-NH_2$ protons drive the *keto-amino* → *enol-imine* arrangement, which introduces enol-imine protons that participate in coupled quantum oscillations at frequencies of $\sim 10^{13}$ $s^{-1}$. Based on experiment, lifetimes of $37^0$ C keto-amino hydrogen bonds are the order of ~ 3000 to ~ 60000 years. Approximate quantum methods are used to obtain a 'rate constant' expression for introducing coherent states via the *keto-amino* → *enol-imine* arrangement. Section V develops a polynomial model (quantum + classical) for phenotypic expression of a $(CAG)_n$ repeat human disease as a function of a $(CAG)_n$ "genetic threshold" becoming populated beyond its evolutionarily allowed limit by time-dependent coherent states. The Conclusion is presented in Section VI.