

È ACCADUTO... / IT HAPPENED...

I miei primi novant'anni

Perugia, 1919. Il fisiologo Osvaldo Polimanti dava vita al suo progetto di fondare un periodico di biologia che avesse come obiettivo “l’occuparsi, almeno nella massima parte, di argomenti generali”. Nasceva *Rivista di Biologia*. E cominciava una storia articolata: dall’adesione plebiscitaria della biologia italiana alla Rivista (erano gli anni quaranta, l’epoca in cui il periodico contava ottanta direttori), all’apertura internazionale e al legame fecondo con il gruppo di Osaka, sotto la guida di Giuseppe Sermonti (anni ottanta), alla caduta sotto i colpi della burocrazia e infine alla rinascita del 1996, con l’editore Tilgher (si veda la sintesi storica apparsa nel fascicolo n. 2 del 1999, in occasione degli ottant’anni della Rivista). In tre anni (1996-1998) la Rivista, sempre sotto la direzione di Sermonti, porta a 0.5 il suo impact factor, che nel 1994 era crollato a 0.03, diventa sostanzialmente anglofona e salpa, tra le prime riviste in Italia, tra le acque, ancora fresche, di Internet.

A questo punto, per sgombrare il campo da ogni sospetto di autoccelebrazione, va detto che la Rivista ha tuttora lasciato inespresse molte potenzialità e ha ancora tanta voglia di migliorarsi. Dunque, più che dei consuntivi, questa è l’ora dei progetti. La Rivista festeggia con orgoglio i suoi primi novant’anni, ringrazia di cuore i lettori che l’hanno fin qui accompagnata nel suo cammino, ma guarda, con entusiasmo, alla prossima tappa del viaggio. [s.t.]

PUNTI DI VISTA / VIEWPOINTS

Why Giant Strong Component Is So Important For Metabolic Networks?Dewu Ding^{2,*} and Lina Li¹*Introduction*

The discovery of functional modules in complex biochemical reaction networks is one of the most important problems for network-based pathway analysis (Papin *et al.* [2004]; Ding *et al.* [2008a]). Ma and Zeng proposed that the metabolic networks could be decomposed (based on their “bow tie” structure) into the following four parts: 1) giant strong component (GSC), 2) substrate subset (S), 3) product subset (P), and 4) isolated subset (IS) (Ma and Zeng [2003a]). This “bow tie” structure of complex biological networks has attracted much attention, and it has been shown that this structure property is functionally meaningful for metabolism, disease and the design principle of biological robustness (Csete and Doyle [2004]; Kitano [2004], [2007]; Zhao *et al.* [2007]; Ding *et al.* [2008b]).

From a global point of view, the giant strong component is the biggest strongly connected component of a metabolic network and global topological structural properties such as so-called “small-world”, “scale-free”, modularity etc. have been thoroughly understood. The results suggest that the giant strong component determine the structure of the entire network at a certain extent (Ma and Zeng [2003a]; Zhao *et al.* [2007]; Ding *et al.* [2008b]).

However, these studies only focused on global topological structure, the local structure is still not completely understood. Herein, the simplest building blocks, network motifs (Milo *et al.* [2002]) have been applied to understand the local structure of complex biological networks. We analyzed network motifs in whole metabolic network and corresponding giant strong component of 10 organisms (*Escherichia coli* K-12 MG1655, *Escherichia coli* K-12 W3110, *Escherichia coli* O157 EDL933, *Escherichia coli*

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O157 Sakai, *Mycobacterium tuberculosis* H37Rv, *Mycobacterium tuberculosis* CDC1551, *Ralstonia solanacearum*, *Salmonella typhi*, *Salmonella typhimurium* and *Vibrio cholerae*). The results suggest that the motifs found are quite consistent between the metabolic network and corresponding giant strong component, which might demonstrate the fundamentality of giant strong component from a local point of view.

Metabolic Networks and Their Giant Strong Components

The metabolic network data were obtained and compiled from chemical reaction database developed by Ma and Zeng [2003b], which is revised based on KEGG database according to the following principles: 1) corrected obvious inconsistencies; 2) confirmed the reversibility of every reaction; 3) excluded the current metabolites and small molecules such as ATP, ADP, NADH and H₂O etc., with the purpose of reflecting biologically meaningful transformations. Subsequently, the metabolic networks are represented by so-called metabolite graph in which the nodes are metabolites and the links are reactions. For example, the irreversible reaction, C00064 + C00026 → C00025 is represented by two directed arcs C00064 → C00025 and C00026 → C00025. We then extracted the giant strong component of each metabolic network (Using Pejak (Batagelj and Mrvar [1998])) and compiled a new excel table for motif detection.

Local Structure Character: Network Motifs

Initially, the concept of network motifs is derived from the investigation of recurring regulation units in gene regulation networks, they are defined to be sub-graphs that occur in a network at frequencies much higher than those found in randomized ones (Milo *et al.* [2002]; Shen-Orr *et al.* [2002]). Network motifs have been thoroughly investigated in gene regulation networks in these years, in both theoretical (e.g., application/construction of mathematical models for describing functions, evolution and dynamics of network motifs) and experimental (e.g., experimental validation for predictive functions of network motifs) fields (Alon [2007]). For example, foregoing research has identified that the feed-forward loop (FFL) is one of the most important network motifs in gene regulation networks (Alon [2006]). Furthermore, they are

also emerging in other biological networks, such as metabolic networks (Zhu and Qin [2005]), protein interaction networks (Yeager-Lotem *et al.* [2004]) and signal transduction networks (Ma'ayan *et al.* [2005]) in recent years. For example, Zhu and Qin [2005] used network motifs to explain conserved patterns in biological networks, and they have shown network motifs to be significant for network structure and design principle.

Motif Detection

Since the concept of network motifs is published, lots of algorithms are proposed for the detection and enumeration of network motifs (Ciriello and Guerra [2008]) and there is a lot of software developed available for the purpose. Herein, we employed FANMOD for motif detection, since it is based on an improved (so-called randesu) algorithm that outperforms congeneric tools such as Mfinder and MAVisto. We searched for all of the 13 three-node motifs (Using FANMOD, with the P-Values < 0.05 and Z-Scores > 2) in these giant strong components.

Generally speaking, the giant strong components often only contain about 25%-35% nodes in metabolic networks. Despite this remarkable difference, our results showed that the simplest network building blocks (i.e. motifs) found are quite consistent (60% or above) between the metabolic network and corresponding giant strong component.

Conclusions

Given that modularity is a fundamental property of metabolic networks, and with the important aid by rapidly developing complex network theory, several modular decomposition methods are proposed for analyzing the structure and function of genome-scale metabolic networks. Among these, “bow tie” structure based decomposition method is particular interesting due to its meaningful function, and global topological structural properties of this character have been thoroughly researched in the past few years. To ulteriorly discover functional information involved in the character, local structure characteristic sub-graph is employed in this study.

By comparatively analyzing frequent sub-graph in metabolic

networks and their giant strong components (GSC) of 10 organisms from different categories, we find that the motifs found are quite consistent between the metabolic network and corresponding giant strong component, which might demonstrate the fundamentality of giant strong component from a local point of view. Furthermore, considering that many isolated reactions are included in the whole metabolic networks, we suggested that analysis of network motifs in giant strong component of metabolic networks might be more helpful than the analysis of the whole metabolic networks.

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A New Light on Yarrell's Law?

Yongsheng Liu

In genetics, Mendel's laws are well known. Less well known is Yarrell's law. This law was named for William Yarrell, a British naturalist and animal breeder. It maintains that a parent of an older breed will have more influence on the character of the offspring than a parent of a young breed (Darwin [1987]). This law was later confirmed by Ivan Michurin, who found that old varieties of fruit plants possess a stronger capacity for transmitting their characters than young varieties. "The older the plant chosen as a progenitor, the greater is the force with which it transmits its genes to the offspring, and conversely, if the plant is young, in its

first year of bearing, and particularly if it is a hybrid of recent origin, its hereditary power reaches a minimum” (Michurin [1949]). Beardmore *et al.* [1975] reported that the heritability of sternopleural chaeta number in *Drosophila melanogaster* is influenced by the age of the parent flies. Their results were surprising in that they demonstrated the heritability to be higher among flies produced from parents which were 14 days or older than those from 3-day-old parents, suggesting that heritability increased with increasing parental age. Lizana and Prado [1994] compared the offspring from crosses between heterozygous individuals of different ages (young x young, young x old, and old x old), and observed an association between adult age and allele frequencies of the offspring. The offspring of the older parents have a greater frequency of the Adf-F allele compared to the offspring of younger parents.

Some possible explanations lie in changes with age in the quantity of genetic materials which pass into gametes. Callan [1967] supposed that age affects the replication or segregation of parts of the genome in such a way as to produce gametes with consistently different amounts of genetic information at different parental ages, possibly by differential activity of master-slave complexes. Lints [1978] suggested that the heritability increase observed in ageing populations may be due to a changing ratio of heterozygotes versus homozygotes. He also considered the age effect on heritability in terms of gene control. Firstly, the information related to genetic control systems varies with the age of the parents in such a way that the older the parents, the better the phenotypic expression of a given set of polygenes in the offspring. Secondly, it could also be assumed that the additivity of action of a given set of polygenes, which determines a quantitative trait, is increased when transmitted by older parents.

Yarrell’s law was of great interest to Charles Darwin, as he was trying to understand why certain breeds seemed to have a greater ability to “impress” their characters on the offspring. He believed that “Yarrell’s law must be partly true” (Darwin [1987]). In his theory of heredity – Pangenesis, he supposed that all cells of the body throw off minute particles or molecules (gemmules) throughout development and these gemmules are able to circulate throughout the body and enter the sex cells. The transmission of characteris-

tics from parent to offspring was explained as a consequence of the incorporation of these gemmules into gametes, and their development in the offspring. Cases in which the characteristics of one parent dominate (Mendelian inheritance) he believed to be a consequence of that parent's gemmules having some advantage in number, affinity, or vigour over those derived from the other parent. The more gemmules there were from one parent, the more that parent's specific characters would predominate – and that, it seemed, also explained the dominance associated with Yarrell's law.

Recently, it has been suggested that Darwin's gemmules is analogous to circulating nucleic acids (Liu [2006]), thus shedding a new light on Yarrell's law. Circulating nucleic acids occur ubiquitously and are bioactive in living organisms. Two sources of circulating nucleic acids have been considered and discussed in the literature: dying cell, whether necrotic or apoptotic, and active nucleic acids release. Apoptosis is the most common form of cell death, continuing throughout life from early stages of embryogenesis to death. It was found that genomic DNA fragments originating presumably from apoptotic cells are always present in tissue fluids and blood plasma (Lichtenstein [2001]). It has been extensively documented that there is an enhanced apoptosis with increasing age (Higami and Shimokawa [2000]). For example, the frequency of apoptotic cells was found to significantly increase in old rats, suggesting that aging itself accelerates the apoptosis (Zhang *et al.* [1995]). Thus it is reasonable to suppose that older animals have higher concentration of circulating nucleic acids. Indeed it has been demonstrated that circulating DNA was significantly associated with age, and increased with increasing age (Chetsanga *et al.* [1975]; Sozzi *et al.* [2003]). Yakubov *et al.* [2007] reported that small DNA fragments in the form of tiny chromatin-like particles naturally present in blood plasma can spontaneously penetrate into human cells and cell nuclei. They proposed that such an innate gene replacement mechanism might function naturally in an organism using its own apoptotic DNA fragments. Garcia-Olmo *et al.* [2000] presented a "genometastasis hypothesis", which suggests that metastasis might occur via transfection of susceptible cells located in distant target organs with dominant oncogenes that derived from the primary tumor and are circulating in the plasma.

Obviously, this hypothesis is consistent with Darwin's Pangenesis.

We may try to explain Yarrell's law by translating Darwin's pangenetic explanation into our modern language. The older parent contains more apoptotic cells, which significantly increases the concentration of circulating nucleic acids. Thus the older parent's circulating nucleic acids have advantage in quantity over those derived from the younger parent. With the establishment that apoptosis is the most common form of cell death and there is an enhanced apoptosis with increasing age, the ability of circulating nucleic acids to be incorporated into gametes and expressed in the progeny, mechanism exists for Yarrell's law.

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Molecular Evidence for the Hadrosaur B. canadensis as an Outgroup to a Clade Containing the Dinosaur T. rex and Birds

Shi Huang

Molecular analysis of collagen sequences from an 80 million year old hadrosaur *B. canadensis* and a 68 million year old dinosaur *T. rex* suggests that the two dinosaurs belong to a clade to the exclusion of birds (Schweitzer *et al.* [2009]; Asara *et al.* [2007]; Asara and Schweitzer [2008]). However, well-established morphological analyses of fossils show that *T. rex* is more closely related to birds than it is to the ornithischian hadrosaur *B. canadensis* (Pisani *et al.* [2002]). The molecular analyses were based on the molecular clock paradigm, which is known to be contradicted by fossil sequences (Huang [2008]; Green *et al.* [2008]). It is therefore necessary to reevaluate the molecular data independent of the molecular clock paradigm.

Here, I analyzed all the collagen sequences reported for *B. canadensis* and *T. rex*. There are a total of four peptides whose sequences are known in the two dinosaurs and extant chicken. But, only one of these is informative as the other three are identical among the three species. For this single informative 18 amino acid peptide (GLPGESGAVGPAGPPGSR), I compared its sequence from all extant species including birds, reptiles, amphibians, fishes, and mammals where the sequence information is available (Table 1). The data show that *T. rex* is identical to *G. gallus* whereas *B. canadensis* differs from *T. rex* and *G. gallus* at residue position 15. An Ile residue at this position is completely conserved in all extant

species of mammals, birds, and reptiles. And yet, *B. canadensis* has a Pro at this position. From the Dayhoff PAM (accepted point mutation) matrix (Dayhoff [1978]), a change from Ile to Pro or vice versa is highly uncommon. Furthermore, not a single extant species from mammals, birds, reptiles, amphibians, and fishes (19 species analyzed) has a Pro at this position.

Table 1 – Sequence alignment of a peptide from collagen alpha 2 type 1.

<i>B. Canadensis</i>	GLPGESGAVGPAGPPGSR
<i>T. rex</i>I...
<i>G. gallus</i>I...
<i>T. guttata</i>	.P.....I...
<i>S. camelus</i>	.P.....I...
<i>A. mississippiensis</i>V..I...
<i>A. carolinensis</i>	.A.....S..I...
<i>H. sapiens</i>	.P.....A..T..I...
<i>M. mullut</i>	.P.....A..T..I...
<i>B. taurus</i>	.P.....A..T..I...
<i>M. americanum</i>	.P..Q...A..T..I...
<i>L. afiricana</i>	.P..Q...A..T..I...
<i>M. musculus</i>	.T.....A..S..I...
<i>R. norvegicus</i>	.P.....A..S..I...
<i>E. telfair i</i>	.P..Q...A..T.SI...
<i>M. domestica</i>	.P.....T.SI...
<i>X. levis</i>	.T.....A..F..L.P.
<i>X. tropicalis</i>	.A.....A..L.AL.P.
<i>R. catesbeiana</i>	.A.....GA..H.PS...
<i>D. rerio</i>	.N..PA..A.AQ..I.A.
<i>O. mykiss</i>	.NS.PA.SA.SQ.AI.A.
<i>P. olivaceus</i>	.IN.VA..S.VQ.AV.A.

These molecular data therefore suggest strongly that *B. canadensis* is an outgroup to a clade containing *T. rex* and birds, fully consistent with the well-established phylogeny based on morphological analyses of fossils (Pisani *et al.* [2002]). The unusual change from a conserved Ile to a Pro also show that *B. canadensis* is genetically more distant to the outgroup fish than extant birds and reptiles, confirming the previous observation that ancient fossil specimens of extinct species are more distant to a simpler outgroup than extant sister species (Huang [2008]; Green *et al.* [2008]). Thus, fossil sequences consistently contradict the molecular clock paradigm and would inevitably lead to absurd conclusions if analyzed under the assumptions of that paradigm.

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LIBRI / BOOKS

Le dimensioni dell'evoluzione

di Paolo Freguglia

Sin dalla formulazione darwiniana, molteplici sono i fattori che determinano l'evoluzione e che contribuiscono quindi alla trattazione teorica di essa. Altrettanto articolati sono i livelli di analisi che dipendono dalla scelta dei fattori considerati, o meglio di sintesi di essi. Pertanto è possibile, per esempio, considerare concetti di livello teorico basilare o – se vogliamo – “rudimentale”, cioè senza approfondire i meccanismi biologici che governano intrinsecamente le dinamiche dell'evoluzione, esaminando piuttosto il comportamento degli individui e dell'ambiente soggetti ad evolversi. In altre parole, non specificando analiticamente il ruolo delle mutazioni, delle ricombinazioni, del potenziale di fitness, dell'influenza dell'ambiente esterno, ecc., ma considerando la loro “risultante” o come si dice, in sintesi, la *perturbing action* che a sua volta fa da pendant con la tendenza generativa (che è anch'essa una *action*) a restare nella specie (quando di specie si può parlare). È un modo di procedere che può sembrare semplicistico. Invece è il risultato di uno schema riduzionista essenzialista che individua i caratteri fenomenologici cruciali della teoria evuzionistica. In quest'ottica si può trattare ad esempio l'evoluzione come una teoria ago-antagonista nei confronti della speciazione, o anche, ma con altri obiettivi, applicare – come è stato già fatto – la *Game Theory*. Questo primo livello teorico-biologico di trattazione non è in contrasto con impostazioni biologicamente più profonde e quindi di livello superiore, in cui invece si considerano altri fattori che nella precedente formulazione venivano sinteticamente compattati in base alla loro azione. Una trattazione consona di livello “superiore” dell'evoluzione deve tener presente anche una classificazione più vasta dei fattori coinvolti. Ha senso così parlare di *dimensioni*, intese come componenti fondamentali dell'evoluzione. Ogni dimensione va vista come un'articolazione funzionale dei suoi componenti. Va da sé che se ci limitassimo ai soli effetti (adeguatamente sintetizzati) di ciascuna di queste dimensioni ci troveremo in una situazione di primo livello ampliata. Ma non è così. Dal momento che lo studio dell'articolazione funzionale di fattori all'interno di una stessa dimensione ovviamente complica le cose. Nell'ampio volume *Evolution in Four Dimensions. Genetic, Epigenetic, Behavioral and Symbolic variation in the History of Life* (Massachusetts Institute of Technology, 2005, tradotto in italiano), Eva Jablonka e Marion J. Lamb propongono appunto quattro dimensioni per descrivere l'evoluzione. La

prima dimensione, dell'ereditarietà e dell'evoluzione, riguarda il sistema genetico, dove si sostiene che non tutte le mutazioni genetiche sono dettate o soggette soltanto al caso e tenendo presente che "il frammento di DNA che costituisce un 'gene' ha significato solo all'interno del sistema [vivente] nel suo insieme e [...] il suo effetto dipende dal contesto in cui si trova". D'altro canto il *genoma* è un sistema organizzato e non una mera raccolta di geni. La seconda dimensione è quella che concerne l'ereditarietà epigenetica, "tramite cui cellule diverse, seppur dotate dello stesso identico DNA, sono in grado di trasmettere le proprie caratteristiche alle cellule figlie". La terza dimensione è quella che riguarda "il modo in cui gli animali tramandano il proprio comportamento e le loro preferenze attraverso l'apprendimento sociale". Infine la quarta dimensione è quella relativa "alla trasmissione dell'informazione per mezzo del linguaggio e di altre forme di comunicazione simbolica". La trattazione di Jablonka e Lamb affronta e coinvolge i concetti più aggiornati e consolidati in merito, come ad esempio quello dell'evolubilità (*evolvability*) mediante la quale si esprime "una maggiore capacità di generare una variazione fenotipica non letale e rilevante, su cui può agire la selezione" (Gerhart e Kirschner (1997)). In altre parole, l'evolubilità descrive la capacità che ha una popolazione di catalizzare il processo di transizione tra minimi fenotipici (adattamento ai cambiamenti ambientali) in modo da stabilizzare il meccanismo di speciazione. Dunque, come dire che gli individui hanno un'intrinseca capacità di modificare l'impatto delle mutazioni nella dinamica evolutiva. Questo concetto è cruciale e viene oggi ben tenuto presente anche nelle modellizzazioni (matematiche).

Il libro di Jablonka e Lamb, a nostro avviso, contiene una ampia gamma di concettualizzazioni, la valenza delle quali è ben giustificata su ricerche, dati e riferimenti biologici. Basti vedere l'amplissima bibliografia. Una trattazione utilissima per chi vuol avere un approccio teorico alla teoria dell'evoluzione, in funzione anche dello stesso approccio modellistico matematico. Bella ed opportuna la Prefazione di Marcello Buiatti.

Eva Jablonka e Marion J. Lamb, *L'evoluzione in quattro dimensioni. Variazione genetica, comportamentale e simbolica nella storia della vita* (tr. N. Colombi, pref. M. Buiatti, illustrazioni A. Zeligowski), UTET, Torino 2007, pp. XXV + 578, € 23.00.

RISVOLTI / FLAPS

Brian Goodwin, *Dovuto alla natura. Riflessioni sulla complessità biologica e culturale*. Aboca Museum, Arezzo 2009, pp. 236.

La nostra cultura scientifica, dalla quale è nata la tecnologia moderna, ha un disperato bisogno di cambiamento. Il lavoro scientifico viene svolto principalmente da gruppi di specialisti, attivi in discipline separate, che cercano risposte a domande estremamente specifiche che hanno ben poco a che fare con il mondo vivente. Negli ultimi anni, però, ha iniziato a prendere piede un approccio più integrato e olistico a come vediamo e comprendiamo il mondo. Autore del libro di grande successo *How the Leopard Changed Its Spots*, l'eminente biologo e matematico Brian Goodwin afferma una visione della natura come una serie di reti complesse e interconnesse di rapporti.

Secondo Goodwin, per lavorare nuovamente insieme alla natura e raggiungere una vera sostenibilità sul nostro pianeta, dobbiamo adottare una nuova scienza, una nuova arte, un nuovo design, un nuovo modello economico e nuovi modelli di responsabilità. Dobbiamo essere preparati a dare alla natura il dovuto: riconoscere che abbiamo un debito con il mondo naturale e rifiutare di sfruttarlo solo per i nostri fini.

In questo libro, Brian Goodwin propone di ripensare e ampliare la visione scientifica in modo tale che natura e cultura siano considerate un processo creativo ininterrotto e unificato, invece che due ambiti separati in cui le peculiarità dell'uomo vengono viste come tratto distintivo che separa l'una dall'altra. I collegamenti tra natura e cultura, esplorati nel corso di tutto il libro, mettono in evidenza come la coerenza, l'interezza e il significato siano termini riconducibili a entrambe, in quanto descrivono processi simili di creatività in ambiti diversi. Attraverso scienza e conoscenza, Goodwin ci porta alla scoperta di una visione olistica, supportata da molti esempi e fondante nuovi modelli di analisi scientifica dei fenomeni biologici.

Stephen Jay Gould, *I Have Landed*. Codice, Torino 2009, pp. 451, € 32,00.

Le persone che hanno avuto la fortuna di conoscere, lavorare o anche solo chiacchierare con Stephen Jay Gould, nonché i milioni di lettori dei suoi libri, ne ricorderanno la travolgente cultura enciclopedica. La curiosità e la passione per ogni espressione della creatività umana – dalla scienza alla politica, dall'arte al baseball, dalla letteratura ai Simpson – sono state infatti la cifra del suo percorso biografico e intellettuale; una divertente e divertita varietà di scrittura che in questa raccolta di saggi trova una delle sue massime espressioni. Gould, scienziato e autore di libri specialistici e divulgativi, fu anche instancabile editorialista per riviste e giornali, tra cui *Natural History*, *Time* e *New York Times*; saggi dove le riflessioni sull'evoluzionismo, e sul suo impatto nella società contemporanea, convivono perfettamente accanto a quelle sui legami tra scienza,

arte e letteratura e tra storia mondiale e personale (l'11 settembre 2001 è stato anche il centesimo anniversario dello sbarco a Ellis Island del nonno di Gould, dal cui diario è tratta la curiosa espressione del titolo). *I have landed* è l'ultima antologia di quegli articoli, curata dallo stesso Gould poco prima della sua prematura scomparsa; uno spaccato completo della sua scrittura, capace di trasmettere il talento, la lievità e l'acume di uno degli intellettuali più influenti del Novecento.

Fritjof Capra, *La botanica di Leonardo. Un discorso sulla scienza della qualità*. Aboca Museum, Arezzo 2009, pp. 84, € 59,00.

Dall'autore del *Tao della Fisica* un'opera inedita che segue il grande successo del suo ultimo libro *La Scienza Universale: arte e natura nel genio di Leonardo*, nel quale il grande uomo del Rinascimento emerge come il primo autentico pensatore sistemico. Uno scienziato capace di sviluppare per la prima volta un metodo sperimentale di osservazione della natura pur mantenendo ed esaltando nella sua arte un profondo rispetto per la vita in ogni sua espressione. In questo testo Capra torna su questi temi con specifico riferimento agli ampi studi di botanica che Leonardo intraprese lungo tutto il corso della sua vita. Dall'osservazione alla puntuale rappresentazione delle piante nelle sue opere, egli trasse interessantissimi spunti da rianalizzare oggi nella prospettiva di quella scienza della qualità, che consentì al grande protagonista del Rinascimento di cogliere la natura nel suo naturale processo del divenire.

L'opera, arricchita da bellissime immagini provenienti dai maggiori Musei del mondo, ripercorre gli studi di Leonardo sulla Botanica, mettendo in evidenza come il suo disegno avesse una solida base "scientifica", capace di rappresentare fedelmente una realtà in costante evoluzione. Il dinamismo della sua rappresentazione testimonia un diverso approccio alla conoscenza della natura, che ci porta a riflettere sulla complessità dei sistemi viventi trovando una sorprendente linea di continuità tra le intuizioni di Leonardo e le più avanzate frontiere della scienza moderna.

Agu Laisk, Ladislav Nedbal and Govindjee (eds.), *Photosynthesis in Silico. Understanding Complexity from Molecules to Ecosystems*. Springer, Berlin-Heidelberg-New York 2009, pp. 520, € 217,36.

Photosynthesis in silico: Understanding Complexity from Molecules to Ecosystems is a unique book that aims to show an integrated approach to the understanding of photosynthesis processes. In this volume – using mathematical modeling – processes are described from the biophysics of the interaction of light with pigment systems to the mutual interaction of individual plants and other organisms in canopies and large ecosystems, up to the global ecosystem issues. Chapters are written by 44 international authorities from 15 countries.

Mathematics is a powerful tool for quantitative analysis. Properly programmed, contemporary computers are able to mimic complicated processes in living cells, leaves, canopies and ecosystems. These simulations – mathematical models – help us predict the photosynthetic responses of modeled systems under various combinations of environmental conditions, potentially occurring in nature, e.g., the responses of plant canopies to globally increasing temperature and atmospheric CO₂ concentration. Tremendous analytical power is needed to understand nature's infinite complexity at every level.

This book is not a list of equations and computer programs, but the emphasis is on analytical ideas facilitating the understanding of complex interactions governing the photosynthetic process on every level and between different levels of hierarchy. The book provides the necessary background on photosynthesis and demonstrates the benefits of the computer-aided quantitative analysis of its reactions; it is designed for graduate students and researchers in plant physiology, functional plant biology, plant biochemistry, systems biology, biophysics, bio-energy and bio-fuel.

Shietada Nakanishi, Ryoichiro Kageyama, Dai Watanabe (eds.), *Systems Biology. The Challenge of Complexity*. Springer, Berlin-Heidelberg-New York 2009, XV, pp. 246, € 135,15.

Biological signaling pathways dynamically interact with one another to form complex information networks intracellularly, intercellularly, and eventually at the level of the organism. Biology and medicine have conventionally focused on identification and characterization of functional elements in biological signaling pathways. Recently, research in this field has pursued a new approach, systems biology, to understand the dynamics, complexity, and physiological functions of the biological signaling networks. Instead of reductionistic analyses or large-scale studies of biomolecules piece by piece, systems biology emphasizes the need for interdisciplinary methods and analysis of the regulation and operation of information networks at the systems level.

The contributors to this book are leading researchers in the rising field of systems biology. Readers will find not only the most recent advances in research, but also the latest information about interdisciplinary methods and related topics.

Jason McDermott, Ram Samudrala, Roger Bumgarner, Kristina Montgomery, Renée Ireton (eds.), *Computational Systems Biology*. Springer, Berlin-Heidelberg-New York 2009, XVIII, pp. 587, 130 illus., € 90,43.

The recent confluence of high throughput methodology for biological data gathering, genome-scale sequencing, and computational processing power has

driven a reinvention and expansion of the way we identify, infer, model, and store relationships between molecules, pathways, and cells in living organisms. In *Computational Systems Biology*, expert investigators contribute chapters which bring together biological data and computational and/or mathematical models of the data to aid researchers striving to create a system that provides both predictive and mechanistic information for a model organism. The volume is organized into five major sections involving network components, network inference, network dynamics, function and evolutionary system biology, and computational infrastructure for systems biology.

As a volume of the highly successful *Methods in Molecular Biology* series, this work provides the kind of detailed description and implementation advice that is crucial for getting optimal results.

Comprehensive and up-to-date, *Computational Systems Biology* serves to motivate and inspire all those who wish to develop a complete description of a biological system.

Ivan V. Maly (ed.), *Systems Biology*. Springer, Berlin-Heidelberg-New York 2009, XII, pp. 500, 138 illus., € 83,15.

The rapidly developing methods of systems biology can help investigators to make inference and predictions from their data that intuition alone would not discern; however, the difficulty lies in the broad knowledge of mathematics and engineering that seems to be required to even evaluate the applicability of the methods to the problem at hand. In *Systems Biology*, scientists who possess that mathematical knowledge and have applied it effectively to various biological problems contribute methods which reflect their experience, crystallized in a form very similar to typical biological laboratory protocols. In order to best aid researchers, the chapters supply the theory behind the method, its step-by-step implementation, and the pitfalls explained thoroughly and from the practical angle.

Cutting-edge and easy to use, *Systems Biology* shatters the perceived insurmountable barrier between the laboratory and systems-biological research techniques.