

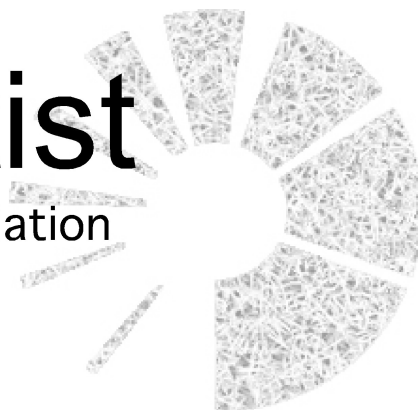
# The Systematist

Newsletter of the Systematics Association

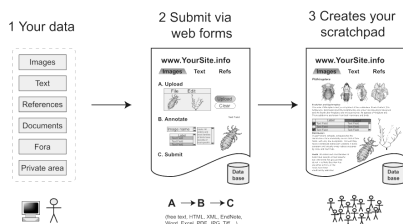
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## **Lead Article: How Many Uses For a Scratchpad?**



***The Sir Julian Huxley Lecture***  
**Joseph Felsenstein**

### ***Inspirations***

**Davide Pisani: a passion for  
Life's Kingdoms**

### ***New Journal***

**Biogeography & Systematics**



### ***Spotlight***

**Francisco Ayala on Evolution vs.  
Creationism**

### ***Book Reviews***

**algae and mosses galore  
advances in biogeography  
gene regulatory networks**

## Editorial

Dear Readers,

Issue 30 of our Newsletter begins with state-of-the-art information technology and its role in promoting web-based approaches to the production, storage, exchange and update of taxonomic data. In an elegant, step-by-step introduction to web-based applications, Roberts et al guide us through the fascinating world of Scratchpads.

Davide Pisani (Maynooth) is the author of our Inspirations column, in which he reveals everything (well, almost everything) about his fascination with the five (or six, or seven) big domains of Life.

The debate on evolution vs. creationism rages on in the pages of the Spotlight article by Francisco Ayala, who draws attention to the widely diverging philosophical connotations embedded in scientific and religious thinking. Ayala details the content of a pamphlet published at the beginning of this year by the National Academy of Sciences (USA) with the aim to promote awareness of evolutionary (in particular) and scientific (more in general) thought, and to counteract creationists' argument in favour of the introduction of intelligent design teaching in US public schools.

We have four wonderful book reviews on subjects as diverse as algae, mosses,

biogeography, and gene regulatory networks

We report the imminent launching of a new journal, Biogeography and Systematics, and draw attention to a special discount price (for members of the SystAss) for the purchase of the Royal Society themed publication on the evolution of animals.

Finally, the speaker for this year's Sir Julian Huxley Lecture (2 July, 2008) is Professor Joe Felsenstein, who will entertain us with the uncertainties that permeate phylogenetic reconstruction and novel statistical methods to address them.

Sadly, this issue also marks the final editorial effort by Ron Jenner. Ron's style and spread of scientific and philosophical knowledge remain unsurpassed. We wish him well in all his future undertakings and we thank him for his outstanding service to the Systematics Association.

The Editors



Cover illustrations: Joe Felsenstein

**The Systematics Association** is committed to furthering all aspects of Systematic biology. It organises a vigorous programme of international conferences on key themes in Systematics, including a series of major biennial conferences launched in 1997. The association also supports a variety of training courses in systematics and awards grants in support of systematics research.

Membership is open to amateurs and professionals with interests in any branch of biology, including microbiology and palaeontology. Members are generally entitled to attend the conferences at a reduced registration rate, to apply for grants from the Association and to receive the Associations newsletter, *The Systematist* and mailings of information.

For information on membership, contact the Membership Secretary, Dr G. Reid ([membership@systass.org](mailto:membership@systass.org)), Department of Botany, Natural History Museum, Cromwell Road, London, SW7 5BD, U.K.

*The Systematist* Newsletter of the Systematics Association.

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# Getting Taxonomy onto the Web

Dave Roberts<sup>1</sup>, Simon D. Rycroft<sup>1</sup>, Irina Brake<sup>1</sup>, Kehan Harman<sup>1</sup>, Ben Scott<sup>2</sup> & Vincent S. Smith<sup>1</sup>

<sup>1</sup>Natural History Museum, London; <sup>2</sup>Dune Media Ltd.

Countless words have been written on the desirability of liberating taxonomy from the vault that is its native habitat, imprisoned on obscure printed pages, and freeing it to take part in the glorious information revolution (Godfray 2002, Wheeler, 2008). Turning this desire into reality faces two major challenges, one technical and the other social.

Encyclopedia of Life, which put information into a standard structure available as web pages, or by the provision of basic tools to allow people to create their own web sites. This article is primarily about this second approach. The first and most obvious hurdle is the lack of a web site and, possibly, the computer skills necessary to manage one. In this day and age computers and disk space are cheap, so the provision of a fairly substantial server able

project EDIT has addressed this and the result is a product called a Scratchpad (<http://scratchpads.eu>).

In a nutshell, Scratchpads are an intuitive web-application, enabling communities of taxonomists to build, share, manage and publish their data on the web (Fig 1). They are available as a hosted web site containing a suite of tools for taxonomists and are a mechanism to facilitate collaboration. Scratchpads are easy to use,

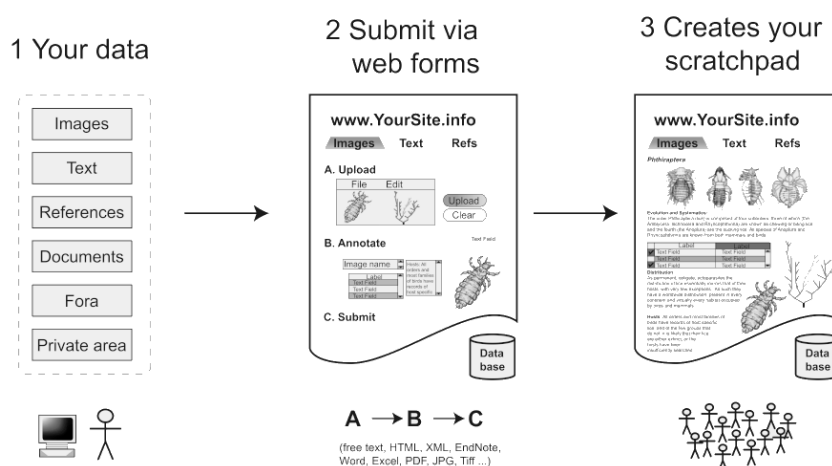


Figure 1. The Scratchpad concept. Your data from a variety of sources are uploaded through the import tools and structured onto web pages.

## Technical challenges

The technical challenge has been approached in two fundamental ways, either by large collaborative projects like Species2000 and

to support many web sites is within the petty-cash range of most large institutions. On the other hand, software and the technical skills needed to manage websites are not to be had so easily: the EU-funded

adaptable to taxonomists' needs, and provide powerful tools for managing biological information.

Taxonomists are good at organising their data, but commonly lack a

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## The Sir Julian Huxley Lecture

**Professor Joseph Felsenstein**

Department of Genome Sciences and Department of Biology  
University of Washington, Seattle, USA

### **Not the fly on the wall: can systematists cope with uncertainty?**

**Wednesday, 2 July 2008, 6pm**

**The Linnean Society, Burlington House, Piccadilly, London**

In reconstruction of molecular phylogenies, biologists have largely shifted their emphasis from inferring a single phylogeny to being comfortable with statistical descriptions of the uncertainty about it, whether by using bootstrapping, jackknifing, or Bayesian posteriors. Similar developments for morphological and behavioral characters have been slower in coming, as there have been fewer defensible statistical models available. The spread of statistical approaches to the comparative method is changing that. I will describe some new developments in statistical models for discrete as well as continuous morphological characters. They can infer correlations of character change across a phylogeny. However these inferences must necessarily be very noisy and uncertain. How will systematists and other evolutionary biologists cope with this uncertainty, if they cannot look forward to further molecular sequencing reducing it? Can we make use of the information without ignoring its uncertainties or overreacting to them? If we cannot hope for an exact account of actually what happened in evolution, is despair inevitable?

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straightforward way to link this information and display the results on the web. Scratchpads contain tools to import data from spreadsheet structures, from well-structured text files, XML output from databases, various image formats and from various reference management packages, like EndNote, BibTeX and ProCite.

The data are imported

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into existing standard content structures, such as bibliographies or classifications, or users can design their own content types for specific purposes.

#### *Getting data in*

The recommended, and simplest, way to import information is to start with the classification.

This can be prepared

in either nested columns in a spreadsheet or as a set of explicit parent-child statements that can be directly imported. Alternatively, classifications can be imported via a web service from ClassificationBank (a service provided by the Universal Biological Indexer and Organizer – uBio, see <http://www.ubio.org>). Once imported, the classification becomes a menu (Fig 2) through which users can navigate the site. This classification acts as a framework to link other data elements held within or external to the Scratchpad. Additional Information (e.g. specimen records, images, maps) loaded into a site are stored in an underlying database (see ‘The small print’ below) and ‘tagged’ with the appropriate taxon names so that they become findable.

#### *Making it visible*

Information can be explored through a series of ‘views’ available for each content type or aggregated on a single page for each taxon through a suite of panes (Panels – Fig 3). These are windows on the underlying data, providing a dynamic view of different content as the user browses through the taxon pages or as more information becomes available. The default set of panels (Fig 4) can be augmented by the Scratchpad

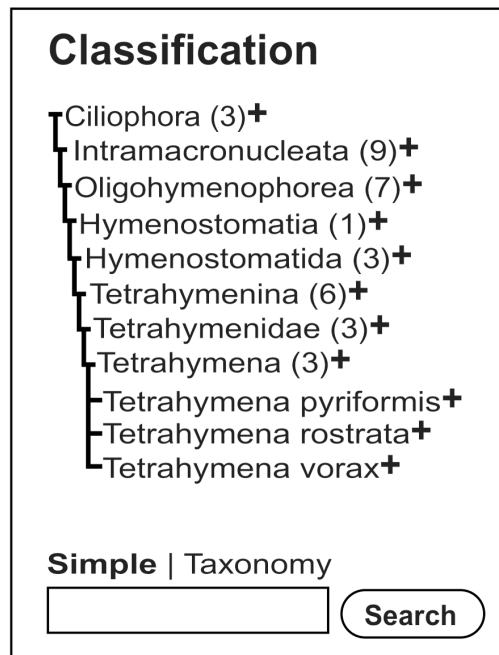


Figure 2. An imported classification of the Ciliates. The main classification was published in 2002 and has been locally modified. This one contains over 2000 names and took about 3 hours to make a well-formed text file from Dennis Lynn's web page (<http://www.uoguelph.ca/~ciliates/classification/genera.html>) that could be imported directly into the Scratchpad environment to act as a scaffold for further information.

owner and the screen layout can be adjusted, forming a customised template through which information about the selected taxon will be displayed. Within panels that recover multiple items, such as images and bibliographic citations, Scratchpad editors can tailor the content by selecting which items to display. For instance, a search for a parasitic taxon will often recover images of the host that are not the focus of the site. Those images can be blocked, thus panels provides an interface that allows users effectively to curate the underlying web of information connected to a page.

#### *Making it citable*

According to some, "if you can't cite it, its not science" (<http://www.editwebrevisions.info/content/meeting-report>). To cite a panels page there is a panel called 'Authors/sources' containing a *create citation* button. Pressing the button creates an archived copy of the taxon page with a permanent web address pointing to this static version of the dynamic page (Fig 5). When an author uses this citation, the reader will be able to see exactly what the author saw.

#### *Learning how to do it*

The system has a collection of

instructional video clips that guide owners through a variety of processes that they will need to customise their site. Each Scratchpad community may need to develop its own customised user help, although as yet few have found it necessary to do so.

#### *The small print*

Scratchpads are built using a content management system (CMS) called Drupal (<http://drupal.org>), a popular open source CMS. It operates under the LAMP architecture (Linux, Apache, My-SQL, PHP) on servers at the Natural History Museum, London. The Scratchpads are backed-up daily on a Tivoli Storage Manager. Each Scratchpad also maintains an internal 'roll back' facility to recover individual pages without disrupting the entire site. Drupal contains a core set of functions that are supplemented by modules for specific purposes. Each Scratchpad is the responsibility of a single named individual, a maintainer, who controls access to the site and can allocate roles to other registered users. By default the roles are editor, contributor and authenticated user. Normally editors can create new pages, contributors can modify existing pages and authenticated users can add comments to pages and the



Figure 3. A panels page showing images, a text description and a citation. As more data are added to the database they would be exposed in these panels automatically.

forum. The maintainer controls which pages are visible to each category of visitor.

Scratchpads do not allow non-administrators to install new modules, or to write their own, because all installed modules are available to all Scratchpads and the development team need to verify that any new module is compatible with those already in use. Those with the relevant skills are welcome to contact the team, via <http://scratchpads.eu/help>, to discuss adding new functions to the system. Users do, however, have a great deal of flexibility over the configuration of their site, its content and the way this is

displayed. Users can also download all the data from their site as a My-SQL dump should they wish to move it or re-use it for another purpose.

### Sociological challenges

#### Share and enjoy

The idea of sharing data has become commonplace in many fields, such as physics and molecular biology, where data are often generated by teams and there is a recognition that the analyses carried out on large data sets is far more powerful than those carried out on small sets. The EDIT *Future Scoping Group* workshop that was held in December 2007 (published here:

<http://ww2.bgbm.org/EditDocumentRepository/Taxonomy21report.pdf>) identified the need for taxonomy to move from an artisanal to an industrial process. To achieve such a goal taxonomists have to employ industry-style methods typified by the production line (again the comparison with physics and molecular biology). There is no doubt that the craftsman-built Daimlers of the early 20th Century were of far better quality than the model-T Fords, but how many Daimlers could be built and how many people could afford to use them? The issues are volume and fitness for purpose.

A first step that helped

several start-up communities has been to work on building shared taxonomic bibliographies. This has already been done for Botany through the TL2 project (<http://tl2.idcpublishers.info>) and superseded by an up to date list maintained by IPNI (the International Plant Names Index, <http://www.ipni.org>), but Zoology has not been so fortunate. Many Scratchpad users have small bibliographic

data sets that collectively form near complete bibliographies for a given taxon. Exposing these on a Scratchpad provides a simple activity that allows users to gain trust in sharing data with their colleagues and builds confidence in using the Scratchpad system. Similarly, many taxonomists have data fragments that have been acquired for some purpose in the past but which will never

now be used for further work. Sharing such snippets through a Scratchpad is a means to make sure that their effort was not wasted while joining in a common goal within a site. It is notable that funding for infrastructure is available, but not for data generation (e.g. iPlant Collaborative, Ledford, 2008). Scratchpads facilitate the accumulation of small quantities of data on an opportunistic basis.

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## **The Systematics Association Publications**

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**Following the acquisition of CRC Press by Taylor & Francis, Systematics Association book production operations have been transferred to the CRC Press offices in Florida. Members of the Systematics Association receive a 25% discount of all Systematics Association volumes published by Taylor & Francis.**

**All volumes published by Taylor & Francis/CRC Press should now be ordered via either the CRC Press offices or the CRC press office in London (details below). The 25% SA members' discount is claimed by using a promotion code, for details of this code please contact Alan Warren, Systematics Association Editor-in-Chief.**

### **ORDERING INFORMATION:**

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### *Whose site is it anyway?*

A key strategy in the project design was that Scratchpads are unbranded. Essentially they are blank templates to be imprinted with each community's individual style. Our aim was that Scratchpads would form a focal point where someone with a level of computer savvy could build a site that the community as a whole would own and nurture. This was well illustrated by one of the first Scratchpads that, while being created in London, was discovered by a laboratory in Norway who e-mailed the maintainer and asked if they could contribute some of their data to the site.

The principal inhibitor to people joining these teams stems from concern that they will not receive credit or recognition for their work, both in terms of personal effort and arguably more importantly in terms of measures that are used for career advancement. It is



Figure 4. The default set of panels. Those in light grey are panes that pull content from the web. All panels are configurable and other panels can be designed and added by the site manager.

important that we as a research community devise a mechanism that measures use-rates for individual's contributions to web-based

environments like the Scratchpads. These need to become similar in application to citation rates and journal rankings such as those

developed by Thomson-ISI.

### *The publication problem*

It is generally agreed that the publication of alpha taxonomy, especially descriptive taxonomy, is becoming increasingly difficult and, except for a few charismatic organisms, high-impact journals are not an option. Putting descriptions into the public domain on web sites is surely an inevitable end-point of the current trend. It is likely that the Zoological Code will be modified to recognise on-line publication at the next review (A. Polaszek, pers. comm). The same issue will be discussed at the next Botanical Congress in 2012. If communal web sites become the new

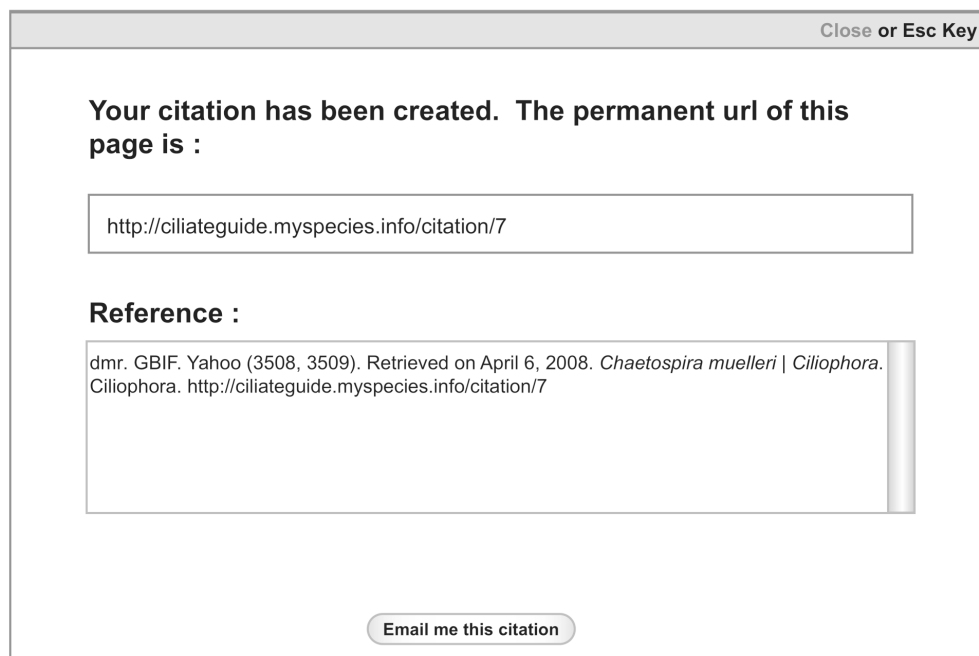


Figure 5. The current result of pressing the *create citation* button. The url presented is an archival copy of the page at the time the button was pressed, so went it is used by an author, the reader will see the author saw. This is the first iteration of this routine and the output format is still under development.



monographs, i.e. the standard work for a particular taxonomic group, for instance The Dipteran Site (<http://www.diptera.org>), then there is a real risk that community behaviour will outstrip the strictures of the codes leading to an anarchic and unregulated nomenclature. But if there are encyclopaedic monographs that are dynamic and authoritative exactly how much of a problem would that be?

#### *The peer review problem*

There is much concern that web-publication, especially though a Scratchpad-type environment, can and will happen without peer review. It is apposite to observe that very few books and monographs are peer-reviewed either, but they still stand as definitive guides to many taxa.

It is also relevant that Wikipedia scored higher than the Encyclopaedia Britannica in an accuracy test (Giles, 2005). We would argue that the taxonomic community is best placed to monitor decision-making in a taxonomic domain, so once a site becomes a standard reference work for a particular group, that same community are best placed to object to controversial decisions and the site forum is the best place to argue the pros and cons in order to achieve consensus.

The basis for this argument is that the debate and conclusion are available to everyone with internet connection in one place, rather than being dispersed into increasingly obscure paper journals. Once again it is imperative that those employing taxonomists recognise the value of these contributions and they count towards career development.

#### *The small print*

Data entered on a Scratchpad remain the property of the contributor under a Creative Commons licence (<http://creativecommons.org>). Recovering an individual's data from a Scratchpad has to be negotiated with the site maintainer, who would be able to download the whole site content and would then need to separate the individual's contribution.

#### **Where are we now?**

The first Scratchpad was introduced in March 2007. By the end of February 2008 there were 55 Scratchpads (rising) that had attracted 503 registered users (rising) in >28 countries, who have collectively built more than 110,000 pages (nodes). Collectively the sites attract approximately 200 unique visitors per day (rising), who each spend an average of 8 minutes (rising) looking at an average of 8.7 pages(rising) each. Of these visitors 54.6% (falling) have never

previously looked at the Scratchpads. In February the Scratchpads attracted a total of 55,772 page-views, reaching a maximum daily peak of 3,690 on 26 February 2008.

#### **In the pipeline**

The EDIT project will be funded until February 2011. Scratchpad development is active and on-going under the rubric of 'release early and release often', which means early adopters can request modifications, and influence design, during the construction phase, rather than being presented with a finished product on a take-it-or-leave it basis. An immediate priority is the provision of an up-to-date help system, which should be available by the time you read this. In addition we are trying to work out how to build a distance learning package for a project under such active development.

Currently the systems work most readily with a single classification that can be locally modified by addition and deletion of content. An obvious requirement is better management of synonyms, which currently are included, but not part of the taxonomy proper, making synonymised content less readily accessible.

The *create citation* button, discussed above, needs to be extended to

individual components, so that downloaded components from a web page take their attribution details and licence requirements.

EDIT's Workpackage 5 (<http://wp5.e-taxonomy.eu>) are developing a Common Data Model that will provide powerful data management services. WP5 are also working on a bibliographic services (from Ex Libris) that will search for web-availability for cited articles.

The data entered into standard Scratchpad structures could be exposed to data harvesters like GBIF and EoL, provided the data owners agree. We are currently writing routines that will make such data harvesting an automatic, background task when it is activated by the site's maintainer.

#### **Your own, your very own ...**

To apply for a Scratchpad you simply complete the application form (<http://scratchpads.eu/apply>). You will need a name and mission statement (200 words that describes your site's scope) and, if you have one, a domain name that will point to your site. We will provide a site to any legitimate group of taxonomists or taxonomic project.

Although we are working to make the administration of Scratchpads as easy as possible, there is a requirement for a certain level

of computer skill. If you are not comfortable with building and maintaining databases, then it is unlikely that you will be able to get the best from a Scratchpad at this stage and you should wait for additional training material. An ideal situation would be for someone with computer expertise to exist for each taxonomic or regional interest group who could take on the responsibility for managing the site.

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# Inspirations

## **Davide Pisani**

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### **How would you summarize yourself in the form of a title of a scientific paper?**

A chimeric multicellular organism, with a complex life cycle, from a mesophilic terrestrial environment of planet Earth. Of course, chimeric here would stress the symbiotic nature of the eukaryotes, and their dual (Archaeobacterial and Eubacterial) ancestry.

### **Summarize the when and where of your academic career**

I did my undergraduate studies in Italy, at the University of Parma. I chose Parma because at that time, Prof. Danilo Mainardi, Italy's most prominent ethologist, was the head of the Department of Biology. My introduction to biology was through the books of Konrad Lorenz (particularly *King Solomon's Ring*), and when I enrolled at university I wanted

to study ethology. It was only during my undergraduate years that I was introduced to the study of evolution. As part of our General Zoology course, we were advised to read Steve Gould's *Wonderful Life* (which had just been translated into Italian – it was 1991). It was Gould's *Wonderful Life* that triggered my interest in the study of evolutionary biology. I completed my studies in ethology: my undergraduate thesis (and my first scientific article) focused on the behavioural ecology of the Italian Ruin Lizard *Podarcis sicula*. For my PhD, I wanted to specialise in evolutionary biology, and particularly in phylogenetics. I thus moved to the University of Bristol, where I obtained my PhD in theoretical phylogenetics under the supervision of Prof. Mike Benton and Dr. Mark Wilkinson. I am now a lecturer on bioinformatics and head of the Evolutionary Biology Laboratory at the National University of Ireland, Maynooth (which is one of the Dublin-area universities).

### **When did you decide to follow the career path you are on now?**

I certainly developed an

interest in zoology after reading *King Solomon's Ring*, in my early teens. However, my interest in evolutionary biology developed only during my university years. Still, to some level, I always wanted to be a scientist, and particularly a zoologist. I often ask myself what might have triggered this interest, and sometimes I think it might have something to do with having watched the TV serial "Born Free", which was on air in Italy in the mid to late seventies. I still remember that as one of my favourite childhood shows, but of course it might well have been that I liked it because it was about African wildlife. Nature or Nurture? Probably both.

### **What are the main goals of your research, and what is your future ambition?**

The main goal of my research is to help uncover the truth about the history of life on Earth, and that is also my ambition. It is amazing how many commonly held concepts about the origin and early evolution of cellular life are questionable if not plain wrong. Take the Tree of Life for example. We often refer to it as if we were talking of a well-supported theory, yet the data supporting this hypothesis are scant at best. People of the like of Lynn Margulis, Jim Lake and Bill Martin (for example) would

say that the “tree of life” is actually not tree-like because the origin of the eukaryotes coincided with a symbiotic event that led to the “fusion” of an archaeobacterium and a eubacterium. The problem is that I think they are right. That is, eukaryotes are chimeric, and the tree of life is actually “a Ring of Life” – to use Jim Lake’s evocative definition. The implications, of this, from the phylogenetic standpoint are huge. Eukaryotes are the only monophyletic “domain” of life, while both Archaeobacteria and Eubacteria are paraphyletic with reference to the eukaryotes. I think all this is just amazing!

**What organisms have you worked on, and which are your favourites?**

During my academic career I have been studying a variety of organisms. Of course, having a background in theoretical phylogenetics has helped me to become a fairly flexible phylogeneticist. My earliest studies focused mostly on fossil vertebrates. I am still involved in the study of vertebrate palaeontology, but these days I engage in fossil-based research through collaborations with palaeontologists at the University of Bristol. I have also worked on sponges, caecilian amphibians, echinoderms, prokaryotes and unicellular eukaryotes. I have

also had involvement in arthropod research for quite a while. I proposed the Myriochelata hypothesis, and I am still working on this group. More generally, current studies in my laboratory focus on prokaryote and eukaryote phylogenetics, the origin of animal phyla, and arthropod interrelationships.

I think all living organisms are interesting, but I particularly like the extremophilic prokaryotes, because everything that can grow optimally in boiling water intrigues me, and the eukaryotes, because of their dual ancestry and their fascinating chimeric nature.

**How many hours per week do you work?**

I guess these days I probably work an average of 50 to 60 hours per week. It is difficult to say. I used to work longer hours, but last summer my first child (Olmo – which is the Italian name of the elm tree) was born, and of course my lifestyle has changed quite drastically.

**What percentage of time do you spend on each of your different responsibilities?**

Since I became a lecturer my administrative and teaching duties have increased significantly. This winter most of my time was spent teaching or supervising undergraduate students. When I am not teaching, and I am done with

the administration, I work in the lab (or I should say in front of my computer). I am lucky that most of my research is computational, so I can often set up analyses in the evening and let them run during the day while I am busy teaching and/or carrying out administrative duties.

**How many people are there in your lab?**

Currently I have only one PhD student in the lab, however a postdoc and a second PhD student will start during the summer. This winter there were five undergraduate students in the lab, while this summer two undergraduate students will join the lab for 10 weeks. These two students are, respectively, from Japan and Uruguay and will be in Ireland to participate in a Summer School of Molecular Evolutionary Research that I have organised together with my colleague James McNerney (also from Maynooth). The school is funded by Science Foundation Ireland, will initially run for three years, and will admit ten undergraduate students per year (which will join various research groups in Maynooth).

**What gives you the most satisfaction and frustration in your job?**

Satisfaction is the discovery, finding out something

unexpected. That is thrilling. Administration is frustrating. I also like to teach quite a lot, and I found supervision of PhD students quite rewarding.

**Do you have any international collaborations?**

I have many collaborators and I think that today you cannot do science without collaborators (national and internationals). I think this is one of the great things in science: it is a multinational collaborative effort. If I can use a sport metaphor, I would say that science is like rugby: it unites people, even when if they are in competition.

Currently, my main international collaborators are Mark Wilkinson, from the NHM in London, Mike Benton from Bristol, and Kevin Peterson from Dartmouth (USA).

**Is there any paper or book that has been very influential for your thinking?**

It depends what you mean with “thinking”. I was urged to become a biologist after having read Konrad Lorentz’s *King Solomon’s Ring*, and an evolutionary biologist after having read Steve Gould’s *Wonderful Life*. So it is clear that these two books had a very strong influence on me. A third book that had a very powerful influence on my life was Nico Tinbergen’s *Curious*

*Naturalists*. Of the three, the one that influenced me the most was Gould’s *Wonderful Life*. Note that I disagree with most of Gould’s ideas. What I think is great in *Wonderful Life* is that it is hugely inspirational, no matter whether you agree with Gould or not. When you read *Wonderful Life*, you feel that sense of awe that you get when reading the great novelists, like Twain and his *Adventures of Huckleberry Finn*, or Kerouac and his *On the Road*. After you read those books you almost feel compelled to hit the road, when you read Gould you almost feel compelled to become an evolutionary biologist. There are many other scientific (and non-scientific) books and papers that I found in some way inspirational. The work of authors of the like of Kimura, Woese, Mayr, Cavalli-Sforza, Simpson, was certainly inspirational. However, I think that I should particularly mention here two authors which I particularly like: George Estabrook and Jim Lake.

Reading George’s papers taught me about mathematical rigor. Notable are his early seventies papers where, together with McMorris and others, he defines the concept of cladistic character within a purely mathematical framework. Reading Jim

Lake’s work taught me about versatility. In fact, I think Jim Lake is quite an exceptional phylogeneticist from this point of view, one who has been able to make significant contributions to both theoretical (e.g. Lake’s *Invariant*, *Paralinear distances*, *Conditioned Reconstruction*, *Top-Down Rooting*) and applied (e.g. the *Ring of Life hypothesis*, the *Eocyte hypothesis*, the *Ecdysozoa hypothesis*, the *Complexity hypothesis*) phylogenetics and evolutionary biology. Some of his papers, especially those relating to the *Ring of Life* and to the *Complexity hypothesis*, are key to most modern discussions on prokaryotic evolution and the origin of the eukaryotes. Of course, the *Ecdysozoa hypothesis* is central to any modern discussion on the evolution of animals. Finally I think that some strictly speaking non-scientific authors also deserve a mention here, as they strongly influenced my thinking. These are (in random order): Cesare Pavese, Henry David Thoreau, John Steinbeck, Jack London, Pablo Neruda, Jack Kerouac, John Stuart Mill, Carlo Rosselli, Gabriel Garcia Marquez, Mark Twain and Ernest Hemingway.

**Who was the most important mentor in your career?**

Mark Wilkinson, probably the best mentor you can hope for.

**How many scientific publications do you have?**

I published 26 peer reviewed scientific publications since 2002.

**Could you nominate any of your discoveries or papers as the most important one, or the one (or several) that you personally like best?**

This has to be the 2007 Molecular Biology and Evolution article on the origin of the eukaryotes. There are many reasons why I think that paper was important. First we performed the largest phylogenomic analysis to date, analysing almost 6000 genes for more than 180 organisms. Note that previous phylogenomic studies rarely analysed more than a few hundred genes. So I think that with this paper (which was co-authored by James McInerney and James Cotton) we reset the standards of what should be considered a phylogenomic analysis. Secondly, this study finally and unequivocally showed that the supertree methods (a class of methods I have been working on since I was a PhD student) can be extremely useful phylogenomic tools. Thirdly, and most importantly, we showed that the eukaryotic genomes are chimeric, and that contrary to common knowledge, most of the genes

in our genomes are of eubacterial origin (a-proteobacterial), rather than of archaeobacterial origin. This of course is an observation of general relevance as it has to do with the nature of eukaryotes and therefore with the nature of humanity.

**Is there a particular contribution you generally bring to collaborative papers?**

I think it is the ability to deal with data sets that most other researchers would just consider to be impossible to analyse. I can easily handle data sets of hundred of taxa and thousands of genes. If you assume an average gene length of 100 amino acids, it means that I can easily deal with data sets of 200 or more species and 600,000 characters. Currently, for example, I am working on a data set of 450 eukaryotic species and 3.6 million sequences. Performing an all-versus-all BLAST analysis of this data set (which is necessary to identify protein families) took 1600 days (CPU-time). That is, if I was running this analysis on a desktop PC it would have taken more than 3 years. Yet, I completed it in just over a week by using a simple divide and conquer approach and distributed computing. Besides, of course, I am a theoretical phylogeneticist by training, and that means that I

can generally help my collaborators decide what is the best strategy to analyse a given data set.

**What skills do you think a successful researcher in your discipline must possess?**

I think the most important skill is multidisciplinary. Today, it is not sufficient to understand the general biology of the organisms you study, you need to understand molecular biology (as data are mostly molecular), you need skills in computational biology and computer sciences (to analyse the data), and an understanding of the Earth history (to place your results in a sensible geological framework). I think that very often the limiting factor for systematists is the lack of computational skills. Unfortunately, the days of the menu driven software are over. Today, you need to be able to compile software (even if you did not write the code). You need to learn how to automate processes in a UNIX environment (you need to learn Shell scripting), and quite often, you need to write some code yourself (for example in PERL or PHYTON) to carry out tasks for which there is no software available.

**Do you have any tips for students aspiring to a career like yours?**

Never give up. The postdoc years in particular can be very hard, you will be moving from town to town, perhaps from one country to the other, without much certainty about your future. This is very frustrating, but the first years after your PhD are essential, so concentrate on the present and do not worry too much about the future. You can always get out of the academia. Choose your post docs wisely, you need to publish as many paper as possible, and in good journals. Try to join a group with a high output of published papers, and with many international collaborators. The latter point is very important because through these collaborators you are quite likely to be able to find your next postdoc.

**What do you think are currently the greatest impediments to achieving a successful career in your field?**

I think funding is our major problem. Obtaining funds is often very difficult, particularly for young researchers, but I also think that this is not necessarily a fault in the system. Scientists should be more aware that Euros (or Pounds) are not from heaven; they come from the taxpayers' pockets. Accordingly, scientists have the moral duty to be careful with this money. It is thus

generally a good idea to think about your projects from two points of view. Think of what you want to do, but think also of what the taxpayers might want from you, because ultimately, they are your employer. So, always ask yourself: in what way can I contribute to the good of the society? This is a key question that sometime scientists forget to ask themselves. If you can come up with ideas that make your work of relevance to society, you will significantly increase your chances of obtaining funds, and I guess in the end you will always feel better with yourself.

## Book Reviews

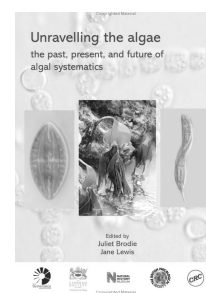
**Unraveling the Algae. The Past, Present, and Future of Algal Systematics**

Brodie, J. & Lewis, J. (eds.).  
CRC Press, Taylor and Francis Group, Boca Raton, FL.,

Systematics Association  
Special Volume 75, 402 pp.  
ISBN: 9780849379895.  
Hardcover: £65.99

For anyone who has spent time in a diverse intertidal community, trying to find and identify the individual algae present, the title of this collection certainly should

resonate. To the uninitiated, it can be difficult simply to disentangle where one individual alga ends and another begins. To the veteran of algal sampling, trouble might lie in teasing apart phenotypic plasticity from species diversity. To experts, trying to tie various algae together in stable and natural systematic frameworks has presented problems at nearly every taxonomic rank. Thus, algal enthusiasts at all levels will find "Unravelling the Algae" a useful resource, especially those hoping to keep pace with the dizzying changes brought on by the use of molecular characters in algal systematics. For most major algal groups, this volume provides a solid history of systematic classification, a detailed explanation of how recent molecular investigations have impacted historical views, and a thoughtful discussion of the additional challenges remaining for researchers in the field.



In their introduction, editors Juliet Brodie and Jane Lewis explain that the book is divided into thematic sections; three introductory chapters intended to frame the complex

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## New Journal

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### Biogeography & Systematics

#### a New Journal for Taxonomists and Biogeographers

Under the auspices of the Systematic and Evolutionary Biogeographical Association (SEBA – <http://www.uac.pt/~seba/>) a new journal, *Biogeography & Systematics*, is to be launched later this year; a call for papers has already been announced (<http://www.uac.pt/~seba/?q=taxonomy/term/21>). The journal is primarily an online production specialising in, but not exclusively, larger monographic studies in biogeography and systematics, as well as history, theory, methodology and epistemology. While the journal will consider papers that focus solely on a particular taxonomic revision of a group, preference will be given to those contributions that provide a biogeographical analysis of an area or the taxon in question.

*Biogeography & Systematics* will initially have 20 copies of each number printed to be deposited in accessible libraries around the world. Thus, the journal will conform to publication requirements as outlined in the International Codes of Zoological and Botanical Nomenclature.

The reasons for starting this journal are many but the driving force is the desire to provide a forum for taxonomists whose studies of a taxonomic group include biogeographic analysis and interpretation and require a greater page number so that primary data and analyses can be included in the body of the paper. Usually, these kinds of studies require new taxa to be named and, after biogeographic analysis, the nodes on a cladogram(s) require proper identification. Many systematics print journals will now no longer publish primary data, relegating such details to online supplementary material. The reasons and consequences of such policies were outlined in a recent paper by José Padial & Ignacio De La Riva, the situation eloquently captured in their title ('Taxonomy, the Cinderella of science, hidden by its evolutionary stepsister', *Zootaxa* **1577**: 1–2, 2007). Their concluding sentence runs: "If taxonomies cannot be included in the main body of phylogenetic or biogeography-oriented papers, they should be published elsewhere as full peer-reviewed articles". That elsewhere is *Biogeography & Systematics*.

David M. Williams<sup>1</sup>, Malte C. Ebach<sup>2</sup> & Dalton Amorim<sup>3</sup>

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issues related to algal systematics, a 13 chapter walk through the various algal phyla and, finally, two chapters that look to the future. There is no doubt some logic to this structure, but many readers (certainly any novice in algal

systematics) might want to rearrange the sampling order just a bit. I would recommend beginning at the end, with "Algal molecular systematics: a review of the past and prospects for the future" (chapter 18) by Medlin, Metfies, John and Olsen.

Although it does provide a nice discussion of current and likely future controversies, such as DNA barcoding, it also offers the most concise and eminently readable general overview of the major methods that have reshaped a good deal of the systematic framework covered in the book. Given that much of the "unravelling" discussed throughout is based on molecular data, I'd recommend diving into this chapter first.

As for the three formal introductory chapters, Charles Delwiche does a particularly effective job (chapter 2) of summarizing complex issues related to how plastid endosymbioses have shaped algal diversity, and outlining remaining areas of controversy. This chapter certainly fulfils the mission intended by the editors. The following two chapters might be better sampled as dessert than as appetizers. Chapter 3 by Cavalier-Smith reviews where various algae fit on the "major branches of the tree of life." It is chocked full of details and nomenclature on numerous eukaryotic taxa, and advances some fairly complicated and often controversial phylogenetic scenarios. Many readers will be better able to follow the arguments, and come to their own well-reasoned conclusions, once they have absorbed information about



the diverse algal groups contained in the rest of the book. Likewise, in chapter 4 David Williams compiles an extensive and scholarly

state of algal systematics across all these phyla is that molecular characters have produced the most satisfying results in groups with the

**algal enthusiasts at all levels will find “Unravelling the Algae” a useful resource, especially those hoping to keep pace with the dizzying changes brought on by the use of molecular characters in algal systematics.**

history of diatom systematics, which makes an excellent companion to the later chapter on diatoms (chapter 13) by Mann and Evans. However, this history is presented to frame a polemic against paraphyletic groupings in classification, an argument readers will more easily digest after first acquiring the solid working knowledge of algal systematics presented in subsequent chapters.

Chapters 5 through 16 are devoted to the current state of knowledge in nearly all major groups of algae; the only notable exception is the Glaucophyta, for which fairly little is known in any case. Just about all authors provide worthwhile up-to-date reviews of recent developments based on molecular phylogenetic analyses. Of course, systematic classifications at certain key levels and in many groups remain in flux, so some chapters are more up to date than others, and a few likely will be somewhat out-of-date in short order. One clear theme that emerges after reading through the current

richest histories of systematics based on cellular and ultrastructural features. For example, chapters 7 by Pröschold and Leliaert and 8 by Hall and Delwiche demonstrate the power of molecular phylogenies when used to test, reinforce and expand the rigorous systematic framework developed from flagellar architecture and patterns of cell division. Likewise, in their discussion of red algal systematics, Maggs, Verbruggen and de Clerck (chapter 6) provide a compelling example of how combining classical observations on fertilization development, later ultrastructural investigations of pit-plugs during cell division, and finally molecular phylogenies, led to a more robust systematic framework for Florideophyte red algae. It is clear that when such “polyphasic” approaches are possible, as Pröschold and Leliaert call them, they have produced systematics at class and ordinal levels that are likely to be stable for the

foreseeable future.

For many algae particularly microalgal phyla, comparably reliable ultrastructural characters have not been available, and a number of chapters covering these groups come to somewhat less satisfying or at least definitive conclusions.

For example, Robert Anderson provides a clear and thorough review of the interplay between structural and molecular characters in chrysophyte and synurophyte algae (chapter 15), and asserts that it is unclear as yet how to resolve discord between the two. As he puts it, “*The eventual resolution of conflicts between morphology and molecules will also require careful reexamination of the organisms, their various life forms, and their sexual reproduction...*” Even well-resolved branching orders leave a great deal to be desired, if they do not help to systematize and understand the underlying biology of the algae in question.

In an outstanding chapter on diatom systematics, Mann and Evans further describe the problem: molecules “*have an almost metaphysical outworking: the data they produce are generally not valued by taxonomists for what they are in themselves, only for what they imply about relationships between different organisms.*” They go on to point out that

*“for the first time in the history of systematics, there is beginning to be a significant divergence between the kinds of characters we use to describe and recognize taxa and the characters that are most effective for determining relationships.”* In a compelling review (chapter 5) on challenges faced in cyanobacterial systematics, Hayes Adel El Semary and Sánchez-Baracaldo, demonstrate that morphospecies are not reliable but that molecule-based classifications create their own problems, and may ultimately bring us no closer to a stable and satisfying resolution. It is clear from these and other chapters, that the ultimate unravelling of much of microalgal systematics will require new and innovative approaches to escape what, at present, may be unresolvable conundrums.

In a brief review, such as this, it is not possible to discuss all the chapters individually, but each has something worthwhile to offer. For example, although one of the shortest, chapter 9 on the chlorarachniophytes by Ishida, Yabuki and Ota, compiles new and exciting genetic and genomic results, many of which have yet to make their ways into textbooks. Parenthetically, this chapter is worth the read just for its quality of writing. Wondering where to find

chlorarachniophytes? Try looking *“In a bright shallow lagoon of a coral reef, among the bushes of tropical green seaweed...”* or *“...among the drifting seaweeds, [where] tiny green single-flagellated plankton swim.”* In addition to many similarly valuable chapters, the volume contains an excellent glossary of both systematic and phycological terms and provides, up front, an easy to find list of abbreviations that will be most helpful to almost all readers.

Because of the dynamic nature of algal systematics, one of the most insightful decisions made by the editors and most of the authors was to provide a thorough and scholarly historical context for the recent developments in each respective group. That is, they explain how the specific algal taxon was organized classically and how systematics may have changed during earlier revolutions based on cytological, ultrastructural or biochemical data. This kind of information can be difficult to locate for many algal groups; prior to this publication, I don't think it could be found for the algae as a whole in a single and handy source. Thus, regardless of further changes brought about by current and emerging technologies, this valuable historical perspective will be

timeless. As an instructor in the biology of algae, that aspect of book itself is worth the sticker price, and guarantees that this volume will have a place on my bookshelf for years to come.

As with efforts to unravel a twisted and knotted telephone cord (my apologies to the cell phone generation ...try substituting an electrical wire or garden hose), many initial steps lead to further and unexpected tangles. For algal systematics, this appears to be most true for questions related to species delimitation, and those at the broadest taxonomic levels. For example, most of the chapters related to groups with serially-derived red algal plastids are framed within the working hypotheses of the Chromalveolata. Recently, the chromalveolate model has come into increasing conflict with both plastid and nuclear characters and its future is uncertain, at least in its current incarnation. In this, and numerous other cases, there is likely to be further unravelling of new tangles that emerged from initial molecular systematic studies.

Far from a weakness, however, delineating current uncertainties is perhaps the greatest strength of this compilation. The editors' stated goal is *“...to inspire the next generation of scientists to study the taxonomy/systematics of*

*algae.*” In laying out both the advances and the difficult challenges that have emerged from molecular studies, they have made the best choices possible. When I first was attracted to the field of phycology, it was because there were really big and exciting questions to be addressed. Many of those same questions, in one form or another, keep me interested to this day. That so many of important issues remain unresolved, from what defines a species for most algae, to how major groups originated from heterotrophic ancestors, is perhaps the best bait to entice the brightest and most free-thinking young researchers to join the ranks of algal systematists. I suspect that this book will be a valuable asset in helping to achieve that goal.

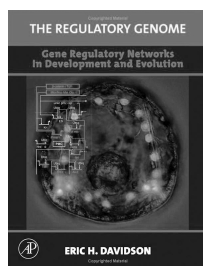
**The Regulatory Genome.  
Gene Regulatory Networks  
in Development and  
Evolution**

Davidson, E. (2006).  
Academic Press, U.S.A. ISBN  
13: 978-0-12-088563-3; ISBN  
10: 0-12-088563-8.  
Hardcover: £43.99

Eric Davidson is no household name in systematics. He is an embryologist at the California Institute of Technology, and he specializes in understanding how the

regulation of gene expression relates to the development of animal form.

A few years ago Davidson and his lab managed to provide the first detailed elucidation of a genomic regulatory network involved in development based on many years of



ingenuous and elegant embryological experiments: the endomesoderm specification network in the sea urchin *Strongylocentrotus purpuratus* (Davidson et al. 2002).

This work becomes of outstanding interest to systematists when placed in an evolutionary context, and this has long been an overarching goal of Davidson who has produced some of the most provocative and imaginative ideas about animal evolution of the last several decades. For example, a 1995 *Science* paper led by Davidson was titled “Origin of bilaterian body plans: evolution of developmental regulatory mechanisms.” This paper explicitly rooted the explanation of the Cambrian radiation of animal body plans in the structure of genetic regulatory mechanisms that underpin embryonic

development. Not surprisingly, the paper has earned a certain amount of notoriety in the field, attracting 213 citations at the date of this writing. Refining and elaborating his thinking to book length, Davidson published *Genomic regulatory systems: development and evolution* in 2001. The last chapter of that book presented a provocative and tantalizing discussion of what the structure of genomic regulatory systems could teach us about animal body plan evolution. However, when the time came to update the book for a second edition a few years later, “everything seemed to have been transformed to another landscape” Davidson writes in the preface of his new book.

So *The regulatory genome* is built upon a stronger empirical foundation than the previous work, incorporating many new insights about the nature of developmental gene regulatory networks. This stronger foundation in the genetic underpinning of development is then mined in the final chapter of the book for new insights about the evolution of animal form. This final chapter by itself fully justifies buying this book.

The first four chapters of the book provide a detailed overview of the nature and functional significance of the

regulatory apparatus that is encoded in the genome. The core components of genomic regulatory architecture are the *cis*-regulatory sequences of genes. These DNA regions regulate the pattern of transcriptional activity of genes in space and time.

The *cis*-regulatory regions consist of modules in which transcription factors can bind, and these regions achieve the regulation of gene activity by functioning as information processing units that integrate the various inputs they receive from combinations of transcriptional activators and repressors. The architecture of gene regulatory networks (GRNs) is defined by the functional relationships between transcription factor encoding genes, and between these and genes encoding signalling molecules. The functional relationships between these genes consist of the interactions of the transcription factors that these genes encode and their *cis*-regulatory regions. The ultimate output of developmental GRNs is the regulation of the expression of genes that do not encode transcription or signalling factors. These genes are therefore located at the periphery of the GRNs, and consist of the protein coding differentiation genes that actually built parts of the phenotype (contractile

proteins in muscle cells, pigment in skin cells).

The final chapter explores the implications of the architecture of GRNs for the evolution of morphology. Here the architecture of GRNs is used as a guide to the likelihood of the occurrence of viable mutations (i.e. those that allow the organisms to survive and reproduce), and the expected magnitude of

phenotypic changes. The most striking of these arguments are summarized in Davidson & Erwin (2006). At one extreme, at the periphery of GRNs, changes in differentiation genes (either in their coding or regulatory sequences) are expected to be both frequent and relatively minor in effect. Because these changes have no downstream consequences for the regulation of gene expression, and thus development, these changes are the stuff of adaptive evolution, often characterizing differences between related species (integument colour). The other extreme are changes in components of GRNs that Davidson & Erwin (2006) call 'kernels.' Kernels are circuits of interacting regulatory genes with the defining criteria that

they influence each other's transcriptional activity, that their coordinated activity is uniquely employed in the development of a certain body part, and that interference with the expression of any one kernel gene destroys kernel function, preventing proper development of the affected body part. Since changes in the expression of kernel genes are likely to lead

**I strongly recommend [the book] to everybody who is interested in the reconstruction of phylogenetic relationships based on morphological and molecular data irrespective of the nature of the organisms he or she is working on.**

to developmental catastrophe, evolution of the dependent body parts may be severely constrained. This is proposed as a mechanistic explanation of the existence and evolutionary inertia of animal body plans characters. The relative evolutionary volatility of body parts may then in large part be due to differences in the regulatory architecture that underpins their development.

This is of course where GRNs become very interesting to us systematists. Davidson in effect proposes that the phenotypic consequences of changes in different parts of GRN architecture roughly correlate with the Linnaean hierarchy. Changes in differentiation genes can occur frequently, and these produce differences

commonly observed between closely related species. Qualitatively different changes in less peripheral parts of GRNs will result in larger phenotypic effects, such as those that roughly separate different families, orders, or classes. Such changes tend to occur less frequently because of the greater likelihood of downstream pleiotropic effects that can disrupt development. These claims put up for discussion a lot of fundamental issues that have already started to be debated (once again in most cases) in the recent literature. Is macroevolution just microevolution writ large, or are they underpinned by qualitatively different kinds of genetic change? Are there marked discontinuities in evolutionary step sizes based on where the regulatory genome is changed by a mutation, and might these correlate with observed differences in the amount of intraspecific phenotypic variation and the step size of morphological transformations at different times in a clade's history? Is, in contrast to what all good neo-Darwinians should assert, homology perhaps more than just historical residue? What are the relative contributions of external selection pressures and internal constraints in determining the direction of evolutionary change? Have there been, as Davidson &

Erwin (2006) claim, no new origins of phylum-level body parts since the Cambrian because of the constraints imposed by GRN kernels?

These fundamental issues are always worth discussing, and they deserve our dedicated attention. However, as Davidson himself candidly admits, there is now a more pressing need for more empirical data. History shows that personal conviction and intuition are insufficient to resolve these issues. Let us hope that the next decade will shed new empirical light on these fascinating fundamentals of systematics.

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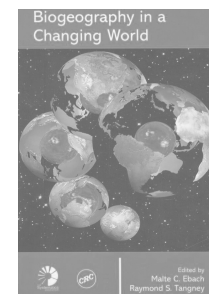
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### Biogeography in a Changing World

Ebach, M. C. & Tangney, R. S. (eds). (2007). Systematics Association Special Volume 74, U.K. ISBN 10: 0-8493-8038-3; ISBN 13: 978-0-8493-8038-9. Hardcover: £47.49

The book 'Biogeography in a Changing World' is in large

part based on the papers presented at a symposium titled 'What is Biogeography?' held in Cardiff in August 2005 as part of the Fifth Biennial Meeting of the Systematics Association. According to the editors of the book, biogeography is suffering from something like an identity crisis, being closely connected to and partly dependent on other biological disciplines (such as ecology, evolution, taxonomy or molecular systematics) but also struggling to maintain a position as an independent discipline with a core of accepted knowledge and



methodological principles that guide research. Contributors to the book are current leading proponents of differing methods in biogeography and the aim of the book was to produce a broad-based perspective on the nature of biogeography offering both historical perspectives and methodological advances as well as a foresight as to what the future might hold for the discipline. Rather worryingly, Adams' foreword and his animation of an expanding

earth featured uncompromisingly on the cover and McCarthy's final chapter, seem at odds with the declared pluralistic approach of the book, and leave the reader with the feeling that perhaps here current geological understanding is being unhinged with the wrong tools.

Given the many definitions in the book for subdisciplines of biogeography, e.g. historical, cladistic, or phylogenetic biogeography, it is obvious that there is no easy answer to the question 'what is biogeography?'. It is also obvious that biogeography as a discipline is severely divided with authors stressing the importance of finding shared patterns of distribution and others focussing on identifying causes of patterns, some stressing the importance of vicariance, and others of dispersal. We find it a pity that Ebach's introductory pages put more effort in carving a deep fracture between disciplines – ultimately pinpointing at the alleged 'faults' of phylogenetics – rather than preparing a constructive framework for a subsequent synthesis. We could not help but sometimes feeling 'attacked' by some authors for being phylogeographers and failing to use terms, concepts, methods and philosophies that are central to biogeography.

However, if such concepts are not without controversy even amongst biogeographers themselves, that should come as no surprise! In our opinion – as fortunately Riddle & Hafner manage to convey in Chapter 7 – genetic tools have the potential to 'solve' or at least circumvent many controversies in biogeography, by discovering patterns (e.g. revealing cryptic species) and at the same time uncovering processes (e.g. direction of gene flow) or to provide a historical biogeography for one (or several species) that may include episodes of vicariance followed by range expansion and dispersal.

The first chapter by Williams is aimed at providing an historical grounding for the book, by focusing on the 'threefold parallelism' between ontogeny, phylogeny and paleontology – championed in particular by Ernst Haeckel at the end of the 19<sup>th</sup> century – and discussing its importance in the development of modern biogeographical thinking. Whilst we believe that an historical perspective is crucial to understand the rise (and fall) of scientific ideas, we also felt that if this chapter had been 60% shorter, it would have provided a much more focused 'rooting' for the subsequent essays. Instead, it offers a huge amount of interesting, yet largely irrelevant, information about

the 'conflicts of intellect' between Haeckel and Agassiz. The conclusion of the chapter, well in line with Ebach's opening, again seems to call for the need for biogeographers to 'stick' to classification of areas, and refrain from using methods aimed at 'discovering ancestry', which – more than three decades after Dobzhansky's famous statement – sounds puzzling to say the least.

In the second chapter, Parenti warns against the philosophy that one aim of historical biogeography is to generate an explanation as well as to discover a pattern. She also warns against a rejection of biogeographic patterns using estimates of divergence times based on molecular data (because calibrations rely for a large part on fossils). She unjustly blames the application of molecular tools to biogeography for reviving untestable hypotheses of center of origin, recognition of ancestors, and dismissal of the importance of Earth history at all levels. However, she admits that molecular data also have great potential to unravel fine scale patterns of relationships among endemic areas, especially throughout the marine realm where they have not been expected. She also calls for a reclassification of global biogeographic regions, which should include

both terrestrial and marine components.

In chapter three, Grehan starts with yet another stern attack of molecular methods (a section entitled 'Molecular Mithology'!) and the defence of systematic 'biogeographic maps', fully independent from a Darwinian approach, as fundamental units of biogeography. He then goes on in the attempt to deconstruct a long-distance dispersal model developed for a genus of daisies. Data from other taxa with similar disjunct distributions are invoked to support a 'fit-for-all' vicariance model possibly consistent with an expanding Earth. Despite the lack of details provided, a number of aspects remain unclarified, and a great extent of the evidence provided could be interpreted in more than one way.

The fourth chapter by Hausdorf & Hennig deals with biotic element analysis and vicariance biogeography. These authors provide a clear argument that it should be tested first whether the clustering of ranges is stronger than expected by chance (thus vicariance should not be predisposed) and describe how this should be done with some clear examples. The appropriate units for this are biotic elements, i.e. groups of taxa with similar ranges, and not areas of endemism because

they cannot be delimited if dispersal occurred. Secondly, another prediction of the vicariance model is tested, namely that closely related species originate on different sides of an emerging barrier. Their case studies indicated that speciation modes other than vicariance were frequent or that the imprint of vicariance on the ranges was often obscured by extensive postspeciation dispersal, regional extinction or sympatric speciation. The methods described in this chapter can help to identify those taxa and areas that are most promising for further analysis of vicariance events.

Chapter 5, by Stuessy, is a clear and useful synopsis on the different processes affecting species and genetic diversity during the four successive phases in the ontogeny of island biogeography. Shifting from the classical McArthur & Wilson's model, the author stresses that diversity never really reaches an equilibrium, and that island-island and/or island-continent comparisons of biological diversity should always take into account the 'ontogenetic phase' of the biotas considered.

According to Sanmartín in chapter 6 historical biogeography aims to infer the distribution history of biotas and to identify the causal factors or processes that have shaped

those distributions over time. She reviews recent methodological developments that are event-based and have led to an extraordinary revolution in biogeographic studies. She convincingly shows that including *all* biogeographic processes into the analysis is the way forward for biogeography. She clearly explains and compares two event-based methods, dispersal-vicariance analysis and parsimony-based tree fitting, and offers practical tips as to when to use which method. She dismisses a common critique against event-based methods (that if the models are wrong, the biogeographic inference would be wrong) by citing Ronquist's (2003) argument in favour of model-based methods in phylogenetic analysis (such as Maximum Likelihood and Bayesian inference) 'ignoring process in the formulation of a method does not make it more objective; the method's performance is still determined by the nature of the evolutionary processes being studied'.

The excellent chapter 7, by Riddle & Hafner, is the only chapter that attempts to bring historical biogeography and phylogeography closer together. The authors identify two promising areas of growth likely to bridge the gap between phylogeographic and area-based biogeography:

statistical phylogeography and comparative phylogeography. Indeed, as neatly synthesized in Figure 7.4, the latter (defined as the geographical comparison of evolutionary subdivision across multiple co-distributed species or species complexes; Arbogast & Kenagy 2001) can generate the hypothesis than can be subsequently tested by the former. The authors also present a case study illustrating the application of a five-step approach to interactively and successfully employ phylogeographic and biogeographic analyses in the study of the warm desert biota of western North America.

As much as chapter 7 seemed to finally come to a fruitful synthesis, we were left bemused by McCarthy's closing contribution. As early as in the abstract, and all the way to the final summary, the author seems to follow a personal agenda to use some selected biogeographic evidence that would uphold the expanding Earth theory. McCarthy argues that for a number of relatively closely related taxa found on both sides of the Pacific Ocean, dispersal interpretations do not fit, whilst a vicariance interpretation of an expanding Earth, featuring a spectacular opening and expansion of the Pacific beginning in the Triassic, would explain all disjunct distributions. Unfortunately, McCarthy does

not adopt a rigorous scientific approach for his paper, especially for scientists that are unfamiliar with the expanding Earth theory. He lists his arguments leaving little room for the consideration of alternative possibilities, even though the explanation provided (the expanding Earth) is by far the least parsimonious. Not only – as noted by Briggs (2004) – can the expanding Earth theory not explain the Precambrian to Paleozoic fossil record of marine life, which provides evidence of extensive oceans, but more importantly, the very geological and physical disciplines that he invokes as support for the theory have long dismissed the expanding Earth as pseudoscience, on the grounds of its disagreement with paleomagnetic estimates of the Earth radius (McElhinney et al., 1978) and its moment of inertia (Williams, 2000). Perhaps even more gravely, expanding Earth assumptions are in contrast with overwhelming evidence of subduction and the basic principles of Einstein's theory of General Relativity, and the Standard Model of particle physics.

McCarthy's final summary should have probably included a fourth point, stating: 'no researcher supporting the expanding Earth theory has hitherto provided any scientifically

sound framework to uphold what essentially are plain speculations and grave assumptions'.

In our opinion, biogeography cannot survive without embracing genetic tools, a bit like systematics has done before. This book was certainly an unconventional read to us and sparked some ideas about focussing more on species with shared distribution patterns in a comparative framework. Yet, we are still unsure as to the real purpose of the book: if its main intent was to bridge different approaches and philosophies currently contributing to biogeographic analysis, and to pave the way for their synthesis and integration, we believe the objectives have not been met, as only one chapter (7) seems to possess such synthetic characteristics. If the goal was instead to simply showcase the current methods in biogeography and forecast its potential future developments, the picture obtained is still that of a field characterised by a deep fracture, across which the 'dispersal' of novel ideas for scientific integration appears strongly hindered.

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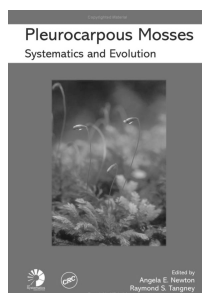
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**Pleurocarpous Mosses**  
Systematics and Evolution  
Newton A. E. & Tangney,  
R.S. (Eds.) (2007) CRC Press,  
Taylor & Francis Group.  
ISBN9780849338564  
(hardcover)  
82£, 149.95\$, 104.99€

The book is the product of a  
symposium on pleurocarpous  
mosses held at the National  
Museum of Wales, Cardiff in  
2004.

Pleurocarpous mosses are the  
largest group of mosses,  
comprising around 6,000 of  
the overall assumed 10,000  
species. By far the largest  
group of pleurocarps, the  
Hypnales underwent a rapid  
radiation and is  
morphologically highly  
plastic, which in the past  
made it a very difficult task to  
reconstruct the phylogeny  
solely based on morphology  
and intuition.

In its history the  
classification of the  
pleurocarpous mosses has  
been subject to great changes  
mainly due to changes in the  
evaluation and interpretation  
of morphological characters.  
At one time sporophyte  
characters were believed to  
provide the most useful  
information for systematics;  
later, gametophyte characters  
were accepted as the most  
important. These points of  
view alternated until



molecular methods were  
available. Only then, when  
more reliable phylogenies  
were available for the first  
time, could morphological  
characters be (re)evaluated.

The book gives an  
overview of the recent  
knowledge of relationships of

the pleurocarpous mosses  
based on molecular data but  
without neglecting the  
morphology, as unfortunately  
happens so often in the recent  
molecular era. In contrast, the  
morphological characters are  
re-evaluated in the light of  
molecular results and much  
interesting congruence is  
found even though there are  
many remaining questions.

The first chapter is  
dedicated to the history of  
pleurocarp classification,  
pointing out the problem that  
the usefulness of  
morphological characters of  
gametophyte and sporophyte  
has been assessed very  
differently in history, leading  
to periodic and quite drastic  
changes in the classification  
of this group. Several aspects  
of this problem are addressed  
in the following chapters.

The next chapters  
throw light on the  
relationships of the earliest-  
diverging lineages of mosses  
in which pleurocarpous  
morphology appeared using  
both molecular and  
morphological data, followed  
by chapters about other basal  
pleurocarpous groups,  
comprising reconstruction of  
their phylogeny and re-  
evaluation of morphological  
characters.

Chapters 6 – 10 focus  
on the relationships within the  
Hypnales, the most derived  
and by far the largest order of  
pleurocarps, primarily based  
on analyses of molecular data

but never neglecting morphology. The main emphasis is put on the relationships within certain families but valuable insights into the backbone phylogeny of the whole pleurocarps are also gained. The strength of these chapters is the use and discussion of many different analytical techniques, like alignment optimization or the use of secondary structure to name only two.

In contrast to the previous chapters the following five (11 – 15) deal mainly with morphology. Morphological characters and their use in pleurocarpous moss systematics are reviewed. Many characters are critically evaluated or re-evaluated regarding homology/homoplasy leading to a new understanding of certain structures. For example, stem structures like pseudoparaphyllia are examined, and the branching architecture of whole plants which is necessary to define pleurocarpy s.str. and for understanding relationships within pleurocarps.

The two following chapters explore the origins of pleurocarpous mosses, the first one by utilizing fossil data and the second by calculations based on molecular data.

In the final two chapters, evolutionary questions are analyzed, one focusing on reconstruction of

morphological character evolution and the other on geographic distribution patterns of pleurocarpous mosses in the Australasian region in comparison with patterns known for angiosperms.

A very extensive and helpful index closes the book.

The technical quality of the book is also very good. It is printed on high quality paper.

Drawings and photographs are mostly of high quality although some of the black and white photographs could benefit from somewhat higher contrast. However, most of the photographs can be found as better full-color versions on the attached CD.

The book comes with a CD-ROM. It provides datasets corresponding to some of the chapters of the book, so that the interested reader can for example run analyses with his own programs and/or personal settings as well as use the datasets as a basis for further research without having to download the data from GenBank. It would be perfect to have data for all chapters but that's unfortunately not the case. Other contents of the CD are full-color versions of many of the B/W-photographs appearing in the book as already mentioned earlier and additional drawings as well as other information referred to

in the text. In order to be able to use the molecular datasets a copy of an alignment editor is included. One folder obviously contains photographs of the symposium and an excursion that took place in its context but there is no other information about their contents than the file-names. Thus, these photos will unfortunately be of use for the participants of the symposium only. A simple text-file with some information about the photos would have been helpful. The CD contains useful data but one cannot help thinking that it was assembled in a hurry.

To summarize, the book covers the current knowledge about the phylogeny of the pleurocarps as well as the ongoing research. It furthermore points at the open questions and discusses possibilities for their solution in the future. A wide range of methods for phylogeny reconstruction is critically discussed. It is not just one of the many books about molecular phylogeny of a certain group of organisms. Its strength is that the focus moves from molecular data to other aspects of biology, showing that molecular and morphological data for example can complement each other leading to a better understanding of the organisms' evolution. This "is a rare type of book for *any*

group of plants” as already Brent Mishler pointed out in the foreword to the book. Looking on the composition of authors it is noticeable that many names appear several times in different combinations demonstrating an extensive network of cooperating researchers, a fact that is surely contributing to the high quality of the book’s content.

The book is a ‘must have’ for all bryologists but I strongly recommend it to everybody who is interested in the reconstruction of phylogenetic relationships based on morphological and molecular data irrespective of the nature of the organisms he or she is working on.

Unfortunately, the high price will discourage many potential readers from buying the book. This is in so far a pity as especially interested students and young scientists would benefit from its contents

## Memorable Quotes

**“ We must remember the distinction between the cart – the explanation – and the horse – the data. And where models are introduced in phylogenetic reconstruction, we should prefer models dictated by features of the data to models derived from explanatory theories. ”**  
(Colin Patterson 1994)

# Spotlight



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## The Missing Link: Science Literacy

Scientists and science educators have a lot to account for. The lack of scientific education, even of the most basic kind, in the United States is appalling; or dreadful if we take into account that our world is becoming increasingly technological and that economic prosperity and jobs depend on a scientifically literate citizenry. According to a Gallup poll of 1,016 US adults, taken in November 2004, 45% of those surveyed favored the statement that “God created human beings in their present form within the last 10,000 years. (38% favored that “Man developed over millions of years, but God guided the process,” and 13% that “Man developed over millions of years from less advanced life forms.”)

The evolution/creationism divide is no less scary. In a CNN/USA Today Gallup poll of 1,001 adults conducted in

March 2005, 76% would not “be upset if public schools in [their] community taught creationism,” but only 63% would not “be upset if the schools taught evolution.” Only 22% would be upset if creationism would be taught, while 34% would be upset if evolution would be taught. Other polls yield similar statistics. There can be no doubt that a crucial link is missing in the US educational system: scientific literacy.

On January 4, 2008, the National Academy of Sciences (NAS) published *Science, Evolution, and Creationism*, which was prepared by a committee of the NAS, as an effort to counteract the widening exertions of antievolutionists seeking to eliminate from public schools the teaching of evolution, or at least, to “balance” it by also teaching creationism and intelligent design. *Science, Evolution, and Creationism* is the third edition of *Science and Creationism*, published in 1984, but sufficiently modified to deserve a new title. A second edition of

*Science and Creationism* was published in 1999.

*Science and Creationism* was prepared in response to statutes passed by the legislatures of the states of Arkansas, first, and Louisiana, shortly thereafter, that required that “creation science” be taught in the public schools together with evolution. The Louisiana “Creation Act” was appealed all the way to the United States Supreme Court, which in 1987 (*Edwards v. Aguillard*) concluded that the Act’s “primary purpose was to change the public school science curriculum to provide persuasive advantage to a particular religious doctrine that rejects the factual basis of evolution in its entirety. Thus, the Act is designed either to promote the theory of creation science that embodies a particular religious tenet or to prohibit the teaching of a scientific theory disfavored by certain religious sects. In either case, the Act violates the First Amendment.”

*Science and Creationism* was made part of an “amicus brief” submitted to the Supreme Court in *Edwards v. Aguillard* by the NAS, with the endorsement of the American Association for the Advancement of Science and other organizations.

In the 1990s, several authors schemed a new tactic to introduce creationism in the schools, or alternatively to

remove the teaching of evolution, by reviving the old “argument from design,” under the moniker of Intelligent Design Theory (ID). The argument from design for the existence of God, based on the complex organization of living things, was elaborated by English clergyman William Paley in his *Natural Theology*, published in 1802. Paley’s argument from design is twofold. The first prong asserts that humans, as well as all sorts of organisms, in their wholes, in their parts, and in their relations to one another and to their environment, cannot have come about by chance, but rather manifest to have been designed for serving certain functions and for certain ways of life. The second prong of the argument is that only an omnipotent Creator could account for the perfection and functional design of organisms. The new advocates of ID modified the second prong of the argument by referring to an unspecified “intelligent designer,” thus avoiding explicit reference to God, so that the argument from design would not necessarily have religious connotations, and thus could be taught in the public schools as an alternative to evolution. This hypocritical subterfuge amounts to nothing else than a charade. On December 20, 2005, John E. Jones III, Federal Judge for the Middle

District of Pennsylvania, issued a 130-page-long decision (*Kitzmiller v. Dover Area School District*) declaring that “The overwhelming evidence at trial established that ID is a religious view, a mere re-labeling of creationism, and not a scientific theory ... ID is not supported by any peer-reviewed research, data, or publications.”

*Science, Evolution, and Creationism* consists of three main chapters. The first chapter briefly describes the process of evolution and the nature of science in contrast to other forms of knowledge. The second chapter surveys the scientific evidence that supports evolution from diverse disciplines that include astronomy, paleontology, comparative anatomy, biogeography, molecular biology, genetics, and anthropology. The third chapter examines intelligent design and other creationist perspectives so as to point out the scientific and legal reasons against teaching creationism in public school science classes. The text concludes with a selection of frequently asked questions and additional readings.

Much has happened in evolutionary biology since the release of the first two editions of *Science and Creationism*. The new edition provides important updates about these developments.

Fossil discoveries have continued to produce new and compelling evidence about evolutionary history. New information and understanding about the molecules that make up organisms has emerged, including the complete DNA sequence of humans. DNA sequencing has become a

paleontology and the older disciplines continues to accumulate, such as the discovery published in 2006 and described in *Science*, *Evolution, and Creationism*, of *Tiktaalik*, a fish that lived in shallow freshwater streams and swamps about 380 million years ago. *Tiktaalik* is a nearly precise intermediate

asserted that “Nothing makes sense in biology except in the light of evolution.” Evolution provides a scientific explanation for why there are so many different kinds of organisms on Earth and gives an account of their similarities and differences (morphological, physiological, and genetic). It accounts for the appearance of humans on Earth and reveals our species’ biological connections with other living things. It provides an understanding of the constantly evolving bacteria and viruses, and enables the development of effective new ways to protect ourselves against the diseases they cause. Evolution has made possible improvements in agriculture and medicine, and has been applied in many fields outside biology, including forensics and software engineering; it has stimulated chemists, for example, to use the principles of natural selection for developing new molecules with specific functions.

**...many people of faith have questions about biological evolution, because they have been told that the scientific understanding of evolution is incorrect or at least doubtful, and that accepting evolution is not compatible with their religious beliefs**

powerful tool for establishing genetic relationships among species. DNA evidence has both confirmed fossil evidence and allowed studies of evolution where the fossil record is still incomplete. An entirely new field, evolutionary developmental biology, enables scientists to study how the genetic changes that have occurred throughout history have shaped the forms and functions of organisms. The study of biological evolution constitutes one of the most active and far-reaching endeavors in all of modern science.

Evolutionists are no longer concerned with obtaining evidence to support the fact of evolution. Rather, evolutionary research nowadays seeks to understand further and in more detail how the process of evolution occurs. Yet the evidence from

between typical fish and the first known four-legged animals, from which would evolve all animals that live on the land, from frogs to reptiles, to birds and to mammals, including humans. No intermediate fossils between humans and apes were known in Darwin’s time. Now, thousands of remains are known that belong to the human lineage after it separated from the lineage that goes to the apes.

Biological evolution is the central organizing principle of modern biology.

Biological evolution is part of a compelling historical narrative that scientists have

**The lack of scientific education, even of the most basic kind, in the United States is appalling; or dreadful if we take into account that our world is becoming increasingly technological and the economic prosperity and jobs depend on a scientifically literate citizenry**

In 1973, the eminent evolutionist Theodosius Dobzhansky famously

constructed over the last few centuries. The narrative begins with the formation of

the universe, the solar system, and the Earth, where conditions occur suitable for life to evolve. There are theories that seek to account for how life originated on Earth, but none of them has gathered enough supporting evidence to be generally accepted by scientists. But natural selection, discovered by Darwin, has been convincingly demonstrated as the process that accounts for the adaptive configuration and function of organisms, for their “design.” Darwin is often credited with providing compelling evidence that evolution has occurred, but Darwin’s greatest contribution to science is not that he accumulated evidence demonstrating the evolution of life, but that he discovered natural selection, the process that accounts for the design of organisms, their wonderful adaptations to survive and reproduce in the environments where they live: wings for flying, legs for running, eyes to see, and kidneys that regulate the composition of the blood.

A strategy of ID proponents and other creationists is to argue that science teachers should teach “critical thinking” and thus that they should present the controversies surrounding evolution. But there is no controversy in the scientific community about whether evolution has occurred. On

the contrary, the evidence supporting the evolution of organisms is both overwhelming and compelling. In the century and a half since Darwin, scientists have uncovered exquisite details about many of the mechanisms that underlie biological variation, inheritance, and natural selection, and they have shown how these mechanisms lead to biological change over time. Because of this immense body of evidence, scientists treat the occurrence of evolution as one of the most securely established of scientific facts. Indeed, critical thinking demands that ID and other creationist proposals be kept out of the science curriculum, because they lack scientific content: they are not scientific theories nor are they supported by any scientific evidence.

Religious authors, and scientists as well, have written eloquently about their awe and wonder at the history of the universe and of life on this planet, explaining that they see no conflict between the evidence for evolution and their belief in God. Authorities of diverse religious denominations have issued statements affirming the compatibility between the tenets of their faith and the acceptance of biological evolution. Science and religion concern different aspects of the human

experience. Scientific explanations are based on evidence drawn from examining the natural world and rely exclusively on natural processes to account for natural phenomena. Scientific explanations are subject to empirical tests by means of observation and experimentation, and are subject to the possibility of modification and rejection. Religious faith, in contrast, does not depend on empirical tests, nor is it subject to the possibility of rejection based on empirical evidence.

Nevertheless, many people of faith have questions about biological evolution, because they have been told that the scientific understanding of evolution is incorrect or at least doubtful, and that accepting evolution is not compatible with their religious beliefs. *Science, Evolution, and Creationism* speaks to these questions. It is written to serve as a source of information and as a resource for people who find themselves embroiled in debates about evolution. It should be helpful to “school board members, science teachers and other education leaders, policy makers, legal scholars, and others in the community who are committed to providing students with quality science education.” Moreover, as stated in the Preface, *Science, Evolution, and Creationism*

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“is also directed to the broader audience of high-school and college students as well as adults who wish to become more familiar with the many strands of evidence supporting evolution and to understand why evolution is both a fact and a process that accounts for the diversity of life on Earth.” Our educational system and society as a whole are best served when we teach science, not religious faith, in science classrooms. That is but one step in the efforts to fill in the missing link of science literacy.

*Science, Evolution, and Creationism* is beautifully produced and illustrated in color and only 70 pages long. An eight-page brochure, adapted from the full-length book, and also beautifully produced in color, is also available from the NAS. The brochure and the full-length document are available for free download and ordering at [http://www.nap.edu/catalog.php?record\\_id=11876](http://www.nap.edu/catalog.php?record_id=11876)

## Calendar

**2 July 2008**

**The Sir Julian Huxley Lecture**  
**Prof. Joe Felsenstein**  
**Talk: Not the Fly on the Wall: Can Systematists Cope With Uncertainty?**

**Linnean Society, London**

**2-4 July 2008**

**10<sup>th</sup> Symposium of the International Organization of Plant Biosystematists**  
**Evolution of Plants in Mountainous and Alpine Habitats**  
**Visoke' Ttatty, Slovakia**

**July 29-August 1r 2008**

**Saltation: Macroevolution by Profound Phenotypic Change Across a Single Generation**  
**Euro Evo Devo 2**  
**Ghent, Belgium**  
**Organizers: Richard Bateman (Kew), Jan Deutsch (Paris)**

**1-3 September 2008**  
**Climate Change and Systematics**

**Organizers:**  
**Trinity College Dublin, on behalf of Systematics Association and Linnean Society**

**3 October 2008**

**Beyond Cladistics – A Festschrift for Chris Humphries**  
**Organizers:**  
**David Williams (dmw@nhm.ac.uk), Paula Rudall**

**19-24 October 2008**

**4<sup>th</sup> International Rubiaceae (Gentianales) Conference,**  
**Jalapa, Veracruz, Mexico**

**2 December 2008**

**10<sup>th</sup> Young Systematists' Forum, Flett Lecture Theatre, The Natural History Museum, London, UK**

**3 December 2008**

**Annual General Meeting and Lecture**

**11-14 August 2009**

**7th Biennial Meeting**  
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