Moving forward in biogeography

With this, the fourth issue of *Biogeografía, Bulletin of the Systematic and Evolutionary Biogeographical Association* (SEBA) continues its aim to provide a voice for biogeographers through access to communication tools and an electronic Bulletin.

In the first three issues, *Biogeografía* has provided a platform for the presentation of a diverse range of perspectives on the relationship between systematics and biogeography from both theoretical and methodological viewpoints. Unlike many journals in the US and UK, *Biogeografía* is not constrained by the editorial requirement of perfect English, or English at all (allowing for Portuguese, Spanish and French contributions), or by particular assumptions about biogeography. If you have opinions or perspectives that you wish to present, *Biogeografía* is a place where they can be expressed – of course so long as it conforms to established principles respectful of etiquette and arguments grounded in presentation of evidence.

Book reviews are also considered an important element of *Biogeografía* as they provide an opportunity for the exploration and questioning of the methods and concepts that are so important for the science of biogeography. Naturally anyone with different views to those expressed in the book reviews is very welcome to contribute counter-points. It is through this process of exchange that biogeography can continue to grow as a science.

In future issues we look forward to encouraging research students as well as established researchers to contribute biographic accounts of their interest in systematics and biogeography with an outline of where they work and what they are working on – especially what excites them about their research subject and in biogeography in general. We will approach individuals for contributions, but please do not wait, contact us if you are interested. Contributions can be small or large, and no limits on images! Moreover, all URLs and emails will be published as active links.

After providing critical help and leadership with establishing *Biogeografía*, Juan Morrone is stepping down from the editorship in order to concentrate on other projects, but we look forward to his continued interest and support for the bulletin. We are very pleased to welcome Ivonne Garzon, a PhD student at the University of New Orleans. She is working on the phylogeny and evolution of life history traits of *Hamadryas* butterflies. Her research can be viewed at [http://biology.uno.edu/igarzon/Research.html](http://biology.uno.edu/igarzon/Research.html)

Please do not forget that SEBA has a website at [http://www.seba.uac.pt](http://www.seba.uac.pt) You will see that Pauline Ladiges, University of Melbourne, was recently awarded the Order of Australia for her service to the advancement of botanical science and research. If you know of any biogeographer receiving a national or other major award for their research please let us know as we would love to list the information on the SEBA website.

John R. Grehan
Malte C. Ebach
Ivonne Garzon
Co-editors, SEBA Bulletin, 2009
The twenty-seventh edition of the Brazilian Congress of Zoology, promoted by the Brazilian Zoological Society (SBZ), was held in Curitiba, Parana in February, 2008. The meeting was attended by more than 4,000 people including researchers, professors, school teachers, graduate and undergraduate students. During the five-day meeting, subjects such as evolution, evo-devo, biodiversity conservation, biogeography, threatened species, DNA barcoding, public health, zoology teaching, invasive species, animal physiology, forensic zoology and others were presented orally or discussed at the symposiums and halls of the convention center.

Indeed, at this events’ edition, biogeography was prominent in many subjects discussed. Presentations at the Neotropical Biogeography Symposium, coordinated by Dalton S. Amorim, were very popular and the full lecture rooms reflected the high interest of the audience and the vibrant curiosity about the theme. Approximately 800 people attended the first symposium day held in the main auditory and approximately 200 people attended the second day that was unfortunately held in a smaller room (Fig. 1).

John R. Grehan (Fig. 2) opened the biogeography symposium with a keynote talk about his own view on panbiogeography. Instead of explaining the audience basic panbiogeographic elements, such as tracks, standard tracks or nodes, Grehan exposed very clearly and objectively the essence of Léon Croizat’s philosophy and examples that illustrated his theory. His narrative about how he, Robin Craw and Michael Heads, at that time, graduate students, found Croizat’s work and started rescuing his thoughts was very inspiring for young biogeographers.

The following lecture was a ‘guideline’ on what to do and what not to do in biogeographic analysis. Dalton S. Amorim (Fig. 3) showed some elements that must appear in a biogeographic study in order to achieve robust and satisfactory results. He called attention for input localities precision, taxon identification and systematic position and asked for criteria on choosing biogeographic methods. One novelty presented by him was the concepts and methods. He reviewed the main biogeographical approaches and presented a well-argued trend towards integrating concepts and methods in evolutionary biogeography. In this way, many approaches can be successively employed and supplementary results achieved in order to rescue biotic components and cenocrons under congruent biogeological scenarios (Morrone 2007, Morrone 2009).

Alexandre C. Ribeiro presented a detail review about the main geological events that affected the formation of drainage basins in Atlantic Forest. This information referred to characid phylogeny to develop a biogeographical scenario for their present distribution.

Claudio J. B. de Carvalho (Fig. 2) presented some biogeographical patterns and processes in Neotropical and Andean regions. His information was based on three families of Diptera, relatively well known in Latin America. The patterns corroborate alternative biotic histories that can be attributed to distinct temporal
concept of ‘allochronic taxa’ – non-contemporary coincident taxa (Amorim et al. 2009), a perspective that provides a detailed and alternative way to approach temporal pseudocongruence in spatial analyses (Donoghue and Moore 2003).

Cladistic biogeography was presented and discussed by Charles M. D. dos Santos. During his lecture, he emphasized the need for phylogeny in biogeographic analysis, as argued in his recently published article (Santos and Amorim 2007). He presented results from his Ph.D. thesis and highlighted the need for Assumption 0 and BPA to be carefully employed in biogeographic analysis.

The second day of the symposium was opened by Juan J. Morrone (Fig. 3), whose lecture was about biogeographical biogeographic scenarios.

The challenges of marine biogeography were presented by Antonio C. Marques. He illustrated some of the difficulties found when analyzing poorly known taxa in a 3D environment. Some preliminary results were shown for jelly fishes sampled in the South Atlantic coast of South America and Antarctica.

A recurrent topic approached at the symposium was the temporal congruence and pseudo congruence, as commented on by Amorim (allochronic), Morrone (cenocrons) and others. Silvio S. Nihei approached the issue by highlighting the temporal factor at delimiting areas of endemism (Nihei 2008). The areas should be considered as hypothesis for a given time interval and the temporal dynamics considered in the biogeographical analysis.

Besides the Neotropical Biogeography symposium, the biogeographic theme was also present in many other symposia, such as Biodiversity conservation, Threatened Brazilian fauna, Cnidaria, Echinodermata, Ichthyology systematics and biogeography, and Bioinvasions. Approximately 130 posters about biogeographic patterns, method applications and taxa spatial distribution (regional to continental scale) were presented during the congress.

The success of the Biogeography Symposium in the Brazilian Congress of Zoology can be credited to the participation of the young Brazilian scientific community. The full rooms, the high attendance and the consolidation of some Brazilian biogeographers and the explosion of students searching for biogeographic training allows us to naturally predict that, in a not too distant future, a Brazilian biogeography meeting will be necessary.

Acknowledgments

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References


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Your chance to tell the world!

Don’t let others hog the limelight. If you are busy working on evolutionary and systematic biogeography then you have something worth saying. Biogeografia is one place you don’t have to worry about what opinion or perspective you might have – as long as it is said in a respectful manner. If you work on some kind of obscure (to everyone else!) plant or bug, addressing some of the conundrums of biogeographic methodology, analyzing the biogeography of a group or region, trying to find that final answer to reconstructing the spatial and biological meaning of life, or you want to write a critique that’s been sitting on the back burner, then we want to hear from you.

Here is also your chance to also write about yourself. We encourage anyone interested to write a biography, whether long or short, on what interests you, how you got interested, where you do your research, and what you hope to do in the future. So much of biogeography that affects each of us as individuals goes unsaid and is lost to history. But perhaps no more!

And remember, the electronic format of Biogeografia means that you can use color images, and there is no restriction on how many you might want to use!

Please send Spanish language contributions to Ivonne Garzon (ivonne.garzon@gmail.com) and English language to John Grehan (jgrehan@sciencebuff.org) or Malte Ebach (mcebach@gmail.com).
Croizat: A Software Package for Quantitative Analysis in Panbiogeography

By Mauro J. Cavalcanti

CROIZAT is a free, user-friendly, cross-platform desktop software package which biologists can use to integrate and analyze spatial data on species or other taxa and to explore geographical patterns in diversity under a panbiogeographic and graph-theoretic approach.

Over the last two decades, Panbiogeography as first conceived by Léon Croizat (1958, 1964, 1976) and further developed by researchers in New Zealand and Latin America (Craw et al. 1999, Llorente et al. 2000) became established as a productive research programme in historical biogeography (Craw & Weston 1984). Panbiogeography provides a method for analyzing the geographic (spatial) structure of distributions in order to generate predictions about the evolution of species and other taxa in space and time.

Panbiogeographic key concepts of track, node, baseline, and main massing have shown to be powerful analytical tools, especially following the mathematical formalization of these concepts with the development of quantitative panbiogeography (Page 1987, Craw 1988, 1989, Henderson 1989, 1991). Such developments were based on the application of concepts and methods from graph theory, for example minimum spanning trees to depict individual tracks in a more rigorous way, clique analysis to identify standard tracks, and nodal analysis to determine the precise location of panbiogeographic nodes. Panbiogeography emphasizes the analysis of raw locality and broader distribution data for taxa and may thus benefit from modern technological advances for the collection, storage, and analysis of such data as the Global Positioning System (GPS) and Geographic Information Systems (GIS) technology (Davis et al. 1990, Haslett 1990, McAllister et al. 1994, Scott & Jennings 1998). Furthermore, besides its academic interest and scientific relevance as a method for the analysis of earth/life historical relationships, panbiogeographic concepts may also be useful to address the critical issue of global biodiversity conservation in a potentially very fast and cost-effective way (Craw et al. 1999, Grehan 1989, 1992, 1993, 1995, 2000, Prevedello & Carvalho 2006).

As of today, there is no standard, general-purpose software for the analysis of distributional data under a panbiogeographic approach. Henderson (2003) wrote a program for plotting biogeographical distribution maps of the New Zealand region which can draw minimum spanning trees for distributions. Rojas (2004, 2007) developed a script for the ArcView GIS (ESRI 1998) for drawing individual and generalized tracks and nodes. However, there are no stand-alone, general-purpose programs specially designed to perform quantitative panbiogeographic analysis and facilitate the fast, interactive acquisition and editing of distribution information on taxa from taxonomic monographs, scientific collections, and electronic databases.

This hampers many research projects adopting a panbiogeographic approach, as well as the more widespread application of panbiogeographic concepts to biodiversity conservation. The availability of a software tool especially designed to address such need would be a welcome development.

Features

The CROIZAT program is based on the same database/analytical tools/map graphics model of many Geographic Information Systems, yet unlike GIS’s, rather than concentrating on database and graphics flexibility, it is designed to perform specialized biological analyses, many of which are not readily available in GIS’s.

Outstanding features of the CROIZAT program include:

• An easy-to-use, interactive graphical user interface, with pulldown menus, dialog boxes, and other standard controls, with almost identical look-and-feel on GNU/Linux, Microsoft Windows, and Apple Macintosh personal computers (Figures 1-3).
• Track analysis, for finding and plotting individual tracks as minimum-spanning trees from a distance matrix among stations.
• Clique analysis, for obtaining the largest cliques of compatible tracks, with randomization tests of significance.
• Nodal analysis, computing the degree of each vertex on a track to allow quantification of node importance.
• Data import in a variety of formats, including tab- and comma-delimited text as generated by all major online biodiversity databases (GBIF, FishNet, FishBase, HerpNet, CROIZAT is a free, user-friendly, cross-platform desktop software package which biologists can use to integrate and analyze spatial data on species or other taxa and to explore geographical patterns in diversity under a panbiogeographic and graph-theoretic approach.

Fig. 1. CROIZAT on GNU/Linux Ubuntu.
MANIS, OBIS, ORNIS), as well as standard GIS shapefiles (Figure 4).

- Locality records are displayed as symbols (squares, circles, crosses, etc) on the map, with different symbols for each species.
- Optional overlay of satellite imagery on maps, using NASA “Blue Marble” images (Figure 5).
- Optional display of rivers and country boundaries.
- Zoom in and out on areas of interest.
- Point, line and fill colours can be set.
- Size, colour and type of symbols can be set.
- Maps can be saved as graphics files, or copied to the clipboard and pasted into other applications.

Additional features (as drawing of generalized tracks from the results of clique analysis, grid analysis for locating of main massings, and data export for displaying distributions and tracks on Google Earth) will be included in future releases.

### Implementation

The CROIZAT program is written in Python, an interpreted, interactive, object-oriented programming language, coupled with the portable, multi-platform wxPython interface management library and other external libraries. Therefore, the program is platform-independent, and runs without modifications on any PC compatible with the x86 architecture, under GNU/Linux, Mac OS X, and MS-Windows.

Minimum spanning trees are computed after Page (1987) using Prim (1957) algorithm. The algorithm in Bron & Kerbosch (1973) are used to find the largest cliques of compatible tracks (as implemented in the CLIQUE program in the PHYLIP package of Felsenstein 1993). Statistical testing of tracks are performed according to Craw (1989) and Henderson (1989, 1991), using regular random graphs generated by the algorithm of Wormwald (1984), with the modifications proposed by Steger & Wormwald (1999) and Kim & Vu (2003). The graph routines are from the NetworkX library (Hagberg et al. 2008). All computations are done in double arithmetic precision using routines from the NumPy library (Oliphant 2007).

Distribution packages for GNU/Linux, Mac OS X and MS-Windows are available for downloading from the program’s website (http://croizat.infobio.net). The CROIZAT program is distributed as free software (Stallman 2004), under the GNU General Public License (GPL).

User support, announcement of updates, and big reports are provided by means of the Panbio-L discussion list (http://groups.google.com.br/group/panbio). Updates and progress reports are also made available via the Twitter service (https://twitter.com/croizat).

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**Fig. 2.** CROIZAT on MS-Windows XP.

**Fig. 3.** CROIZAT on Mac OS X Tiger.

**Fig. 4.** CROIZAT data import wizard under MS-Windows XP.

**Fig. 5.** Distribution of Zygodontomys rodents in northern South America represented as a track graph computed by CROIZAT (with satellite image background).
Conclusions

CROIZAT provides a freely available, user-friendly software package which biologists can use to integrate and analyze spatial information on species or other taxa and to explore geographical patterns in diversity, rarity and conservation priorities, under a panbiogeographic approach. It is expected that it will help disseminate the interest for Panbiogeography as a comprehensive and innovative programme of scientific investigation and the application of the panbiogeographic approach to the analysis of distribution patterns of organisms, especially in connection with the potentially quite useful but as yet underexplored uses of this approach in biodiversity conservation.

Acknowledgements

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References


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Archipiélago cubano, Biogeografía Histórica y Complejidad

by Tania Escalante

La complejidad puede entenderse como un fenómeno compuesto de varios elementos o partes, y como un concepto aplicable a un asunto en el cual hay que considerar muchos aspectos, por lo que no es fácil de comprender o resolver (RAE 2001, Moliner 2007). Sin embargo, el mismo concepto de complejidad no es tan simple de definir, y de hecho, se ha desarrollado toda una teoría de la complejidad para entender el mundo (Cornejo-Álvarez 1997). La biogeografía, por sí misma, desde siempre ha sido una ciencia compleja, ya que el estudio de la biodiversidad en el espacio geográfico ha incluido la integración de diferentes conceptos y métodos. En este libro, Fontenla y López señalan que, además, los objetos de estudio de la biogeografía son sistemas dinámicos complejos. De hecho, Croizat (1964) propuso que la evolución orgánica es función del espacio, el tiempo y la forma (quizá también una alusión a la concepto de complejidad), y que los nodos pana biogeográficos son áreas complejas, donde se encuentran diferentes fragmentos ancestrales geológicos y bióticos (Morrone y Crisci 1995).

Por otro lado, el estudio de las islas oceánicas ha sido de gran interés para los biogeógrafos, puesto que son objetos visibles y discretos que la mente puede seleccionar y comprender, y aportan información de procesos evolutivos y ecológicos (MacArthur y Wilson 1967, Pozo y Llorente-Bousquets 2001). Las Antillas han sido objeto de varios estudios biogeográficos dada su riqueza biótica y su naturaleza archipelágica (Trejo-Torres 2003). Además, se consideran uno de los “puntos calientes” o hotspots de biodiversidad identificados en el mundo, con cerca de 230,000 km2 de extensión (http://www.biodiversityhotspots.org/Pages/default.aspx). El archipiélago cubano forma parte de las Antillas Mayores, y está integrado por dos islotes principales: la Isla de Cuba y la Isla de la Juventud, además de cuatro mil pequeñas islas, islotes y cayos. Su biodiversidad se caracteriza por su gran diversidad de ecosistemas presentes y el alto grado de endemismo de sus recursos bióticos (datos del Informe Nacional a la Cuarta COP del Convenio sobre Diversidad Biológica, http://www.ecosis.cu/cenbio/cenbio.htm).

El presente libro precisamente se enmarca dentro del concepto de la complejidad subyacente en la biogeografía histórica del archipiélago cubano. Está estructurado en una introducción y seis capítulos, cada uno de ellos destinado a la comprensión de las polémicas actuales de la biogeografía, tal como lo señalan sus autores. La introducción incluye una amplia disertación profunda y filosófica de la complejidad y de cómo ha sido abordada en los estudios de la biogeografía de las Antillas.

El capítulo 1, titulado “La gran herencia”, inicia con un análisis de la labor científica, el conocimiento y la sustitución de paradigmas. También los autores hablan de la causalidad, la simplicidad y las explicaciones de los hechos. El capítulo 2 está dedicado a “reflexiones entre el orden y el caos”, un análisis sobre la complejidad y los sistemas; de hecho, los autores asumen como “casi un axioma escuchar o leer que la complejidad se encuentra entre el orden y el caos” (ítalicas en el original). Así, los autores guían a los lectores hacia un encuentro de una ciencia que estudia sistemas complejos y no lineales con cualidades emergentes, de tal manera que llegan al concepto de fractal. Al finalizar el capítulo 2, los autores además muestran un triángulo, donde cada uno de los ángulos representa el espacio, el tiempo y el sentido, con la palabra complejidad en el centro. Haciendo alusión a esta figura, explican que es la dimensión ontológica de la realidad de los sistemas complejos vivos, ya que todo proceso u objeto existe en un espacio, en un tiempo y de una forma determinada (el sentido) – cabe mencionar que todo el libro contiene figuras que representan tríadas –. No es sorprendente que esta figura sea muy parecida a la que presentó Morrone (2004) – así como tampoco es sorprendente encontrarse precisamente esta misma figura en la página 323, refiriéndose a las dimensiones de la diversidad biológica: espacio, tiempo y forma (sensu Croizat 1964), donde la biogeografía es la disciplina que pone mayor énfasis en el espacio y el tiempo.

El tercer capítulo está dedicado a la percepción del mundo real por parte del observador y de la causalidad. El capítulo cuarto, titulado “la evolución orgánica en el ojo de la complejidad” es quizá uno de los más interesantes. En él, los autores inician con las importantes y únicas aportaciones de Darwin no solo a la ciencia, sino también a la cultura. Dedican un apartado a la selección natural y a la ortogénesis de Croizat, y otro más a la adaptación y al concepto de nicho. Además, mencionan la complejidad genética, morfológica, organística y ambiental. Finalmente, tratan el problema de la especie; en este sentido, los autores hacen uso de la teoría presentada en los capítulos anteriores para asegurar que una especie es “un resultado de un evento filogenético, emergente de la divergencia de procesos de información entre linajes”.

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Después de los primeros cuatro capítulos, en el quinto por primera vez aparece en el título la palabra biogeografía. En mi opinión, los autores intentaron generar polémica y reflexión sobre el tema que abordarían en el capítulo fundamental del libro. Los primeros renglones de éste, que es el capítulo más extenso, se refieren a una definición sencilla o simple de la biogeografía, pero explican más adelante que evidentemente es compleja. De esta manera, nuevamente los autores hacen referencia a las cualidades emergentes, los sistemas y las jerarquías para definir al espacio biogeográfico. Lo mismo ocurre cuando definen al área de distribución como “un fenómeno emergente, probabilístico y dinámico”, o cuando se refieren a los términos patrón y proceso, siendo estos últimos manifestaciones multi-causales subyacentes en los patrones observados. Así, se hace alusión a los procesos que modifican la distribución geográfica de los taxones: dispersión, vicarianza y extinción, y a los principales enfoques biogeográficos históricos: dispersalismo y vicariancismo. Respecto al descubrimiento de las relaciones entre las áreas geográficas, los autores coinciden en que estas son reticuladas (es decir, complejas) más que divergentes, y la necesidad de utilizar métodos que la puedan descubrir cuando no existen arreglos necesariamente jerárquicos. En cuanto a la panbiogeografía y la ortogénesis de Croizat, también son analizadas a la luz de la teoría de sistemas complejos. Finalmente, también la dispersión es tratada en este sentido, al hablar del movimiento como un flujo infodinámico.

Después de un extenso análisis conceptual de la biogeografía histórica a la luz de la teoría de la complejidad, el último y sexto capítulo está dedicado al archipiélago de Cuba. Un concepto que es de reciente utilización y propuesto por uno de los autores es el de “atractor biogeográfico”, que es bien representado por el concepto de área de endemismo. El apartado de áreas de endemismo se encuentra bien documentado con una regionalización botánica de Cuba, así como un análisis de conectividad de los diferentes distritos, lo que permite identificar “meta-atractores”. En el caso de los trazos generalizados, se identificaron ocho de ellos, los cuales se presentan ilustrados, así como los trazos individuales que los componen. También se muestran los 25 nodos donde convergen los trazos generalizados, y analizan los trazos generalizados en relación con la –de nuevo compleja – historia geológica de Cuba, que incluye procesos de fusión y fragmentación de tierras, fluctuaciones en el nivel de mar y movimientos verticales. Para algunos taxones, se comparan sus relaciones filogenéticas con sus trazos individuales para inferir procesos. Para terminar este capítulo, los autores retoman nuevamente el propósito de la ciencia y la teoría de los sistemas complejos para encaminar a la biogeografía a una práctica trans-disciplinaria, donde no existe una causa universal, sino una red causal.

Al final del libro, se presenta una serie de notas y aclaraciones de los diferentes temas, junto con una amplia bibliografía. Sin dudas es un libro que requiere ser leído con detenimiento y apertura a nuevas ideas y a una visión diferente de la biogeografía histórica.

Referencias

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Never Never Land

BY DALTON DE SOUZA AMORIM


“(…) but on the whole the Neverlands have a family resemblance, and if they stood still in a row you could say of them that they have each other’s nose, and so on” (Peter Pan, J.M. Barrie).

Many scientists perform “analyses”—they find a “problem” and apply a method to go from data to inference. Good papers of this style would consider the implications of the results, but in many cases the scientific implications are frequently not much more than the results themselves. These scientists believe in objectivity. Someone else developed the methods they employ and they have faith in their methods—or at least use them for the sake of simplicity (e.g., editors accept them easily). Some other scientists are interested in conflicting inferences, sometimes originated from competing methods, even if editors don’t care for it. Advances may come from considerations about the methods, i.e., in their underlying assumptions and way of performing calculations. This is a more difficult task. Some scientists look even more deeply. They know that the very problems posed, definitions, criteria of truth etc. vary according to biases, emphases, personal interests, and vision of the world. They set the fundamentals of mainstream research and direct the minds and projects of hundreds of scientists (and editors) that happily apply these methods or discuss their details. In fact, most scientists really don’t care much about what is going on in the basement. Understanding the foundations of any area of research is indeed a difficult goal. The roots of any recent area of research may extend to the past for decades (or centuries) and quite often the subtle, philosophical issues and the real reasons for important shifts in an area are not clearly published nor publicly declared. Sometimes they are merely suggested within introductory sentences of prologues and prefaces, final comments, and discourses; but usually proliferate in undocumented informal talks and discussions.

Based on its title, Foundations of Systematics and Biogeography, by Williams & Ebach (2008) —[from hereon referred to as W&E]—should get to the roots of comparative biology. The book is prefaced by Gareth Nelson. Chapter 1, Introduction, has an overview of Systematics. Chapter 2, Systematics as Problem-solving, is a short chapter dealing with the underlying problems of Systematics and the kinds of answers it raises. Chapter 3, The Archetype, begins to deal with a detailed historical reappraisal of Comparative Biology, and this chapter is dedicated to Goethe’s ideal morphology. Chapter 4, Ernst Haeckel and Systematische Phylogenie, addresses the question of representing historical entities using “phylogenetic trees”, with a focus on Haeckel’s contribution and some additional comments on some authors preceding Charles Darwin, such as Louis Agassiz, Heinrich Bronn, and the linguist August Schleicher. In these early days of the evolutionary era, the profile of an evolutionary Paleontology began to be constructed through these contributors. Chapter 5, German Development of Morphology: From Ernst Haeckel to Willi Hennig, has a detailed overview of the developments of systematics after Haeckel, especially among German authors, including Hans Spemann, Adolf Naef, Joseph Kälin, Arnold Lang, Adolf Remane, Rainer Zangerl, Konrad Lorenz, and Willi Hennig. The text also examines pre-Darwinian authors, such as Richard Owen and E. Ray Lankester. The discussion presented in this chapter deals with the relationship between evolution, phylogeny, evidence of phylogeny, and classification. Chapter 6, Pattern Cladistics, is centered on what is considered by the authors to be a stem of evolutionary thought of its own, cladistics, through the works of Erik Stensio, Erik Jarvik, Lars Brundin, Collin Patterson, Gareth Nelson, and Norman Platnick, along with comments on other authors such as Daniele Rosa, Leon Croizat, Ernst Mayr, George Gaylord Simpson. Chapter 7, Homologies and Homology, deals with one of the central issues of the book and of comparative biology, that of homology itself. The subject finds further development on Chapter 8, Discovering Homologues, with a discussion on the relationships of what the authors understands as cladistics, phylogenetics, and phenetics. The history of matrices used in systematic analyses is briefly examined with respect to the early contributions of the entomologist Robin John Tillyard. Chapter 9, Homology and Systematics, considers the connection between homology, relationship, and classification, with notes on William Sharp MacLeay, Richard Owen, John Obadiah Westwood, and Hugh Edwin Strickland. Chapter 10, Homology and Transformation, addresses the concept of transformation in its material, logical, phylogenetic, and ontogenetic contexts with respect to the contributions of St. George Mivart, Carl Gegenbauer, Geoffroy de Saint Hilaire, Oscar Hertwig, Warren H. Wagner Jr., Olivier Rieppel, Walter Zimmermann, and Michael T. Ghiselin. Chapter 11, Character Conflict, represents a more technical part of the book. This chapter deals with conflicting evidence and therefore the questions of parsimony and related issues, as congruence, compatibility, and component analysis. Chapter 12, The Analyses of Relationships, actually deals with
the problem of three-item analyses, deepening the discussion of the previous chapter. Chapter 13, Biogeographical Relationships, Evolution, and Classification, deals with the underlying questions and answers biogeography. The Epilogue provides closure with a final synthesis of the message behind the entire book.

This book has very important qualities and is definitely worthy of being read and studied. A major contribution of the book is, in my view, the recovery of forgotten or hidden authors that identified and articulated the problems, concepts, and methods of comparative biology as we know it in the present. The book expands, in some aspects, Nelson & Platnick’s (1981) Systematics and Biogeography. Whatever the stage we may now be in the understanding of the concepts of sameness, similarity, affinity, homology, analogy, evolution, taxon, monophyly, classification etc., it is the result of a long process of polishing that, in modern science, goes back to the 18th century. The history of comparative biology has a lot more to it than Darwin, and it is really not possible to understand the conflicts among major recent currents of systematic thought without addressing its deeper origin and gradual development. Nevertheless, the historical understanding of comparative biology is by and large overlooked in our practice of science—which is typically ignorant and boldly devoid of culture (maybe still as a consequence of the positivistic approach of the nature of science) —resulting in a superficial understanding of tasks, concepts, and methods.

Throughout the book, the earlier roots of the main concepts of comparative biology are addressed, as well as the use of trees as representations of affinity and the use of matrices etc. Perhaps even more important, the connections and conflicts between idealistic morphology, evolutionary morphology, and logical transformation are illuminated. Among older authors, I would just mention that Lamarck would deserve more extensive consideration, and the contributions of Pierre Louis Maupertuis and Gottfried Leibniz should have been included.

Other interesting aspects of the book are worth comment. One of the most important concerns is the nature of phenetics. It is rather well known that phenetics originated in the 1950s due to doubts about the ability to reconstruct phylogenetic relationships from traditional methods—as well as some excitement about the role that computer calculations could bring to taxonomy by providing “objectivity”. Since its beginning phenetics has been infused with a statistical perspective that is divorced from an evolutionary biology. Not able to see anything anew beyond idealistic morphology in the time of evolutionary taxonomy, pheneticists adhered to a naïve view of the nature of taxa and of similarity. Phenetics has been always devoid of any underlying biological ontology. The lack of a time-scale in phenetic taxonomy is explicit: “Taxonomic relationships are evaluated purely on the basis of the resemblances existing now in the material in hand.” (Sneth & Sokal 1973, W&E p. 142). In practice, phenetics deals with a merely topological and operational comparison of recent specimens, free from any evolutionary concerns. Actually, paraphrasing Bather (1927, W&E p. 167), phenetics lost the way set by the transformation of “a professed abstraction” underlying the concept of archetype “into a presumed concrete existence”, underlying the concept of ancestor.

On an even more fundamental level of discussion, it seems fair to say that phenetics is actually the ultimate nominalism applied to taxonomy. It would be a natural consequence, see-
book is successful in presenting critical discussion on many of fundamental issues in systematics.

Having said some good (and meritorious) words about the book, it is also necessary now to consider some of its deficiencies. Despite the excellent historical review of systematics, I get the impression that the book is actually trying to sell a new story—that of a (renewed) pattern cladistics as if it were the history of systematics itself, with different heroes and villains. At the end, much of the historical reappraisal of W&E's book intends to reveal a supposed opposition between "transformational-systematics" and "pattern-systematists", associating Gareth Nelson to Goethe's idealistic morphology.

To verify whether Gary Nelson would be happy to be associated to idealistic morphology we could just ask him. But as to the question of whether or not the division between transformational and pattern systematics has any meaning at all—opinions of course could differ. The biggest problem, in my view, however, concerns the role the book attributes to time in systematics, everything else being seen as a consequence. Under the name of pattern cladistic systematics following W&E seems to be devoid of a temporal dimension (or at least of its implications).

The book also deeply depreciates the role Willi Hennig had in the development of systematics. The main reason is that Hennig would be actually associated with the "transformationism" in comparative biology. It is legitimate that one may not be interested on matters of transformation, as well as one may just not be interested on the biogeographical or biochemical questions underlying data, but it this is entirely different from saying that time has nothing to do with the very nature of systematics, and thereby promoting a rehabilitated idealistic morphology out of its historical context.

Part of W&E criticisms of Hennig's original reasoning is correct: the idea that the determination of character polarity (or character transformation) is prior to the establishment of the groups is really mistaken. It has been clear since Nixon & Carpenter (1993) that moving from an unrooted to a rooted cladogram with the establishment of outgroups simultaneously brings about character polarity (apomorphy) and monophyly of taxa (synapomorphies or secondary homologies). In other words, inferences about homology (=synapomorphy or taxon inference) provide the source of evidence for transformation series, not the other way around.

However, the role of outgroups is very clear in Hennig's method. "Prior apomorphies" are just a shortcut due to informal outgroup comparison. In Hennig's systematics as well as subsequent phylogenetic reconstruction, the idea of outgroup has been a central concept. Interestingly enough, outgroups are absent in phenetics. The very idea of outgroups is justifiable in cladistic analyses only because it introduces the idea of a time span, i.e., of establishing a root to cladograms or, in other words, relative antiquity of clades. It is a logical consequence of a cladogram bearing a time scale that, once outgroups root analyses, time cannot be disengaged from systematic reasoning or from the systematic endeavor. Pattern cladistics did not (until now) give up the use of outgroups and rooted trees. The fact that ad hoc hypotheses of character transformation are not acceptable sources of tree reconstruction does not imply that character transformation is not a legitimate and necessary by-product of systematic analyses. Transformation series is a corollary of the use of outgroups.

On page 137, W&E seem to be arguing that the absence of a notion of transformation in Goethe's and Owen's works would give support for a "pattern" systematics: "Owen (…) did not see the necessity for evolutionary mechanisms when classifying organisms or even understanding their morphology. (…) Goethe too saw no point in creating hypotheses about how things came to be. Experience of the phenomenon was what mattered most." First, this is exegetic. Second, the reasoning is really not good. One could say that Goethe's and Owen's ignorance about an evolutionary perspective (or about whatever else) would be enough support for a denial of any evolutionary interest in systematics. And finally, the use of the word phenomenon here may become quite tricky, since it can take as to φαίνω, appearance and, hence, similarity, in a phonetic perspective.

The multifaceted discussion on homology is also interesting. W&E ignore the concept of character, only commenting on "character phylogeny". Paradoxically, in my opinion their discussion actually contributes to a better understanding of the material aspects of homology comparison. Homologies are the material aspects or parts of organisms compared (Nelson 1989, p. 131), homology been the relation between homologues, which is a very clarifying position. Characters, as a consequence, are not the physical structures, as often referred to in the literature, but the differences between the conditions shown by actual specimens (Amorim 2002). Platnick (1979, p. 542) had already dealt with this in a very clear way: "A character is thus a theory, a theory that two attributes which appear different in some way are nonetheless the same (or homologous). As such, a character is not empirically observable; hence any (misguided) hope to reduce taxonomy to mere empirical observation seems futile". Individuals do not exhibit characters, but homologues, or character conditions or structures. Characters (even though pattern cladistics may not be interested in it) are the shifts or modifications of homologues over time. As Platnick (1979) said, they are also hypotheses or part of the hypotheses underlying homologies.

The discussion about the criteria concerning the establishment of homology—i.e., of a relation between parts—also misses some important points. As commented above, it is now well known that the establishment of the relation between homologues as a homology of its own, i.e., as a synapomorphy, is secondary in the analyses, when meets the criterion of congruence. This means that before having an inference about homology, we really don't know whether we are dealing with homologues or with mere similarity. But how do we know that homologues are really comparable? In other words, how do we decide if structures are to be compared? In fact, before a given analysis of congruence, parsimony analyses at higher levels are needed to indicate whether the compared structures themselves are comparable. This is already seen back in the work of Owen, as W&E show (p. 165), "Owen recognized (…) that the first stage in effective comparison of organisms was to identify the parts that might reasonably be considered the same." In other words, secondary hypotheses of homology at higher levels of analyses generate the primary hypotheses of homology for analyses at lower levels. Pushing the comparisons to extremes, the head of a cat is comparable to the head of a dog because it is the most parsimonious overall solution, homology between frontal bones being a consequence; cell 4d of one embryo is compared to cell 4d in another embryo because it is the most parsimonious solution. Not because of any criteria of similarity. This means that homology and homologues are, after all, nothing but parsimony hypotheses. The implication is that homology is logically and methodologically subordinate to parsimony, notwithstanding the relationship
between homology and taxa established later in the analysis. A proper consideration of parsimony is one of the most noticeable issues missing from discussion in the book. Also, a number of questions posed in the literature by Steve Farris, as well as by other authors dealing with the problem of parsimony (e.g., Sober 1983), were not included. Independently of the question of the epistemological nature of phylogenetic hypotheses (see Fitzhugh 2005a,b, 2006), parsimony has been the most important conceptual and methodological development of systematics under the phylogenetic perspective proposed by Hennig. If parsimony was not seen to have the status of a distinct issue this should have been properly justified in a discussion.

There are also some important missing phylogenetic developments prior to Hennig that were not referred to in the book. Frederick Wallace Edwards, an eminent English dipterist, began to distinguish between different kinds of similarities (Edwards 1925), of which Hennig was obviously aware. And the German paleontologist Anton Handlirsch proposed a historical relationship between the Linnaean categories and geological eras (Handlirsch, 1925), an idea later improved on by Hennig (1966). Many important concepts used by Hennig were derived from Karl Ludwig von Bertalanffy (1932, 1942). Hennig was very fair giving due credit to his sources. It could be just as obvious to say that Hennig was not entirely original, as neither was Linnaeus or Darwin. So what? Hennig was not the only researcher to help the development of a phylogenetic method or related concepts. The importance of Hennig’s opera came from his ability to present systematics under an integrated perspective—goals, concepts, methods and implications of Systematics. A phylogenetic systematics organized the disorder that similarity alone was not enough to perform. No authors prior to Hennig, “transformationists” or “idealists”, were able to offer such construction. With patterns recovered, the entirety of biology could be understood under a temporal, phylogenetic perspective—and even conflicting reconstructions could be understood within this context. A number of subtle and interesting problems of homology and phylogenetic reconstruction began to be dealt with in all spheres of biological literature from biochemistry to behavior.

Against this background the book may be unfair relegating Hennig to the level of a Haeckelian transformationism. In particular, the labeling Hennig a “transformationist” in W&E and, hence, considering him injudicious in the development of evolutionary thought, is a bit puzzling to me. Of course there were a lot of naive ideas about transformation in the literature—as there still is. Under a modern, post-Hennigian perspective, there is no material transformation (as in ontogenesis): information endures through transformation over time. That is all. “Hennig’s revolution” (if we could separate it from other “parallel” developments, such as that of Stensiö—something that Brundin may have anticipated?) in the 1960s and 1970s was an integral part of the argument against a phenetic systematics and the “old paleontological systematics” (actually, gradism renamed). It is historically incorrect to rewrite history to now characterize it as a mistaken branch of systematic thinking.

Getting rid of the idea of transformation—and of its connected logical implications, such as characters, ground-plan reconstructions, common ancestry (even not being recognizable among fossil specimens), vicariance events etc.—is connected with the elimination of the time scale in systematics. Paradoxically, this would remove the underlying evolutionary ontology from pattern cladistics. This problem is met in a mysterious statement where W&E conclude that: “The difference between phenetics and cladistics is, as has always been, the algorithms rather than the basic unit” (p. 149). This is contradictory. From other parts of the book one would conclude that the main difference between phenetics and cladistics is the meaning of the units, something applicable even at the species level (Santos & Amarim 2007). If the ontological perspective is the same and the differences relate merely to algorithms, W&E’s pattern cladistics would be phenetics in camouflage—an expression used by Farris (1990) in another context. In knowing David Williams and Malte Ebach personally I am sure that this is not their view of systematics. To me there is something wrong with the importance they give to the problem of time in systematics and, hence, their notion of transformation.

Some other comments worth making: The excellence of the text in the first chapters contrasts with the writing of the technical chapters (11 and 12). Definitions in these two chapters are largely wanting and patience to convert ideas in an understandable text seems to have vanished. Another point is that a new pattern cladistics appears to come through in this book because it would not insist on the idea that shared 0’s would generate any hypothesis of homology. An exception, however, is the relation between Table 11.13 and Figure 11.11, based on old fashioned three-item analysis. But the discussion of three-item data is deceptive. A sounder development of the matter, that could raise the discussion to a clarifying level, is knowingly wanting: “The details below should be understood as a guide rather than a definite account (...) [that] has yet to be written.” This is a pretty limited view for a book on the “Foundations of Systematics”, and one trying to show that pattern cladistics should be seen as the appropriate perspective for systematics.

W&E’s discussion of the differences between the topological results of parsimony analyses and the results of three-item analyses is interesting. They say (p. 213) that three-item data “...can be fitted to a cladogram(s) using any conventional parsimony programs...” Further on, they state that “As in standard parsimony analyses, the optimal tree is the shortest in length.” and that “...parsimony programs are adequate for finding optimal tree with these data.” Hence, results from three-item analysis in taxonomy would add restrictions to topologies coming out from usual parsimony analyses (i.e., in the selection of subsets of trees). If better developed, this could have been a major contribution from the book by providing some additional tools to the usual phylogenetic analyses. But this by no means justifies the recognition of an “alternative” school of systematics or an alternative method of phylogenetic reconstruction. The differences between parsimony and three-item analysis seems to be restricted to one of dealing with information, not of method, concept or ideology—unless the underlying ontologies of the two “schools” are really different.

Chapter 13, on biogeography, is pretty weird. Compared to the part of the book on systematics, it is surprisingly shallow from a historical point of view, and superficial in addressing conceptual issues and problems of method. Ideas on the geographical distribution of organisms developed before the 18th century, e.g., St. Augustine and José d’Acosta (Papavero et al., 1995a,b) were left behind. A deeper consideration of Wallace is wanting and many pre-Croizatian and post-Croizatian authors are also missing. It is also hard to understand the emphasis given to the 19th century literature on the geography of Man. The inability to remove creationist models from biogeographical reconstructions in the second half of the 19th century should be seen as just that: “This view seems to be little more than inheritance from the special creationists” (Clements 1909, W&E,
p. 242). That should be all. But for reasons that are not stated clearly this outdated dispersalist discussion about geographical origin of Man is mixed in with a critique of the goals, concepts, and methods of modern biogeography. Many aspects of modern analytical biogeography were largely ignored, so the goal of the book—fundamentals—is still a long way off concerning biogeography.

Again there seems to be a question of an agenda underneath the book that is not easy to understand. The temporal aspect of comparative biology seems to have been removed from biogeography, reducing it to the mere finding of patterns. Time span in biogeography unavoidably implies some kind of explanatory hypotheses—i.e., event (of vicariance or dispersion)—something that W&E appear to want to avoid. On page 240, W&E state “Whatever the mechanism [dispersal or vicariance], it does not—nor can it—assist in the discovery of a biotic classification.” That seems to be pretty much fair. Much of the literature since Croizat has demonstrated that inferred patterns indicate the most probable cause, not the other way around. But then, “Vicariance, in the sense of a vicariant event”, is impossible to define as every event carries a unique explanation. In order to make ‘dispersal’ and ‘vicariance’ meaningful, it should be described as a descriptive term.” (p. 241). It seems, from the perspective of the book, that it is not a question of how inferences are made, but a question of complete denial of any kind of evolutionary (systematic or biogeographical) inference.

W&E’s book is, for me not about the foundations of systematics and biogeography, even though knowledgeable readers will really benefit from its reading. It seems to me that this is a book trying to justify a new version of pattern cladistics—but on mistaken grounds and to which a connection is proposed to exist with idealist morphology. Systematics in the absence of a time scale not only lacks ‘sense’—it is logically equivocal. Transformation series—and the entire set of historical explanations it may bring to biology—are the corollary of rooted trees. Epistemology has been telling science to focus on the proposition of explanatory universal models. But with W&E’s version of systematics and biogeography, with patterns devoid of a time scale and its corollaries, what kind of science do we have in hand?

The pagination of the index is almost entirely displaced by one or two pages, making it a bit difficult to find passages. I really enjoyed reading the book and it will be an obligatory reading for students in my lab. I don’t agree with the general underlying message, but this does not reduce the importance of the debate behind the book. It is a vigorous treatment of the roots of comparative biology, something we really are in need of in times of theory-free “molecular systematics” (see Nelson & Ladiges 2009).

References


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