Introduction

A. Schmidt-Rhaesa

in The Evolution of Organ Systems

This introductory chapter provides definitions and explains the scope of the book. It explains how conclusions are drawn from trees, how they are used to build these trees, why gametes are included, and the limitations of the topics considered. Previously, there have been many approaches to explain the evolution of organ systems, but these were restricted to particular systems. Other approaches have reconstructed phylogeny derived from the one organ system instead of reconstructing the evolution of this organ system from a tree based on all available data.

Perspectives in Animal Phylogeny and Evolution

Alessandro Minelli

Animal phylogeny is currently undergoing a major revolution due to the availability of an exponentially increasing amount of molecular data and the application of novel methods of phylogenetic reconstruction, as well as the many spectacular advances in palaeontology and molecular developmental biology. Traditional views of the relationships among major phyla have been shaken up and new, often unexpected, relationships are now being considered. At the same time, the emerging discipline of evolutionary developmental biology, or evo-devo, has offered new insights into the origin and evolvability of major traits of animal architecture and life cycle. All these developments call for a revised interpretation of the pathways along which animal structure and development has evolved since the origin of the Metazoa. This book
takes on this challenge, successfully integrating morphological, fossil, and molecular evidence to produce a novel reinterpretation of animal evolution. Central to the book's approach is an evo-devo perspective on animal evolution (with all the fresh insights this has given into the origin of animal organization and life cycles), complementary to the more traditional perspectives of pattern (cladistics, comparative anatomy, and embryology), mechanisms (developmental biology), and adaptation (evolutionary biology). The book advocates the need to approach the study of animal evolution with a critical attitude towards many key concepts of comparative morphology and developmental biology. Particular attention in the book is paid to the evolution of life cycles and larval forms.

Perspectives
ZHENG YANG

in Computational Molecular Evolution

Published in print: 2006 Published Online: April
Publisher: Oxford University Press
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Item type: chapter

This chapter discusses current challenges and future perspectives of the field. Topics covered include theoretical issues in phylogeny reconstruction, computational issues in analysis of large and heterogeneous data sets, genome rearrangement data, and comparative genomics.

Ancestry
Xiaoming Wang, Richard H. Tedford, Blaire Van Valkenburgh, and Robert K. Wayne

in The Biology and Conservation of Wild Canids

Published in print: 2004 Published Online: September 2007
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DOI: 10.1093/acprof:oso/9780198515562.003.0002
Item type: chapter

This chapter discusses the evolutionary history, molecular systematics, and evolutionary ecology of canids. Topics covered include the Hesperocyoninae, Borophaginae, and Caninae subfamilies; morphological and molecular phylogenies; and iterative evolution of hypercarnivory.
The field of systematics has developed remarkably over the last few decades. A multitude of new methods and contributions from diverse biological fields — including molecular genetics and developmental biology — have provided a wealth of phylogenetic hypotheses, some confirming traditional views and others contradicting them. There is now sufficient evidence to draw up a ‘tree of life’ based on fairly robust phylogenetic relationships. This book aims to apply these new phylogenies to an evolutionary interpretation of animal organ systems and body architecture. Organs do not appear suddenly during evolution: instead they are composed of far simpler structures. In some cases, it is even possible to trace particular molecules or physiological pathways as far back as pre-animal history. What emerges is a fascinating picture, showing how animals have combined ancestral and new elements in novel ways to form constantly changing responses to environmental requirements. The book starts with a general overview of animal systematics to set the framework for the discussion of organ system evolution. The chapters deal with the general organization, integument, musculature, nervous system, sensory structures, body cavities, excretory, respiratory and circulatory organs, the intestinal and reproductive system, and spermatozoa. Each organ system is presented with its function, the diversity of forms that are realized among metazoan animals, and the reconstruction of its evolution.

Color Vision
Thomas W. Cronin, Sönke Johnsen, N. Justin Marshall, and Eric J. Warrant
in Visual Ecology
This chapter addresses why animals have evolved different numbers, ranges, and placements of spectral channels in their color-vision systems. It also examines the factors, such as water transmission, visual task, phylogeny, and activity patterns, that drive the evolution of such diverse modes of seeing color. Even in the absence of any color sense, trees are still visible, as most of the information in natural scenes can
be gained from achromatic cues alone. Color vision, however, gives an animal more information, allowing it to make quicker and more informed decisions. The chapter attempts to disentangle man's experience of color from that of other animals to provide an objective measure of what color vision is and how evolution has molded its variety of forms.

Introduction – Blueprint of a Bird (Bauplan/Body plan)
J. Eduardo P. W. Bicudo, William A. Buttemer, Mark A. Chappell, James T. Pearson, and Claus Bech

in Ecological and Environmental Physiology of Birds
Published in print: 2010 Published Online: May 2010
Item type: chapter

This chapter focuses on the characterization of birds as a group; why they differ from other vertebrates; and how they have evolved. The most recent evolutionary trees of birds are provided, as well as the most recent findings with regard to the origin of birds, a still unsettled matter. Feathers constitute a distinctive feature of birds; the evolutionary implications of feathers and their importance for the group are discussed. The origin and evolution of flight is presented together with a description of the energy requirements for flight. Migration as one of the most impressive aspects of the aerial lifestyle of many birds is thoroughly discussed, including its evolutionary aspects. Flightlessness is presented as an uncommon, but pervasive avian phenomenon.

Estimating the history of mutations on a phylogeny
Jonathan P. Bollback, Paul P. Gardner, and Rasmus Nielsen

in Ancestral Sequence Reconstruction
Published in print: 2007 Published Online: September 2008
Item type: chapter

Evolution has left its signature on the molecules and morphology of living organisms. Ancestral reconstruction offers an excellent tool for understanding the process of evolution using comparative information. Methods for ancestral reconstruction have generally focused on reconstructing the ancestral states at the internal nodes of a phylogeny. Often, we are not interested in particular nodes of the phylogeny but the whole history of a character. This chapter focuses on a Bayesian method for estimating these histories, or mutational
paths, on phylogenies. Mutational path methods differ most notably from other approaches in their ability to estimate not only the ancestral states at the internal nodes of a phylogeny, but also the order and timing of mutational changes across the phylogeny. The chapter provides a concise introduction to the statistical tools needed for sampling mutational paths on a phylogeny.

**Adaptation**

Lee Cronk and Beth L. Leech

in *Meeting at Grand Central: Understanding the Social and Evolutionary Roots of Cooperation*

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DOI: 10.23943/princeton/9780691154954.003.0002
Item type: chapter

This chapter examines the concept of adaptation and how it is applied (and sometimes misapplied) to cooperation. It starts with George C. Williams's idea that adaptation is a “special and onerous concept that should be used only where it is really necessary,” which he articulated in *Adaptation and Natural Selection*. It then considers different levels of explanation that help clarify the notion of adaptation, fortuitous benefits and by-product mutualism in relation to adaptation, and the link between adaptation and natural, artificial, social, and sexual selection. It also explores how phylogeny constrains natural selection, the ways that adaptations solve specific problems found in specific environments, and how adaptation influences judgment. Finally, it analyzes the role of culture and language in adaptation and evolutionary explanations of morality.

**Blanford's foxes**

Eli Geffen

in *The Biology and Conservation of Wild Canids*

Published in print: 2004 Published Online: September 2007
DOI: 10.1093/acprof:oso/9780198515562.003.0011
Item type: chapter

While the morphology typical of canids adapts them to endurance running, and consequently to life in open habitats, a few species have specialized to other habitats such as rainforests, or even to climbing trees or cliffs. The cliff-dwelling Blanford's fox (Vulpes cana) is one of these exceptional canid species. This chapter presents an overview of
the Blanford's fox's phylogeny and taxonomic status, recent distributional changes, the behavioural ecology of a population studied in Israel, and its conservation status.

**Statistical Theory and Methods for Evolutionary Genomics**

Xun Gu

Published in print: 2010 Published Online: January 2011
Item type: book

Evolutionary genomics is a relatively new research field with the ultimate goal of understanding the underlying evolutionary and genetic mechanisms for the emergence of genome complexity under changing environments. It stems from an integration of high throughput data from functional genomics, statistical modelling and bioinformatics, and the procedure of phylogeny-based analysis. This book summarises the statistical framework of evolutionary genomics, and illustrates how statistical modelling and testing can enhance our understanding of functional genomic evolution. The book reviews the recent developments in methodology from an evolutionary perspective of genome function, and incorporates substantial examples from high throughput data in model organisms. In addition to phylogeny-based functional analysis of DNA sequences, the book includes discussion on how new types of functional genomic data (e.g., microarray) can provide exciting new insights into the evolution of genome function, which can lead in turn to an understanding of the emergence of genome complexity during evolution.

**Introduction**

Quentin Cronk

in The Molecular Organography of Plants

Published in print: 2009 Published Online: May 2009
Item type: chapter

This introductory chapter chronicles in general the enormous increase in complexity in plants since plants colonized the land, and the consequences of this for terrestrial ecosystems. The principles of developmental biology and morphological evolution are briefly covered as an introduction to the study of the evolution of developmental mechanisms in plants (plant evo-devo). Important concepts such as organ homology, heterochrony, heterotopy, and homeosis are discussed.
in relation to plant evolution and empirical plant morphology. Examples are given of how plants achieve evolutionary innovation at the molecular level, as well as regressive evolution (organ loss and reversion of character states). Finally, the chapter concludes with a reflection on some morphological preoccupations of the last century by examining the work of Corner and Sporne.

The phylogenetic frame
A. Schmidt-Rhaesa

in The Evolution of Organ Systems

This chapter presents the available data for the reconstruction of a tree. It shows that there is a robust backbone, along with several areas of uncertainty. Such controversies are discussed which provide alternative interpretations of the evolution of organ systems. The chapter starts with some general remarks on the current problems of phylogeny reconstruction. The phylogenetic relationships of all major taxa are then discussed in detail. This gives a presentation of the tree that is used as a basis for the book. Not one particular tree is used, but several areas are considered, in particular the position of acoelomorphs, the Ecdysozoa/Articulata debate, and the position of tentaculate taxa are regarded as not fully settled and treated with care.

Preview
Anne E. Magurran

in Evolutionary Ecology: The Trinidadian Guppy

This opening chapter sets the scene by evaluating the significance of the guppy system as a tool for investigations in evolutionary ecology. It traces the growth of studies on the guppy, and illustrates how they have mirrored and indeed shaped shifting trends in the field. It provides a historical perspective showing why the species has become such an important model for evolutionary biologists. Pioneering work in many important areas such as sperm competition, sexual selection, and reproductive isolation has been done in the context of the guppy system.
Key questions are identified and the book's structure briefly explained. The chapter also provides a general introduction to the species and addresses the following topics: taxonomic status, basic biology, natural range of guppy, reasons for emphasis on populations in Trinidad, and advantage of manipulations in the wild.

Transport and Introduction
Tim M. Blackburn, Julie L. Lockwood, and Phillip Cassey

in Avian Invasions: The Ecology and Evolution of Exotic Birds

This chapter considers the first two steps on the invasion pathway: transport and introduction. It starts by summarizing why what we know about the history of avian invasions leads us to expect non-randomness in the transport and introduction processes. It proceeds to review evidence for non-randomness in the types of birds that get transported and introduced, where they are transported and introduced to, and finally changes in the identity of these bird species through time. Non-randomness in transport and introduction are considered together because there is little information on them as separate processes. The chapter concludes by outlining the significant consequences transport and introduction have for the study of subsequent invasion stages.

Assembling the spiralian tree of life
Gonzalo Giribet, Casey W. Dunn, Gregory D. Edgecombe, Andreas Hejnol, Mark Q. Martindale, and Greg W. Rouse

in Animal Evolution: Genomes, Fossils, and Trees

The advent of numerical methods for analyzing phylogenetic relationships, along with the study of morphology and molecular data, have driven our understanding of animal relationships for the past three decades. Within the protostome branch of the animal tree of life, these data have sufficed to establish two major clades; Ecdysozoa, a clade of animals that all moult, and Spiralia (often called Lophotrochozoa), a clade whose most recent common ancestor had spiral cleavage. In this chapter, we outline the current knowledge of protostome
relationships and discuss future perspectives and strategies to increase our understanding of relationships within the main spiralian clades. Novel approaches to coding morphological characters are a pressing concern, best dealt with by scoring real observations on species selected as terminals. Methodological issues, such as the treatment of inapplicable characters and the coding of absences, may require novel algorithmic developments. Taxon sampling is another pressing issue, as terminals within phyla should include enough species to represent their span of anatomical disparity. Furthermore, key fossil taxa that can contribute novel character state combinations, such as the so-called 'stem-group lophotrochozoans', should not be neglected. In the molecular forum, EST-based phylogenomics is playing an increasingly important role in elucidating animal relationships. Large-scale sequencing has recently exploded for Spiralia, and phylogenomic data are lacking from only a few phyla, including the three most recently discovered animal phyla (Cycliophora, Loricifera, and Micrognathozoa). While the relationships between many groups now find strong support, others require additional information to be positioned with confidence. Novel morphological observations and phylogenomic data will be critical to resolving these remaining questions. Recent EST-based analyses underpin a new taxonomic proposal, Kryptrochozoa (the least inclusive clade containing the Brachiopoda and Nemertea).

The origins and evolution of the Ecdysozoa

Maximilian J. Telford, Sarah J. Bourlat, Andrew Economou, Daniel Papillon, and Omar Rota-Stabelli

in Animal Evolution: Genomes, Fossils, and Trees

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Ecdysozoa is a clade composed of eight phyla, three of which — arthropods, tardigrades, and onychophorans — share segmentation and have appendages, and the remaining five — nematodes, nematomorphs, priapulids, kinorhynchs, and loriciferans — are worms with an anterior proboscis or introvert. Ecdysozoa contains the vast majority of animal species and there is a great diversity of body plans among both living and fossil members. The monophyly of the clade has been called into question by some workers based on analyses of whole genome datasets and we review the evidence that now conclusively supports the unique origin of these phyla. Relationships within Ecdysozoa are also controversial and we discuss the molecular and morphological evidence for several monophyletic groups within this superphylum.
Primate Classification and Diversity
Matt Cartmill

in Primate Neuroethology

This chapter discusses current understanding of primate phylogeny. It argues that a cladistic approach based on genetics, supplemented by morphological and behavioral data, offers unique promise for organizing relationships among living primates, as well as their pattern of descent from a common ancestor. Understanding evolutionary relationships within the Order Primates is a key starting point for the comparative study of primate behavior and neurobiology.

Beyond linear sequence comparisons: the use of genome-level characters for phylogenetic reconstruction
Jeffrey L. Boore and Susan I. Fuerstenberg

in Animal Evolution: Genomes, Fossils, and Trees

The first whole genomes to be compared for phylogenetic inference were those of mitochondria, which provided the first sets of genome-level characters for phylogenetic reconstruction. Most powerful among these characters has been comparisons of the relative arrangements of genes, which have convincingly resolved numerous branching points, including some that had remained recalcitrant even to very large molecular sequence comparisons. Now the world faces a tsunami of complete nuclear genome sequences. In addition to the tremendous amount of DNA sequence that is becoming available for comparison, there is also the potential for many more genome-level characters to be developed, including the relative positions of introns, the domain structures of proteins, gene family membership, presence of particular biochemical pathways, aspects of DNA replication or transcription, and many others. These characters can be especially convincing because of their low likelihood of reverting to a primitive condition or occurring independently in separate lineages, so reducing the occurrence of homoplasy. The comparisons of organelle genomes pioneered the way for using such features for phylogenetic reconstructions, and it is almost certainly true, as ever more genomic sequence becomes available, that further use of
genome-level characters will play a big role in outlining the relationships among major animal groups.

**Darwin and development: Why ontogeny does not recapitulate phylogeny for human concepts**

Frank C. Keil and George E. Newman

in *The Making of Human Concepts*

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Item type: chapter

This chapter argues that human cognitive development tells us a great deal about what makes human thinking qualitatively unique, but it does so in the same way that current evolutionary biologists explain how organisms are particularly well adapted to niches; that is, the way in which human concepts are specialized, rather than the product of a linear increase in complexity. The chapter outlines a few key developmental transitions that are commonly assumed in human cognitive development and then demonstrates how these ontogenetic distinctions fail to contribute to our understanding of cross-species differences.