

Methodology

1. When Clocks Collide, By Christopher A. Brochu

The conflict is a matter of interpretation, and as long as competing hypotheses are not completely understood, the magnitude of the “conflict” will be exaggerated. As seen in the papers in this issue, we still have a long way to go to resolve some of the inconsistencies between sources of information—but an integrative approach holds the greatest promise in achieving the one goal of understanding the history of life as thoroughly as possible. Page 1.

2. Missing Links, By Kevin Padian

This brings us to a very important distinction in tracing lineages. The title of this book is *Missing Links*. I have seldom, if ever, heard a professional paleontologist refer to any specimen as a “missing link.” In most respects, paleontology largely gave up the literal search for “missing links” decades ago. (Here, by “missing links” I mean transitional forms, direct ancestors, specific critters that fill gaps in lineages.) So, in a book intended for students who don’t know much about the subject, why focus on an outmoded concept? Page 620

3. Origin And Early Evolution Of The Amniotes, By David S Berman

Cladistic analyses of Paleozoic tetrapod relationships have yielded dramatically contradictory results (Gauthier et al., 1988; Carroll, 1995; Laurin and Reisz, 1995, 1997; Laurin, 1998), despite the use of similar computerized algorithms and extremely large data sets. Major sources of this problem, according to Carroll (1995), can be attributed to: 1) the lack of at least some data from all known taxa and 2) the lack of more information of more plesiomorphic members of recognized clades that are not known from their presumably earlier fossil record. Thus, if any of the recent cladistic analyses of late Paleozoic tetrapod relationships are used to construct a morphological series that traces the early evolutionary changes of a particular region of the tetrapod skeleton to its culmination in the amniote condition, the result is often, predictably, questionable. Page 938

Potentially important to the controversy of the phylogenetic position of the baphetids is the recent description by Lombard and Bolt (1995) of the Lower Carboniferous amphibian *Whatcheeria*, which in their phylogenetic scheme was placed tentatively as the first outgroup of the anthracosaurs. Page 952

With the additional consideration of the diadectomorphs, his phylogeny encountered further problems, and he was unable to resolve the relationships between the three taxa. The final solution was an unresolved trichotomy. Page 953

4. Systematic Paleontology, By Jonathan M. Adrain

How do we generate phylogenies? Debate, of course, rages on this issue. Page 1056

Resolution of the **debate** over whether phylogeny should be read from the rocks is central to the future development of paleontological systematics. Page 1057

5. Evidence for Punctuated Gradualism, By Bjorn A. Malmgren

One of the fundamental problems in this **debate** is the lack of well-conceived studies employing detailed morphologic measurement and a rigorous biometric testing strategy. We believe that much more time should be devoted to generating real data on real evolutionary lineages than to endless theoretical discussions on hypothetical evolutionary models. Thus, instead of forcing our data to fit preconceived models, we would prefer to formulate the models from real- world paleontologic data. Page 377

6. Extinction, By Andy Purvis

The **debate** continues, with key points of contention including (1) the rate at which non-deleterious mutations arise, (2) the extent to which “deleterious” mutations provide evolutionary potential in changing environments, and (3) how conservative to be when faced with such uncertainties. Page 1125

7. The shape of life, By Matthew A. Wills

Whether this disparity was generated in the time permitted by a literal reading of the body fossil record, or over a more protracted period extending far back into the Precambrian is still hotly **debated**. Page 1150

8. Phylogeny of g-proteobacteria, By James R. Brown

Because of HGT, there are intense **debates** in the evolutionary biology community as to whether or not the faithful reconstruction of the universal tree of life is possible. Page 464

9. From 2R to 3R, By Axel Meyer

However, the relative importance of both gene duplication and divergent transcriptional regulation in explaining the evolution of biological complexity remains a subject of vigorous **debate**. Page 937

10. Effects of sequence alignment, By Nick Goldman

There has been much **debate** about the best procedures for molecular phylogenetic inference, that is, estimation of evolutionary relationships from genetic sequence data. These discussions have been predominantly based on comparisons of different methods for estimating evolutionary trees from aligned DNA, RNA, or amino acid sequences. Page 287

Perhaps because of longstanding **debate**s regarding phylogeny estimation methodology, variation in the results of this final stage of analyses has received by far the most attention. Page 288

11. Molecular Evolution, By Ross J. MacIntyre

Since then, the clock's existence has been the subject of considerable analysis and **debate**. Page 700

12. Reproductive mode and speciation, By David W. Zeh

How new species arise during evolution is one of the most fundamental but highly contentious issues in biology. Speciation occurs when populations diverge sufficiently to become reproductively isolated; but is this isolation initiated by pre-fertilization barriers to gene flow or by postzygotic genetic incompatibility? There is currently little consensus regarding the answer to this question, and much **debate** over the relative importance of mutation accumulation, sexual selection, selfish genetic elements and intergenomic conflict in the speciation process. Page 938

13. Reconstructing evolutionary relationships, By Carlos Briones

Nonetheless, these analyses have also resulted in major, ongoing, taxonomic **debates** (Bromham and Penny, 2003; Doolittle, 1999; Huynen et al., 1999; Mayr, 1998; Woese, 2000; Wolf et al., 2002). At the base of the controversy lies the fact that tree reconstruction is affected by horizontal gene transfer, which is currently acknowledged as a driving force of prokaryotic evolution (Clarke et al., 2002; Kurland et al., 2003; Nesbo et al., 2001; Ochman et al., 2000) and may even involve lateral transfer of rRNA operons (Perez-Luz et al., 1998; Yap et al., 1999). Other discrepancies are related to the constancy of the rate of the molecular clock among different genes and organisms, and to the influences that population size and fixation of mutations with a selective effect have on the divergence of sequences (Bromham and Penny, 2003). Moreover, the release of complete genome sequences from over 200 organisms has fueled this **debate** by showing that phylogenies constructed with many universally distributed genes may exhibit important differences with the rRNA-based universal tree. Page 372

14. Evolution of a complex minisatellite, By Paula Barros

The reconstruction of the phylogenetic history of a microsatellite locus is a very challenging task. Currently, we do not know the nature of the substitution process that might operate at these loci, or how insertion and deletions arise in each case, and therefore, statements of homology—the alignment—are very uncertain. Page 493

In this case we are not confident enough in our estimate to enter into this **debate**, as the estimation of allelic phylogenies from microsatellite loci is still a very difficult undertaking. The analysis of the homology between the great apes and humans revealed that the highest homology in the organization of MsH43 was between orang-utan and humans. This result does not agree with the standard phylogeny of primates. Page 493

15. Lusitania revisited, By Graham Rowe

However, interesting questions still await resolution. Lusitanian distributions of fauna and flora in western Europe, for example, have puzzled biogeographers for more than 150 years. Lusitanian species have highly disjunct distributions in Ireland and in Iberia, often with few or no other populations inbetween. Despite much **debate**, no agreed explanation for Lusitanian distributions has yet emerged. Page 335

16. Gene tree parsimony, By James A. Cotton

Of the few remaining criticisms, most are reflections of a wider **debate**, that between consensus and “total-evidence” methods for using multiple sources of evidence in phylogenetic reconstruction. We revisit this **debate** briefly, to suggest that these criticisms are not decisive in deciding between gene tree parsimony and uninode coding methods. A further subset of the criticisms are aimed at only a particular implementation of the gene tree parsimony method—that of the program GENETREE (Page, 1998), and overlook a number of recent algorithmic developments. Page 298, 299

The **debate** over whether to combine data from multiple different sources of evidence in a single data matrix for phylogenetic analysis has been on-going for over a decade (for reviews see de Queiroz et al., 1995; Huelsenbeck and Bull, 1996). Three different opinions have been reflected in the literature. Page 300

There has been a long **debate** between proponents of these methods for dealing with multiple data sources in systematics. Page 300

In the sense that one uses the sequence data directly and the other considers tree from the separate data partitions, gene tree parsimony and uninode coding represent alternative sides of the **debate** over combined analysis vs. Consensus methods. Simmons and Freudenstein's criticisms #4 and #5 reflect this **debate**—a **debate** that is still active (Levausser and Lapointe, 2001) and can hardly be considered a decisive criticism of gene tree parsimony. Page 301

17. Tempo of speciation, By Hendrik-Jan Megens

Molecular systematics is frequently beset with phylogenetic results that are not fully resolved. Researchers either state that the absence of resolution is due to character conflict, explosive speciation, or some combination of the two, but seldom do they carefully examine their data to distinguish between these causes. Page 1181

Despite careful phylogenetic analysis using multiple gene regions and thousands of base pairs, the historical relationships of many groups of organisms remain unresolved (e.g., Arnaiz-Villena et al., 1999; Lessa and Cook, 1998; Waits et al., 1999). These enigmatic cases have led researchers to postulate rapid radiation events, where the lack of characters supporting an internal node is explained by insufficient time for substitutions to occur (Mardulyn and Whitfield, 1999; Waits et al., 1999). Page 1182

18. Why weight?, By Karl M. Kjer

Philosophical issues aside, the **debate** over phylogenetic methods could be considered a **debate** over the best treatment of homoplastic data, since non-homoplastic data are likely to reveal phylogenetic patterns accurately by most reasonable methods (Hillis et al., 1994; Simon et al., 1994). Page 999

19. Letter to the Editor, By Tan Siew Hoong Denise

Most biologists agree that species occupy “a pivotal position in all aspects of biology” (Cracraft, 2000), but despite decades of **debate** it appears unlikely that biologists will ever settle on a single species concept (Wheeler and Meier, 2000). Page 688

Given that a resolution of the species concept **debate** is not in sight, we thus urge all authors who propose new species to be explicit about which species concept they use. Page 689

20. Implications for Character Weighting, By Gerhard Haszprunar

Throughout a long-lasting history of **debate** (as reviewed by Boyden, 1943; Remane, 1989; Rieppel, 1988, 1994; Panchen, 1992) most biologists agree that it is essential for phylogenetics to analyze similarities in order to distinguish homologies from analogies (or homoplasies in general). There is, however, no general agreement about the optimal method of inference of homology. Page 333

21. Recovery of fusion genomes, By C. Donovan Bailey

Current **debate** surrounding the origin of this complex assemblage of genes focuses on the competing causal mechanisms (e.g., Spring, 2003). Page 264

22. Falsifications and corroborations, By Kevin G. Helfenbein

Though there has been much **debate** regarding the nature of the relationship between Darwinian evolutionary theory and systematics, particularly as to whether one justifies the other (see, for example, Brower, 2000), there is no denying a relationship. Page 275

23. Analysis of the *Bufo gargarizans*, By Jinzhong Fu

Although what constitutes a species is a subject of intense **debate**, there is a general agreement that species are segments of evolutionary lineages (deQueiroz, 1998). Page 211

24. mtDNA and microsatellite loci, By Nicolás M. Suárez

The definition of taxonomic units has been under **debate** for Decades. Page 562

25. 10 years after Avise, By M. J. Hickerson

While such simulation testing of NCPA has provoked **debate** (Beaumont, 2008b; Garrick et al., 2008; Knowles, 2008; Templeton, 2004, 2009a,b), it is also a sign that the field is becoming a more statistically rigorous endeavor and that empiricists are coming to recognize that equating genealogical pattern with demographic and evolutionary processes can lead to over interpretation when ignoring coalescent stochasticity in the data. Page 293

26. Vicariance or parapatry?, By Florence Tellier

The role of demographic history versus selection for creating these patterns has always puzzled evolutionists and the **debate** about sympatric and allopatric speciation remains controversial (Bolnick and Fitzpatrick, 2007; Fitzpatrick et al., 2008). Page 679

27. Implications for DNA barcoding, By Amanda D. Roe

Using only mitochondrial characters has always been controversial (Dunn, 2003; Lipscomb et al., 2003; Seberg et al., 2003; Tautz et al., 2003), and recent **debates** have been particularly heated (Moritz and Cicero, 2004; Ebach and Holdrege, 2005; Hebert and Gregory, 2005; Meyer and Paulay, 2005; Will et al., 2005) in light of the increasing popularity of projects such as the Consortium for the Barcode of Life (<http://barcoding.si.edu/>). Page 325

28. DNA sequence library, By Torbjørn Ekrem

Many of the central issues in antagonist **debates** about the ‘promise and perils’ of DNA barcoding (Besansky et al., 2003; Blaxter, 2004; Hebert and Gregory, 2005; Lorenz et al., 2005; Moritz and Cicero, 2004; Wheeler, 2005; Will and Rubinoff, 2004; Will et al., 2005) are essentially rooted in phylogenetics. Page 540

29. Letter to the editor, By John S. Sparks

It is obvious from this symposium volume and the studies cited within, that the methods for DNA taxonomy alone, or its integration into taxonomy as a whole, are still a topic of considerable **debate**. Page 901

30. Base Compositions of Genes Encoding, By Rachael A. Ream

There is a long-standing **debate** in molecular evolution concerning the putative importance of GC content in adapting the thermal stabilities of DNA and RNA. Page 105

31. Caenorhabditis elegans Genome, By Asher D. Cutter

However, much **debate** exists about whether natural selection mediates such redundancy (Lynch and Conery 2000; Kondrashov et al. 2002; Wagner 2002), and it has been argued that this could result from many duplicates actually representing pseudogenes (Reece-Hoyes et al. 2007). Page 1206

32. Evolutionary Divergence, By Fabia U. Battistuzzi

Molecular and nonmolecular time estimates do not always agree, and their differences have fuelled **debates** on possible biases inherent in both types of data and the methods of analyses (Ayala 1999; Smith and Peterson 2002; Graur and Martin 2004; Hedges and Kumar 2004; Reisz and Muller 2004; Blair and Hedges 2005; Pulquerio and Nichols 2007; Peterson et al. 2008). Page 1289

33. More Genes or More Taxa?, By Antonis Rokas

The relative contribution of taxon number and gene number to accuracy in phylogenetic inference is a major issue in phylogenetics and of central importance to the choice of experimental strategies for the successful reconstruction of a broad sketch of the tree of life. Maximization of the number of taxa sampled is the strategy favored by most phylogeneticists, although its necessity remains the subject of **debate**. Page 1337

34. Evolution of Proteins, By Bernardo Lemos

However, the relationship between evolutionary variation in gene expression and protein sequence is controversial. Page 1345

35. Human and Mouse Malaria, By Cristian I. Castillo-Davis

Although there is still much **debate** concerning the process by which initially identical duplicate genes come to diverge in sequence and function, it is certain that after duplication, the resulting genes are subject to either one of two fates: silencing of one copy by degenerative mutations or preservation of both copies via natural selection. Page 1424

36. Gene Regulatory Network, By Rory Johnson

Consequently, **debate** continues as to the relative contributions to evolution from regulatory versus coding DNA mutation (Hoekstra and Coyne 2007). Page 1491

37. Tropomyosin Genes in Metazoans, By Manuel Irimia

Much of the **debate** about the emergence of new functions has focused on two possibilities: changes in gene expression patterns across environmental conditions, developmental stages, tissues, or subcellular locations; or emergence of new genic products, primarily by genomic duplication and/or alternative splicing (AS). Page 1504 Whether morphological innovation arises mainly through the recruitment of nearly unchanged proteins and functional gene networks or through changes in protein functions is the subject of a hot **debate** (Wagner and Lynch 2008), and only few examples of protein neofunctionalization were reported in recent literature. Page 1515

38. Toll-Like Receptor Multigene, By Miguel Alcaide

However, the ability of MHC diversity to explain the entirety of wildlife immunogenetics has been the subject of **debate**, and investigation of other candidate genes for immunoeology has been encouraged (Acevedo-Whitehouse and Cunningham 2006; Radwan et al. 2009). Page 1713

39. Programmed Genetic Instability, By Yongzhong Zhao

A longstanding **debate** in evolutionary biology concerns how species of increasing structural complexity maintain their capacity for genetic variation—and, hence, adaptation and divergence—despite a predictably increasing need for genetic fidelity (Gulick 1893; Gould JL and Gould CG 1997). Page 1737

40. Gene Family Size, By Feng-Chi Chen

The evolution of duplicate genes, however, is an issue of **debate**. Page 1750

41. The Impact of Fossils, By Laura A. Hug

In any case, the relative validity of fossil versus molecular divergence date estimation continues to be **debated**. Page 1889

The positive impact of increased taxon sampling on phylogeny determination has often been posited (Delsuc, Brinkmann and Philippe 2005), although there has been considerable **debate** over the relative impacts of taxon versus site inclusion (Hedtke, Townsend and Hillis 2006). Page 1890

This indicates that the **debate** surrounding the method of constraining fossils in molecular clock analysis (Graur and Martin 2004; Hedges and Kumar 2004; Reisz and Muller 2004; Blair and Hedges 2005; Glazko, Koonin and Rogozin 2005) is justified; molecular clock studies would benefit from greater caution taken when implementing these constraints. Page 1893

Considerable **debate** has surrounded the use of single versus multiple fossil constraints on molecular dating analyses (e.g. see Graur and Martin 2004; Hedges and Kumar 2004). Page 1893

42. Domesticated Transposase Genes, By Rebecca K. Cowan

While transposons have traditionally been viewed as genomic parasites or ‘‘junk DNA,’’ the discovery of transposon-derived host genes has fueled an ongoing **debate** over the evolutionary role of transposons. Page 2084

43. Evidence from Published Sequences, By Emmanuel D. Ladoukakis

The question of whether animal mitochondrial DNA (mtDNA) undergoes recombination has recently been the subject of intense **debate**. Page 2127

44. Estimation of Phylogenetic Inconsistencies, By Victor Soria-Carrasco

Whereas gene transfer within the same species or between closely related species is well-known and cellular mechanisms to favor it have been described, the evolutionary significance of the transfer of genes between distant species is a matter of controversy, and there is an active **debate** about whether the latter type of transfer is quantitatively anecdotal (Glansdorff 2000; Kurland 2005) or reflects a paradigm shift in prokaryotic evolution (Gogarten et al. 2002; Baptiste et al. 2005). Page 2319

45. Evolution of Transcription Factors, By Richard Jovelin

Whether phenotypic evolution proceeds predominantly through changes in regulatory sequences or changes in protein sequences has ignited an intense **debate**, with the argument in favor of the cis-regulatory hypothesis focusing on the prediction of strong conservation of TF function (Carroll 2005, 2008; Hoekstra and Coyne 2007; Wray 2007; Stern and Orgogozo 2008). Page 2373

46. Determinants of Protein Evolution, By Eric A. Franzosa

The effect of protein-core size on protein evolution has been studied by multiple groups, resulting in **debate** as to its mechanisms and significance (Bloom et al. 2006; Lin et al. 2007; Zhou et al. 2008). Page 2392

47. 16 Yeast Genomic Variables, By Fabian J. Theis

There has been much **debate** as to whether proteins involved in many interactions evolve more slowly, with some studies confirming this trend (Fraser et al. 2002), whereas others rejecting it (Batada et al. 2006). Page 2506

48. Hot Spots in the Human Genome, By Mikael Brandstrom

The study of the relationship between microsatellite polymorphism and recombination is relevant to this **debate** because if recombination drives microsatellite evolution through a mutagenic effect, recombination rate should be correlated with microsatellite variability. Page 2579

49. Histories of Dioxygen Reductases, By Celine Brochier-Armanet

Understanding the origin and evolution of cellular processes is fundamental to understand how biological activity has shaped the history of our planet. Among these, aerobic respiration is probably one of the most **debated**. Page 285

Our study of O2Red is a good example and allowed bringing an updated insight on a long-standing **debate** around the origin and evolution of enzymes involved in a fundamental energy conversion process such as aerobic respiration. Page 295

50. Genes Involved in HIV Pathogenesis, By Millan Ortiz

There is **debate** about the best handling of short deletions or insertions in the analysis of sequence evolution (Loytynoja and Goldman 2008). Page 2867

51. Large-Scale mtDNA Screening, By Qing-Peng Kong

However, it has to be pointed out that although there are some **debates** on the accuracy of molecular dating with the rho statistic (Cox 2008), the estimated ages of the basal lineages only provide a rough time range when they began to differentiate and may serve as some kind of circumstantial evidence in support of their long-time existence in the region. Page 519

52. Faster-Z Evolution, By Judith E. Mank

These studies provide a broad consensus for Faster-X Evolution; however, the underlying evolutionary mechanism remains a subject of **debate**. Page 661

53. Multiple Evolutionary Rate Classes, By Christopher Oldmeadow

The proportion of functional sequence in the human genome is currently a subject of **debate**. Page 942

Despite the vast amount of analysis of the human genome, it is unclear what proportion is functional. Page 942

54. Accuracy in AFLP Data Sets, By Maria Jesus Garcia-Pereira

Although it is generally accepted that AFLPs may not provide an accurate estimate of species phylogeny when genetic divergence is too high, it is still a matter of **debate** where this limit is (Meudt and Clarke 2007). Page 989

55. Microsatellites Within Genes, By You-Chun Li

Debates over whether SSRs play any functional role in organism development, adaptation, survival, and evolution are never-ending. Page 991

56. Animal Mitochondrial DNA, By Emmanuel D. Ladoukakis

The question of whether animal mitochondrial DNA (mtDNA) undergoes recombination has recently been the subject of intense **debate**. Page 2127

57. American Arabis divaricarpa, By Marcus A. Koch

Although molecular clock hypotheses are still under **debate**, for ITS a substitution rate of approximately 0.5% to 2.5% nucleotide divergence per 1 million years can be assumed. Page 347

58. Splicing in Phylum Rotifera, By Natalia N. Pouchkina-Stantcheva

The lack of sequence conservation and the apparently sporadic occurrence of trans-splicing among different phyla have prompted **debate** about its evolutionary origin. Page 1482

59. Evidence to Date the Tree of Life, By Michael J. Benton

Current **debate**s about which are the “best” fossil dates for calibration move to consideration of the most appropriate constraints on the ages of tree nodes. Page 26

This date was based on the age of the oldest members of the synapsid and diapsid clades (Benton 1990), and yet these basal fossils have been **debated**, as has the dating of the rocks from which they come. Page 26

So, **debates** about the superiority of one “calibration” date or another are irrelevant in the context of a search for the most appropriate distribution of dates and minimum and maximum constraints—the only bad dates are those that predate the evolutionary event upon which they are supposed to provide a minimum constraint. Page 26

It is still **debated** whether an analysis based on many genes and few dates or few genes and many dates is preferable. Page 26

However, the phylogenetic position of the plesiadapiforms is **debated**—they were probably close relatives of primates, but not primates proper (Bloch and Boyer 2002). Page 32

The age of these deposits has been much **debated** (Dyke and Van Tuinen 2004), and they fall either below or above the KT boundary (65.5 MYA 6 0.3 Myr). Page 37

The topology of the basal region of the cladogram around the split of Archosauromorpha and Lepidosauromorpha has been agreed (although some higher parts of the cladogram are still much **debated**, especially the placement of Sauropterygia and Ichthyosauria). Page 38

The most ancient lepidosauromorph is **debated**—Benton (1993, p. 688) indicated that Saurosternon bainii, sole representative of the Saurosternidae, may be the oldest, but he was uncertain. Page 38

The age of the Joggins Formation has been much **debated**, and figures in the range from 320 to 305 MYA have been cited recently. Page 39

Dating the earliest record of successive sister taxa is complicated by long-standing **debate** over the relative phylogenetic position and monophyly of the various groups. Page 44

60. Evolutionary and Functional Relationships, By Gipsi Lima-Mendez

These showed that similar morphology does not imply genetic similarity or vice versa, raising serious **debate** on the validity of the ICTV taxonomy (Hendrix et al. 2000; Brussow and Hendrix 2002; Lawrence et al. 2002; Nelson 2004). Page 762

61. Programmed Genetic Instability, By Yongzhong Zhao

A longstanding **debate** in evolutionary biology concerns how species of increasing structural complexity maintain their capacity for genetic variation—and, hence, adaptation and divergence—despite a predictably increasing need for genetic fidelity (Gulick 1893; Gould JL and Gould CG 1997). Page 1737

62. Evolution of Transcription Factors, By Richard Jovelin

Whether phenotypic evolution proceeds predominantly through changes in regulatory sequences or changes in protein sequences has ignited an intense **debate**, with the argument in favor of the cis-regulatory hypothesis focusing on the prediction of strong conservation of TF function (Carroll 2005, 2008; Hoekstra and Coyne 2007; Wray 2007; Stern and Orgogozo 2008). Page 2373

Methodology

63. Supermatrix Rooted Triples, By Michael DeGiorgio

Though statistical power generally increases with the size of a data set, the accuracy of concatenation is currently under **debate**. Page 552

64. Tropomyosin Genes in Metazoans, By Manuel Irimia

Much of the **debate** about the emergence of new functions has focused on two possibilities: changes in gene expression patterns across environmental conditions, developmental stages, tissues, or subcellular locations; or emergence of new genic products, primarily by genomic duplication and/or alternative splicing (AS). Page 1504 Whether morphological innovation arises mainly through the recruitment of nearly unchanged proteins and functional gene networks or through changes in protein functions is the subject of a hot **debate** (Wagner and Lynch 2008), and only few examples of protein neofunctionalization were reported in recent literature. Page 1515

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