

Research article

Open Access

Uncovering the mutation-fixation correlation in short lineages

Eric J Vallender^{1,2} and Bruce T Lahn*¹

Address: ¹Howard Hughes Medical Institute, Department of Human Genetics, and Committee on Genetics, University of Chicago, USA and ²New England Primate Research Center, Harvard Medical School, USA

Email: Eric J Vallender - eric_vallender@hms.harvard.edu; Bruce T Lahn* - blahn@bsd.uchicago.edu

* Corresponding author

Published: 21 September 2007

Received: 7 July 2007

BMC Evolutionary Biology 2007, 7:168 doi:10.1186/1471-2148-7-168

Accepted: 21 September 2007

This article is available from: <http://www.biomedcentral.com/1471-2148/7/168>

© 2007 Vallender and Lahn; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract

Background: We recently reported a highly unexpected positive correlation between the fixation probability of nonsynonymous mutations (estimated by ω) and neutral mutation rate (estimated by K_s) in mammalian lineages. However, this positive correlation was observed for lineages with relatively long divergence time such as the human-mouse lineage, and was not found for very short lineages such as the human-chimpanzee lineage. It was previously unclear how to interpret this discrepancy. It may indicate that the positive correlation between ω and K_s in long lineages is a false finding. Alternatively, it may reflect a biologically meaningful difference between various lineages. Finally, the lack of positive correlation in short lineages may be the result of methodological artifacts.

Results: Here we show that a strong positive correlation can indeed be seen in short lineages when a method was introduced to correct for the inherently high levels of stochastic noise in the use of K_s as an estimator of neutral mutation rate. Thus, the previously noted lack of positive correlation between ω and K_s in short lineages is due to stochastic noise in K_s that makes it a far less reliable estimator of neutral mutation rate in short lineages as compared to long lineages.

Conclusion: A positive correlation between ω and K_s can be observed in all mammalian lineages for which large amounts of sequence data are available, including very short lineages. It confirms the authenticity of this highly unexpected correlation, and argues that the correction likely applies broadly across all mammals and perhaps even non-mammalian species.

Background

Point mutations in coding regions of genes can be classified into two categories: synonymous and nonsynonymous. In mammals, synonymous mutations are largely neutral, though they may sometimes experience weak selection [1]. Nonsynonymous mutations, in contrast, are frequently subject to strong selection. The rate of fixed synonymous (or nonsynonymous) substitutions is often denoted as K_s (or K_a). K_s is typically treated as a reasonable proxy for neutral mutation rate, and the K_a/K_s ratio

(abbreviated ω) is often used as a measure for the fixation probability of nonsynonymous mutations scaled to neutral expectation.

Recently, we discovered a strong positive correlation between ω and K_s in several mammalian lineages, arguing that the fixation probability of nonsynonymous mutations in a gene is positively correlated with the gene's neutral mutation rate [2]. This finding is highly unexpected under the classical neutral theory of molecular evolution,

which argues that the fixation probability of nonsynonymous mutations is determined by (and serves as an estimator for) selective pressure, and as such, should be independent of neutral mutation rate [3-5]. Conventionally, therefore, ω should not show any positive correlation with K_s , and in fact, simulations demonstrate that only an inverse correlation should in theory exist between ω and K_s due to a mathematical artifact [2] (see below). The observation of a strong positive correlation between ω and K_s therefore challenges the current paradigm of molecular evolution, and necessitates a reexamination of the widely held assumption that ω is determined primarily by selective pressure independent of neutral mutation rate.

There is, however, an important caveat to this finding. The positive correlation between ω and K_s was observed in mammalian lineages with relatively large sequence divergence, specifically, the human-mouse, human-rabbit, and mouse-rat lineages [2] (the average K_s of these lineages being 0.48, 0.38 and 0.18, respectively), but not found in the human-chimpanzee or the human-macaque lineages, which have much lower levels of sequence divergence (the average K_s being 0.012 and 0.063, respectively). Instead, an inverse correlation between ω and K_s was seen in these latter short lineages [2]. This is troubling because it leaves open the possibility that the positive correlation between ω and K_s observed in long lineages may actually be an artifact associated with the imprecise calculation of K_a or K_s . In particular, multiple hits at any given nucleotide position can occur with high probability in long lineages. Such multiple hits, difficult to correct since only one or zero changes can be observed at a given nucleotide position, can constitute a major source of error in the calculation of K_a and, even more so, K_s . It is formally possible, therefore, that errors stemming from the improper correction of multiple hits along with some other unknown factors have systematically biased the calculation of K_a and K_s in long lineages, in a manner that creates an artifactual positive correlation between ω and K_s .

We have argued previously that this inverse correlation may be due to the effect of stochastic noise on K_s , which affects short lineages more profoundly than long lineages. Specifically, stochastic deviation of K_s from the true underlying neutral mutation rate (μ) represents a much greater fraction of μ in short lineages as compared to long lineages, and our simulations showed that this could indeed lead to a strong inverse correlation between ω and K_s in very short lineages such as the human-chimpanzee lineage because K_s is also used as the denominator in the calculation of ω (which equals K_a/K_s) (see Supplementary Material in [2]).

If the failure to observe a positive correlation between ω and K_s in short lineages is indeed due to the inherently

high levels of stochastic noise affecting K_s in short lineages, then a reasonable correction of noise in K_s might be able to bring out the positive correlation again. Here, we show that by introducing a method that corrects for stochastic noise in K_s , a strong positive correlation between ω and K_s indeed becomes observable in short lineages. This result strengthens the authenticity of this highly unexpected correlation, and argues that a biological mechanism (rather than a methodological artifact) is relating the fixation probability of nonsynonymous mutations to mutation rate.

Results

We generated a set of 6,779 genes each with orthologs from five primate and rodent species for which large-scale genome sequences are currently available: human, chimpanzee, rhesus macaque, mouse, and rat. A subset of 5,831 genes also included orthologs from dog. To ensure that the current data set was consistent with our earlier results based on a separately derived data set [2], we sought to recapitulate the positive correlation between ω and K_s in human-mouse and mouse-rat comparisons. Indeed, for both lineages, a highly robust correlation exists and binning of genes creates a visually striking representation of the correlation (Additional file 1). We also plotted human-dog and mouse-dog values and observed correlations similar to that seen in the human-mouse lineage (data not shown). To ensure that the correlation is not restricted to genes with orthologs in all the species sampled, we also obtained data sets containing only pairwise orthologs. Again, we observed correlations that are essentially the same as that seen in the five- or six-way ortholog sets (data not shown).

We then considered the human-chimpanzee and human-macaque ortholog pairs within the complete data set. As expected for these short lineages, plotting ω against K_s showed that not only is there not a positive correlation, but there is a strong inverse correlation between these two parameters for the human-chimpanzee lineage (Additional file 2). We have speculated previously that this inverse correlation is due to the inherently high levels of stochastic variation in K_s when it is used as a proxy for neutral mutation rate in short lineages [2]. If this is correct, then the strength of the inverse correlation should be stronger in the human-chimpanzee lineage than in the human-macaque lineage because the former is shorter and therefore suffers from an even higher level of stochastic noise in K_s . This is precisely what we observed (Additional file 2). Indeed, the general finding is that as evolutionary distance of a lineage decreases (and hence the stochastic noise associated with K_s relative to neutral mutation rate increases), the relationship between ω and K_s goes from a strong positive correlation in the case of

long lineages progressively toward a strong inverse correlation in the case of very short lineages.

In molecular evolutionary studies, K_s is frequently used as a proxy for neutral mutation rate (μ). It is often forgotten, however, that mutational events are a discreet process and as such are subject to stochastic variation. Over short periods of evolutionary time, this stochastic variation is often large relative to the true underlying neutral mutation rate. As evolutionary time lengthens and the number of mutational events increases, stochastic variation decreases relative to neutral mutation rate. This is clearly demonstrated by computer simulations in our previous study [2].

High levels of stochastic noise in K_s can lead to an artifactual inverse correlation because K_s is in both parameters being corrected, and it is the denominator of ω . Mathematically, by just correcting for noise on the x-axis (K_s), the artifactual inverse correlation should go away even if there is still considerable noise on the y-axis. This prediction was clearly borne out by our previous simulation studies [2]. We therefore decided to focus on devising a means to correct for noise in K_s only, and to examine if such correction can eliminate the artifactual inverse correlation between ω and K_s in short lineages. This may reveal the underlying positive correlation, if any, that has been obscured.

One way to accomplish this is to use the K_s value from orthologs of the same gene but in a longer lineage (i.e., K_s between a pair of species with greater divergence time). Indeed, when we plotted ω of the human-chimpanzee lineage against K_s of the corresponding human-mouse lineage, not only did the inverse correlation disappear, but a positive correlation as typically observed in long lineages was seen (Figure 1). The same result should, and did, occur when human-macaque ω was plotted against human-mouse K_s (Figure 1). We note that an implicit assumption in this approach is that the neutral mutation rate of a gene is correlated across different mammalian lineages [6-9]. Although the existence of such a correlation has been contentious [6,7,10], we were able to verify it in our data set independent of GC content, including not only K_s but also K_4 (Additional file 3).

In a similar manner, it is possible to correct for variation in ω apart from K_s . By using the K_s value from the human-chimpanzee lineage but ω from human-mouse, we were also able to observe the positive correlation (Figure 2). It is interesting to note the differences between these two approaches. When K_s is corrected, the positive correlation appears more robust than when ω is corrected. This is likely due to the fact that K_s is used as the denominator in the calculation of ω .

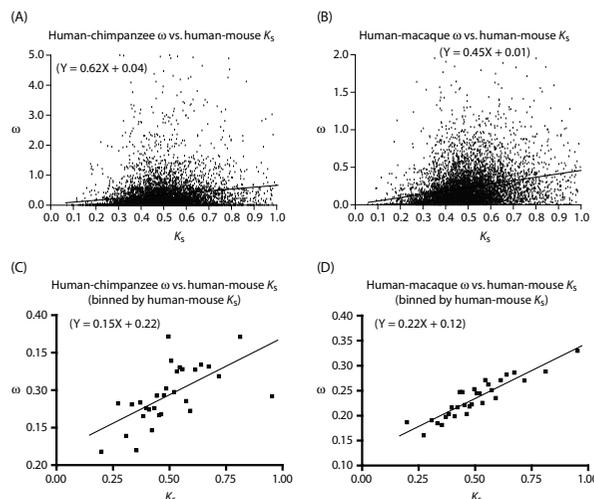


Figure 1
Positive correlation between ω of the short human-chimpanzee or human-macaque lineage and K_s of the long human-mouse lineage. In cases where genes are binned, all the genes used in the analysis are divided into bins based on ascending K_s (i.e., the first bin contains genes with the lowest K_s values and the last bin contains genes with the highest K_s values, etc.). There are 200 genes per bin except for the last bin, which contains whatever number of remaining genes that is 200 or less.

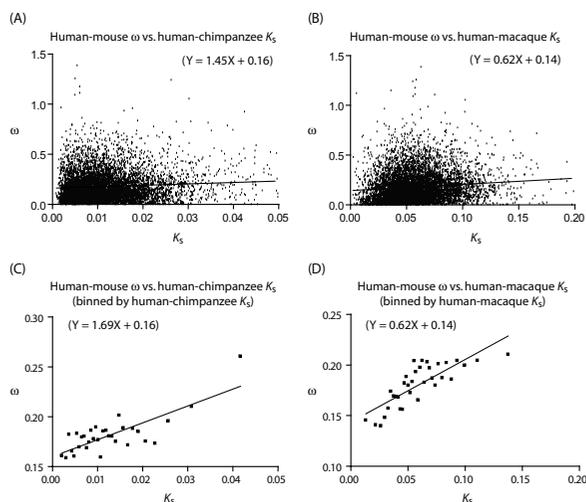


Figure 2
Positive correlation between ω of the long human-mouse lineage and K_s of the short human-chimpanzee or human-macaque lineage. The binning of genes follows the convention in Figure 1.

In the above analyses, the lineage used to calculate ω is entirely subsumed by the lineage used to calculate K_s (e.g., when human-chimp ω was plotted against human-mouse K_s). This may introduce confounding effects. We therefore also plotted human-chimp or human-macaque ω against mouse-dog K_s . We found that a rather similar positive correlation between ω and K_s exists despite a complete lack of shared descent between the lineage used to calculate ω and the lineage used to calculate K_s (Figure 3)

In the initial analysis, ω of a short lineage is plotted against K_s of a long lineage. This reveals a positive correlation presumably because K_s of the long lineage is a more accurate estimator of neutral mutation rate than K_s of the short lineage even for the short lineage. The ideal situation, however, is to plot ω of a short lineage against K_s of the same short lineage, and do so in a manner that corrects for the stochastic noise in K_s . One approach to correct for the noise in K_s affecting individual genes is to bin genes and plot the bin-average ω against bin-average K_s . Given that K_s of the long lineage is a more accurate proxy for neutral mutation rate, we binned genes based on K_s in the long lineage even though bin-average ω and K_s values were all derived from the short lineage. Using this approach, we first plotted bin-average ω against bin-average K_s in the human-chimpanzee lineage, using human-mouse K_s to bin genes. This revealed a robust positive correlation between ω and K_s (Figure 4). A similar positive correlation was seen between bin-average ω and K_s in the human-macaque lineage when human-mouse K_s was again used to bin genes (Figure 4). Comparable results

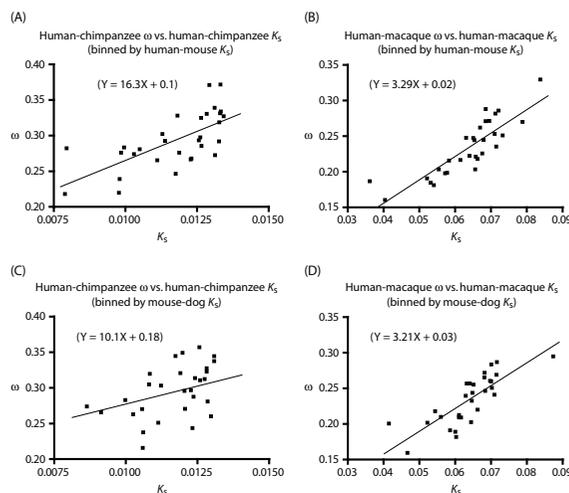


Figure 4
Positive correlation between bin-average ω of a short lineage and bin-average K_s of that same short lineage when genes are binned by K_s of a long lineage. The binning of genes follows the convention in Figure 1.

were also obtained for either the human-chimpanzee or human-macaque lineage when mouse-dog K_s was used to bin genes.

We note that the accuracy of K_a and K_s can be compromised by polymorphisms and that the effect is stronger for short lineages. This is because in short lineages, a considerable fraction of observed sequence differences between two reference genomes may actually be polymorphisms rather than fixed divergence. As such, K_a and K_s values calculated from two closely related reference genomes are inflated. This is especially true for K_a because a significant fraction of nonsynonymous polymorphisms can be slightly deleterious mutations destined for elimination before they can reach fixation [11]. This may contribute to the poor quality of K_s in approximating μ and K_a/K_s in approximating selective pressure, and thus the erosion of the positive correlation in short lineages. What remains clear, however, is that polymorphisms are an unlikely source of the positive correlation between ω and K_s . This is because in long lineages, the effect of polymorphisms on K_a and K_s is negligible given that only a tiny fraction of the observed sequence differences between two reference genomes are due to polymorphisms, and yet that a robust positive correlation between ω and K_s can be seen in long lineages. This effectively rules out polymorphisms as a major contributing factor to the correlation.

Discussion

In this study, we show that the positive correlation between ω and K_s is not restricted to specific mammalian

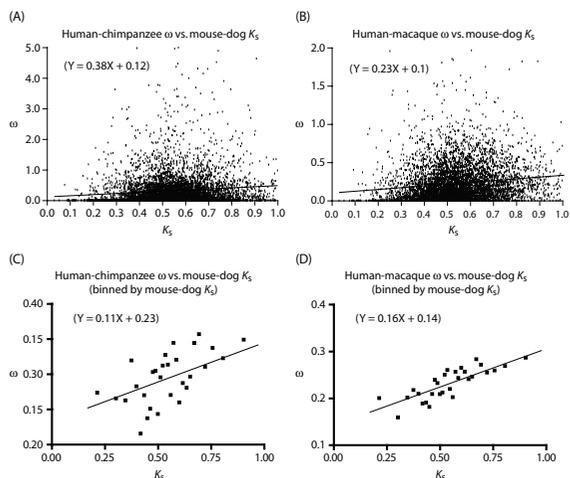


Figure 3
Positive correlation between ω of the short human-chimpanzee or human-macaque lineage and K_s of the long mouse-dog lineage. The binning of genes follows the convention in Figure 1.

lineages. Rather, the correlation can be observed across all mammalian species for which large-scale genome sequence data are available. It is particularly interesting that the correlation can be observed even in very short lineages once measures are taken to correct for the stochastic noise in K_s . This argues that the failure to observe a positive correlation between ω and K_s in short lineages in our previous study is indeed due to noise in K_s as we had speculated [2]. We note that the calculation of K_a and K_s is minimally confounded by the occurrence of multiple hits in short lineages. The ability to observe a strong positive correlation between ω and K_s in very short lineages therefore argues that the correlation is not an artifact stemming from the improper correction of multiple hits in the calculation of K_a and K_s . Our current study thus bolsters the authenticity of this correlation while demonstrating its broad applicability across the mammalian tree.

Another important message from the study is that K_s in long lineages may provide a much better estimator of neutral mutation rate than K_s in short lineage. This occurs because of the large amount of stochastic variation in K_s relative to the true underlying neutral mutation rate in short lineages than in long lineages. Indeed, when estimating neutral mutation rate of a gene in a short lineage, it may be more accurate to use the observed K_s of that gene in a long lineage (scaled down proportional to the genome-average differential in sequence divergence of the two lineages) than to use the observed K_s from the short lineage. This study and our unpublished data confirm that neutral mutation rate can remain relatively stable across different mammalian lineages [8,9].

Neither the previous long-lineage study nor the current short-lineage study alone is sufficient to eliminate methodological artifacts from consideration. In the study of long lineages, the correlation is complicated by possible difficulties in correcting for multiple hits, though the stochastic noise in K_s and the effect of polymorphisms are not major issues. In the study of short lineages, the converse situation is true. It is thus gratifying that a strong positive correlation between ω and K_s can be observed not only for long lineages, but also for short lineages after noise in K_s is corrected. Together, these results argue that the correlation is the result of a biological mechanism rather than a methodological artifact.

It is as yet unclear why there should exist such a strong positive correlation between ω and K_s . Neither this study nor our previous study provides a definitive mechanism by which this correlation may occur, though several models have been proposed. Perhaps ω is reflective of some combined effect of selective pressure and neutral mutation rate, or perhaps selective pressure and neutral mutation rate influence each other in some way [2]. It was

speculated that the occurrence of intragenic compensatory mutations, which is supported by some theoretical and empirical studies [12-14], may contribute to the former scenario [2]. It was also suggested that modulated mutability may contribute to the latter scenario [2], that is, the correlation may be partly due to the fact that genes with conserved functions have evolved lower neutral mutation rates over evolutionary time [15-17]. These speculations notwithstanding, the biological mechanism responsible for the correlation remains unclear.

Given the presence of the correlation in all the mammalian lineages for which there is sufficient genome sequence data, including very short lineages, it now seems clear that the correlation is indeed the result of a biologically meaningful process. The stage is set for future studies to identify the mechanisms underpinning this enigmatic correlation.

Methods

Using data from Ensembl v36 [18], sequences were obtained for: human, *Homo sapiens* (NCBI 35); chimpanzee, *Pan troglodytes* (PanTro 1.0); rhesus macaque, *Macaca mulatta* (Mmul 1.0); mouse, *Mus musculus* (NCBI m34); rat, *Rattus norvegicus* (RGSC 3.4); and dog, *Canis familiaris* (CanFam 1.0). Genes were clustered into orthologous groups using reciprocal best BLAST hits following established methods [19-21]. We further attempted to ensure proper alignments by imposing maximum acceptable K_s cut-offs at roughly three standard deviations above average for all alignments. Sequences were curated for length differences and for poor alignment. This resulted in 5,831 orthologous groups containing a member from each of the six species with reasonable alignment and 6,779 orthologous groups containing all five primate and rodent species. Ortholog groups, alignments, and evolutionary estimates used in this study can be obtained through the SPEED database [21].

In-frame alignments of orthologs were performed using The Wisconsin Package v10.2 <http://www.accelrys.com/>. Evolutionary parameters were estimated using the Li method [22], though the results obtained were comparable (positive linear correlations between ω and K_s) when other methods such as PAML [23,24] were used.

Competing interests

The author(s) declare that there are no competing interests.

Authors' contributions

EJV and BTL designed the project, performed analysis and wrote the paper. EJV performed bioinformatic data mining. Both authors have read and approved the final manuscript.

Additional material

Additional file 1

Supplementary Figure 1. Positive correlation between ω and K_3 for the human-mouse lineage and the mouse-rat lineage.

Click here for file

[http://www.biomedcentral.com/content/supplementary/1471-2148-7-168-S1.pdf]

Additional file 2

Supplementary Figure 2. Lack of positive correlation between ω and K_3 in the human-chimpanzee lineage and the human-macaque lineages.

Click here for file

[http://www.biomedcentral.com/content/supplementary/1471-2148-7-168-S2.pdf]

Additional file 3

Supplementary Figure 3. Correlation of K_3 or K_4 between different lineages.

Click here for file

[http://www.biomedcentral.com/content/supplementary/1471-2148-7-168-S3.pdf]

Acknowledgements

We thank L. Hurst and A. Kondrashov who served as constructive reviewers of the manuscript.

References

- Chamary JV, Parmley JL, Hurst LD: **Hearing silence: non-neutral evolution at synonymous sites in mammals.** *Nat Rev Genet* 2006, **7(2)**:98-108.
- Wyckoff GJ, Malcom CM, Vallender EJ, Lahn BT: **A highly unexpected strong correlation between fixation probability of nonsynonymous mutations and mutation rate.** *Trends Genet* 2005, **21(7)**:381-385.
- Ohta T: **Slightly deleterious mutant substitutions in evolution.** *Nature* 1973, **246(5428)**:96-98.
- Kimura M: **Evolutionary rate at the molecular level.** *Nature* 1968, **217(129)**:624-626.
- Kimura M: **The Neutral Theory of Molecular Evolution.** Cambridge, UK, Cambridge University Press; 1983.
- Bulmer M, Wolfe KH, Sharp PM: **Synonymous nucleotide substitution rates in mammalian genes: implications for the molecular clock and the relationship of mammalian orders.** *Proc Natl Acad Sci U S A* 1991, **88(14)**:5974-5978.
- Mouchiroud D, Gautier C, Bernardi G: **Frequencies of synonymous substitutions in mammals are gene-specific and correlated with frequencies of nonsynonymous substitutions.** *J Mol Evol* 1995, **40(1)**:107-113.
- Makalowski W, Boguski MS: **Evolutionary parameters of the transcribed mammalian genome: an analysis of 2,820 orthologous rodent and human sequences.** *Proc Natl Acad Sci U S A* 1998, **95(16)**:9407-9412.
- Kumar S, Subramanian S: **Mutation rates in mammalian genomes.** *Proc Natl Acad Sci U S A* 2002, **99(2)**:803-808.
- Williams EJ, Hurst LD: **Is the synonymous substitution rate in mammals gene-specific?** *Mol Biol Evol* 2002, **19(8)**:1395-1398.
- Rocha EP, Smith JM, Hurst LD, Holden MT, Cooper JE, Smith NH, Feil EJ: **Comparisons of dN/dS are time dependent for closely related bacterial genomes.** *J Theor Biol* 2006, **239(2)**:226-235.
- Kimura M: **The role of compensatory neutral mutation in molecular evolution.** *J Genet* 1985, **64**:7-19.
- Kimura M: **Diffusion models in population genetics with special reference to fixation time of molecular mutants under mutational pressure.** In *Population Genetics and Molecular Evolution* Edited by: Ohta T, Aoki K. New York, New York, Springer-Verlag; 1985:19-39.
- Choi SS, Li W, Lahn BT: **Robust signals of coevolution of interacting residues in mammalian proteomes identified by phylogeny-aided structural analysis.** *Nat Genet* 2005, **37(12)**:1367-1371.
- Cox EC: **On the organization of higher chromosomes.** *Nat New Biol* 1972, **239(92)**:133-134.
- Kondrashov AS: **Modifiers of mutation-selection balance: general approach and the evolution of mutation rates.** *Genet Res* 1995, **66**:53-69.
- Chuang JH, Li H: **Functional bias and spatial organization of genes in mutational hot and cold regions in the human genome.** *PLoS Biol* 2004, **2(2)**:E29.
- Birney E, Andrews D, Caccamo M, Chen Y, Clarke L, Coates G, Cox T, Cunningham F, Curwen V, Cutts T, Down T, Durbin R, Fernandez-Suarez XM, Flicek P, Graf S, Hammond M, Herrero J, Howe K, Iyer V, Jekosch K, Kahari A, Kasprzyk A, Keefe D, Kokocinski F, Kulesha E, London D, Longden I, Melsopp C, Meidl P, Overduin B, Parker A, Proctor G, Pric A, Rae M, Rios D, Redmond S, Schuster M, Sealy I, Searle S, Severin J, Slater G, Smedley D, Smith J, Stabenau A, Stalker J, Trevanion S, Ureta-Vidal A, Vogel J, White S, Woodwark C, Hubbard TJ: **Ensembl 2006.** *Nucleic Acids Res* 2006, **34(Database issue)**:D556-61.
- Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA: **The COG database: an updated version includes eukaryotes.** *BMC Bioinformatics* 2003, **4**:41.
- Tatusov RL, Koonin EV, Lipman DJ: **A genomic perspective on protein families.** *Science* 1997, **278(5338)**:631-637.
- Vallender EJ, Paschall JE, Malcom CM, Lahn BT, Wyckoff GJ: **SPEED: a molecular-evolution-based database of mammalian orthologous groups.** *Bioinformatics* 2006, **22(22)**:2835-2837.
- Li WH: **Unbiased estimation of the rates of synonymous and nonsynonymous substitution.** *J Mol Evol* 1993, **36(1)**:96-99.
- Goldman N, Yang Z: **A codon-based model of nucleotide substitution for protein-coding DNA sequences.** *Mol Biol Evol* 1994, **11(5)**:725-736.
- Nei M, Gojobori T: **Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions.** *Mol Biol Evol* 1986, **3(5)**:418-426.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

