Refining Convergent Rate Analysis with Topology in Mammalian Longevity and Marine Transitions

Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.06.434197v1
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Features of the Sentence Audit:

The Sentence Audit combines two complementary proofreading approaches:

1. Each sentence of your text is parsed and displayed in isolation for focused inspection.
2. Each individual sentence is further parsed into Minimal Sentence Components for a deeper review of the clarity, composition and consistency of the language you used.

The Minimal Sentence Components shown are the smallest coherent elements of each sentence of your text as derived from it's conjunctions, prepositions and selected punctuation symbols (i.e. commas, semicolons, round and square brackets).

The combined approaches ensure easier, faster, more effective proofreading.

Comments and Caveats:

• The sentence parsing is achieved using a prototype natural language processing pipeline written in Python and may include occasional errors in sentence segmentation.

• Depending on the source of the input text, the Sentence Audit may contain occasional html artefacts that are parsed as sentences (E.g. "Download figure. Open in new tab").

• Always consult the original research paper as the true reference source for the text.

Contact Information:

To get a Manuscript Microscope Sentence Audit of any other research paper, simply forward any copy of the text to John.James@OxfordResearchServices.com.

All queries, feedback or suggestions are also very welcome.

Research Paper Sections:

The sections of the research paper input text parsed in this audit.

Section No.	Headings	Sentences
Section: 1	Abstract	12
Section: 2	Introduction	15
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title

Refining Convergent Rate Analysis with Topology in Mammalian Longevity and Marine Transitions

S1 [001] Abstract

S1 [002] The quest to map the genetic foundations of phenotypes has been empowered by the modern diversity, quality, and availability of genomic resources.

> The quest ...
> ... to map the genetic foundations ...
> ... of phenotypes has been empowered ...
> ... by the modern diversity, ...
> ... quality, ...
> ... and availability ...
> ... of genomic resources.

S1 [003] Despite these expanding resources, the abundance of variation within lineages makes the association of genetic change to specific phenotypes improbable.

> Despite these expanding resources, ...
> ... the abundance ...
> ... of variation ...
> ... within lineages makes the association ...
> ... of genetic change ...
> ... to specific phenotypes improbable.

S1 [004] Drawing such connections requires an a priori means of isolating the associated changes from background genomic variation.

> Drawing ...
> ... such connections requires an a priori means ...
> ... of isolating the associated changes ...
> ... from background genomic variation.

S1 [005] Evolution may provide these means via convergence; i.e., the shared variation that may result from replicate evolutionary experiments across independent trait occurrences.

> Evolution may provide these means ...
> ... via convergence; ...
> ... i.e., ...
> ... the shared variation ...
> ... that may result ...
> ... from replicate evolutionary experiments ...
> ... across independent trait occurrences.

S1 [006] To leverage these opportunities, we developed TRACCER: Topologically Ranked Analysis of Convergence via Comparative Evolutionary Rates.

> To leverage these opportunities, ...

... we developed TRACCER: ...

... Topologically Ranked Analysis ...

... of Convergence ...

... via Comparative Evolutionary Rates.

S1 [007]   As compared to current methods, this software empowers rate convergence analysis by factoring in topological relationships, because variation between phylogenetically proximate trait changes is more likely to be facilitating the trait.

As compared ...

... to current methods, ...

... this software empowers rate convergence analysis ...

... by factoring ...

... in topological relationships, ...

... because variation ...

... between phylogenetically proximate trait changes is more likely ...

... to be facilitating the trait.

S1 [008]   Pairwise comparisons are performed not with singular branches, but in reference to their most recent common ancestors.

Pairwise comparisons are performed not ...

... with singular branches, ...

... but in reference ...

... to their most recent common ancestors.

S1 [009]   This ensures that comparisons represent identical genetic contexts and timeframes while obviating the problematic requirement of assigning ancestral states.

This ensures ...

... that comparisons represent identical genetic contexts ...

... and timeframes ...

... while obviating the problematic requirement ...

... of assigning ancestral states.

S1 [010]   We applied TRACCER to two case studies: marine mammal transitions, an unambiguous trait which has independently evolved three times, as well as the evolution of mammalian longevity, a less delineated trait but with more instances to compare.

We applied TRACCER ...

... to two case studies: ...

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... as well ...

... as the evolution ...

... of mammalian longevity, ...

... a less delineated trait ...

... but with more instances ...

... to compare.

S1 [011]   TRACCER, by factoring in topology, identifies highly significant, convergent genetic signals in these test cases, with important incongruities and statistical resolution when compared to existing convergence approaches.

> TRACCER, ...
>
> ... by factoring ...
>
> ... in topology, ...
>
> ... identifies highly significant, ...
>
> ... convergent genetic signals ...
>
> ... in these test cases, ...
>
> ... with important incongruities ...
>
> ... and statistical resolution ...
>
> ... when compared ...
>
> ... to existing convergence approaches.

S1 [012]   These improvements in sensitivity and specificity generate refined targets for downstream analysis of convergent evolution and identification of genotype-phenotype relationships.

> These improvements ...
>
> ... in sensitivity ...
>
> ... and specificity generate refined targets ...
>
> ... for downstream analysis ...
>
> ... of convergent evolution ...
>
> ... and identification ...
>
> ... of genotype-phenotype relationships.

S2 [013]   Introduction

S2 [014]   When challenged with similar selective pressures, independent lineages may converge on similar adaptations to those challenges (Losos, 2011).

> When challenged ...
>
> ... with similar selective pressures, ...
>
> ... independent lineages may converge ...
>
> ... on similar adaptations ...
>
> ... to those challenges ...
>
> ... (Losos, 2011).

S2 [015]   A myriad of complex mutations can be sufficient to produce such adaptive traits, but the stochastic nature of evolution begets that such adaptive traits will tend to manifest parsimoniously, particularly given the genetic constraints and largely similar toolkits of life (Rosenblum et al., 2014).

> A myriad ...
>
> ... of complex mutations can be sufficient ...
>
> ... to produce ...
>
> ... such adaptive traits, ...
>
> ... but the stochastic nature ...
>
> ... of evolution begets ...
>
> ... that such adaptive traits will tend ...
>
> ... to manifest parsimoniously, ...

... particularly given the genetic constraints ...

... and largely similar toolkits ...

... of life ...

... (Rosenblum et al., 2014).

S2 [016]   Given these developmental and physiological constraints in organisms, the convergent evolution of traits will tend towards similar molecular mechanisms, providing a valuable map for phenotype to genotype inferences, recently coined "forward genomics" (Currie, 2013; Hiller et al., 2012).

Given these developmental ...

... and physiological constraints ...

... in organisms, ...

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... providing a valuable map ...

... for phenotype ...

... to genotype inferences, ...

... recently coined "forward genomics" ...

... (Currie, 2013; ...

... Hiller et al., 2012).

S2 [017]   However, while the parsimonious path to the same adaptive phenotype may tread upon the same genetic elements or pathways, the specific molecular changes may evolve in unique ways.

However, ...

... while the parsimonious path ...

... to the same adaptive phenotype may tread ...

... upon the same genetic elements ...

... or pathways, ...

... the specific molecular changes may evolve ...

... in unique ways.

S2 [018]   Given a convergent trait, the molecular similarities will be shaped both by the genetic context and the precision required; there are countless ways to disrupt a pathway or knockout a gene, but there may only be a handful to specifically compromise a hydrophobic pocket, and only one to create a disulfide bridge between two domains.

Given a convergent trait, ...

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... by the genetic context ...

... and the precision required; ...

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... or knockout a gene, ...

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... to create a disulfide bridge ...

... between two domains.

End of Sample Audit