A Manuscript Microscope 'Sentence Audit' of:

Post-transcriptional regulation of Leishmania fitness gain

What is the Manuscript Microscope Sentence Audit?

The Manuscript Microscope Sentence Audit is a research paper introspection system that parses the text of your manuscript into minimal sentence components for faster, more accurate, enhanced proofreading.

Why use a Sentence Audit to proofread your manuscript?

- Accelerated Proofreading: Examine long technical texts in a fraction of the usual time.
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Bonus 3: Improved Reputation: Become known for rigorously precise publications.

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Manuscript Authors: Laura Piel, K. Shanmugha Rajan, Giovanni Bussotti, Hugo Varet, Rachel Legendre, Caroline Proux, Thibaut Douché, Quentin Giai-Gianetto, Thibault Chaze, Barbora Vojtkova, Nadav Gordon-Bar, Tirza Doniger, Smadar Cohen-Chalamish, Praveenkumar Rengaraj, Céline Besse, Anne Boland, Jovana Sadlova, Jean-François Deleuze, Mariette Matondo, Ron Unger, Petr Volf, Shulamit Michaeli, Pascale Pescher & Gerald F. Späth

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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	11
Section: 2	Introduction	16
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title # Post-transcriptional regulation of Leishmania fitness gain

S1 [001] Abstract

S1 [002] The protozoan parasite Leishmania donovani causes fatal human visceral leishmaniasis in absence of treatment.

The protozoan parasite Leishmania donovani causes fatal human visceral leishmaniasis ...

... in absence ...

... of treatment.

S1 [003] Genome instability has been recognized as a driver in Leishmania fitness gain in response to environmental change or chemotherapy.

Genome instability has been recognized ...

... as a driver ...

... in Leishmania fitness gain ...

... in response ...

... to environmental change ...

... or chemotherapy.

S1 [004] How genome instability generates beneficial phenotypes despite potential deleterious gene dosage effects is unknown.

How genome instability generates beneficial phenotypes ...

... despite potential deleterious gene dosage effects is unknown.

S1 [005] Here we address this important open question applying experimental evolution and integrative systems approaches on parasites adapting to in vitro culture.

Here we address this important open question applying experimental evolution ...

... and integrative systems approaches ...

... on parasites adapting ...

... to in vitro culture.

S1 [006] Phenotypic analyses of parasites from early and late stages of culture adaptation revealed an important fitness tradeoff, with selection for accelerated growth (fitness gain) impairing infectivity (fitness costs).

Phenotypic analyses ...

... of parasites ...

... from early ...

... and late stages ...

... of culture adaptation revealed an important fitness tradeoff, ...

... with selection ...

... for accelerated growth ...

... (fitness gain) ...

... impairing infectivity ...

... (fitness costs).

S1 [007] Comparative genomics, transcriptomics and proteomics analyses revealed a complex regulatory network driving parasite fitness, with genome instability causing highly reproducible, gene dosage-dependent changes in protein linked to post-transcriptional regulation.

Comparative genomics, ...
... transcriptomics ...
... and proteomics analyses revealed a complex regulatory network driving parasite fitness, ...
... with genome instability causing highly reproducible, ...
... gene dosage-dependent changes ...
... in protein linked ...
... to post-transcriptional regulation.

S1 [008] These in turn were associated with a gene dosage-independent reduction in flagellar transcripts and a coordinated increase in abundance of coding and non-coding RNAs known to regulate ribosomal biogenesis and protein translation.

These ...
... in turn were associated ...
... with a gene dosage-independent reduction ...
... in flagellar transcripts ...
... and a coordinated increase ...
... in abundance ...
... of coding ...
... and non-coding RNAs known ...
... to regulate ribosomal biogenesis ...
... and protein translation.

S1 [009] We correlated differential expression of small nucleolar RNAs (snoRNAs) with changes in rRNA modification, providing first evidence that Leishmania fitness gain may be controlled by post-transcriptional and epitranscriptomic regulation.

We correlated differential expression ...
... of small nucleolar RNAs ...
... (snoRNAs) ...
... with changes ...
... in rRNA modification, ...
... providing first evidence ...
... that Leishmania fitness gain ...
... may be controlled ...
... by post-transcriptional ...
... and epitranscriptomic regulation.

S1 [010] Our findings propose a novel model for Leishmania fitness gain, where differential regulation of mRNA stability and the generation of fitness-adapted ribosomes may potentially filter deleterious from beneficial gene dosage effects and provide proteomic robustness to genetically heterogenous, adapting parasite populations.

Our findings propose a novel model ...
... for Leishmania fitness gain, ...
... where differential regulation ...
... of mRNA stability ...
... and the generation ...

... of fitness-adapted ribosomes ...
... may potentially filter deleterious ...
... from beneficial gene dosage effects ...
... and provide proteomic robustness ...
... to genetically heterogenous, ...
... adapting parasite populations.

S1 [011] This model challenges the current, genome-centric approach to Leishmania epidemiology and identifies the Leishmania non-coding small RNome as a potential novel source for biomarker discovery.

This model challenges the current, ...
... genome-centric approach ...
... to Leishmania epidemiology ...
... and identifies the Leishmania non-coding small RNome ...
... as a potential novel source ...
... for biomarker discovery.

S2 [012] Introduction

S2 [013] Parasitic protozoa of the genus Leishmania are the etiologic agents of a spectrum of severe diseases known as leishmaniases that cause substantial human morbidity and are among the five most serious parasitic diseases worldwide.

Parasitic protozoa ...
... of the genus Leishmania are the etiologic agents ...
... of a spectrum ...
... of severe diseases known ...
... as leishmaniases ...
... that cause substantial human morbidity ...
... and are ...
... among the five most serious parasitic diseases worldwide.

S2 [014] Today, almost 1 billion people are at risk of Leishmania infection in close to 100 endemic countries throughout tropical and subtropical regions, with over 12 million people diagnosed with the infection [1].

Today, ...
... almost 1 billion people are ...
... at risk ...
... of Leishmania infection ...
... in close ...
... to 100 endemic countries ...
... throughout tropical ...
... and subtropical regions, ...
... with over 12 million people diagnosed ...
... with the infection ...
... [1].

S2 [015] Leishmaniasis represents a global public health challenge: recurrent epidemics are observed in South America, the Maghreb, Middle East, East Africa and India, and Leishmania infection has been declared an emerging disease in the EU and South East Asia [1, 2].

Leishmaniasis represents a global public health challenge: ...
... recurrent epidemics are observed ...
... in South America, ...
... the Maghreb, ...
... Middle East, ...
... East Africa ...
... and India, ...
... and Leishmania infection has been declared an emerging disease ...
... in the EU ...
... and South East Asia ...
... [1, 2]...
... .

S2 [016] In absence of treatment, visceral leishmaniasis (VL - also known as Kala Azar) is the most severe and fatal form of the disease, caused either by Leishmania (L.) donovani or L. infantum.

In absence ...
... of treatment, ...
... visceral leishmaniasis ...
... (VL - also known ...
... as Kala Azar) ...
... is the most severe ...
... and fatal form ...
... of the disease, ...
... caused either ...
... by Leishmania ...
... (L.) ...
... donovani ...
... or L. infantum.

S2 [017] Most Leishmania species show a digenic life cycle comprising two major developmental stages that infect two distinct hosts.

Most Leishmania species show a digenic life cycle comprising two major developmental stages ...
... that infect two distinct hosts.

S2 [018] The motile, extracellular promastigote form of Leishmania proliferates inside the digestive tract of the sand fly insect vector, while the non-motile, intracellular amastigote form develops and proliferates inside fully acidified, macrophage phagolysosomes of mammalian hosts.

The motile, ...
... extracellular promastigote form ...
... of Leishmania proliferates ...
... inside the digestive tract ...
... of the sand fly insect vector, ...
... while the non-motile, ...
... intracellular amastigote form develops ...

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

To get the full audit of this text (or any other research paper),
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John.James@OxfordResearchServices.com
