A Manuscript Microscope 'Sentence Audit' of:

Computationally reconstructed interactome of Bradyrhizobium diazoefficiens USDA110 reveals novel functional modules and protein hubs for symbiotic nitrogen fixation

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: Review long technical papers in a fraction of the usual time.
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Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.06.434201v1

Manuscript Authors: Jun-Xiao Ma, Yi Yang, Guang Li & Bin-Guang Ma

Audit Date: 19/03/21 **Audit Identifier:** GH7SB8V9R941MM4 **Code Version:** 3.6

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 conjuctions, prepositions and selected punctuation symbols (i.e. commas, semicolons, square and rounded brackets).

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

Comments and Caveats:

• The sentence parsing is achieved using a prototype python natural language processing pipeline and may result in occasional sentence segmentation or parsing errors.

• 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 of 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	1. Introduction	24
N/A	--- --- --- --- --- --- ---	0
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The Sentence Audit Of The Research Paper

Title

Computationally reconstructed interactome of Bradyrhizobium diazoefficiens USDA110 reveals novel functional modules and protein hubs for symbiotic nitrogen fixation

S1 [001] Abstract

S1 [002] Symbiotic nitrogen fixation is an important part of the nitrogen biogeochemical cycles and the main nitrogen source of the biosphere.

Symbiotic nitrogen fixation is an important part of the nitrogen biogeochemical cycles ...

... and the main nitrogen source ...

... of the biosphere.

S1 [003] As a classical model system for symbiotic nitrogen fixation, rhizobium-legume systems have been studied elaborately for decades.

As a classical model system ...

... for symbiotic nitrogen fixation, ...

... rhizobium-legume systems have been studied elaborately ...

... for decades.

S1 [004] Detailed panorama about the molecular mechanism of the communication and coordination between rhizobia and host plants is becoming clearer.

Detailed panorama ...

... about the molecular mechanism ...

... of the communication ...

... and coordination ...

... between rhizobia ...

... and host plants is becoming clearer.

S1 [005] For more systematic insights, there is an increasing demand on new studies integrating multi-omics information.

For more systematic insights, ...

... there is an increasing demand ...

... on new studies integrating multi-omics information.

S1 [006] Here we present a comprehensive computational framework, integrating the reconstructed protein interactome of B. diazoefficiens USDA110 with its transcriptome and proteome data, to study the complex protein-protein interaction (PPI) network involved in the symbiosis system.

Here we present a comprehensive computational framework, ...

... integrating the reconstructed protein interactome ...

... of B. diazoefficiens USDA110 ...

... with its transcriptome ...

... and proteome data, ...
... to study the complex protein-protein interaction ...
... (PPI) ...
... network involved ...
... in the symbiosis system.

S1 [007] We reconstructed the interactome of B. diazoefficiens USDA110 by computational approaches.

We reconstructed the interactome ...
... of B. diazoefficiens USDA110 ...
... by computational approaches.

S1 [008] Based on the comparison of interactomes between B. diazoefficiens USDA110 and other rhizobia, we inferred that the slow growth of B. diazoefficiens USDA110 may owe to the requirement of more protein modifications and further identified 36 conserved functional PPI modules.

Based ...
... on the comparison ...
... of interactomes ...
... between B. diazoefficiens USDA110 ...
... and other rhizobia, ...
... we inferred ...
... that the slow growth ...
... of B. diazoefficiens USDA110 may owe ...
... to the requirement ...
... of more protein modifications ...
... and further identified 36 conserved functional PPI modules.

S1 [009] Integrated with transcriptome and proteome data, interactomes representing free-living cell and symbiotic nitrogen-fixing (SNF) bacteroid were obtained.

Integrated ...
... with transcriptome ...
... and proteome data, ...
... interactomes representing free-living cell ...
... and symbiotic nitrogen-fixing ...
... (SNF) ...
... bacteroid were obtained.

S1 [010] Based on the SNF interactome, a core-sub-PPI-network for symbiotic nitrogen fixation was determined and 9 novel functional modules and 11 key protein hubs playing key roles for symbiosis were identified.

Based ...
... on the SNF interactome, ...
... a core-sub-PPI-network ...
... for symbiotic nitrogen fixation was determined ...
... and 9 novel functional modules ...
... and 11 key protein hubs playing key roles ...
... for symbiosis were identified.

S1 [011] The reconstructed interactome of B. diazoefficiens USDA110 may serve as a valuable reference for studying the mechanism underlying the SNF system of rhizobia and legumes.

The reconstructed interactome ...
... of B. diazoefficiens USDA110 may serve ...
... as a valuable reference ...
... for studying the mechanism underlying the SNF system ...
... of rhizobia ...
... and legumes.

S2 [012] 1. Introduction

S2 [013] In most cases, rhizobia are a group of gram-negative soil bacteria within the family Rhizobiaceae.

In most cases, ...
... rhizobia are a group ...
... of gram-negative soil bacteria ...
... within the family Rhizobiaceae.

S2 [014] They can colonize roots of legumes, establish symbiotic relationship with them and perform nitrogen fixation.

They can colonize roots ...
... of legumes, ...
... establish symbiotic relationship ...
... with them ...
... and perform nitrogen fixation.

S2 [015] This kind of symbiotic nitrogen-fixing (SNF) system can convert inorganic nitrogen to organic nitrogen and constitute an important part of the biogeochemical cycle1.

This kind ...
... of symbiotic nitrogen-fixing ...
... (SNF) ...
... system can convert inorganic nitrogen ...
... to organic nitrogen ...
... and constitute an important part of the biogeochemical cycle1.

S2 [016] As the type strain of Bradyrhizobium, an important genus of rhizobia, B. diazoefficiens USDA110 (formerly known as B. japonicum USDA110) 2 can establish a symbiotic relationship with Glycine max (soybean).

As the type strain ...
... of Bradyrhizobium, ...
... an important genus ...
... of rhizobia, ...
... B. diazoefficiens USDA110 ...
... (formerly known ...
... as B. japonicum USDA110) ...
... 2 can establish a symbiotic relationship ...

... with Glycine max ...

... (soybean).

S2 [017] The G. max – B. diazoefficiens system has been an important model for the study of SNF system 3,4.

The G. max – B. diazoefficiens system has been an important model ...

... for the study ...

... of SNF system 3,4.

S2 [018] In addition, given the efficient SNF ability of B. diazoefficiens USDA1105, it is widely used in agriculture and environmental engineering 6,7.

In addition, ...

... given the efficient SNF ability ...

... of B. diazoefficiens USDA1105, ...

... it is widely used ...

... in agriculture ...

... and environmental engineering 6,7.

S2 [019] Owing to its importance, various biological characteristics of B. diazoefficiens have been extensively studied for decades, especially its SNF mechanism such as the information exchange between B. diazoefficiens and G. max during the process of establishing symbiosis 8,9.

Owing ...

... to its importance, ...

... various biological characteristics ...

... of B. diazoefficiens have been extensively studied ...

... for decades, ...

... especially its SNF mechanism ...

... such as the information exchange ...

... between B. diazoefficiens ...

... and G. max ...

... during the process ...

... of establishing symbiosis 8,9.

S2 [020] The genome of B. diazoefficiens reference strain USDA110 was completely sequenced in 2002 10 and corresponding high-throughput omics studies were performed in recent years 11–17.

The genome ...

... of B. diazoefficiens reference strain USDA110 was completely sequenced ...

... in 2002 10 ...

... and corresponding high-throughput omics studies were performed ...

... in recent years 11–17.

S2 [021] Although a large amount of knowledge has been obtained through these studies, contribution of the protein-protein interaction (PPI) network of this species in SNF mechanism remains elusive.

Although a large amount ...

... of knowledge has been obtained ...

... through these studies, ...

End of Sample Audit

This is a truncated Manuscript Microscope Sample Audit.

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