Translational activation by an alternative sigma factor in Bacillus subtilis

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.
- Superior Proofreading: Detect subtle errors that are invisible to traditional methods.
- Focused Proofreading: Inspect each individual sentence component in isolation.
- Reliable Proofreading: Ensure every single word of your manuscript is correct.
- Easier Proofreading: Take the hardship out of crafting academic papers.

Bonus 1: Improved Productivity: Rapidly refine rough drafts to polished papers.
Bonus 2: Improved Authorship: Cultivate a clear, concise, consistent, writing style.
Bonus 3: Improved Reputation: Become known for rigorously precise publications.

Manuscript Source: https://www.biorxiv.org/content/10.1101/2021.03.06.434181v1

Manuscript Authors: Dylan M. McCormick, Jean-Benoît Lalanne, Tammy C. T. Lan, Silvi Rouskin

& Gene-Wei Li

Audit Date: 22/03/21 Audit Identifier: 766E6KT89Q10S75 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 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	7
Section: 2	INTRODUCTION	18
N/A		0

Translational activation by an alternative sigma factor in Bacillus subtilis

S1 [001] ABSTRACT

S1 [002] Sigma factors are an important class of bacterial transcription factors that lend specificity to RNA polymerases by binding to distinct promoter elements for genes in their regulons.

Sigma factors are an important class ...
... of bacterial transcription factors ...
... that lend specificity ...
... to RNA polymerases ...
... by binding ...
... to distinct promoter elements ...
... for genes ...
... in their regulons.

S1 [003] Here we show that activation of the general stress sigma factor, σB, in Bacillus subtilis paradoxically leads to dramatic induction of translation for a subset of its regulon genes.

Here we show ...
... that activation ...
... of the general stress sigma factor, ...
... σB, ...
... in Bacillus subtilis paradoxically leads ...
... to dramatic induction ...
... of translation ...
... for a subset ...
... of its regulon genes.

S1 [004] These genes are translationally repressed when transcribed by the housekeeping sigma factor, σA , owing to extended RNA secondary structures as determined in vivo using DMS-MaPseq.

These genes are translationally repressed ...
... when transcribed ...
... by the housekeeping sigma factor, ...
... σA, ...
... owing ...
... to extended RNA secondary structures ...
... as determined in vivo ...
... using DMS-MaPseq.

S1 [005] Transcription from σB -dependent promoters liberates the secondary structures and activates translation, leading to dual induction.

Transcription from σB -dependent promoters liberates the secondary structures and activates translation, ...

- ... leading ...
 ... to dual induction.
- S1 [006] Translation efficiencies between σB and σA -dependent RNA isoforms can vary by up to 100-fold, which in multiple cases exceeds the magnitude of transcriptional induction.

Translation efficiencies between σB - and σA -dependent RNA isoforms can vary by up to 100-fold, which in multiple cases exceeds the magnitude of transcriptional induction.

S1 [007] These results highlight the role of long-range RNA folding in modulating translation and demonstrate that a transcription factor can regulate protein synthesis beyond its effects on transcript levels.

These results highlight the role ...
... of long-range RNA folding ...
... in modulating translation ...
... and demonstrate ...
... that a transcription factor can regulate protein synthesis ...
... beyond its effects ...
... on transcript levels.

S2 [008] INTRODUCTION

S2 [009] Transcriptional regulation by sigma factors is a hallmark of bacterial gene expression.

Transcriptional regulation ...
... by sigma factors is a hallmark ...
... of bacterial gene expression.

S2 [010] Sigma factors bind to the core RNA polymerases, forming holoenzymes that can initiate transcription at sites with well-defined sequences.

Sigma factors bind ...
... to the core RNA polymerases, ...
... forming holoenzymes ...
... that can initiate transcription ...
... at sites ...
... with well-defined sequences.

S2 [011] In B. subtilis, most genes are transcribed by the housekeeping sigma factor σA, and some are additionally or exclusively transcribed by alternative sigma factors that control specific processes such as sporulation and motility (Haldenwang 1995; Helmann 2019).

```
In B. subtilis, ... ... most genes are transcribed ... ... by the housekeeping sigma factor \sigma A, ...
```

```
... and some are additionally ...
... or exclusively transcribed ...
... by alternative sigma factors ...
... that control specific processes ...
... such as sporulation ...
... and motility ...
... (Haldenwang 1995; ...
... Helmann 2019).
```

S2 [012] The alternative sigma factor σB is involved in the general stress response (Haldenwang and Losick 1979; Hecker et al. 2007; Price 2014; Haldenwang 1995) and initiates transcription for over two hundred genes with well-defined promoter sequences (Nicolas et al. 2012; Petersohn et al. 1999; Zhu and Stülke 2018).

The alternative sigma factor obsis involved ...
... in the general stress response ...
... (Haldenwang ...
... and Losick 1979; ...
... Hecker et al. 2007; ...
... Price 2014; ...
... Haldenwang 1995) ...
... and initiates transcription ...
... for over two hundred genes ...
... with well-defined promoter sequences ...
... (Nicolas et al. 2012; ...
... Petersohn et al. 1999; ...
... Zhu ...
... and Stülke 2018).

S2 [013] Induction of transcription leads to corresponding increases in RNA levels (Figure 1A).

```
Induction ...
... of transcription leads ...
... to corresponding increases ...
... in RNA levels ...
... (Figure 1A).
```

S2 [014] Translational regulation is also widespread in B. subtilis, although it is not typically thought to be controlled by transcription factors.

```
Translational regulation is also widespread ...
... in B. subtilis, ...
... although it is not typically thought ...
... to be controlled ...
... by transcription factors.
```

S2 [015] Differential translation among genes in the same operon is largely driven by differences in mRNA secondary structure (Burkhardt et al. 2017) and is important for stoichiometric production of proteins in the same complex or metabolic pathway (Lalanne et al. 2018; Li et al. 2014).

```
Differential translation ...
... among genes ...
... in the same operon is largely driven ...
```

```
... by differences ...
... in mRNA secondary structure ...
... (Burkhardt et al. 2017) ...
... and is important ...
... for stoichiometric production ...
... of proteins ...
... in the same complex ...
... or metabolic pathway ...
... (Lalanne et al. 2018; ...
... Li et al. 2014).
```

S2 [016] Translation can be additionally regulated by RNA-binding proteins or riboswitches that modulate the accessibility of the ribosome binding sites on the mRNA (Breaker 2018; Yakhnin et al. 2004, 2007).

Translation can be additionally regulated ...
... by RNA-binding proteins ...
... or riboswitches ...
... that modulate the accessibility ...
... of the ribosome binding sites ...
... on the mRNA ...
... (Breaker 2018; ...
... Yakhnin et al. 2004, 2007).

S2 [017] Operons are often controlled both transcriptionally and translationally (Figure 1A), but seldomly by the same regulator (Bastet et al. 2018; Chauvier et al. 2017; Hollands et al. 2012).

Operons are often controlled both transcriptionally ...
... and translationally ...
... (Figure 1A), ...
... but seldomly ...
... by the same regulator ...
... (Bastet et al. 2018; ...
... Chauvier et al. 2017; ...
... Hollands et al. 2012).

S2 [018] Here we show that the transcription factor σB not only activates transcription, but also derepresses translation for a subset of its regulon genes.

```
Here we show ... ... that the transcription factor \sigma B not ... ... only activates transcription, ... ... but also derepresses translation ... ... for a subset ... ... of its regulon genes.
```

S2 [019] Using Rend-seq (end-enriched RNA-seq) (Lalanne et al. 2018) and ribosome profiling, we identified 12 genes whose apparent translation efficiency is increased substantially during σB activation.

```
Using Rend-seq ...
... (end-enriched RNA-seq) ...
... (Lalanne et al. 2018) ...
```

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), forward a copy of the research paper to John James at John.James@OxfordResearchServices.com