Reviewer’s report

Title: Screening for Mouse Genes Lost in Mammals with Long Lifespans

Version: 0 Date: 18 Jul 2019

Reviewer: Joseph Romano

Reviewer's report:

The authors describe new methods and software for identifying gene loss that leads to anomalous lifespan in certain species of animals.

The content is interesting and important, and it integrates topics from numerous fields of biology. However, the paper itself is fairly unpolished and needs heavy structural and stylistic editing before I can be able to adequately assess the underlying scientific content.

Major issues:
- Extensive editing for grammar and style needs to be performed before the paper is ready for publication. There also seems to be some other remaining artifacts from translation to english, such as the cyrillic text in the last line of page 2.
- The discussion section is far too lengthy, and mostly consists of descriptions of genes that were identified by the software. While this information is likely useful, the discussion should be shortened to contain only the most salient points related to your findings. Extra narrative describing the genes can be moved to supplemental resources.
- Similarly, the background section is too long and needs to be condensed to the most important points. There is currently way too much detail on orthology and specific biochemical mechanisms.
- It doesn't feel like you adequately motivate focusing on gene loss alone, rather than both gene loss and gene duplication. Maybe you cover this in depth elsewhere, but aside from some vague mentions on page 3 and a set of references on the top of page 4, it is not clear why you only consider gene loss.
- The flow and ordering of the paper has flaws. The entire first subsection of "Results" is not results at all - it is a mix of background and methods (in fact, the methods described here are more informative than what you included in the "Methods" section of the paper). This is not the only area where such issues are apparent.
- Even if it is described in previous papers, your narrative description of the algorithm used by lossgainRSL is hard to follow as a reader. Please include a structured description of the algorithm (e.g., in pseudocode). Edits made to grammar and style should also help make it easier to follow in the text, as requested above.

Minor issues:
- Several areas in "Background" need citations (for example, the claim that naked mole rats and humans have anomalous lifespans).
- The paper is presented in the context of detecting genes related to lifespan, but the authors keep referring to other characteristics, such as warm vs cold blood. While it is important to mention that this
was a previous application of the software, continually referencing it tends to detract from the focus of the current paper. Furthermore, why is it reasonable to assume the software should translate to the new task (long- vs. short-lived Euarchontoglires species)? Did you have to make any alterations to the underlying model to make it work with the gerontogene task versus previous applications?
- It would be a good idea to include a permanent link to the software (e.g., via a FigShare citation) rather than a link to an institutional website (which can---and often do---change).
- Synteny needs to be defined in "Background"
- Why did you choose to limit species to Euarchontoglires? Is it simply because it is the most specific clade that includes both mole rats and primates?

Level of interest
Please indicate how interesting you found the manuscript:
An article of importance in its field

Quality of written English
Please indicate the quality of language in the manuscript:
Not suitable for publication unless extensively edited

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