

Peer Review

Review of: "CSMA: An ImageJ Plugin for the Analysis of Wound Healing Assays"

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The “CSMA: An ImageJ Plugin for the Analysis of Wound Healing Assays” preprint proposes a new image analysis tool called CSMA for monitoring the repair of a cell mat wound in culture. CSMA is programmed in Python with Java scripts for use as an ImageJ plugin, making it easy for non-programmers to implement. The authors illustrate CSMA's performance on data they have produced and on a public dataset. They compare it to two other software packages, HTM and MRI. The advantage of CSMA is that it includes cells that persist within the injured area. The additional precision provided by CSMA makes it possible to show an exponential modelling of the healing speed rather than a linear modelling in two phases. However, some information is missing to demonstrate that this software is better than the existing ones.

Exponential modelling:

The introduction emphasises the interest of cellular wound models in biology, the ways in which they can be produced and analysed. The biological players involved in wound healing are listed in detail and documented in the state-of-the-art literature. We would therefore expect a more detailed discussion of the exponential modelling of the speed of wound healing from a biological point of view. Is this modelling new? What biological information does it provide about the repair mechanism? This modelling also seems to be more appropriate for images analysed by the MRI tool (figure S4), suggesting that it has probably already been considered.

Many injury images in the literature show no residual cells. How are the velocity curves modelled in this case?

Benchmark

A list of 8 automatic or semi-automatic software packages is given in the introduction for analysing images of scarring over time. This list contains both an uncited publication and a publication cited 310

times in PubMed. Again, in the introduction, the authors criticise the failure of some software to take account of cells persisting inside the wounded area, without specifying which ones on the list, and they illustrate this criticism with software that is not on the list, HTM (nor on the references). Note that the second tool used for the benchmark, MRI, is not mentioned in the list either. Justifying the choice of tools in the list and benchmark would allow us to better measure the contribution of the CSMA software.

FAIR practices:

Datasets: The link to the public dataset from another article does not work:

At https://ganymed.math.uni-heidelberg.de/victoria/supplementary_data_migration_quantification_scratch_assays.shtml s.shtml.

I couldn't find a link to examine the new dataset.

Code: "The image analysis tool is available as the ImageJ plugin for Windows and a source code with UI for Linux and macOS." On Git, there is installation documentation for Windows but nothing for running the source code in Linux and macOS. I didn't find the .jar plugin in Git. CSMAenv_installer: it doesn't install.

At least part of the code has been turned into a comment. The code is not easy to understand.

Conclusion: I haven't tested CSMA.

Parameters: Table 2 in the article details the parameters chosen by the user without any explanation. There is no documentation about them on Git.

Conclusion:

There is a lack of comparative elements to assess the contribution of CSMA in relation to what already exists. Some observations could be better highlighted, particularly from a biological point of view. Finally, I recommend following the FAIR rules, a best practice necessary for the success of a tool like CSMA.

Form

The author's name Bobodilla ref 14 is missing an a.

The years of publication are not mentioned in the bibliography.

MRI platform asks to be cited as such:

You can use the tool's resource id (see scicrunch.org): (Wound Healing Tool, RRID:SCR_025260)

Declarations

Potential competing interests: No potential competing interests to declare.