

## PUT THE TITLE OF YOUR EXCITING PROJECT HERE

YOUR NAME<sup>1</sup>, COAUTHOR ONE<sup>2</sup>, AND COAUTHOR TWO<sup>1,3</sup>

<sup>1</sup>The first affiliation in the list.; [your@email.address](mailto:your@email.address)

<sup>2</sup>Another affiliation can be put here.

<sup>3</sup>And generally as many affiliations as you like.

*Received YYYY MM DD; accepted YYYY MM DD; published YYYY MM DD*

You have completed the reproduction pipeline and are ready to configure and implement it for your own research. This template reproduction pipeline and document contains almost all the elements that you will need in a research project containing the downloading of raw data, processing it, including them in plots and report, including this abstract, figures and bibliography. If you use this pipeline in your work, don't forget to add a notice to clearly let the readers know that your work is reproducible. If this pipeline proves useful in your research, please cite Akhlaghi and Ichikawa (2015).

*Keywords:* Add some keywords for your research here.

*Reproducible paper:* Generated from reproduction pipeline v1-55-ge5b66d9 and Gnuastro 0.7.86-ea793. Pipeline available at: <https://link-to.the/git/repo-of-your-pipeline>.

### 1. CONGRATULATIONS!

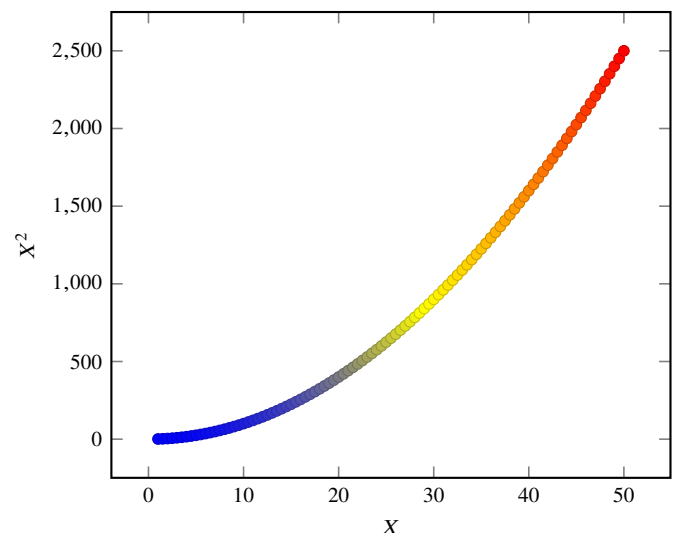
Congratulations on running the reproduction pipeline! You can now follow the checklist in the `README.md` file to customize this pipeline to your exciting research project.

Just don't forget to *never* use any numbers or fixed strings (for example database urls like <https://some.webpage.com/example/server>) directly within your  $\LaTeX$  source. Read them directly from your configuration files or outputs of the programs as part of the reproduction pipeline and import them into  $\LaTeX$  as macros through the `tex/pipeline.tex` file. See the several examples within the pipeline for a demonstration. For some recent real-world examples, the reproduction pipelines for Sections 4 and 7.3 of Bacon et al. (2017) are available at [zenodo.1164774](https://zenodo.org/record/1164774)<sup>1</sup>, or [zenodo.1163746](https://zenodo.org/record/1163746)<sup>2</sup>. Working in this way, will let you focus clearly on your science and not have to worry about fixing this or that number/name in the text.

Just as a demonstration of creating plots within  $\LaTeX$  (using the PGFPlots package), in Figure 1 we show a simple plot, where the Y axis is the square of the X axis. The minimum value in this distribution is 1.000, and 2500.000 is the maximum. Take a look into the  $\LaTeX$  source and you'll see these numbers are actually macros that were calculated from the same dataset (they will change if the dataset, or function that produced it, changes).

The PDF file of Figure 1 is available in the directory `reproduce/BDIR/tex/build/tikz/` and can be used in other contexts (for example slides). If you want to directly use the PDF file in the figure without having to let TikZ decide if it should be remade or not, you can also comment the `makepdf` macro at the top of this  $\LaTeX$  source file.

PGFPlots is a great tool to build the plots within  $\LaTeX$  and removes the necessity to add further dependencies (to create the plots) to your reproduction pipeline. High-level language



**Figure 1:** A very basic  $X^2$  plot for demonstration.

libraries like Matplotlib do exist to also generate plots. However, bare in mind that they require many dependencies (Python, Numpy and etc). Installing these dependencies from source (after several years when the binaries are no longer available in common repositories), is not easy and will harm the reproducibility of your paper.

Furthermore, since PGFPlots is built by  $\LaTeX$  it respects all the properties of your text (for example line width and fonts and etc), so the final plot blends in your paper much more nicely. It also has a wonderful manual<sup>3</sup>.

This pipeline also defines two  $\LaTeX$  macros that allow you to mark text within your document as *new* and *notes*. For example, **this text has been marked as new.** [While this one is marked as *tonote*.] If you comment the line (by adding a '%' at the start of the line or simply deleting the line) that defines

<sup>1</sup> <https://gitlab.com/makhlaghi/muse-udf-origin-only-hst-magnitudes>

<sup>2</sup> <https://gitlab.com/makhlaghi/muse-udf-photometry-astrometry>

<sup>3</sup> <http://mirrors.ctan.org/graphics/pgf/contrib/pgfplots/doc/pgfplots.pdf>

`highlightchanges`, then the one that was marked `new` will become black (totally blend in with the rest of the text) and the one marked `tonote` will not be in the final PDF. You can thus use `highlightchanges` to easily make copies of your research for existing coauthors (who are just interested in the new parts or notes) and new co-authors (who don't want to be distracted by these issues in their first time reading).

## 2. NOTICE AND CITATIONS

To encourage other scientists to publish similarly reproducible papers, please add a notice close to the start of your paper or in the end of the abstract clearly mentioning that your work is fully reproducible.

For the time being, we haven't written a specific paper only for this reproduction pipeline, so until then, we would be grateful if you could cite the first paper that used the first version of this pipeline: Akhlaghi and Ichikawa (2015).

After publication, don't forget to upload all the necessary data, software source code and the reproduction pipeline to a long-lasting host like Zenodo (<https://zenodo.org>).

### References

- Akhlaghi, M. and T. Ichikawa (Sept. 2015). *ApJS*, 220, 1.  
Bacon, R. et al. (Nov. 2017). *A&A*, 608, A1.