

### SMAUG Toolbox: Version History

- April 15<sup>th</sup>, 2020, Version 1.0.0: Initial release!
  - Includes functionality for Segment Clustering as described in Bamberger et al. 2020 [[doi.org/10.1021/acs.jpcc.0c03612](https://doi.org/10.1021/acs.jpcc.0c03612)], other clustering modes, and several simple analysis tools (histograms, etc.).
- July 28<sup>th</sup>, 2020, Version 1.0.1: Minor bug fixes
  - Fixed typos in tutorials
  - Fixed minor bug in y-axis label and lin/log assumptions in displayTraces.m
  - Minor improvement to DisplacementHistogram\_AtCut.m
  - Added the "spring" color map used in figures in Bamberger et al. 2020
  - Clarified language in tutorials regarding loading in datasets
  - Fixed rare bug in chop\_TSO\_first\_cross.m
  - Added links to Bamberger et al. 2020
- June 2<sup>nd</sup>, 2021, Version 1.1.0: Added suite of grid-based analysis tools; other minor changes
  - These grid-based analysis tools are designed for identifying rare behaviors in single-molecule data, as described in Bamberger et al. 2021 [<https://arxiv.org/abs/2105.13521>]. Two new tutorials have been added to explain how these new tools work
  - Fixed minor (and rare) error in linear fitting of tunneling sections
  - Added label to color bar in time histogram, changed default traces per bin
  - Minor changes to automatic name generation for datasets in dataset library
  - Minor changes to iterative fitting functions (do not impact results)
  - Improved the RUN\_ME function so that it still works if you download this repository from GitHub using the web interface
  - Added code of contact as suggested by GitHub