

SEPIA is a QSM pipeline processing tool to connect various toolboxes, such as MEDI, FANSI, STI Suite and SEGUE, in a single framework.

Its graphical user interface provides an intuitive way to build a pipeline, with the ability to combine methods across toolboxes.

Additionally, extra utility functions such as bipolar gradient readout correction, alternative spatial reweighting or reference regions are provided to achieve highquality QSM results in a more accessible manner.

SEPIA uses standard units for its outputs to facilitate communication across multiple toolboxes. Full documentation is available online, including detailed explanations of the interface, as well as tutorials to help you building your first QSM pipeline.

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For seasoned researchers in QSM processing, SEPIA can also benefit your research since it can be run entirely by script. Therefore, it can easily be added to your existing workflow. Moreover, the pipeline configuration file provides a clean structure about how the pipeline is set up. This is particularly useful when optimising your pipeline, as changes of method and parameters can be easily monitored, and to ensure your results are reproducible.

SEPIA – A Pipeline Processing Tool for QSM	
Use SEPIA to share your method! Be part of the solution • and benefit from other existing tools Your method, Your way • develop in your favourite way: all you need is a wrapper to communicate with SEPIA	 myQSM.m chi = myQSM(localField,mask,matrixS Sepia_handle_panel_qsm_myQSM.m b = sepia_handle_panel_qsm_myQSM.m [chi] = Wrapper_QSM_myQSM.m [chi] = Wrapper_QSM_myQSM(localFir
Easy Integration • plug-in to SEPIA with 3 simple scripts (+1 for GUI), put them together with SEPIA and you are all set ③ Let's make SEPIA better together	Documentation
New Top: All - Answered Unanswered Label - C: Search all discussion - - - Categories + - - - Oo View all + - - - Monouncements + - - - Optimized parameters + - - - Optimized parameters + - - - Optimized parameters + - - -	Links: Download: github.com/kschan0214/sepia Documentation: <u>sepia-</u> <u>documentation.readthedocs.io/en/latest/</u> Publication: Chan, KS., Marques, J.P., 2021. SEPIA— Susceptibility mapping pipeline tool for phase images. Neuroimage 227, 117611.

Having a new method is great, but it gets even better when more people are using it! Use SEPIA as a platform to share your latest development with the MR community. Your method can be seamlessly integrated into the existing pipeline in SEPIA together with other phase processing algorithms corresponding to different tasks.

Adding a new method in SEPIA is very straightforward: keep your method as it is and just create a wrapper function to get the input data from SEPIA and send back the result when the process is finished. Then copy everything to the SEPIA add-on folder and the integration is done!

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We believe SEPIA can simplify the workflow and improve the accessibility to advanced QSM processing methods. If you have any questions regarding SEPIA usage or ideas on how to improve it, please leave your comment in the GitHub discussion forum.