Addition to Simulated Analysis of Linear Reversible Enzyme Inhibition with SCILAB

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ⓢ *Supporting Information*

In the article Simulated Analysis of Linear Reversible Enzyme Inhibition with SCILAB,[1] the Supporting Information included the script *hyp_reg*, which is devoted to hyperbolic fitting of rate data and runs for SCILAB 5.4.1 and earlier versions. This script was based on the built-in SCILAB function *fit_dat*, which was removed in SCILAB 5.5.1. To ensure compatibility with further SCILAB versions we provide an actualized version of *hyp_reg*, named *hyp_reg_new*, which is based on the SCILAB function *datafit*. The run process of *hyp_reg _new* is identical as described before for *hyp_reg*.[1]

■ ASSOCIATED CONTENT

ⓢ Supporting Information

The file *hyp_reg_new.sce,* based on the SCILAB function *datafit*. This material is available via the Internet at http://pubs.acs.org.

■ REFERENCES

(1) Antuch, M.; Ramos, Y.; Álvarez, R. Simulated Analysis of Linear Reversible Enzyme Inhibition with SCILAB. *J. Chem. Educ.* **2014**, *91* (8), 1203−1206.