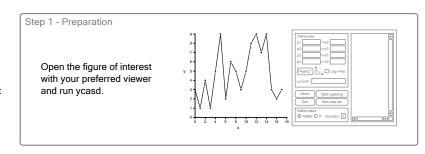
Ycasd - a tool for capturing and scaling data from graphical representations

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Mathematical modelling of biological processes often requires a large variety of different data sets for parameter estimation and validation. It is common practice that clinical data are not available in raw formats but are provided as graphical representations. Hence, in order to include these data into environments used for model simulations and statistical analyses, it is necessary to extract them from their presentations in the literature. For this purpose, we developed the freely available software yeasd. On the basis of an example, we demonstrate how to use it.

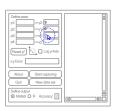


Step 2 - Define axes coordinates

Define axes coordinates y2, y1, x1 and x2 by typing in the values 9,0,0 and 18, respectively.







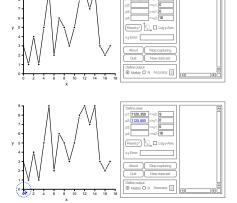


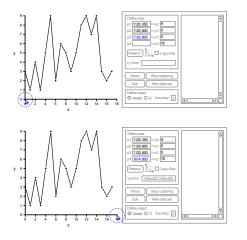
Push "Start capturing" and capture the four pixels p1 to p4 defining the axis intercepts by

simply left clicking on the axes.

Step 3 - Define axes pixel

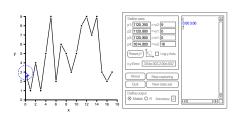


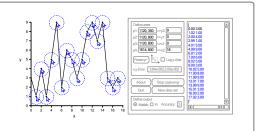




Step 4 - Capture data

While clicking on every data point of the figure, the coordinates are calculated with respect to the axes definition and displayed in the output box.





Step 5 - Define output

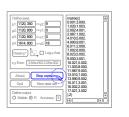
Try to modify the output style, e.g. by changing it to an R matrix and increasing the output accuracy to 3.





Step 6 - Finish

Push "Stop capturing" to inactivate capturing of data. All coordinates can be copied from the output box to the clipboard for further processing.



For more details regarding our tool, a comparison with other publically available tools or a short summary of our experiences with yeasd please have a look at http://www.biomedcentral.com/1471-2105/15/219 \Leftrightarrow

