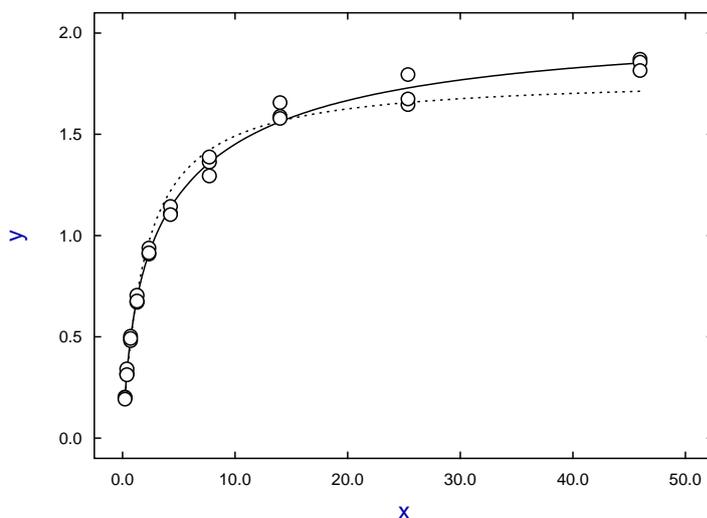


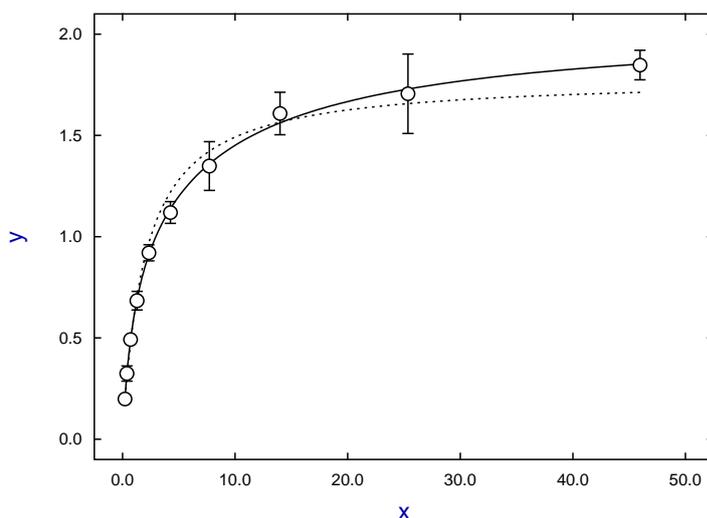


The Scatchard plot was used historically to estimate binding constants by extrapolation, but nowadays parameter estimation and model discrimination would be performed using nonlinear regression and statistical analysis. However, the plot is still sometimes used to illustrate deviations from Michaelis-Menten kinetics or one-site binding (Childs, R.E and Bardsley, W.G. (1976) *J. Theor. Biol.* **63**, 1 – 18). This can be demonstrated by opening program **mmfit** and fitting first one then a sum of two Michaelis-Menten functions. Program **mmfit** provides an option to visualize a Scatchard plot but, to use additional features, the data would be transferred directly to advanced editing leading to the following plots. The first plot shows all the data, while the second results from interactive calculation of error bars for 95% confidence limits.

Data, Best-Fit Curve and Previous Fit

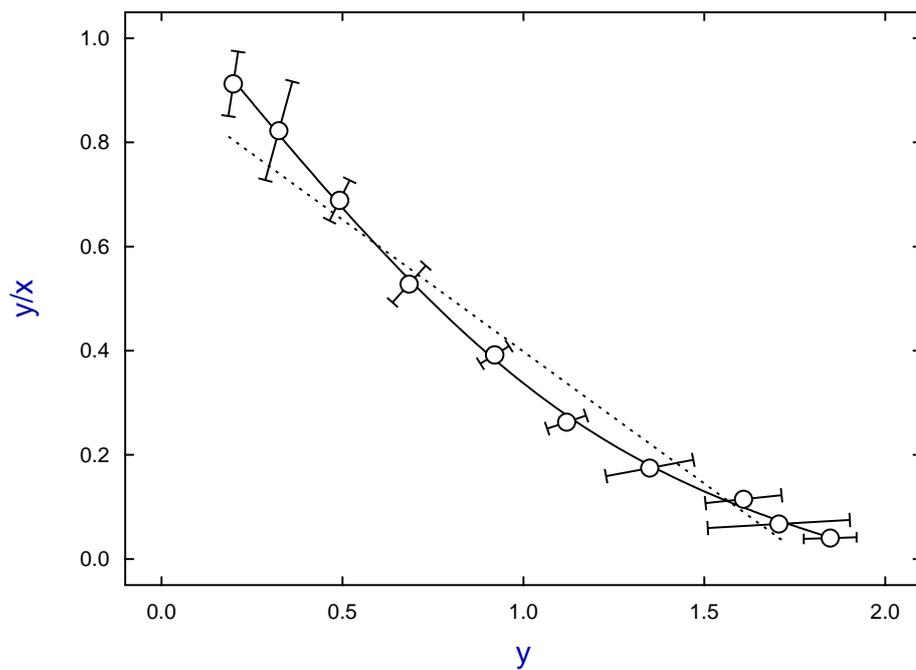


Data, Best-Fit Curve and Previous Fit



Selecting the Scatchard transformation then leads to the next graph where the best-fit curve is a conic section.

Scatchard Plot



For further illustration, the configuration file `w_simfig1.cfg` was installed, followed by minor editing to create the next plot.

Scatchard Plot for Two Binding Sites

