

Instructions for "rocclod.m"

"rocclod" derives a smooth ROC estimate for a biomarker subject to a limit of detection, either a lower or an upper.

INPUT ARGUMENTS:

xcen: a column with the scores of the healthy.

ycen: a column with the scores of the diseased.

statusx: refers to xcen and it is a column taking the value -1 for a left censored measurement due a lower LOD, 0 for an exactly observed measurement, and 1 for a right censored measurement due to an upper LOD.

statusy: refers to ycen and it is a column taking the value -1 for a left censored measurement due a lower LOD, 0 for an exactly observed measurement, and 1 for a right censored measurement due to an upper LOD.

method: can only be one the following: 'BC', 'GG', 'kernelBC', 'kernelGG', 'HCNS'. 'BC' refers to the power normal fit a.k.a. Box-Cox, 'GG' refers to the generalized gamma based ROC, 'kernelBC' refers to the kernels for which the power normal fit has been used to perform multiple imputation to the hidden tails of each distribution. An average of 30 kernel smoothed ROC estimates in then produced to be the final estimate. kernelGG: same as kernelBC but the GG is considered for the multiple imputation. HCNS: refers to the spline method as described in the paper with automatic knot selection.

init: initial values that apply only for the BC and kernelBC methods. If this argument is not reached then the means and std of the complete data are taken for initial values of the four parameters of the two groups. For the lambda 1 is the default initial value. This argument can either not be reached at all or it can be set to []. If provided it should contain a row vector of 5 values: a guess for mx, sx, my, sy and lambda with that order. For the GG and kernelGG methods initial values are based on the fit of a Weibull. The HCNS does not require initial values.

OUTPUT ARGUMENTS:

rochat: a function handle that refers to the selected by the user methodology.

AUChat: the area under the rochat.

rocnaive: a function handle that refers to the Naive Empirical ROC.

AUCnaive: the area under rocnaive.

exitflag: s scalar that is equal to 1 if the selected method has converged and zero otherwise.

EXAMPLE: see "example_of_software" file for a reproducible example.

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Any use of this software implies reference to the relevant paper:
"Estimation of smooth ROC curves for biomarkers with limits of detection"
by Leonidas E. Bantis, Qingxiang Yan, John V. Tsimikas and Ziding Feng.

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