

Description

ROC analysis quantifies the accuracy of diagnostic tests or other evaluation modalities used to discriminate between two states or conditions, which are here referred to as normal and abnormal or control and case. The discriminatory accuracy of a diagnostic test is measured by its ability to correctly classify known normal and abnormal subjects. For this reason, we often refer to the diagnostic test as a classifier. The analysis uses the ROC curve, a graph of the sensitivity versus $1 - \text{specificity}$ of the diagnostic test. The sensitivity is the fraction of positive cases that are correctly classified by the diagnostic test, whereas the specificity is the fraction of negative cases that are correctly classified. Thus the sensitivity is the true-positive rate, and the specificity is the true-negative rate.

There are six ROC commands:

Command	Entry	Description
<code>roccomp</code>	[R] roccomp	Tests of equality of ROC areas
<code>rocgold</code>	[R] roccomp	Tests of equality of ROC areas against a standard ROC curve
<code>rocfit</code>	[R] rocfit	Parametric ROC models
<code>rocreg</code>	[R] rocreg	Nonparametric and parametric ROC regression models
<code>rocregplot</code>	[R] rocregplot	Plot marginal and covariate-specific ROC curves
<code>roctab</code>	[R] roctab	Nonparametric ROC analysis

Postestimation commands are available after `rocfit` and `rocreg`; see [R] [rocfit postestimation](#) and [R] [rocreg postestimation](#).

Both nonparametric and parametric (semiparametric) methods have been suggested for generating the ROC curve. The `roctab` command performs nonparametric ROC analysis for a single classifier. `roccomp` extends the nonparametric ROC analysis function of `roctab` to situations where we have multiple diagnostic tests of interest to be compared and tested. The `rocgold` command also provides ROC analysis for multiple classifiers. `rocgold` compares each classifier's ROC curve to a "gold standard" ROC curve and makes adjustments for multiple comparisons in the analysis. Both `rocgold` and `roccomp` also allow parametric estimation of the ROC curve through a binormal fit. In a binormal fit, both the control and the case populations are normal.

The `rocfit` command also estimates the ROC curve of a classifier through a binormal fit. Unlike `roctab`, `roccomp`, and `rocgold`, `rocfit` is an estimation command. In postestimation, graphs of the ROC curve and confidence bands can be produced. Additional tests on the parameters can also be conducted.

ROC analysis can be interpreted as a two-stage process. First, the control distribution of the classifier is estimated, assuming a normal model or using a distribution-free estimation technique. The classifier is standardized using the control distribution to $1 - \text{percentile value}$, the false-positive rate. Second, the ROC curve is estimated as the case distribution of the standardized classifier values.

Covariates may affect both stages of ROC analysis. The first stage may be affected, yielding a covariate-adjusted ROC curve. The second stage may also be affected, producing multiple covariate-specific ROC curves.

The `rocreg` command performs ROC analysis under both types of covariate effects. Both parametric (semiparametric) and nonparametric methods may be used by `rocreg`. Like `rocfit`, `rocreg` is an estimation command and provides many postestimation capabilities.

The global performance of a diagnostic test is commonly summarized by the area under the ROC curve (AUC). This area can be interpreted as the probability that the result of a diagnostic test of a randomly selected abnormal subject will be greater than the result of the same diagnostic test from a randomly selected normal subject. The greater the AUC, the better the global performance of the diagnostic test. Each of the ROC commands provides computation of the AUC.

Citing a lack of clinical relevance for the AUC, other ROC summary measures have been suggested. These include the partial area under the ROC curve for a given false-positive rate t [$pAUC(t)$]. This is the area under the ROC curve from the false-positive rate of 0 to t . The ROC value at a particular false-positive rate and the false-positive rate for a particular ROC value are also useful summary measures for the ROC curve. These three measures are directly estimated by `rocreg` during the model fit or postestimation stages. Point estimates of ROC value are computed by the other ROC commands, but no standard errors are reported.

See [Pepe \(2003\)](#) for a discussion of ROC analysis. Pepe has posted Stata datasets and programs used to reproduce results presented in the book (<https://www.stata.com/bookstore/pepe.html>).

References

- Cook, J. A., and A. Rajbhandari. 2018. `heckroccurve`: ROC curves for selected samples. *Stata Journal* 18: 174–183.
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- Luque-Fernandez, M. A., D. Redondo-Sánchez, and C. Maringe. 2019. `cvauroc`: Command to compute cross-validated area under the curve for ROC analysis after predictive modeling for binary outcomes. *Stata Journal* 19: 615–625.
- Pepe, M. S. 2003. *The Statistical Evaluation of Medical Tests for Classification and Prediction*. New York: Oxford University Press.

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