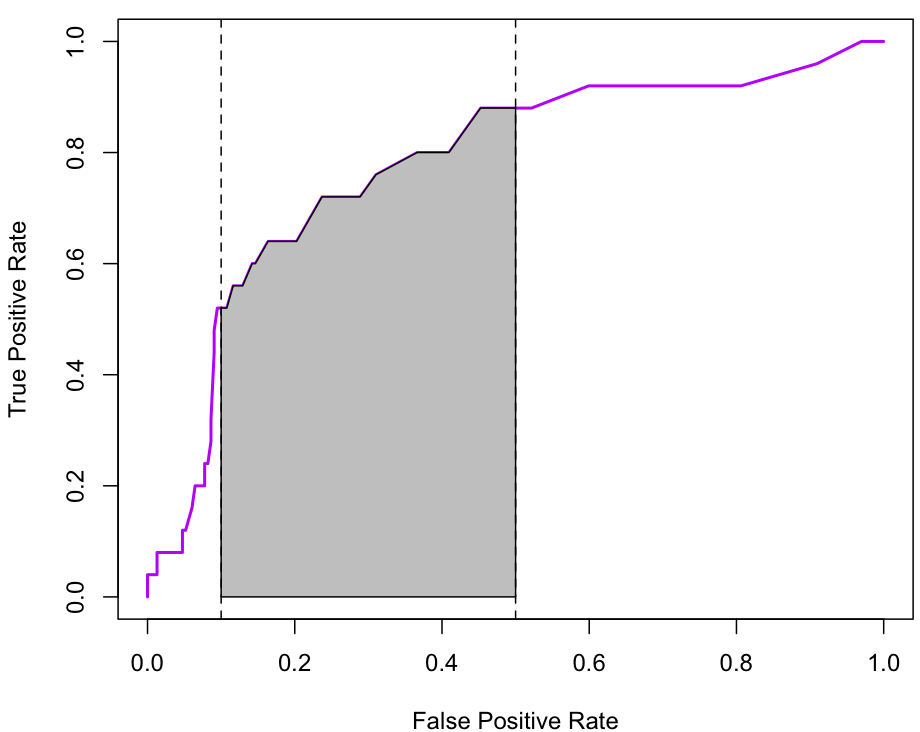
Advanced R

Exercises for Session 4: Objects and Methods.

1. (a) Write a summary() method for the S3 ROC curve object that calculates the *partial area under the curve* (pAUC). That is, given an upper and lower endpoint for the false positive rate (x-axis), it computes the area under the curve between the upper and lower endpoints. The endpoints should default to 0 and 1, and the user should be able to specify both, just one, or neither.



*Shaded area is partial AUC between false positive rates of 0.1 and 0.5*

(b) Repeat for the S4 ROC curve objects. For debugging, try using trace() with the signature= argument set to follow the S4 methods.

2. ROC curves are also useful for summarizing logistic regression models. Given a logistic regression model object model of class glm, we can extract the predicted values with fitted(model) and the observed binary outcome with model$y and then use the same computations to produce an ROC curve for the model.

(a) Write a function that computes the ROC curve for a logistic regression model.

(b) Write a *generic* function ROC() with methods that compute the ROC curve when the user supplies *either* a continuous test variable and binary outcome *or* a glm object.

3. The data file sequence.rda has DNA sequences for 5000 people and 4028 *rare* sequence variants (simulated using MaCS). The Matrix package provides tools for handling sparse (ie, mostly zero) matrices. Compare the time and memory taken for

crossprod(sequence)

and

library(Matrix)

M<-Matrix(sequence)

crossprod(M)

Look at the class of M and the methods available for that class. What can you find out about how M is actually stored internally?