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In regression we have: (which allows for writing R^2 differently)

LHS is logit transform of π

(Linear) logistic regression

Linearity assumptions (for LS regression)

Scatterplot

Diagram

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The following removes col. upo3:

For J>2

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adds log(03) as a col. and removes 03

Likelihood (for Bernoulli x then for Binomial)



(In-sample) R2 in R

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LOOCV in R





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Nadaraya Watson (normal kernel)



Non-parametric regression in R

(Cross-validated LOOCV) R2 in R

Multinomial logistic regression

will give the probability of heart disease (N/m)



Does indicator variable affect thorax length?

Reject H0 if Pr(>F) <= 0.05

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where the probabilities of each class are stored in the columns (columns same order as levels (…)) but we can also achieve logistic regression by using dummy encoding and glm:

Order data

Local polynomial

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MARS in R

Q-Q plot

Smoothing splines



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ROC and Misclassification graph in R



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We can then find their R2 as follows:

TODO: Hat matrix (serie 5 methods and non-parametric regression)

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TODO: Equivalent ways of calculating LOOCV using hat matrix and manually computation

Bootstrap in R



which plots the TPR vs FPR. To plot the misclassification rate as a function of threshold prob. (i.e., after this it is considered positive)

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MARS fits a function of the form





K-Fold CV in R

Mallows Cp statistic

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which is prop. to Cp(M):

The MSE can be estimated by:

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Poly. regression using a polynomial of degree d (no interaction term):

Neural Networks (1 Layer with q units)

R2 describes the proportion of the total variation of the response Y around its mean Y bar which is explained by the regression Y hat.

To get the weights use summary(Nfit). R prefixes input variables with *i* and hidden unit with *h*.To get the error use sum(residuals(Nfit)2)

Make sure to scale the data (except for response) to avoid getting stuck in the flat regions of the sigmoid function. Weight decay is good as it reduces the dependency on the starting values and reduces the importance of choosing the # of hidden units

and f0 is typically identity for regression and sigmoid for classification. We can add a linear regression component (skip conxn):

Alternatively,

where

Add anova table and f-test and interpretation

We can also get the 3D plots (effect of the interaction of 2 terms on the response) using

summary (mars fit) gives the importance of each variable. If we fitted a model of degree 2, then we can get the graphs of the response variables as a function of each predictor variable as follows:

Cp in R (note: object is of type fit, and sigma can be found using sigma(fit))

Note that the linear regression model does not assume a normal distribution for the predictors, but a skewed distribution and outliers often result in  
regression solutions that are largely determined by very few points.

Forward selection (in case p, the nr. of predictors vars. Is too large for exhaustive search):

1) start with smallest model

2) add predictor which reduces the MSE the most

3) repeat 2 until all predictors or large nr. of predictors selected (now a seq. models is produced)

4) choose the model in the seq. which has smallest Cp statistic.

Backward selection is obvious.

Tukey Anscombe is residuals versus fitted values. Q-Q is empirical quantiles vs standard normal quantiles.

Forward and backward selection in R

Maybe add all-subsets regression in R (from HW2)?

Whereas Q-Q plot is given by

For lm, Tukey Anscombe is given by



To plot the same thing but for lm use:

Bootstrapping LDA/QDA

To plot the splines do:

Generalized additive model in R

And then pred.cv <- prediction (all.y.pred, all.y.true) and proceed as normal (but add avg = “threshold” for ROC and avg = “vertical” for misclassification) use add = T to add them to same plot. One can specify the cost for FN and FP using cost.fp = 0.8, cost.fn = 1.2 as args to performance().

To plot the average ROC (across all folds) initialize a vector of lists and assign them as follows:



Decision boundary plot in R



Decision boundary between class 0 and 1:

QDA Classifier (more easily overfits if p is big)

if the covariance matrix ∑ is diagonal and const. then w is parallel to the line connecting µ0 and µ1



Prediction of LDA found by taking argmax: of:

LDA Classifier

Bayes Risk Bayes Classifier

Expected size of out-of-bootstrap sample [roughly 1/3 of points will be out of sample]:

“basic” = “Reversed quantile”

“norm” = “Normal”

“perc” = “Quantile”



is equivalent to using a neural network (note results may differ due to different seed). Optimization in R

Assume we have a fct. like this for the neg. log likelihood which we want to minimize (case of binomial distribution of response and logist. regr.),

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Then the following will return the vector beta (same as that of logistic regression),

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Trees (CART)

The cost function is: (note that the size of the tree is the # of leaves, n, and that for a binary tree # of nodes = 2n - 1 ). For regression, R(T), can be -2\*(log likelihood)=sum of squares as in the case for regression or the misclassification rate for classification



**Pros** of trees: Interpretable, can deal with missing values using “surrogate” split, does automatic variable selection.

**Cons**: piecewise constant (for probability estimate or regression). Unstable split: if a split is “wrong”, then all of the splits below it will be “wrong”.

CART in R

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cp stands for cost complexity pruning (i..e penalizes large trees -> higher cp means shorter trees. cp = alpha/R(0)).

Plotting can be done as follows (note that each node will display J numbers for each category which falls into this region in the order given by levels(data$var)):

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**One-standard-error rule**: Find the model with the lowest cross-validation error. Then choose the simplest model, which is at most one standard-deviation worse than that model.

To prune the tree according to this rule, we need cross validation error of the tree, use (ignore relative error column):

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