Advanced R Programming for Bioinformatics.

Exercises for session 8: Interfacing to C.

**1.** The files nnfind.c, bin\_heap.c, bin\_heap.h, item.h implement an algorithm based on k-d trees for finding nearest neighbours. Write an R interface to the functions in nnfind.c:

void within\_neighbours(const double \*X, int \*pNx, const int \*pp,

int \*neighbours, double \*dists)

and

void between\_neighbours(const double \*X, int \*pNx,

const double \*Y, const int \*pNy, const int \*pp,

int \*neighbours, double \*dists)

In these functions X and Y are matrices of points in p-dimensional space, \*pNx is the number of rows in X, \*pNy is the number of rows in Y, \*pp is the dimension of the space (number of columns in X and Y), neighbours is used to return the row number of the nearest neighbour (from 0 to (n-1)) and dists returns the distance to the nearest neighbour.

The difference between the two functions is that within\_neighbours finds the nearest neighbour in X of each point in X and between\_neighbours finds the nearest neighbour in X of each point in Y. This means that neighbours and dists have length \*pNx in within\_neighbours and \*pNy in between\_neighbours.

The row numbers returned are C row numbers from 0 to (n-1); you need to add 1 to get R row numbers.

Test the code by drawing a scatterplot and connecting each point to its nearest neighbour (with segments()). A nice data example is data(faithful)

**2**. A `box-car’ filter is a simple smoother; on a scatterplot of (X1, Y1), (X2, Y2), … (Yn, Xn), it provides a smooth line illustrating how Y changes with X. Formally, for given radius *r*, at point *x* it is evaluated as;  
  
 ,  
  
in other words, it is the average of the Y’s that have X’s within *r* of *x*. Typically, we evaluate the box-car filter at x=X1, X2, … Xn.  
  
(continues…)

In R, one simple way to implement the box-car filter is the following;

boxcar <- function(Y, X, radius, n=length(Y)){

y.smooth <- rep(0,n)

x <- 0

for (i in 1:n){

count <- 0

x <- X[i]

for (j in 1:n){

if(abs(X[j]-x)<radius){

count <- count+1

y.smooth[i] <- y.smooth[i] + Y[j]

}

}

y.smooth[i] <- y.smooth[i]/count

}

y.smooth

}

Try this code, for n=1000 data points, and then n=10,000. What takes the time? Code this approach in C, and see how much faster it becomes.

For keen people; a preliminary sort of the data enables you to implement this filter without the double loop; think of ‘sliding’ a window of radius r along the sorted X values. Implement the filter using this observation, and see what speed improvement you can achieve.