Optimisation Prac 2

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Simulated Annealing

Changing the solution to the travelling salesman problem

In this case we will change the way that the moves are made to change the order of the cities

```
# load data
y <- as.matrix(eurodist)
```

```
# function to initialise cities
get_initial_x <- function(ncity){
  tour <- sample(1:ncity)
  # ensure tour returns to first city
  tour <- c(tour, tour[1])

  return(tour)
}

# get initial tour:
cur_tour <- get_initial_x(nrow(y))
```

```
# define an evaluation function
evaluate_x <- function(dists, tour){
  sum(dists[cbind(tour[-length(tour)], tour[-1])])
}
```

We will change the function that perturbs by setting it to choose 2 random indeces and swopping the cities related to those cities.

```
perturb_x <- function(tour){

  # select two indeces at random
  i_j <- sample(1:(length(tour)), 2, replace = F)
  # swop the cities at these indeces
  ## select city i
```

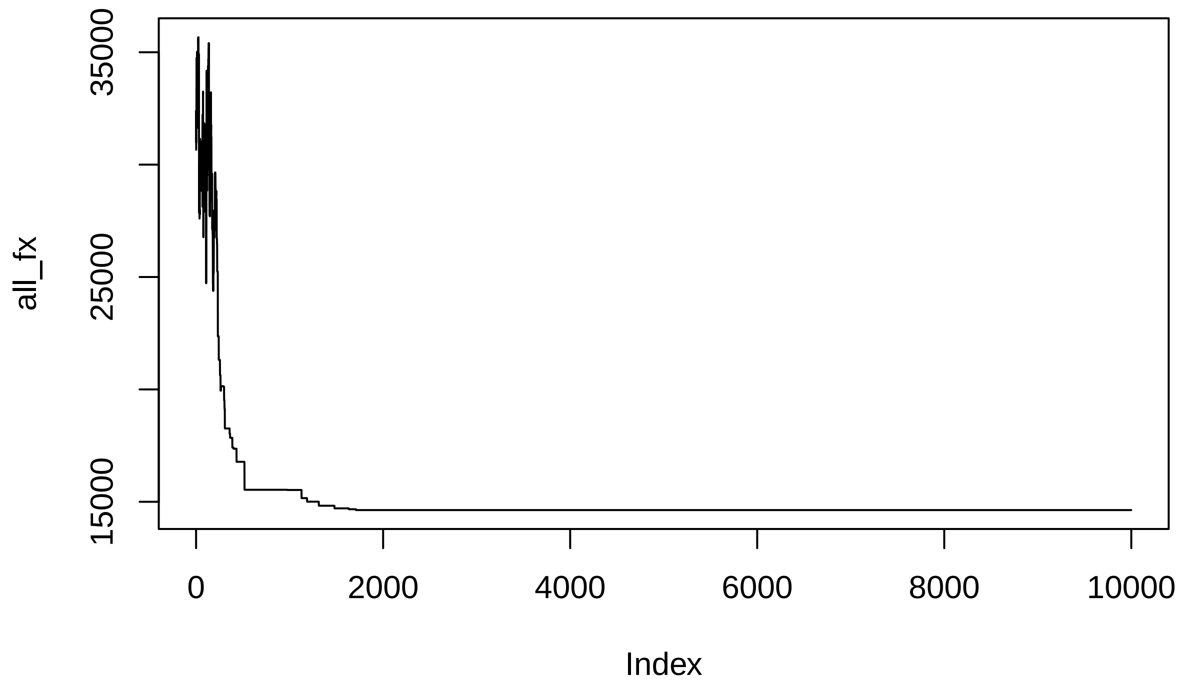
```r
  city_i <- tour[i_j[1]]
  ## select city j
  city_j <- tour[i_j[2]]
  ## swop them
  tour[i_j[1]] <- city_j
  tour[i_j[2]] <- city_i

  return(tour)
}
```

```r
# set start temperature and geometric cooling factor
set.seed(100) # for repeatability
start_temp <- 50000
temp_factor <- 0.98
```

```r
# get an initial solution
cur_x <- get_initial_x(ncol(y))
# evaluate the solution
cur_fx <- evaluate_x(dists = y, tour = cur_x)
```

```r
# initialize results data frames
all_fx <- c()
all_x <- data.frame()
# for a fixed number of iterations
for(i in 1:10000){

  # generate a candidate solution
  prop_x <- perturb_x(cur_x)

  # evaluate the candidate solution
  prop_fx <- evaluate_x(dists = y, tour = prop_x)

  # calculate the probability of accepting the candidate
  anneal_temp <- start_temp * temp_factor ^ i
  accept_prob <- exp(-(prop_fx - cur_fx) / anneal_temp)

  # accept or reject the candidate
  if(runif(1) < accept_prob){
   cur_x <- prop_x
   cur_fx <- prop_fx
  }

  # store all results
  all_fx <- c(all_fx, cur_fx)
  all_x <- rbind(all_x,cur_x)

}
```

```r
plot(all_fx,type="l")
```



The best tour returned by the simulated annealing algorithm is given below.

```
best_solution <- which.min(all_fx)
best_tour <- all_x[best_solution,]
best_solution
```

```
## [1] 1710
```

```
best_tour
```

```
##      X10L X1L X16L X14L X12L X7L X20L X15L X4L X19L X18L X2L X17L X9L X8L X3L
## 1710   11   3    4    5   12   9   14    2  15   19    1  21   17  16  10  10
##      X21L X6L X11L X13L X5L X10L.1
## 1710    6  18   13    8   7     20
```

```
colnames(y)[as.numeric(best_tour)]
```

```
##  [1] "Hook of Holland" "Brussels"        "Calais"          "Cherbourg"
##  [5] "Lisbon"          "Gibraltar"       "Madrid"          "Barcelona"
##  [9] "Marseilles"      "Rome"            "Athens"          "Vienna"
## [13] "Munich"          "Milan"           "Hamburg"         "Hamburg"
## [17] "Cologne"         "Paris"           "Lyons"           "Geneva"
## [21] "Copenhagen"      "Stockholm"
```

Changing the solution to the Soduko problem

```
# create a Sudoku puzzle
s <- matrix(0,ncol=9,nrow=9)
s[1,c(6,8)] <- c(6,4)
s[2,c(1:3,8)] <- c(2,7,9,5)
s[3,c(2,4,9)] <- c(5,8,2)
s[4,3:4] <- c(2,6)
s[6,c(3,5,7:9)] <- c(1,9,6,7,3)
s[7,c(1,3:4,7)] <- c(8,5,2,4)
```

```r
s[8,c(1,8:9)] <- c(3,8,5)
s[9,c(1,7,9)] <- c(6,9,1)

s
```

```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
##  [1,]    0    0    0    0    0    6    0    4    0
##  [2,]    2    7    9    0    0    0    0    5    0
##  [3,]    0    5    0    8    0    0    0    0    2
##  [4,]    0    0    2    6    0    0    0    0    0
##  [5,]    0    0    0    0    0    0    0    0    0
##  [6,]    0    0    1    0    9    0    6    7    3
##  [7,]    8    0    5    2    0    0    4    0    0
##  [8,]    3    0    0    0    0    0    0    8    5
##  [9,]    6    0    0    0    0    0    9    0    1
```

```r
# define the spaces that can be changed
free_spaces <- (s == 0)
free_spaces
```

```
##        [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8]  [,9]
##  [1,]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE FALSE  TRUE
##  [2,] FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE
##  [3,]  TRUE FALSE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE FALSE
##  [4,]  TRUE  TRUE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [5,]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
##  [6,]  TRUE  TRUE FALSE  TRUE FALSE  TRUE FALSE FALSE FALSE
##  [7,] FALSE  TRUE FALSE FALSE  TRUE  TRUE FALSE  TRUE  TRUE
##  [8,] FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE
##  [9,] FALSE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE FALSE
```

```r
get_initial_x <- function(s){

  # identify free spaces
  free_spaces <- (s == 0)
  # fixed non-free spaces
  cur_x <- s
  # randomly choose a number between 1 and 9 for free spaces
  cur_x[free_spaces] <- sample(1:9, sum(free_spaces), replace=T)

  return(cur_x)
}

# create the initial solution:
init_x <- get_initial_x(s)
```

These functions will stay the same.

```r
# function to count duplicates:
count_duplicates <- function(x)
{
  n_dup <- length(x) - length(unique(x))
  return(n_dup)
}

# sum duplicates accross rows, columns and blocks:
```

```r
evaluate_x <- function(x){

  # within-row duplications
  row_dups <- sum(apply(x,1,count_duplicates))

  # within-col duplications
  col_dups <- sum(apply(x,2,count_duplicates))

  # within-block duplications
  block_dups <- 0
  for(i in 1:3){
    for(j in 1:3){
      small_x <- x[(3*(i-1) + 1):(3*i), (3*(j-1) + 1):(3*j)]
      thisblock_dups <- count_duplicates(as.vector(small_x))
      block_dups <- block_dups + thisblock_dups
    }
  }

  total_dups <- row_dups + col_dups + block_dups

  return(total_dups)

}

# evaluate performance of the initial solution:
evaluate_x(init_x)
```

```
## [1] 76
```

We will change the perturbing in this problem to replace one of the free_spaces values in the column and row that has the most duplicates with a random draw. The idea is that if we target the most problematic columns first, the algorithm should run faster.

```r
perturb_x <- function(x, free_spaces)
{
  # find column with the largest number of duplicates
  max_col_index <- which.max(apply(init_x, 2, count_duplicates))

  # select a free site
  row_index <- sample(1:9,1,prob=free_spaces[,max_col_index])
  # change that site at random
  x[row_index, max_col_index] <- sample(1:9,1,replace=T)

   # find row with the largest number of duplicates
  max_row_index <- which.max(apply(init_x, 1, count_duplicates))

  # select a free site
  col_index <- sample(1:9,1,prob=free_spaces[max_row_index,])

  # change that site at random
  x[max_row_index, col_index] <- sample(1:9,1,replace=T)

  return(x)
}
```

We now apply simulated annealing to solve the Sudoku puzzle, starting by setting a start temperature and geometric cooling factor.

```r
set.seed(100) # for repeatability
start_temp <- 1e3
temp_factor <- 0.995
```

We'll generate a new initial solution and evaluate, just to keep this whole code block self-contained.

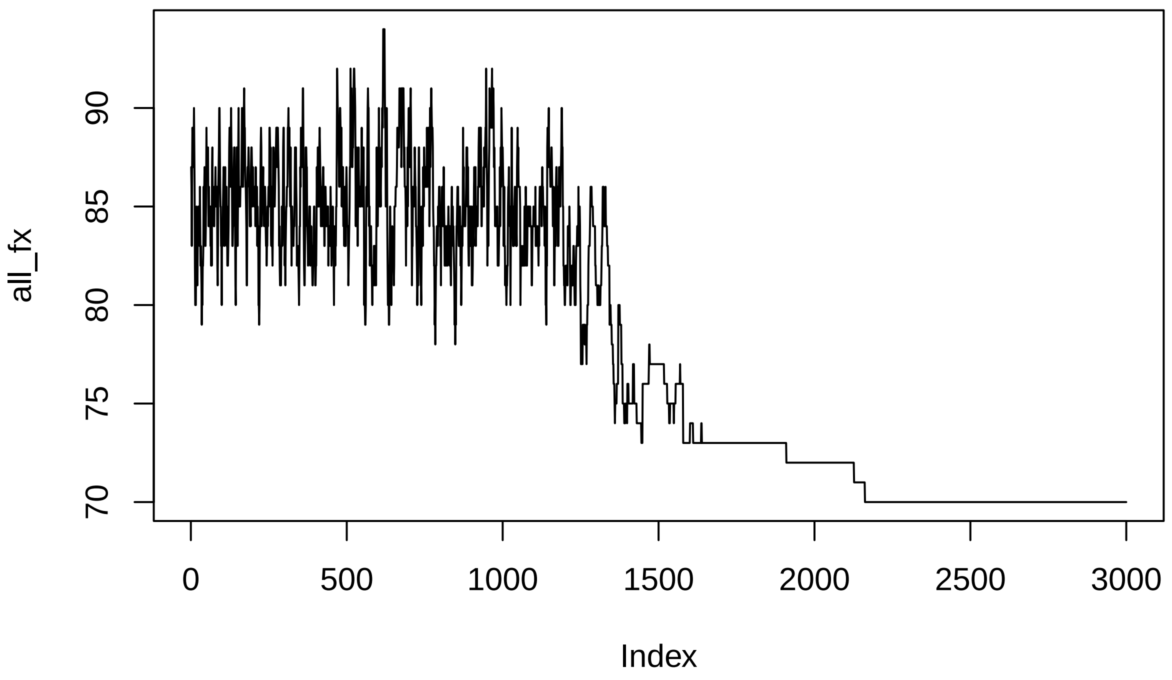
```r
cur_x <- get_initial_x(s)
cur_fx <- evaluate_x(cur_x)
```

We now apply the simulated annealing algorithm.

```r
# initial results data frames
all_fx <- c()
all_x <- data.frame()
# for a fixed number of iterations
for(i in 1:3000){

  # generate a candidate solution
  prop_x <- perturb_x(cur_x, free_spaces = free_spaces)

  # evaluate the candidate solution
  prop_fx <- evaluate_x(prop_x)

  # calculate the probability of accepting the candidate
  anneal_temp <- start_temp * temp_factor ^ i
  accept_prob <- exp(-(prop_fx - cur_fx) / anneal_temp)

  # accept or reject the candidate
  if(runif(1) < accept_prob){
    cur_x <- prop_x
    cur_fx <- prop_fx
  }

  # store all results
  all_fx <- c(all_fx, cur_fx)
  all_x <- rbind(all_x,as.vector(cur_x))

}
```

We plot the solution quality over time.

```r
plot(all_fx,type="l")
```



From the above plot we can see that this peturbing function actually performs worse than the previous model.

Genetic Algorithms

Changing the solution to the traveling salesman problem

```r
# Generate initial population of solutions (given number of cities and size of popn)
initial_pop = function(varsize, popsize){
  # sample 1:21 popsize number of times
  pop0 <- matrix(NA, popsize, varsize)
  for(i in 1:popsize){
    pop0[i,] <- sample(1:nrow(y), replace = F)
  }
  return(pop0)
}
```

```r
# evaluate the total distance for each item in the population
evaluate_pop = function(pop, y){
  # y is the distance matrix

  # create empty eval vector:
  evals = rep(0,nrow(pop))
  for(i in 1:nrow(pop)){
    # sum pairwise distances between city for each population member
    evals[i] <- sum(y[cbind(pop[i,][-length(pop[i,])], pop[i,][-1])])
  }
  return(evals)
}
```

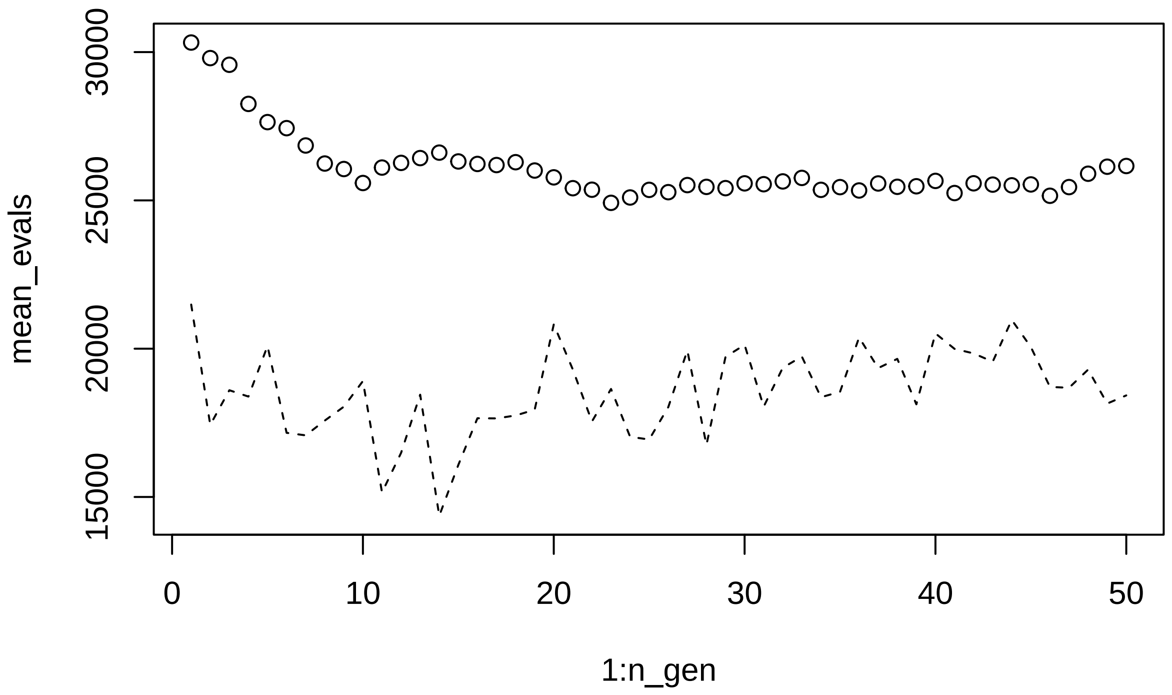
```r
# Function for selection (outputs = parents)
# proportional to fitness
select = function(pop,fitness){
  newpop = matrix(NA, nrow(pop), ncol(pop))
  # randomly select how many you want to change
  # note: change the prob to be inverted (smaller distances have greater prob)
  probabilities <- dnorm(scale(fitness))
  picks = sample(1:nrow(pop), prob = probabilities, replace = T)
  for(i in 1:length(picks)){
    # replace the columns newpop with the random draw of the old population
    newpop[i, ] = pop[picks[i], ]
  }
  return(newpop)
}
```

```r
# Function for crossover step (outputs = offspring_crossover)
#uniform crossover
crossover = function(parents){
  popsize = nrow(parents)
  varsize = ncol(parents)
  # Pick parents to mate randomly
  parent_pairs = matrix(sample(1:popsize), popsize/2, 2)
  # Initialise offspring
  offsprings = matrix(NA, popsize, varsize)
  for(i in 1:nrow(parent_pairs)){
    # Get parents
    p1 = parents[parent_pairs[i,1], ]
    p2 = parents[parent_pairs[i,2], ]
    # Make kids
    c1 = rep(NA, varsize)
    c2 = rep(NA, varsize)
    # Apply uniform crossover to get kids
    for(j in 1:varsize){
      if(runif(1) <= 0.5){
        c1[j] = p1[j] # c1's jth element is same as p1's jth element
        c2[j] = p2[j]
      }else{
        c2[j] = p1[j]
        c1[j] = p2[j]
      }
    }
    # Store kids
    offsprings[2*i-1, ] = c1
    offsprings[2*i, ]   = c2
  }
  return(offsprings)
}
```

```r
# Function for mutation step (outputs = offspring_mutation) (no changes made)
#scramble mutation
mutation = function(offspring_crossover,mutation_rate=0.05){
  # Initialise mutations
  mutations = matrix(NA, nrow(offspring_crossover), ncol(offspring_crossover))

  for(i in 1:nrow(offspring_crossover)){
    persontomutate = offspring_crossover[i,]
    if(runif(1) <= mutation_rate){
      # Select two elements
      picks = sort(sample(1:ncol(offspring_crossover),
                          2, replace = FALSE))
      # Get sub-set
      temp = persontomutate[picks[1]:picks[2]]
      # Reshuffle
      temp = sample(temp, length(temp), replace = FALSE)
      # Add mutation
      persontomutate[picks[1]:picks[2]] = temp
      mutations[i,] = persontomutate
    }else{
      mutations[i,] = persontomutate
    }
  }
  return(mutations)
}
```

```r
# Function for replacement (outputs = new population)
#generational replacement
replace = function(parents,offspring_mutation){
  return(offspring_mutation)
}
```

```r
## putting it all together
#pts = c(10, 20, 15, 2, 30,10, 30)
#wts = c(1, 5, 10, 1, 7, 5, 1)
set.seed(10)
n_pop = 100
n_vars = ncol(y)
this_pop = initial_pop(varsize=n_vars,popsize=n_pop)

min_evals = c()
mean_evals = c()
n_gen = 50

for(gen in 1:n_gen){
  evals = evaluate_pop(pop=this_pop, y=y)
  next_parents = select(pop=this_pop,fitness=evals)
  offspring_crossover = crossover(parents=next_parents)
  offspring_mutation = mutation(offspring_crossover,mutation_rate=0.05)
  this_pop = replace(next_parents, offspring_mutation)
  min_evals = c(min_evals,min(evals))
  mean_evals = c(mean_evals,mean(evals))
}

plot(1:n_gen,mean_evals,
     ylim=c(min(c(min_evals,mean_evals)),max(c(min_evals,mean_evals))))
lines(1:n_gen,min_evals,lty=2)
```


mean_evals
1:n_gen
15000
20000
25000
30000
0
10
20
30
40
50