MSc Statistical Programming 2023 Assessed Practical Assignment

P151

November 19, 2023

0.1 British House Prices

Figure 1 below displays the evolution of House Prices in England over time.

Figure 1: Average House Price in England Over Time

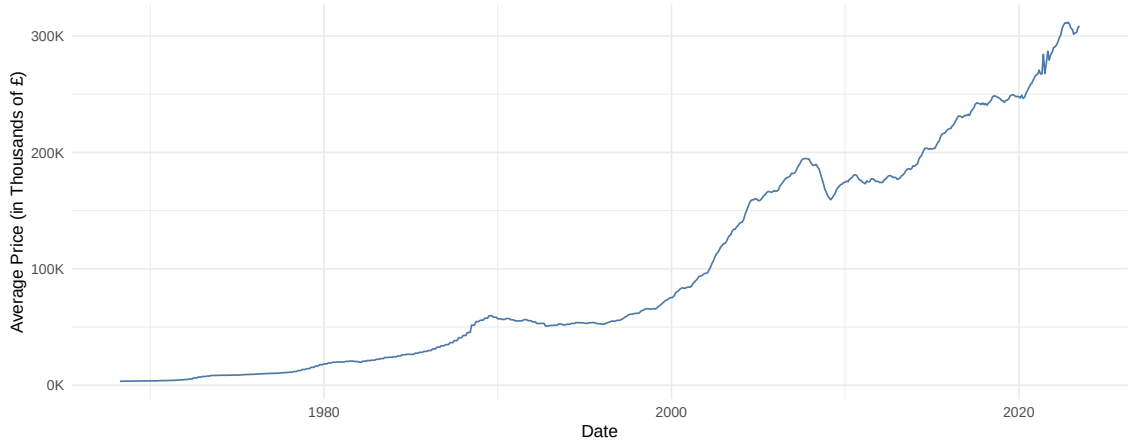


Figure 2 below additionally displays the evolution of House Prices in the Oxford Regions as well as England as a whole over time.

Figure 2: Comparison of Average House Prices between England and Oxford Regions

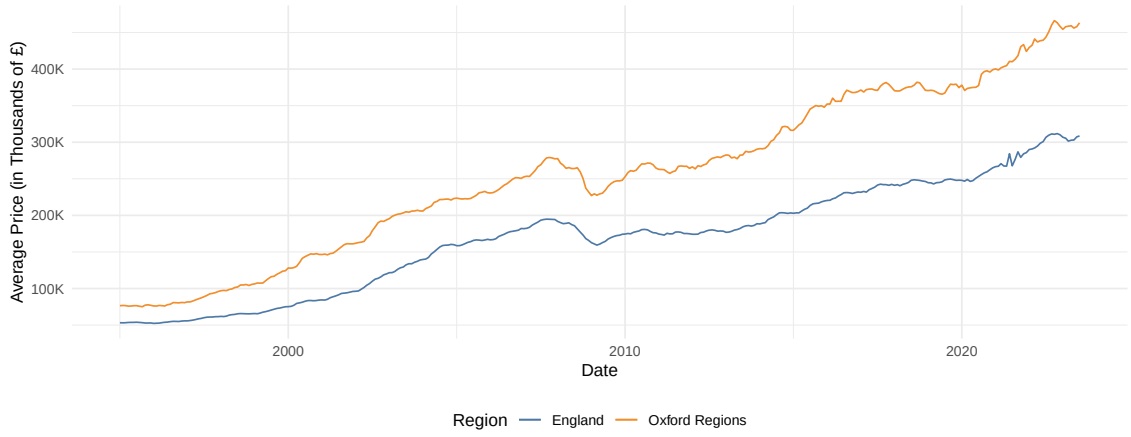


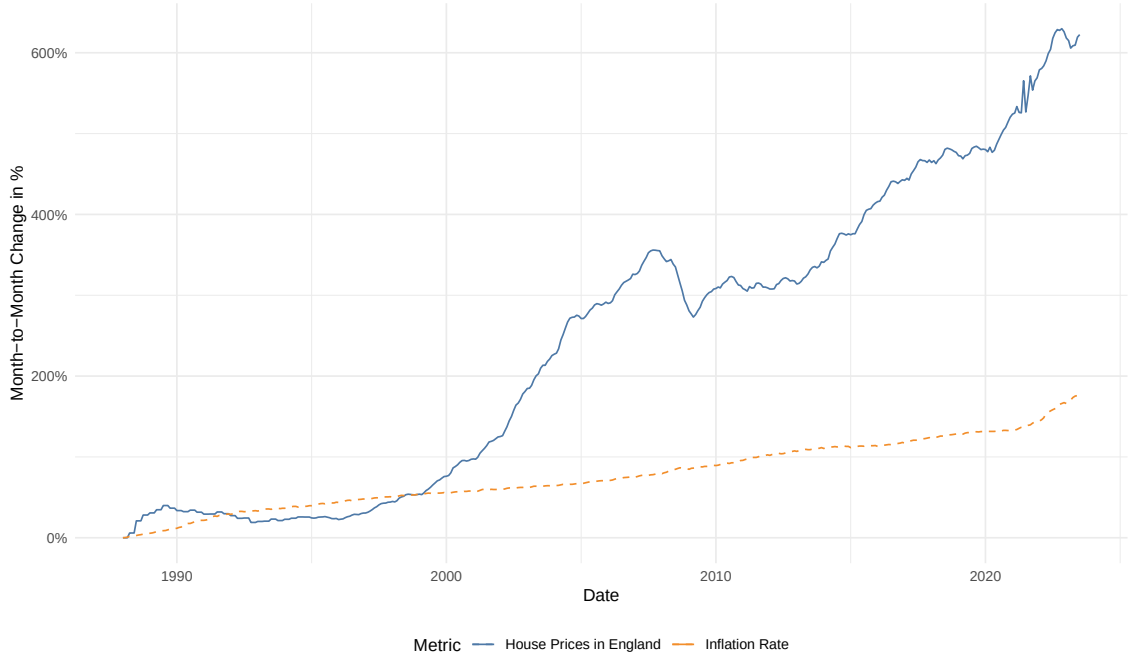
Table 1 below shows that of the ten regions with the highest median of the ratio $\frac{regional\ average\ house\ price}{average\ house\ price\ in\ England}$. Perhaps unsurprisingly, we can see that the ten most expensive regions by this metric are geographically concentrated in London and its suburbs, and that no Oxford Regions are included.

Table 1: Ten Highest Median Ratios of Average House Prices

	Region Name	Median Ratio	Initial Price	Final Price	% Increase	Oxford?
1	Kensington and Chelsea	4.59	182694.83	1344669.00	636.02	FALSE
2	City of Westminster	3.24	133025.28	954356.00	617.42	FALSE
3	Camden	2.92	120932.89	828389.00	585.00	FALSE
4	Hammersmith and Fulham	2.79	124902.86	798537.00	539.33	FALSE
5	City of London	2.56	91448.98	905489.00	890.16	FALSE
6	Richmond upon Thames	2.51	109326.12	770107.00	604.41	FALSE
7	Elmbridge	2.34	106524.00	678279.00	536.74	FALSE
8	Islington	2.32	92516.49	710181.00	667.63	FALSE
9	Wandsworth	2.15	88559.04	632895.00	614.66	FALSE
10	Mole Valley	1.98	101899.76	563083.00	452.59	FALSE

Figure 3 below compares the month-on-month percentage increase in House Prices in England to monthly inflation, defined as the percentage increase in the monthly Consumer Price Index over the period in which data for both is available. We can see that like in most countries, the increase in the average price of a house has drastically outpaced the general cost-of-living increase since the year 2000.

Figure 3: Percentage Increase in House Prices compared to Inflation Rate



1 Chromosome Painting

1.1 Implementation of Forward Algorithm

```
# Function to calculate emission probability (eq. 3)
emission_probability <- function(observed, reference, error = 0.1) {
  return ((1 - error)^(observed == reference) * error^(observed != reference))
}

# matrices alpha and beta , both with K rows and T columns
forward <- function(haps, hap, error = 0.1) {
  K <- nrow(haps)
  T <- ncol(haps)

  # Initialize alpha matrix
  alpha <- matrix(0, nrow = K, ncol = T)

  # Compute initial and emission probabilities
  pi <- 1 / K  # (eq. 1)
  for (k in 1:K) { # (eq. 4)
    alpha[k, 1] <- pi * emission_probability(hap[1], haps[k, 1], error)
  }

  # Induction step to compute (eq. 5)
  for (t in 2:T) {
    for (k in 1:K) {
      transition_sum <- 0
      for (i in 1:K) {
  A_ik <- ifelse(i == k, (1 - 0.999) / K + 0.999, (1 - 0.999) / K) # (eq. 2)
  transition_sum <- transition_sum + alpha[i, t - 1] * A_ik
  }
      b_kt <- emission_probability(hap[t], haps[k, t], error)
      alpha[k, t] <- transition_sum * b_kt
    }
  }

  return(alpha)
}
```

1.2 Unit Test for Forward Algorithm Implementation

```
test_that("alpha matrix has expected form when haps and hap always match", {
  K <- 10  # Number of rows in haps
  T <- 15  # Number of columns in haps = length of hap
  e <- 0.1  # Error rate (= default value)

  # Create haps and hap such that they always match (both all 0)
```

```
  haps <- matrix(0, nrow = K, ncol = T)
  hap <- rep(0, T)

  # Run the forward function
  alpha <- forward(haps, hap, error = e)

  # Check first column
  expected_first_column <- rep((1 - e) / K, K)
  expect_equal(alpha[, 1], expected_first_column)

  # Check all other columns
  for (t in 2:T) {
    expect_equal(alpha[, t], alpha[, t - 1] * (1 - e), tolerance = 1e-5)
  }
})

## Test passed
```

1.3 Implementation of Backward Algorithm

```
backward <- function(haps, hap, error = 0.1) {
  K <- nrow(haps)
  T <- ncol(haps)

  # Initialize beta matrix (eq. 6)
  beta <- matrix(0, nrow = K, ncol = T)
  beta[, T] <- 1  # Set last column to 1

  # Induction step (eq. 7)
  for (t in (T-1):1) {
      for (k in 1:K) {
        sum_transition <- 0
        for (i in 1:K) { # (eq. 2)
          A_ki <- ifelse(k == i, (1 - 0.999) / K + 0.999, (1 - 0.999) / K)
          b_i_t_plus_1 <- emission_probability(hap[t+1], haps[i, t+1], error)
          sum_transition <- sum_transition +
              A_ki * b_i_t_plus_1 * beta[i, t+1]
        }
        beta[k, t] <- sum_transition
      }
    }

  return(beta)
}
```

1.4 Implementation of Gamma Function

```
gamma <- function(haps, hap, error = 0.1) {
  K <- nrow(haps)
  T <- ncol(haps)

  # Compute alpha and beta matrices
  alpha <- forward(haps, hap, error)
  beta <- backward(haps, hap, error)

  # Compute normalization factor (denominator)
  norm_factor <- sum(alpha[, T])

  # Initialize gamma matrix
  gamma_matrix <- matrix(0, nrow = K, ncol = T)

  # Update gamma values (eq. 8)
  for (t in 1:T) {
    for (k in 1:K) {
      gamma_matrix[k, t] <- (alpha[k, t] * beta[k, t]) / norm_factor
    }

  return(gamma_matrix)
  }
}
```

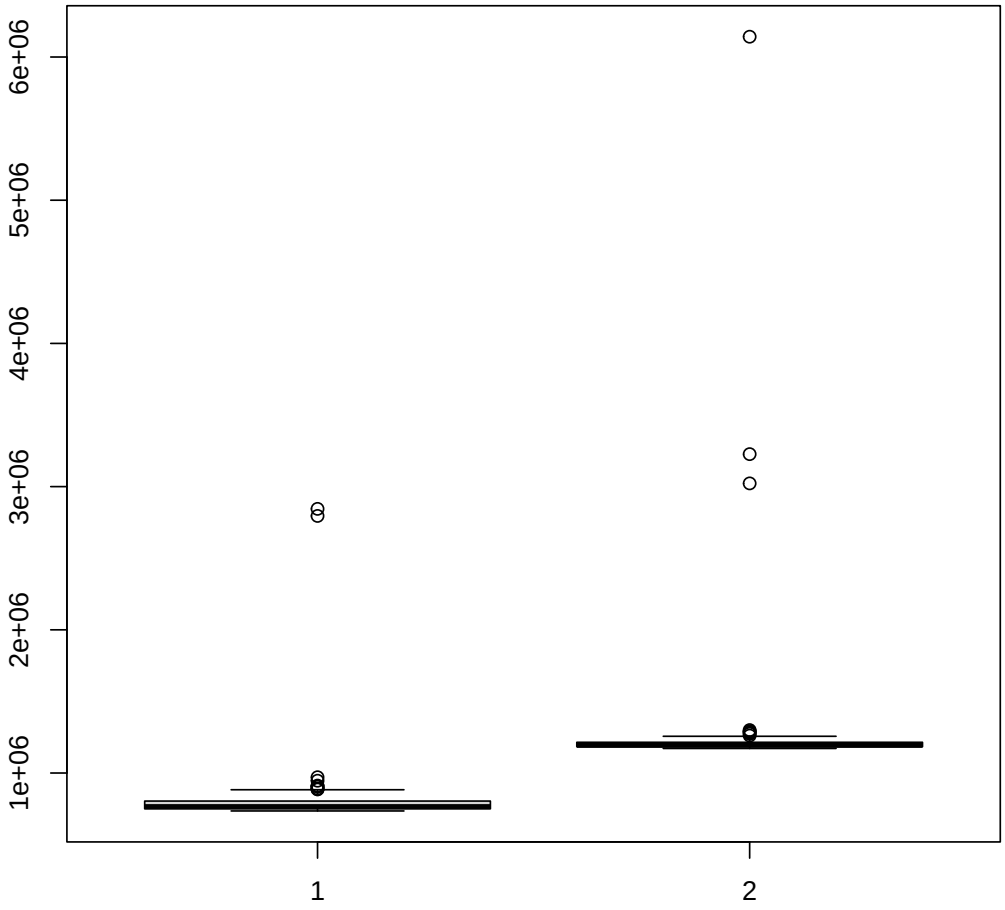
1.5 Unit Test for Gamma Function Implementation

```
test_that("column sums of gamma matrix sum to 1", {
  set.seed(42)  # For reproducibility
  K <- 10  # Number of rows in haps
  T <- 15  # Number of columns in haps = length of hap
  e <- 0.1  # Error rate (= default value)

  # Create random haps and hap with 0 or 1 entries
  haps <- matrix(sample(0:1, K * T, replace = T), nrow = K, ncol = T)
  hap <- sample(0:1, T, replace = T)

  # Run the gamma function
  gamma_matrix <- gamma(haps, hap, error = e)

   # Check total sum
  total_sum <- sum(gamma_matrix)
  expect_equal(total_sum, 1, tolerance = 1e-5)
})

## Test passed
```

1.6 Computational Complexity of Forward and Backward Algorithms

1. The forward algorithm has a time complexity of $\mathcal{O}(K^2 \cdot T)$ as for each time step t, it iterates over K states, and within each state again iterates over K states to compute the transition probabilities.
2. The backward algorithm has an identical time complexity of $\mathcal{O}(K^2 \cdot T)$ as it performs the same iterations, just in a different oder.

```
# Define a small test case
K <- 10  # Number of haplotypes
T <- 10  # Length of each haplotype
error <- 0.1

# Generate random haplotypes for testing
haps <- matrix(sample(0:1, K * T, replace = T), nrow = K, ncol = T)
hap <- sample(0:1, T, replace = T)

# Benchmark the forward function
forward_benchmark <- microbenchmark(
  forward(haps, hap, error),
  times = 100
)

## Warning in microbenchmark(forward(haps, hap, error), times = 100): less
accurate nanosecond times to avoid potential integer overflows

# Benchmark the backward function
backward_benchmark <- microbenchmark(
  backward(haps, hap, error),
  times = 100
)

# Print the results
print(forward_benchmark)

## Unit: microseconds
##                       expr     min       lq     mean   median       uq      max
##  forward(haps, hap, error) 735.007 750.0335 825.6592 765.2445 804.1125 2844.621
##  neval
##    100

print(backward_benchmark)

## Unit: milliseconds
##                        expr      min       lq     mean   median       uq
##  backward(haps, hap, error) 1.171411 1.184182 1.289618 1.193449 1.214502
##       max neval
##  6.141759   100

# Optional: Compare the performance visually using boxplots
boxplot(forward_benchmark$time, backward_benchmark$time)
```


6e+06
5e+06
4e+06
3e+06
2e+06
1e+06
1
2