MSc Statistical Programming 2023 Assessed Practical Assignment

P151

November 24, 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

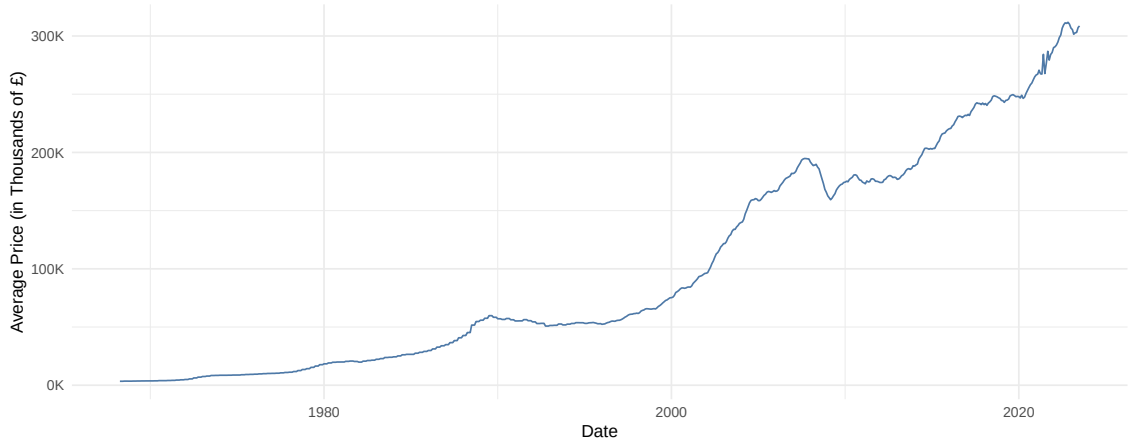


Figure 2 below additionally displays the evolution of House Prices in the Oxford Regions as well as England as a whole over time.

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

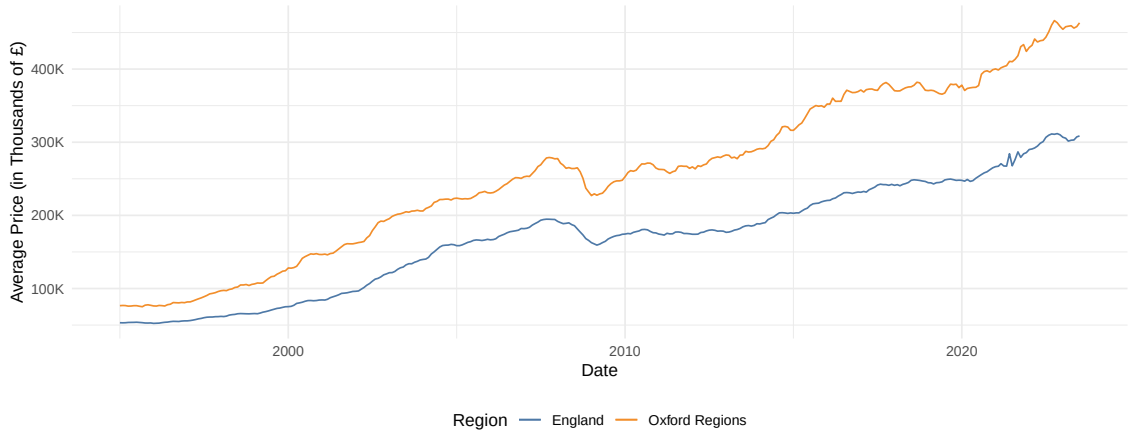


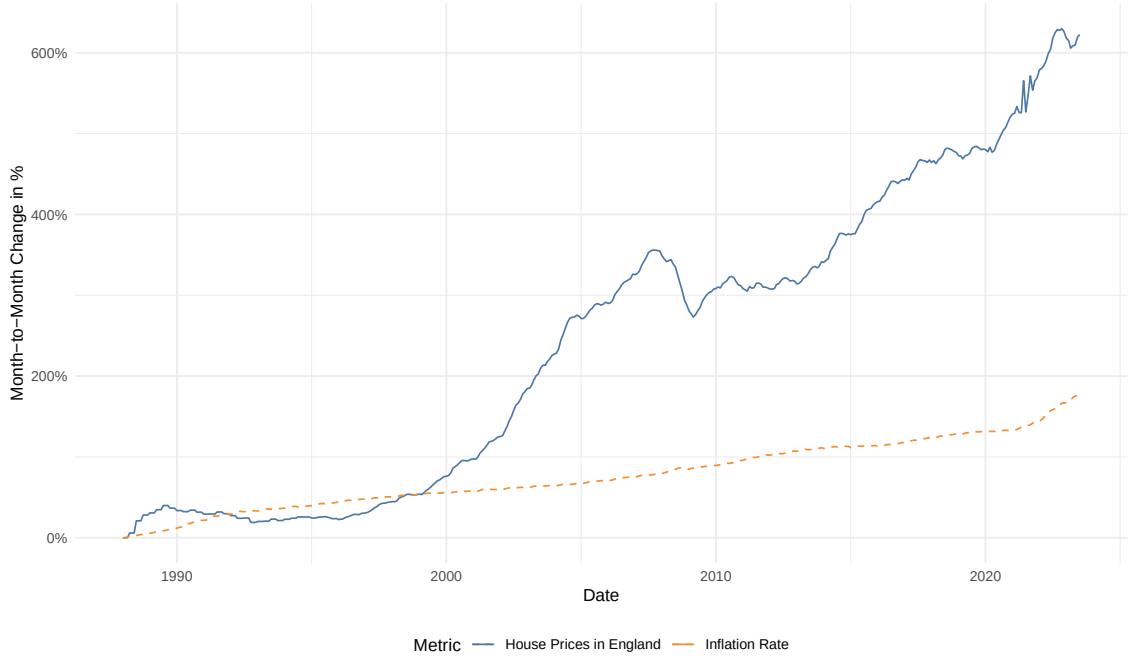
Table 1 below shows that of the ten regions with the highest median of the ratio $\frac{regional\ average\ house\ price}{average\ house\ price\ in\ England}$. Perhaps unsurprisingly, we can see that the ten most expensive regions by this metric are geographically concentrated in London and its suburbs, 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

```r
# 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

```r
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

```r
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

```r
# 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_that("column sums of gamma matrix all equal 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 = TRUE), nrow = K, ncol = T)
  hap <- sample(0:1, T, replace = TRUE)

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

  # Check that each column sum is close to 1
  for (t in 1:T) {
    expect_equal(sum(gamma_matrix[, t]), 1, tolerance = 1e-5)
  }
})

## Test passed
```

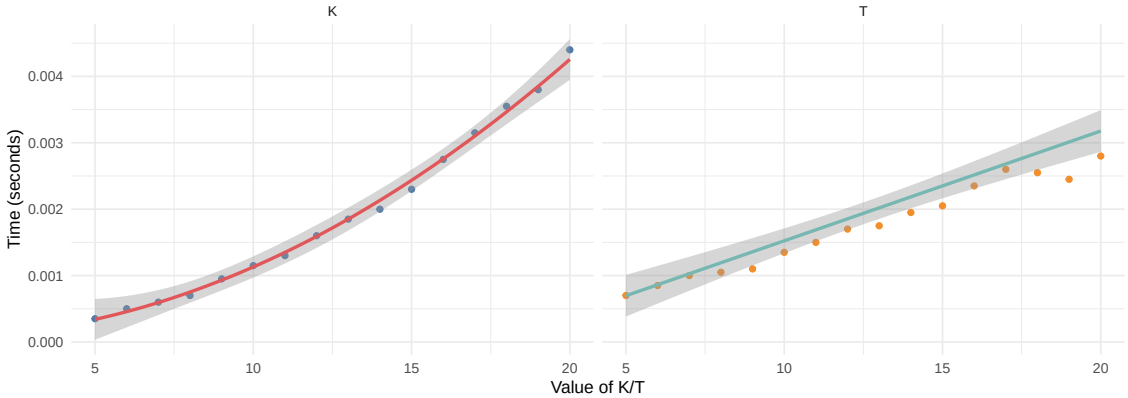
1.6 Computational Complexity of `forward` and `backward` Algorithms

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.

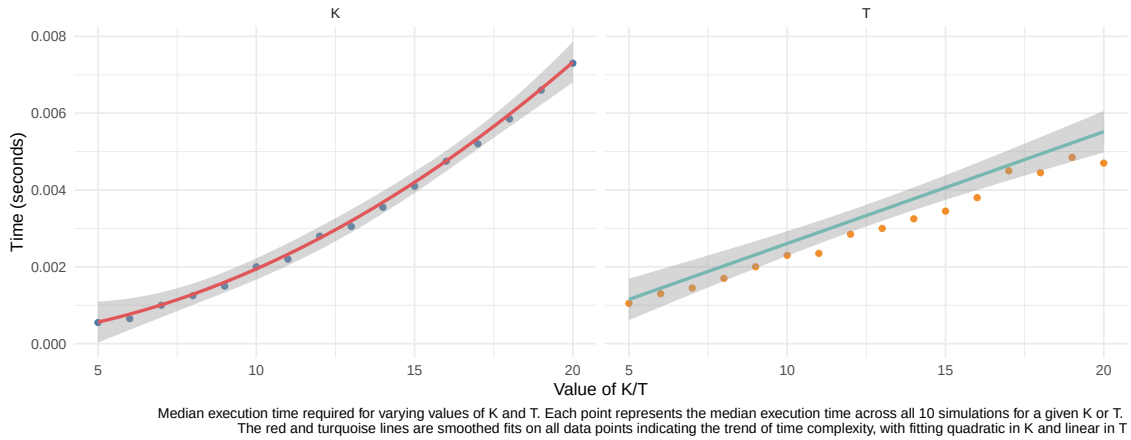
Figures 4 and 5 below show benchmark results for both the forward and backward algorithms, executed 10 times each for all $K \times T$ with $K, L = 5, \ldots, 20$. The fitted lines for the median execution time for each value of K and T, respectively, look polynomial in K and linear in T.

Figure 4: Benchmark Results for **`forward`** Algorithm



Median execution time required for varying values of K and T. Each point represents the median execution time across all 10 simulations for a given K or T. The red and turquoise lines are smoothed fits on all data points indicating the trend of time complexity, with fitting quadratic in K and linear in T

Figure 5: Benchmark Results for `backward` Algorithm



Median execution time required for varying values of K and T. Each point represents the median execution time across all 10 simulations for a given K or T. The red and turquoise lines are smoothed fits on all data points indicating the trend of time complexity, with fitting quadratic in K and linear in T

1.7 Implementation of `forward2` Algorithm

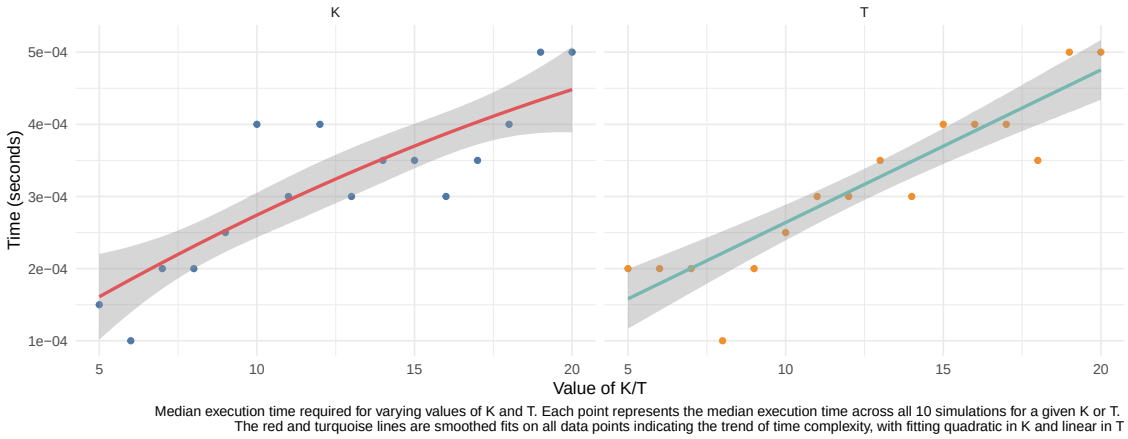
```r
forward2 <- function(haps, hap, error = 0.1) {
  K <- nrow(haps)
  T <- ncol(haps)
  alpha <- matrix(0, nrow = K, ncol = T)
  pi <- 1 / K

  for (k in 1:K) {
    alpha[k, 1] <- pi * emission_probability(hap[1], haps[k, 1], error)
  }

  for (t in 2:T) {
    phi <- sum(alpha[, t - 1]) * (1 - 0.999) / K
    for (k in 1:K) {
      A_ik <- ifelse(k == k, (1 - 0.999) / K + 0.999, (1 - 0.999) / K)
      b_kt <- emission_probability(hap[t], haps[k, t], error)
      alpha[k, t] <- (phi + 0.999 * alpha[k, t - 1]) * b_kt
    }
  }

  return(alpha)
}
```

```r
test_that("forward and forward2 produce the same outputs", {
  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)

  # Generate example data
```

```
  haps <- matrix(sample(0:1, K * T, replace = TRUE), nrow = K)
  hap <- sample(0:1, T, replace = TRUE)

  # Run both functions
  alpha_forward <- forward(haps, hap, e)
  alpha_forward2 <- forward2(haps, hap, e)

  # Check if the outputs are equal
  expect_equal(alpha_forward, alpha_forward2, tolerance = 1e-5)
})

## Test passed
```

The `forward2` algorithm has a time complexity of $\mathcal{O}(K \cdot T)$ as it computes the initial probabilities ($\mathcal{O}(K)$) and then for each time step t, it sums over all K states ($\mathcal{O}(K)$) and computes equation (14) ($\mathcal{O}(1)$). Since the main loop runs for each time step T, and within each time step, two $\mathcal{O}(K)$ operations are performed (one for summing alpha and one for the loop over K), the overall complexity of the forward2 function is $\mathcal{O}(K \cdot T)$. Figure 6 below displays this improved performance.

Figure 6: Benchmark Results for `forward2` Algorithm



1.8 Implementation of `backward2` Algorithm

```
backward2 <- 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. 14)
  for (t in (T-1):1) {
```

```
    # Calculate the phi term which is constant for all k (eq. 13)
    phi <- sum(beta[, t+1] * sapply(1:K, function(i) emission_probability(hap[t+1], haps[
    for (k in 1:K) { # Update beta for each k using the phi term and the specific transit
      beta[k, t] <- phi + 0.999 * beta[k, t+1] * emission_probability(hap[t+1], haps[k, t
    }
  }

  return(beta)
}
```

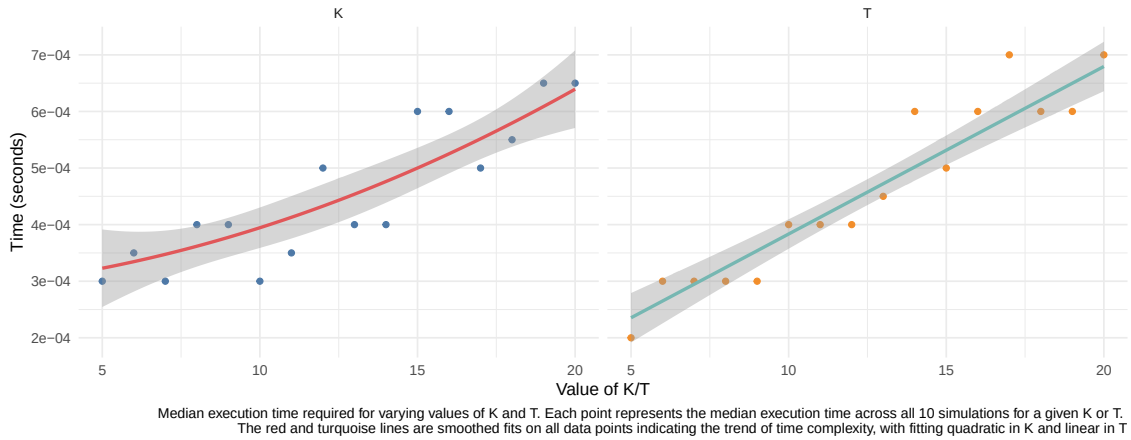
```
test_that("backward and backward2 produce the same outputs", {
  set.seed(42)  # For reproducibility
  K <- 10  # Number of rows in haps
  T <- 15  # Number of columns in haps = length of hap
  e <- 0.1  # Error rate (= default value)

  # Generate example data
  haps <- matrix(sample(0:1, K * T, replace = TRUE), nrow = K)
  hap <- sample(0:1, T, replace = TRUE)

  # Run both functions
  beta_backward <- backward(haps, hap, e)
  beta_backward2 <- backward2(haps, hap, e)

  # Check if the outputs are equal
  expect_equal(beta_backward, beta_backward2, tolerance = 1e-5)
})

## Test passed
```

The `backward2` algorithm has a time complexity of $\mathcal{O}(K \cdot T)$ as it computes the initial probabilities ($\mathcal{O}(K)$) and then for each time step t, it sums over all K states ($\mathcal{O}(K)$) and computes equation (14) ($\mathcal{O}(1)$). Since the main loop runs for each time step T, and within each time step, two $\mathcal{O}(K)$ operations are performed (one for summing alpha and one for the loop over K), the overall complexity of the forward2 function is $\mathcal{O}(K \cdot T)$. Figure 7 below displays this improved performance.

1.9 Implementation of `gamma2` Function

```
gamma2 <- function(haps, hap, error = 0.1) {
  K <- nrow(haps)
  T <- ncol(haps)

  # Compute alpha and beta matrices using forward2 and backward2
  alpha <- forward2(haps, hap, error)
  beta <- backward2(haps, hap, error)
```

Figure 7: Benchmark Results for `backward2` Algorithm



Median execution time required for varying values of K and T. Each point represents the median execution time across all 10 simulations for a given K or T. The red and turquoise lines are smoothed fits on all data points indicating the trend of time complexity, with fitting quadratic in K and linear in T

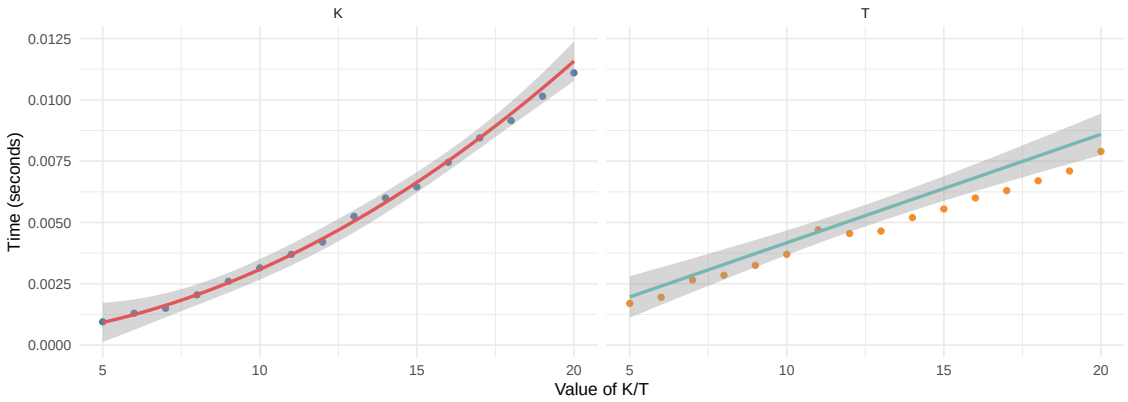
```
  # Compute normalization factor (denominator)
  norm_factor <- sum(alpha[, T])

  # 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)
}
```

```
test_that("gamma and gamma2 produce the same outputs", {
  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)

  # Generate example data
  haps <- matrix(sample(0:1, K * T, replace = TRUE), nrow = K)
  hap <- sample(0:1, T, replace = TRUE)

  # Run both functions
  gamma_matrix <- gamma(haps, hap, e)
  gamma_matrix2 <- gamma2(haps, hap, e)

  # Check if the outputs are equal
```

```
  expect_equal(gamma_matrix, gamma_matrix2, tolerance = 1e-5)
})

## Test passed
```

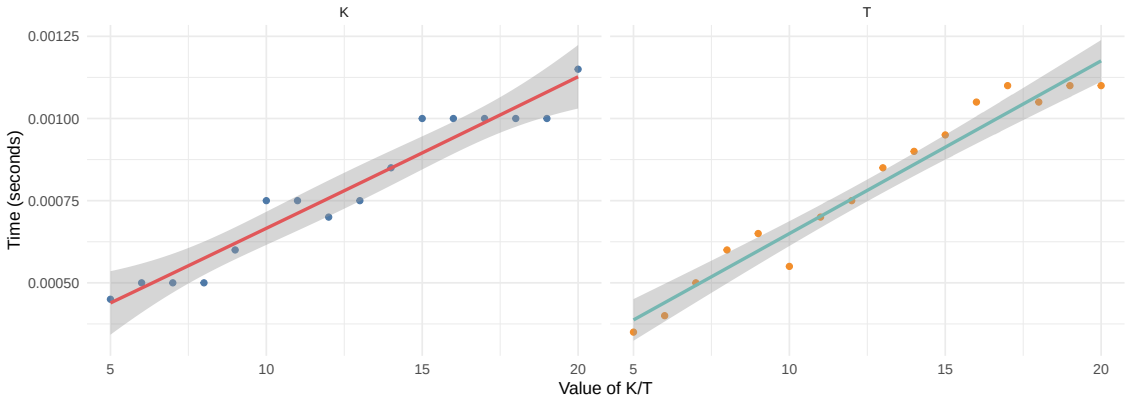
Figures 8 and 9 below show that the empirical time complexity of `gamma` and `gamma2` indeed matches the reasoning laid out above.

Figure 8: Benchmark Results for `gamma` Function



Median execution time required for varying values of K and T. Each point represents the median execution time across all 10 simulations for a given K or T. The red and turquoise lines are smoothed fits on all data points indicating the trend of time complexity, with fitting quadratic in K and linear in T

Figure 9: Benchmark Results for `gamma2` Function



Median execution time required for varying values of K and T. Each point represents the median execution time across all 10 simulations for a given K or T. The red and turquoise lines are smoothed fits on all data points indicating the trend of time complexity, with fitting quadratic in K and linear in T

```r
# Extract the first 5 target haplotypes
first_5_haps <- samples_raw[1:5, ]

paint_and_sum <- function(target_hap, ref_panel) {
  gamma_results <- gamma2(ref_panel, target_hap, error = 0.1)

  # Sum contributions from YRI and CEU haplotypes
  yri_sum <- rowSums(gamma_results[grepl("YRI", rownames(ref_panel)), ])
  ceu_sum <- rowSums(gamma_results[grepl("CEU", rownames(ref_panel)), ])

  return(list(YRI = yri_sum, CEU = ceu_sum))
}

# Apply function to first 5 target haplotypes (parallelized)
first_5_painted <- mclapply(1:nrow(first_5_haps), function(i) {
  paint_and_sum(first_5_haps[i, ], refpanel_raw)
}, mc.cores = detectCores())

compile_results_matrix <- function(painted_results) {
  results_matrix <- matrix(nrow = length(painted_results), ncol = 3)
  colnames(results_matrix) <- c("Sum_YRI", "Sum_CEU", "Percentage_YRI")

  # Loop through each list of results and calculate the sum of YRI, CEU,
  # percentage of YRI
  for (i in seq_along(painted_results)) {
    sum_yri <- sum(painted_results[[i]]$YRI)
    sum_ceu <- sum(painted_results[[i]]$CEU)
    total_sum <- sum_yri + sum_ceu
    percentage_yri <- (sum_yri / total_sum) * 100

    results_matrix[i, ] <- c(sum_yri, sum_ceu, percentage_yri)
  }

  colnames(results_matrix) <- c("Sum YRI", "Sum CEU",
                                "Percentage of YRI in Total")
  return(results_matrix)
}

painted <- compile_results_matrix(first_5_painted)
```

Table **??** below shows that among the first 5 target haplotypes, haplotypes 2 and 5 show a high contribution of YRI haplotypes. Target haplotype 5 suggests an entirely African genetic background over the investigated chromosome.

	Sum YRI	Sum CEU	Percentage of YRI in Total
1	46.12	70.88	39.42
2	98.58	18.42	84.26
3	30.18	86.82	25.80
4	71.69	45.31	61.27
5	116.46	0.54	99.54