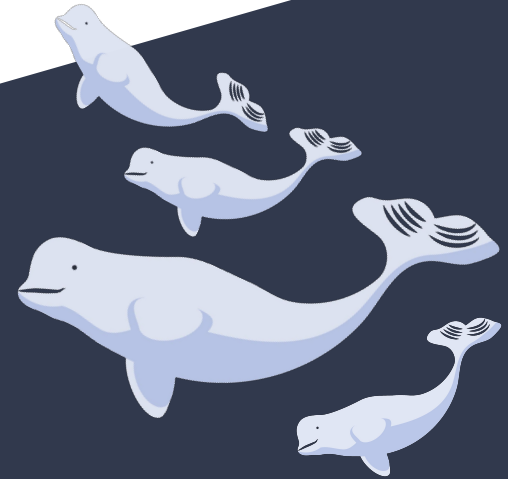
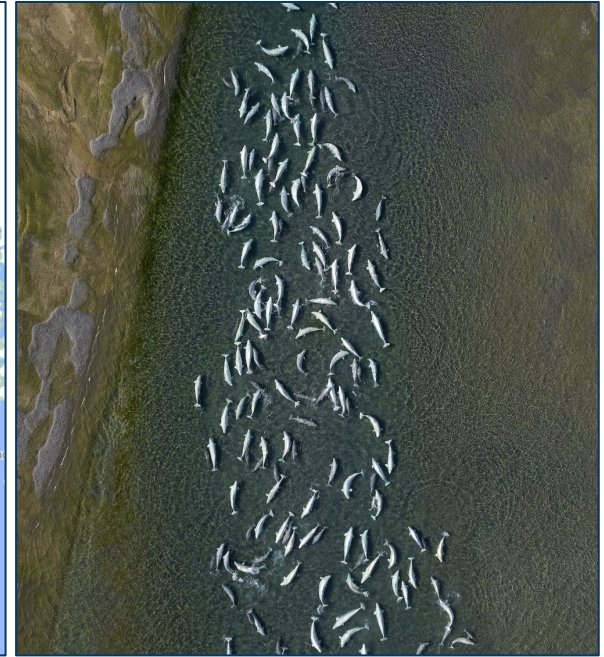
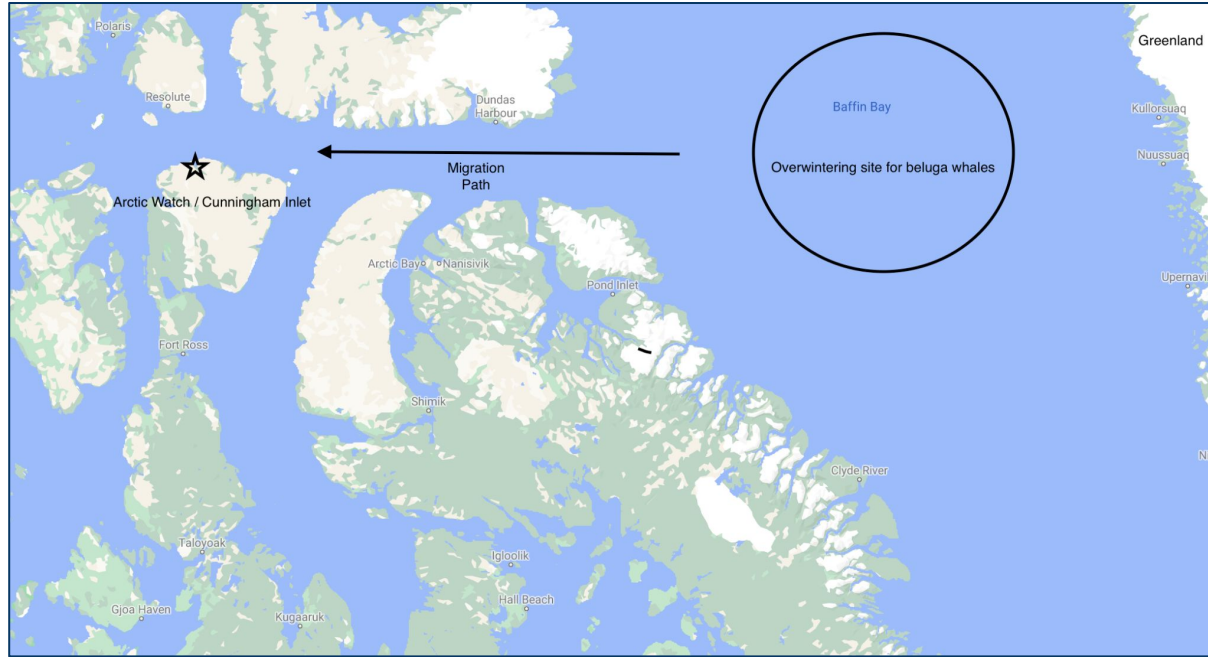


Beluga whales migration from Greenland to Cunningham Inlet

Spatial Population Dynamics



A bit about the migration



- Taxic movement for birthing, nursing, moulting, and socialisation in warmer waters during summer (July-August)
- Water in the inlet is 10 degrees warmer than the overwintering site
- Warm water allows for calves to survive better post birth as they have yet to accumulate the fat layers required to live in colder waters

Source: <https://weberarctic.com/stories/the-belugas-of-cunningham-inlet>

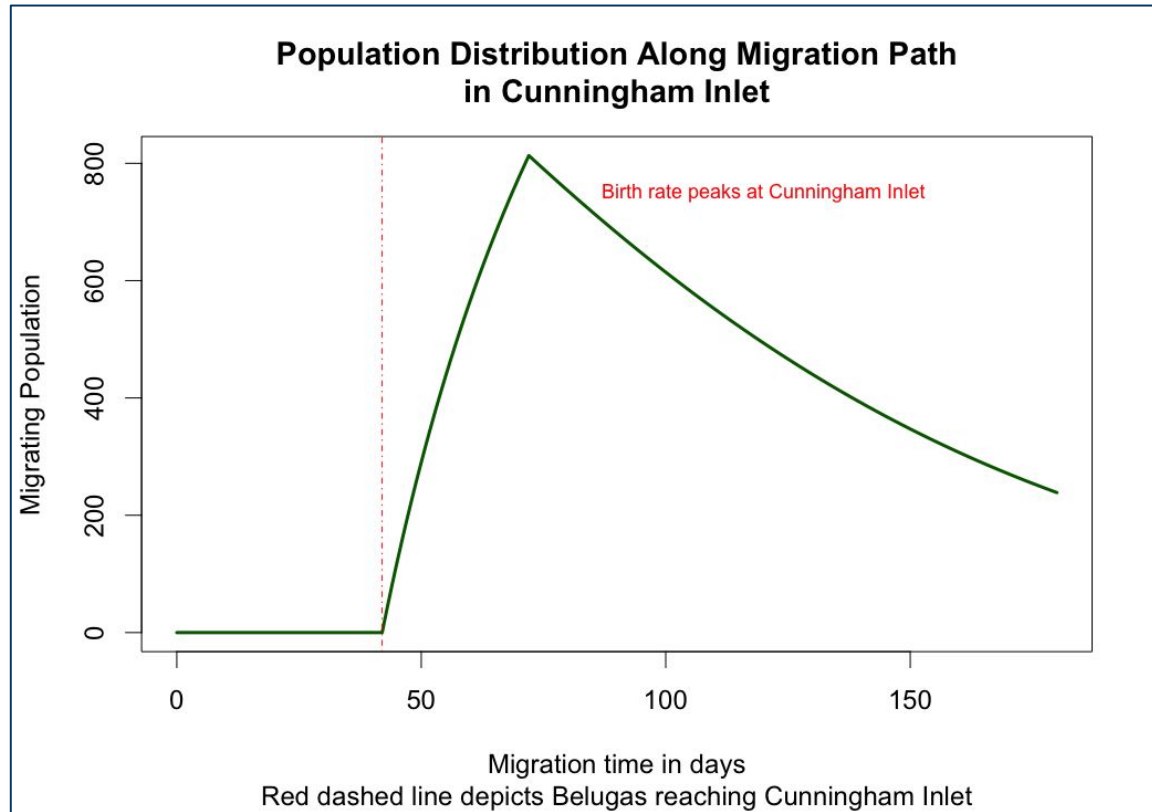
Parameters and steady-state population sizes

Location	Patch 1 Greenland waters	Patch 2 Cunningham Inlet, North Canada
Maximum intrinsic growth rate (r_{\max}) <i>per year</i>	$r_{\max 1} \Rightarrow 0.25$	$r_{\max 2} \Rightarrow 0.75$
Carrying capacity (K)	10,000	3,000
Size of migrating population (N)	5000	Initially, it is zero
Intrinsic growth rate (r) <i>per year</i>	$r_1 \Rightarrow r_{\max 1} (1 - (N_1 / K_1)) = 0.125$	$r_2 \Rightarrow r_{\max 2} (1 - (N_2 / K_2)) = 0.750$
Distance from Patch 1 to 2 (d)	500 miles	
Time taken for migration (t)	6 weeks \Rightarrow 42 days	
Physical movement rate (m)	$m \Rightarrow d/t = 500/42 = 11.9$ miles per day	
Ecological movement rate (g)	$m ((r_2 - r_1) / 365) = 0.203$ per day	
Population size at equilibrium	$K_1 (1 - (g/r_{\max 1})) \approx 9185$	$K_2 / 2 (1 + \sqrt{1 + (4((g / r_{\max 2}) - (g^2 / r_{\max 2}^2))))})$ $= 3077.33$

Migration: Patch 1 to Patch 2

Greenland to Cunningham Inlet, North Canada

Patch 1 population	$dN_1/dt \Rightarrow r_1 N_1 - g N_1$
Patch 2 population	$dN_2/dt \Rightarrow r_2 N_2 + g N_1$
<p>Each Beluga typically spends 7 to 10 days in Cunningham Inlet, engaging in self-care activities and the birthing and nursing process.</p> <p>Due to the limited food options in this area, they rely on deeper seas and bays for hunting and feeding once their calves are strong enough to swim out with them.</p> <p>This migration is one of the most extraordinary natural phenomena that occurs every year, attracting many explorers to the site.</p>	



Extended Model – Migration: Patch 2 to Patch 3

Cunningham Inlet to Hudson Bay, Northeastern Canada

Population size in:

- Greenland
- Cunningham Inlet
- Hudson Bay

Patch 1
population

$$dN_1/dt \Rightarrow r_1 N_1 - g_{12} N_1$$

Patch 2
population

$$dN_2/dt \Rightarrow r_2 N_2 + g_{12} N_1 - g_{23} N_2$$

Patch 3
population

$$dN_3/dt \Rightarrow r_3 N_3 + g_{23} N_2$$

Population remaining in Greenland grows at its own pace over time and so does the native Hudson Bay population.

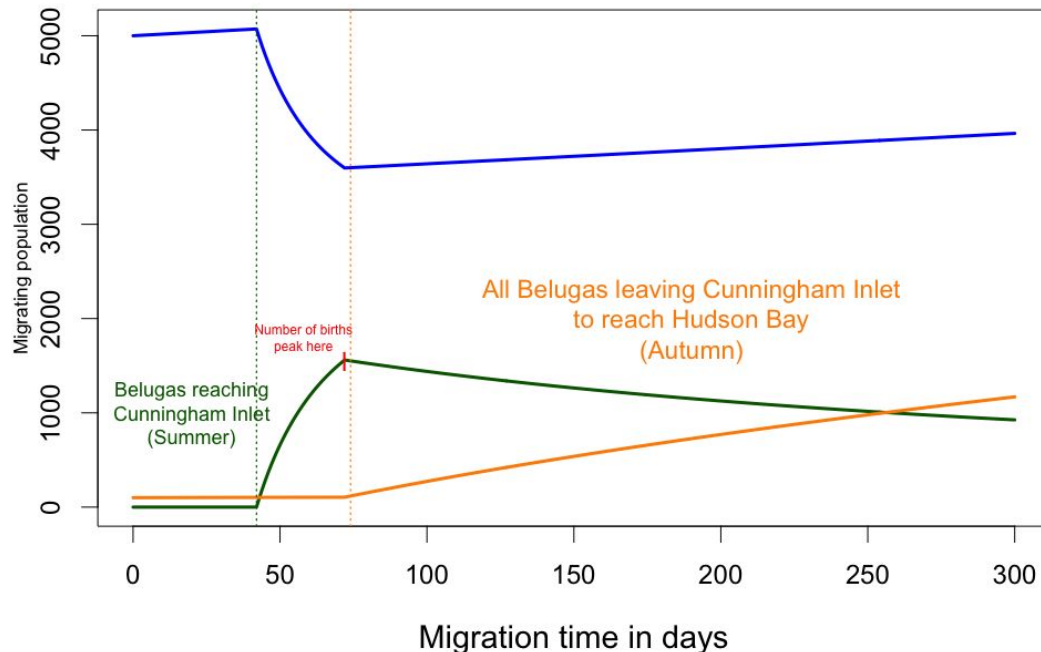
However, influx from the Cunningham inlet adds up to the activity of Belugas in Hudson bay where they feed with their newly born calves during autumn.

Hudson Bay waters are rich in nutrients and thus marine life at this time which is a good source of nutrition for these whales.

While Cunningham Inlet is a safe haven for these Belugas as there are no possibilities of their predation there, polar bears hunt belugas in Hudson Bay which can further add to the population dynamics there (it was not included in the model this time though).

Inspiration: <https://www.youtube.com/watch?v=NJ08zvLDCmM>

Population Distribution Along Migration Path



Mathematical Biology

Weekly Exercise 7

Swati Tak

2023-10-17

Parameters and equilibrium conditions

```
library(deSolve)

# Setting parameter values
K1 <- 10000      # Carrying capacity in Greenland
K2 <- 3000       # Carrying capacity in Cunningham Inlet

r_max1 <- 0.25   # Maximum intrinsic growth rate in Greenland
r_max2 <- 0.75   # Maximum intrinsic growth rate in Cunningham Inlet

N1 <- 5000       # Initial population in Greenland (patch 1)
N2 <- 0          # Initial population in Cunningham Inlet (patch 2)

duration_12 <- 42 # Duration of migration in days from patch 1 to 2
dist_12 <- 500    # Distance between Greenland and Cunningham Inlet in miles

# Calculations

## Intrinsic growth rate in Greenland
r1 <- (r_max1 * (1 - (N1/K1)))/365 # Growth rate per day

## Intrinsic growth rate in Cunningham Inlet
r2 <- (r_max2 * (1 - (N2/K2)))/365 # Growth rate per day

## Movement rates from patch 1 to 2
m12 <- dist_12/duration_12 # Physical movement rate miles per day
g12 <- (r2 - r1)*m12 # Ecological movement rate per day from patch 1 to 2

# Equilibrium conditions for movement for patch 1 to 2

## Equilibrium pop in Greenland waters
N1_eq <- K1*(1 - (g12/r_max1))

## Equilibrium pop in Cunningham Inlet during summer
N2_eq <- 0.5 * K2 * (1 + sqrt(1 + (4*g12/r_max2) - (4*g12^2/r_max2^2)))

cat("Equilibrium population sizes for patch 1 and 2 are", N1_eq, "and", N2_eq, ", respectively.")
```

Equilibrium population sizes for patch 1 and 2 are 9184.605 and 3077.33 , respectively.

Model 1: Migration from Patch 1 Greenland to Patch 2 Cunningham Inlet

```
# Set initial conditions and parameters
initial_state <- c(N1 = N1, N2 = N2)
parameters <- c(
  K1 = K1,          # Carrying capacity patch 1 - Greenland
  K2 = K2,          # Carrying capacity patch 2 - Cunningham Inlet
  r1 = r1,          # Intrinsic growth rate patch 1
  r2 = r2,          # Intrinsic growth rate patch 2
  g12 = g12,        # Rate of ecological movement from patch 1 to 2
  m12 = m12
)

# Time points for simulation
time <- seq(0, 180, by = 1) # Times in days

# Define the model
model <- function(time, state, parameters) {
  with(as.list(c(state, parameters)), {

    r1 <- (r_max1 * (1 - (N1/K1)))/365 # Growth rate per year
    r2 <- (r_max2 * (1 - (N2/K2)))/365 # Growth rate per year
    g12 <- (r2 - r1) * m12 # Ecological movement rate per day from patch 1 to 2

    dN1_dt <- (r1 * N1) - (g12 * N1)
    dN2_dt <- 0 # In the beginning, no belugas in Cunningham Inlet

    # Check if belugas have reached patch 2
    if (time >= 42) {
      # Once the belugas reach Cunningham Inlet, their number increases there
      dN2_dt <- (r2 * N2) + (g12 * N1)
    }

    if (time >= 72) {
      # After some time, the number decreases as belugas start leaving for feeding
      dN2_dt <- (r2 * N2) - (g12 * N2)
    }

    return(list(c(dN1_dt, dN2_dt)))
  })
}

# Apply the model
output <- ode(initial_state, time, model, parameters, method = "ode45")

# Create a data frame to store the results
results <- data.frame(
  time = output[, 1],
  N1 = output[, 2],
```

```

N2 = output[, 3]
)

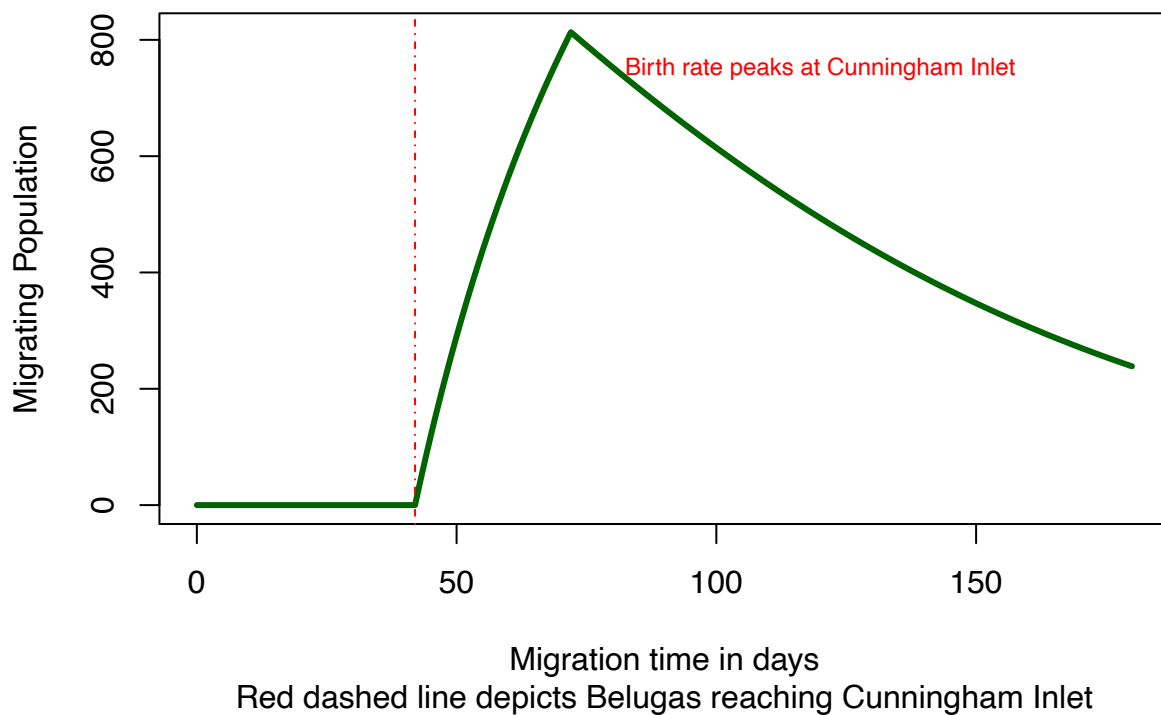
# Plot of N(x) versus x in patch 2
plot(results$time, results$N2, type = "l", col = "darkgreen",
      xlab = "Migration time in days",
      ylab = "Migrating Population",
      main = "Population Distribution Along Migration Path\in Cunningham Inlet",
      sub = "Red dashed line depicts Belugas reaching Cunningham Inlet",
      lwd=3,
      lty=1)

abline(v=42, lwd=1, lty=4, col="red")

# Add the text label at the vertical line
# text(120, 750, "Birth rate peaks at Cunningham Inlet", col = "red", cex=1)
text(120, 750, "Birth rate peaks at Cunningham Inlet", col = "red", cex=0.75)

```

Population Distribution Along Migration Path in Cunningham Inlet



Model Extension – Patch 3 – The Hudson Bay, Northeastern Canada

```

# Parameters and initial conditions
K1 <- 10000      # Carrying capacity in Greenland
K2 <- 3000      # Carrying capacity in Cunningham Inlet

```



```

K3 <- 10000          # Carrying capacity in Hudson Bay

r_max1 <- 0.25        # Maximum intrinsic growth rate in Greenland
r_max2 <- 0.75        # Maximum intrinsic growth rate in Cunningham Inlet
r_max3 <- 0.25        # Maximum intrinsic growth rate in Hudson Bay

N1 <- 5000           # Initial population in Greenland patch 1
N2 <- 0              # Initial population in Cunningham Inlet patch 2
N3 <- 100            # Initial population of Belugas in Hudson bay

duration_12 <- 42     # Duration of migration in days from patch 1 to 2
duration_23 <- 60     # Duration of migration in days from patch 2 to 3

dist_12 <- 500        # Distance between Greenland and Cunningham Inlet in miles
dist_23 <- 1000       # Distance from Cunningham Inlet to Hudson Bay (miles)

# Calculations
m12 <- dist_12/duration_12 # Physical movement rate from patch 1 to 2
m23 <- dist_23/duration_23 # Physical movement rate from patch 2 to 3
Total = N1 + N2 + N3 # Total size of population overall at all times

## Set initial conditions and parameters
initial_state <- c(N1 = N1, N2 = N2, N3 = N3, Total = Total)
parameters <- c(
  K1 = K1,          # Carrying capacity patch 1 - Greenland
  K2 = K2,          # Carrying capacity patch 2 - Cunningham Inlet
  K3 = K3,          # Carrying capacity patch 3 - Hudson Bay
  m12 = m12,
  m23 = m23
)

## Time points for simulation
time <- seq(0, 300, by = 1) # Times in days

## Define the extended model
model <- function(time, state, parameters) {
  with(as.list(c(state, parameters)), {

    r1 <- (r_max1 * (1 - (N1/K1)))/365 # Growth rate per day - Greenland
    r2 <- (r_max2 * (1 - (N2/K2)))/365 # Growth rate per day - Cunningham Inlet
    r3 <- (r_max3 * (1 - (N3/K3)))/365 # Growth rate per day - Hudson Bay

    m12 <- dist_12/duration_12
    m23 <- dist_23/duration_23

    g12 <- m12*(r2 - r1) # Ecological movement rate per day from patch 1 to 2
    g23 <- m23*(r3 - r1) # Ecological movement rate per day from patch 2 to 3

    dN1_dt <- (r1 * N1)
    dN2_dt <- 0
    dN3_dt <- (r3 * N3)
  }
}

```

```

# Check if belugas have reached patch 2
if (time >= 42 && time < 72) {
  # Belugas leaving Greenland waters for migration
  dN1_dt <- (r1 * N1) - (g12 * N1)
  # Once the belugas reach Cunningham Inlet, their number grows there
  dN2_dt <- (r2 * N2) + (g12 * N1)
  # Belugas already living in Hudson bay grow at their own rate
  dN3_dt <- (r3 * N3)
}

# After some time
if (time >= 72) {
  # Number decreases in Cunningham Inlet as belugas start leaving
  # toward Hudson Bay for hunting and feeding
  dN2_dt <- (r2 * N2) - (g23 * N2)
  # Additional influx in Hudson bay starts from Cunningham Inlet
  dN3_dt <- (r3 * N3) + (g23 * N2)
}

# The total population should keep increasing
# as deaths, predation, etc., are not included
Total = dN1_dt + dN2_dt + dN3_dt

return(list(c(dN1_dt, dN2_dt, dN3_dt, Total)))
})

}

## Apply the extended model
output <- ode(initial_state, time, model, parameters, method="ode45")
head(output)

```

```

##      time      N1 N2      N3    Total
## [1,]    0 5000.000  0 100.0000 5100.000
## [2,]    1 5001.712  0 100.0678 5101.780
## [3,]    2 5003.425  0 100.1357 5103.560
## [4,]    3 5005.137  0 100.2036 5105.341
## [5,]    4 5006.849  0 100.2716 5107.121
## [6,]    5 5008.562  0 100.3396 5108.901

```

```
tail(output)
```

```

##      time      N1      N2      N3    Total
## [296,]  295 3956.034 933.7615 1150.977 6040.772
## [297,]  296 3957.671 932.0961 1154.662 6044.430
## [298,]  297 3959.309 930.4369 1158.341 6048.088
## [299,]  298 3960.948 928.7839 1162.015 6051.747
## [300,]  299 3962.586 927.1370 1165.683 6055.407
## [301,]  300 3964.225 925.4962 1169.346 6059.067

```

```

# Create a data frame to store the results
results <- data.frame(
  time = output[, 1],
  N1 = output[, 2],
  N2 = output[, 3],
  N3 = output[, 4]
)

# par(cex=1.5)

# Plotting the results with different colors and labels
matplot.0D(output, which = list(c(1,2,3)),
  lwd = 3,
  lty = 1,
  col = c("blue", "darkgreen", "darkorange"),
  xlab="Migration time in days",
  ylab = "Migrating population",
  main="Population Distribution Along Migration Path",
  cex.lab=1.2,
  legend="none")

# Add a legend
legend("topright", title="Population size in:",
  legend = c("Greenland", "Cunningham Inlet", "Hudson Bay"),
  col = c("blue", "darkgreen", "darkorange"), lty = 1, lwd = 3)

abline(v=42, lty=3, lwd = 1.2, col="darkgreen")
text(20, 1000, "Belugas reaching\nCunningham Inlet\n(Summer)",
  cex=0.75, col="darkgreen")

points(72, 1550, pch="l", col="red")
text(58, 1800, "Number of births\npeak here",
  cex=0.5, col="red")

abline(v=74, lty=3, lwd = 1.2, col="darkorange")
text(190, 2000,
  "All Belugas leaving Cunningham Inlet\nto reach Hudson Bay\n(Autumn)",
  cex=0.95, col="darkorange")

```

Population Distribution Along Migration Path

