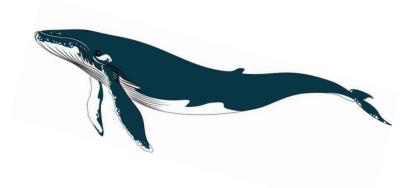
# Somatic Growth Modelling



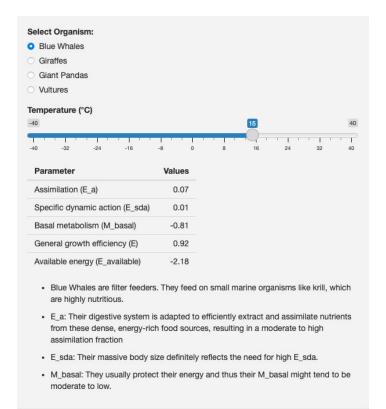


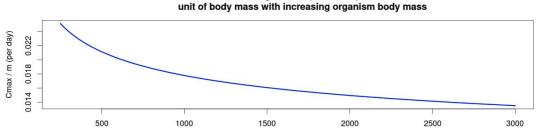






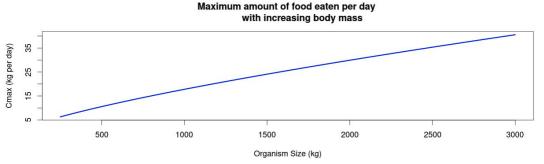






Maximum daily consumption rate per

Organism Size (kg)



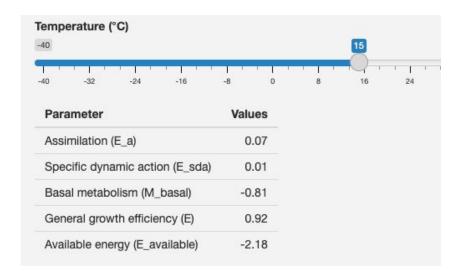
# If temperature "T" changes ...

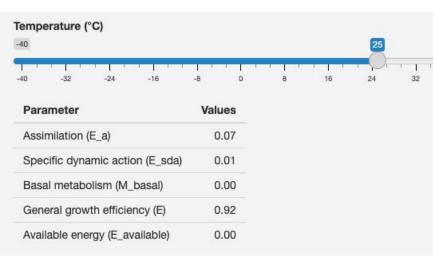
### # Basal metabolic rate changes

$$k = k_0 \cdot (0.01 \cdot (T - 25))$$

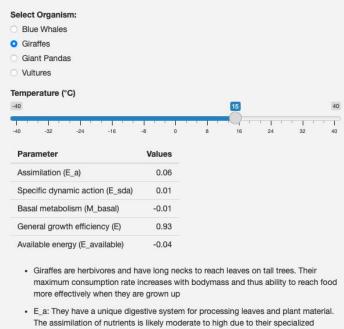
### # Feeding level changes too

$$f = f_0 \cdot (0.01 \cdot (T - 25))$$





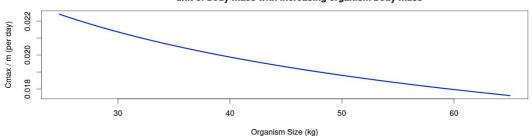
### **Giraffes**



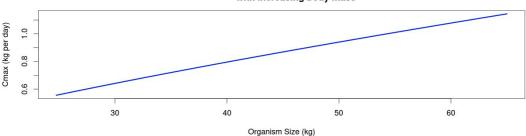
- digestive system developed for fibrous vegetation.
- E\_sda: Considering their huge bodies and long-neck adaption, their specific dynamic action need it moderate to high.
- . M\_basal: They are fairly active in their pursuit of green leaves, so their M\_basal might be moderate as well



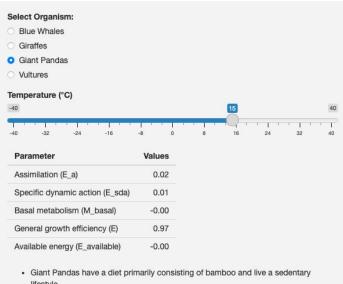
#### Maximum daily consumption rate per unit of body mass with increasing organism body mass



#### Maximum amount of food eaten per day with increasing body mass



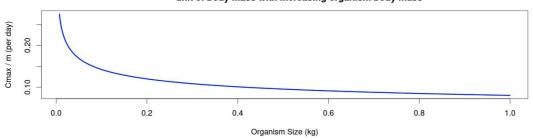
## **Giant Pandas**



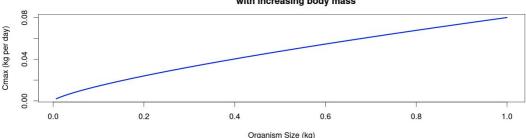
- lifestyle.
- E\_a: A bamboo diet usually has low nutrition value and their digestive system is also moderately active, therefore they assimilate moderate to low levels of consumed food.
- E\_sda: Pandas consume a large amount of bamboo for energy, with a good portion of their diet allocated for the creation of new biomass.
- . M\_basal: Their M\_basal does not need to be high as they are not much active



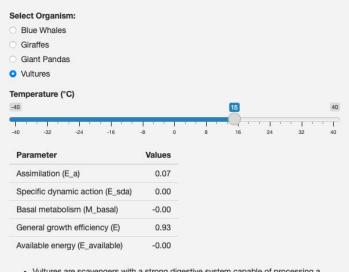
#### Maximum daily consumption rate per unit of body mass with increasing organism body mass



#### Maximum amount of food eaten per day with increasing body mass



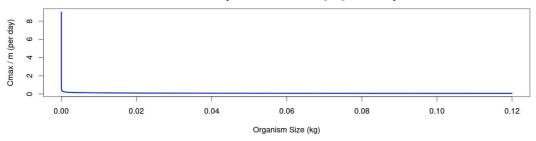
## **Vultures**



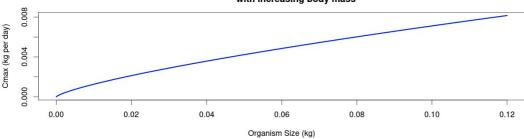
- Vultures are scavengers with a strong digestive system capable of processing a variety of foods, including carrion.
- E\_a: Their digestive system is specialized to efficiently extract and assimilate nutrients from diverse and sometimes challenging food sources, likely resulting in a high assimilation fraction.
- E\_sda: Vultures, as scavengers, typically do not require a significant amount of new biomass synthesis.
- M\_basal: Meat-eating vultures can get enough nutrition even with a small fraction of food consumed for staying alive and active.



### Maximum daily consumption rate per unit of body mass with increasing organism body mass



#### Maximum amount of food eaten per day with increasing body mass



```
# Somatic Growth Model
# Load necessary libraries
library(shiny)
library(deSolve)
# Define UI
ui <- fluidPage(</pre>
  titlePanel("Somatic Growth Model"),
  sidebarLayout(
    sidebarPanel(
      selected = "Blue Whales"),
      sliderInput("temperature", "Temperature (°C)", min = -40, max = 40, value = 25),
      tableOutput("organism_details"),
      uiOutput("organism_description"),
      tableOutput("attribute_table"),
    ),
   mainPanel(
      plotOutput("cmax_m_plot"),
      plotOutput("cmax_plot")
    )
  )
)
# Define server logic
server <- function(input, output) {</pre>
  observe({
    # Simulation based on user input
    organism <- switch(input$organism,</pre>
                       "Blue Whales" = list(m_0 = 3000, m_mature = 130000, m_max =
150000, h = 0.1, f = 0.8, E_a = 0.07, E_{sda} = 0.007, k = 0.02, k_r = 0.25),
                       "Vultures" = list(m_0 = 0.12, m_mature = 10, m_max = 14, h =
0.04, f = 0.2, E_a = 0.07, E_sda = 0.004, k = 0.005, k_r = 0.05),
                       "Giraffes" = list(m_0 = 65, m_mature = 1500, m_max = 1900, h =
0.05, f = 0.4, E<sub>a</sub> = 0.06, E<sub>sda</sub> = 0.006, k = 0.003, k<sub>r</sub> = 0.08),
                       "Giant Pandas" = list(m_0 = 1, m_mature = 120, m_max = 150, h =
0.08, f = 0.6, E_a = 0.02, E_sda = 0.006, k = 0.001, k_r = 0.10)
    # Input temperature
    T <- input$temperature
    # Basal metabolism constant changes with temperature
   k \leftarrow organism k * (0.01 * (T - 25))
    f \leftarrow organism f * (0.01 * (T - 25))
    # Calculations for chosen species
    E_growth <- (1 - organism$E_a - organism$E_sda) # Energy efficiency for overall</pre>
growth
   M_basal <- k * (organism$m_0 ^ 0.75) # Basal metabolism
    Cmax_0 <- organism$h * (organism$m_0 ^ 0.75) # Maximum consumption rate</pre>
    C <- f * Cmax_0 # Consumption rate</pre>
    fc <- organism$k / (E_growth * organism$h) # Critical feeding level, fraction of
Cmax used for basal metabolism
    A <- E_growth * organism$h * (f - fc) # General constant
    E_available <- (E_growth * C) - M_basal # Available energy</pre>
    H < - 0
    # Model parameters and initial states
    initial_state <- c(m = organism$m_0)</pre>
    parameters <- c(k_r = organism$k_r, A = A, m_mature = organism$m_mature, m_max =
organism$m_max)
    # Time sequence
    times <- seq(0, 500, by = 1)
    # Define the somatic growth model
```

```
sg_model <- function(time, state, parameters) {</pre>
      with(as.list(c(state, parameters)), {
        dmdt \leftarrow A * (m ^ 0.75) - (H * (m - m_mature) * k_r * m)
        if (m >= m_mature && m < m_max) {</pre>
          H <- 1
        } else {
          H < - 0
        if (m \ge m_max) {
          dmdt <- 0
        list(dmdt)
      })
    }
    # Apply the somatic growth model
    somatic_growth <- ode(y = initial_state, times = times, func = sg_model, parms =</pre>
parameters)
    sg <- as.data.frame(somatic_growth)</pre>
    # Calculations for organism details table
    Assimilation <- organism$E_a
    Specific.dynamic.action = organism$E_sda
    Basal.metabolism = M_basal
    Available.energy = E_available
    # Generate content for organism_details table
    organism_details <- data.frame(</pre>
      Parameter = c("Assimilation (E_a)", "Specific dynamic action (E_sda)", "Basal
metabolism (M_basal)", "General growth efficiency (E)",
                     "Available energy (E_available)"),
      Values = c(Assimilation, Specific.dynamic.action, Basal.metabolism, E_growth,
                 Available.energy)
    )
    # Display organism details table
    output$organism_details <- renderTable({</pre>
      organism_details
    })
    # Additional calculations for the plots and table
    Cmax \leftarrow organism$h * (sg$m ^ 0.75)
    Cmax_over_m <- Cmax / sg$m</pre>
    # Plot Cmax/m versus m
    output$cmax_m_plot <- renderPlot({</pre>
      par(cex=1.5)
      plot(sg$m, Cmax_over_m, xlab = "Organism Size (kg)", ylab = "Cmax / m (per day)",
           type = "1", col = "blue", lwd = 3, main = "Maximum daily consumption rate per
           unit of body mass with increasing organism body mass")
    })
    # Plot Cmax versus m
    output$cmax_plot <- renderPlot({
      par(cex=1.5)
      plot(sg$m, Cmax, xlab = "Organism Size (kg)", ylab = "Cmax (kg per day)", type =
"1", col="blue", lwd=3, main = "Maximum amount of food eaten per day
           with increasing body mass")
    output$organism description <- renderUI({
      desc <- switch(input$organism,</pre>
                      "Blue Whales" = c("Blue Whales are filter feeders. They feed on
small marine organisms like krill, which are highly nutritious.",
                                         "E_a: Their digestive system is adapted to
efficiently extract and assimilate nutrients from these dense, energy-rich food sources,
resulting in a moderate to high assimilation fraction",
                                         "E_sda: Their massive body size definitely
```

```
reflects the need for high E sda.",
                                       "M_basal: They usually protect their energy and
thus their M basal might tend to be moderate to low.
                     "Giraffes" = c("Giraffes are herbivores and have long necks to
reach leaves on tall trees. Their maximum consumption rate increases with bodymass and
thus ability to reach food more effectively when they are grown up",
                                    "E_a: They have a unique digestive system for
processing leaves and plant material. The assimilation of nutrients is likely moderate
to high due to their specialized digestive system developed for fibrous vegetation.",
                                    "E_sda: Considering their huge bodies and long-neck
adaption, their specific dynamic action need it moderate to high.",
                                    "M_basal: They are fairly active in their pursuit of
green leaves, so their M_basal might be moderate as well"
                     "Giant Pandas" = c("Giant Pandas have a diet primarily consisting
of bamboo and live a sedentary lifestyle.",
                                        "E_a: A bamboo diet usually has low nutrition
value and their digestive system is also moderately active, therefore they assimilate
moderate to low levels of consumed food.",
                                        "E sda: Pandas consume a large amount of bamboo
for energy, with a good portion of their diet allocated for the creation of new
biomass.",
                                        "M basal: Their M basal does not need to be high
as they are not much active"
                     "Vultures" = c("Vultures are scavengers with a strong digestive
system capable of processing a variety of foods, including carrion.",
                                    "E_a: Their digestive system is specialized to
efficiently extract and assimilate nutrients from diverse and sometimes challenging food
sources, likely resulting in a high assimilation fraction.",
                                    "E_sda: Vultures, as scavengers, typically do not
require a significant amount of new biomass synthesis.",
                                    "M_basal: Meat-eating vultures can get enough
nutrition even with a small fraction of food consumed for staying alive and active
                     )
      )
     description <- paste("<ul>",
                           sapply(desc, function(point) {
                             paste("", point, "")
                           }), ""
      )
     HTML(description)
    })
 })
}
# Run the application
shinyApp(ui = ui, server = server)
# install.packages('rsconnect')
# library(rsconnect)
 # if(!require("devtools"))
    install.packages("devtools")
 # devtools::install github("rstudio/rsconnect")
# install.packages("renv")
# renv::init()
# renv::snapshot()
# renv::restore()
# rsconnect::deployApp(appDir = "/Users/swati/Desktop/Mathematical Biology/Somatic
```

Growth")