Tuesday, 13 December 2022 - Melbourne

Metabolic Chamber Simulation

On Monday (12/12/2022), Nat and I were working on the chamber simulation. Natalie had developed a custom function for endoR that includes a specific thermoregulatory sequence for green ringtail possums. However, there were some problems related to some problems with the ZEN variable. The function was not running. We need to try to include the thermoregulatory sequence gradually to detect where the error was.

Without the custom thermoregulatory sequence, the metabolic chamber experiment captures the pattern fairly accurately. However, we need to work out the correct sequence to be able to implement natural conditions.

Once we fixed the code, we noticed that the values estimated were not accurate. They did not make sense. There was a strong threshold after 25 degrees that induced a biphasic pattern in the metabolic response.

In order to try finding where the error is, we explore the influence of each module within the function, providing the observed data to the simulation. We included the observed core temperature, ambient temperature, and metabolic rate. Then we sequentially set one of these parameters to constants to see the influence of the real data on the chamber simulation.

Nat provided a code with the original thermoregulatory sequence, but a small modification. She included a line to correct posture (PVEN) in line 600.

The function run to detect the changes metabolic responses depending on the data input is:

endoR\_devel\_f1(

# ENVIRONMENT

TA = TAs[x], VEL = VEL, RH = hum[x], # OPTION 1: DYNAMIC HUMIDITY

#TA = TAs[x], VEL = VEL, RH = 40, # OPTION 2: STATIC HUMIDITY

# CORE TEMPERATURE

TC = TCs[x], TC\_MAX = TC\_MAXs[x], TC\_INC = TC\_INC, # OPTION 1: TC PER OBSERVATION

#TC = fur[[34,6]], TC\_MAX = fur[[35,6]], TC\_INC = 0.05, # OPTION 2: AVERAGE TC; TC\_MAX = 40.8 (KROCKENBERGER ET AL 2012)

# SIZE AND SHAPE

AMASS = AMASS, SHAPE = SHAPE, SHAPE\_B = SHAPE\_B, SHAPE\_B\_MAX = SHAPE\_B\_MAX,

UNCURL = UNCURL, SAMODE = SAMODE, PVEN = PVEN,

# FUR PROPERTIES

DHAIRV = DHAIRV, LHAIRD = LHAIRD, LHAIRV = LHAIRV, ZFURD = ZFURD,

ZFURV = ZFURV, RHOD = RHOD, RHOV = RHOV, REFLD = REFLD, DHAIRD = DHAIRD,

# PHYSIOLOGICAL RESPONSES

PCTWET = PCTWET, PCTWET\_INC = PCTWET\_INC, PCTWET\_MAX = PCTWET\_MAX,

PCTBAREVAP = 5, AK1 = AK1, AK1\_INC = AK1\_INC, AK1\_MAX = AK1\_MAX,

#Q10 = Q10s[x], QBASAL = QBASAL, DELTAR = DELTAR, PANT\_INC = PANT\_INC, # OPTION 1: Q10 PER OBSERVATION

Q10 = fur[[42,6]], QBASAL = QBASAL, DELTAR = DELTAR, PANT\_INC = PANT\_INC, # OPTION 2: Q10 WITH THE CHANGE IN MET. RATE BETWEEN 30-35 DEG C.

PANT\_MAX = PANT\_MAX, EXTREF = EXTREF, PANT\_MULT = PANT\_MULT)

}) # run endoR across environments

Next, we provide the results of each combination. The code for the sequence refers to the option that is turned on. For example, 1.1.1 means that all the dynamic data is provided (all option 1 are on); in the same vein, 1.2.1 would mean that core temperature is provided as a constant (option 2) instead of dynamic (option 1).

1\_1\_1:

* Metabolic rate seems to be a bit underestimated at 35 degrees.
* Evaporative water loss is underestimated at 30 degrees.
* Body temperature overlap between observed and predicted because the actual data is provided.
* Minute volume is underestimated at 30 degrees.

