R and Bacon plus R and Clam (at end)

Start R

Change to Bacon Directory *File pulldown menu (C:/Bacon)*

>source(‘Bacon.R’) *starts the program with a greeting*

>Bacon() runs the default MSB2K core with all defaults

>Cores() shows the cores in the Bacon folder

Parameters for U1357 dates (depths in cm) – note that quotes (“) need to be (")

> Bacon("U1357B") *will run the file but will produce errors without setting some parameters, e.g.*

>dR=1200

>dSTD=100

>thick=100

>acc.mean=0.63

>res=30

Note: these parameters can also be set in the Bacon() command line, e.g.:

> Bacon("U1357ARescaled", cc=2, cc2="Marine13", mem.strength=6, thick=100, acc.mean=0.65, mem.mean=0.8, res=30, d.min=0, C14.border=rgb(0, 0, 0, 1), C14.col=rgb(0, 0, 1, 1))

Or

> Bacon("U1357C", cc=2, cc2="Marine13", mem.strength=2, thick=30, acc.mean=0.65, mem.mean=0.6, res=10, d.min=0, C14.border=rgb(0, 0, 0, 1), C14.col=rgb(0, 0, 1, 1))

Note:

dR=XXXX sets total reservoir age

dSTD=XXX sets error in reservoir age measurement

thick=XXX sets the number of sections of equal thickness the core is divided into (default is 5 (cm)). Ideally you divide the core up into between 10 and 200 sections. For long cores and low values of thick, the calculation will take a LONG time so choose a number for thick that will divide the core up into less than 200 sections, e.g. 100 for a 180 m corer will yield 180 sections.

acc.mean=XX (in years/cm)…..so for U1357 use 0.5 or 0.65 (closest to average sed rate)

res=XX somehow sets the resolution by adjusting section thickness in a fashion different from thick…….not sure what the difference is but the guide suggests starting with res-50 for long cores.

mem.strength=XX (default = 4) but higher numbers assume that sedimentation rates don’t change as much……

Note: Some of the Bacon work suggests that I may be better off calibrating with d.R=1200+/-100 years.

Clam:

Chdir to clam

>source(‘clam.R’)

clam("U1357", cc=2, cc2="Marine13.14C")