

# Harvey Lake Core (HGC2) Chronology

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## Prep Workspace

We will be using rbacon to create Bayesian age-depth models

```
library("rbacon")
```

The following command will create a new folder called “Bacon\_runs” in the working directory. Follow the direction for making data available for Bacon.

```
Bacon()
```

The following command will show you the cores available for analysis.

```
Bacon_runs()
```

## Calibrate Dates

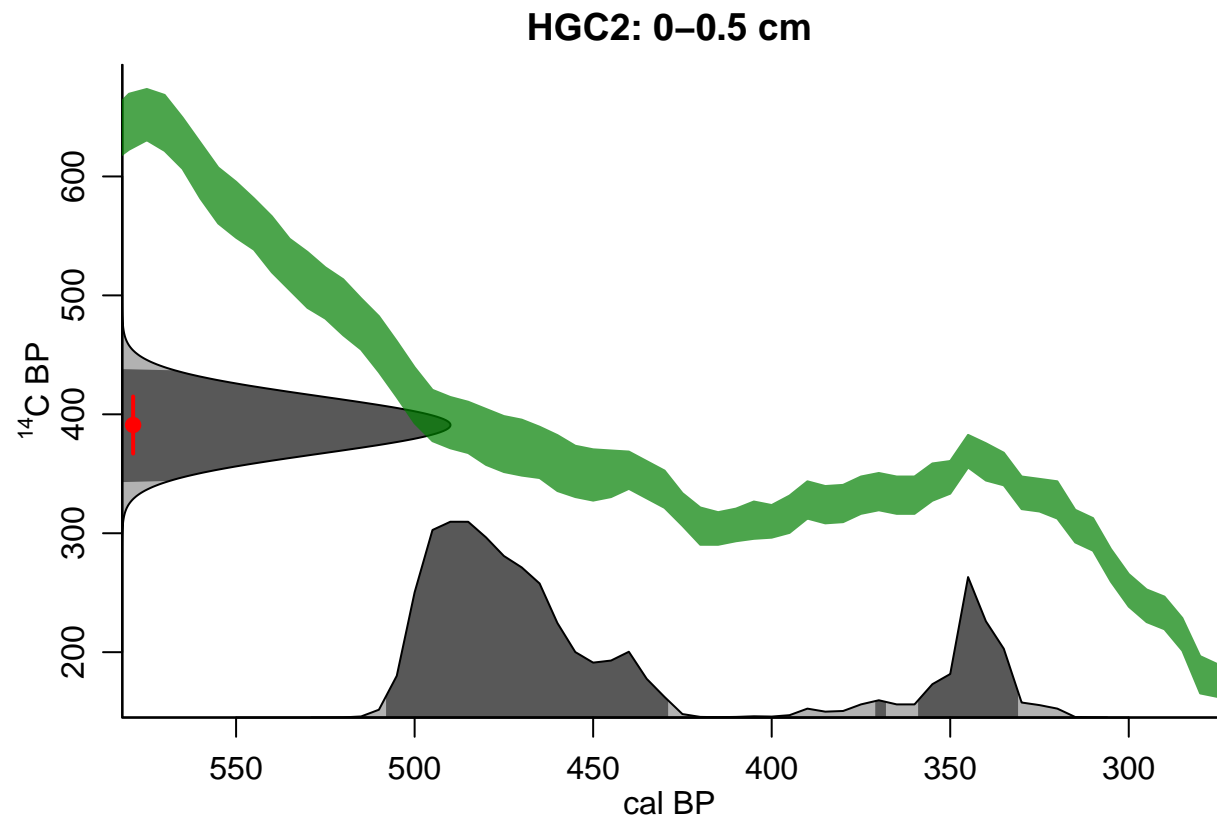
We can use “clam” to show use how are dates are calibrated using the IntCal13 curve. The following code will generate a figure showing the age distribution for each date.

```
library("clam")
```

UOC8525

```
calibrate(cage = 391, error = 24, title = "HGC2: 0-0.5 cm")
```

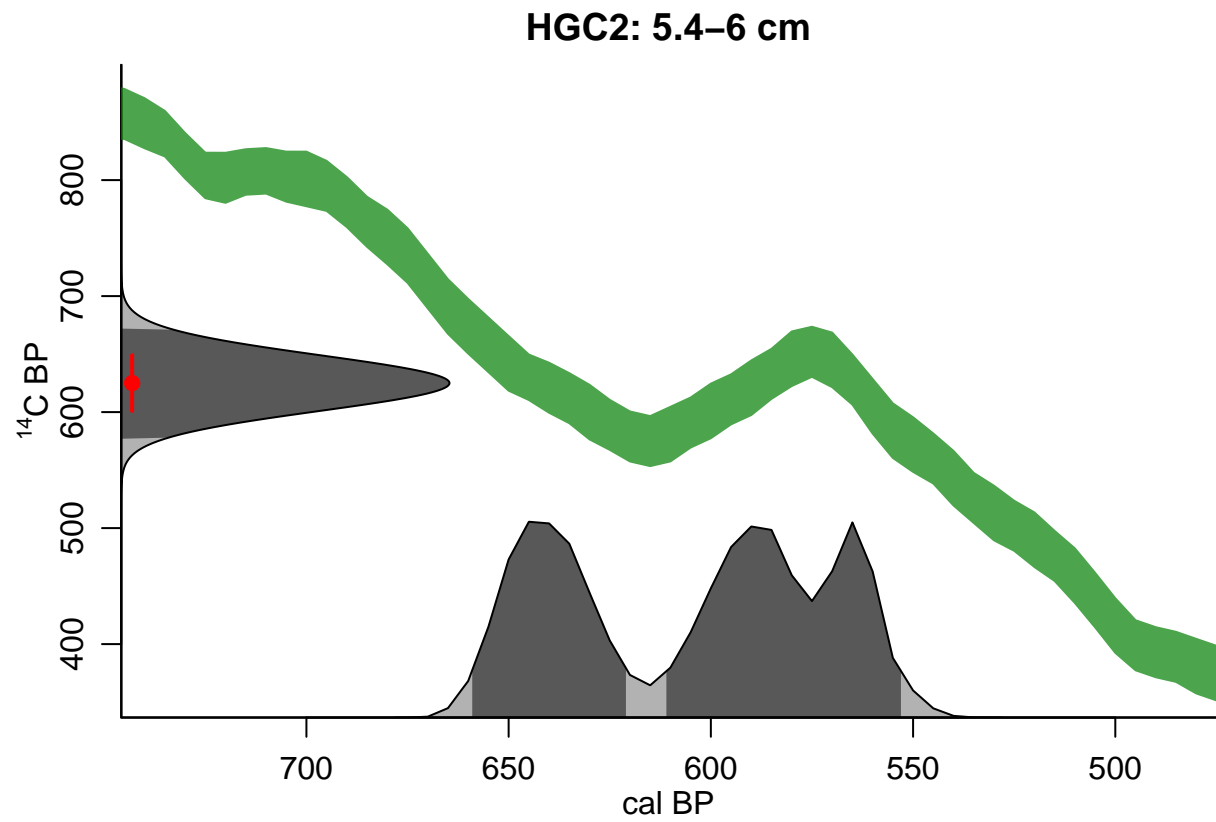
```
##
## min  max prob
## 331  359    17.2
## 368  371     0.6
## 429  508    77.2
```



UOC8526

```
calibrate(cage = 625, error = 24, cc = 1, title = "HGC2: 5.4-6 cm")
```

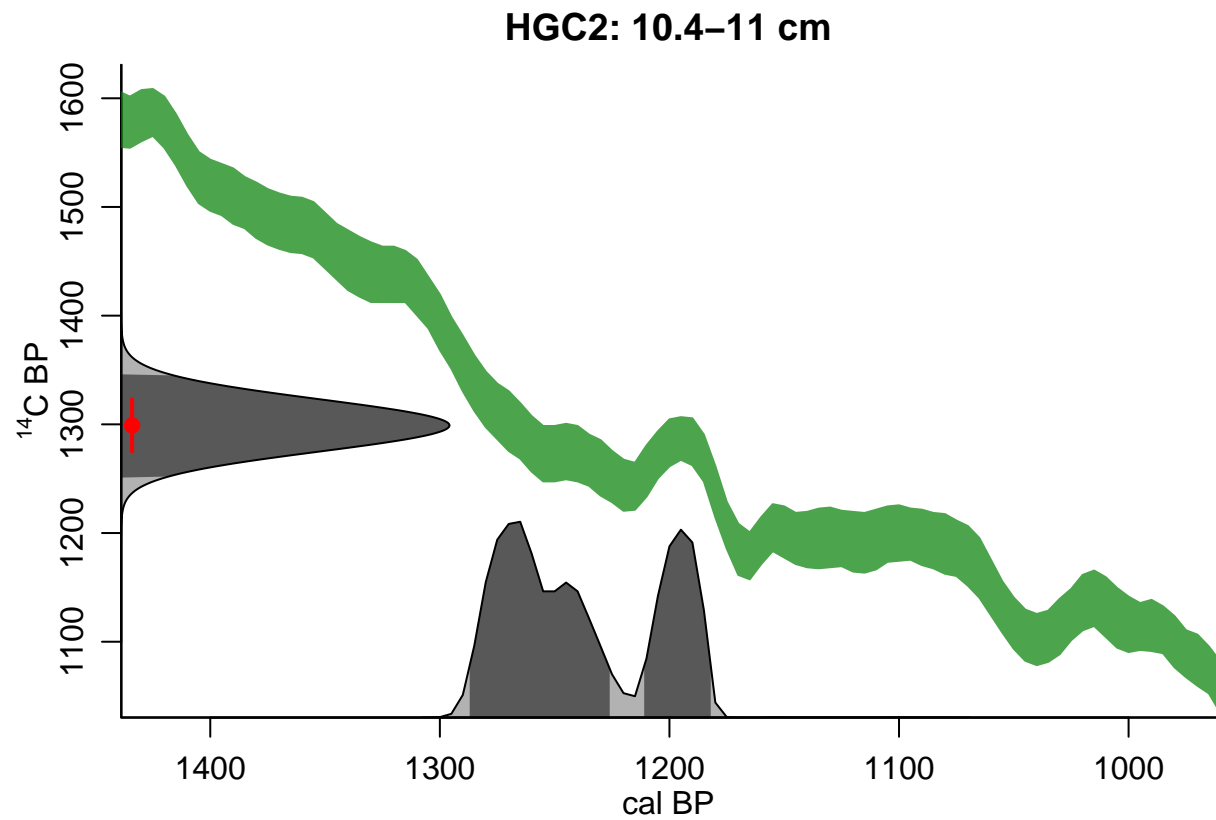
```
##
## min max prob
## 553 611    57.4
## 621 659    37.4
```



UOC8527

```
calibrate(cage = 1299, error = 24, cc = 1 , title = "HGC2: 10.4-11 cm")
```

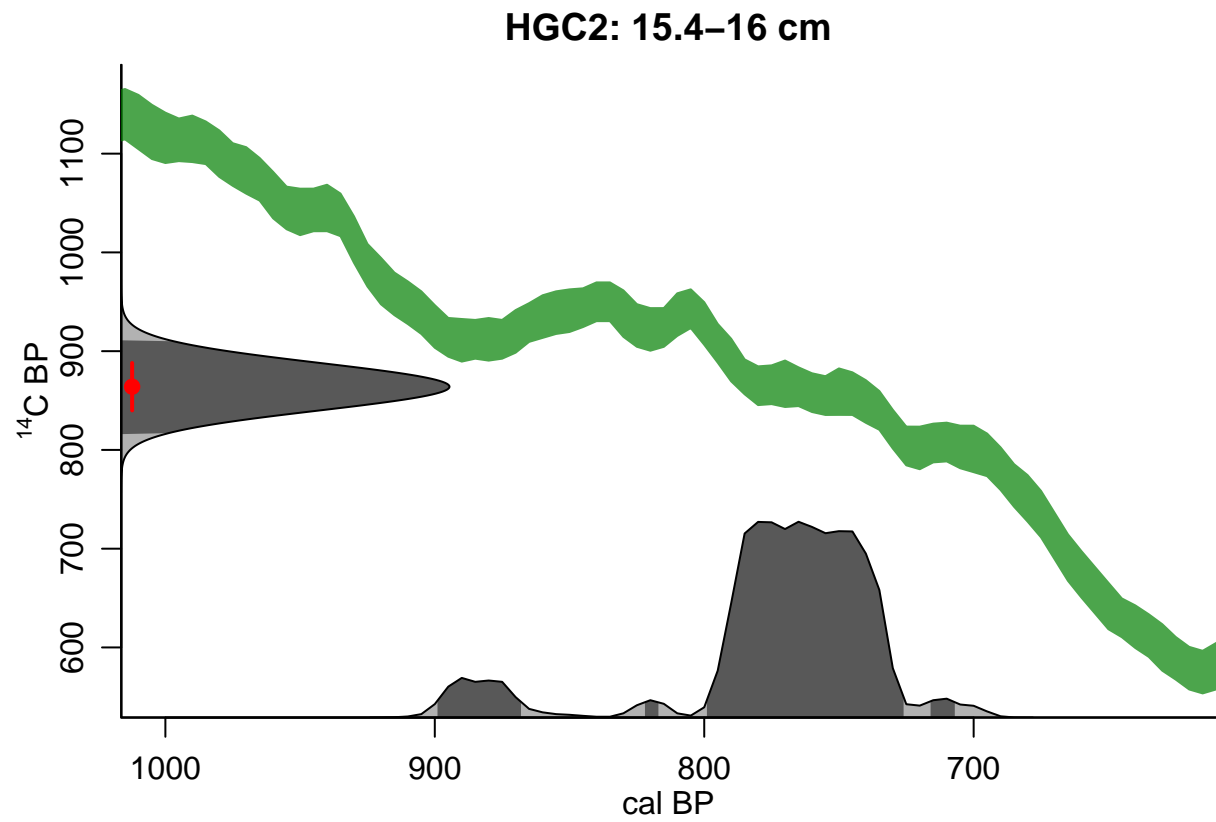
```
##
## min max prob
## 1182 1211 31.3
## 1226 1287 63.3
```



UOC8528

```
calibrate(cage = 864, error = 24, cc = 1, title = "HGC2: 15.4-16 cm")
```

```
##
## min  max prob
## 707  716    1.3
## 726  799    85
## 817  822    0.7
## 868  899    7.8
```

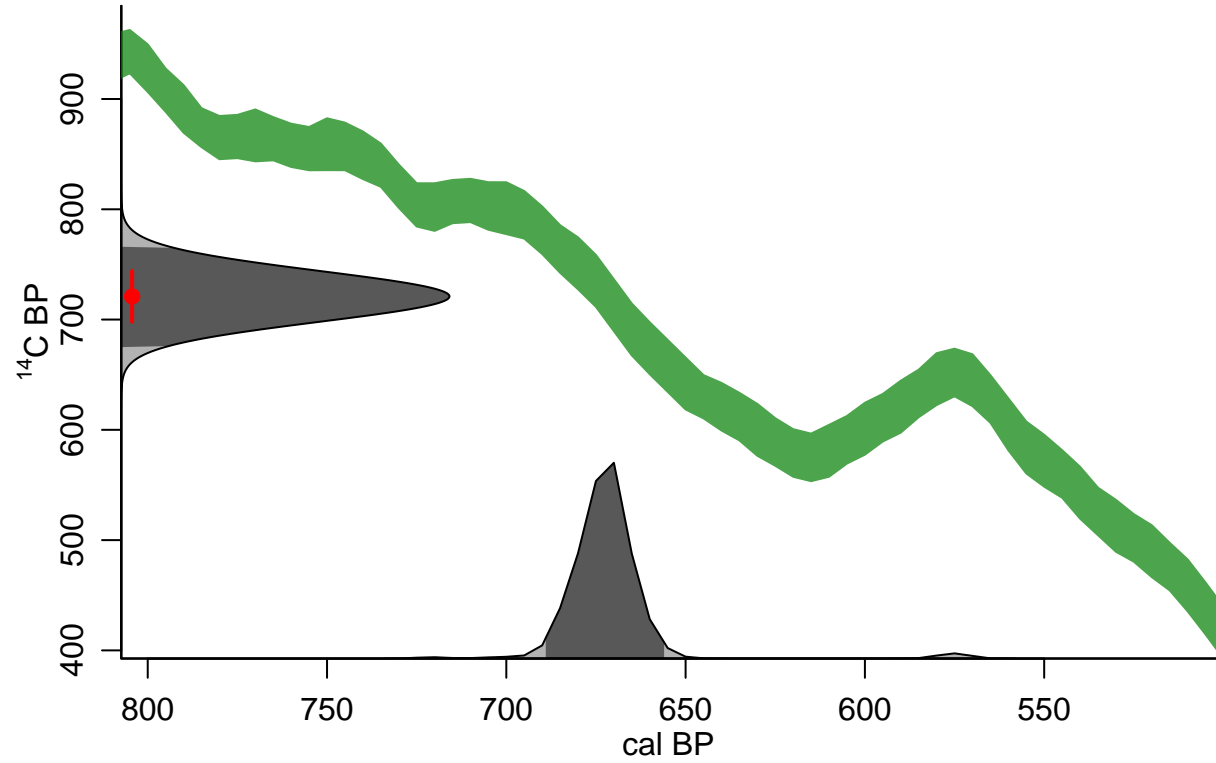


UOC6358

```
calibrate(cage = 721, error = 23, cc = 1, title = "HGC2: 17-17.5 cm")
```

```
##
## min  max prob
## 656  689    95
```

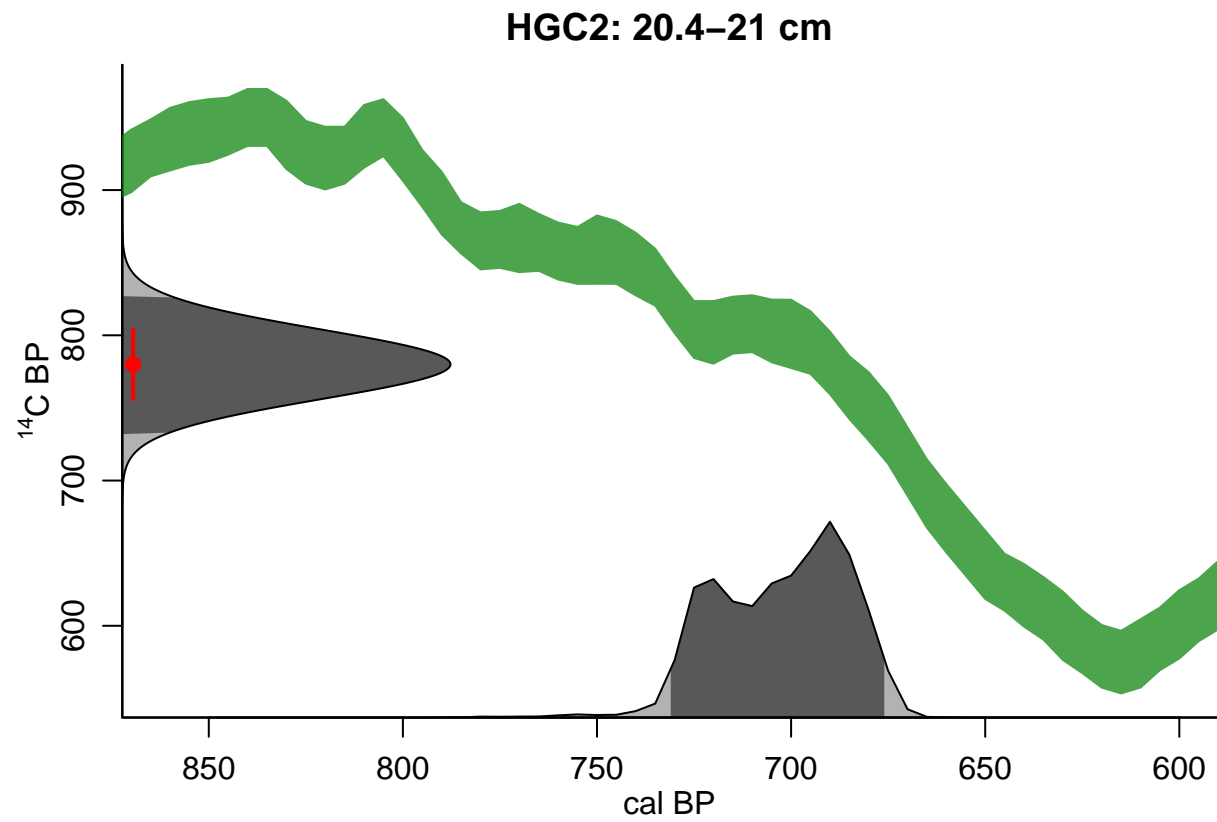
## HGC2: 17–17.5 cm



UOC8529

```
calibrate(cage = 780, error = 24, cc = 1, title = "HGC2: 20.4-21 cm")
```

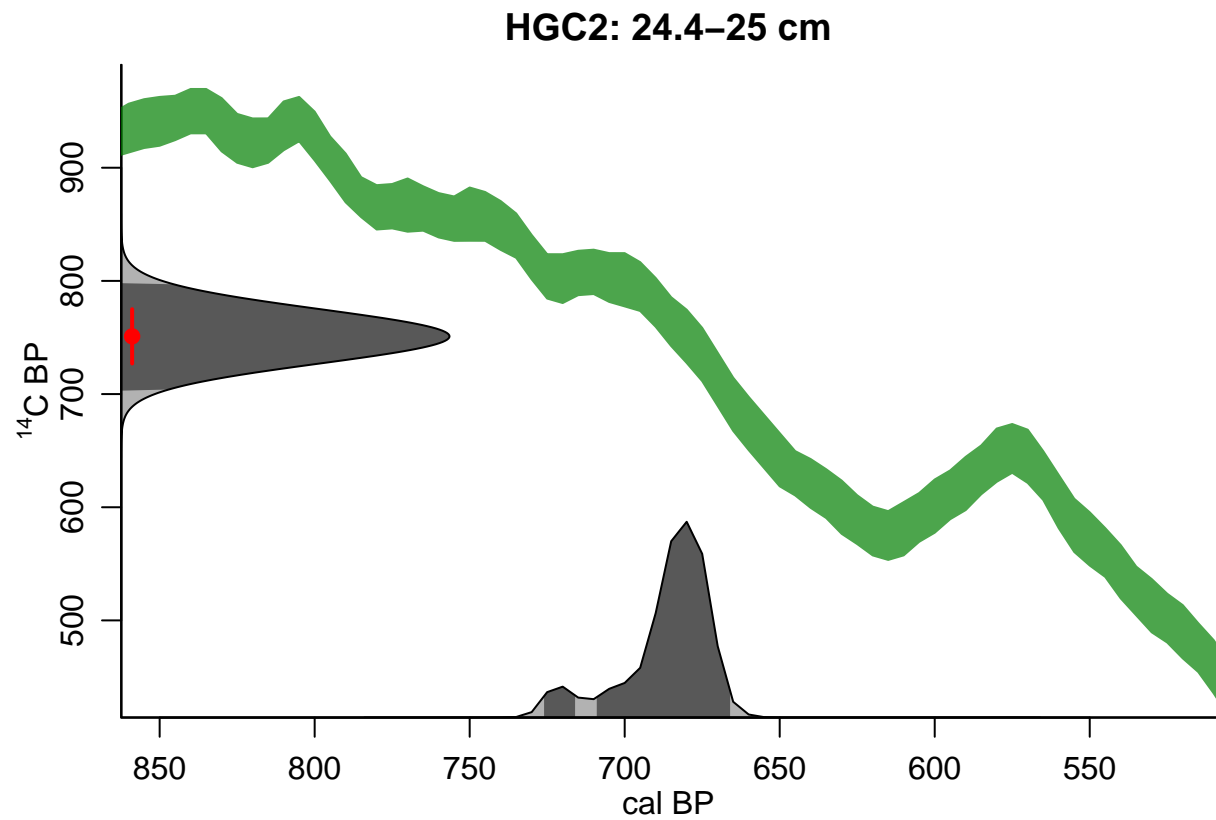
```
##
## min  max prob
## 676  731    95
```



UOC8530

```
calibrate(cage = 751, error = 24, cc = 1, title = "HGC2: 24.4–25 cm")
```

```
##
## min  max  prob
## 666  709   88.6
## 716  726    6.2
```

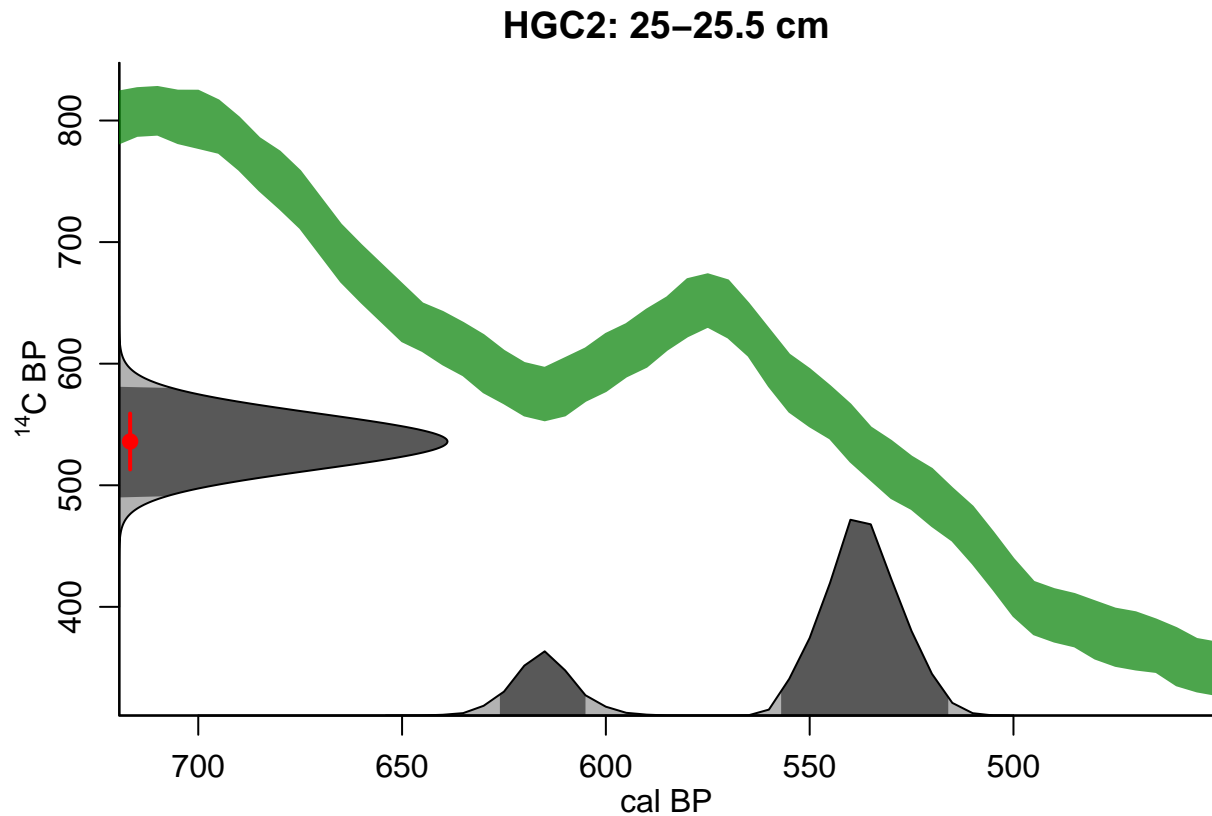


UOC6359

```
calibrate(cage = 536, error = 23, cc = 1, title = "HGC2: 25-25.5 cm")
```

```
##
## min max prob
## 516 557    78.2
## 605 626    16.6
```





## Age Depth Models

Version 000: all dates included

```
Bacon("HGC2_v000") # acc.mean 5 yr/cm; thick 1; 26 sections
```

Version 001: excluded UOC-8527, 6359

```
Bacon("HGC2_v001",
      acc.mean = 35,
      thick = 3,
      acc.shape = 1.5,
      mem.strength = 5,
      mem.mean = 0.5)
```

Version 002: version 001 + reservoir 8525

```
Bacon("HGC2_v002",
      d.min = 0,
      d.max = 25,
      d.by = 0.1,
      acc.mean = 20,
      thick = 1,
      acc.shape = 1.5,
```

```
mem.strength = 10,  
mem.mean = 0.3) # 26 sections
```

## Age Depth Model Evaluation

We want to model how deposition rate (yr/cm) and total chronological error vary in the HGC2 core. Total chronological error is simply the max age estimate for an interval minus the minimum age estimate for an interval.

Read in the age-depth model results

```
ages_000 <- read.table(file = "Bacon_runs/HGC2_v002/HGC2_v002_26_ages.txt"  
  , header = TRUE)
```

Load libraries

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
  
## The following objects are masked from 'package:stats':  
##  
##   filter, lag  
  
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(forecast)
```

```
## Registered S3 method overwritten by 'xts':  
##   method      from  
##   as.zoo.xts zoo  
  
## Registered S3 method overwritten by 'quantmod':  
##   method      from  
##   as.zoo.data.frame zoo  
  
## Registered S3 methods overwritten by 'forecast':  
##   method      from  
##   fitted.fracdiff   fracdiff  
##   residuals.fracdiff fracdiff
```

Calculate deposition rate (yr/cm) and total chronological error

```
ages_001 <- ages_000 %>%  
  mutate(diff_median = median - lag(median)) %>%  
  mutate(diff_depth = depth - lag(depth)) %>%  
  mutate(depo_cm = (diff_median/diff_depth)/10) %>%  
  mutate(depo_mean5cm = ma(depo_cm, order = 5)) %>%  
  mutate(tce = max - min)
```

## Plot Age Depth Model Evaluation

We will be creating stratigraphic plots (vs depth) of two parameters: deposition rate (yr/cm) and total chronological error (years). First we will organize the plot parameters and then create the plot

Format dataframe for plotting by selecting columns to be plotted and using the depth as the row names.

```
plot_data <- ages_001[,c(1,9,10)]
row.names(plot_data) <- ages_001$depth
plot_data$depth <- NULL
```

Define labels and ticks for x and y axes. Depo = deposition rate; tce = total chronological error.

```
# Info needed for y-axes
library("matrixStats")
```

```
##
## Attaching package: 'matrixStats'

## The following object is masked from 'package:dplyr':
##
##      count
```

```
colMins(as.matrix(plot_data), na.rm = TRUE)
```

```
## [1] 1 112
```

```
colMaxs(as.matrix(plot_data), na.rm = TRUE)
```

```
## [1] 2.8 173.0
```

```
depo.ylim <- c(0,3)
depo.yticks <- seq(0,3, by = 1)

tce.ylim <- c(100,200)
tce.yticks <- seq(100, 200, by = 25)
```

```
# Info needed for x-axis
row.names(plot_data)
```

```
## [1] "0" "0.1" "0.2" "0.3" "0.4" "0.5" "0.6" "0.7" "0.8" "0.9"
## [11] "1" "1.1" "1.2" "1.3" "1.4" "1.5" "1.6" "1.7" "1.8" "1.9"
## [21] "2" "2.1" "2.2" "2.3" "2.4" "2.5" "2.6" "2.7" "2.8" "2.9"
## [31] "3" "3.1" "3.2" "3.3" "3.4" "3.5" "3.6" "3.7" "3.8" "3.9"
## [41] "4" "4.1" "4.2" "4.3" "4.4" "4.5" "4.6" "4.7" "4.8" "4.9"
## [51] "5" "5.1" "5.2" "5.3" "5.4" "5.5" "5.6" "5.7" "5.8" "5.9"
## [61] "6" "6.1" "6.2" "6.3" "6.4" "6.5" "6.6" "6.7" "6.8" "6.9"
## [71] "7" "7.1" "7.2" "7.3" "7.4" "7.5" "7.6" "7.7" "7.8" "7.9"
## [81] "8" "8.1" "8.2" "8.3" "8.4" "8.5" "8.6" "8.7" "8.8" "8.9"
## [91] "9" "9.1" "9.2" "9.3" "9.4" "9.5" "9.6" "9.7" "9.8" "9.9"
## [101] "10" "10.1" "10.2" "10.3" "10.4" "10.5" "10.6" "10.7" "10.8" "10.9"
```

```
## [111] "11"      "11.1" "11.2" "11.3" "11.4" "11.5" "11.6" "11.7" "11.8" "11.9"
## [121] "12"      "12.1" "12.2" "12.3" "12.4" "12.5" "12.6" "12.7" "12.8" "12.9"
## [131] "13"      "13.1" "13.2" "13.3" "13.4" "13.5" "13.6" "13.7" "13.8" "13.9"
## [141] "14"      "14.1" "14.2" "14.3" "14.4" "14.5" "14.6" "14.7" "14.8" "14.9"
## [151] "15"      "15.1" "15.2" "15.3" "15.4" "15.5" "15.6" "15.7" "15.8" "15.9"
## [161] "16"      "16.1" "16.2" "16.3" "16.4" "16.5" "16.6" "16.7" "16.8" "16.9"
## [171] "17"      "17.1" "17.2" "17.3" "17.4" "17.5" "17.6" "17.7" "17.8" "17.9"
## [181] "18"      "18.1" "18.2" "18.3" "18.4" "18.5" "18.6" "18.7" "18.8" "18.9"
## [191] "19"      "19.1" "19.2" "19.3" "19.4" "19.5" "19.6" "19.7" "19.8" "19.9"
## [201] "20"      "20.1" "20.2" "20.3" "20.4" "20.5" "20.6" "20.7" "20.8" "20.9"
## [211] "21"      "21.1" "21.2" "21.3" "21.4" "21.5" "21.6" "21.7" "21.8" "21.9"
## [221] "22"      "22.1" "22.2" "22.3" "22.4" "22.5" "22.6" "22.7" "22.8" "22.9"
## [231] "23"      "23.1" "23.2" "23.3" "23.4" "23.5" "23.6" "23.7" "23.8" "23.9"
## [241] "24"      "24.1" "24.2" "24.3" "24.4" "24.5" "24.6" "24.7" "24.8" "24.9"
## [251] "25"
```

```
xlim <- c(0,25)
xticks <- seq(0, 25, by = 1)
```

Define x and y axes values for parameters.

```
depo.x <- row.names(plot_data)
depo.y <- plot_data[,1]

tce.x <- row.names(plot_data)
tce.y <- plot_data[,2]
```

Stratigraphic plots of deposition rate and total chronological error

```
# Open new plot and define dimensions
plot.new()
layout(matrix(c(1,1,2,2), 2, 2, byrow = TRUE),
        widths=c(3,3), heights=c(2,2))

# Deposition Rate
plot(depo.x, depo.y
     , type = "l", lwd = 3
     , xaxt = "n", xlim = xlim, xlab = ""
     , ylim = depo.ylim, yaxt = "n", ylab="")
)
axis(2, at=depo.yticks, labels=depo.yticks, cex.axis = 1.25)
title(main = "HGC2 Age-Depth Model Evaluation", ylab = "Deposition rate (yr/cm)", cex.lab = 1.25)

# Total Chronological Error
plot(tce.x, tce.y
     , type="l", lwd = 3, col="red"
     , xaxt = "n", xlim = xlim, xlab = ""
     , ylim = tce.ylim, yaxt = "n", ylab="")
)
axis(2, at=tce.yticks, labels=tce.yticks, cex.axis = 1.25)
axis(1, at=xticks, labels=xticks, cex.axis = 1.25)
title(ylab = "Total Chronological Error (years)", xlab = "Depth (cm)", cex.lab = 1.25)
```

