

Probabilistic models of seasonal *Bison* exploitation based on fetal prey osteometry and reproductive phenology: SUPPLEMENTAL METHODS

Ryan P. Breslawski

Tomasin Playford

Email: rbreslawski@smu.edu
Phone: +1(801)884-9451
Department of Anthropology
Southern Methodist University
PO Box 750 336
Dallas, TX 75275-0235
United States

Saskatchewan Archaeological Society
#1-1730 Quebec Avenue
Saskatoon, Saskatchewan S7K 1V9
Canada

2017

1. Skeletal Growth Models	S1
2. PSMFB.R Guide	S6
2.1. Getting started	S6
2.2. Choosing a conception distribution	S7
2.3. Entering osteometric information	S9
2.4. Evaluating a hypothesized date range	S12
2.5. Obtaining a single SODE from two or more elements	S13

1. Skeletal Growth Models

Skeletal growth models for fetal bison were developed using fetal bison growth functions (Gogan et al., 2005) in combination with osteometric data on fetal growth in domestic Jersey cattle (Richardson et al., 1990). This section corresponds with the *est.function* function in the PSMFB.R program. Each time PSMFB.R runs, *est.function* executes the algorithmic equivalent of the methods described here. This supplemental section explains how the skeletal cattle metrics were scaled to the fetal bison growth functions. This was done by linking models from each study through crown-rump length (CRL), a body length metric that was presented in each publication.

Gogan et al. (2005) present functions that relate fetal weight (g) to gestation age. They also present functions relating fetal CRL to fetal weight. There is no function relating CRL directly to gestation age. To create functions relating CRL to gestation age, RPB first considered Gogan et al.'s (2005:1724) observation that weight is equal to $CRL^{2.95}$. However, this relationship scales differently between bison herds. Gogan et al. developed these functions based on data from five Yellowstone National Park (YNP) herds, labelled, A, B, C, D, and E. Herd A was observed in 1940-1941, when YNP bison received supplemental winter feed. Herds B-E were observed in 1988-2002, when no supplemental winter feeding occurred. They present the weight-CRL relationships graphically for each herd (Gogan et al., 2015:1722), but do not state herd-specific scaling values. To estimate these scaling values, RPB first set weight to 35,000 g for each herd:

$$35,000 = CRL_h^{2.95} / s_h$$

Equation 1

Where CRL_h is the average fetal CRL for herd h when weight is 35,000 g, and s_h is the scaling factor for herd h . The 35,000 g weight was selected as it is the maximum y-axis value presented for this relationship in Gogan et al. (2005:1722), making the CRL value at this weight easy to visually estimate from the plotted relationship. RPB visually estimated CRL_h at 35,000 g for each herd based on Figure 2 in Gogan et al. (2005:1722). This allowed me to solve for s_h (Table S1). During these estimations, RPB treated herds C and E as one group since the relationships were visually indistinguishable in the plot. Henceforth, herds will be referenced as A, B, CE, and D.

Table S1. Visually estimated CRL values at 35,000 g (CRL_h) and scaling factors (s_h) for each herd.

Herd	CRL_h (mm)	s_h
A	835.25	11,893
B	907.24	15,193
CE	879.71	13,859
D	912.04	15,416

RPB translated herd weights to herd CRL values. To do so, RPB first considered the weight-age functions presented by Gogan et al. (2005:1722). They present these functions for male and female bison in both modern and historic contexts to account for differences in supplemental winter feeding practices. Age is presented in units of days. Their functions use the cube root of weight, so the right side of the equation is cubed here to keep weight consistent with other parts of this section:

$$\text{Modern female weight} = (57.26 / (1 + (age / 275.71)^{-2.05}))^3$$

Equation 2

$$\text{Modern male weight} = (66.79 / (1 + (age / 300.66)^{-2.04}))^3$$

Equation 3

$$\text{Historic female weight} = (67.54 / (1 + (age / 302.53)^{-2.04}))^3$$

Equation 4

$$\text{Historic male weight} = (80.82 / (1 + (age / 334.26)^{-2.03}))^3$$

Equation 5

An age vector of 1:320 days was passed through Equations 2-5. This yielded 320 age-dependent weights for each sex in each period (historic and modern). RPB then passed the four weight vectors into an equation that solves for CRL based on weight. This equation is rearranged from Equation 1, and parameters are herd specific:

$$CRL_{sh} = \sqrt[2.95]{s_h \times w_s}$$

Equation 6

Where w_s is a sex-specific weight vector (dependent on modern or historic context), s_h is the herd-specific scaling value (Table S1), and CRL_{sh} is a 320-bin vector of sex- and herd-specific CRL values. For herd A, CRL_{sh} was calculated with the historic male and female weights, and for herds B, CE, and D, CRL_{sh} was calculated with the modern male and female weights. Within each herd, both sex-specific vectors were averaged to estimate a mean herd-specific CRL vector.

RPB then estimated skeletal metrics for cattle using the data presented by Richardson et al. (1990). They present fetal biometrics at gestation ages of 100 days (six fetuses), 140 days (seven fetuses), 160 days (seven fetuses), 180 days (seven fetuses), 220 days (nine fetuses), and 260 days (eleven fetuses). The biometrics include CRL, tibial diaphysis length, and radial diaphysis length. RPB used the mean CRL values and the 95% tolerance limits for osteometrics at each gestation age. These tolerance limits capture 95% of the predicted osteometric variability at a given gestation age (i.e., variability contained within 1.96 standard deviations of the population mean). About 1 in 20 metric values would be expected to fall outside of these limits. Given the number of elements modelled in this study (211 between the archaeological and UWAR specimens), 95% tolerances would likely fail to capture the true gestation age for several specimens. As such, these tolerances were adjusted to 99.7% (within three standard deviations of the population mean). These more conservative tolerances produce a wider range of osteometric variability for a given gestation age, but only about 1 in 370 specimens are expected to fall outside of these tolerances. The probability that every specimen in a sample falls within these limits exceeds 0.5 for up to 256 observations. This is in contrast with the 95% tolerances, where the probability that every specimen falls within the limits stays above 0.5 for sample sizes of up to only 13.

RPB fit generalized logistic growth functions to the tolerance values using R's *nls* function (Table S2; Figure S1a,b). During model fitting, each tolerance value was weighted by the sample size of fetuses that contributed to its estimation:

$$metric = K / ((1 + Qe)^{-B \times age})$$

Equation 7

Table S2. Parameter estimates and standard errors for fetal cattle growth metrics (mm).

Metric		<i>K</i>	<i>Q</i>	<i>B</i>
Tibial diaphysis length	99.85% tolerance limit	265.1 ± 15.61	76.3 ± 7.7	1.9E-2 ± 9.8E-4
	0.15% tolerance limit	242.6 ± 26.8	78.9 ± 10.8	1.9E-2 ± 1.5E-3
Radial diaphysis length	99.85% tolerance limit	194.5 ± 11.2	68.2 ± 8.7	2.0E-2 ± 1.2E-3
	0.15% tolerance limit	178.9 ± 24.4	61.7 ± 10.5	1.8E-2 ± 1.9E-3
CRL	mean	1174.0 ± 57.5	23.2 ± 1.7	1.6E-2 ± 8.4E-4

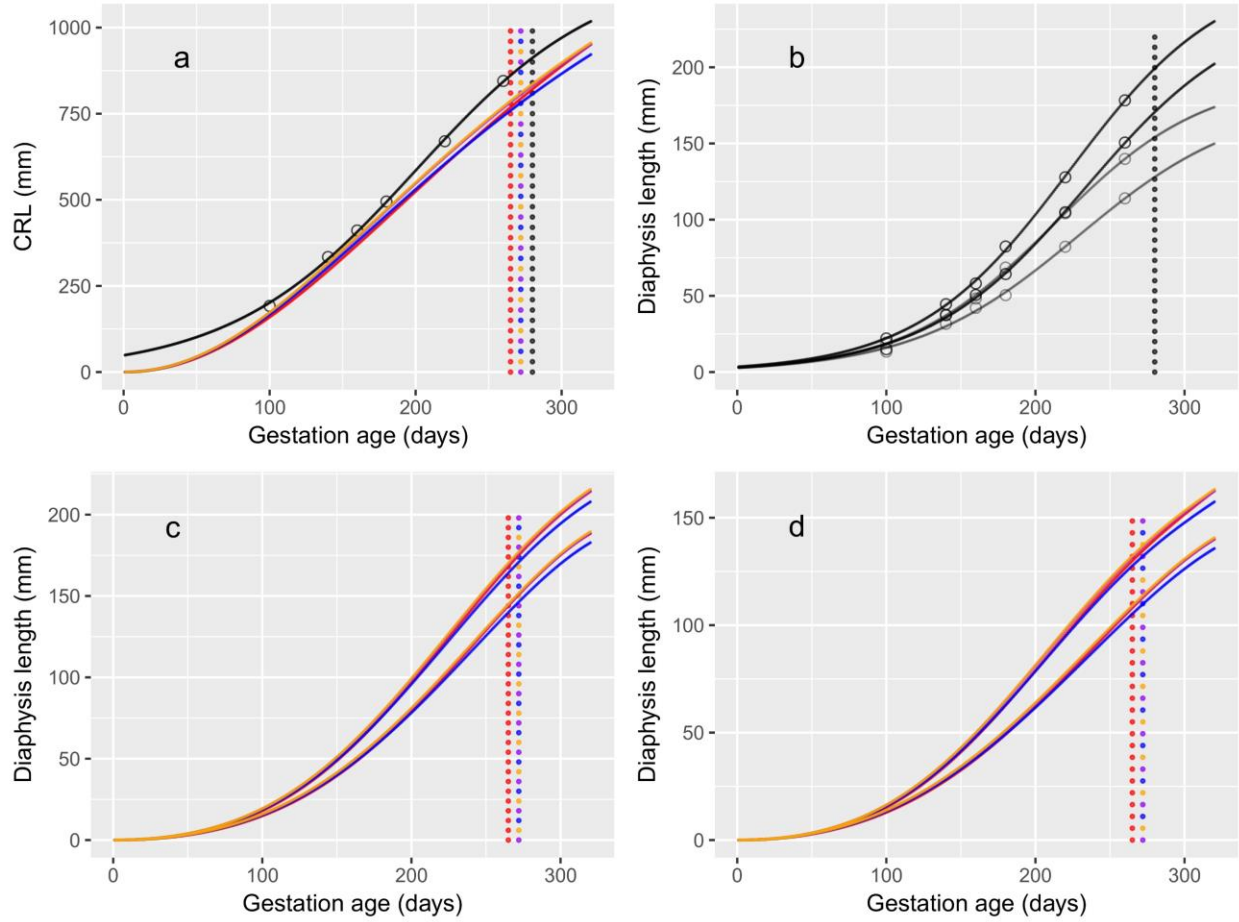


Figure S1. Fetal biometrics simulated over 320 days: (a) mean CRL for bison and cattle, (b) 99.7% tolerances for tibial (black) and radial (grey) diaphysis lengths in cattle, (c) 99.7% tolerances for bison tibial diaphysis lengths, and (d) 99.7% tolerances for bison radial diaphysis lengths. Black and grey lines are cattle growth and open circles correspond to observations published in Richardson et al. (1990). Other line colors correspond to YNP bison herds published in Gogan et al. (2005): red = herd A; purple = herd B; blue = herd CE; orange = herd D. Vertical dotted lines mark average gestation lengths: grey = 280 days for Jersey cattle; red = 265 days for historic YNP bison; purple, blue, and orange = 272 days for modern YNP bison.

Metric vectors were then simulated for ages of 1:320 days with each growth model. Osteometric mean vectors were generated by averaging the tolerance vectors for each element. Each tolerance vector was converted to a proportion of the mean for each element ($OP_{0.15t}$ and $OP_{99.85t}$ for the 0.15% and 98.85% tibia tolerances; $OP_{0.15r}$ and $OP_{99.85r}$ for the 0.15% and 99.85% radius tolerances). Averaged element metrics vectors were transformed into proportions of mean CRL (CP_t for the tibia and CP_r for the radius).

Prior to scaling the cattle osteometrics to fetal bison growth, RPB adjusted the cattle vectors to account for gestation length differences between taxa. The mean gestation length for Jersey cattle is 280 days (Norman et al., 2009:2261), whereas it is 265 days for historic bison and 272 days for modern bison (Gogan et al., 2005). First, a 320-bin vector was created that scales 320 days at a 280-day gestation length into 320-bin vectors for 272- and 265-day gestation lengths:

$$age_{period} = (agec/280) \times GL_{period}$$

Equation 8

Where age_{period} is a vector of gestation ages for bison within a period (modern or historic), $agec$ is a vector of gestation ages for domestic cattle, and GL_{period} is the gestation length for bison specific to modern or historic herds.

Using R's *lm* function, RPB parameterized a series of quintic polynomial functions to describe the relationships between the rescaled age vectors and the metric proportion vectors (i.e., $OP_{0.15t}$, $OP_{99.85t}$, $OP_{0.15r}$, $OP_{99.85r}$, CP_t , and CP_r). All quintic functions produced adjusted R^2 values exceeding 0.999, indicating that they provide accurate descriptions of the relationships between rescaled age vectors and metric proportion vectors. These functions allowed for metric proportion vectors to be simulated for 1:320 days under the bison gestation lengths rather than the 280-day cattle gestation length. Variable names for the rescaled metric proportion vectors received the prefix *R*.

The CRL vectors for bison herds A-E were multiplied by RCP_t , and RCP_r to produce two new vectors for each herd. Herd A was multiplied by the metric proportion vectors scaled by historic gestation lengths and herds B-E were multiplied by the metric proportion vectors scaled by modern gestation lengths. This produced mean osteometric vectors for each element within each herd. The mean osteometric vectors were multiplied by $ROP_{0.15t}$, $ROP_{99.85t}$, $ROP_{0.15r}$, and $ROP_{99.85r}$ to produce 99.7% osteometric tolerance limits for each element within each herd (Figure S1c,d). For each day in 1:320, RPB obtained the maximum 99.85% osteometric value and the minimum 0.15% osteometric value between herds for both radial and tibial diaphyses. This yields 99.7% tolerance limits for the range of metric variability through the gestation period between the YNP herds. These tolerance limits are not continuous functions, but discrete values corresponding to whole days of growth in the gestation period.

Using these models of tibial and radial diaphysis growth, RPB estimated similar growth models for the scapula, humeral diaphysis, and femoral diaphysis. To do so, RPB evaluated the metric relationships between these elements with 21 fetal bison skeletons curated at the University of Wyoming Archaeological Repository (UWAR) and another fetal bison skeleton from YNP. The metric values for these skeletons are stored as vectors within PSMFB.R: *hl* contains humerus lengths, *rl* contains radius length, *fl* contains femur lengths, *tl* contains tibia lengths, and *sl* contains scapula lengths. Occasionally, broken/weathered surfaces or missing specimens prevented measurement, in which case the vectors contain 'NA' values. The *lm* function was used to evaluate the relationships between these metrics, with tibial diaphysis length as a predictor for femoral diaphysis length and radial diaphysis length as a predictor for the other two forelimb element metrics. The linear model intercepts were set at zero to ensure that metric values in one element always correspond with positive values in another element (i.e., the linear models will not predict negative metric values). None of these models were fit to the full sample of right and left elements for all 22 fetuses due to sporadic 'NA' values. The models indicate strong predictive relationships between these metrics (Table S3).

Table S3. Linear models for the relationships between length metrics.

Model	<i>n</i>	β and std. error	Adjusted R^2
humeral diaphysis length = $\beta \times$ radial diaphysis length	38	1.023 ± 0.004	>0.999
scapula length = $\beta \times$ radial diaphysis length	22	1.159 ± 0.006	>0.999
femoral diaphysis length = $\beta \times$ tibial diaphysis length	38	0.908 ± 0.004	>0.999

Application of these linear models to the 99.7% tolerance growth vectors for radial and tibial diaphysis lengths generated generated 99.7% tolerance growth vectors for humeral diaphysis, scapula, and femoral diaphysis lengths. Thus, each osteometric has two 320-bin vectors simulating the 99.7% limits of growth over 320 gestation days. Although the average bison gestation length is shorter than 320 days, these growth vectors can accommodate fetuses that have been gestating longer than that average. Graphical representations of these vectors are shown in Figures 4 and 5 of the main text.

2. PSMFB.R Guide

2.1. Getting started

Download the PSMFB.R file to a directory that you prefer to work from. To execute the program, you will need to download and install R (<https://www.r-project.org/>). Users who prefer to use RStudio can also run PSMFB.R through this interface (<https://www.rstudio.com/>). On some machines, users may notice that graphical outputs display slower in RStudio than in R. Start an R session and install the following packages from a CRAN mirror: *ggplot2*, *gridExtra*, *reshape2*, *stringi*, and *smoother*. Without these packages, PSMFB.R will experience errors and stop.

To run PSMFB.R, use the *source* command from the R or RStudio console. You can type `source("filepath/PSMFB.R")`, or set the working directory to the file location and type `source("PSMFB.R")`. After pressing [enter], the program will execute and display introductory information. There are three paragraphs of text outlining the program. You can cycle through these by pressing any key.

```
R version 3.3.2 (2016-10-31) -- "Sincere Pumpkin Patch"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> source("PSMFB.R")
```

Running PSMFB.R from the R console with the working directory set to the file location.


```

> source("PSMFB.R")
Loading required package: TTR

**** PSMFB.R **** PSMFB.R **** PSMFB.R ****
*** Probabilistic Seasonality Models for Fetal Bison Osteometrics ***

- Built in R version 3.3.2 -- 'Sincere Pumpkin Patch'
- Last updated on March 15, 2017.
- Report bugs or make suggestions: rbreslawski@smu.edu
- Required packages: ggplot2, gridExtra, reshape2, stringi, smoother
PSMFB.R provides numerical and graphical season of death estimates (SODEs)
for fetal bison specimens based on radius, humerus, scapula, tibia, and
femur osteometrics.

Press any key to continue.

```

Initial block of introductory text when PSMFB.R is executed.

```

The program will first prompt you to select a baseline distribution for the begin-
ning of the gestation period. These distributions are based on observations of modern
bison, and you may select whichever distribution is most applicable to the ecological
context of the bison specimens that you are analyzing. In many cases, the ecological
contexts of bison populations are uncertain (i.e., archaeological and paleontological
studies), and for these cases there are 'generalized' distributions that pool observ-
ations from multiple herds rather than any one modern herd.

Press any key to continue.

After a baseline distribution for the beginning of the gestation period is select-
ed, you will be prompted to enter the number of skeletal specimens to be analyzed as
well as metric values (in mm) for the lengths of each element. Alternatively, you will
be given the option to upload a csv table of elements and metric values. After metrics
have been entered or uploaded, the program will plot and print SODEs for each element.

Following these SODEs, you will be presented with options for further analysis. One
of these options allows you to specify a date interval for a 'season of death' hypothesis.
The program returns a SODE based probability that elements fall within this hypothesized
interval (with graphical output). Additionally, you may combine multiple elements from a
single fetus into a single more informed SODE. SODEs based on multiple elements can be
subjected to further analyses.

Press any key to begin.

```

The final two blocks of introductory text.

2.2. Choosing a conception distribution

After cycling through the introductory text, the program will prompt you to select a conception schedule. Fourteen conception distributions are displayed as text with a leading index value, [i]. Additionally, the program produces a graphical representation of each conception distribution. You will need to expand the plotting window to read these plots (otherwise, the text and geometry runs together). The plots may not display immediately, but they should load in less than one minute. If they do not display immediately, do not resize the blank plotting window, as this may cause an error. After the plots have loaded, it is safe to resize the plotting window.

The odd index numbers correspond to sample data, and the even index numbers correspond to 3-week smooths of these data as approximations of the underlying distributions from which the samples were drawn. In the main paper, the bulk of the analyses were completed with conception distribution 2, but the modern YNP fetus example was completed with conception distribution 4. The first 10 distributions correspond to the fetal biometric estimations of conception dates. Distributions 11-14 correspond to

behavioral observations related to rutting activity, which may also be associated with the probability of conception. When you have decided on a conception distribution, type the corresponding index number next to the prompt and hit [enter]. If you enter an integer outside of 1-14 or any other invalid character, you will receive an error message and the opportunity to re-enter your index of choice.

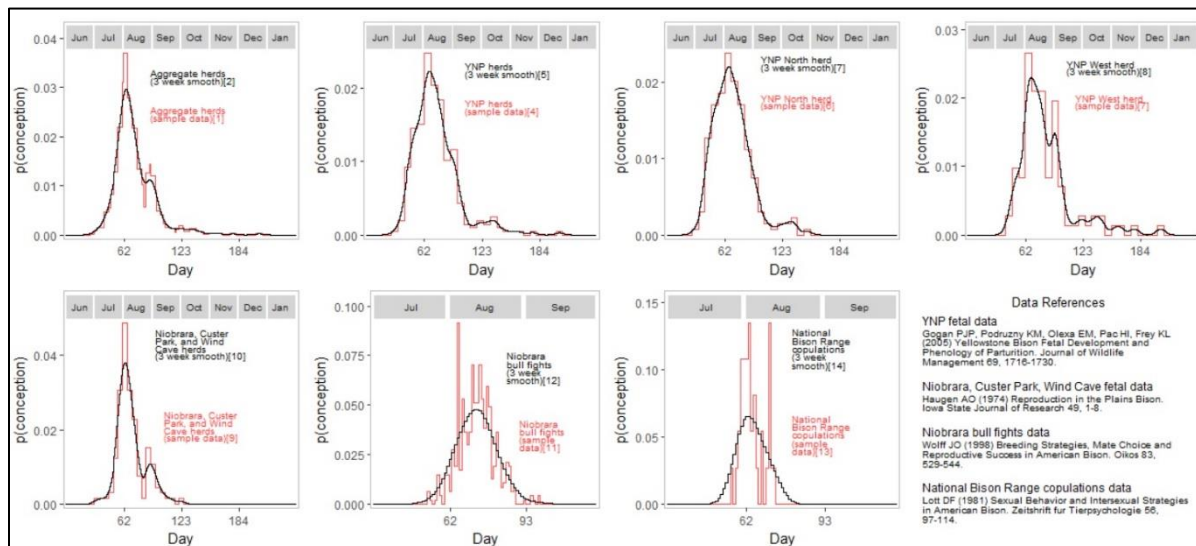
```
[1] Aggregated YNP, Custer State Park, and wind cave herds, based on fetal data (n = 428) [sample data].
[2] Aggregated YNP, Custer State Park, and wind cave herds, based on fetal data (n = 428) [3 week smooth].
[3] YNP western and northern herds, based on fetal metrics (n = 297) [sample data].
[4] YNP western and northern herds, based on fetal metrics (n = 297) [3 week smooth].
[5] YNP northern herd, based on fetal metrics (n = 192) [sample data].
[6] YNP northern herd, based on fetal metrics (n = 192) [3 week smooth].
[7] YNP western herd, based on fetal metrics (n = 105) [sample data].
[8] YNP western herd, based on fetal metrics (n = 105) [3 week smooth].
[9] Custer State Park and wind cave, based on fetal metrics (n = 131) [sample data].
[10] Custer State Park and wind cave, based on fetal metrics (n = 131) [3 week smooth].
[11] Niobrara bull fights (n = 1088)[sample data].
[12] Niobrara bull fights (n = 1088)[3 week smooth].
[13] National Bison Range copulations (n = 37)[sample data].
[14] National Bison Range copulations (n = 37)[3 week smooth].

select a conception distribution (refer to plots for visual reference, expand or zoom
for a better view of each calendar model. Y-axis days are zeroed on June 1). The aggreg-
ated fetal samples gives the most 'generalized' distribution (Index 1). The smoothed
version of this distribution approximates the population from which the sample data were
drawn (Index 2).

Generating conception calendar plots...

Calendar index (integer value):
```

Conception distribution options displayed on the R console. Calendar index (integer value): will not display until the associated plots have loaded.



Conception distribution plots in an expanded plotting window.

After selecting a conception distribution, the program will prompt you to display the growth curves for each element. If you wish to display the curves, type `y0` and press [enter]. If you wish to display the growth curves with the UWAR fetal metrics printed over these curves, type `y1` and press [enter]. If you want to skip this step, you can press any other key to proceed. If you display a growth curve plot, you will be prompted to press another key to proceed after the plot has been generated.

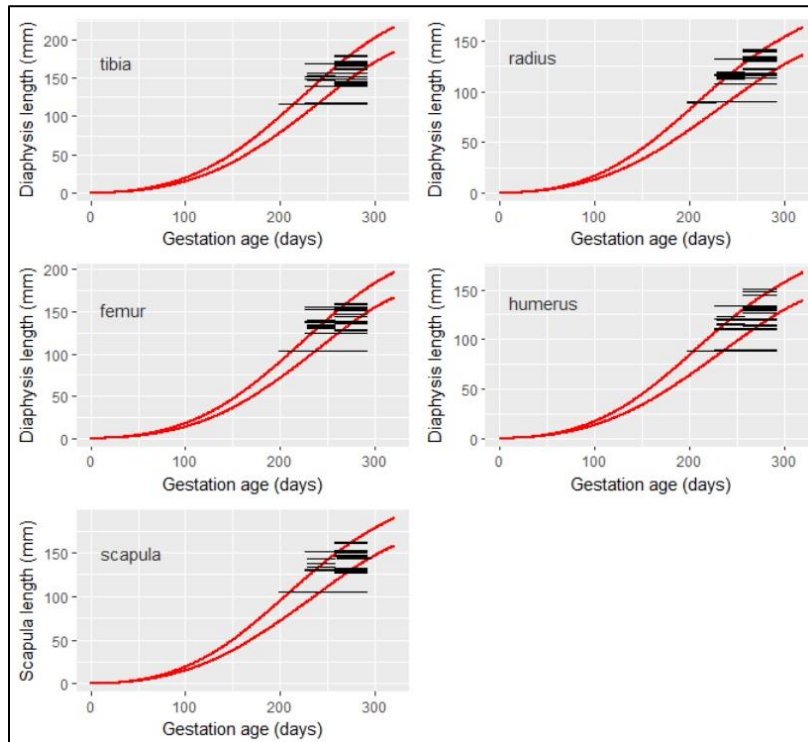

```

Calendar index (integer value): 2
Model conception calendar 2 successfully selected.

Would you like to plot the growth curves?
[y0] Plot growth curves.
[y1] Plot growth curves overlaid with UWAR fetal metrics.
[any other key] Do not display a plot.
y1
Press any key to continue.

```

Growth curve plotting options displayed in the R console. Here, the user has opted to display the growth curves with the UWAR fetal metrics (y1). The program is waiting for the user to press another key to proceed.



Growth curve plot with UWAR fetal metrics (y1).

2.3. Entering osteometric information

After selecting a conception distribution, the program will prompt you to enter metric data. These data are entered as individual specimen lengths in units of mm. The first prompt asks whether you would like to enter values manually through the R console (m) or upload a csv table of metric values (u). If a character other than u or m is entered, the program will display an error message and prompt you to re-enter a method for data entry.

If manual entry is selected (m), the program will prompt you to enter the number specimens that are included. Enter a positive integer x indicating the number of entries that you will make. The program will then repeat a prompt x times that requires you to enter an element type and its associated length metric. Valid element types include *scapula*, *humerus*, *radius*, *femur*, and *tibia*. Do not capitalize or abbreviate element types. The program can read length entries in whole mm (e.g., 93) or entries with sub-mm digits (e.g., 93.44). After all specimens have been entered, the program will display season of death estimates (SODEs) as text descriptions and plots.

If data are uploaded rather than entered through the R console (u), the program will first display text that describes how the table should be formatted. The table should be saved as a csv file with two columns; the first column is for element types and the second column is for length metrics. Element types and length metrics should be formatted as specified in the preceding paragraph. The program also reads the first row as a header. If the first row of your table includes data instead of a header, this row will be excluded from analysis. To upload the csv table, press any key; this will open a window to navigate to the csv file. If data are incorrectly formatted, the program will display an error and give you the opportunity to upload a correctly formatted table. If you cancel out of the file navigation window, the program will stop. After a correctly formatted table has been uploaded, the program will display season of death estimates (SODEs) as text descriptions and plots.

```
would you like to manually enter metric values for each specimen ('m')
or upload an existing csv table of elements with metric values ('u')? m

How many specimens will be input (enter an integer)? 4

Valid element types: 'radius', 'humerus', 'scapula', 'tibia', or 'femur'.
Press ENTER after each entry.

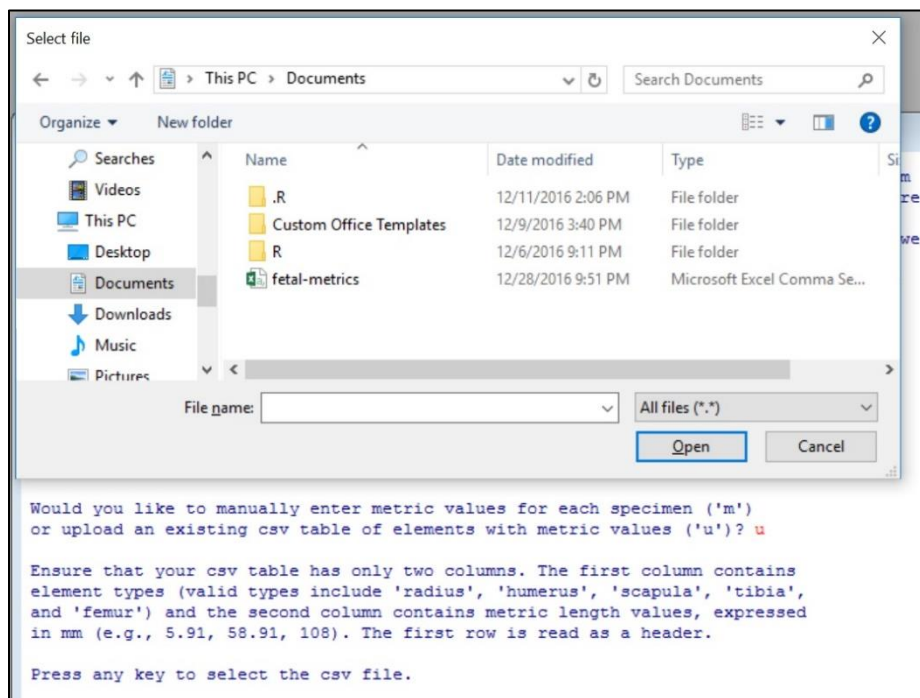
What type of element is entry 1? femur
Enter the length of this element in mm (format xx.xx): 91.16

What type of element is entry 2? tibia
Enter the length of this element in mm (format xx.xx): 106.04

What type of element is entry 3? tibia
Enter the length of this element in mm (format xx.xx): 102.61

What type of element is entry 4? scapula
Enter the length of this element in mm (format xx.xx): 95.51
```

R console display showing prompts for manual specimen entry where the user has entered four specimens.

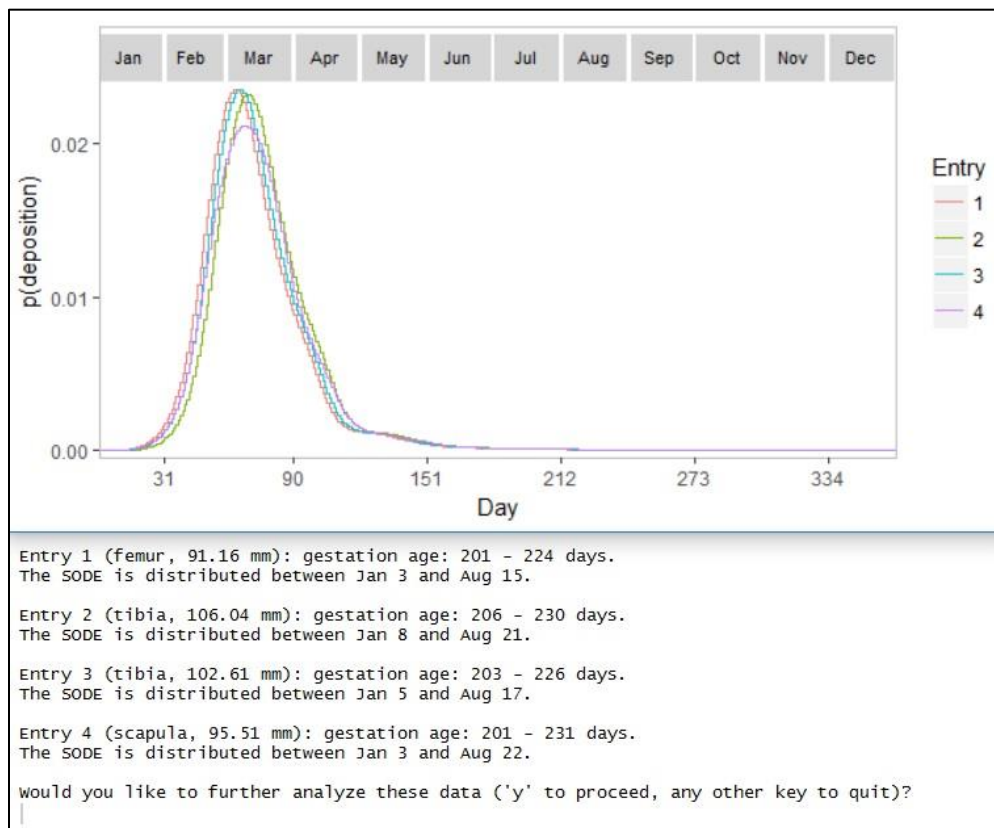


R console display overlaid by a file navigation window that has opened as a result of the user opting to upload a csv table of length metrics.

During either manual data entry or a csv upload, the program might present an error indicating that a metric value is outside of the modelled range of fetal bison metrics. This error indicates that for an entry, the value was either too large or small to fit within the bounds of the growth models. In most cases, this will arise if a value is too large. If such an error displays, ensure that the entry is indeed a fetal element as opposed to a calf element that falls outside of the range of modelled metrics. The program cannot proceed with metric values that exceed the range of modelled values.

After all length metrics have been successfully entered, the program will display SODEs. In the R console, text will specify the gestation age range associated with each entry as well as the dates that bound its SODE. The plotting window will show how the probability of deposition varies across each entry's SODE. Plotted SODEs are distinguished by color. The plot legend may not display SODE colors in the standard R interface, although the colors will be visible in a saved PDF. The legend should display SODE colors in the RStudio plotting window if the extent of the window is expanded sufficiently.

Finally, the program will prompt you to further analyze the SODEs. If you would like to obtain the probability that any fetal elements fall within a specific date interval, or if you would like to use multiple SODEs to generate a posterior SODE (the latter option is only available if you have SODEs for at least two specimens), type `y` and hit [enter]. If you do not want to do any further analysis, press any other key to exit the program



R console displaying SODEs for four elements. The console is overlaid by a plot showing the SODE distributions.

```
would you like to further analyze these data ('y' to proceed, any other key to quit)? y

['c'] obtain a single SODE from multiple elements. If multiple
      elements are from a single fetus, they should represent the same
      death date. This function constrains the gestation age range from
      multiple elements to obtain a narrow and more informative SODE.
['i'] Find the probability that one or more elements share a death date
      within a date interval or at any point during the year.
[any other key] Quit, no further analyses.
```

R console displaying options for a user that has indicated that they would like to perform further analyses with the SODEs (y). The option to generate a posterior SODE is available since the user is examining SODEs from more than one element.

2.4. Evaluating a hypothesized date range

Entering `i` allows you to assess the probability that one or more elements were deposited within a hypothesized date range or the probability that one of more elements were deposited on the same date. This analysis first prompts the user to indicate which entries they would like to include in the analysis. These must be entered as comma-and-space-separated positive integers. Press [enter] when you have finished.

The program will prompt you to indicate the dates that bound your hypothesis. Dates are indexed as 1:365, and a list of indexed dates prints out for easy reference. Enter only two dates, separated by a comma and space. If you do not have a specific hypothesized date range, but would still like to obtain the probability that two elements were deposited on the same date, type `1, 365` and press [enter].

The R console and plotting window will return several items. First, the R console displays the probability that the elements were deposited on the same date within the hypothesized date interval. If there was no hypothesized date interval, then the R console displays that probability that the elements were deposited on the same date across the entire year. Next, the R console displays the probability that all elements were deposited within the date interval. This differs from the first probability in that the elements may have been deposited on different dates within the hypothesized interval. This second probability is not displayed if a hypothesized date range was not specified.

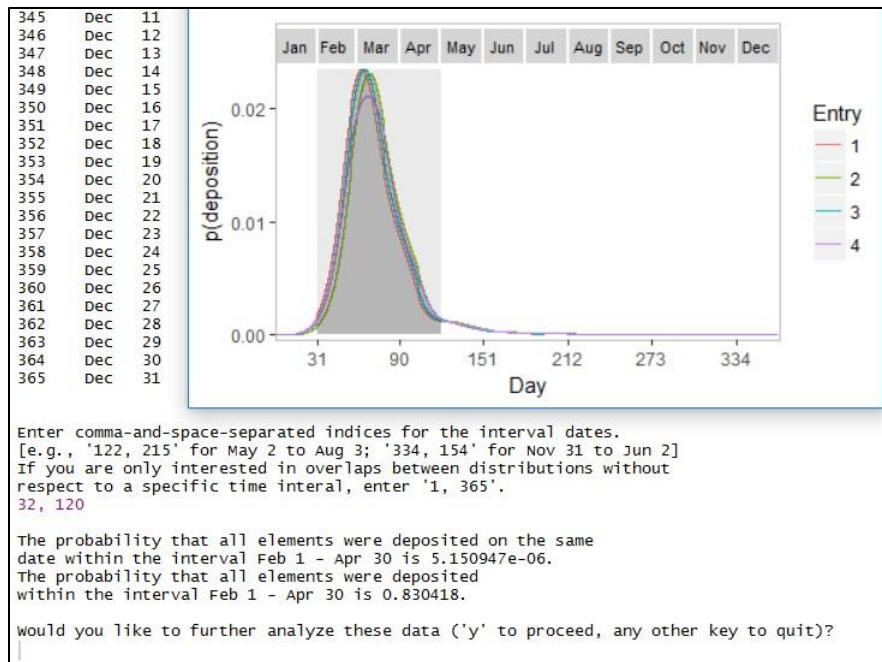
The plotting window will display color-differentiated SODE distributions for the selected elements. The plot legend may not display SODE colors in the standard R interface, although the colors will be visible in a saved PDF. The legend should display SODE colors in the RStudio plotting window if the extent of the window is expanded sufficiently. A transparent red polygon indicates the hypothesized date interval. Semi-transparent red geometry indicates where at least one SODE overlaps the hypothesized interval. Opaque red geometry indicates where all SODEs overlap the hypothesized interval. Finally, you will be presented with the option to exit the program or to undertake more analyses (e.g., evaluate other date intervals or obtain a posterior SODE).

```
i

** ANALYSIS: DATE INTERVALS AND SODE OVERLAPS**

Enter comma-and-space-separated indices for the SODEs that
you would like to include. [e.g., '1, 3, 8, 26, 15']
1, 2, 3, 4
```

R console display showing a user that has entered four SODEs to be included in the analysis.



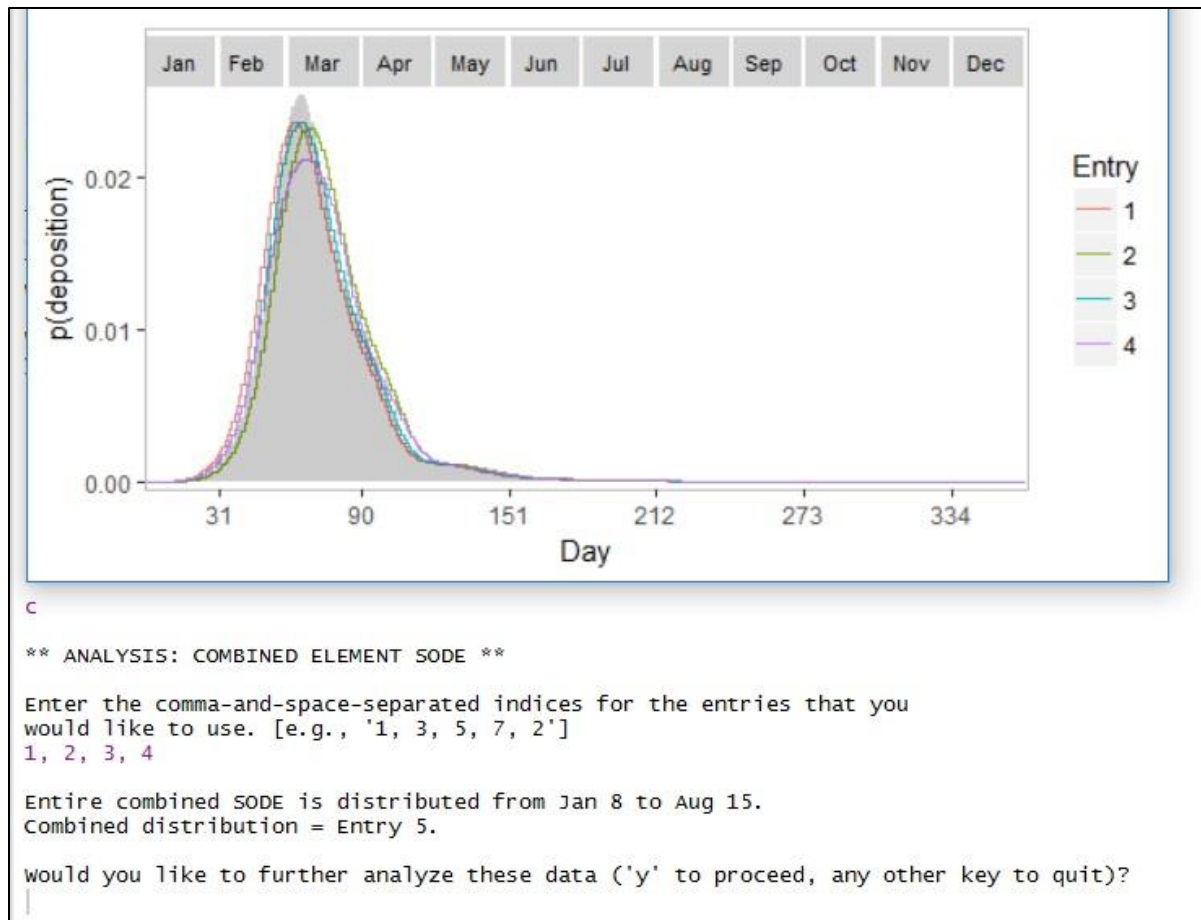
R console results overlaid with plotting window output. The user hypothesized a date interval of February 1 through April 30 (as indicated by the indices 32, 120). The console displays the probability that all four elements were deposited on the same date within the interval, as well as the probability that all elements were deposited on any date within the interval. The plotting window displays each SODE with the hypothesized date interval indicated by a transparent red rectangle. The semi-transparent regions show where at least one SODE overlaps the hypothesized interval. The opaque red region shows where all SODEs overlap the hypothesized interval.

2.5. Obtaining a single SODE from two or more elements

If you have entered two or more elements, the program presents the option to obtain a combined SODE from multiple elements. This analysis assumes that the two elements originate from a single fetus, and therefore can be used to obtain a better constrained gestation age. This is accomplished by setting the minimum gestation age to the largest between-element minimum gestation age and by setting the maximum gestation age to the smallest between element maximum gestation age.

The analysis prompts you to indicate the entries to be used to calculate the combined element SODE. Type these numbers, separated by commas and spaces, and press [enter]. The R console then displays the dates bounding the posterior SODE as well as a new entry designation. The combined element SODE is stored as a new entry so that it can be used for other analyses, such as finding the probability that it falls within a hypothesized date interval. The plotting window will display color-differentiated SODE distributions for the selected elements. The plot legend may not display SODE colors in the standard R interface, although the colors will be visible in a saved PDF. The legend should display SODE colors in the RStudio plotting window if the extent of the window is expanded sufficiently. The posterior SODE is represented by a semi-transparent grey distribution.

After obtaining the posterior distribution, the program presents the user with the option to quit or proceed with further analyses, such as evaluating hypothesized date intervals.



R console results overlaid with plotting window. The user included all four elements for the combined SODE analysis. The console displays the dates bounding the combined element SODE and its entry designation. The plotting window displays each color-differentiated SODE with the combined SODE symbolized by a semi-transparent grey fill.