

Review of R and RStudio

EES 5891-03

Bayesian Statistical Methods

Jonathan Gilligan

Class #5: Thursday, September 08 2022

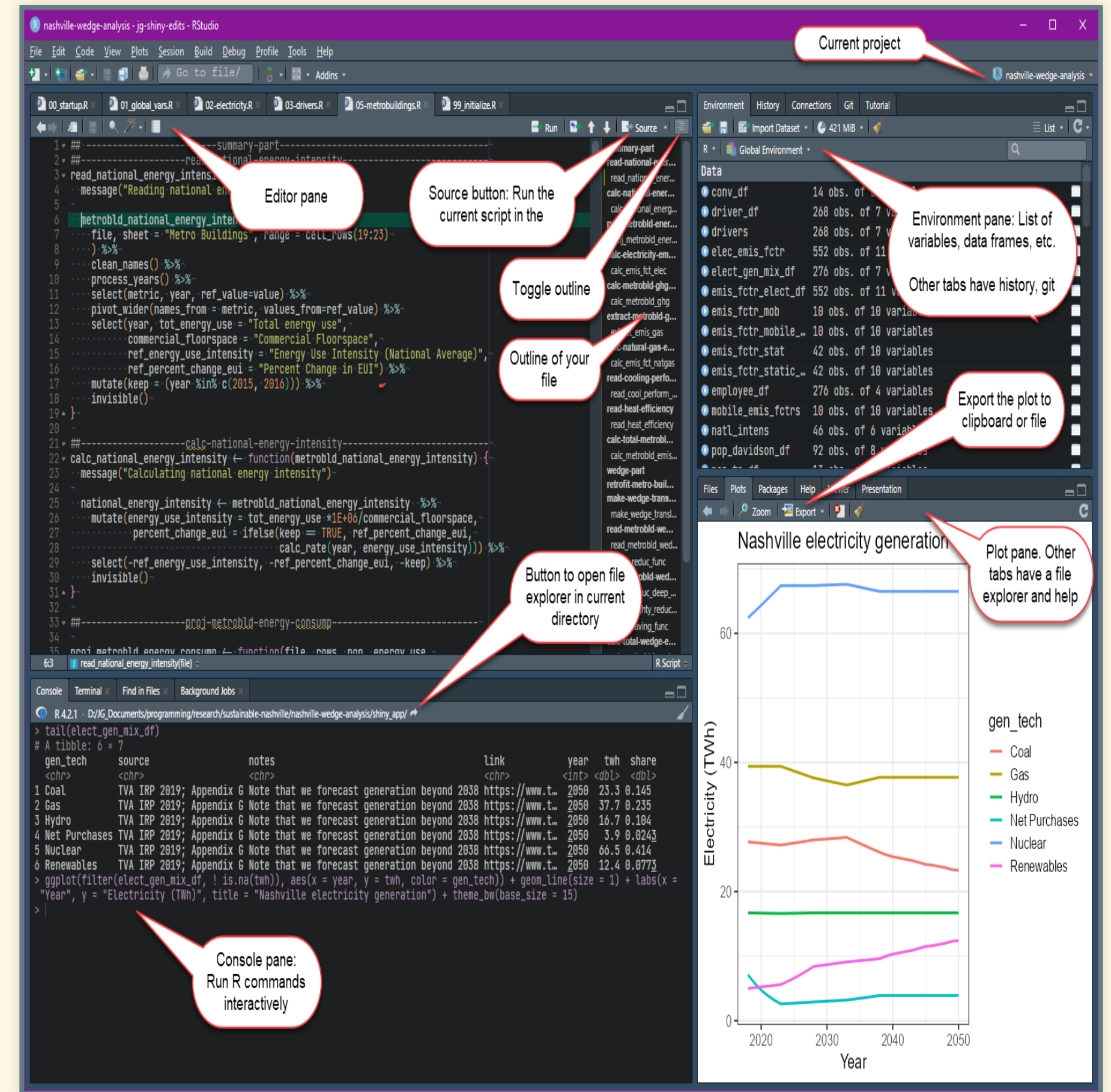
Announcement

- I have updated the instructions for configuring R and downloading necessary packages (in Homework #1 and on the “Tools” page of the web site).
- The `rethinking` package now uses `cmdstanr` as its default for Monte Carlo sampling, instead of `rstan`. `cmdstanr` is more reliable and up to date; `rstan` is being phased out.

Overview of Rstudio

RStudio Window layout

- Project oriented
 - A project is a directory with a group of related files (R, data, etc.)
 - A project can be managed with [git](#) for revision control
 - Create a new project:
 - Create a new directory for a project
 - Create a project in an existing directory
 - Download a project from GitHub or another external source, using [git](#)
- Online help and cheatsheets
- Window layout
 - Four panes:
 1. Editor pane (edit R scripts, text files, etc.)
 2. Console and Terminal pane (interactively run R commands, etc.)
 3. Files, Plots, Packages, Help, etc.
 - You can export plots to the clipboard or files.
 4. Environment, History, Git, etc.



R Language

R Language

- R is flexible
- Two approaches
 - Base R
 - Very flexible and powerful
 - Sometimes confusing and verbose
 - Nothing special about data frame (`data.frame`)
 - Tidyverse (`library(tidyverse)`)
 - Unified philosophy of data analysis
 - Canonical reference: [R for Data Science](#)
 - Oriented toward `data.frames` (and `tibbles`)
 - Principles of “Tidy Data”
 - Consistent approach makes it easy to figure out how to do what you want to do.
 - Download extensive cheatsheets via RStudio help menu.

Graphics

- Base R

- `plot` command

```
plot(x, y) # plot y vs. x with points
plot(x, y, type = "l") # plot with a line
plot(height ~ weight, data = df) # with a data.frame
```

- Tidyverse/`ggplot2` (`library(tidyverse)` or `library(ggplot2)`)

- `ggplot` command

```
data(Howell1)
ggplot(Howell1, aes(x = weight, y = height)) +
  geom_point() +
  labs(x = "weight (kg)", y = "height (cm)",
       title = "!Kung San height and weight")
ggplot(Howell1, aes(x = weight, y = height)) +
  geom_point(aes(shape = male, size = age),
            "color = "magenta") +
  labs(x = "weight (kg)", y = "height (cm)",
       title = "!Kung San height and weight")
```

- Philosophy: Grammar of Graphics

- online manual <https://ggplot2-book.org/>
- data, mapping (aesthetics), layers (geometries), scales, coordinates, facets, and themes
- You can combine and adjust these different parts separately.

Data

- Base R
 - Separate 1-dimensional lists or vectors of data
 - 2D (or higher) arrays: `data.frame`, `array`, `matrix`
 - Index rows and columns `Howell1[107, 3]`
 - `Howell1[107,]` for all columns of the row
 - `Howell1[, "height"]` for all rows of the "height" column
 - `Howell1[c(1, 3, 5), 10:15]` to get rows 1, 3, and 5 of columns 10–15.
 - `Howell1["age" >= 18, c("height", "weight")]`
- Tidyverse (`library(tidyverse)`)
 - `data.frame`
 - `tibble` (an enhanced `data.frame`)
 - Select columns:

```
select(Howell1, height, weight, age)
select(Howell1, -male, -age)
```

 - Select all columns that start with "foo_" but don't end with "bar"

```
select(my_data, starts_with("foo_"),
      -ends_with("bar"))
```
 - Select rows:

```
filter(Howell1, age >= 18, male)
```


Tidyverse Data Manipulations

- Modifying data: `mutate`

```
mutate(Howell1, hgt_std = (height - mean(height)) /  
sd(height),  
      wt_std = (weight - mean(weight)) /  
sd(weight))
```

- Summarizing data

```
summarize(d, height = mean(height), weight =  
mean(weight))  
d_tmp <- group_by(d, male)  
d_tmp <- summarize(d_tmp, height = mean(height),  
                  weight = mean(weight))  
d_tmp <- ungroup(d_tmp)
```

- Pivot tables: `pivot_longer`, `pivot_wider`
 - Example using `relig_income` data

Pipe operator

- It can get confusing to combine multiple commands

```
ungroup(summarize(group_by(filter(Howell1, age >= 18), male),  
  height = mean(height), weight = mean(weight)))
```

- Pipe commands allow us to break this up:

```
Howell1 %>% filter(age >= 18) %>%  
  group_by(male) %>%  
  summarize(height = mean(height), weight = mean(weight)) %>%  
  ungroup()
```

- The pipe operator `%>%` sends its input (what's on the left) to the first argument of the function on the right.
 - `Howell1 %>% filter(age >= 18)` is the same as `filter(Howell1, age >= 18)`
 - `Howell1 %>% filter(age >= 18) %>% group_by(male)` is the same as `group_by(filter(Howell1, age >= 18), male)`

Sampling from models

- Base R

```
mdl <- quap(alist(  
  height ~ dnorm(mu, sigma),  
  mu <- a + b * weight,  
  a ~ dnorm(178, 20),  
  b ~ dlnorm(0, 1)  
  sigma ~ dunif(0, 50)  
), data = d2)  
w_lst <- data.frame(weight = seq(30, 70, by =  
5))
```

- Sample from posterior predictive distribution for data (e.g., `height`):

```
extract.samples(mdl, 1000)
```

- Sample from posterior of model link (`mu`):

```
link(mdl, w_lst)
```

- Tidyverse (`library(tidyverse)`)

```
library(tidybayes)  
library(tidybayes.rethinking)
```

- Sample from posterior predictive distribution for data (e.g., `height`):

```
predicted_draws(w_lst, mdl, ndraws = 1000,  
                value = "height")  
add_predicted_draws(mdl, w_lst, ndraws = 1000,  
                    value = "height")
```

- Sample from posterior of model link (`mu`):

```
linpred_draws(w_lst, mdl, ndraws = 1000,  
              value = "height")  
add_linpred_draws(mdl, w_lst, ndraws = 1000,  
                  value = "height")
```

- `add_` versions are the same, but reverse the order of the first two arguments (model object and new data).

Splines

Splines

- Originally from mechanical drafting splines
- Arbitrary smooth curve
- Complexity:
 - Physical splines: “ducks” or “whales”
 - Mathematical splines: “knots”
- Splines are a special case of a class of models called *generalized additive models* (GAMs).



Splines in Statistical Regression

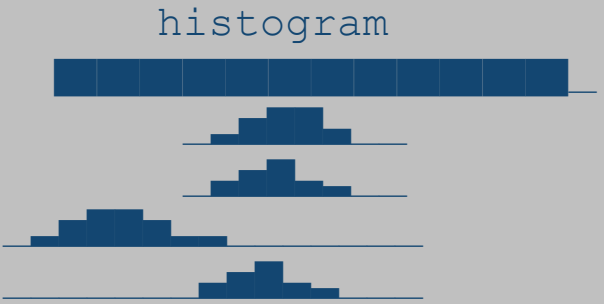
- Cherry blossom data
 - Over 1000 years of historical records for timing of full-blossoming of cherry trees
 - Y. Aono & S. Saito, *Int. J. Biometeorology* **54**, 211 (2010).
 - No changes for most of history, but pronounced trend in 20th century (global warming).
- Spline regression:
 - *Basis splines*: for the i th point, x_i

$$\mu_i = \alpha + \sum_{j=1}^{n_{\text{knots}}} w_j B_{i,j}$$

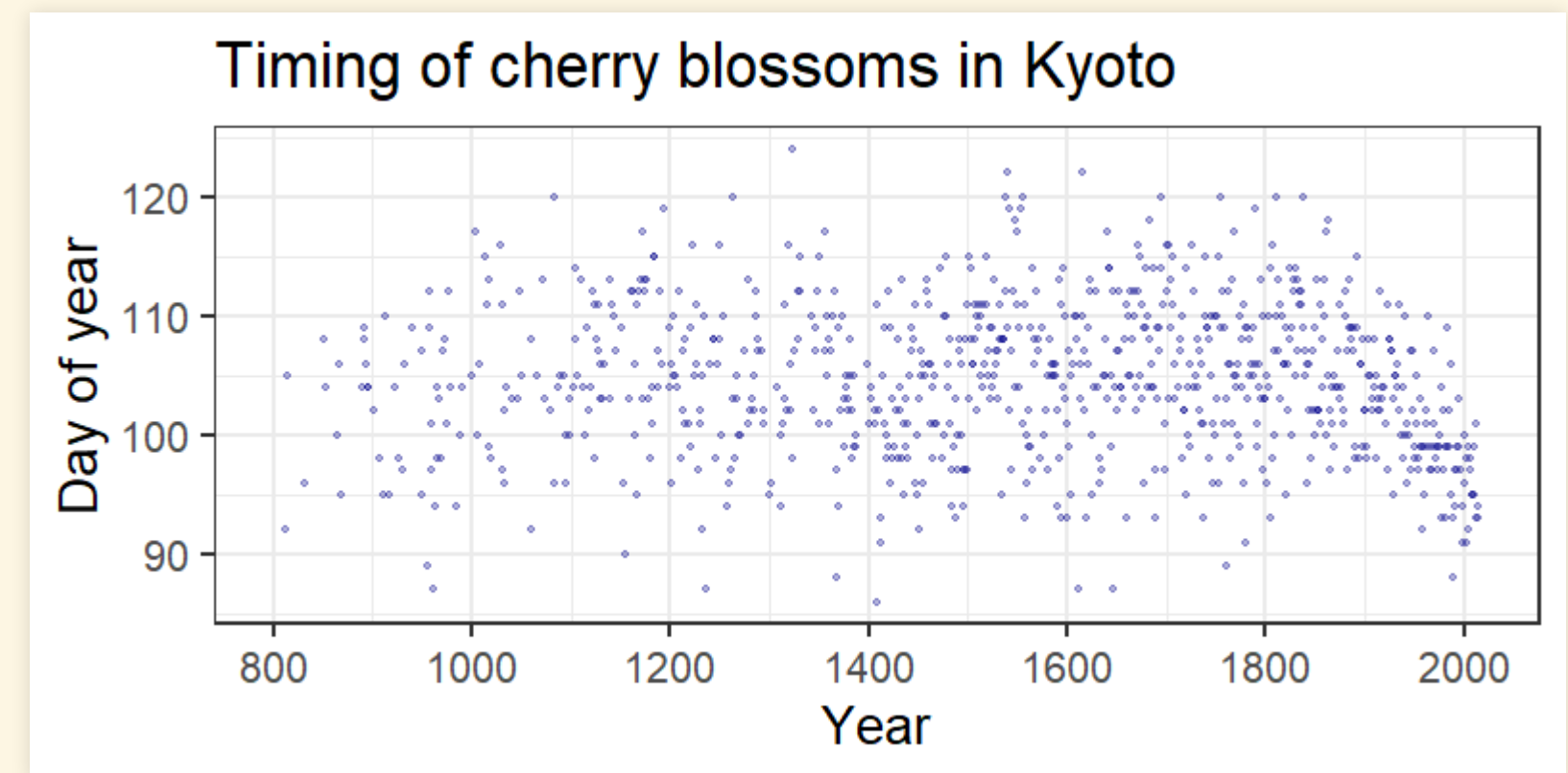
n_{knots} = # knots, w_j = weight for knot j ,
 $B_{i,j}$ = i th row of j th basis function (matrix with one row for each x value, and n_{knots} columns).

```
data(cherry_blossoms)
d <- cherry_blossoms
precis_show(precis(d, digits = 2))
```

```
## 'data.frame': 1215 obs. of 5 variables:
##      mean      sd  5.5%  94.5%
## year   1408.00 350.88 867.77 1948.23
## doy    104.54   6.41  94.43  115.00
## temp     6.14   0.66   5.15   7.29
## temp_upper 7.19   0.99   5.90   8.90
## temp_lower 5.10   0.85   3.79   6.37
```

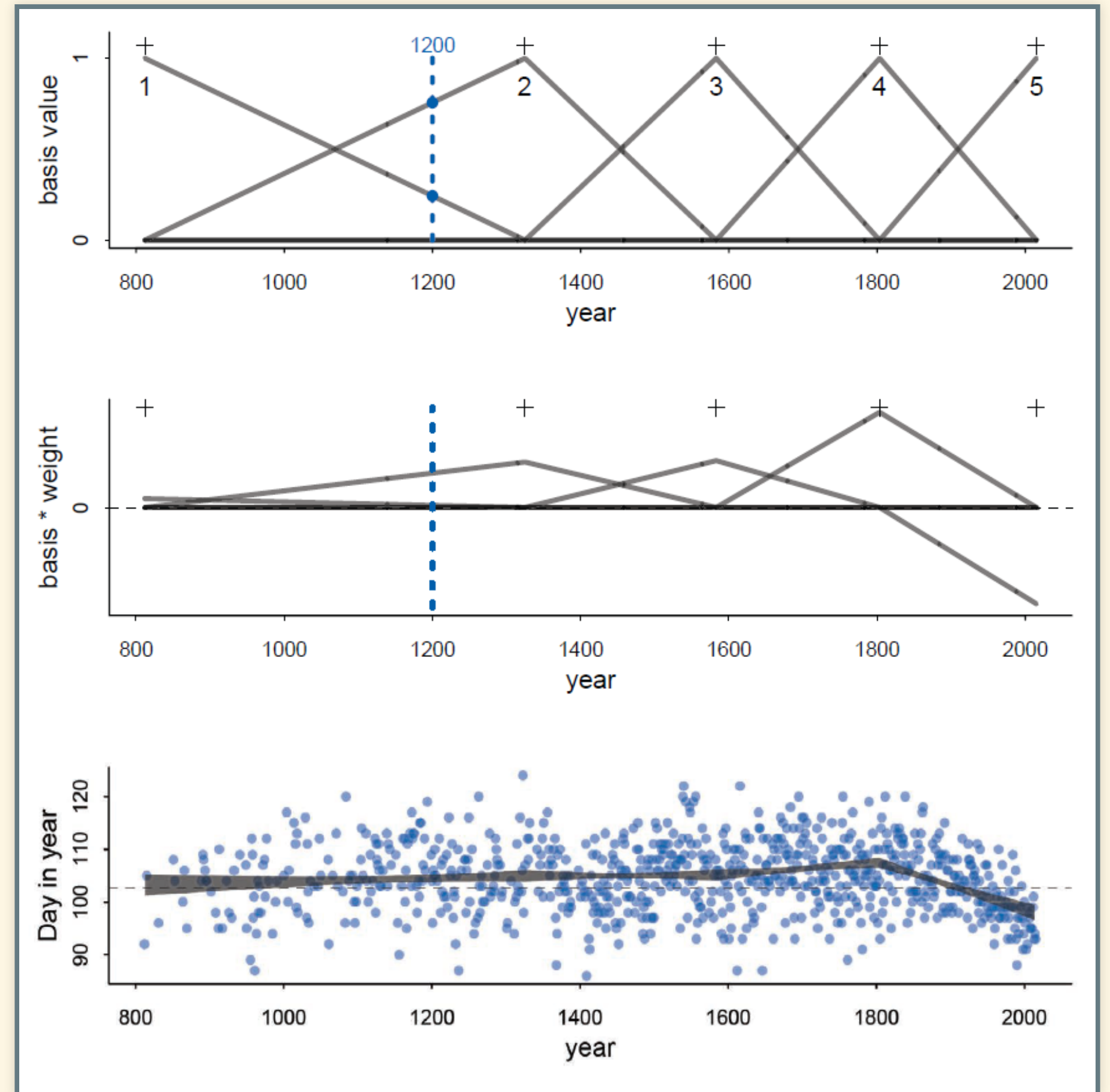
A histogram showing the distribution of five variables: year, doy, temp, temp_upper, and temp_lower. The year variable has a very wide distribution from approximately 800 to 2000. The other variables (doy, temp, temp_upper, temp_lower) have much narrower distributions, mostly concentrated between 800 and 1400.

```
ggplot(d, aes(x = year, y = doy)) +
  geom_point(color = "darkblue", size = 1, alpha = 0.3) +
  scale_x_continuous(breaks = seq(600, 2200, by = 200)) +
  labs(x = "Year", y = "Day of year",
       title="Timing of cherry blossoms in Kyoto")
```



Linear Basis Spline

- Linear basis functions $B_j(x)$
 - 5 knots
 - Piecewise linear
 - At most 2 functions are nonzero for any x .
- Model fits weights w_j for each basis function



Cubic Basis Spline

- 15 knots
 - Equal # of years with data between knots.
- Cubic functions
- Only 3 have nonzero values for any x .

```
library(splines)
d2 <- filter(d, ! is.na(doy)) # omit missing values
n_knots <- 15
knot_list <- quantile(d2$year,
                      probs=seq(0,1, length.out =
                                n_knots))

# Create basis function matrix
B <- bs(d2$year, knots = knot_list[-c(1,n_knots)],
        degree = 3, intercept = TRUE)

mdl <- quap(
  alist(
    D ~ dnorm(mu, sigma),
    mu <- a + B %*% w, # %*% is matrix multiplication
    a ~ dnorm(100, 10),
    w ~ dnorm(0, 10),
    sigma ~ dexp(1)
  ),
  data = list(D = d2$doy, B = B),
  start = list(w = rep(0, ncol(B)))
)
```

