# Review of R and RStudio

EES 5891-03

Bayesian Statistical Methods

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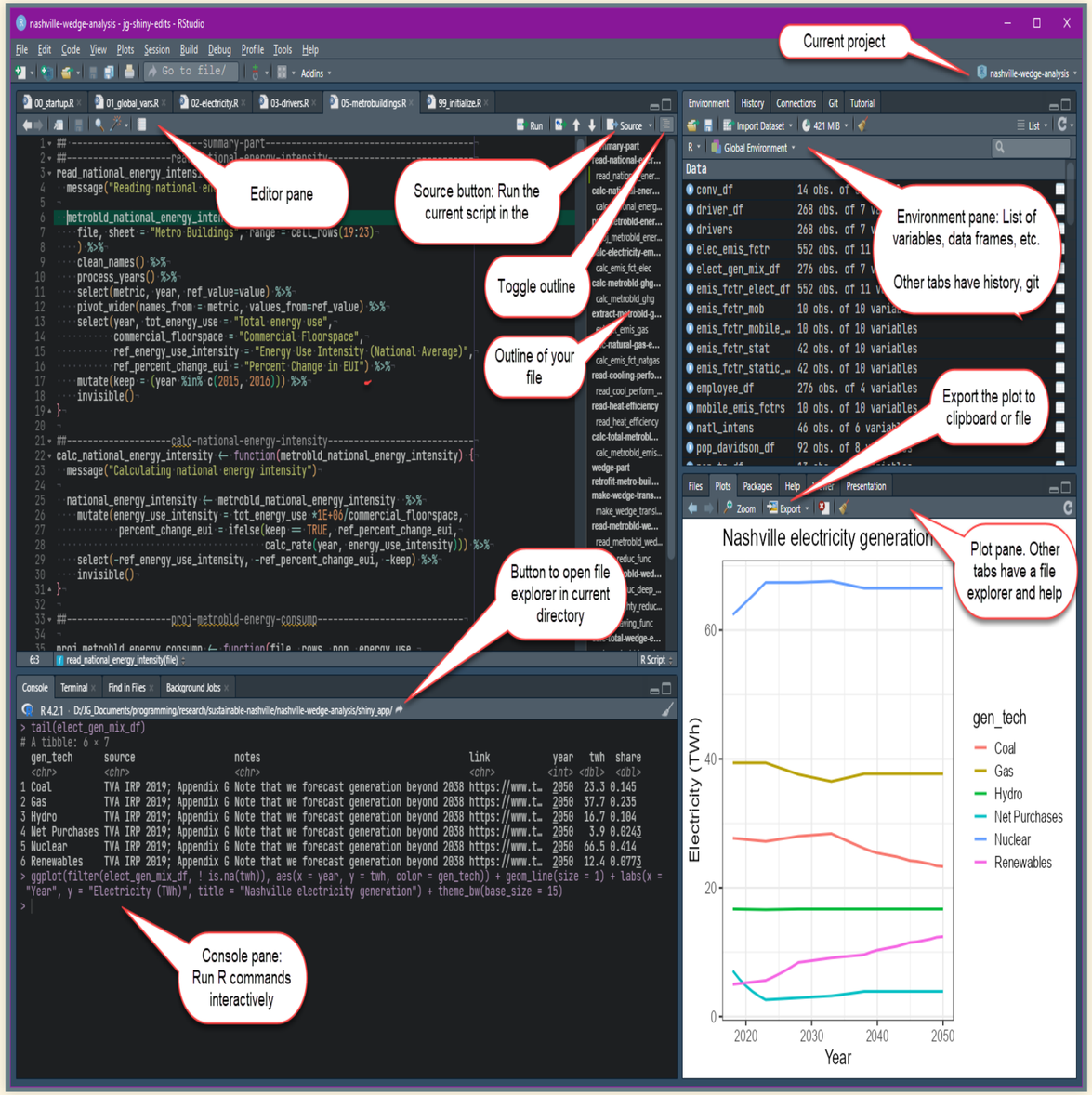
# Announcement

- 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 framse (`data.frame`)
  - Tidyverse (`library(tidyverse)`)
    - Unified philosophy of data analysis
      - Canonical reference: R for Data Science
      - Oriented toward `data.frame`s (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 it 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_list)
```

- 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).

(Photos: Rain Noe, When Splines Were Physical Objects)

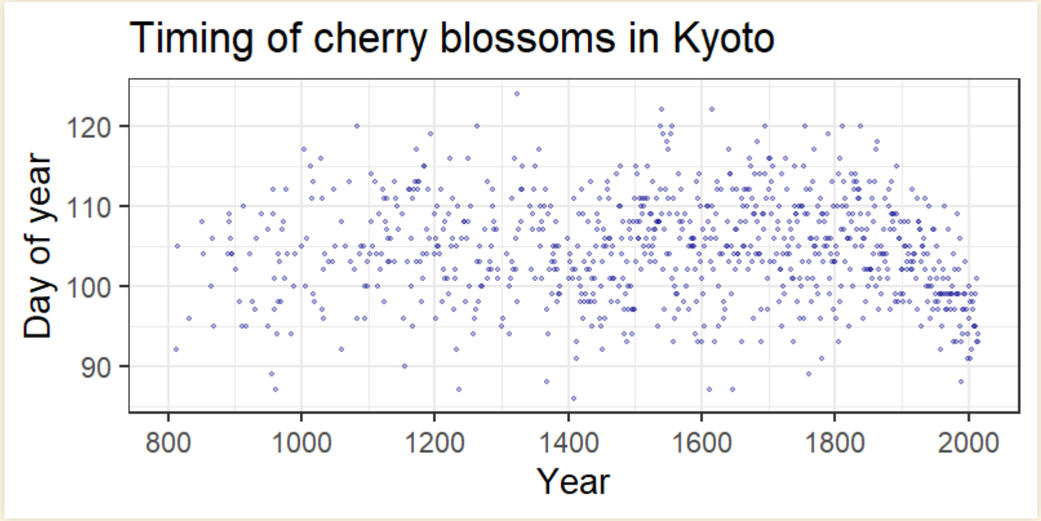
# Splines in Statistical Regression

- 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, $x_i$ $$ \mu_i = \alpha + \sum_{j = 1}^{n_{\text{knots}}} w_j B_{i,j} \\ $$ $n_{\text{knots}}$ = # 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 $n_{\text{knots}}$ columns).

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

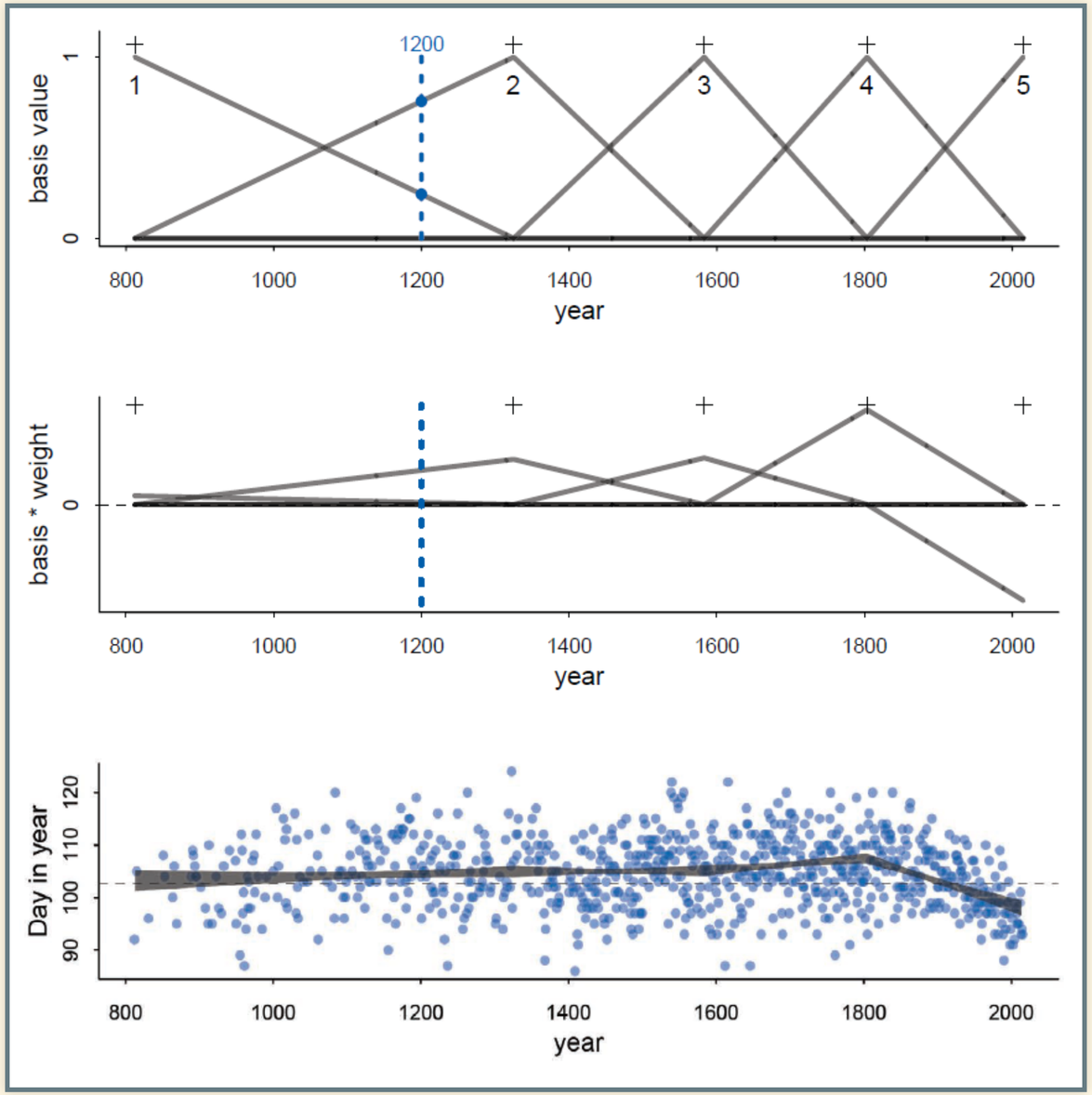
```
## 'data.frame': 1215 obs. of 5 variables:
##                mean      sd   5.5%   94.5%     histogram
## year       1408.00 350.88 867.77 1948.23
## doy         104.54   6.41  94.43  115.00
## temp          6.14   0.66   5.15    7.29
## temp_upper    7.19   0.99   5.90    8.90
## temp_lower    5.10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

```
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)))
)
```