SMLP 2022 Set up

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Set-up

This script can be run prior to starting the book "An Introduction to Bayesian Data Analysis for Cognitive Science" by Bruno Nicenboim, Daniel Schad, and Shravan Vasishth. The code is based on https://vasishth.github.io/bayescogsci/book/software-needed.html

Required packages

Required pacakges hosted on CRAN are installed below.

```
# if all else fails, just run this line:
install.packages(c(#"SIN", # SIN package was removed from the CRAN repository
    "MASS", "dplyr", "tidyr", "purrr", "extraDistr", "ggplot2", "loo", "bridgesampling", "brms", "bayespl

Some required packages aren't available on CRAN. They are installed below.

#From https://github.com/stan-dev/rstan/wiki/RStan-Getting-Started
# run the next line if you already have rstan installed
# remove.packages(c("StanHeaders", "rstan"))
install.packages("rstan", repos = c("https://mc-stan.org/r-packages/", getOption("repos")))

# run the nextline if you don't have 'devtools' already installed
# install.packages("devtools")
devtools::install_github("bnicenboim/bcogsci")

# and cmdstanr (https://mc-stan.org/cmdstanr/)
remotes::install_github("stan-dev/cmdstanr")
```

Loading packages in subsequent scripts

After you've first installed all packages, you can use the following code at the beginning of each subsequent script, which will check that will load the required packages, or install them if they are missing from the library. This step only works after the developer packages have been installed. Try 'Session > Restart R' and thenr unning this code chunk to see if it works,

```
if (!require(x, character.only = TRUE)) {
    install.packages(x, dependencies = TRUE)
    library(x, character.only = TRUE)
}
}

# this is also required, taken from the textbook

## Save compiled models:
rstan_options(auto_write = FALSE)
## Parallelize the chains using all the cores:
options(mc.cores = parallel::detectCores())
# To solve some conflicts between packages
select <- dplyr::select
extract <- rstan::extract</pre>
```

IF the code above gives you trouble, just use the chunk below. It is taken from the textbook.

```
library(MASS)
## be careful to load dplyr after MASS
library(dplyr)
library(tidyr)
library(purrr)
library(extraDistr)
library(ggplot2)
library(loo)
library(bridgesampling)
library(brms)
library(bayesplot)
library(tictoc)
library(hypr)
library(bcogsci)
library(lme4)
library(rstan)
library(cmdstanr)
library(rootSolve)
## Save compiled models:
rstan_options(auto_write = FALSE)
## Parallelize the chains using all the cores:
options(mc.cores = parallel::detectCores())
# To solve some conflicts between packages
select <- dplyr::select</pre>
extract <- rstan::extract</pre>
```