vaccine_delay_fits

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Some initial settings and version check

```
source("global_util.R")

version_check("sircovid", "0.13.15")
version_check("spimalot", "0.7.11")
```

Specify the MCMC parameters

```
date <- "2021-09-13"
model_type <- "BB"

#Some data streams are unreliable for the last few days. Define how many days here.
trim_deaths <- 4
trim_pillar2 <- 5

## MCMC control (only applies if short_run = FALSE)
burnin <- 500
n_mcmc <- 1500
chains <- 4
kernel_scaling <- 0.2
```

spim_check_region checks if the target region is a valid NHS region in dataset.

```
#Checks current region is valid
region <- spimalot::spim_check_region(region, FALSE)
```

spim_fit_pars_load loads the parameters. This function loads the data in *parameters* folder and conducts some pre-processing.

```
#Checks and assembles all the outputs from vaccine_delay_parameter_fits task
#Output pars is a list containing:
#info - the loaded info.csv
#prior - the loaded prior.csv
#proposal - the loaded proposal.csv
#transform - the functions in transform.R
#raw - exact output of first 3 csvs, without any treatment
```

```r
#base - the baseline.rds object
#mcmc - some sort of initialisation object built from the above to pass to the mcmc
pars <- spimalot::spim_fit_pars_load("parameters", region, "central",
                                     kernel_scaling)

restart_date <- readRDS("parameters/base.rds")[[region[[1]]]]$restart_date
```

This command sets the parameters for the MCMC. This function invokes mcstate::pmcmc_control

```r
#This sets up a lot of pmcmc controls, checks iterations are compatible etc.
control <- spimalot::spim_control(
  short_run, chains, deterministic, date_restart = restart_date,
  n_mcmc = n_mcmc, burnin = burnin)
```

```
## Running on 1 workers with 1 threads
```