

# Favipiravir PLATCOV

James Watson

```
knitr::opts_chunk$set(cache = T, cache.comments = FALSE,  
  echo = F, include = TRUE,  
  fig.width = 8, fig.height = 8,  
  fig.pos = 'H', dev = 'png', dpi = 300)
```

Loading required package: StanHeaders

Loading required package: ggplot2

rstan (Version 2.21.7, GitRev: 2e1f913d3ca3)

For execution on a local, multicore CPU with excess RAM we recommend calling  
options(mc.cores = parallel::detectCores()).

To avoid recompilation of unchanged Stan programs, we recommend calling  
rstan\_options(auto\_write = TRUE)

```
-- Attaching packages ----- tidyverse 1.3.2 --  
v tibble  3.2.1      v dplyr   1.1.2  
v tidyr   1.2.1      v stringr 1.5.0  
v readr   2.1.3      v forcats 0.5.2  
v purrr   0.3.5  
-- Conflicts ----- tidyverse_conflicts() --  
x tidyr::extract() masks rstan::extract()  
x dplyr::filter()  masks stats::filter()  
x dplyr::lag()     masks stats::lag()
```

Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':

group\_rows

```
platform      -
arch           aarch64-apple-darwin20
os            aarch64
os            darwin20
system        aarch64, darwin20
status
major         4
minor         2.2
year          2022
month         10
day           31
svn rev       83211
language      R
version.string R version 4.2.2 (2022-10-31)
nickname      Innocent and Trusting
```

```
R version 4.2.2 (2022-10-31)
Platform: aarch64-apple-darwin20 (64-bit)
Running under: macOS Ventura 13.5.2
```

Matrix products: default

```
BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRlapack.dylib
```

locale:

```
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] RColorBrewer_1.1-3  finalfit_1.0.6      kableExtra_1.3.4
[4] forcats_0.5.2       stringr_1.5.0       dplyr_1.1.2
[7] purrr_0.3.5         readr_2.1.3         tidyr_1.2.1
[10] tibble_3.2.1        tidyverse_1.3.2     rstan_2.21.7
[13] ggplot2_3.4.0       StanHeaders_2.21.0-7
```

loaded via a namespace (and not attached):

[1] httr_1.4.4	splines_4.2.2	jsonlite_1.8.4
[4] viridisLite_0.4.1	modelr_0.1.10	RcppParallel_5.1.5
[7] assertthat_0.2.1	stats4_4.2.2	googlesheets4_1.0.1
[10] cellranger_1.1.0	yaml_2.3.6	lattice_0.20-45
[13] pillar_1.9.0	backports_1.4.1	glue_1.6.2
[16] digest_0.6.31	rvest_1.0.3	colorspace_2.0-3
[19] Matrix_1.5-1	htmltools_0.5.4	pkgconfig_2.0.3
[22] broom_1.0.2	haven_2.5.1	webshot_0.5.4
[25] scales_1.2.1	processx_3.8.0	svglite_2.1.1
[28] tzdb_0.3.0	timechange_0.1.1	googledrive_2.0.0
[31] generics_0.1.3	ellipsis_0.3.2	withr_2.5.0
[34] cli_3.6.1	survival_3.4-0	magrittr_2.0.3
[37] crayon_1.5.2	readxl_1.4.1	evaluate_0.19
[40] ps_1.7.2	mice_3.15.0	fs_1.5.2
[43] fansi_1.0.4	xml2_1.3.3	pkgbuild_1.4.0
[46] tools_4.2.2	loo_2.5.1	prettyunits_1.1.1
[49] hms_1.1.2	gargle_1.2.1	lifecycle_1.0.3
[52] matrixStats_0.63.0	munSELL_0.5.0	reprex_2.0.2
[55] callr_3.7.3	compiler_4.2.2	systemfonts_1.0.4
[58] rlang_1.1.0	grid_4.2.2	rstudioapi_0.14
[61] rmarkdown_2.19	boot_1.3-28	gtable_0.3.1
[64] codetools_0.2-18	inline_0.3.19	DBI_1.1.3
[67] R6_2.5.1	gridExtra_2.3	lubridate_1.9.0
[70] knitr_1.41	fastmap_1.1.0	utf8_1.2.3
[73] stringi_1.7.8	parallel_4.2.2	Rcpp_1.0.10
[76] vctrs_0.6.2	dbplyr_2.2.1	tidyselect_1.2.0
[79] xfun_0.35		

Warning in checkStrict(plot\_serial\_data): global variables used: daily\_VL, ID, log10\_viral\_load, Time, Timepoint\_ID, Trt, trt\_color

Warning in checkStrict(calculate\_fever\_clearance): global variables used: ID, Time

## Load data

Set up analysis

## Make modified intention to treat population

mITT population

Intervention	FALSE	TRUE
Favipiravir	0	114
Fluoxetine	2	116
Ivermectin	2	44
Molnupiravir	0	66
Nirmatrelvir	0	90
No study drug	4	198
Remdesivir	0	67

## Baseline characteristics

### Fit models

Analysis dataset contains 695 patients and 12472 datapoints (10387 above LLOD, 83%)

There are a total of 695 patients in the database with a total of 12472 PCRs analysable  
 16.72% of samples are below LOD  
 check stan data formatting:

We are running all models with 4 chains and 2000 samples for each chain, discarding 1000 for

main model selection

Warning in brewer.pal(n = nrow(model\_settings), name = "Set1"): minimal value for n is 3, re

Table 1: Baseline characteristics in mITT population

Dependent: Trt		No study drug	Ivermectin	Remdesivir	Favipiravir	Fluoxetine	Mo
Site	br003	25 (12.6)	0 (0.0)	9 (13.4)	16 (14.0)	12 (10.3)	
	la008	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.9)	
	pk001	4 (2.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.7)	
	th001	164 (82.8)	40 (90.9)	54 (80.6)	96 (84.2)	101 (87.1)	
	th057	3 (1.5)	2 (4.5)	2 (3.0)	2 (1.8)	0 (0.0)	
	th058	2 (1.0)	2 (4.5)	2 (3.0)	0 (0.0)	0 (0.0)	
Age	Mean (SD)	30.1 (7.6)	30.0 (7.0)	30.1 (8.2)	30.2 (7.5)	29.5 (7.7)	
Sex	Female	128 (64.6)	24 (54.5)	35 (52.2)	71 (62.3)	82 (70.7)	
	Male	70 (35.4)	20 (45.5)	32 (47.8)	43 (37.7)	34 (29.3)	
BMI	Mean (SD)	23.1 (4.1)	22.3 (3.2)	22.7 (3.1)	23.1 (3.7)	22.3 (3.5)	
Weight	Mean (SD)	62.8 (13.5)	61.6 (12.3)	63.9 (11.0)	63.0 (13.6)	59.6 (11.3)	
Baseline.viral.load	Mean (SD)	5.4 (1.3)	5.6 (1.2)	5.5 (1.1)	5.5 (1.0)	5.6 (1.3)	
Variant	BA.1	13 (6.6)	14 (31.8)	20 (29.9)	21 (18.4)	0 (0.0)	
	BA.2	52 (26.3)	18 (40.9)	37 (55.2)	42 (36.8)	25 (21.6)	
	BA.5	41 (20.7)	0 (0.0)	0 (0.0)	32 (28.1)	29 (25.0)	
	BA.2.75	43 (21.7)	0 (0.0)	0 (0.0)	5 (4.4)	34 (29.3)	
	XBB	10 (5.1)	0 (0.0)	0 (0.0)	0 (0.0)	9 (7.8)	
	Delta	10 (5.1)	12 (27.3)	10 (14.9)	11 (9.6)	0 (0.0)	
	BA.4	2 (1.0)	0 (0.0)	0 (0.0)	3 (2.6)	0 (0.0)	
	BQ.1	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.7)	
	XBB.1.5-like	24 (12.1)	0 (0.0)	0 (0.0)	0 (0.0)	14 (12.1)	
	FL.4	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.9)	
	-	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	2 (1.7)	
	EG.2	1 (0.5)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	
	XBB.1.5.39	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	
Symptom_onset	Mean (SD)	2.2 (0.8)	2.3 (0.8)	2.4 (0.8)	2.1 (0.7)	2.1 (0.8)	
Vaccinated	Yes	197 (99.5)	43 (97.7)	64 (95.5)	112 (98.2)	116 (100.0)	
	No	1 (0.5)	1 (2.3)	3 (4.5)	2 (1.8)	0 (0.0)	
Fever_Baseline	0	154 (77.8)	31 (70.5)	48 (71.6)	88 (77.2)	85 (73.3)	
	1	44 (22.2)	13 (29.5)	19 (28.4)	26 (22.8)	31 (26.7)	
	(Missing)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	

## Plot treatment effect

