

RESEARCH

A sample article title

Jane E. Doe^{???}, John R.S. Smith^{?,??}

^{??} Correspondence: ??
^{??} Department of Science,
University of Cambridge, London,
UK
Full list of author information is
available at the end of the article

Abstract
First part title: Text for this section.
Second part title: Text for this section.
Keywords: sample; article; author

Content
Text and results for this section, as per the individual journal’s instructions for authors.

Section title
Text for this section...

Sub-heading for section
Text for this sub-heading...

Sub-sub heading for section
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Sub-sub-sub heading for section Text for this sub-sub-sub-heading...
In this section we examine the growth rate of the mean of Z_0 , Z_1 and Z_2 . In addition, we examine a common modeling assumption and note the importance of considering the tails of the extinction time T_x in studies of escape dynamics. We will first consider the expected resistant population at vT_x for some $v > 0$, (and temporarily assume $\alpha = 0$)

$$E[Z_1(vT_x)] = \int_0^{v\wedge 1} Z_0(uT_x) \exp(\lambda_1) du.$$

If we assume that sensitive cells follow a deterministic decay $Z_0(t) = xe^{\lambda_0 t}$ and approximate their extinction time as $T_x \approx -\frac{1}{\lambda_0} \log x$, then we can heuristically estimate the expected value as

$$\begin{aligned} E[Z_1(vT_x)] &= \frac{\mu}{r} \log x \int_0^{v\wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du. \end{aligned} \tag{1}$$

Thus we observe that this expected value is finite for all $v > 0$ (also see [?, ?, ?, ?, ?, ?]).

```

eset_Mvals <- read_rds("../data/formatted/eset_Mvals_clean.rds")
f_dat <- fData(eset_Mvals)
sum(f_dat$CVprobe >= 100)
## [1] 5532
sum(f_dat$CVprobe < 100)
## [1] 684481
eset_Mvals <- eset_Mvals[f_dat$CVprobe < 100,]
core_vars <- c("ID", "SITE", "V3AGE1")
outcome_var <- c("CYCRPJH", "CYTNFR2JH", "CYIFNGJH", "CYIL1BJH", "CYIL6JH", "CYTNFJH")

p_dat1 <- pData(eset_Mvals)
pheno <- read_csv("../data/pheno/INFLAME.CSV") %>%
  select(ID, SITE, CYCRPJH, LALYMP)

##
## -- Column specification -----
## cols(
##   .default = col_double(),
##   SITE = col_character(),
##   ID = col_character()
## )
## i Use 'spec()' for the full column specifications.
phenoV3 <- read_csv("../data/pheno/v3feb21.csv", guess_max = 4682)
##
## -- Column specification -----
## cols(
##   .default = col_double(),
##   ID = col_character(),
##   V3DATE = col_character(),
##   V3HVDATE = col_character(),
##   SITE = col_character(),
##   GISEDOD = col_character(),
##   CISTAFF = col_character(),
##   LSSTAFF = col_character(),
##   TMSTAFF = col_character(),
##   TBSTAFF = col_character(),
##   HWSTAFF = col_character(),
##   GSSTAFF = col_character(),
##   NFCSTAFF = col_character(),
##   NFWSTAFF = col_character(),
##   BPAASTAF = col_character(),
##   NPSTAFF = col_character(),
##   BPSTAFF = col_character(),
##   SCSTAFF = col_character(),
##   SCUSTAFF = col_character(),
##   V3AMSTF = col_character(),
##   TMTIMEM = col_time(format = "")

```

```
## # ... with 1 more columns
## )
## i Use 'spec()' for the full column specifications.
phenoV3 <- phenoV3 %>%
  select(ID, HWBMI, TURSMOKE, V3AGE1)
pheno2 <- inner_join(pheno, phenoV3, by = "ID") %>%
  mutate(SITE = as.factor(SITE),
         TURSMOKE = factor(as.character(TURSMOKE), levels = c("0", "1", "2"),
                           labels = c("never", "former", "current")))
  )

#Work on CRP right now. Make loop for other inflammatory markers later.
p_dat <- p_dat1 %>%
  left_join(pheno2, c("Sample_Name" = "ID")) %>%
  arrange(sampOrder)
map_int(p_dat, function(x) sum(is.na(x)))

#Must remove missings from eset and pData
mykeep <- !is.na(p_dat$SITE) & !is.na(p_dat$V3AGE1) & !is.na(p_dat$HWBMI) & !is.na(p_dat$TURSMOKE)
eset_Mvals_mod <- eset_Mvals[, mykeep]
p_dat <- p_dat[mykeep, ]
dim(eset_Mvals_mod)

dim(p_dat)

#Make table 1
p_dat %>%
  summarize(mean_CRP = mean(CYCRPJH), sd_CRP = sd(CYCRPJH)) %>%
  kable()
```

mean_CRP	sd_CRP
3.010294	4.000611

Appendix

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Acknowledgements

Text for this section...

Funding

Text for this section...

Abbreviations

Text for this section...

Availability of data and materials

Text for this section...

Ethics approval and consent to participate

Text for this section. . .

Competing interests

The authors declare that they have no competing interests.

Consent for publication

Text for this section. . .

Authors' contributions

Text for this section . . .

Authors' information

Text for this section. . .

Author details

?? Department of Science, University of Cambridge, London, UK. ?? Institute of Biology, National University of Sciences, Kiel, Germany.

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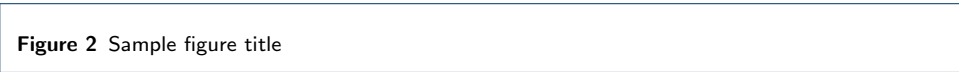
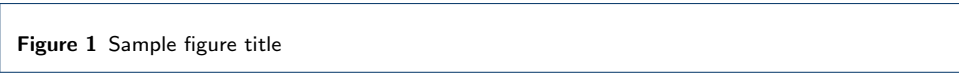
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Figures



Tables

Table 1 Sample table title. This is where the description of the table should go

	B1	B2	B3
A1	0.1	0.2	0.3
A2
A3

Additional Files

Additional file 1 — Sample additional file title
Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title
Additional file descriptions text.