



Journal of Statistical Software

MMMMMM YYYY, Volume VV, Issue II.

doi: 10.18637/jss.v000.i00

Time invariant analysis of epidemics with EpiCompare

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Abstract

The abstract of the article.

Keywords: keywords, not capitalized, Java.

1. Introduction

This is the Section 1. This template demonstrates some of the basic LaTeX that you need to know to create a JSS article.

1.1. Code formatting

In general, don't use Markdown, but use the more precise LaTeX commands instead:

- Java
- `plyr`

One exception is inline code, which can be written inside a pair of backticks (i.e., using the Markdown syntax).

If you want to use LaTeX commands in headers, you need to provide a `short-title` attribute. You can also provide a custom identifier if necessary. See the header of Section 2 for example.

2. R code

Can be inserted in regular R markdown blocks.

hags hags hags [Neal and Roberts \(2004\)](#)

```
R> x <- 1:10
R> x
```

```
[1] 1 2 3 4 5 6 7 8 9 10
```

2.1. Features specific to rticles

- Adding short titles to section headers is a feature specific to **rticles** (implemented via a Pandoc Lua filter). This feature is currently not supported by Pandoc and we will update this template if **it is officially supported in the future**.
- Using the `\AND` syntax in the `author` field to add authors on a new line. This is a specific to the `rticles::jss_article` format.

In this section, we highlight a number of the functionalities available in EpiCompare. These functionalities include data cleaning, visualization, simulation, and comparison, in accordance with the data analysis pipeline REF??. We show a full data analysis from beginning to end that can be accomplished in a streamlined and standardized manner.

2.2. Data and EDA

We analyze an outbreak of measles in the town of Hagelloch, Germany from 1861-1862, a data set organized by [Pfeilsticker \(1863\)](#). The data was later made visible by [Oesterle \(1992\)](#) and made available in an R by [Meyer, Held, and Höhle \(2017\)](#). The Hagelloch data includes a rich set of features including household members, school level, household locations, date of first symptoms (prodromes), date of measles rash, and even the alleged infector. Because of these rich features, this data set has been an ideal testing ground methodology in infectious disease epidemiology and is used in work by [Neal and Roberts \(2004\)](#); [Britton, Kypraios, and O'NEILL \(2011\)](#); [Groendyke, Welch, and Hunter \(2012\)](#); [Becker, Birger, Teillant, Gastanaduy, Wallace, and Grenfell \(2016\)](#).

```
R> devtools::load_all()
R> library(ggplot2)
R> library(tidyr)
R> library(dplyr)
R> library(knitr)
R> library(kableExtra)
```

```
R> hagelloch_raw %>% select(PN, NAME, AGE, SEX, HN, PRO, ERU, IFTO) %>%
+   head(5) %>% kable(format = "latex", booktabs = TRUE, caption = "Cool table") %>%
+   kable_styling(position = "center")
```

- thing

Table 1: Cool table

PN	NAME	AGE	SEX	HN	PRO	ERU	IFTO
1	Mueller	7	female	61	1861-11-21	1861-11-25	45
2	Mueller	6	female	61	1861-11-23	1861-11-27	45
3	Mueller	4	female	61	1861-11-28	1861-12-02	172
4	Seibold	13	male	62	1861-11-27	1861-11-28	180
5	Motzer	8	female	63	1861-11-22	1861-11-27	45

References

- Becker AD, Birger RB, Teillant A, Gastanaduy PA, Wallace GS, Grenfell BT (2016). “Estimating enhanced prevaccination measles transmission hotspots in the context of cross-scale dynamics.” *Proceedings of the National Academy of Sciences*, **113**(51), 14595–14600.
- Britton T, Kypraios T, O’NEILL PD (2011). “Inference for epidemics with three levels of mixing: methodology and application to a measles outbreak.” *Scandinavian Journal of Statistics*, **38**(3), 578–599.
- Groendyke C, Welch D, Hunter DR (2012). “A network-based analysis of the 1861 Hagelloch measles data.” *Biometrics*, **68**(3), 755–765.
- Meyer S, Held L, Höhle M (2017). “Spatio-Temporal Analysis of Epidemic Phenomena Using the R Package surveillance.” *Journal of Statistical Software*, **77**(11), 1–55. doi:10.18637/jss.v077.i11.
- Neal PJ, Roberts GO (2004). “Statistical inference and model selection for the 1861 Hagelloch measles epidemic.” *Biostatistics*, **5**(2), 249–261. ISSN 14654644. doi:10.1093/biostatistics/5.2.249.
- Oesterle H (1992). “Statistische Reanalyse einer Masernepidemie 1861 in Hagelloch.”
- Pfeilsticker A (1863). “Beiträge zur Pathologie der Masern mit besonderer Berücksichtigung der statistischen Verhältnisse.” URL <http://www.archive.org/details/beitrgezurpatho00pfeigoog>.

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