

WholeTale Workshop, Chicago, Sept 13 2018

Reproducible Document Stack

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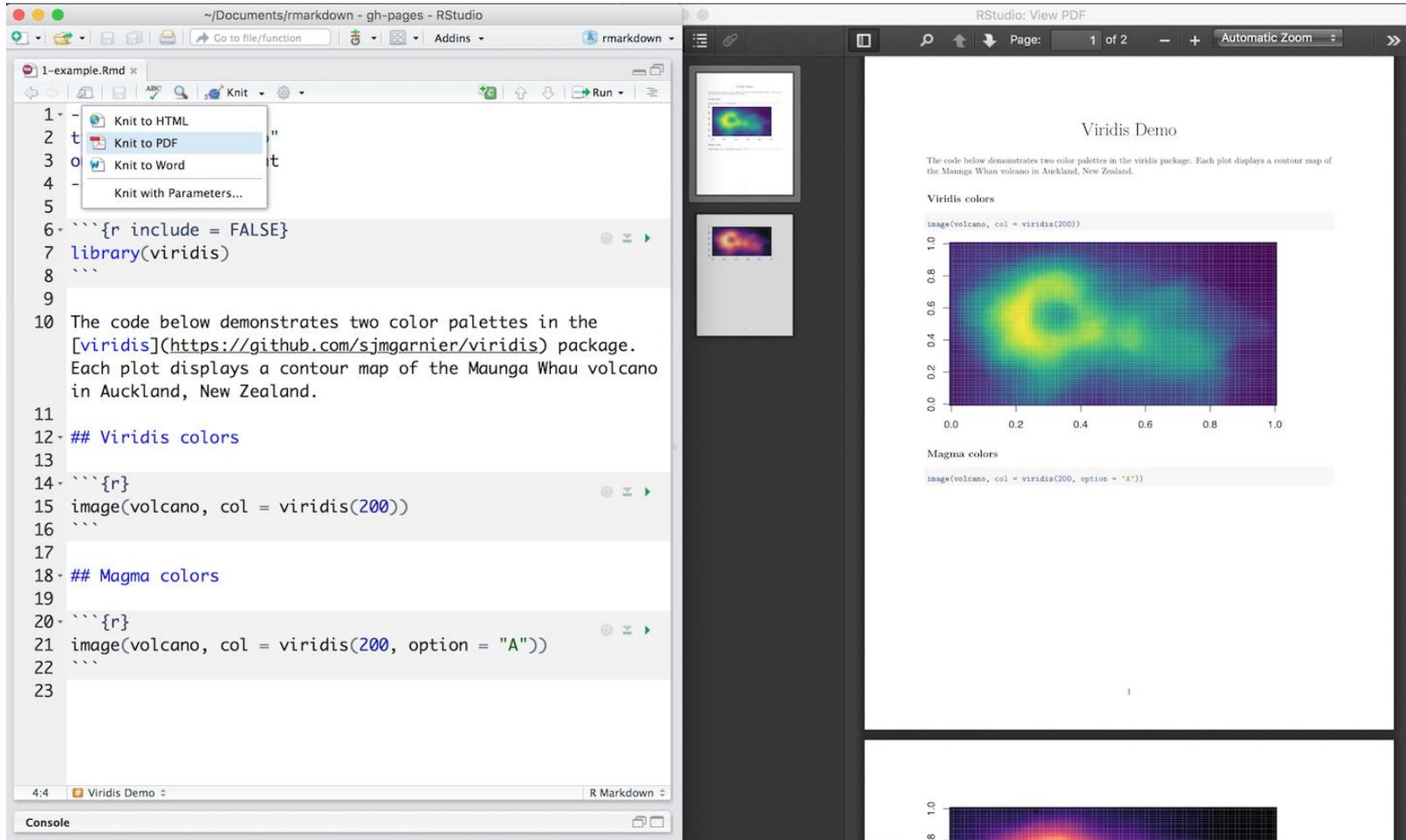


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that encourages and recognises the most
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Is this you?

Is this you?



The image shows a screenshot of the RStudio interface. On the left, the R Markdown editor is open, displaying a document titled "1-example.Rmd". A context menu is open over the document, showing options: "Knit to HTML", "Knit to PDF" (which is highlighted), "Knit to Word", and "Knit with Parameters...". The R code in the document includes:

```
1 -  
2 t "  
3 O t  
4 -  
5 -  
6 ```{r include = FALSE}  
7 library(viridis)  
8 ```  
9 -  
10 The code below demonstrates two color palettes in the  
11 [viridis](https://github.com/sjmgarnier/viridis) package.  
12 Each plot displays a contour map of the Maunga Whau volcano  
13 in Auckland, New Zealand.  
14 -  
15 ## Viridis colors  
16 -  
17 ```{r}  
18 image(volcano, col = viridis(200))  
19 ```  
20 -  
21 ## Magma colors  
22 -  
23 ```{r}  
24 image(volcano, col = viridis(200, option = "A"))  
25 ```  
26 -
```

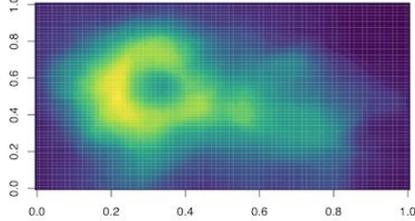
On the right, the RStudio PDF viewer is open, showing the rendered PDF document titled "Viridis Demo". The PDF content includes:

Viridis Demo

The code below demonstrates two color palettes in the viridis package. Each plot displays a contour map of the Maunga Whau volcano in Auckland, New Zealand.

Viridis colors

```
image(volcano, col = viridis(200))
```

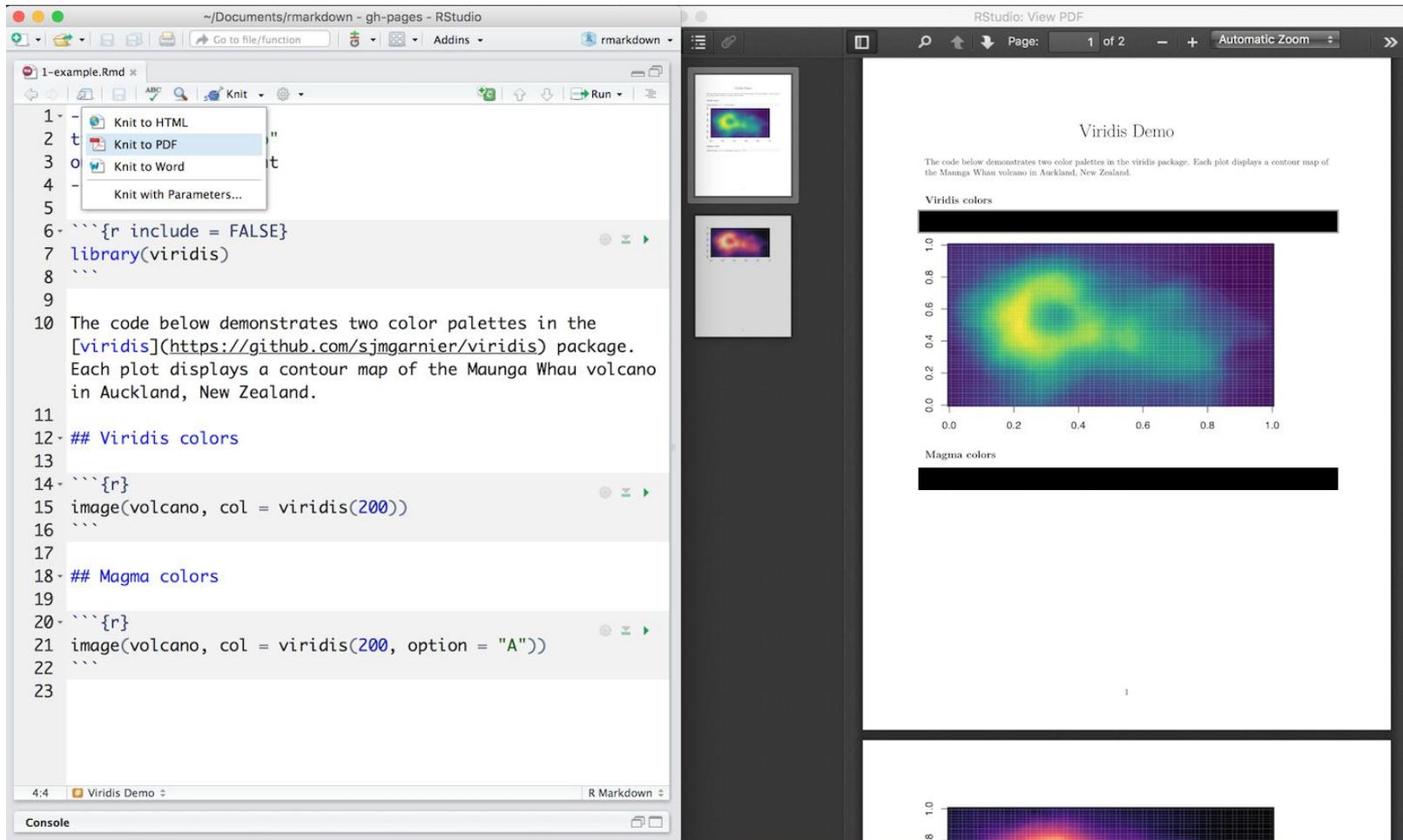


Magma colors

```
image(volcano, col = viridis(200, option = "A"))
```

The PDF viewer shows two small thumbnail images of the volcano contour maps on the left side of the page. The main plot area shows a large contour map of the volcano using the viridis color palette. The x and y axes of the plot range from 0.0 to 1.0. Below the main plot, there is a smaller, partially visible plot showing the volcano contour map using the magma color palette.

Is this you?



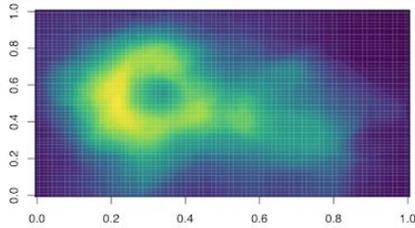
The image shows a screenshot of the RStudio interface. On the left, the R Markdown source file is open, showing code for generating a PDF. A context menu is open over the code, with 'Knit to PDF' selected. The code includes a pre-rendered plot, a text block, and two more pre-rendered plots. The text block describes the viridis package and the Maunga Whau volcano. The right pane shows the rendered PDF, titled 'Viridis Demo', which contains the same content as the source file, including the two color palettes and the contour map.

```
1 -  
2 t "  
3 O t  
4 -  
5  
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Viridis Demo

The code below demonstrates two color palettes in the [viridis](https://github.com/sjmgarnier/viridis) package. Each plot displays a contour map of the Maunga Whau volcano in Auckland, New Zealand.

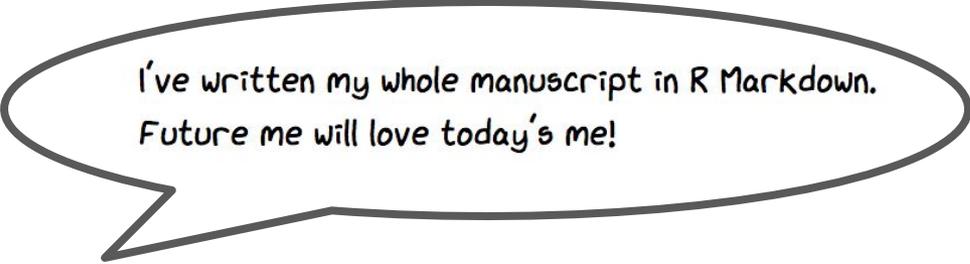
Viridis colors



Magma colors

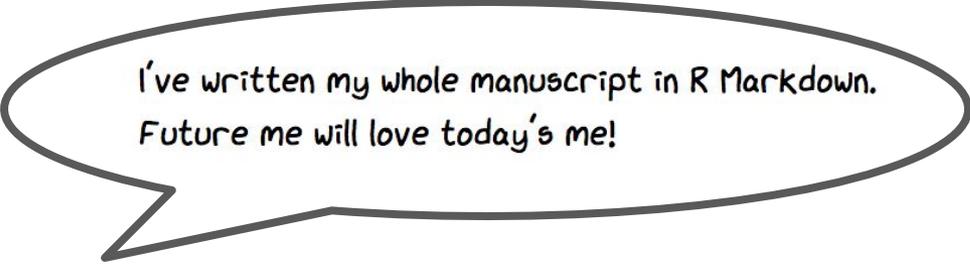


Is this you?

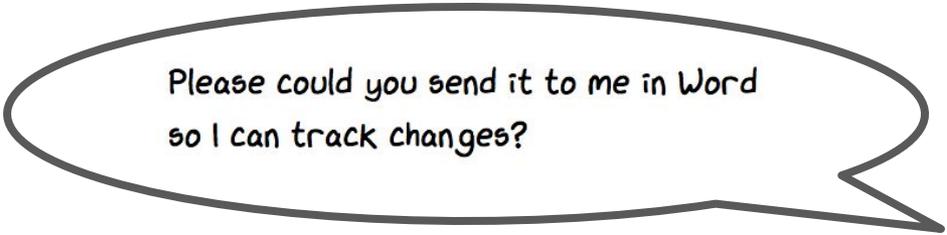


I've written my whole manuscript in R Markdown.
Future me will love today's me!

Is this you?



I've written my whole manuscript in R Markdown.
Future me will love today's me!



Please could you send it to me in Word
so I can track changes?

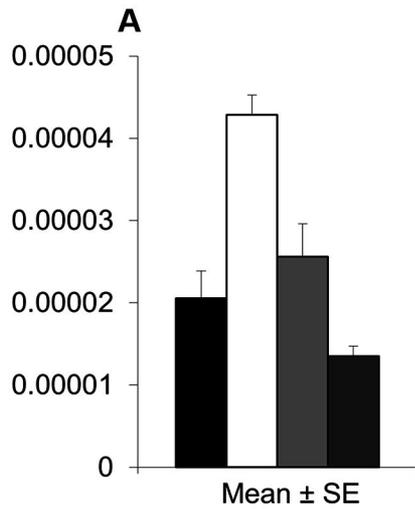
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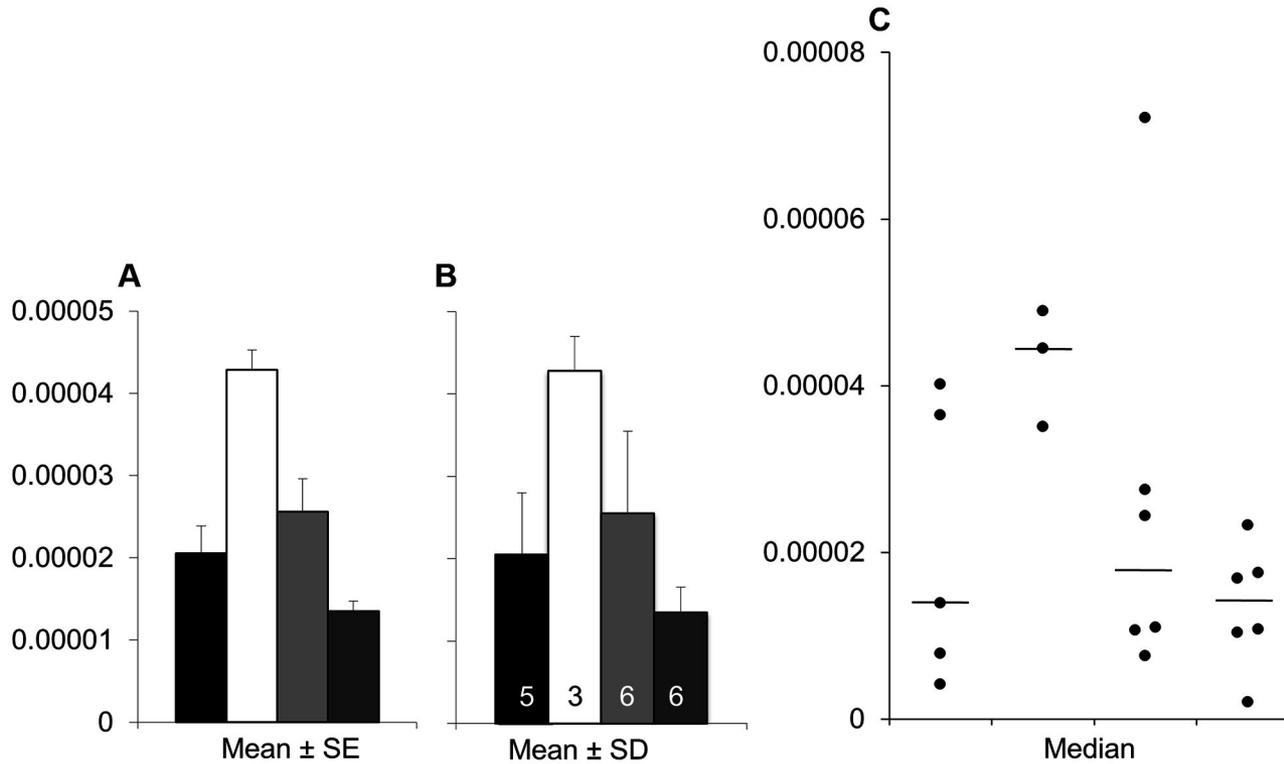
Please could you send it to me in Word
so I can track changes?

`$%*!@#!*$&%`

Is this you?



Is this you?



Is this you?

LIKELIHOOD YOU WILL GET CODE WORKING
BASED ON HOW YOU'RE SUPPOSED TO INSTALL IT:



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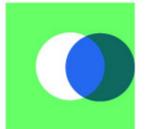


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Publish reproducible articles



- XML-based for scholarly publishing
- Avoid fragmentation, maintain clarity: dataset X —*script* Y—> result Z
- Play first in the browser before committing to local use
- Connect Excel clickers with iPython notebook coders

Learn more about Stencila:

elifesciences.org/labs/c496b8bb/stencila-an-office-suite-for-reproducible-research

Recent progress

- Stencila have improved support for R and Python code in reproducible articles and R Markdown and Jupyter converters
- Substance have built the first reader interface; eLife are conducting user tests now

DEMO

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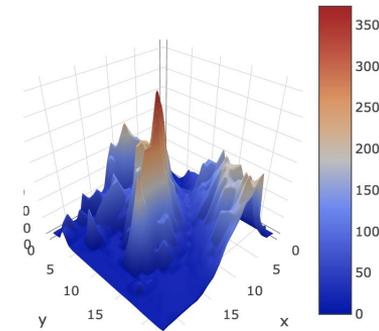
Recent progress

- Stencila have improved support for R and Python code in reproducible articles and R Markdown and Jupyter converters
- Substance have built the first reader interface; eLife are conducting user tests now
- The first reproducible article is being prepared (see <https://github.com/stencila/examples/tree/master/elife-30274>)

Figure 2

Formula for: Plotly

status: ready



Digital gene expression analysis.

P493-6 cells grown in the presence of tetracycline (Tet) for 72 hr for repression of the conditional *pmyc-tet* construct, were switched into Tet-free growth medium to induce c-Myc expression. Cells were cultured in two separate lots of serum. Transcripts/cell estimates from NanoString nCounter gene expression assays (1369 genes assay) for active (left) and silent (right) genes at 0, 1, and 24 hr after release from Tet. Active genes expressed greater than one transcript/cell. Silent genes expressed less than 0.5 transcript/cell. Box and whisker plots with median represented as the line through the box and whiskers representing values within 1.5 IQR of the first and third quartile. Cells grown in serum lot one: active genes = 708, silent genes = 580. Cells grown in serum lot two: active genes = 719, silent genes = 573. Confirmatory analysis is reported in [Table 1](#) and exploratory statistical analysis is reported in [Table 2](#) and [Table 3](#). Additional details for this experiment can be found at <https://osf.io/fn2y4/>.

You can help

- Share your use case
- Provide feedback
- Learn about progress and opportunities to help

Sign up: elifesci.org/RDSupdates

This will take you to a form asking for your consent to be added to a mailing list for ~monthly emails with updates about this project, including calls for contributions and feedback.

Funding, exposure and mentorship

Supporting the open source community through the eLife Innovation Initiative

Get involved elifesci.org/innovate



#eLifeSprint. Credit: Orquidea Real Photobook - Julieta Sarmiento Photography @orquidea.real.pho



Questions?

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