

Reproducibility in an Office World

Noam Ross



New York R Conference

May 2019



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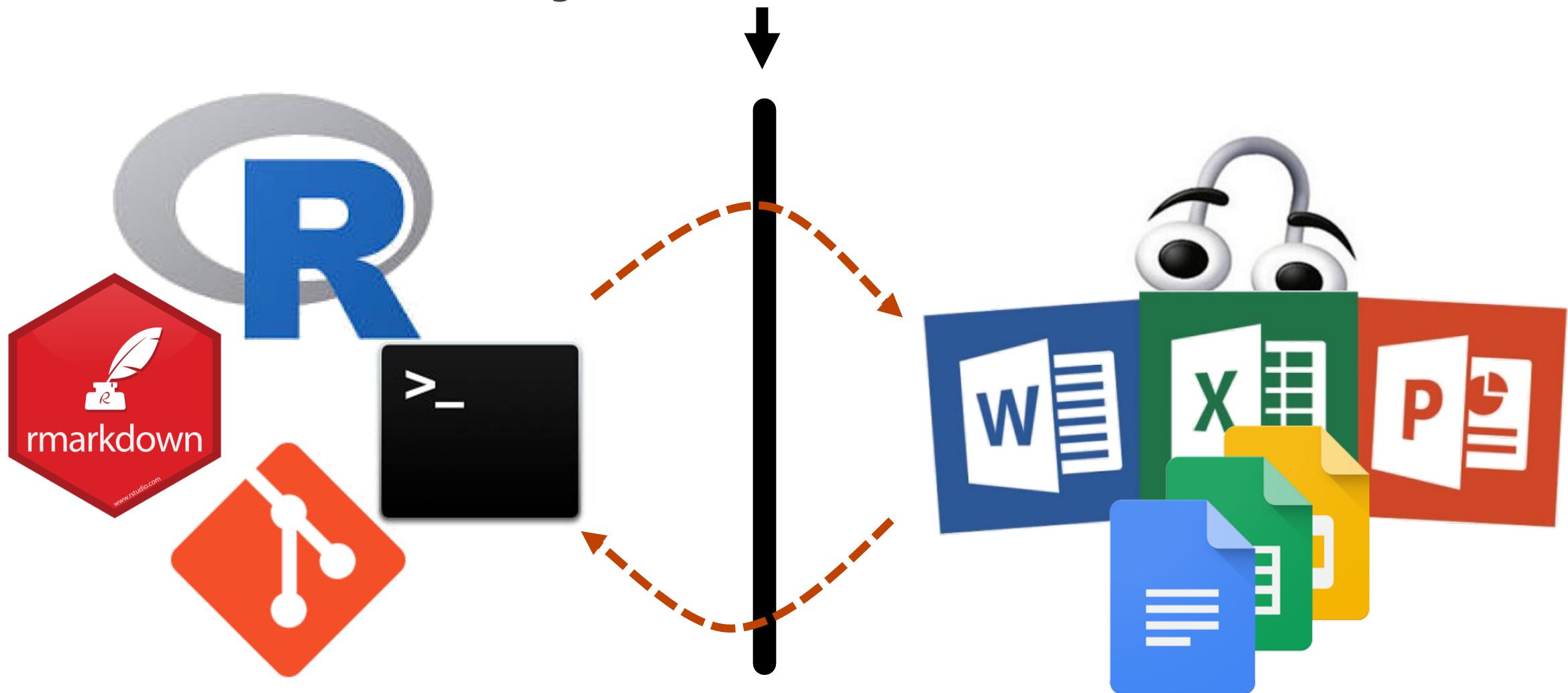


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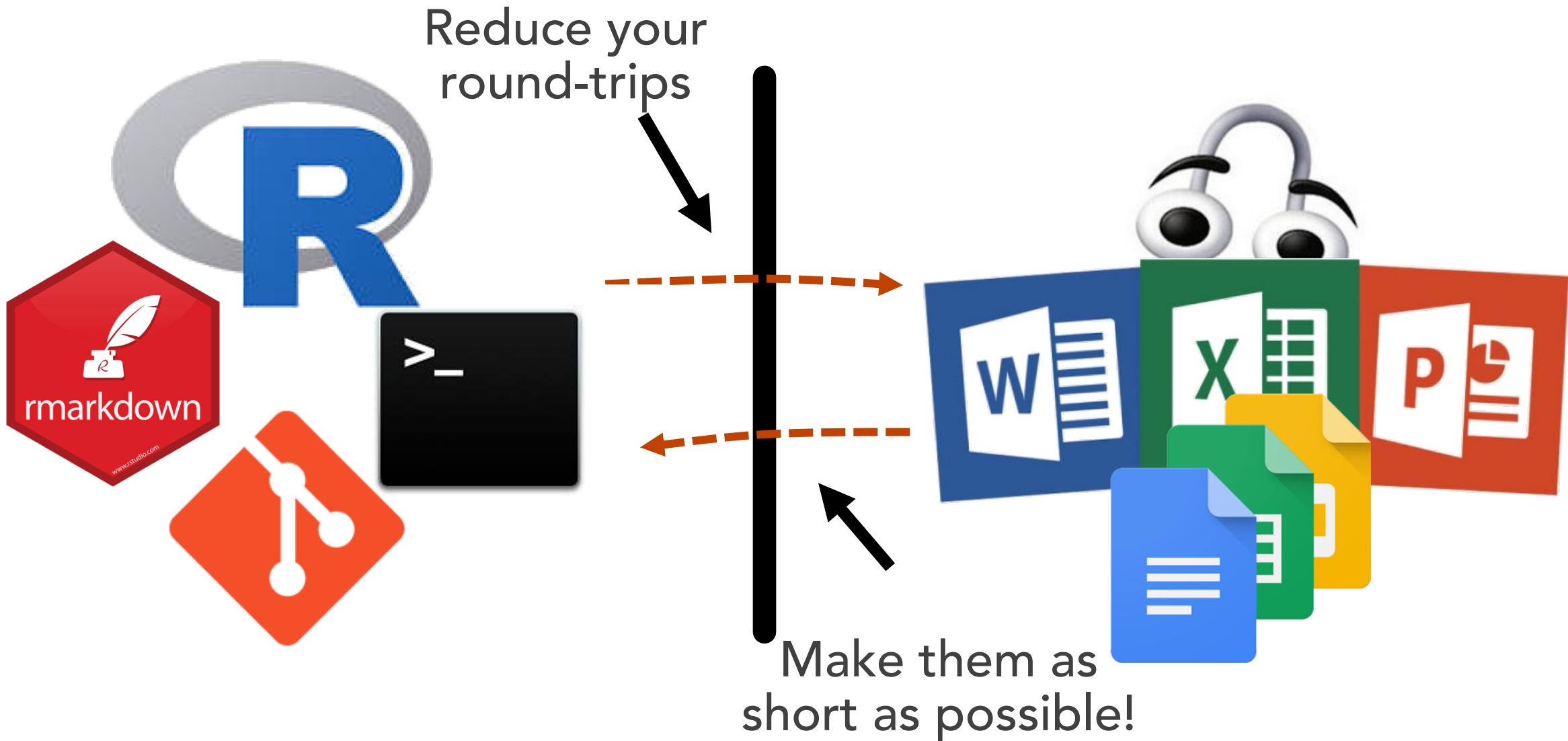
The Two Realms of Workflows



Valley of Heartbreak



Avoiding the Valley of Heartbreak



Web and
programmatic outputs

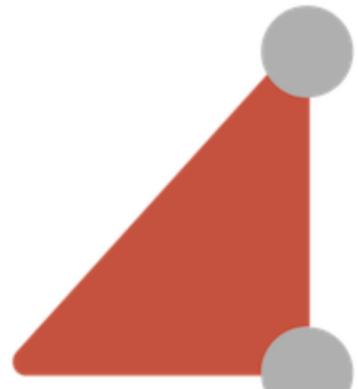


Documents and further iterated outputs

 noamross / rchie

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rchie: An R parser for ArchieML

repo status Active CRAN 1.0.0 build passing  build passing  codecov 93%

"Structured text, for an unstructured world."

This package is a wrapper for [archieml-js](#), a parser for the New York Times' ArchieML markup format. ArchieML is designed for non-coders writing documents that need to include some structured data, especially writers producing structured text that will be rendered on website or interactive graphics. Learn more about ArchieML's syntax and use cases at <http://archieml.org/>, and see examples of its use [here](#).

noamross.github.io/rchie



Web and
programmatic outputs



Documents and further
iterated outputs



The Officeverse / Gohelverse

officer

mschart

rvg

flextable

officedown: github.com/davidgohel/officedown

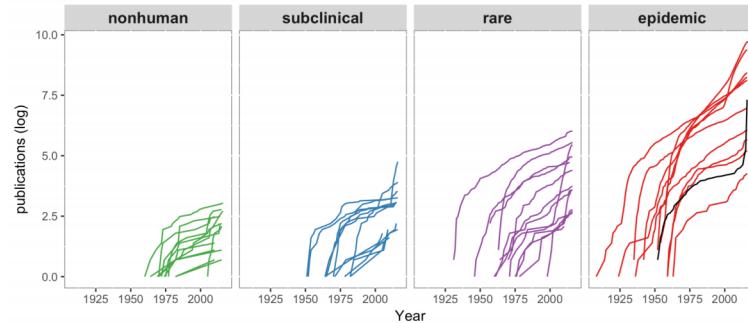
David Gohel (@DavidGohel)



Identifying the Next Zika: An Analysis of Understudied Flaviviruses

The ongoing Zika virus epidemic was declared a public health emergency of international concern by WHO in February 2016, due to its rapid spread and link to birth defects. Despite discovery in 1947, evidence of human infection, and close relation to high-impact human viruses like Dengue and Yellow Fever, the study of Zika remained limited until the Yap Island, Micronesia outbreak in 2007¹ (Figure 1). The pandemic spread of Zika emphasizes the need to better understand the distribution, host range, and epidemic potential of other understudied flaviviruses².

The PREDICT-2 Modeling & Analytics team compiled a database of all known natural host and vector species for the 53 ICTV-recognized viruses³ in the genus Flavivirus. In total, 1,768 flavivirus-host associations (including 317 unique mammal species and 743 bird species) and 309 flavivirus-vector associations (149 unique insect vector species) were identified. We then calculated the taxonomic breadth and geographic range of each flavivirus in order to inform both current and potential risks of flavivirus spillover and spread.



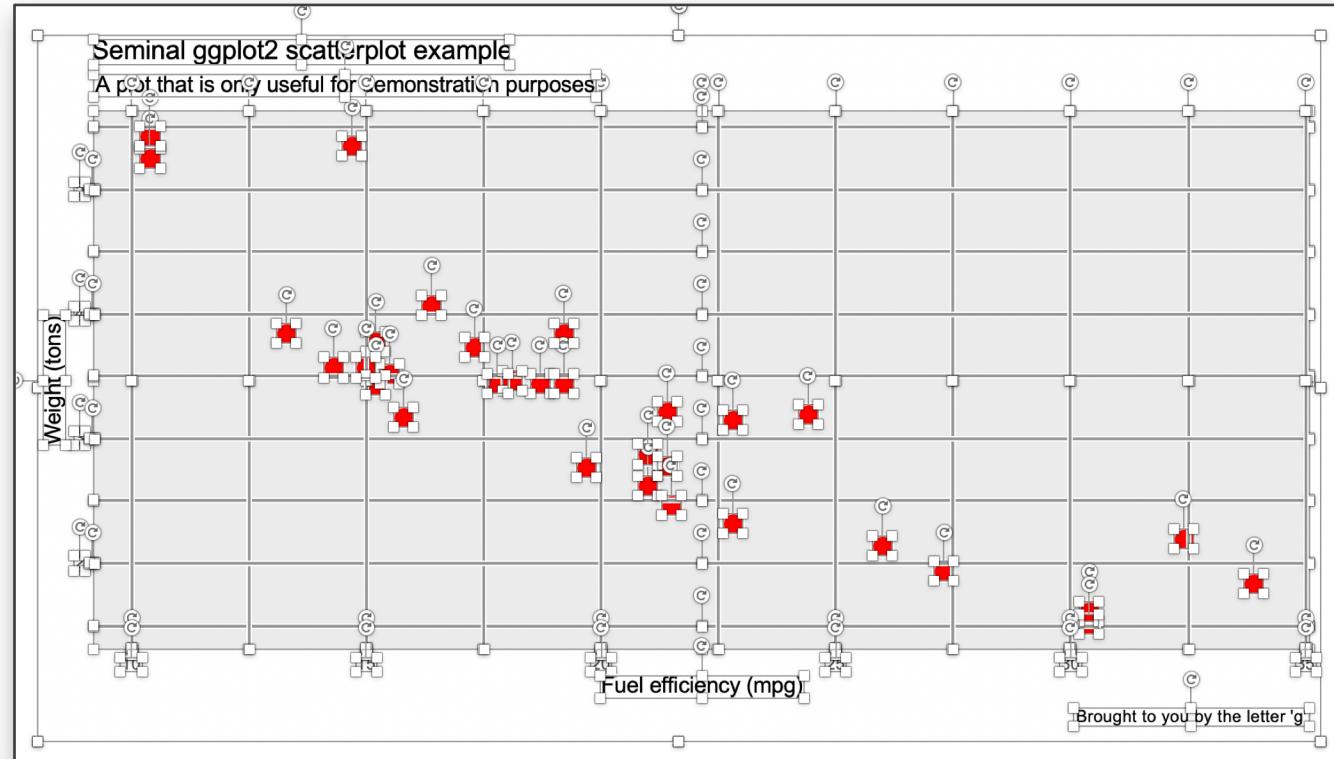
April 16, 2018

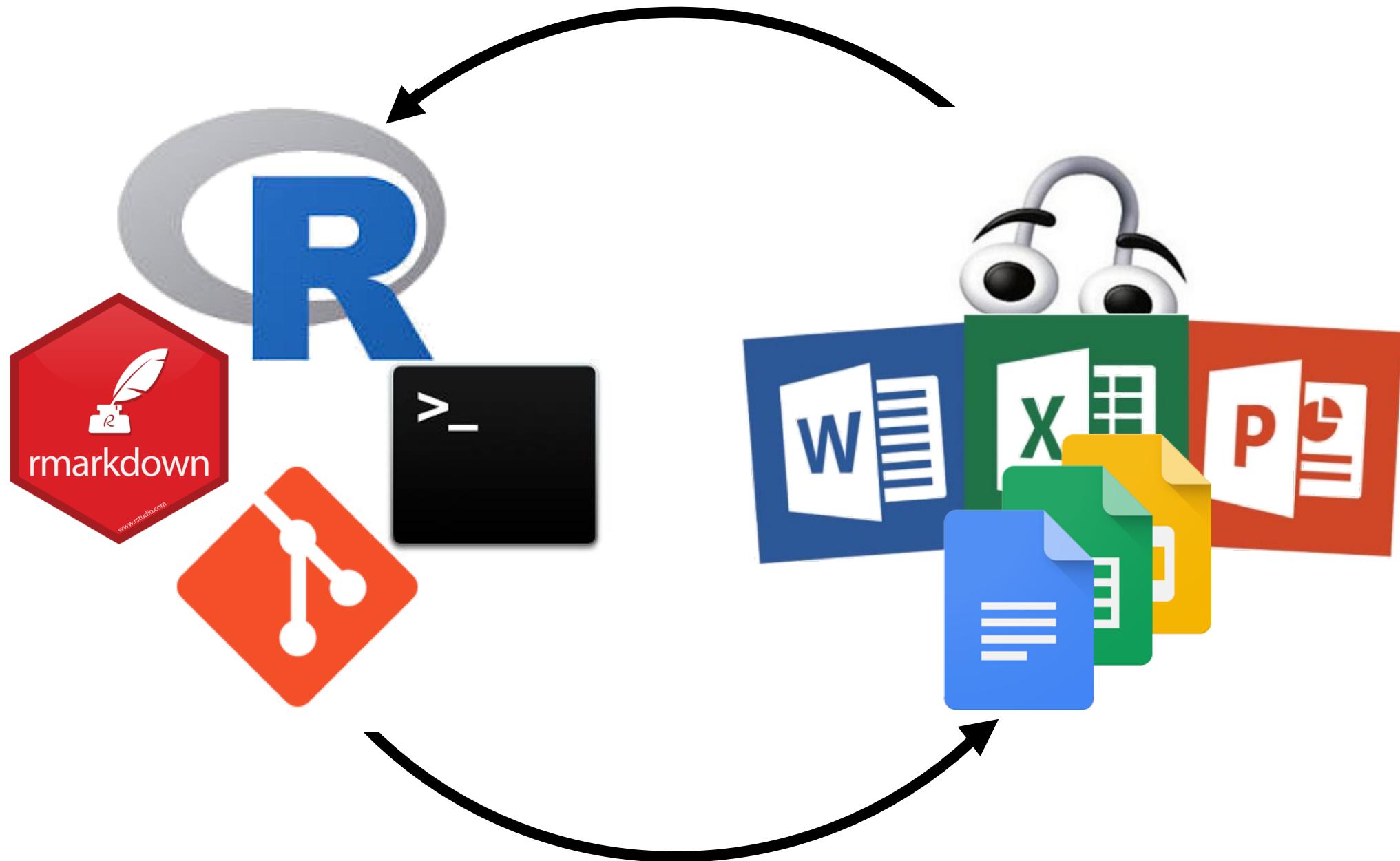
For details on methods or analysis contact:
PREDICTmodeling@ecohealthalliance.org

Figure 1: Publication effort 1900-2016 of each flavivirus (n = 53). Publication counts per virus retrieved from Web of Science on 10/27/16. Virus color based on human impact: nonhuman viruses = green, subclinical viruses (detected only via serology) = blue, rare viruses (<20 pathogenic cases) = purple, epidemic viruses (>20 pathogenic cases) = red. Zika is colored black to emphasize the sharp rise in publications after its human impact changed to epidemic in 2007.

In order to control for the effect of research effort and understand the relative importance of host and vector breadth in the zoonotic potential of Flaviviruses, we developed a generalized linear model of likelihood a virus is zoonotic. We simplify host and vector breadth to the lowest taxonomic group that encompasses all known natural host or vector species. Both non-human host breadth ($p = 0.02$) and vector breadth ($p = 0.03$) were significant in determining if a virus is classified as zoonotic, so these variables were used to prioritize viruses for more research (Table 1). Using the IUCN mammalian range and BirdLife spatial files, we created a unique vertebrate host distribution layer for each flavivirus, and combine these to produce a global map of known flavivirus diversity in wild mammals and birds (Figure 2).

Of the 53 flaviviruses, 37 (70%) have been detected in humans, and 25 of these human-







Invertible Reproducible Documents

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Code

Issues 64

Pull requests 0

Projects 0

Wiki

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#76

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Code

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Reversible Reproducible Documents

noamross.github.io/redoc



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The road ahead for redoc

robustness and more edge-case testing

opinionated and sensible defaults

officedown and other format integration

citations?

Google Docs support?

noamross.github.io/redoc/CONTRIBUTING.html

Thank you!



@noamross



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And thanks to:

Yihui Xie+ (knitr, rmarkdown)

David Gohel (officer, officedown)

John Macfarlane (pandoc)

Brodie Gaslam (diffobj)

...and many more