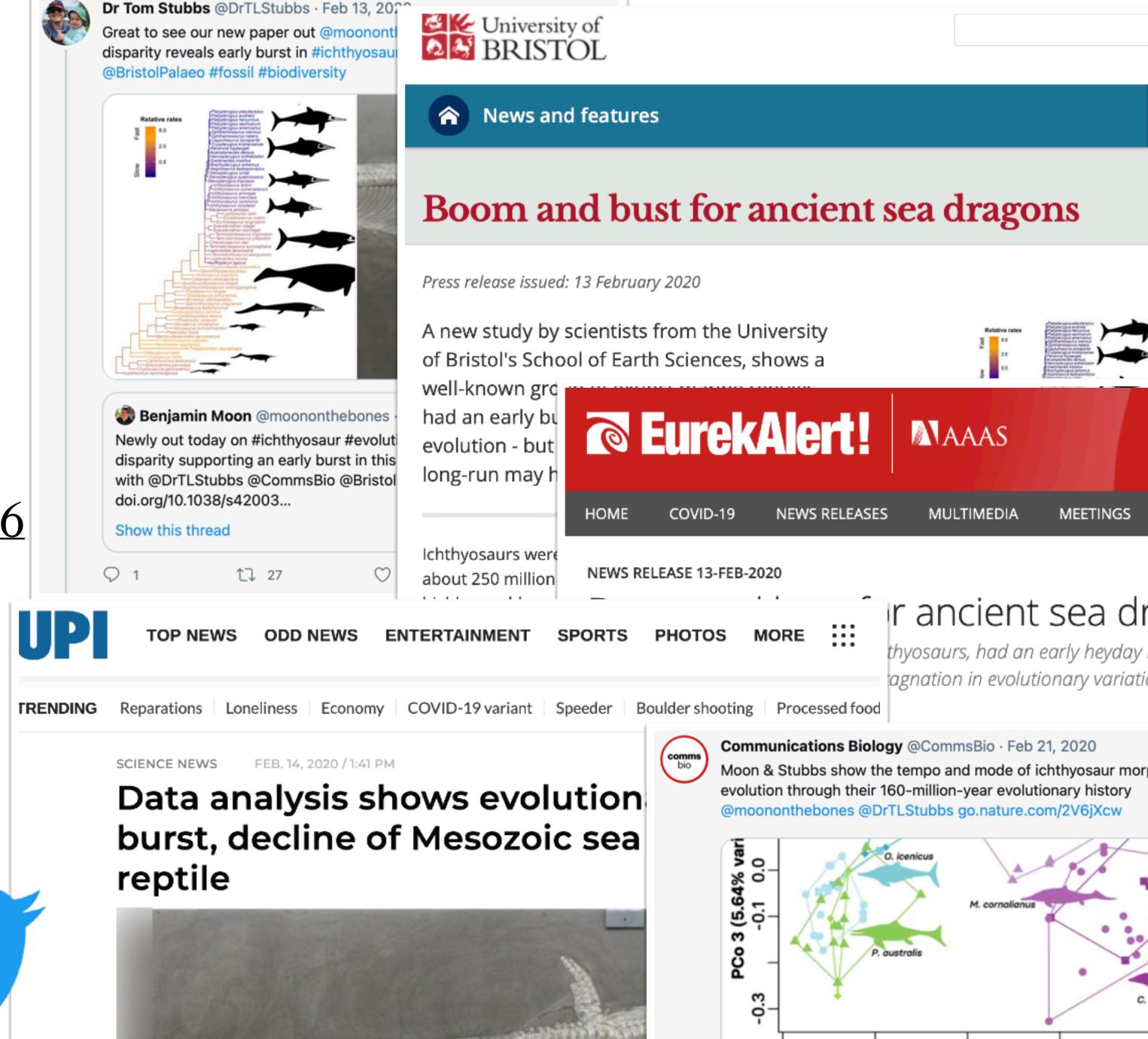
Reach

Open science

- Open Access publication
 - Communications Biology
 - DOI: 10.1038/s42003-020-0779-6
- Open review
- Press release
 - Twitter
 - Popular in Japan



0.0 0.2 PCo 1 (26% variance)

-0.4

-0.2

Lessons

Future considerations

- We used raw scripts
 - Text, code with RMarkdown
- Development environment
 - Package control with renv
- Replication and teaching
 - Online version with Binder

```
kable(caption = "**Shareholder quorum subsampled divers
                                                                       rough
         the Cenozoic.** Diversity is counted in each stage. The
         collections used for each bin is indicated.")
                                                            ■ Lines s
     2 ## Diversity through time ##
  370 Diversity shows a generally increasing trend between 60-20 Ma.
       Substantial simultaneous changes in raw species diversity most likely
       represent changes in the collection regime: either due to increased
       sampling effort or preservation rate. Patterns of diversity general
       match between raw species diversity and subsampled diversity, al
       at different scales of resolution. Notable differences occur in
       substantial increase in raw species diversity of Bryozoa in the
       Oligocene onwards that is not present in subsampled diversity,
       stasis in Gastropoda at the same time compared to an increase ir
                                                                         rmarkdown
       subsampled diversity.
     2 ```{r ggplot_pbdb_diversity, fig.cap = "**Species diversity through
       the later Palaeogene.** Diversity is counted from raw occurrence
       ranges in 0.5 my slices (A) and shareholder quorum subsampled
       diversity in stage-level bins (B). The vertical yellow band indicates
       the Eocene-Oligocene transition (34-33.5 Ma). The number of
       collections included in each bin is indicated in the top panel of B.",
       fig.show = "hold"}
     3 pbdb_diversity_labels <-</pre>
      4 c("Diversity", names(taxon_matching))
     5 event_ages <-
                                              # big events in the Palaeogene
         tribble(
            ~event, ~xmax, ~xmin, ~hjust,
           "PETM", 55.6, 55.4, 0.7,
           "<u>EECO</u>", 53.3, 49.1, 0.5,
           "EOT", 34.0, 33.5, -0.2
      shelf-diversity-over-eot-analyses.Rmd[+] utf-8 △ ¥ rmd 36% 370:619
21 >
71835:R [-]
                                                                         21:1
                                                    2021-03-24 Wed 16:47:16
© 24/03, 4:47 pm
                    ~/O/C/t/revision
```

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