

Demo Manuscript

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2 ABSTRACT

3 Hello, this is the abstract.

4 **Keywords:** keyword1, kw2, kw3... have to have at least 5, max 8

5 Hello, world!

1 INTRODUCTION

6 Here are some things to consider:

7 1. We don't know what's happening

8 2. Neither does anyone else

9 Also important:

10 • this creates an unordered list

11 • and this is the second item.

12 This is how links work: [link text](#)

13 We can also include code snippets:

```
# Exemplary python code
print("Hello World!")
print("2 + 5 = " + (2+5))
with open('testfile.fa', 'w') as file:
    file.write("Hello, world")
print("Done")
```

2 RMARKDOWN

14 Now for some really kewl stuff: We load a file in R:

```
annotation_quantities =
  read.csv('../.../data/mocks/processed/annotation_quantities.csv', header=
rice = subset(annotation_quantities, genome=='rice' & source=='GOMAP')
```

15 And now we can actually use it:

```
head(annotation_quantities)
```

```
16 ##      genome      source n_c n_f n_p n_genes
17 ## 1 maize_v3      GOMAP  95  56 169      11
18 ## 2 maize_v3 Gramene49   63  83  74      11
19 ## 3 maize_v3 Phytozome   14  67  59      11
20 ## 4 maize_v4      GOMAP  52  65 213      11
21 ## 5      rice      GOMAP  60  67 223      11
```

```
summary(annotation_quantities$n_c)
```

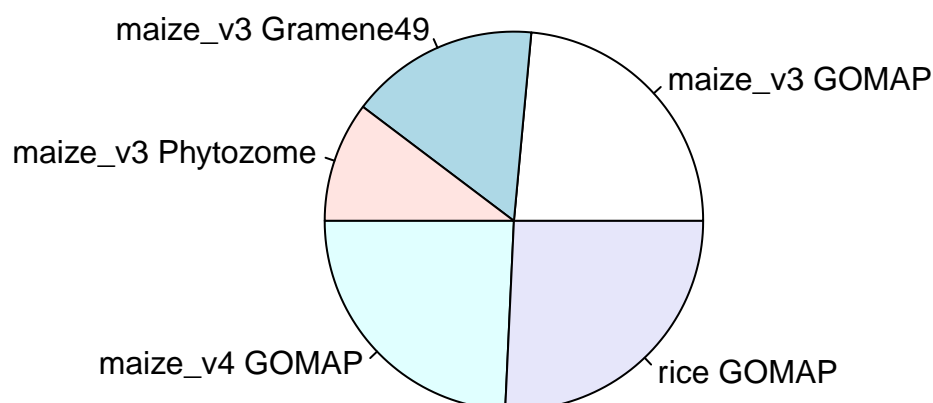
```
22 ##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
23 ##      14.0   52.0    60.0   56.8   63.0   95.0
```

24 The annotation set for rice had a total of 60 annotations for cellular component.

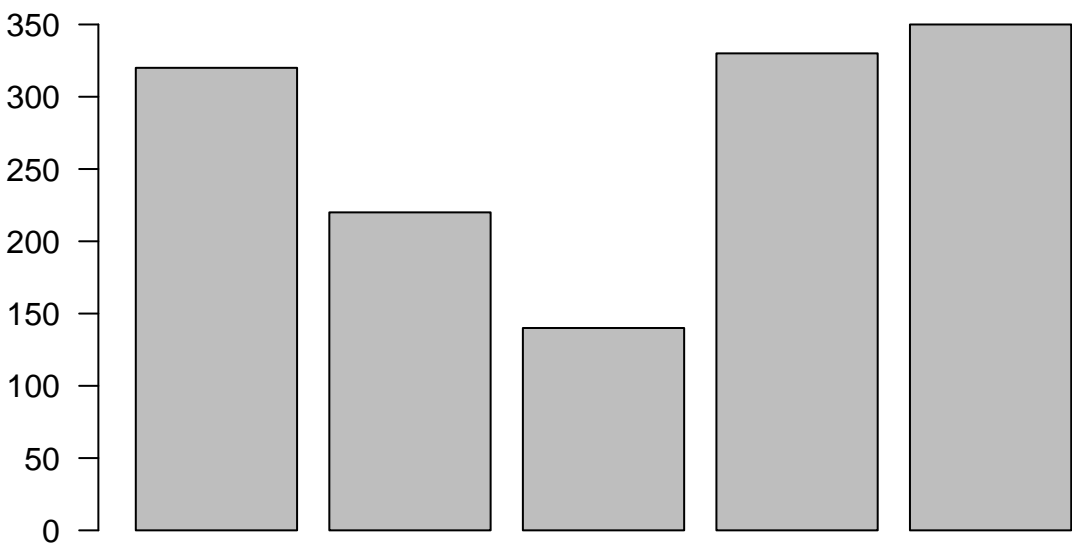
25 2.1 Plots

26 We can even plot the data:

```
a = annotation_quantities
pie(a$n_c+a$n_f+a$n_p, labels=paste(a$genome, a$source))
```



```
barplot(a$n_c+a$n_f+a$n_p, las=2)
```



Now here is an actual figure I’ve been working on:

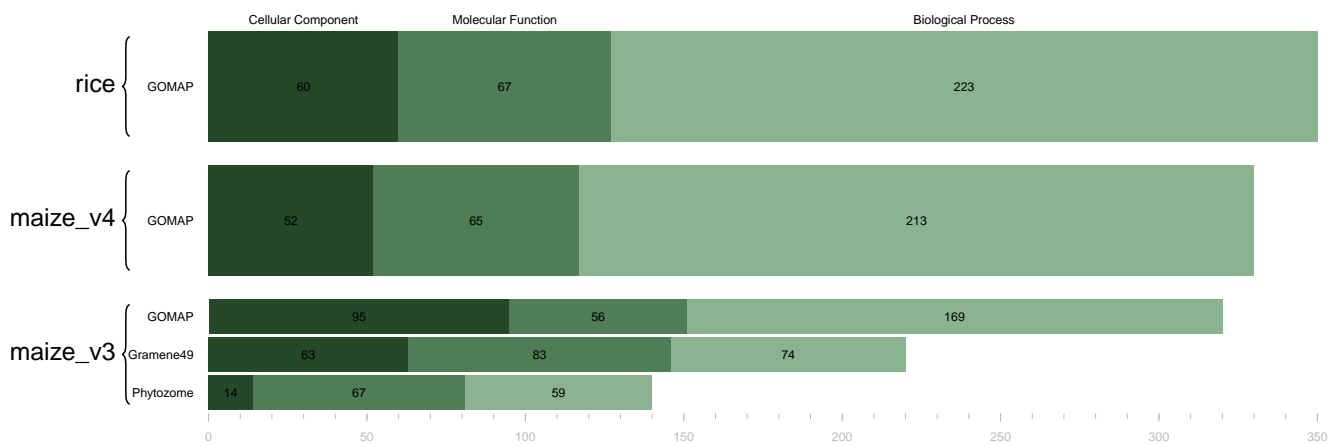


Figure 1. Quantitative lalala