

# ML Code Completeness Checklist Analysis

This notebook contains the ML Code Completeness analysis for NeurIPS 2019 repositories.

For a run & rendered version of this notebook please see: [code\\_checklist-analysis.pdf](#).

Official repositories for NeurIPS 2019 papers fetched from: <https://papers.nips.cc/book/advances-in-neural-information-processing-systems-32-2019>

A random 25% sample has been selected and manually annotated according to the 5 criteria of the ML Code Completeness Checklist. The result has been saved into `code_checklist-neurips2019.csv`.

```
library(tidyverse)

## -- Attaching packages -----
## v ggplot2 3.2.1      v purrr  0.3.3
## v tibble  2.1.3      v dplyr  0.8.4
## v tidyr   1.0.2      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.4.0

## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(ggplot2)
library(MASS)

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##   select

library(RColorBrewer)

t = read_csv("code_checklist-neurips2019.csv")

## Parsed with column specification:
## cols(
##   url = col_character(),
##   stars = col_double(),
##   python = col_double(),
##   training = col_double(),
##   evaluation = col_double(),
##   pretrained_model = col_double(),
##   results = col_double(),
##   dependencies = col_double()
## )

cat("Number of rows:", nrow(t), "\n")

## Number of rows: 221
```

We'll focus only on Python repositories, since this is the dominant language in ML and repositories in other languages tend to have a smaller number of stars just because the community is smaller.

```
t = t[t$python==1,]
cat("Number of rows:", nrow(t), "\n")
```

```
## Number of rows: 200
```

Next, we calculate the score as a sum of individual checklist items and calculate summary stats.

```
t$score = rowSums(t[,4:8])
```

We group repositories based on their score and calculate summary stats.

```
cat("Spread of values in each group:\n")
```

```
## Spread of values in each group:
```

```
summaries = tapply(t$stars, t$score, summary)
names(summaries) = paste(names(summaries), "ticks")
print(summaries)
```

```
## $`0 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.0     0.0     1.5    14.5    10.0    89.0
##
## $`1 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.00     0.00     5.00   11.94    11.00   59.00
##
## $`2 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.00     4.00    15.00   43.17    30.00   654.00
##
## $`3 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.00     6.00    19.00  171.15    75.75  6082.00
##
## $`4 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.00    22.25    62.50  457.88   148.50  5114.00
##
## $`5 ticks`
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      16.00    93.25   196.50 2664.89   517.00 36549.00
```

```
cat("Proportion of repos in each group:\n")
```

```
## Proportion of repos in each group:
```

```
props = tapply(t$stars, t$score, length)
props = props/sum(props)
names(props) = paste(names(props), "ticks")
print(props)
```

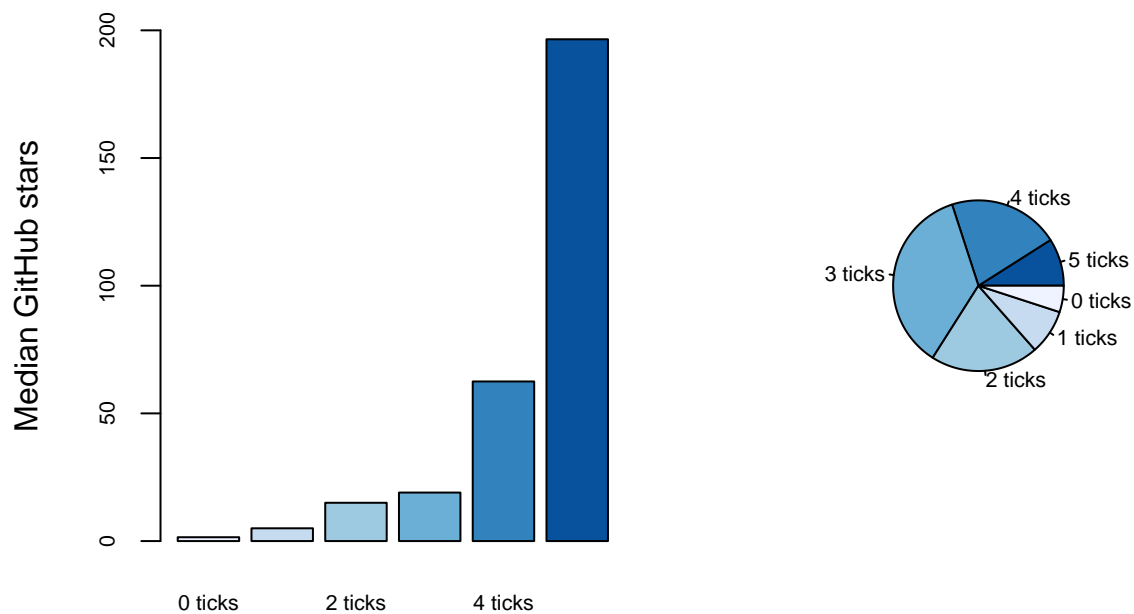
```
## 0 ticks 1 ticks 2 ticks 3 ticks 4 ticks 5 ticks
##  0.050   0.085   0.205   0.360   0.210   0.090
```

```
# Extract medians
medians = unlist(lapply(tapply(t$stars, t$score, summary), function(x) x["Median"]))
names(medians) = paste(sub(".Median", "", names(medians)), "ticks")
```

Generate summary graphs.

```
par(oma=c(0,1,0,1))
layout(matrix(c(1,2), 1, 2, byrow = TRUE), widths=c(3,2))
barplot(medians,
        xlab="",
        ylab="Median GitHub stars", ylim=c(0,200),
        col=brewer.pal(6, "Blues"), cex.axis=0.7, cex.names=0.7)
mtext("GitHub repos grouped by number of ticks on ML code checklist", side=1, line=3, cex=0.8)

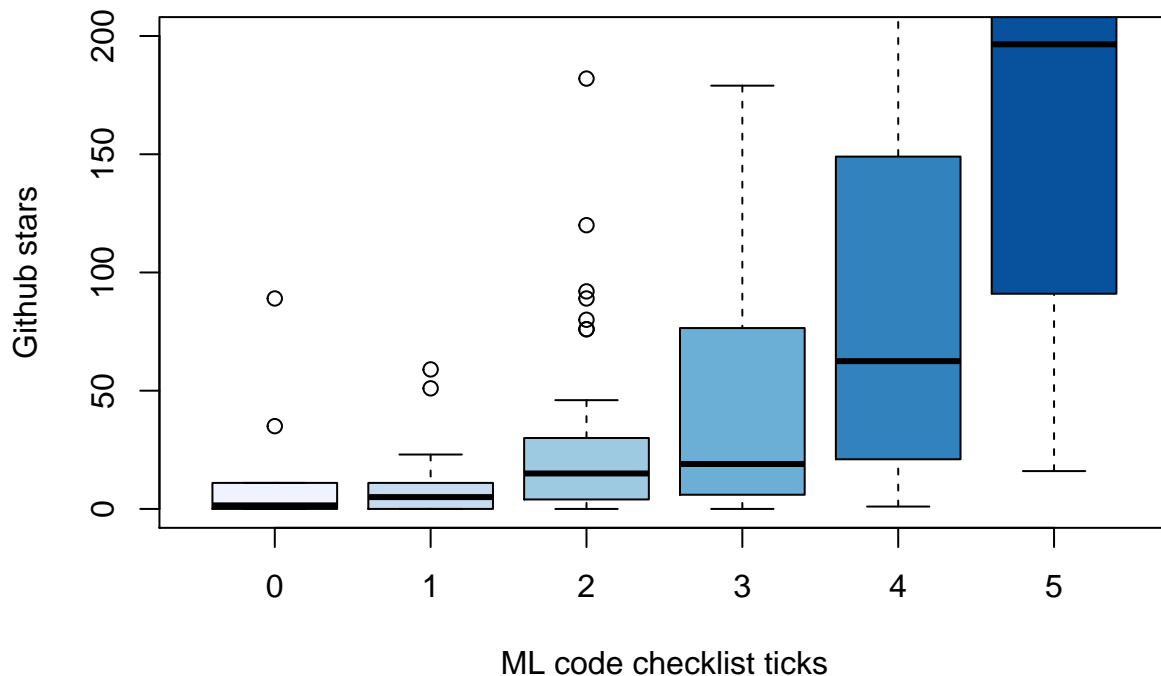
pie(rev(props), col=rev(brewer.pal(6, "Blues")), cex=0.7)
mtext("Proportion of repositories in each group", side=1, line=3, cex=0.8)
```



GitHub repos grouped by number of ticks on ML code checklist

Compare using box plots.

```
tp = t
tp$score = as.factor(tp$score)
par(mfrow=c(1,1))
boxplot(stars~score, data=t, ylim=c(0,200), col=brewer.pal(6, "Blues"),
        xlab="ML code checklist ticks", ylab="Github stars")
```



Fit robust regression and test significance of results

```
print(summary(rlm(stars~training+evaluation+pretrained_model+results+dependencies, data=t)))
```

```
##
## Call: rlm(formula = stars ~ training + evaluation + pretrained_model +
## results + dependencies, data = t)
## Residuals:
##      Min       1Q   Median       3Q      Max
## -118.293  -25.391   -7.406   36.218 36414.707
##
## Coefficients:
##              Value      Std. Error t value
## (Intercept)   -1.0246     11.5557   -0.0887
## training       24.3908     11.8245    2.0627
## evaluation    -12.0504      8.8434   -1.3626
## pretrained_model 70.3466      9.1685    7.6726
## results       36.7966      8.8318    4.1664
## dependencies  15.8344      9.2208    1.7172
##
## Residual standard error: 40.03 on 194 degrees of freedom
```

```
for(i in 0:4){
  cat("\nScore5 vs Score", i, "\n")
  print(wilcox.test(t$stars[t$score==5], t$stars[t$score==i]))
}
```

```
##
## Score5 vs Score 0
## Warning in wilcox.test.default(t$stars[t$score == 5], t$stars[t$score == :
## cannot compute exact p-value with ties
##
## Wilcoxon rank sum test with continuity correction
```

```
##
## data:  t$stars[t$score == 5] and t$stars[t$score == i]
## W = 174, p-value = 5.943e-05
## alternative hypothesis: true location shift is not equal to 0
##
##
## Score5 vs Score 1

## Warning in wilcox.test.default(t$stars[t$score == 5], t$stars[t$score == :
## cannot compute exact p-value with ties

##
## Wilcoxon rank sum test with continuity correction
##
## data:  t$stars[t$score == 5] and t$stars[t$score == i]
## W = 300, p-value = 1.279e-06
## alternative hypothesis: true location shift is not equal to 0
##
##
## Score5 vs Score 2

## Warning in wilcox.test.default(t$stars[t$score == 5], t$stars[t$score == :
## cannot compute exact p-value with ties

##
## Wilcoxon rank sum test with continuity correction
##
## data:  t$stars[t$score == 5] and t$stars[t$score == i]
## W = 677, p-value = 4.1e-07
## alternative hypothesis: true location shift is not equal to 0
##
##
## Score5 vs Score 3

##
## Wilcoxon rank sum test with continuity correction
##
## data:  t$stars[t$score == 5] and t$stars[t$score == i]
## W = 1082, p-value = 1.22e-05
## alternative hypothesis: true location shift is not equal to 0
##
##
## Score5 vs Score 4

## Warning in wilcox.test.default(t$stars[t$score == 5], t$stars[t$score == :
## cannot compute exact p-value with ties

##
## Wilcoxon rank sum test with continuity correction
##
## data:  t$stars[t$score == 5] and t$stars[t$score == i]
## W = 528.5, p-value = 0.01551
## alternative hypothesis: true location shift is not equal to 0
```

## Session information

```
sessionInfo()
```

```

## R version 3.6.2 (2019-12-12)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.3
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] RColorBrewer_1.1-2 MASS_7.3-51.4      forcats_0.4.0      stringr_1.4.0
## [5] dplyr_0.8.4      purrr_0.3.3      readr_1.3.1      tidyr_1.0.2
## [9] tibble_2.1.3      ggplot2_3.2.1      tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.0.0 xfun_0.12      haven_2.2.0      lattice_0.20-38
## [5] colorspace_1.4-1 vctrs_0.2.3    generics_0.0.2    htmltools_0.4.0
## [9] yaml_2.2.1      rlang_0.4.4    pillar_1.4.3     withr_2.1.2
## [13] glue_1.3.1      DBI_1.1.0      dbplyr_1.4.2     modelr_0.1.6
## [17] readxl_1.3.1    lifecycle_0.1.0 munsell_0.5.0     gtable_0.3.0
## [21] cellranger_1.1.0 rvest_0.3.5     evaluate_0.14     knitr_1.28
## [25] fansi_0.4.1     broom_0.5.4     Rcpp_1.0.3        scales_1.1.0
## [29] backports_1.1.5 jsonlite_1.6.1  fs_1.3.1          hms_0.5.3
## [33] digest_0.6.25   stringi_1.4.6   grid_3.6.2        cli_2.0.1
## [37] tools_3.6.2     magrittr_1.5    lazyeval_0.2.2    crayon_1.3.4
## [41] pkgconfig_2.0.3 xml2_1.2.2      reprex_0.3.0      lubridate_1.7.4
## [45] assertthat_0.2.1 rmarkdown_2.1   httr_1.4.1        rstudioapi_0.11
## [49] R6_2.4.1        nlme_3.1-142    compiler_3.6.2

```