Untitled

# Enables using readLines(knitr::purl(knitr::current\_input(),documentation=1,quiet=T)) to include code at end of document (otherwise 'duplicate labels' error)  
  
 options(knitr.duplicate.label = 'allow')

packages <- c("base"  
 ,"tidyverse"  
 ,"bookdown"  
 ,"knitr"  
 ,"fs"  
 ,"devtools"  
 ,"fastcluster"  
 ,"cluster"  
 ,"randomForest"  
 ,"DBI"  
 )  
  
 purrr::walk(packages,library,character.only=TRUE)

## -- Attaching packages --------------------------------------------------------------------------------------------------------- tidyverse 1.3.0 --

## v ggplot2 3.3.2 v purrr 0.3.4  
## v tibble 3.0.3 v dplyr 1.0.0  
## v tidyr 1.1.0 v stringr 1.4.0  
## v readr 1.3.1 v forcats 0.5.0

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

## Warning: package 'fs' was built under R version 4.0.3

## Loading required package: usethis

##   
## Attaching package: 'fastcluster'

## The following object is masked from 'package:stats':  
##   
## hclust

## randomForest 4.6-14

## Type rfNews() to see new features/changes/bug fixes.

##   
## Attaching package: 'randomForest'

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

## The following object is masked from 'package:ggplot2':  
##   
## margin

testUnderscore <- "Alinytjara Wilu\u1E5Fara"

I wonder if this will work: Alinytjara Wiluṟara.

#-------Load functions-------  
   
 commonFiles <- path("..","template","toCommon")  
   
 if(file.exists(commonFiles)){  
   
 files <- dir\_ls(commonFiles)  
 newFiles <- files %>% gsub(commonFiles,path("common"),.)  
 dir\_create("common")  
 walk2(files,newFiles,file\_copy,overwrite=TRUE)  
   
 }  
   
 source("common/functions.R") # these are generic functions (e.g. vec\_to\_sentence)

#---------References-------  
   
 packageBibFile <- "packageCitations.bib"  
   
 write\_bib(packages  
 ,file=packageBibFile  
 ,tweak=TRUE  
 ,width=1000  
 )  
   
 refs <- fix\_bib(packageBibFile,isPackageBib = TRUE)  
   
 #fix\_bib("common/refs.bib")

# Document

plot(cars[,1:2])



Figure 1 caption

cars blah blah

plot(iris[,3:4])

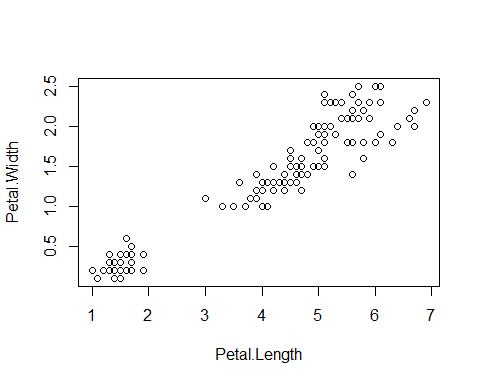


Figure 2 caption

iris blah blah Figure @ref(fig:chunk1).

Very very open grassland: always *Asparagus asparagoides with emergent frequent* \_Asparagus declinatus\_ and occasional *Acacia retinodes*, *Olea europaea,* \_Pinus halepensis\_, \**Osteospermum moniliferum*.

iris %>%  
 dplyr::sample\_n(15) %>%  
 dplyr::mutate(Species = if\_else(Species == "setosa"  
 , paste0("\*\_",Species,"\_")  
 , as.character(Species)  
 )  
 ) %>%  
 kable(caption = "Ecosystem description: floristics"  
 , format = "markdown"  
 , booktabs = TRUE  
 )

Ecosystem description: floristics

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species |
| 6.6 | 2.9 | 4.6 | 1.3 | versicolor |
| 6.2 | 2.2 | 4.5 | 1.5 | versicolor |
| 5.4 | 3.4 | 1.7 | 0.2 | \**setosa* |
| 6.5 | 2.8 | 4.6 | 1.5 | versicolor |
| 4.6 | 3.4 | 1.4 | 0.3 | \**setosa* |
| 6.1 | 2.8 | 4.7 | 1.2 | versicolor |
| 7.2 | 3.0 | 5.8 | 1.6 | virginica |
| 6.8 | 3.2 | 5.9 | 2.3 | virginica |
| 5.5 | 3.5 | 1.3 | 0.2 | \**setosa* |
| 6.4 | 2.8 | 5.6 | 2.2 | virginica |
| 6.4 | 2.7 | 5.3 | 1.9 | virginica |
| 6.9 | 3.1 | 5.4 | 2.1 | virginica |
| 4.7 | 3.2 | 1.3 | 0.2 | \**setosa* |
| 5.4 | 3.9 | 1.3 | 0.4 | \**setosa* |
| 5.5 | 2.4 | 3.7 | 1.0 | versicolor |

Some text with a citation (Xie 2014; Xie 2015; Xie 2020a).

Another citation (Liaw and Wiener 2002; Breiman *et al.* 2018).

Accents on author name (Müllner 2013; Müllner 2018).

What about cluster (Maechler *et al.* 2019).

A citation from common/refs.bib rather than packageCitations.bib:

* book section (Hobbs *et al.* 2013)
* journal (Hobbs and Norton 1996)
* report (Rogers 2010)
* book (Robinson *et al.* 1996)

# Appendix

## ----GlobalOptions------------------------------------------------------------  
   
 # Enables using readLines(knitr::purl(knitr::current\_input(),documentation=1,quiet=T)) to include code at end of document (otherwise 'duplicate labels' error)  
  
 options(knitr.duplicate.label = 'allow')  
  
  
  
## ----setup--------------------------------------------------------------------  
  
 packages <- c("base"  
 ,"tidyverse"  
 ,"bookdown"  
 ,"knitr"  
 ,"fs"  
 ,"devtools"  
 ,"fastcluster"  
 ,"cluster"  
 ,"randomForest"  
 ,"DBI"  
 )  
  
 purrr::walk(packages,library,character.only=TRUE)  
   
 testUnderscore <- "Alinytjara Wilu\u1E5Fara"  
   
  
  
## ----functions----------------------------------------------------------------  
  
 #-------Load functions-------  
   
 commonFiles <- path("..","template","toCommon")  
   
 if(file.exists(commonFiles)){  
   
 files <- dir\_ls(commonFiles)  
 newFiles <- files %>% gsub(commonFiles,path("common"),.)  
 dir\_create("common")  
 walk2(files,newFiles,file\_copy,overwrite=TRUE)  
   
 }  
   
 source("common/functions.R") # these are generic functions (e.g. vec\_to\_sentence)  
  
  
  
## ----references---------------------------------------------------------------  
  
#---------References-------  
   
 packageBibFile <- "packageCitations.bib"  
   
 write\_bib(packages  
 ,file=packageBibFile  
 ,tweak=TRUE  
 ,width=1000  
 )  
   
 refs <- fix\_bib(packageBibFile,isPackageBib = TRUE)  
   
 #fix\_bib("common/refs.bib")  
  
  
  
## ----chunk1, fig.cap = "Figure 1 caption"-------------------------------------  
  
 plot(cars[,1:2])  
  
  
  
## ----chunk2, fig.cap = "Figure 2 caption"-------------------------------------  
  
 plot(iris[,3:4])  
  
  
  
## ----chunk3-------------------------------------------------------------------  
 iris %>%  
 dplyr::sample\_n(15) %>%  
 dplyr::mutate(Species = if\_else(Species == "setosa"  
 , paste0("\*\_",Species,"\_")  
 , as.character(Species)  
 )  
 ) %>%  
 kable(caption = "Ecosystem description: floristics"  
 , format = "markdown"  
 , booktabs = TRUE  
 )  
  
  
  
## ----code, code = readLines(knitr::purl(knitr::current\_input(),documentation=1,quiet=T)), echo = TRUE, eval=FALSE----  
##   
## # Need to include options(knitr.duplicate.label = "allow") prior to knitting.  
##   
## # From https://github.com/yihui/knitr/issues/332  
##   
  
  
## ----packages-----------------------------------------------------------------  
  
 kable(tibble(package = packages) %>%  
 dplyr::mutate(citation = map\_chr(package,cite\_package,brack = FALSE)) %>%  
 dplyr::left\_join(as\_tibble(devtools::session\_info(include\_base = TRUE)$packages)) %>%  
 dplyr::select(package,citation,loadedversion,date,source)  
 , caption = paste0("R "  
 , cite\_package("base")  
 , " packages used in the production of this report"  
 )  
 )

## Packages

kable(tibble(package = packages) %>%  
 dplyr::mutate(citation = map\_chr(package,cite\_package,brack = FALSE)) %>%  
 dplyr::left\_join(as\_tibble(devtools::session\_info(include\_base = TRUE)$packages)) %>%  
 dplyr::select(package,citation,loadedversion,date,source)  
 , caption = paste0("R "  
 , cite\_package("base")  
 , " packages used in the production of this report"  
 )  
 )

## Joining, by = "package"

R (R Core Team 2020) packages used in the production of this report

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| package | citation | loadedversion | date | source |
| base | R Core Team (2020) | 4.0.2 | 2020-06-22 | local |
| tidyverse | Wickham (2019); Wickham *et al.* (2019) | 1.3.0 | 2019-11-21 | CRAN (R 4.0.2) |
| bookdown | Xie (2020b); Xie (2016) | 0.20 | 2020-06-23 | CRAN (R 4.0.2) |
| knitr | Xie (2020a); Xie (2015); Xie (2014) | 1.29 | 2020-06-23 | CRAN (R 4.0.2) |
| fs | Hester and Wickham (2020) | 1.5.0 | 2020-07-31 | CRAN (R 4.0.3) |
| devtools | Wickham *et al.* (2020) | 2.3.1 | 2020-07-21 | CRAN (R 4.0.2) |
| fastcluster | Müllner (2018); Müllner (2013) | 1.1.25 | 2018-06-07 | CRAN (R 4.0.0) |
| cluster | Maechler *et al.* (2019) | 2.1.0 | 2019-06-19 | CRAN (R 4.0.2) |
| randomForest | Breiman *et al.* (2018); Liaw and Wiener (2002) | 4.6-14 | 2018-03-25 | CRAN (R 4.0.2) |
| DBI | R Special Interest Group on Databases (R-SIG-DB) *et al.* (2019) | 1.1.0 | 2019-12-15 | CRAN (R 4.0.2) |

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