

# The CMapBox User's Guide

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**February 22, 2019**

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## 1 Introduction

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The CMapBox package provides efficient and powerful functions for pharmacogenomic data analysis...

## 2 Installation and Settings

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CMapBox requires that several packages be installed. All dependencies are available from CRAN or Bioconductor:

```
if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")  
BiocManager::install("CMapBox", version = "3.8")
```

The package can also be installed directly from GitHub using devtools:

```
#install devtools if required  
install.packages("devtools")  
  
#install Xeva as:  
devtools::install_github("bhklab/CMapBox")
```

Load Xeva into your current workspace:

```
library(CMapBox)
```

Load the dataset you wish to analyze:

```
#data(brca)  
#print(brca)
```

### 3 SessionInfo

```

sessionInfo()

## R version 3.5.2 (2018-12-20)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Linux Mint 18.3
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
##  [1] LC_CTYPE=en_CA.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_CA.UTF-8      LC_COLLATE=en_CA.UTF-8
##  [5] LC_MONETARY=en_CA.UTF-8  LC_MESSAGES=en_CA.UTF-8
##  [7] LC_PAPER=en_CA.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_CA.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats      graphics grDevices utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] Biobase_2.42.0      BiocGenerics_0.28.0 CMapBox_0.0.0.9000
## [4] knitr_1.21
##
## loaded via a namespace (and not attached):
##  [1] gtools_3.8.1      tidyselect_0.2.5   fgsea_1.8.0
##  [4] xfun_0.4          slam_0.1-44        sets_1.0-18
##  [7] purrr_0.3.0       lattice_0.20-38    colorspace_1.4-0
## [10] htmltools_0.3.6   yaml_2.2.0         marray_1.60.0
## [13] rlang_0.3.1       pillar_1.3.1       glue_1.3.0
## [16] piano_1.22.0      BiocParallel_1.16.5 bindrcpp_0.2.2
## [19] plyr_1.8.4        bindr_0.1.1         stringr_1.3.1
## [22] munsell_0.5.0     gtable_0.2.0       caTools_1.17.1.1
## [25] evaluate_0.12     highr_0.7           Rcpp_1.0.0
## [28] KernSmooth_2.23-15 relations_0.6-8     scales_1.0.0
## [31] BiocManager_1.30.4 limma_3.38.3        gdata_2.18.0
## [34] gridExtra_2.3     gplots_3.0.1.1     fastmatch_1.1-0
## [37] BiocStyle_2.10.0  ggplot2_3.1.0       digest_0.6.18
## [40] stringi_1.2.4     dplyr_0.7.8         grid_3.5.2
## [43] tools_3.5.2       bitops_1.0-6        magrittr_1.5
## [46] lazyeval_0.2.1    tibble_2.0.1        cluster_2.0.7-1
## [49] crayon_1.3.4      pkgconfig_2.0.2     Matrix_1.2-15
## [52] data.table_1.12.0 assertthat_0.2.0    rmarkdown_1.11
## [55] R6_2.3.0          igraph_1.2.2        compiler_3.5.2

```